

European Conference on Complex Systems' 09

University of Warwick, September 21-25, 2009

Programme & Abstracts

Welcome Addresses

The European Conference on Complex Systems 2009

It is a great pleasure to present this year's conference on Complex Systems located at the University of Warwick. We are very grateful to the Complex Systems Society (CSS) for inviting Warwick to host this event. The University of Warwick has recently developed a strong research capacity in Complex Systems Science. We would like to thank the university for the continuing support of this relatively new way to approach scientific problems. We all hope ECCS'09 will become a successful event triggering new discussion and research. The strong international embedding of the conference in Europe and beyond can be seen by exploring the fascinating ECCS'09 programme covering nearly all sciences. Here we would like to thank all visiting scientists whether young or experienced for supporting the conference with much enthusiasm.

Many thanks also to all the members of the local organisation committee at Warwick and the Open University. Without their help and commitment a conference on this scale would have been impossible to set up. As the conference is highly interdisciplinary we have been fortunate to benefit from experienced track and co-track chairs having the necessary background in their established field of research while being open to the other sciences at the same time. Here my special thanks goes to François Képès, our programme chair, who had the challenging task of establishing the necessary communication between all of our different research themes. Many thanks also to the track and co-track chairs for setting up the respective programmes of high scientific quality.

A conference like ECCS'09 cannot exist without financial and administrative support. We would like to thank the University of Warwick, our Vice-Chancellor Nigel Thrift, the CSS, the Open University, the EPSRC, the BBSRC, the European Commission, the abaci partnership, the London Mathematical Society, Springer-Verlag, and IOP Publishing.

We are currently living in a world of both immense richness and immense problems. The human race has become so influential in all areas that it can determine the global fate in the years to come. The scientific development with all its necessary controversies is still giving hope to overcome some of the more serious global problems we are facing. New scientific solutions to problems on small and large scales will help us all, spanning from new technologies in biology, medicine or engineering to the understanding of the dynamics of cities, the global market or the society as a whole. ECCS'09 will host a round table discussion on the 'Complexity of Global Change' to which I would like to invite all interested visitors. The ECCS conference series will for sure continue to bring scientists together working on such global challenges. The strength of complex systems research is its unique combination of theory, simulation and data acquisition, in nearly all fields of science. I would like to wish all ECCS'09 participants a successful and inspiring time during their stay at Warwick University.

Coventry, September 2009

Markus Kirkilionis

ECCS'09 Conference Organising Chair

Towards a Science of Complex Systems

Following the success of reductionist approaches in many scientific fields, and despite the recent possibility of accumulating massive data sets, there are new kinds of problems in which it is impossible to predict the behaviour of a system from a description of its components and their interactions. To tackle these new problems, complex systems approaches have shown great promise around the turn of the century, in establishing scientific methods that could successfully be applied across a variety of application fields. More recently, the trend has been of more deeply anchoring these approaches into the intricacies of each particular application field. This trend constantly reflects back into transversal approaches, by increasing the opportunities for renewed inspiration from the application fields. So far, many studies in complex systems science follow either a network-based or an agent-based approach. We shall likely witness increased hybridization between these two complementary approaches, for more realistic modelling that would involve both privileged interactions between specific agents and an organization of agents in space. Finally, we can currently distinguish an increased focus on the design of complex systems, undoubtedly a consequence of past analytical work that improved our understanding of their underlying principles.

Since its inception in 2004, the European Conference on Complex Systems has established itself as the major scientific conference in this highly cross-disciplinary field. It reached as early as 2005 a world-wide scope despite its name.

Again this year, with over 290 scientific contributions, the ECCS'09 constitutes a rich testimony to the liveliness of the community involved in the exploration and design of complex systems. The Programme Committee has assigned these contributions to six tracks: Policy, Planning & Infrastructure, Collective Human Behaviour and Society, Interacting Populations and Environment, Complexity and Computer Science, From Molecules to Living Systems, Mathematics and Simulation. One advantage of rotating the ECCS among European cities is that each session has a slightly different local flavour. This year, Mathematics makes a notable contribution to the Warwick flavour. In addition to these track contributions, 12 Satellite meetings adaptively emphasize a wide variety of topics or concerns.

I take this opportunity to warmly thank the track Chairs, co-Chairs and Referees, the Programme Committee members and the Satellite meetings organizers, who have ensured that this Conference would meet the highest standards. I am also grateful to the Conference Steering Committee and to the Complex Systems Society for their wisdom and advice at crucial moments. Last but not least, I gratefully acknowledge the wonderful support of the Conference Organization Committee and of its Chair, Markus Kirkilionis.

Évry, September 2009

François KEPES

ECCS'09 Programme Committee Chair

Conference Venue

University of Warwick (Zeeman Building), Coventry, CV4 7AL, United Kingdom

Conference Organising Chair

Markus Kirkilionis (University of Warwick)

Conference Programme Chair

François Képès (Genopole®, Évry)

Event Manager

Aude Exbrayat

Complex Systems Society International Steering Committee

Markus Kirkilionis (Warwick; Chair 2008-10), Fatihcan Atay (Leipzig), Jürgen Jost (Leipzig), Scott Kirkpatrick (Jerusalem), David Lane (University of Modena and Reggio Emilia), Andreas Lorincz (Hungarian Academy of Sciences), Denise Pumain (Sorbonne), Felix Reed-Tsochas (Oxford), Eörs Szathmáry (Collegium Budapest, Hungary), Stephan Thurner (Wien), Paul Verschure (Barcelona), Alessandro Vespignani (Indiana, ISI), Riccardo Zecchina (Torino).

ECSS'09 Programme Committee

François Képès (Genopole; Chair), Paul Bourguine (Paris), Jeffrey Johnson (OU), Sorin Solomon (Hebrew University), Markus Kirkilionis, Robin Ball (Warwick).

- **Track A, Policy, Planning and Infrastructure:** Jeffrey Johnson (Chair, Open University), Arnaud Banos (Strasbourg, France)
- **Track B, Collective Human Behaviour and Society:** Felix Reed-Tsochas (Chair, Oxford), Edmund Chattoe-Brown (University of Leicester), Frances Griffiths (University of Warwick)
- **Track C, Interacting Populations and Environment:** Markus Kirkilionis (Chair, University of Warwick)
- **Track D, Complexity and Computer Science:** András Lörincz (Chair, Eötvös Loránd University), Paul Verschure (Zurich)
- **Track E, From Molecules to Living Systems:** Mark Chaplain (Chair, University of Dundee), Wolfgang Marwan (Max Planck Institute, Magdeburg)
- **Track F, Mathematics and Simulation:** Holger Kantz (Chair, Max Planck Institute, Dresden), Fatihcan Atay (Max Planck Institute, Leipzig), Matteo Marsili (Trieste)

ECSS'09 Local Organising Committee

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Poster Prize Committee

François Képès (Genopole, Chair)

Fatihcan Atay (Leipzig)

Paul Bourguine (Paris)

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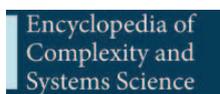
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Society



Monday, 21 September, 2009

08:15	Registration opens (The Street)					
09:00-10:20	Welcome address, Professor Nigel Thrift, Vice-Chancellor of the University of Warwick (MS.02) Plenary Session 1: Tony Prescott (MS.02)					
10:20-10:50	Coffee Break (The Street)					
10:50-12:30 *	Track A Policy, Planning and Infrastructure (MS.04)	Track B Collective Human Behaviour and Society (MS.02)	Track C Interacting Populations and Environment (MS.05)	Track D Complexity and Computer Science (B3.03)	Track E From Molecules to Living Systems (MS.03)	Track F Mathematics and Simulation (MS.01)
12:30-14:00	Lunch (The Street)					
14:00-16:00 *	Track A Policy, Planning and Infrastructure (MS.04)	Track B Collective Human Behaviour and Society (MS.02)	Track C Interacting Populations and Environment (MS.05)	Track D Complexity and Computer Science (B3.03)	Track E From Molecules to Living Systems (MS.03)	Track F Mathematics and Simulation (MS.01)
16:00-17:00	Poster Session & Tea Break (The Street)					
17:00-18:00	Plenary Session 2: Dirk Helbing (MS.02)					
18:00-19:30	<i>Dinner @ Rootes Restaurant</i>					
19:30-21:30	Public Event on “The Complexity of Global Change” (Theatre of the Arts Centre)					

* GENESYS Workshop runs in parallel to the Track Sessions (B3.02)

Tuesday, 22 September, 2009

09:00-10:00	Plenary Session 3: Michael Batty (MS.02)					
10:00-10:30	<i>Coffee Break (The Street)</i>					
10:30-12:30 *	Track A Policy, Planning and Infrastructure (MS.04)	Track B Collective Human Behaviour and Society (MS.02)	Track D Complexity and Computer Science (B3.03)	Track E From Molecules to Living Systems (MS.03)	Track F Mathematics and Simulation (MS.01)	
12:30-14:00	<i>Lunch (The Street)</i>					
14:00-16:00 *	Track A Policy, Planning and Infrastructure (MS.04)	Track B Collective Human Behaviour and Society (MS.02/MS.05)	Track D Complexity and Computer Science (B3.03)	Track E From Molecules to Living Systems (MS.03)	Track F Mathematics and Simulation (MS.01)	
16:00-17:00	Poster Session & Tea Break (The Street)					
17:00-18:00	Plenary Session 4: Michael Dawson (MS.02)					
18:00-19:00	Plenary Session 5: Nigel Gilbert (MS.02)					
19:00-20:30	<i>Dinner @ Rootes Restaurant</i>					
20:30-22:00	Complex Systems Society Council meeting (Rootes Building)					

* GENESYS Workshop runs in parallel to the Track Sessions (B3.02)

Wednesday, 23 September, 2009

09:00-10:00	<p>Satellite Meetings</p> <ul style="list-style-type: none"> • GENESYS • COSI-ICT'09: Complex Systems for Socially Intelligent ICT • MOAN-CB: Modelling and Analysis of Cell Behaviour 	<ul style="list-style-type: none"> • Statistical Mechanics of Molecular and Cell Biology • Dynamics on and of Complex Networks III • PhD 'In progress' workshop
10:00-10:30	<i>Coffee Break (The Street)</i>	
10:30-12:30	<p>Satellite Meetings</p> <ul style="list-style-type: none"> • GENESYS • COSI-ICT'09: Complex Systems for Socially Intelligent ICT • MOAN-CB: Modelling and Analysis of Cell Behaviour 	<ul style="list-style-type: none"> • Statistical Mechanics of Molecular and Cell Biology • Dynamics on and of Complex Networks III • PhD 'In progress' workshop • Cell Biology and Imaging Technologies
12:30-14:00	<i>Lunch (The Street)</i>	
14:00-16:00	<p>Satellite Meetings</p> <ul style="list-style-type: none"> • COSI-ICT'09: Complex Systems for Socially Intelligent ICT • MOAN-CB: Modelling and Analysis of Cell Behaviour 	<ul style="list-style-type: none"> • Statistical Mechanics of Molecular and Cell Biology • Dynamics on and of Complex Networks III • Cell Biology and Imaging Technologies
16:00-17:00	Poster Session & Tea Break (The Street)	
17:00-18:40	<p>Satellite Meetings</p> <ul style="list-style-type: none"> • COSI-ICT'09: Complex Systems for Socially Intelligent ICT • MOAN-CB: Modelling and Analysis of Cell Behaviour 	<ul style="list-style-type: none"> • Statistical Mechanics of Molecular and Cell Biology • Dynamics on and of Complex Networks III • Cell Biology and Imaging Technologies
19:00-22:00	<p><i>Springer Reception & Conference Dinner (Panorama Room - Rootes Building)</i></p> <p>After Dinner Talk: Ian Stewart "What the Frog's Eye Tells the Mouse's Ear"</p>	

See individual schedules for each Satellite meeting in the programme

Thursday, 24 September, 2009

09:00-10:00	Satellite Meetings	<ul style="list-style-type: none"> • Putting Complexity to work - Supporting the Practitioners • Information, Computation and Complex Systems • PATRES workshop • Networks: Dynamics and Flows 	<ul style="list-style-type: none"> • EmergeNET3: Emergence and Networks • Dynamics on and of Complex Networks III • Cell Biology and Imaging Technologies • PhD 'In progress' workshop
10:00-10:30	Coffee Break (The Street)		
10:30-12:30	Satellite Meetings	<ul style="list-style-type: none"> • Putting Complexity to work - Supporting the Practitioners • Information, Computation and Complex Systems • PATRES workshop • Networks: Dynamics and Flows 	<ul style="list-style-type: none"> • EmergeNET3: Emergence and Networks • Dynamics on and of Complex Networks III • Cell Biology and Imaging Technologies • PhD 'In progress' workshop
12:30-14:00	<i>Lunch (The Street)</i>		
14:00-16:00	Satellite Meetings	<ul style="list-style-type: none"> • Putting Complexity to work - Supporting the Practitioners • Information, Computation and Complex Systems • PATRES workshop 	<ul style="list-style-type: none"> • EmergeNET3: Emergence and Networks • Networks: Dynamics and Flows
16:00-16:30	Poster Session & Tea Break (The Street)		
16:30-18:00	Satellite Meetings	<ul style="list-style-type: none"> • Putting Complexity to work - Supporting the Practitioners • Information, Computation and Complex Systems • PATRES workshop 	<ul style="list-style-type: none"> • EmergeNET3: Emergence and Networks • Networks: Dynamics and Flows
18:00-19:00	EPSRC Showcase Poster Session & Reception (Digital Laboratory)		
19:00-20:30	<i>Dinner @ Rootes Restaurant</i>		

See individual schedules for each Satellite meeting in the programme

Friday, 25 September, 2009

09:00-10:00	Plenary Session 6: Peter Deuffhard (MS.02)					
10:00-10:30	Coffee Break (The Street)					
10:30-12:30	Track B Collective Human Behaviour and Society (MS.02)	Track C Interacting Populations and Environment (MS.05)	Track D Complexity and Computer Science (DigiLab Auditorium)	Track E From Molecules to Living Systems (MS.03)	Track F Mathematics and Simulation (MS.01)	
12:30-14:00	DigiLab Tour, <i>Lunch</i> (The Street/DigiLab)					
14:00-15:45	Funding Opportunities Plenary Discussions (MS.02)					
15:45-16:20	<i>Tea Break</i> (The Street)					
16:20-17:00	Plenary Session 7: Alfonso Jaramillo (MS.02)					
17:00-18:00	Poster Prize (MS.02) Plenary Session 8: Robert MacKay Closing remarks					

Programme

Monday, September 21, 2009

08:15 : Registration opens (The Street)

09:00-10:20 : Welcome address. Plenary Session 1 (MS.02)

Professor Nigel Thrift, Vice-Chancellor of the University of Warwick

Feeling it. Exploring brain complexity through active touch in animals and robots

Tony Prescott

53

10:20-10:50 : Coffee Break (The Street)

10:50-12:30 : Track Sessions

Track A - Policy, Planning and Infrastructure (Session: Policy and Management I) (MS.04)

Welcome from Track Chairs

Jeff Johnson, Arnaud Banos, Theo Zamenopoulos

10:50-11:30 Business, transport and the environment: the policy challenge

Brian Collins (Invited talk)

56

11:30-11:50 Towards policy for firm and supply network coevolution: A study of commercial aerospace manufacturing

Liz Varga, Peter Allen, Mark Strathern, Chris Rose-Anderssen, James Baldwin, Keith Ridgway

57

11:50-12:10 Why conceptual design matters in policy formulation: A case for an integrated use of complexity science and engineering design

Araz Taeihagh, Zun Wang, René Bañares-Alcántara

57

12:10-12:30 A complexity approach for policy in an informed society. Insights from regional case studies

Sylvie Occelli

57

Track B - Collective Human Behaviour and Society (MS.02)

10:50-11:30 A general evolutionary model of long-tailed distributions in the social sciences

Alex Bentley, Paul Ormerod, Michael Batty

63

11:30-11:50 Small worlds of conceptual connections: Structural properties of concept networks designed for learning physics

Ismo Koponen, Maija Pehkonen

64

11:50-12:30 Patents in new technologies

Miguel Ferreira, Bruno Oliveira, Alberto Pinto

64

Track C - Interacting Populations and Environment (MS.05)

10:50-11:10 Introduction by Track Chair

Markus Kirkilionis

11:10-12:10 The complexities of predicting pandemic influenza
Matt Keeling (Invited talk)

Track D - Complexity and Computer Science (B3.03)

10:50-11:10 Big Crunch in Computer Science: Introduction and Overview
András Lőrincz **75**

11:10-11:50 BitTorrent - from swarms to collectives
David Hales (Invited talk) **75**

11:50-12:30 A new class of cellular automata: How spatio-temporal delays affect dynamics and improve computation
Thimo Rohlf, Jürgen Jost **75**

Track E - From Molecules to Living Systems (MS.03)

10:50-11:30 Modelling Complexity in Solid Tumours
Helen Byrne (Invited talk) **80**

11:30-12:10 Autocorrelation function analysis of subcutaneous glucose profiles: an exploratory study
Tim Holt, Luca Sbano, Frances Griffiths, Simon Gray **81**

12:10-12:30 Model human heart or brain signals
Çağlar Tuncay **81**

Track F - Mathematics and Simulation (MS.01)

10:50-11:30 Predictive analysis for social dynamics
Richard Colbaugh, Kristin Glass **87**

11:30-12:10 Studying Lyon's Vélo'V: A statistical cyclic model
Pierre Borgnat, Patrice Abry, Patrick Flandrin, Jean-Baptiste Rouquier **87**

12:10-12:30 Analyzing the impact of network clustering on bond percolation and k-core sizes
Sergey Melnik, James Gleeson **88**

GENESYS Workshop (Day 1) (B3.02)

Tutorials: introduction to Genetical Genomics and network inference. These tutorials are aimed to introduce the area of the GENESYS workshop and provide a start point for the rest of the meeting.

10:50-11:40 Tutorial on eQTL
Enrico Petretto

11:40-12:30 Tutorial on gene networks
Ernst Wit

12:30-14:00 : Lunch (The Street)

14:00-16:00 : Track Sessions

Track A - Policy, Planning and Infrastructure (Session: Policy and Management II) (MS.04)

- 14:00-14:40 The Dynamics of Skyscrapers
Michael Batty (Invited talk) 58
- 14:40-15:00 Spatial analysis of dynamic movements of Vélo'v, Lyon's shared bicycle program
Pierre Borgnat, Eric Fleury, Céline Robardet, Antoine Scherrer 58
- 15:00-15:20 Delivering complex services
Mairi Macintyre, Jannis Angelis, Jag Dhaliwal, Glenn Parry 58
- 15:20-15:40 The self-organization and sustainable development of the global system: model and the main principle of the Simulation Modeling
Dmitry Chistilin 59
- 15:40-16:00 Grand challenges for complex systems research
Lex Zandee, Natasa Golo-Tosic 59
-

Track B - Collective Human Behaviour and Society (MS.02)

- 14:00-14:40 The application of complex systems concepts in a military context
Anthonie van Lieburg, Nanne Le Grand, Martijn Schut 64
- 14:40-15:00 The influence of social network topology in a opinion dynamics model
Simone Righi, Timoteo Carletti 65
- 15:00-15:40 The instability of downside risk measures
Istvan Varga-Haszonits, Imre Kondor 65
- 15:40-16:00 An empirical model for electronic submissions to conferences
Patrick Flandrin 65
-

Track C - Interacting Populations and Environment (MS.05)

- 14:00-14:40 Origins of Taylor's power law for fluctuation scaling in complex systems
Agata Fronczak, Piotr Fronczak 70
- 14:40-15:00 Complex network structure and transmission dynamics
Thomas House, Geoff Davies, Leon Danon, Matt Keeling 71
- 15:00-15:20 Disease outbreak dynamics: modelling and simulation for complex realities
Bahaa Abdel Hamid, Amy Griffin, Peter Durr 71
- 15:20-16:00 Poster advertisement
-

Track D - Complexity and Computer Science (B3.03)

- 14:00-14:40 Random hypergraphs and their applications
Guido Caldarelli, Gourab Ghoshal, Vinko Zlatic, Mark Newman 76

14:40-15:00 Pervasive Adaptation <i>Ben Paechter</i>	76
15:00-15:20 Online clustering with CFinder <i>Andras Barta, Gergely Palla, Péter Pollner, Tamás Vicsek</i>	76
15:20-16:00 Poster advertisement	
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Track E - From Molecules to Living Systems (MS.03)	
14:00-14:20 Agent Based algorithm for the study of molecular self-organisation <i>Sara Fortuna, Alessandro Troisi</i>	82
14:20-14:40 The function of communities in protein interaction networks <i>Anna Lewis, Mason Porter, Nick Jones, Charlotte Deane</i>	82
14:40-15:40 Poster advertisement	
<hr/>	
Track F - Mathematics and Simulation (MS.01)	
14:00-14:40 Cluster synchronization in complex networks of coupled non-identical maps <i>Wenlian Lu, Bo Liu, Tianping Chen</i>	88
14:40-15:20 Adaptive Dynamics of Realistic Small-World Networks <i>Olof Mogren, Oskar Sandberg, Vilhelm Verendel, Devdatt Dubhashi</i>	88
15:20-16:00 Poster advertisement	
<hr/>	
GENESYS Workshop (Day 1) (B3.02)	
14:00-15:00 Gene networks from eQTL; are we there yet? <i>Rebecca Doerge</i>	
15:20-16:00 TBC <i>Nico Katsanis</i>	
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16:00-17:00 : Poster Session & Tea Break (The Street)	
17:00-18:00 : Plenary Session 2 (MS.02)	
Cooperation, Norms and Revolutions: A Unified Game-Theoretical Approach <i>Dirk Helbing</i>	
18:00-19:30 : Dinner @ Rootes Restaurant	
19:30-21:30 : Public Event on “The Complexity of Global Change” (Theatre of the Arts Centre)	

Tuesday, September 22, 2009

09:00-10:00 : Plenary Session 3 (MS.02)

Evolution, Cities and Planning: Exemplars from the Sciences of Complexity
Michael Batty 53

10:00-10:30 : Coffee Break (The Street)

10:30-12:30 : Track Sessions

Track A - Policy, Planning and Infrastructure (Session: Spatial Analysis and Modelling) (MS.04)

10:30-11:10 Exploring the possibility-cone of urban development
Alan Wilson, Joel Dearden (Invited talk) 60

11:10-11:30 The law of inhabitant travel distance distribution
Liang Liu, Francesco Calabrese, Assaf Biderman, Carlo Ratti 60

11:30-11:50 Modelling Dynamic Demand Responsive Transport using an Agent Based Spatial Representation
Didier Josselin, Christophe Lang, Nicolas Marilleau 61

11:50-12:10 Slowing down urban networks to fight urban sprawl: agent based approach
Arnaud Banos 61

12:10-12:30 Highway Traffic Forecasting. Beyond Complex to Complicated
Eddie Wilson 61

Track B - Collective Human Behaviour and Society (MS.02)

10:30-11:10 Fitting the Log Periodic Power Law to financial crashes: a critical analysis
David Brée, Nathan Joseph 65

11:10-11:30 Altruism and reputation: cooperation within groups
Przemyslaw Gawronski, Malgorzata Krawczyk, Krzysztof Kułakowski 66

11:30-12:10 Mutual information to assess structural properties in dynamic networks
David Rodrigues, Jorge Louçã 66

12:10-12:30 An individual-based model of collective attention
Mehdi Moussaid, Dirk Helbing, Guy Theraulaz 66

Track D - Complexity and Computer Science (B3.03)

10:30-11:10 Self Organization and Learning in Cellular Robotics
Michele Sebag 77

11:10-11:50 Swarms of Flying Robots for Communication Networks
Sabine Hauert 77

11:50-12:30	An allostatic control model for robot behavior regulation <i>Marti Sanchez, Ulysses Bernardet, Paul Verschure</i>	77
<hr/>		
Track E - From Molecules to Living Systems (MS.03)		
10:30-10:50	The viability theory to control complex food processes <i>Mariette Sicard, Nathalie Perrot, Cedric Baudrit, Romain Reuillon, Paul Bourgine, Isabelle Alvarez, Sophie Martin</i>	82
10:50-11:10	Tag-statistics in complex networks <i>Gergely Palla, Illés J. Farkas, Péter Pollner, Imre Derenyi, Tamás Vicsek</i>	82
11:10-11:30	Multiclock discrete models of biological systems <i>Nolwenn Le Meur, Michel Le Borgne, Jérémy Gruel, Nathalie Théret</i>	83
11:30-11:50	Timing of molecular processes in a synchronous Boolean model of genetic regulatory network <i>Alex Graudenzi, Roberto Serra, Marco Villani, Chiara Damiani, Annamaria Colacci, Stuart Kauffman</i>	83
<hr/>		
Track F - Mathematics and Simulation (MS.01)		
10:30-11:10	The Complex Universe: recent experiments and theoretical challenges <i>Luciano Pietronero, Francesco Sylos Labini</i>	89
11:10-11:30	Collective observables in repeated experiments. The case of population dynamics. <i>Timoteo Carletti, Duccio Fanelli</i>	89
11:30-11:50	Overlapping Communities, Link Partitions and Line Graphs <i>Tim Evans, Renaud Lambiotte</i>	90
11:50-12:10	Self-Organization of Formations and Swarms of Agents <i>Gilles Labonte, Giovanni Fusina, Gerard Pieris, Bumsoo Kim</i>	90
12:10-12:30	Critical behaviour in toroidal plasma confinement by 3-D magnetic fields <i>Mathew McGann, Robert Dewar, Stuart Hudson, Matthew Hole</i>	90
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GENESYS Workshop (Day 2) (B3.02)		
10:30-11:10	Modelling networks: top-down or bottom-up? <i>Ernst Wit</i>	
11:10-11:50	Reverse engineering switching transcription factor activities from microarray data <i>Guido Sanguinetti</i>	
11:50-12:20	Reverse-Engineering Gene Regulatory Networks From Microarray Data with Dynamic Bayesian Network <i>Andrea Ravi</i>	
12:20-12:30	Discussion	
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12:30-14:00 : Lunch (The Street)

14:00-16:00 : Track Sessions

Track A - Policy, Planning and Infrastructure (Session: Networks I) (MS.04)

14:00-14:40 Robustness of Trans-European Gas Networks: The Hot Backbone

Rui Carvalho, Lubos Buzna, Falvio Bono, Eugenio Gutiérrez, Wolfram Just, David Arrow-smith **62**

14:40-15:00 A self-repairing solution for the resilience of networks to attacks and failures

Nicolas Brax, Frédéric Amblard **62**

15:00-15:20 Separating internal and external fluctuation in distributed Web-based services

Sara Casolari, Marco Villani, Michele Colajanni, Roberto Serra **63**

15:20-15:40 The information dynamics of cascading failures in energy networks

Joseph Lizier, Mikhail Prokopenko, David Cornforth **63**

15:40-16:00 Modelling packet pair dispersion in multi hop network with correlated traffic

Péter Hága, Péter Mátray, István Csabai, Gábor Vattay **63**

Track B - Collective Human Behaviour and Society

Parallel session 1 (MS.02)

14:00-14:40 Openness Leads to Opinion Stability and Narrowness to Volatility

Sylvie Huet, Guillaume Deffuant **67**

14:40-15:00 Cognitive similarity, tie creation, and tie strength: Network and content analysis of an online forum

Pietro Panzarasa, Bernard Kujański **67**

15:00-15:40 Risk and beliefs updating mechanisms for contingent claims valuation in incomplete markets

Lampros Boukas, Diogo Pinheiro, Alberto Pinto, Stylianos Xanthopoulos, Athanasios Yannacopoulos **67**

15:40-16:00 Phase diagram of a Schelling segregation model

Laetitia Gauvin, Jean Vannimensus, Jean Pierre Nadal **68**

Parallel session 2 (MS.05)

14:00-14:20 Social norms, Emotions and cooperation in groups

Phan Denis, Waldeck Roger **68**

14:20-14:40 Boolean Network and Simmelian Tie in the Co-Author Model: A Study of Dynamics and Structure of a Strategic Alliance Model

Laurent Tambahong **68**

14:40-15:00 Network Decomposition: An Information Theoretical Approach

Masatoshi Funabashi **68**

15:00-15:20 Effects of Authority on Consensus Formation for Continuous Opinions in an Adaptive Network <i>Brenton Pettejohn, <u>Mark D. McDonnell</u></i>	69
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Track D - Complexity and Computer Science (B3.03)	
14:00-14:40 Creating Complex Systems by Integrating Desktop and Service Grids <i>Gábor Terstyánszky</i>	78
14:40-15:00 Achieving Consensus Among Agents – opinion-dynamics meets belief revision <i>Bruce Edmonds</i>	79
15:00-15:40 A Formal Language Theoretic Approach to Distributed Computing on Dynamic Networks <i>Katalin Anna Lázár</i>	79
<hr/>	
Track E - From Molecules to Living Systems (MS.03)	
14:00-14:20 The Effect of Spatial Organisation in Response Threshold Models for Social Insects <i>Konrad Diwold, Alexander Scheidler, Martin Middendorf</i>	83
14:20-14:40 A stochastic model of myxobacteria explains several features of motility and development <i>Antony Holmes, <u>Sara Kalvala</u>, David Whitworth</i>	84
14:40-15:00 Systems Chemistry: Mechanosensitive Self-replication <i>Sjibren Otto, Jacqui Carnall, Chris Waudby, Jerome Peyralans, Marc Stuart</i>	84
15:00-15:20 A mechanism of cancer robustness: the small complex system TE-TA-P [Telomeres-Telomerase-Proliferation] <i>Jean Deschatrette, Olivier C Martin, <u>Claire Wolfrom</u></i>	84
15:20-15:40 On the Nuclear-Network Dynamics able to convert the Molecular Mechanisms into Biological Information <i>Walter Riofrio</i>	85
<hr/>	
Track F - Mathematics and Simulation (MS.01)	
14:00-14:20 Quantifying structure in networks <i>Eckehard Olbrich, Thomas Kahle, Nils Bertschinger, Nihat Ay, Jürgen Jost</i>	91
14:20-14:40 On the fate of perturbations in critical random Boolean networks <i>Chiara Damiani, Alex Graudenzi, Marco Villani, <u>Roberto Serra</u>, Annamaria Colacci, Stuart Kauffman</i>	91
14:40-15:00 Optimal Control of Electrostatic Self-Assembly of Binary Monolayers <i>Nickolay Shestopalov, Graeme Henkelman, Travis Powell, Gregory Rodin</i>	91
15:00-15:20 Statistical characterisers of transport in a communication network <i>Neelima Gupte, Satyam Mukherjee, Gautam Mukherjee</i>	91

15:20-15:40	Toward a knowledge integration for representing food processes <i>Cedric Baudrit, Mariette Sicard, Pierre-Henri Wuillemin, Nathalie Perrot</i>	92
<hr/>		
GENESYS Workshop (Day 2) (B3.02)		
14:00-14:40	Simulating the bacteriophage lambda genetic switch <i>Rosalind Allen</i>	
14:40-15:20	Experimental target identification of microRNA-140 <i>Tamas Dalmay</i>	
15:20-16:00	Genetic causes of transcript abundance variation in <i>C. elegans</i> <i>Matt Rockmann</i>	
<hr/>		
16:00-17:00 : Poster Session & Tea Break (The Street)		
17:00-18:00 : Plenary Session 4 (MS.02)		
	The Ever-Changing Sea: Physico-Biological Systems Still Eluding Prediction <i>Michael Dawson</i>	54
18:00-19:00 : Plenary Session 5 (MS.02)		
	Middle Range Models: Modelling Real World Social Processes <i>Nigel Gilbert</i>	55
19:00-20:30 : Dinner @ Rootes Restaurant		
20:30-22:00 : Complex Systems Society Council meeting (Rootes Building)		

Wednesday - Thursday, September 23 - 24, 2009

GENESYS Workshop (Day 3) (for Day 1 and Day 2 schedules see timetables for Monday, Sept 21 and Tuesday, Sept 22)

Organisers: DJ de Koning (The Roslin Institute and R(D)SVS, University of Edinburgh), Chris Haley (MRC Human Genetics Unit and The Roslin Institute), Tim Aitman (MRC Clinical Sciences Centre and Imperial College, London), Arnis Druka and Robbie Waugh (Scottish Crops Research Institute, Dundee), John Whittaker (GlaxoSmithKline, Harlow), Dirk Husmeier (Biomathematics and Statistics Scotland, Edinburgh), Chris Rawlings (Rothamsted Research, Harpenden)

The goal of the GENESYS network is to promote the required integration between genetics, bioinformatics and mathematics to facilitate the reverse-engineering of regulatory networks using genetic mapping data and high throughput data, such as transcriptomics. This is an important step toward systems biology approaches where these regulatory networks will be refined and evolve into quantitative models of regulation.

Sept 23 (B3.02)

09:00-09:40 Arne Gjuvland (Cigene) "Causally cohesive genotype-phenotype models - systems biology meets genetics"

09:40-10:10 Yang Li (Groningen University) "Causal inference in genome-wide association and linkage studies: a quantitative genetic perspective"

10:10-10:30 Coffee break

10:30-11:10 Sacha Ott (Warwick University) "Transcriptional regulatory networks from the viewpoint of sequence analysis"

11:10-11:40 Matthieu Vignes (INRA) "From gene clustering to genetical genomics: using or reconstructing biological networks"

11:40- 12:30 General discussion and closure

COSI-ICT'09: Workshop on Complex Systems for Socially Intelligent ICT

Organiser: Jeffrey Johnson (Open University and and ASSYST Project)

Sept 23 (MS.05)

09:00-09:30 Jeff Johnson, ASSYST "Introduction to the COSI-ICT Satellite Meeting"

09:30-10:30 COSI-ICT Integrated Project Presentation 1 (A presentation by the partners explaining their project and progress to data)

10:30-11:00 Coffee break

11:00-12:00 COSI-ICT Integrated Project Presentation 2 (A presentation by the partners explaining their project and progress to data)

12:00-13:00 COSI-ICT Integrated Project Presentation 3 (A presentation by the partners explaining their project and progress to data)

13:00-14:30 Lunch

14:30-15:30 COSI-ICT Integrated Project Presentation 4 (A presentation by the partners explaining their project and progress to data)

15:30-16:00 COSI-ICT and Social Networks - Submitted Presentations

16:00-16:30 Coffee break

16:30-17:30 Simulations and Movies

17:30-18:00 Discussion of the Programme (Jose Fernandez-Villacanas - FET Proactive)

18:00 Drinks reception hosted by ASSYST

MOAN-CB: Modelling and Analysis of Cell Behaviour

Organisers: Frank Bruggeman (VU Amsterdam) and Jaco van de Pol (U Twente)

This workshop will be devoted to computational support for Systems Biology. Our aim is to bring together people from bioinformatics, computer science and biology. In particular, we focus on modeling and analysis techniques for various regulatory networks. Examples are genetic regulation, metabolic processes, and signalling pathways within a cell. The interaction between such networks is of special interest. The workshop is organised by the EC-MOAN project, and consists of presentations from people both within and outside the project.

Sept 23 (MS.01)

09:00-10:00 EC-MOAN session 1: Modelling

09:00-09:20 "Goals and Results of the EC-MOAN project" Jaco van de Pol (U Twente, NL)

09:20-09:40 "Omnipresent two-component signaling governs swift and robust responses even at low molecule numbers" Frank J. Bruggeman (VU Amsterdam, NL)

09:40-10:00 "Modelling ammonium assimilation regulation in *Escherichia coli*" Hongwu Ma (Edinburgh University, UK)

10:00-10:30 Coffee break

10:30-11:30 Session: Methodology

10:30-11:00 "BioModel Engineering and its role in Systems Biology" David Gilbert (Brunel University, UK)

11:00-11:30 "Sound identification and model merging when studying type 2 diabetes" Gunnar Cedersund (Linköping University, SE)

11:30-12:30 Session: Stochastic Process Algebra

11:30-11:50 "Stochastic automata for replication, translation and translesion synthesis" Erik de Vink (TU Eindhoven, NL)

11:50-12:10 "Process algebraic modelling and analysis of signalling pathway crosstalk" Robin Donaldson (Glasgow University, UK)

12:10-12:30 "Modelling scaffold-mediated crosstalk between the cAMP and the Raf-1/MEK/ERK pathways" Oana Andrei (Glasgow University, UK)

12:30-14:00 Lunch break

14:00-15:00 EC-MOAN session 2: Analysis

14:00-14:20 "Qualitative analysis of carbon starvation response in *E. coli*" Valentina Baldazzi (INRIA Grenoble, FR)

14:20-14:40 "On Computational Analysis of Large ODE Models" David Safranek (Masaryk University, Brno, CZ)

14:40-15:00 "Modeling kinase signalling pathways in cells using UPPAAL" Rom Langerak (U Twente, NL)

15:00-16:30 Session: Quantitative Analysis

15:00-15:30 "A general computational method for robustness analysis with applications to synthetic gene networks" Gregory Batt (INRIA Rocquencourt, FR)

15:30-16:00 "Executing Multicellular Development: Quantitative Predictive Modelling of *C. elegans* Vulva" K. Anton Feenstra (VU Amsterdam, NL)
16:00-16:30 "Modelling biochemical pathways with Bio-PEPA and CTMCs" Jane Hillston (Edinburgh University, UK)
16:30-17:00 Tea break
17:00-18:00 Panel Discussion

Statistical Mechanics of Molecular and Cell Biology

Organisers: R.C. Ball, R. MacKay, M. Nicodemi (Warwick), M. Mubilia (Leeds), P. Sorba (Annecy)

As detailed high quality experimental data are becoming available today, Statistical Mechanics has a key role in the development of quantitative approaches to describe Biological Systems, providing the theoretical background for the physical description of interacting many-body systems. Our satellite aims to cover new developments and challenges in such a rapidly growing interdisciplinary research area. It will also provide a unique opportunity to participate to the ECCS'09 broader context and its other related topical satellites. It will bring together researchers working in disciplines ranging from biology, to chemistry, computer science, engineering, mathematics and physics.

Sept 23 (MS.04)

8:50 Welcome

8:50 M. Caselle "Feed-forward loops in the human regulatory network"

9:15 C. Lesieur "Protein oligomers: a good example of complex Interaction Networks"

9:40 J.-F. Joanny "Mechanics and growth of tissues"

10:05 Coffee break

10:30 U. Gerland "Statistical Physics of Nucleosome Positioning"

10:55 A. Gamba "Universal features of cell polarization processes"

11:20 M. Howard "Probing a mechanical bottleneck in FcgR phagocytosis by imaging and mathematical modelling"

11:45 C. Molina-Paris "Stochastic modelling of T cell diversity"

12:10 M. Nicodemi TBA

12:35 Lunch

14:00 M. Cates "Dynamics of Bacterial Suspensions"

14:25 T. Duke TBA

14:50 D. Marenduzzo "Modelling soft active matter: bacterial fluids and actin networks"

15:15 A. McKane "Amplified Biochemical Oscillations in Cellular Systems" 15:40 R. Zecchina TBA

16:05 Coffee break - Posters

17:00 M. Mubilia "Oscillations in evolutionary models with co-dominant dynamics"

17:25 T. Liverpool "From microscopics to hydrodynamics in active filament suspensions"

17:50 M.H. Jensen "Feed-Back Networks and Oscillations in Time and Space"

Dynamics on and of Complex Networks-III

Organisers: Fernando Peruani (Service de Physique de l'Etat Condense (CEA), Paris Ile-de-France), Niloy Ganguly (Indian Institute of Technology, Kharagpur), Andreas Deutsch (Technical University of Dresden, Germany), Eric Fleury (Ecole Normale Supérieure de Lyon)

Large-scale networks with complex interaction patterns between elements are found in abundance in both nature and man-made systems (e.g., genetic pathways, ecological networks, social networks, networks of scientific collaboration, WWW, peer-to-peer networks, power grid etc.). The main aim of this workshop is to explore the statistical dynamics *on* and *of* such networks. Dynamics on networks refers to the different types of so called processes (e.g. proliferation, diffusion etc.) that take place on networks. The functionality/efficiency of such processes is strongly affected by the topology as well as the dynamic behavior of the network. On the other hand, Dynamics of networks mainly refers to various phenomena (for instance self-organization) that go on in order to bring about certain changes in the topology of the network.

It has become clear that the stability and robustness of highly dynamical networks as in ad-hoc networks of mobile agents, and study of dynamical process on transport networks are the hottest new theoretical challenges for Complex Network research. Accordingly, Dynamics On and Of Complex Networks III will focus on these topics.

Sept 23 (MS.02)

Social networks

9:00 Guillaume Chelius "Monitoring Patient - Health Care Workers Interactions in a Hospital Environment"

9:30 Jean-Loup Guillaume "Community stability on pseudo-dynamics graphs"

10:00 Kimmo Kaski "Social networks: can they be modeled?"

10:30 - 11:00 Coffee Break

Spreading processes on networks

11:00 Bruno Goncalves "Complex Techno-Social Networks for Epidemic Forecasting"

11:30 Niloy Ganguly "Epidemic spreading of information in moving agent systems: Technological and Biological applications"

12:00 Anne-Ly Do "Adaptive network approach to the collective motion of self-propelled agents"

12:30 - 14:00 Lunch Break

Cellular Automata

14:00 Bastian Chopard "Spontaneous formation of submarkets in a simple economical model on an irregular topology"

14:30 Nazim Fates "Cellular automata on irregular networks: when topology modifications trigger qualitative changes of dynamics"

15:00 Andras Czirok "Vascular network formation by collective cell motility"

General properties

15:30 Joydeep Chandra "Analyzing Flood Based Searching in Unstructured P2P Networks"

16:00 - 16:30 Coffee Break

16:30 Hans Herrmann "Robustness of social networks"

17:15 Fernando Peruani "Revisiting complex network robustness"

17:45 Bivas Mitra "Understanding the Emergence of Superpeer Networks: A Complex Network

Approach"

18:15 Lionel Tabourier "Generating Random graphs with given constraints"

Sept 24 (MS.02)

Biology and Networks

9:00 Mogens H. Jensen "Repressor-lattices: Coupled Feed-Back Loops in Space"

9:45 Tiago P. Peixoto "Boolean networks with reliable dynamics"

10:15 Andreas Deutsch "Analyzing emergent behaviour in cellular automaton models of cancer invasion"

10:45 - 11:15 Coffee Break

11:15 Florian Greil "Scale-free critical Boolean networks Theory"

11:45 Camille Roth "Reciprocal influence of social and semantic patterns in a dynamic blog network"

12:15 Tyll Krueger "Communication and knowledge transfer on complex networks"

PhD 'In Progress' Workshop

Organisers: Iain Kusel (Design Group, Open University), Martine Barons (Complexity Science Centre and DTC, Warwick University), Andrea Apolloni (NDSSL, VirginiaTech)

The idea of the satellite is to give MSc and PhD students studying within the domain of Complexity Science a platform to present their research question, approach and results at an early point in their research career to an interdisciplinary and supportive group. The broader aim is that beginning researchers are exposed to a wide number of research questions and methodologies within Complexity Science and are allowed to network with potential colleagues.

Sept 23 (A1.01)

09:00-09:20 Opening comments (Goals of workshop, CSS and PhD in progress activities)

09:20-09:40 Neural network machine learning with a complex intervention for back pain

Martine J. Barons

94

09:40-10:00 Developing Sensory Augmentation in Urban Environments for People with Visual Impairment

Anthony Johnston

95

10:00 - 10:30 Coffee break

10:30-10:50 Competition between sexual and asexual reproduction: a model for geographic parthenogenesis

Yixian Song, Irene Ament, Stefan Scheu, Barbara Drossel

95

10:50-11:10 An agent-based model of immune cell trafficking, inflammation and HIV spread.

Kate Wendelsdorf

96

11:10-11:30 Minimizing genome complexity by reductive evolution

Sven Deitz

96

12:10-12:30 Questions and discussion

Sept 24 (A1.01)

09:00-09:20 Deriving Neighborhood Properties of Real Networks with Given Degree Distribution
Joydeep Chandra **96**

09:20-09:40 Stability Analysis of Superpeer Networks in the Framework of Complex Networks
Bivas Mitra **97**

10:00 - 10:30 Coffee break

10:30-10:50 *Iain Kusel*

10:50-11:10 Opinion Formation in Social Systems
Abhishek Mukhopadhyay **97**

11:10-11:30 Opinion Formation in Social Systems
Paul Chapron **97**

12:10-12:30 Questions and discussion

Cell Biology and Imaging Technologies

Organiser: Colin Robinson (Warwick)

Sept 23 (MS.03)**Special session from Jeol and Gatan on electron microscopy/tomography**

11:00 Andy Yarwood (Jeol): An overview of current TEM tomography techniques and software

12:30 Paul Spellwood (Gatan). Title TBA

Synopsis: Tomography has undergone a famine to feast transition over the last decade. 10 years ago, Electron Tomography was in the domain of a few dedicated researchers prepared to put a lot of effort in to collecting datasets of images that could be used for reconstructing a 3D image of the sample. The technique was seen as a black art and equally the reconstruction of the images was a long and complex process with many errors due to inaccuracies in the alignment of the data. Now, the modern user is spoilt for choice with a range of options available for both collection and reconstruction. From relatively costly but simple commercial solutions through to complex but ultimately flexible academic freeware, the choices are now abundant. It is still a relatively lengthy process but no longer shrouded in mystery and confusion. This talk outlines the development of Electron Tomography and the current options available

12:30-14:00 Lunch

Symposium session I

14:00 Helen Saibil (Birkbeck College) Electron microscopy of molecular and cellular machinery

14:40 Corinne Smith (Warwick). Unwinding the clathrin cage - kinetic and structural measurements of the action of Hsc70 on clathrin assemblies

15:20 Judy Armitage (Oxford) Protein localisation and dynamics in bacterial motility measured by single molecule microscopy

16:00 Tea and posters

17:00 Short talk

17:20 Short talk

17:40 Close

Sept 24 (MS.03)

Symposium session II

09:00 Lorenzo Frigerio (Warwick). Reticulons and plant endoplasmic reticulum morphology

09:40 Short talk

10:00 Coffee

10:30 David Stephens (Bristol). Organization and mechanisms of membrane trafficking - COPII-dependent export from the ER

11:10 Martin Pool (Manchester). Role of ribosomal components in protein targeting and membrane protein integration at the ER

11:50-12.10 Short talks

Information, Computation and Complex Systems

Organiser: Karoline Wiesner (University of Bristol)

This workshop will bring together mathematicians and scientists to discuss methods and applications of information theory to complex systems. This includes the perspective of complex systems as computers.

Sept 24 (MS.01)

Session 1

09:00-09:40 Kristian Lindgren - Information-theoretic quantification of order and disorder

09:40-10:00 Robin Ball - Complexity vs emergence: Quantifying emergence in term of persistent mutual information

Session 2

10:30-11:10 James P. Crutchfield - The past and the future in the present

11:10-11:50 Susanne Still - Interactive learning

11:50-12:10 Joseph T. Lizier - Coherent local information dynamics in complex computation

12:10-12:30 Alexander Gegov - Advanced modelling of complex systems by rule based networks

Session 3

14:00-14:30 Mario Rasetti - Information science at the boundary between quantum and living matter

14:30-15:00 Nils Bertschinger - Dynamics and information: Memory in recurrent neural networks

15:00-15:20 Daniel Polani - Empowerment: Guiding adaptation through potential information flows

15:20-15:40 Eckehard Olbrich - How should complexity scale with system size?

15:40-16:00 Karoline Wiesner - Measures of complexity and information erasure

16:15-17:30 Tea + Discussion "Information theory: What it can and cannot do for complex systems" with J.P. Crutchfield, K. Lindgren, R. MacKay, and S. Still

EmergeNET3: Emergence and Networks

Organisers: Lee Cronin (University of Glasgow) and Rebecca Mancy

EmergeNET3: Emergence and Networks focuses on a key element of complex systems theory, that of networks, and explores their role in understanding emergent phenomena. Networks can be used to represent the links between elements of a system, and therefore provide a structure for understanding emergence. But network structures themselves can also emerge. EmergeNET3 is aims to discuss and develop these ideas in a broad range of application areas from the sciences to the social sciences and beyond.

Sept 24 (MS.05)

09:00-10:00 **Session 1**

20 min. Opening Address - Lee Cronin, Rebecca Mancy, Yasmin Merali, Cristina Cerulli

40 min. Jim Crutchfield - Is Anything Ever New?

10:30-12:30 **Session 2: Emergence in social sciences and linguistics**

40 min. Yasmin Merali - Emergence and Persistence

20 min. Jean Boulton - Complexity and emergence

20 min. Helen Ashman - The convergence of users and the emergence of semantics on the Web

20 min. Poster advertisements

14:00-16:00 **Session 3: Social and biological networks**

20 min. Jorge Louca - Detecting emerging structures in informal communication networks

20 min. Pietro Cipresso - Physiologically driven affective agents in simulated networks

20 min. Thimo Rohlf - Emergent network structure, evolvable robustness and non-linear effects of point mutations in an artificial genome model

40 min. Yves Demazeau - Organizational dynamics in agent based systems and applications

17:00-19:00 **Session 4: Networked robots**

40 min. Alan Winfield - Modelling emergence in wirelessly networked swarms of mobile robots

20 min. EmergeNET Business Meeting

Posters

- Pedro Pablo (University of Hull) Emergent product-service systems in one non-hierarchical community
- Torbjorn Dahl (University of Wales, Newport) Self-organising division of labour
- Andres Vejar & Ivan Gomez-Castano (UMR, CNRS-UHP Nancy & Universidad de Antioquia, Columbia) Reparation as an emergent process in metabolic networks
- Massimiliano Zanin & Andres Vejar (INNAXI Foundation & Research Institute and UMR, CNRS-UHP Nancy, France) The Emergence of Transportation Networks
- Irina Neaga & Michael Henshaw (Loughborough University) Developing an adaptive and interoperable metasystem for assuring information security within a highly complex networking environment
- Daniel Morrison (University of Glasgow) Understanding and Communicating Emergence

Putting Complexity to Work - Supporting the practitioners

Organisers: Patrick Beautelement (The abaci Partnership LLP)

The focus of this one-day workshop is: How to harness the insights coming out of complexity science more effectively? How to put them to work in support of practitioners who deal with complex realities in their day-to-day activity, as in business strategy development; health care; humanitarian aid; social and cultural engagement; local and regional planning; sustainable development etc.

Sept 24 (D1.07 Complexity Seminar Room - follow signs to Complexity Centre via Conference Office)

09:00-10:00 Session 1

20 min. Introduction and Workshop Aims

40 min. Scene Setter "Practical Complexity - Do we know what we need to do?" - Speaker TBC

10:30-12:30 Session 2

40 min. Eileen Conn - Living Systems "Community engagement - a social eco-system dance"

40 min. Anna Plodowski - Peckham Power Project "Putting Complexity to Work in Community Projects"

40 min. Group work - Session 1 - "Challenges and Advice to Complexity Science from the Practitioners"

14:00-16:00 Session 3

20 min. Findings from Group Work Session 1

40 min. David Palmer, Institute of Directors, "The Commercial Benefits of Embracing Complexity"

40 min. W.H. Erik de Man - "Trans-disciplinary working - Bridging the Gap between Practitioners and Complexity Scientists"

20 min. Scene setting for Group Work Session 2

17:00-19:00 Session 4

40 min. Group Work - Session 2 - "Addressing the Challenges"

40 min. Findings from Group Work Session 2

20 min. Concluding presentation - Lucian Hudson - "What is to be done? Goodbye to Lenin, and putting complexity to work"

20 min. Decide Follow-on actions for White paper

PATRES Workshop: Computing action policies that insure resilience of social and ecological systems

Organisers: Guillaume Deffuant (Cemagref, France) and Nigel Gilbert (University of Surrey, Guildford, UK)

Resilience is generally defined in the framework of dynamic system theory (attractors, attraction domains, bifurcations): a system is resilient to a perturbation when this perturbation keeps the system in domains of attractors where the system shows the desired properties or functions. However, this definition has two strong limitations: (i) It supposes no possibility to modify the dynamics, whereas socio-ecological systems often involve stakeholders and managers who want to define efficient policies of action. (ii) It supposes that a set of the dynamics attractors show the desired properties, whereas these properties could appear only at non-equilibrium states.

This workshop will demonstrate how new methods, based on viability theory, can overcome these limitations and provide means to compute action policies favouring the recovery from perturba-

tions, and maintain some systems in a desired non-equilibrium state.

This approach has nevertheless drawback: it is very demanding computationally. This is a strong limitation on applying it to complex models from ecology, cognitive science or sociology. This is why the workshop will also introduce methods to simplify complex models. These methods, inspired from physics, can, under certain conditions, derive simple dynamical systems (involving a small set of synthetic variables) representing the main features (patterns) of the dynamics observed on a complex individual or agent based model.

Sept 24 (B3.02)

Morning

- What is resilience? Review, critical assessment, and outlook (Volker Grimm, Camille Roth and Sophie Martin)
- Viability and resilience, concepts from a toy example (Sophie Martin and Guillaume Deffuant)
- Computing viability and resilience, the bottleneck of dimensionality (Laetitia Chapel and Guillaume Deffuant)
- The macro description of individual based models (Federico Vazquez, Cristobal Lopez and Maxi San Miguel)
- Bridging the gap between structurally realistic models and viability theory in savanna ecosystems (Justin M. Calabrese and Volker Grimm)

Afternoon

- Bacterial biofilms (Jean-Denis Mathias and Nabil Mabrouk)
- Viability and resilience in the dynamics of language competition (Xavier Castello and Maxi San Miguel)
- Resilience in the dynamics of collaborative Web communities: Three case studies (Dario Taraborelli, Camille Roth and Nigel Gilbert)
- Resilience and viability problems in social dilemma modelling (David Chavalarias and Laetitia Chapel)
- Panel discussion

Networks: Dynamics and Flows

Organisers: Markus Kirkilionis (Warwick) and Ian Stewart (Warwick)

The theory of networks is a unifying theme throughout Complexity Science and Systems Biology. There is a large class of network problems where a non-static situation has to be considered. In a wider context these are situations where the interaction between the system components has to incorporate different feedback loops, or the interaction is regulated. In this workshop we will concentrate on rate-based deterministic, stochastic and game-theoretic (i.e. involving local optimisation and learning) dynamical networks, and dynamics of network structures (changing connection strengths, addition and deletion of nodes). Phenomena to be addressed include synchronisation, robustness, computational capabilities and qualitative behaviour dependent on the network topology.

This satellite connects into the main NET2009 workshop, 28 Sept - 2 Oct 2009 at Warwick Maths Institute.

Sept 24 (B3.03)

14:00-14:20 From static to dynamic networks - Outlook to NET2009

Markus Kirkilionis

14:20-15:00 Studying the structure and dynamics of organisational networks in the wild <i>Felix Reed-Tsochas</i>	98
15:00-15:40 Mathematical Tools for Studying Collective Behavior in Dynamical Networks <i>Fatihcan M. Atay</i>	98
16:00-16:30 Coffee break	
16:30-17:10 Detailed Modelling of Gene Regulatory Networks <i>Markus Kirkilionis</i>	98
17:10-17:50 Epigenomics and Morphodynamics <i>François Képès</i>	99

Sept 23, 19:00-22:00 : Springer Reception & Conference Dinner (Panorama Room -
Rootes Building)
After Dinner Talk: What the Frog's Eye Tells the Mouse's Ear
Ian Stewart **56**

Sept 24, 18:00-19:00 : EPSRC Showcase Poster Session & Reception (Digital Laboratory)

Friday, September 25, 2009

09:00-10:00 : Plenary Session 6 (MS.02)

Medical Simulation Challenges Mathematical Modelling

Peter Deuffhard

55

10:00-10:30 : Coffee Break (The Street)

10:30-12:30 : Track Sessions

Track B - Collective Human Behaviour and Society (MS.02)

10:30-11:10 Publish or Perish: some collective implications

David Chavalarias, Vincent Gardelle

69

11:10-11:30 The tragedy of the commons in a multi-population complementarity game

Wei Li, Jürgen Jost

69

11:30-12:10 Dynamic communities in multichannel data: An application to the foreign exchange market during the 2007–2008 credit crisis

Daniel Fenn, Mason Porter, Mark McDonald, Stacy Williams, Neil Johnson, Nick Jones

70

12:10-12:30 Evolutionary Complex Systems in Molecular Biology and Social Systems: Similar Processes and Models?

Carl Henning Reschke

70

Track C - Interacting Populations and Environment (MS.05)

10:30-10:50 The impact of concurrent and transient contacts on HIV epidemics

Christel Kamp

71

10:50-11:10 How interaction between co-evolving agents shape temporal mode and structure of the interaction network in a simple ecological mode

Dominic Jones, Henrik Jeldtoft Jensen, Paolo Sibani

72

11:10-11:30 Worldwide spread of the unfolding swine flu epidemic: early assessment and predictions

Paolo Bajardi, Duygu Balcan, Vittoria Colizza, Bruno Goncalves, Hao Hu, Daniela Paolotti, Chiara Poletto, Nicola Perra, Jose Ramasco, Michele Tizzoni, Wouter Van den Broeck, Alessandro Vespignani

73

11:30-11:50 Correlations and stochastic fluctuations in the SIR model

Andrea Parisi, Ana Nunes

73

11:50-12:10 Challenges Arising During the Analysis of Crude Oils and Environmental Samples

Mark P. Barrow, John V. Headley, Kerry M. Peru

73

Track D - Complexity and Computer Science (Digilab Auditorium)

10:30-11:10 Can Robots Communicate?

Jürgen Jost, Eckehard Olbrich, Nils Bertschinger

79

11:10-11:30	The Peace Mediator Effect <i>Andrea Guazzini, Graziano Barnabei, Timoteo Carletti, Franco Bagnoli, Daniele Vilone</i>	80
11:30-11:50	Detecting overlapping communities in graphs <i>Qinna Wang, Eric Fleury</i>	80
11:50-12:30	Security Challenges in Clouds <i>Sadie Creese, Paul Hopkins</i>	
<hr/>		
Track E - From Molecules to Living Systems (MS.03)		
10:30-10:50	Spatially Averaged Microscale Model for quantifying Methemoglobin Anemia <i>Saikat Chakraborty, Srimoyee Bhattacharya</i>	85
10:50-11:10	Constraint-based modeling of the Drosophila Gap-gene regulatory network <i>Eric Fanchon, Fabien Corblin, Laurent Trilling</i>	86
11:10-11:30	Regulatory networks and connected components of the neutral space <i>Gunnar Boldhaus, Konstantin Klemm</i>	86
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14:00-15:45 : Funding Opportunities in Complex Systems Science & Plenary Discussions (CRP Forum) (MS.02)

Participants:

Markus Kirkilionis and Jeffrey Johnson (coordinators)

Jose Fernandez-Villacanas (EC, ICT)

Ana Helman (European Science Foundation)

Raphael Laurent (EC, ERA-NET)

Colin Miles (BBSRC)

Gavin Salisbury (EPSRC, representing EPSRC/Complexity-NET/ERA-NET)

The CRP Forum is supported by the ASSYST coordination action inside the 7th Framework Programme.

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 Eileen **Conn**, Living Systems Research, London
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 of Strathclyde
 Jim **Crutchfield**, Complexity Sciences Center,
 Univ. California at Davis
 Dr Andras **Czirok**, Dept of Anatomy; Univer-
 sity of Kansas Med Ctr
 Lawrence **Dack**, Niteworks
 Torbjorn **Dahl**, UoW, Newport
 Dr Tamas **Dalmay**, University of East Anglia
 Dr. W.H. Erik **de Man**, The Netherlands
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 Yves **Demazeau**, University Of Grenoble
 Julien **Derr**, Harvard University
 Prof. Peter **Deuffhard**, Zuse Institute Berlin
 (ZIB)
 Andreas **Deutsch**, Centre for Information Ser-
 vices and HPC, Technical University Dresden
 Marina **Diakonova**, Complexity Science DTC
 Peter **Dick**, Department of Health
 Sven **Dietz**, BSSE, ETH Zurich
 Konrad **Diwold**, University of Leipzig
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 ratory
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 sterdam
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 China
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 ing Technology
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 Physique
 Pr. Eric **Fleury**, ENS Lyon / INRIA
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 sity of Warwick
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 saw University of Technology
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 Ottawa
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 ences
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 Univ. Laval
 Tobias **Galla**, University of Manchester
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 ENS, PARIS
 Emil **Gegov**, Brunel University
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 versity of Portsmouth
 Eva **Gehrmann**, TU Darmstadt
 Hans **Geiselman**, Univ. of Genoble
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 (LMU), Germany
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 York

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 ogy
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 Danuta **Makowiec**, Gdansk University
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Mario **Nicodemi**, Complexity Science, Warwick

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Matt **Oates**, Bristol Centre for Complexity Sciences

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Supreecha **Rimratchada**, University of Leeds

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Dipl. Phys. Yixian **Song**, Institute of condensed matter physics, TU Darmstadt

Prof Susan **Stepney**, York Centre for Complex Systems Analysis

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Dr. Roger **Waldeck**, Telecom Bretagne and Université Européenne de Bretagne

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Tristan **Webb**, Complexity Science DTC

Kate **Wendelsdorf**, Network Dynamics Simulation Science Lab, Virginia Tech

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Stefan **Wieland**, CFTC, University of Lisbon

Dr. Karoline **Wiesner**, Complexity Centre, Univ. of Bristol

Dr R. Eddie **Wilson**, Bristol Centre for Complexity Science

Prof Alan **Winfield**, Bristol Robotics Lab, UWE bristol

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Dr Theodore **Zamenopoulos**, The Open University

Dr. Lex **Zandee**, NWO

Christoph **Zimmer**, BioQuant, University of Heidelberg

Information for Participants

Travel

Venue of the conference (Zeeman Building, University of Warwick) is no 35 on the campus map (upper right corner).

Check-in for the conference accommodation is in the Rootes Social Building (building no 49 on the campus map).

Note that the University is **not** in the town of Warwick (which is about 8 miles away), and it is **not** the same as Coventry University (which is a different university, located in the centre of Coventry). This is important when telling taxi drivers where you want to be (University of Warwick in Coventry).

How to get here: <http://www2.warwick.ac.uk/about/visiting/directions/>

Bus from Coventry City Centre

Both bus service 12 and 12A run from the city centre bus station, Pool Meadow, out to the University Central Campus passing the Westwood campus en route (travel time approx. 25 minutes) – both display University of Warwick or Leamington as destination. Exit either at the UoW Gatehouse or main bus stop. These are operated by Travel Coventry (part of National Express) and timetable information can be found at www.travelcoventry.co.uk.

Travel Coventry buses do not usually give change so make sure you have the correct amount available before making your journey.

Taxi

There is a taxi rank at the University. They are usually by Rootes Social, but with the works on the Piazza, the rank may be on Health Centre Road - if you are facing Costcutter, Health Centre Road is the second street on your left (the first is not really a street, rather the back entrance to the supermarket). Should you need to call a taxi, please find below 3 phone numbers: there are many others, this is just a sample.

- Central of Coventry 024 7633 3333
- City Cabs 024 7622 2222
- Trinity Street Taxis 024 7663 1631

Disclaimer: The Coventry taxis firms listed on this page are for your information. UoW does not endorse any particular taxi or minicab firms in Coventry and is not responsible for the facilities and services of companies listed.

Parking

Residential guests can park in car parks 7, 8 and 15, but vehicles can be left overnight only in car parks 7 and 15. An exit code for car park 15 must be obtained from Rootes Reception at check-in.

Road works: There will be road works on University Road from Tuesday 22 September which are likely to cause some disruption to taxis and buses, so please allow extra time.

Accommodation

Upon arrival, please check in the Rootes Social Building Reception for instructions (building no. 49). This is also the place to ask about car parking, left luggage, etc.

Workshop registration

Registration will take place

- on Sunday Sep 20 in the Rootes building atrium area between 15:00 and 21:00,
- on Monday Sep 21 in the main Atrium of the Zeeman building between 8:30 and 10:00.
- The rest of the week you can register in Zeeman B1.37, from 9:30 to 14:00.

Computing facilities

During the conference all attendees can connect to the conference network

WiFi at <https://wg-conf1.warwick.ac.uk>

Please note: support for raw smtp (outbound) traffic not assured. You have been assigned a personal user code, which you can find in your conference pack. If that really doesn't work, please try **login**: phhgae or phhxab; **password**: eccs09@Warwick via WiFi 'hotspot'.

Meals

During the conference, lunches and coffee/tea will be provided in the 'Street' on the ground floor of the Zeeman building.

On Sunday Evening, the Bar Fusion in Rootes Social Building will be open. Please note that a Sunday evening meal is not included in the conference registration fee nor in the accommodation package.

Monday through Friday evenings, those who are staying overnight can obtain dinner in Rootes Restaurant (included in DB&B rates); others wishing to join this dinner should enquire at the ground floor reception desk in Rootes Building for tickets.

The main Conference Dinner Wed evening will be on the top floor of Rootes.

Messages

The telephone number for colleagues or family to leave an **urgent** message for you during office hours is 02476 151062.

Emergency numbers

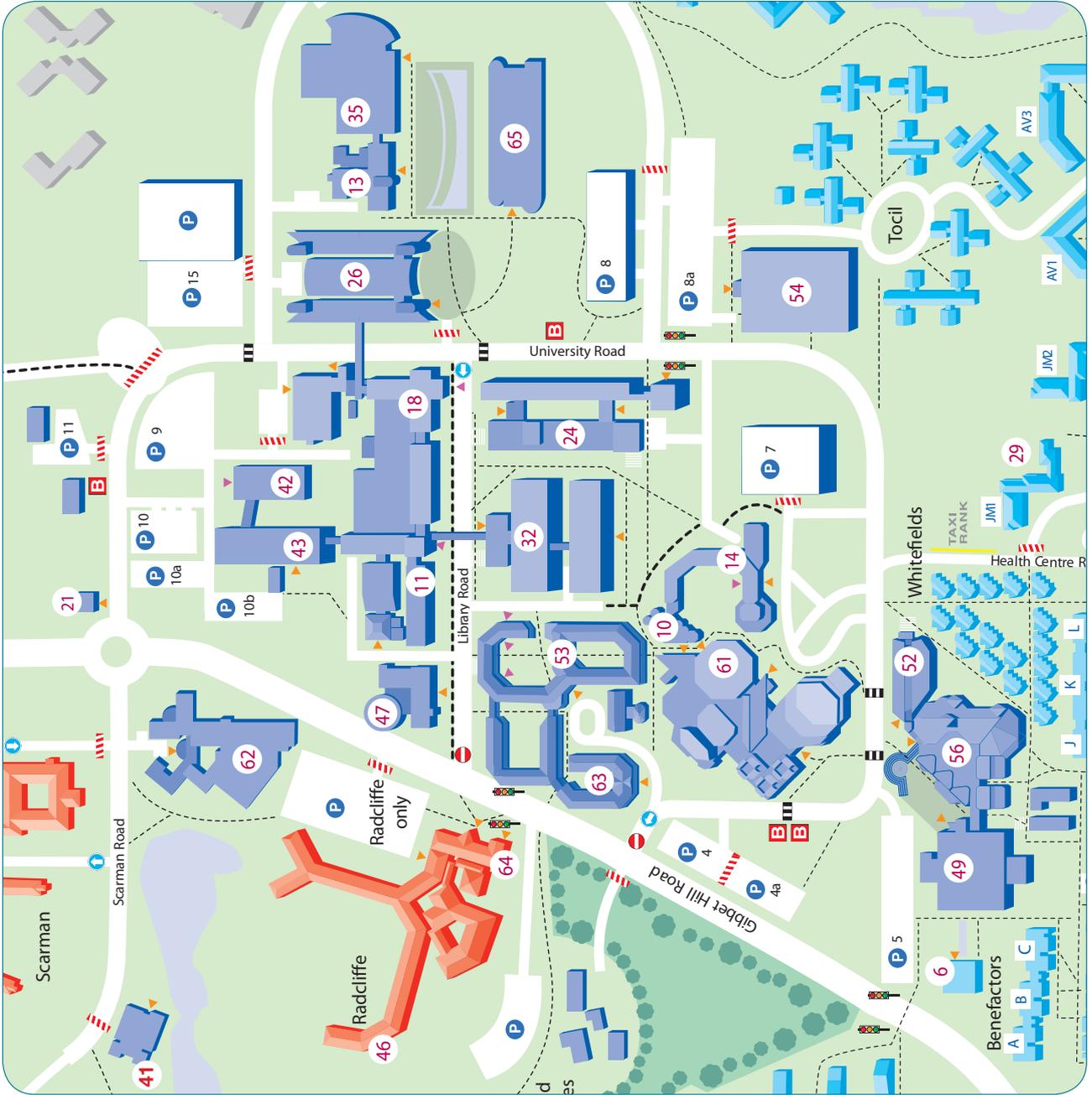
Delegates in need of emergency assistance should contact Security on internal extension 22222 or 22083 (externally 024 76 522 222 or 024 76 522 083).



61. Warwick Arts Centre



49. Rootes Building, Conference Park



35. Zeeman Building

Building Key	
4	Arthur Vick
6	Benefactors
10	Chaplaincy
11	Sciences
13	Computer Science
14	Coventry House
18	Engineering
21	Gatehouse
22	Health Centre
24	Humanities Building
26	International Manufacturing Centre
29	Jack Martin
32	Library
35	Mathematics & Statistics
43	Physics
46	Radcliffe
47	Ramphal Building
49	Rootes
52	Retail Outlets
56	Banks
53	Social Studies
54	Sports Centre
56	Students' Union
61	Warwick Arts Centre
62	Warwick Business School (WBS)
63	Main Reception
63	WBS Social Studies
64	WBS Teaching Centre
65	International Digital Laboratory

List of Abstracts

Feeling it. Exploring brain complexity through active touch in animals and robots

Tony Prescott

Plenary Session 1

The systems approach in the brain sciences has demonstrated that there is no straightforward decomposition of the brain into modules, or even a simple means to separate brain from the body (in control terms), or the body from the environment. So how should we proceed? Our approach has been to investigate a complete sensorimotor loop, specifically, the guidance of exploratory behaviour by tactile sensing signals. We have focused on the rat vibrissal (whisker) system as a model. The neurobiology of this system indicates multiple layers of control, that can be loosely mapped to the different levels of the neuraxis, and that exhibit both some redundancy and some modularity. Neuroethological experiments show a tight coupling between sensory signals and active control of the movement and positioning of the sensors. Electrophysiological and modelling studies suggest a system that is capable of rapidly extracting relevant affordances for action, rather than constructing complex internal representations of the external world. These ideas will be illustrated with examples from our research on active touch sensing in animals and in biomimetic robots.

Evolution, Cities and Planning: Exemplars from the Sciences of Complexity

Michael Batty

Plenary Session 3

Since the time of Newton, there have been speculations that a social physics developed in analogy to classical mechanics and thermodynamics has applicability to city systems with respect to how we might understand their structure and interactions. Since the time of Darwin, similar analogies have been drawn between cities and evolution, particularly with respect to their growth and form. Indeed, the father of town planning in Britain, Patrick Geddes, began his career as a biologist under the Huxley and Sanderson, close friends of Darwin in the 1870s in London. His book *Cities in Evolution* (Geddes, 1915) resonates strongly with early ideas of evolution based on notions that change in cities is driven from the bottom up, by individuals and groups, leading to the emergence of spatial order and pattern at larger scales, reflecting the long standing synergy and dichotomy in the complexity sciences between local action and global order. Indeed, it is Geddes who is accredited with bringing the term local-global into common parlance through his writings about planning and ecology at many scales.

This paper is more of an essay in which I will sketch some of this history in the field of urban studies and city planning, beginning with early ideas in social physics and evolution, and then sketching the first foray into a city science built around ‘the systems approach’ which became popular in social sciences some 50 years ago. The rudimentary theories and models then treated cities as structures in equilibrium and a variety of gravitational and potential models were developed to measure interactions between static locational entities such as populations, retail centres, and related urban phenomena. This static simplification of what even then was widely regarded as dynamic was forged because there was so little science in city planning. There was a view that something, anything that provided a stronger basis for understanding cities was essential and consequently the models that were developed in hindsight now appear naïve in that cities are manifestly dynamic as Geddes and many others always knew.

However those who worked in this field did not stand still. Throughout the 1970s and 1980s, cities were articulated in dynamic terms, with ideas from irreversible thermodynamics, from catastrophe and bifurcation theory and even from chaos being fashioned as analogues for how urban processes might work themselves out in space. Notions about growth and form came back onto the agenda with scaling and self-similarity being aggressively pursued through work on size distributions, spatial similarity and fractal patterns, and self-organised criticality. General notions of emergence, path dependence and historical

contingency are now also being embraced in a wider science of cities. These developments like those during the earlier era of the systems approach are laced with ideas from simulation, econometrics and a variety of computer and statistical techniques required to operationalise and test the empirical veracity of the theories and models suggested.

This arsenal of theory and models is now being slowly forged into a more robust science of which a good example is in the science of networks. Although this science which has rapidly become synonymous with complexity theory is of very wide applicability, city systems with their focus on interaction and their translation into location and space are pivotal. Part of the attraction of network science in explaining city forms and patterns is the fact that cities tend to be more accessible than other physical and social systems in terms of their data and the way we might observe and measure their content. Networks are a key cornerstone of this wider science but there is a view that there is some convergence between many of the methods of the complexity science and more traditional theories that have tended to articulate urban form and structure. Even qualitative thinking which still dominates our theories and understanding of cities is slowly being fashioned in a language and ideology more consistent with what has been happening in complexity theory.

So my essay will present some of this history. It will also grapple with the underlying notion that in cities, our prime purpose for their study has never been based on understanding for its own sake. It is intimately engaged in policy. What complexity science is now showing quite vividly that there are ways in which we might intervene in their control and management somewhat less than tradition has dictated and that there are ways in which large changes can engender small effects. This is primarily due to the notion that in planning cities – in making them more liveable, sustainable, more equitable, and more efficient – we need to go with the flow, intervene less and achieve more, more subtly and less intrusively. The science that is being created has many of these hallmarks.

The Ever-Changing Sea: Physico-Biological Systems Still Eluding Prediction

Michael Dawson

Plenary Session 4

In 1962, during an address to the British Association in Manchester entitled "Man and the Beneficent Sea", Sir Alister Hardy emphasized the difficulties of studying "the ever-changing sea". He opined that "there will no doubt be many new ways in which we shall be able to increase the harvest of the sea when we come to have a greater knowledge of it" and he concluded that "the biologists and the physical oceanographers are now ready to come together to give us one dynamic picture of [the ocean's] month-by-month changes . when this is done and the environment is studied as a changing physico-biological whole . man [will] fully inherit the Earth by understanding its better half."

How do things stand nearly 50 years later - 40 years after establishment of the US National Oceanic and Atmospheric Administration and 15 years after opening of the UK National Oceanography Centre - with unprecedented datasets available from, for example, 107 km of survey from Hardy's continuous plankton recorder and three decades of biological and physical satellite oceanography? Over 60% of assessed fish stocks require rebuilding, the most progressive approach to marine management is area closure, and we have only just passed the point of coarsely matching physical oceanographic connections with patterns of gene flow in some marine animals. Why have we fallen so far short of Hardy's expectations? For sure, some reasons are socio-political and economic, some are technological, but what I will focus on here is our approach to understanding the physico-biological marine systems. Hardy contended that the seas provided a particularly difficult challenge for study because they are always on the move, the ocean is vast, and it mostly hidden from normal human perception. Many have concluded, like Hardy, that it is "useless to think of [the oceans] as we think of the terrestrial world" and it has, indeed, at least proven very difficult

to do so. By reference to two projects we are undertaking on two vastly different scales - one across the ca. 2000 km California Current Ecosystem, the other within hectare-sized marine lakes - I will explore some of the conceptual limitations that have been placed on marine evolutionary biology and marine ecology and argue that a broader perspective and greater synthesis using existing and new analytical techniques may provide the next major advance in our understanding of the ever-changing sea.

Middle Range Models: Modelling Real World Social Processes

Nigel Gilbert

Plenary Session 5

What happens when one tries to follow the numerous methodological prescriptions about how one should develop an agent-based model, such as ‘keep it simple’, ‘identify macro-level stylised facts’, ‘model micro-level behaviour’, ‘develop iteratively’ and so on? This talk will show that these prescriptions do work, but the kind of model they produce is somewhat different to many that are to be found in the literature. The point will be illustrated with two models, in which the aim was to get some deeper understanding of events that having been dominating the headlines. The first model simulates the instabilities displayed in the housing market in England (and elsewhere in the developed world). The model incorporates a simplified version of the actual processes of buying and selling that households typically engage in and demonstrates that the observed aggregate performance of the housing market can be reproduced without resort to conventional economic assumptions about markets. The second concerns the effects of the ‘bonus culture’ that is alleged to be a root cause of the credit crisis. I conclude that although highly abstract models of social phenomena and highly descriptive models of specific situations have their place, there is room also for ‘middle-range’ models in helping to understand the complexities of the social world and its impacts on us.

Medical Simulation Challenges Mathematical Modelling

Peter Deuffhard

Plenary Session 6

Realistic and reliable medical simulation is a rich source of mathematically challenging problems. Just think of computerized tomography originating from medical imaging problems, which, in turn, influences the state-of-the-art of medical imaging. Since this problem class has been well-known for quite a time, it will not be touched in this talk. Rather, the author will exemplify the title by mathematical challenges that have come up in recent work of his research groups at ZIB. First, computational drug design will be surveyed, which has led to a change of mathematical modelling from molecular dynamics (MD) to conformation dynamics (CD), which, in turn, has led to the suggestion of new potential drugs. Second, dynamic contact problems arising in the simulation of the motion of joints (such as the human and sheep knee) will be treated, which has led to the suggestion of a new numerical integrator, the contact-stabilized Newmark method, and a corresponding novel surprising underlying theory.

Towards the Automatic Design of Biological Systems with Targeted Function

Alfonso Jaramillo

Plenary Session 7

We have developed a new computational design methodology for the de novo design of proteins and nucleic acids, and their networks. We will discuss our recent experimental validations where we have synthesized a new thermostable chorismate mutase with a minimal amino acid alphabet, a thioredoxin protein with additional esterase activity or peptides that bind to MHC-I proteins. Afterwards, we will

present our automated procedure to design genetic circuits, composed of predefined genetic parts, having a desired time-response and a degree of robustness. We will then discuss our designs for new transcriptional devices having a targeted switching or oscillatory behavior. Finally, we will present another computational procedure we have created for de novo design of metabolic pathways using a retrosynthetic algorithm. This tool will allow grafting new bioproduction pathways into a given cellular chassis or to find new degradation pathways for bioremediation applications.

Space-time Phases and the Mathematics of Emergence

Robert MacKay

Plenary Session 8

A complex system consists of many interdependent components, e.g. molecules and photons in the atmosphere-ocean-eco-system, people and goods in an economy. Some components may be fixed in space, others are mobile. Some may be “passive” whereas others may be adaptive or goal-oriented.

From prescribed external inputs and microscopic laws for its realisations (weather), may emerge one or more probability distributions (climates). For dynamical systems (deterministic or stochastic) with spatial extent, I call them “space-time phases”.

In the trivial case of independent components, the space-time phases are products of probability distributions for the dynamics of the components. Thus, I quantify the emergence of a space-time phase by its distance to the set of product distributions, in a suitable metric. The interest lies in what sorts of correlations it expresses.

Many systems have unique space-time phase, but structural properties or the idealisation of infinite spatial extent can produce more than one, including non-trivial collective behaviour. I say a system exhibits strong emergence if it has more than one space-time phase and quantify the strong emergence by the diameter of the set of phases. On the other hand, there may be systems with no space-time phase.

As parameters are varied, the set of space-time phases may undergo smooth movements separated by qualitative changes (“phase transitions”).

Control (e.g. traffic lights) can have large effects on space-time phases.

Lastly, there are many questions about design principles for complex systems, e.g. optimisation, resilience.

Reference: R.S.MacKay, *Nonlinearity in Complexity Science*, *Nonlinearity* 21 (2008) T273-281

What the Frog’s Eye Tells the Mouse’s Ear

Ian Stewart

After-Dinner Talk

How *Batrachomyomachia* and *Froschmäusekrieg* relate to *A New Kind of Science*, and the incalculable consequences.

Business, transport and the environment: the policy challenge

Brian Collins

Track A - Policy, Planning and Infrastructure

Prof. Brian Collins, (Chief Scientific Advisor to the Department for Transport and to the Department of Business, Innovation and Skills) will make a presentation on the need for the development and implementation of complex systems models in order to support national infrastructure policy decisions. His presentation will demonstrate graphically why this is so, showing the multiplicity of factors that are involved in, and impact on, different types of infrastructure such as transport, waste, water and power and

in problems such that of climate change. In order to be able to make better policy decisions government needs these new methods of analysis to estimate the trade-offs and constraints for different stakeholders, sectors and regions affected by the many policies and decisions government must make.

Towards Policy For Firm and Supply Network Coevolution: A Study of Commercial Aerospace Manufacturing

Liz Varga, Peter Allen, Mark Strathern, Chris Rose-Anderssen, James Baldwin, Keith Ridgway

Track A - Policy, Planning and Infrastructure

Firm and supply network coevolution was constrained in the past by national policy allowing the home country to control the effects of production. In a globalized environment where firms are geographically dispersed, inter-firm activity accommodates diverse national policies. This study is based in the commercial aerospace manufacturing sector dominated by a duopoly: Boeing in America and Airbus in Europe. These firms and their supply networks have many similarities largely as a consequence of globalization, but as we witness further coevolutionary activity which is moving manufacturing and assembly to low cost economies, the question for policy is how might inter-firm activity be directed by policy to address global environmental concerns relating to the effects of production and use of jetliners?

Why conceptual design matters in policy formulation: A case for an integrated use of complexity science and engineering design

Araz Taeihagh, Zun Wang, René Bañares-Alcántara

Track A - Policy, Planning and Infrastructure

We believe complexity science and engineering design have much to offer for addressing problems faced in policy design and formulation. Adopting tools and techniques developed in these fields can provide insights for the development of methodologies, help in avoiding common pitfalls and minimize the time required for development of solutions. The introduction of a systematic approach for exploring alternative policies using a computational methodology that utilizes integration of diverse techniques such as backcasting, conceptual design, network analysis and agent-based modelling will help in decomposing the problem into subproblems with more manageable size, and accelerate and improve the effectiveness of the process of policy-making. We present a case for policy formulation and analysis in transport sector for achieving CO₂ emission targets for the UK. In particular, our ideas are based on the Hierarchical Design Method for the conceptual design of chemical processes (Douglas, 1988) and use of complexity science techniques such as network analysis and agent-based modelling. A six-step framework has been proposed and is being implemented. A library of policy measures and networks of their relations have been developed and through the analysis of these networks and the internal properties of the policy measures, using an agent-based modeling paradigm, policy alternatives are being formulated. This research constitutes the first step towards the development of a generic family of software systems to support design of policies for different sectors. The results will assist in technology transfer and have the potential to significantly improve the development of policy alternatives, accelerate the design of policies and improve their chance of success.

A complexity approach for policy in an informed society. Insights from regional case studies

Sylvie Occelli

Track A - Policy, Planning and Infrastructure

Notwithstanding over the last decades progress of ICT applications has been astonishing their impact on policy making is still limited. This calls for a more thorough examination of the linking between policy

knowledge requirements and ICT tools. The paper is a contribution to this endeavour. Two regional policy programs recently carried out in Piedmont are briefly recalled as their discussion can help addressing these issues. An illustration of the rationale of the two policy programs is given. Then some interpretative keys for understanding the relationships between policy knowledge requirements and ICT tools are suggested.

The Dynamics of Skyscrapers

Michael Batty

Track A - Policy, Planning and Infrastructure

If you rank order the size of objects or artefacts such as building heights, city populations, firm revenues, individual incomes, and like phenomena, the distributions can often be approximated by a power law. This might appear mysterious in that the regularity of such distributions is so strong that some such as Krugman have been led to remark, for cities, that “we are in the frustrating position of having a striking empirical regularity with no good theory to account for it”. The origins of such scaling clearly depend on competition against a background of scarce resources which imply that fewer large objects can exist than small objects and that this process of ‘sorting out’ those into big and small depends on growth processes where the probability of an object growing gets increasingly smaller as the object gets bigger.

In this paper, I review what is known about building heights – skyscrapers and high rise building greater than 35 metres in height – for a series of world cities, focusing on their scaling and their allometry. I also note the dynamics of this kind of building that is relatively stable with respect to scaling over time but subject to considerable micro irregularities and volatilities as cities appear compete with each other for rank with respect to high buildings in the entire system. As Krugman suggests “This simple regularity is puzzling” but more so is the volatility that occurs within the envelop of macro regularity. All this is clearly a signature of the kind of complexity that characterises systems where competition and growth dominate the organisation of activities.

Spatial analysis of dynamic movements of Vélo’v, Lyon’s shared bicycle program

Pierre Borgnat, Eric Fleury, Céline Robardet, Antoine Scherrer

Track A - Policy, Planning and Infrastructure

Public transportation systems like Lyon’s bicycle community sharing program can be considered as a complex system composed of interconnected stations that exchange bicycles. Such system generates digital footprints that reveals the activity in the city over time and space and make possible their analyze. In this paper, the analysis deals with the spatial understanding and visualization of bicycle trips. We first study the activity in each station separately and then identify the main characteristics of the flow between stations.

Delivering Complex Services

Mairi Macintyre, Jannis Angelis, Jag Dhaliwal, Glenn Parry

Track A - Policy, Planning and Infrastructure

Applying customer focused management approaches to public sector issues are often problematic for a number of reasons. Previous work claims management has either only made a weak attempt at suggesting that methods need to be adapted to situations when clearly in some instances no amount of adaptation would make an approach effective; cultural acceptability is often only pinned on once a process based system has been defined, thus giving a process centred approach as opposed to an experience centred approach. This is not in line with patient centred/client centred service provision and in some cases just not an appropriate method for design of the service intervention. This work posits that private sector is more

complicated than complex and understanding both this distinction and its consequences are critical to developing the correct approach for operational design. Management approaches to operations such as lean are designed to deal with complicated systems, when the public sector is a series of complex systems, thus often rendering such solutions ineffectual. For some services that are so complex in nature and the value is nearly exclusively determined by the experience that no amount of process improvement will improve the overall behavioural outcomes of a service based system. Systems theory offers up an alternative approach because it classes systems into simple, complicated and complex, and acknowledges the importance of first determining the type of system one is dealing with, prior to applying solutions. Operations Management is concerned with the design, implementation and sustainability of systems. There has been little work that offers consequential implications for management of complex or complicated systems. This research offers an initial framework to help determine an approach to managing value creation in complex systems and an initial method of determining to what extent a system is complex. Case studies have been used to provide data and come from both public and private sectors.

The self-organization and sustainable development of the global system: model and the main principle of the Simulation Modeling

Dmitry Chistilin

Track A - Policy, Planning and Infrastructure

The phenomenon of states changes of the world economy during the last 200 years shows that there is a certain 70-year regularity in its development, which is expressed in increased structural complexity of the global economic system every 70 years. The development happens after certain periods of bifurcation (up to 50 years) accompanied by the lower rates of economic development, and periods of adaptation (up to 20 years) with the higher rates. The theoretical justification of this process shows that the increased structural complexity of the global economic system is the external manifestations of the self-organization process in a large complex system we call the “world economy”. This process of development is based on two fundamental laws of nature: the principle of minimum dissipation of resources, and the law of conservation of economic potential; and is realized via two types of development mechanisms – bifurcation and adaptation. Formation of the world system model should rest on applying the natural laws of development, and lead towards the creation of a complex, two-level (regional and global) structure with the institution of geopolitical pluralism, based on implementing the “principle of minimum dissipation”. This will contribute to the development of the global system on the conflict-free base.

Grand challenges for complex systems research

Lex Zandee, Natasa Golo-Tosic

Track A - Policy, Planning and Infrastructure

Complexity is one the strategic research themes for the Dutch National Research Council (NWO). These strategic themes provide a response to important current issues in society and are based on clear prompts for new research in relevant areas. Partly stimulated by the present financial and economic crisis, companies and governmental institutions have changed their view on methods required to understand processes and systems. Complexity based analysis is becoming involved in outlining public policy in different areas. Companies and institutions from several fields participate in the Dutch complexity programme and have provided different research questions relating to public policy in the fields of financial, transportation, climate, IT and control systems. For instance, Dutch National Bank (DNB), Dutch National Railway System (NS) and the Dutch National Weather Forecast (KNMI) take part and have formulated policy related issues such as:

How does a growing complex network between banks, investors and trading institutions affect financial

stability?

How to deduct decisions about network capacity from individual passenger preference?

What does the complexity aspect of climate imply for our future?

How to approach social sensor computing, the ultimate interaction between different complex networks? These questions are in seemingly unrelated fields but it has become clear that, to be successful in providing solutions, it is necessary to form a broad research community on a national level. Therefore the NWO strategic theme is a joint initiative of the research councils for Physical Sciences, Social Sciences, Earth and Life Sciences, Chemical Sciences and the Technology Foundation. Although, in the Netherlands, already several institutes are involved with Complex Systems research, such as EURANDOM, CENDEF and ICMS, the formation of a national community has advantages compared to local research centres. For instance, a national community forms a good point of departure in the relation with industry organisations and the European Complexity community gathered in Complexity-NET. A Dutch steering committee has been formed involving researchers coming from different universities and many different scientific disciplines to govern, together with NWO, the theme development. The committee produced the theme document outlining important sub-themes and related challenges. “Predictability”, “Complex Networks” and “From micro to macro” have been selected as the sub-themes by the committee. Thereupon, the steering committee has taken the lead in setting up a national Complexity educational programme for PhDs. The PhDs will be involved in this multidisciplinary programme next to the standard programme within their own research schools.

Exploring the possibility-cone of urban development

Alan Wilson, Joel Dearden

Track A - Policy, Planning and Infrastructure

The complexity of urban systems means that forecasting how they will evolve is a significant challenge. In this paper we explore how path dependence affects their development by constructing a “possibility cone” - an envelope that contains feasible possible futures for a given urban system. Following Wilson (2008) we characterise the factors that influence this cone as “urban DNA”. Taking this analogy further we look at the idea of urban genetic medicine and ask the question: what interventions would be required to move an urban system into a new possibility cone. These ideas are explored using a stochastic version of the archetypal aggregate retail model using data for the South Yorkshire retail system. We produce a visual representation of the cone of development using a parallel coordinates plot to allow easier interpretation of the results.

The law of inhabitant travel distance distribution

Liang Liu, Francesco Calabrese, Assaf Biderman, Carlo Ratti

Track A - Policy, Planning and Infrastructure

In order to find the unified law in inhabitant travel distance distribution and explain it, in this paper we first do the statistics and regression of travel survey data in USA, UK, Germany, Denmark and Finland. And find they have the same distribution law, which means there is the same law dominating human travel. And we then explore the theoretical reason of this law. We compare the urban passenger flow system to a macro system consist of a large amount of particle system, which could be described using two macro value, namely, ‘system energy’—average travel distance and ‘system temperature’—the geometric average value of the sum of travel distance and constant value a . Under the constraint of these two macro feature, according to maximum entropy law, we derive the theoretical distribution model which is the same form as the empirical distribution. Then we carry out the statistics test for the theoretical distribution model, and the result shows the theoretical model could describe the phenomenon very well. This study

further investigates the real meaning of parameter a, b, c in the travel distance law. Through compare the change trends of parameter a, b, c, we claim that a is urban walking parameter, b is urban form compact parameter; c is the urban travel radius parameter. Finally we qualitatively analyzing the impact of land use control, car use control and transport mode composition to these three parameters. This study shows that we could dynamically monitor the macro status of urban passenger flow system under pervasive computing environment. And we could use parameter a, b, c to reflect the change of walking environment, urban form compactness and urban travel radius to evaluate different urban transport policy and strategy.

Modelling Dynamic Demand Responsive Transport using an Agent Based Spatial Representation

Didier Josselin, Christophe Lang, Nicolas Marilleau

Track A - Policy, Planning and Infrastructure

Our purpose is to discuss how useful can be an agent based representation for modelling a high dynamic system of transport called ‘Demand Responsive Transport’ (DRT). We first give a few definitions of DRT and also enhance what are the relevant key components of such a transport service. We present what could be an appropriate representation of a dynamic DRT based on Multi Agent Systems, using UML that handles the objects we identified and their properties. Two examples are then given and discussed and a more general model is provided.

Slowing down urban networks to fight urban sprawl: agent based approach

Arnaud Banos

Track A - Policy, Planning and Infrastructure

Due to their hierarchised structure, road networks intrinsically favour the use of car, especially for the longest distances. Indeed, being hierarchised by speed, their level of performance increases with the distance travelled. This “speed metric” ensures travellers the possibility to drive farther without necessarily increasing their transportation time in the same proportion. It may be possible to generate a different metric, able to invert the current ratio of efficiency between the different types of automobile travels, that is to say favouring the efficiency of short-range trips and therefore promoting higher densities and functional proximities in urban design according to the hypothesis of the rational locator. An agent based model, S3 (Smart Slow Speed) was designed in order to explore this specific issue. By imposing stops (traffic lights) on a network, with locations and durations following stochastic distributions, it allows assessing the possible impact of various configurations on traffic conditions. Introducing carefully constructed slow metrics could help equilibrate the highly biased competition between non-motorized modes, public transport on one hand and private car on the other hand.

Highway Traffic Forecasting. Beyond Complex to Complicated

Eddie Wilson

Track A - Policy, Planning and Infrastructure

Since the mid-1990s, there has been intense activity in the physics community in classifying and modelling spatiotemporal patterns in highway traffic. The most well-known patterns are ‘stop-and-go’ waves (sometimes referred to as ‘phantom jams’ in the popular media) which propagate against the driving direction with a remarkably robust speed in the range 15–20 km/h. At first sight, highway traffic is thus an almost perfect example of a ‘complex system’, since a large collection of similar agents (vehicles, drivers) interact to produce macroscopic patterns with characteristic scales many times the range of the interac-

tion. My question is whether this ‘complex systems’ approach can make a useful contribution to practical highway engineering problems, in particular short-term traffic forecasting and control.

On the M42 motorway close to the University of Warwick, the UK government has installed the ‘Active Traffic Management’ system in which temporary speed limits and hard-shoulder running are enacted during peak periods. As inputs, these control systems have what is probably the highest density of traffic measurement devices in the world. We are presently collecting spatiotemporal profiles for macroscopic variables such as speed, flow etc. with unprecedented resolution, for the full 17km of highway, as well as trajectory data for individual vehicles driving through a special 1.5km stretch with extra instrumentation.

Trajectory data in particular show us that traffic is not merely complex but also complicated — the variations between individual driver behaviours are huge, and in particular how this heterogeneity effects lane occupancy and platoons has a critical effect on flow breakdown which cannot be understood from aggregate data alone. Moreover, in addition to uncertainty at the microscopic level, we find that day-to-day differences in capacity and hence macroscopic patterns are often driven by external factors such as the weather. In this respect, crude statistical tools may give a better forecast of flow breakdown than a complex microsimulation or PDE model — and I will give some concrete examples of how these forecasts may be achieved using simple clustering and nearest neighbour techniques.

Robustness of Trans-European Gas Networks: The Hot Backbone

Rui Carvalho, Lubos Buzna, Falvio Bono, Eugenio Gutiérrez, Wolfram Just, David Arrowsmith

Track A - Policy, Planning and Infrastructure

Here we uncover the load and vulnerability backbones of the Trans-European gas pipeline network. Combining topological data with information on inter-country flows, we estimate the global load of the network and its vulnerability to failures. To do this, we apply two complementary methods generalized from the betweenness centrality and the maximum flow. We find that the gas pipeline network has grown to satisfy a dual-purpose: on one hand, the major pipelines are crossed by a large number of shortest paths thereby increasing the efficiency of the network; on the other hand, a non-operational pipeline causes only a minimal impact on network capacity, implying that the network is error-tolerant. These findings suggest that the Trans-European gas pipeline network is robust, i.e. error-tolerant to failures of high load links.

A self-repairing solution for the resilience of networks to attacks and failures

Nicolas Brax, Frédéric Amblard

Track A - Policy, Planning and Infrastructure

Robustness against failures and attacks is an important characteristic for real networks. Although methods have been proposed making networks more resistant, they are often designed to rehash networks before issues occur. In this paper, we investigate three dynamic methods making the network being able to repair itself while under massive attacks and failures. We consider two different topologies, Erdos – Renyi random graphs and Barabasi – Albert scale-free networks, and find out that a local strategy is able to maintain, at least for a moment, the network relatively connected. We believe this rewiring algorithm interesting because it might be not very difficult to implant in real networks and it provides a dynamic response while other arrangements are taken to answer the threat or the issues.

Separating internal and external fluctuation in distributed Web-based services

Sara Casolari, Marco Villani, Michele Colajanni, Roberto Serra

Track A - Policy, Planning and Infrastructure

The observable behavior of a complex system reflects the mechanisms governing the internal interactions between the system's components and the effect of external perturbations. We investigate the behavior of a distributed system providing Web-based services and the effects of the impact of external request arrivals on the internal system resources; the results of our study are of primary importance for taking several runtime decisions on load and resource management. Here we show that by capturing the simultaneous activities of several performance indexes of the Web-based system nodes we can separate the internal dynamics from the external fluctuations. For every internal performance index, we are able to determine the origin of fluctuations, finding that while all the considered performance indexes of the application server have robust internal dynamics, the CPU utilization and the network throughput of the Web and database servers are mainly driven by external demand.

The information dynamics of cascading failures in energy networks

Joseph Lizier, Mikhail Prokopenko, David Cornforth

Track A - Policy, Planning and Infrastructure

Small failures in electrical energy networks can lead to cascading failures that cause large and sustained power blackouts. These can disrupt important services and cost millions of dollars. It is important to understand these events so that they may be avoided. We use an existing model for cascading failures to study the information dynamics in these events, where the network is collectively computing a new stable distribution of flows. In particular, information transfer and storage across the network are shown to exhibit sensitivity to reduced network capacity earlier than network efficiency does, and so could be a useful indicator of critical loading. We also show that the local information dynamics at each node reveals interesting relationships between local topological features and computational traits. Finally, we demonstrate a peak in local information transfer in time coinciding with the height of the cascade's spread.

Modelling packet pair dispersion in multi hop network with correlated traffic

Péter HÁga, Péter Mátray, István Csabai, Gábor Vattay

Track A - Policy, Planning and Infrastructure

We introduce a general framework for packet-pair Internet measurements. The framework enables traffic flows to enter and leave the measurement path at arbitrary hops. The novelty of this approach is that it takes into account correlated background traffic flows, which we consider as pseudo probe packets. We present a hop-by-hop iteration method to approximate the packet-pair dispersion curve. It is shown that the introduced model describes correctly the data collected in packet level simulations. Our results are valid for both fluid and granular background traffic models. The motivation of this study is to understand the role of traffic flow correlations and give insights into the network traffic patterns.

A general evolutionary model of long-tailed distributions in the social sciences

Alex Bentley, Paul Ormerod, Michael Batty

Track B - Collective Human Behaviour and Society

Studies of collective human behavior in the social sciences, often grounded in details of actions by individuals, have much to offer 'social' models from the physical sciences concerning elegant statistical regularities. Drawing on behavioral studies of social influence, we present a parsimonious, stochastic

model, which generates an entire family of real-world right-skew socio-economic distributions, including exponential, winner-take-all, power law tails of varying exponents and power laws across the whole data. The widely used Albert-Barabasi model of preferential attachment is simply a special case of this much more general model. In addition, the model produces the continuous turnover observed empirically within those distributions. Previous preferential attachment models have generated speci-

fic distributions with turnover using arbitrary add-on rules, but turnover is an inherent feature of our model. The model also replicates an intriguing new relationship, observed across a range of empirical studies, between the power law exponent and the proportion of data represented.

Small Worlds of Conceptual Connections: Structural Properties of Concept Networks Designed for Learning Physics

Ismo Koponen, Maija Pehkonen

Track B - Collective Human Behaviour and Society

The knowledge structures of physics are often described as webs or networks, where concepts and principles are linked to other concepts and principles. Consequently, in teaching and education effort has been paid on developing instructional strategies based on graphical representations of knowledge – concept graphs or concept maps – that help students to create organized knowledge structures. It is suggested here that the graphical representations designed for purposes of learning and instruction can be quite naturally seen and analyzed as concept networks and also analyzed in terms of network and graph theory. In this study we analyze the structure of concept networks designed by physics instructors as well as advanced students for purposes of learning electrodynamics. It is shown, that the structure of such designed networks share many properties with small world networks and with pseudo-random graphs with fixed degree distribution. It is shown that the properties of the designed concept networks can be understood to large degree as a result how degree distribution is connected to the design principles. Moreover, the important concept in the network can be discerned on basis of their structural properties. The results open up new possibilities to understand the students' learning process of organized knowledge structures and help to find better way to foster the formation of such knowledge structures.

Patents in new Technologies

Miguel Ferreira, Bruno Oliveira, Alberto Pinto

Track B - Collective Human Behaviour and Society

We present a new R&D investment function in a Cournot competition model inspired in the logistic equation. We do a full characterization of the associated game and study the short and long term economical effects derived from using this new R&D investment function. In particular, we find the existence of regions with multiple Nash investment equilibria. For low production costs, that can correspond to the production of old technologies, the long term economical effects are not very sensitive to small changes in the efficiency of the R&D programs neither to small changes in the market structure. However, for high production costs, that can correspond to the production of new technologies, the long term economical effects are very sensitive to small changes in the efficiency of the R&D programs and also to small changes in the market structure.

The application of complex systems concepts in a military context

Anthonie van Lieburg, Nanne Le Grand, Martijn Schut

Track B - Collective Human Behaviour and Society

Military peacekeeping and reconstruction missions become increasingly more complex. This complexity

becomes apparent not only in the large number and variety in actors and domains but also in the intrinsic non-linear dynamics encountered in mission areas. To aid in a better understanding of this complexity we study the potential value of complex systems concepts in this context. This paper describes some of our preliminary insights and discusses some of the remaining challenges from an application point of view.

The influence of social network topology in a opinion dynamics model

Simone Righi, Timoteo Carletti

Track B - Collective Human Behaviour and Society

We investigate an opinion dynamics model with continuously defined affinities and opinions. We focus here on the effects of the affinity matrix's topology on the dynamical evolution and on the scale properties of the model measured through numerical simulations and fittings. We study through a set of statistical network measures, namely mean path, mean degree and clustering, different network topologies. We observe that the model's dynamics eventually leads to a uniformization of the different topologies.

The instability of downside risk measures

Istvan Varga-Haszonits, Imre Kondor

Track B - Collective Human Behaviour and Society

We study the feasibility and noise sensitivity of portfolio optimization under some downside risk measures (Value-at-Risk, Expected Shortfall, and semivariance) when they are estimated by fitting a parametric distribution on a finite sample of asset returns. We find that the existence of the optimum is a probabilistic issue, depending on the particular random sample, in all three cases. At a critical combination of the parameters of these problems we find an algorithmic phase transition, separating the phase where the optimization is feasible from the one where it is not. This transition is similar to the one discovered earlier for Expected Shortfall based on historical time series. We employ the replica method to compute the phase diagram, as well as to obtain the critical exponent of the estimation error that diverges at the critical point. The analytical results are corroborated by Monte Carlo simulations.

An empirical model for electronic submissions to conferences

Patrick Flandrin

Track B - Collective Human Behaviour and Society

Electronic submission to a conference is a process that is known to evolve nonlinearly in time, with a dramatic increase when approaching the deadline. A model has recently been proposed by Alfi et al. (Nature Physics, 2007) for such a process, and the question of its universality has been raised. This problem is revisited here from a data analysis and modeling point of view, on the basis of a larger data set. A new model is proposed that better describes the total evolution of the process (including saturation) and allows for a running prediction of the total number of submissions.

Fitting the Log Periodic Power Law to financial crashes: a critical analysis

David Brée, Nathan Joseph

Track B - Collective Human Behaviour and Society

A number of recent papers claim that a Log Periodic Power Law (LPPL) fitted to financial market bubbles that precede large market falls or "crashes", contain parameters that are confined within certain ranges. The mechanism that has been claimed as underlying the LPPL, is based on influence percolation

and a martingale condition. This paper examines these claims and the robustness of the LPPL for capturing large falls in the Hang Seng stock market index, over a 30-year period, including the current global downturn. We identify 11 crashes on the Hang Seng market over the period 1970 to 2008. The fitted LPPLs have parameter values within the ranges specified post hoc by Johansen and Sornette (2001) for only seven of these crashes. Interestingly, the LPPL fit could have predicted the substantial fall in the Hang Seng index during the recent global downturn. We also find that influence percolation combined with a martingale condition holds for only half of the pre-crash bubbles previously reported. Overall, the mechanism posited as underlying the LPPL does not do so, and the data used to support the fit of the LPPL to bubbles does so only partially.

Altruism and reputation: cooperation within groups

Przemyslaw Gawronski, Malgorzata Krawczyk, Krzysztof Kułakowski

Track B - Collective Human Behaviour and Society

In our recent model, the cooperation emerges as a positive feedback between a not-too-bad reputation and an altruistic attitude. Here we introduce a bias of altruism as to favorize members of the same group. The matrix $F(i,j)$ of frequency of cooperation between agents i and j reveals the structure of communities. The Newman algorithm reproduces the initial bias. The method based on differential equations detects two groups of agents cooperating within their groups, leaving the uncooperative ones aside.

Mutual information to assess structural properties in dynamic networks

David Rodrigues, Jorge Louçã

Track B - Collective Human Behaviour and Society

This article proposes applying the variation of information measure from Information Theory to evaluate macro-level properties characterising dynamic networks. This measure is used to evaluate different clusters given by the agglomerative hierarchical clustering algorithm of Clauset, Newman and Moore (2004), concerning a case study of the multi-agent based network model of a university email service. The variation of information measure is shown to be capable of assessing the outcome of simulating the dynamics of networks, in terms of its macro-level properties.

An individual-based model of collective attention

Mehdi Moussaid, Dirk Helbing, Guy Theraulaz

Track B - Collective Human Behaviour and Society

In our modern society, people are daily confronted with an increasing amount of information of any kind. As a consequence, the attention capacities and processing abilities of individuals often saturate. People, therefore, have to select which elements of their environment they are focusing on, and which are ignored. Moreover, recent work shows that individuals are naturally attracted by what other people are interested in. This imitative behaviour gives rise to various herding phenomena, such as the spread of ideas or the outbreak of commercial trends, turning the understanding of collective attention an important issue of our society. In this article, we propose an individual-based model of collective attention. In a situation where a group of people is facing a steady flow of novel information, the model naturally reproduces the log-normal distribution of the attention each news item receives, in agreement with empirical observations. Furthermore, the model predicts that the popularity of a news item strongly depends on the number of concurrent news appearing at approximately the same moment. We confirmed this prediction by means of empirical data extracted from the website digg.com. This result can be interpreted from the point of view of competition between the news for the limited attention capacity of individuals. The proposed

model, therefore, provides new elements to better understand the dynamics of collective attention in an information-rich world.

Openness Leads to Opinion Stability and Narrowness to Volatility

Sylvie Huet, Guillaume Deffuant

Track B - Collective Human Behaviour and Society

We propose a new opinion dynamic model based on the experiments and results of Wood et al (1996). We consider pairs of individuals discussing on two attitudinal dimensions, and we suppose that one dimension is important, the other secondary. The dynamics are mainly ruled by the level of agreement on the main dimension. If two individuals are close on the main dimension, then they attract each other on the main and on the secondary dimensions, whatever their disagreement on the secondary dimension. If they are far from each other on the main dimension, then too much proximity on the secondary dimension is uncomfortable, and generates rejection on this dimension. The proximity is defined by comparing the opinion distance with a threshold called attraction threshold on the main dimension and rejection threshold on the secondary dimension. With such dynamics, a population with opinions initially uniformly drawn evolves to a set of clusters, inside which secondary opinions fluctuate more or less depending on threshold values. We observe that a low attraction threshold favours fluctuations on the secondary dimension, especially when the rejection threshold is high. The trajectories of the model can be related to some stylised facts.

Cognitive similarity, tie creation, and tie strength: Network and content analysis of an online forum

Pietro Panzarasa, Bernard Kujawski

Track B - Collective Human Behaviour and Society

Through the lens of a network and content analysis of an online forum, this paper explores how cognitive similarity between nodes affects network dynamics. The objective is to show that there is a cognitive component to the creation of social ties and their strength. Ties among users have a two-fold nature: social and cognitive. While social ties stem from communication, cognitive ties reflect users' similarity in terms of the semantic proximity of the words they post. Results indicate that cognitive similarity is a critical catalyst for network dynamics. Cognitively similar users are more likely to create a social tie with each other than dissimilar ones. Moreover, social ties between similar users tend to be stronger than ties between dissimilar ones

Risk and beliefs updating mechanisms for contingent claims valuation in incomplete markets

Lampros Boukas, Diogo Pinheiro, Alberto Pinto, Stylianos Xanthopoulos, Athanasios Yannacopoulos

Track B - Collective Human Behaviour and Society

We review two scenarios for the determination of asset prices in an incomplete market. One scenario is based on the update of the attitude towards risk of the agents involved on the trading of such assets, whereas the other scenario is based on the update of their beliefs about the future states of the world. Furthermore, we briefly describe dynamic mechanisms that model the convergence of the buyer's and the seller's prices of a contingent claim in an incomplete market to a unique price and discuss the stability of these mechanisms as well as their robustness with respect to random perturbations.

Phase diagram of a Schelling segregation model

Laetitia Gauvin, Jean Vannimenus, Jean Pierre Nadal

Track B - Collective Human Behaviour and Society

The collective behavior in a variant of Schelling's segregation model is characterized with methods borrowed from statistical physics, in a context where their relevance was not conspicuous. A measure of segregation based on cluster geometry is defined and several quantities analogous to those used to describe physical lattice models at equilibrium are introduced. This physical approach allows to distinguish quantitatively several regimes and to characterize the transitions between them, leading to the building of a phase diagram. Some of the transitions evoke empirical sudden ethnic turnovers. We also establish links with 'spin-1' models in physics. Our approach provides generic tools to analyze the dynamics of other socio-economic systems.

Social norms, Emotions and cooperation in groups

Phan Denis, Waldeck Roger

Track B - Collective Human Behaviour and Society

A large body of literature in experimental economics is concerned by cooperative behavior in a public good context. Several factors are considered to be important for sustaining cooperative behaviour. These are among others, the net gain from cooperation, privacy of decision, social disapproval or the existence of a punishment mechanism. We propose to discuss the impact of these features on cooperation within the frame of a single model. Specifically, we consider that individuals support some moral costs from deviating from cooperative behavior. It is shown that a polymorphic equilibrium with cooperation and defection exist: players with high moral costs cooperate while those with low moral costs defect. The equilibrium with cooperative behavior depend on the distribution of moral cost in the society. We show how attractiveness of the group, gain from cooperation or the distribution of moral cost affects the equilibrium probability of cooperation.

Boolean Network and Simmelian Tie in the Co-Author Model: A Study of Dynamics and Structure of a Strategic Alliance Model

Laurent Tambayong

Track B - Collective Human Behaviour and Society

This article explains the mechanisms of how a simple simulated game-theoretic network model could generate a phase evolution model of an industry as well as possibly explain and integrate numerous of empirical findings. In particular, it explains the resulting structure based on the dynamics of simulated Co-Author Model (CAM), which tests the Resource Based View and the Liability of Smallness Hypothesis on how firms use their network resources to overcome their smallness. These explanations not only could answer the criticism that a simulation model is merely a toy model without much realism but could also explain and give insights to theory development in strategic alliance research. In this article, classified as a Boolean network with 2 inputs, CAM's dynamics result in an equilibrium structure that could then be explained by the Simmelian tie.

Network Decomposition: An Information Theoretical Approach

Masatoshi Funabashi

Track B - Collective Human Behaviour and Society

We consider the graph representation of the stochastic model with n binary variables, and develop an

information theoretical framework to measure the degree of interactions existing between subsystems as well as the ones represented by each edge of the graph representation. A case study on political weblog data is demonstrated.

Effects of Authority on Consensus Formation for Continuous Opinions in an Adaptive Network

Brenton Prettejohn, Mark D. McDonnell

Track B - Collective Human Behaviour and Society

Consensus formation for continuous opinions has recently been shown by Kozma and Barrat to be more likely in adaptive networks, where agents can dynamically alter their neighbours, when compared with the static case. Here we extend such an adaptive network model by introducing a parameter representing each agent's level of 'authority,' based on their opinion relative to the overall opinion distribution. This variable influences how opinions change after interactions between neighbours, skewing opinion convergence towards those agents with higher levels of authority. Simulation results show that this model of authority provides a significantly more efficient consensus process that is argued to be more analogous to a 'real life' scenario.

Publish or Perish: some collective implications

David Chavalarias, Vincent Gardelle

Track B - Collective Human Behaviour and Society

There have been an increasing pressure on scholars these last several years to publish work constantly to further or sustain a career in academia. What are the implications on the social game underlying collective elaboration of scientific theories? In this paper we try to sketch the consequences of such pressure at the collective level in terms of science dynamics and quality of published works. For this purpose, we propose a formalization of popper's epistemology that is further studied via multi-agents modeling.

The tragedy of the commons in a multi-population complementarity game

Wei Li, Jürgen Jost

Track B - Collective Human Behaviour and Society

We study a complementarity game with multiple populations whose members' offered contributions are put together towards some common aim. When the sum of the players' offers reaches or exceeds some threshold K , they each receive K minus their own offers. Else, they all receive nothing. Each player tries to offer as little as possible, hoping that the sum of the contributions still reaches K , however. The game is symmetric at the individual level, but has many equilibria that are more or less favorable to the members of certain populations. In particular, it is possible that the members of one or several populations do not contribute anything, a behavior called defecting, while the others still contribute enough to reach the threshold. Which of these equilibria then is attained is decided by the dynamics at the population level that in turn depends on the strategic options the players possess. We find that defecting occurs when more than 3 populations participate in the game, even when the strategy scheme employed is very simple, if certain conditions for the system parameters are satisfied. The results are obtained through systematic simulations.

Dynamic communities in multichannel data: An application to the foreign exchange market during the 2007–2008 credit crisis

Daniel Fenn, Mason Porter, Mark McDonald, Stacy Williams, Neil Johnson, Nick Jones

Track B - Collective Human Behaviour and Society

We study the cluster dynamics of multichannel (multivariate) time series by representing their correlations as time-dependent networks and investigating the evolution of network communities. We employ a node-centric approach that allows us to track the effects of the community evolution on the functional roles of individual nodes without having to track entire communities. As an example, we consider a foreign exchange market network in which each node represents an exchange rate and each edge represents a time-dependent correlation between the rates. We study the period 2005-2008, which includes the recent credit and liquidity crisis. Using dynamical community detection, we find that exchange rates that are strongly attached to their community are persistently grouped with the same set of rates, whereas exchange rates that are important for the transfer of information tend to be positioned on the edges of communities. Our analysis successfully uncovers major trading changes that occurred in the market during the credit crisis.

Evolutionary Complex Systems in Molecular Biology and Social Systems: Similar Processes and Models?

Carl Henning Reschke

Track B - Collective Human Behaviour and Society

This paper explores how a systemic evolutionary view, which argues that evolution is a knowledge generating process, and conceptually or mathematically related perspectives can contribute to an integrated perspective on the evolution of information organization by linking perspectives from biology and the social sciences. The paper uses the illustrative example of punctuation patterns in pharmaceutical innovations as a starting point for discussing a number of theoretical models and perspectives with respect to their suitability for such an integrated perspective. These models, if sufficiently correct representations of the characteristics of and tools for research into evolutionary development processes should play a role in explaining the molecular make-up of human organisms. Thus they also must find a reflection in the history and characteristics of pharmaceutical research as well as the more general characteristics of knowledge processes. The implied circularity of scientific concepts used for analysis and processes operating in the evolution of biological organisms and of knowledge indicates the relativity and reflexivity of knowledge which is seen as expression of evolutionary processes of knowledge growth in the social domain being 'eigenprocesses' of evolutionary development from inanimate matter to the social domain.

Origins of Taylor's power law for fluctuation scaling in complex systems

Agata Fronczak, Piotr Fronczak

Track C - Interacting Populations and Environment

Taylor's fluctuation scaling has been observed in many natural and man-made systems revealing an amazing universality of the law. To explain the origins of the law, a number of theoretical approaches have been considered. However, due to the lack of supporting real-world data and limited interdisciplinary applicability, none of these approaches has attracted any considerable attention. Here we give strong theoretical foundations for the origins and abundance of Taylor's fluctuation scaling in different complex systems. The universality of our approach is validated against real world data ranging from bird and insect populations through human chromosomes and traffic intensity in transportation networks to stock market dynamics. Using fundamental principles of information theory and equilibrium statistical physics, we prove that Taylor's law results from the maximum entropy principle and the well-defined density of

states function of a system that gives the number of states characterized by the same value of a macroscopic parameter (i.e., the number of birds observed in a given area or daily activity in the stock market measured in millions of dollars).

Complex network structure and transmission dynamics

Thomas House, Geoff Davies, Leon Danon, Matt Keeling

Track C - Interacting Populations and Environment

Networks have become an indispensable tool in modelling infectious diseases, with the structure of epidemiologically relevant contacts known to affect both the dynamics of the infection process and the efficacy of intervention strategies. One of the key reasons for this is the presence of clustering in contact networks, which is typically analysed in terms of prevalence of triangles in the network. We present a more general approach, based on the prevalence of different four-motifs, in the context of ODE approximations to network dynamics. This is shown to outperform existing models for a range of small world networks.

Disease outbreak dynamics: modelling and simulation for complex realities

Bahaa Abdel Hamid, Amy Griffin, Peter Durr

Track C - Interacting Populations and Environment

Epidemic spread is a complex process that is governed by individual behaviour, contact patterns and population flow among different geographic regions (Colizza et al., 2007). Such a process involves several heterogeneous actors evolving and interacting with each other and with their environment, leading to the continuous emergence of spatio-temporal patterns of disease spread across large-scale geographic environments. In an outbreak situation, decision makers are presented with a complex decision making process as different decisions have to be made during different stages of the outbreak with different data items available during these stages. A major challenge in this context is providing reliable decision support in a timely manner during various stages of the outbreak by matching the appropriate modelling approach to the currently available data set. In this paper we offer a novel multi-resolution approach for spatial modelling and simulation of complex outbreak dynamics. Our approach takes advantage of the formalisms of several modelling methodologies: Equation Based Modelling (EBM), Cellular Automata (CA) and Agent Based Modelling (ABM) along with that of Geographic Information Science, in order to develop an integrated spatial modelling framework for outbreak dynamics. Our framework addresses the problem of differing data availability during the progress of an outbreak. Practical implementation of the framework is illustrated with reference to the development of the Epidemic Spatial Decision Support System (ESDSS) and the application of the system to a typical outbreak situation.

The impact of concurrent and transient contacts on HIV epidemics

Christel Kamp

Track C - Interacting Populations and Environment

While HIV has a worldwide appearance there is a large variability with respect to its prevalence as a consequence of regional differences in the spreading dynamics: In pandemic regions transmissions via heterosexual contacts are much more prominent than in regions where the epidemics is contained to some extent in high risk groups. Therefore insights into the interdependencies between contact patterns and the epidemics are essential for an understanding of the observed variability in prevalence and the implementation of customised intervention strategies. We introduce a mathematical model that allows us to study epidemic spreading of HIV on a network formed by transient partnership relations with arbitrary heterogeneity among individuals with respect to the concurrency of their partnerships. Aside from these

topological characteristics the model also considers the infectious profile of HIV and the background population dynamics which is relevant due to the prolonged course of disease. Our approach facilitates an analysis of the changes in contact patterns during the epidemics and shows under which circumstances new infections from early or latently infected individuals dominate. The model is applied to an exemplary study of two scenarios with identical numbers of lifetime partners but different levels of concurrency. It shows how concurrent partnerships boost the spreading of HIV and promote the spreading during the highly infectious initial stage of disease. Transient contacts add further transmissions from the later stages of disease. A shift towards this route of transmission occurs during the maturation of the epidemics. This again shows that spreading of HIV can only be understood in the context of the underlying epidemic network which has to be taken into account for customised intervention strategies.

How interaction between co-evolving agents shape temporal mode and structure of the interaction network in a simple ecological mode

Dominic Jones, Henrik Jeldtoft Jensen, Paolo Sibani

Track C - Interacting Populations and Environment

We would like to submit this long abstract in place of a paper as the work itself is to be published elsewhere. We have confirmed that this is ok with the organisers.

Understanding systems level behaviour of many complex interacting agents is very challenging for various reasons: the interacting components can lead to hierarchical structures with different causes at different levels. We use the Tangled Nature model to discuss the co-evolutionary aspects connecting the microscopic level of the individual to the macroscopic systems level. At the microscopic level the individual agent may undergo evolutionary changes due to "mutations of strategies". The micro-dynamics always run at a constant rate. Nevertheless, the systems level dynamics exhibit a completely different type of mode characterised by intermittent abrupt dynamics where major upheavals keep throwing the system between meta-stable configurations. These dramatic transitions are described by a log-Poisson time statistics characteristic of record dynamics. The long time effect is a collectively adapted network.

Identifying universal features of ecosystem dynamics has been a long-standing goal in ecology. Increasingly the focus has been on the network properties of the ecosystem, or more precisely the trophic net defined by the mass flows between the species constituting the ecosystem. However empirical evidence at the resolution needed to verify any particular claim remains out of reach for most studies. For ecologists these quantities are both of theoretical and practical interest. From a theoretical point of view it would be nice to find some governing principle of ecological dynamics, while practically speaking there is a need to establish a good measure of ecosystem health and maturity.

We study how ecological measures of ecosystem development evolve in the Tangled Nature model. It is the network of interactions between extant species that evolves over time so we concentrate on the temporal behaviour of the mutual information of the network - a concept derived from ecological work. In particular, we investigate a seeming paradox in ecosystem development - that to become more efficient, ecosystems must become more brittle.

We divide the system into a core of viable species and a periphery of mutants. We show that the mutual information of these two subcomponents evolve in different ways - the core becomes more correlated over time, whereas the periphery becomes progressively less correlated. This gives rise to the non-stationary dynamics observed in the model - particularly increasing stability and increasing mean population. Finally, we relate this back to the detail of the microscopic dynamics, showing how the shape of reproduction function gives rise to some of the macroscopic behaviour.

Worldwide spread of the unfolding swine flu epidemic: early assessment and predictions

Paolo Bajardi, Duygu Balcan, Vittoria Colizza, Bruno Goncalves, Hao Hu, Daniela Paolotti, Chiara Poletto, Nicola Perra, Jose Ramasco, Michele Tizzoni, Wouter Van den Broeck, Alessandro Vespignani

Track C - Interacting Populations and Environment

We present an analysis of the first 5 weeks of the worldwide evolution of the swine flu epidemic after the announcement by WHO in late April of the emergence of a novel influenza A virus. A global epidemic and mobility (GLEaM) modeler was used to assess the early spread of the epidemic and generate future projections of its impact and spread at the global scale. The computational model is based on a stochastic metapopulation approach that integrates detailed demographic data worldwide with long-range airline traffic and short-range commuting patterns. The model was seeded by fixing the initial conditions as based on the early data as of April 25 on the probable origin of the outbreak in Mexico, and calibrated to the observed epidemic pattern. Real-time projections on a 2 weeks time window for iterative calibrations were made available by online posting (www.gleamviz.org). The *a posteriori* comparison between real-time projections and occurrence of confirmed cases shows a good agreement in reproducing the geographical spreading pattern of the epidemic. Data on the arrival times in several countries in the early period of the outbreak was then used to fit the model to the observed spreading of the virus in order to estimate the reproductive number of the epidemic. Results are obtained for longer term predictions considering seasonal aspects, and the effect of the use of antiviral drugs as available for each country.

Correlations and stochastic fluctuations in the SIR model

Andrea Parisi, Ana Nunes

Track C - Interacting Populations and Environment

Stochastic SIR simulations show that demographic noise amplified by resonance with the system's natural frequency can generate a pattern of recurrent epidemics in long time series. We report on recent numerical and analytical results that show that temporal and spatial correlations enhance the amplitude and the coherence of such fluctuations. In particular, the fluctuation spectrum of long time series of stochastic SIR simulations with deterministic recovery or with small world spatial effects exhibits significant changes with respect to the power spectrum of the standard SIR model.

Challenges Arising During the Analysis of Crude Oils and Environmental Samples

Mark P. Barrow, John V. Headley, Kerry M. Peru

Track C - Interacting Populations and Environment

Consumption of crude oil continues to grow, while production from some of the world's largest oil fields are in decline. Crude oil is the essential basis for fuels, plastics, solvents, waxes, lubricants, pesticides, and medicines. Whilst alternative sources of energy are being investigated, world-wide dependence upon petroleum will therefore not cease for the foreseeable future.

As consumption increases, there are increased pressures upon production of crude oil and the subject of when production of this limited resource will peak remains controversial. New sources of oil are required as a result, although discoveries of new oil fields peaked prior to the 1970s, and the petroleum industry must increasingly turn to "opportunistic oil," where the quality is regarded as lower. Sources of oil that were once regarded as non-viable are now being used, amongst the famous well-known of which are the oil sands of Athabasca, Canada. These oil sands are believed to represent 174 billion barrels of bitumen when using existing technology, making it the second largest known reserve in the world, and Canada is now the largest foreign supplier of crude oil to the US, with Saudi Arabia now positioned in second place. It is not

surprising, therefore, that there is currently an “oil rush” taking place in Athabasca, with multinational oil companies seeking to utilize the resources.

Crude oils are highly complex mixtures, typically containing tens of thousands of components, and each oil field has an identifying “fingerprint.” Previously, it has only been possible to partially characterize a crude oil, due to limitations of the scientific instrumentation available. Mass spectrometry can be used to determine the mass-to-charge ratio (m/z) of components within a sample, including complex mixtures. Once a mass spectrum has been acquired, it is possible to assign an elemental composition to each of the peaks observed. Thus, in this manner, it is possible to characterize the many components present within a given sample. It is only with the advent of state-of-the-art varieties of the technique, based upon Fourier transform ion cyclotron resonance (FTICR) mass spectrometry, that ultra-high resolution and mass accuracy have been possible. These performance characteristics are essential when characterizing a sample as complex as a petroleum-related mixture, and the study of such samples using FTICR mass spectrometry has accelerated since the end of the 1990s. In addition to the hardware required in order to be able to analyze petroleum-related samples, there has been a need for further development of software for the processing of data, once acquired. Once the analysis has been performed, however, there is a need for improved methods for visualizing the data, in order to best convey the results to the corresponding audience. A variety of graphical representations have been developed, but there is always the compromise between simplicity and information content which must be considered.

Within a crude oil, many classes of compound will be present (such as sulfur-containing species or acidic species), and within each of these classes there will be further varieties of molecule, as determined by a more detailed analysis of their size and structure (such as number of carbon atoms, heteroatom content, and more). One of the classes of interest is the “naphthenic acids.” These species have been loosely defined, although most commonly described by the general empirical formula: $C_nH_{2n+z}O_2$, where z is a negative, even integer and is often referred to as the “hydrogen deficiency.” Naphthenic acids present a number of challenges. Two of the most important problems posed include these species involvement in the corrosion of refinery apparatus and their toxicity towards aquatic wildlife. The oil industry has, for many years, relied upon the “total acid number” (TAN) as a figure for determining the naphthenic acid content of an oil. The TAN of an oil is measured by determining the number of milligrams of potassium hydroxide required to neutralize 1 g of crude oil. The presence of other acidic or basic species within an oil can make this figure unreliable, and it is only comparatively recently, however, that the oil industry has begun to look to other methods for characterizing the naphthenic acid content of different oils. This issue also serves to highlight that, when investigating complex mixtures, one class of compound cannot be studied in isolation; the “whole picture” must be considered.

The extraction of oil from the oil sands of Athabasca places severe burdens upon the environment. Approximately three barrels of water are consumed per barrel of oil produced, affecting the aquatic environment. Waste water from the processing is often stored within tailings ponds, and it is known that some of the waste products present within these waters, such as naphthenic acids, can be toxic towards aquatic wildlife. While ambient levels of naphthenic acids in Alberta rivers are generally below 1 mg/L, levels in tailings pond waters may reach 110 mg/L, which eventually leaks into the rivers or leaches into groundwater.

In similarity with studies of corrosion, there is need for further research into correlation of toxicity with the specific compounds present in a sample. One challenge posed is how best to represent the data in an easy-to-use format, whilst minimizing the amount of information lost. It is necessary to be able to compare the contents of different samples in order to look for trends. Further complications, however, arise when considering the effects of the environment when investigating the bioavailability and toxicity of the naphthenic acids. Transport of the acids in soil and groundwater, the effects of salinity, and bioremediation are all believed to play important roles. The complexity of the subject thus becomes clearer.

In previous decades, one of the most significant factors limiting the ability to characterize petroleum-related samples was the availability of appropriate instrumentation. As FTICR mass spectrometry developed, advances in software were required in order to handle the complex data sets resulting from the analyses of such samples. When studying complex mixtures from the petroleum industry and/or the environment, two of the current challenges posed include: the need to develop better methods for data visualization and the need to advance understanding of the correlation between the whole of a sample (and its environment) and undesirable phenomena such as corrosion and toxicity.

Big Crunch in Computer Science: Introduction and Overview

András Lörincz

Track D - Complexity and Computer Science

This track is about a most exciting topic of our days. Computer science had its Big Bang about 60 years ago. During the years, it has become one of the main driving forces of all fields of science and it has been evolving steadily within the different disciplines. Achievements of the individual disciplines have been posing new questions for computer science and today we are witnessing the Big Crunch: experiences, knowledge, and discoveries of the different disciplines have become the main driving forces of computer science. This is the subject of this track. Among other things, we shall hear about network of grids, (flying) swarms, collectives, robot control, robot communication, neural, neurocognitive, and graphical approaches to distributed computations on distributed sensory information and databases, including issues related to adaptation and learning.

BitTorrent - from swarms to collectives

David Hales

Track D - Complexity and Computer Science

Everyone has heard about the "Pirate Bay" and how P2P file sharing communities are going to destroy Hollywood. But what is going on beyond the controversy and media hype? I will discuss how P2P file sharing is moving from single files to media communities and towards cohesive social collectives. I will indicate how ideas from social and complexity science have /may shape the design of P2P systems. I will argue that due to the massive and "clean" datasets we can collect detailing node behaviour that such emerging collectives offer the potential of a global socio-economic experiment from which complexity, social and computer scientists can learn new principles. I will discuss deployed and on-going work within the context of the tribler.org Bittorrent media client. Specifically I will cover: an overview of the architectural details and challenges in tribler, self-organising aspects like the gossip-based peer sampling service, potential application of economic and social theories.

A new class of cellular automata: How spatio-temporal delays affect dynamics and improve computation

Thimo Rohlf, Jürgen Jost

Track D - Complexity and Computer Science

Delays in signal transmission are found in many complex systems in nature, e.g. as a consequence of spatial distance between the elements the system consists of. Cellular Automata (CAs) are paradigmatic examples of spatially extended, decentralized discrete dynamical systems. Here, we investigate for the first time the effect of spatio-temporal delay depending linearly on the distance between cells in synchronously updated CAs. We find that delays induce distinctive transitions between different classes of dynamical behavior, and on average tend to increase the space-time entropy of CA patterns. This effect increases

with the number k of different states cells can take. Finally, we show that delays substantially improve the capacity of CAs to solve complex tasks in distributed computation: solutions are found faster, and they are more accurate and more robust than solutions found for CAs without delays.

Random hypergraphs and their applications

Guido Caldarelli, Gourab Ghoshal, Vinko Zlatic, Mark Newman

Track D - Complexity and Computer Science

In the last few years we have witnessed the emergence, primarily in on-line communities, of new types of social networks that require for their representation more complex graph structures than have been employed in the past. One example is the folksonomy, a tripartite structure of users, resources, and tags – labels collaboratively applied by the users to the resources in order to impart meaningful structure on an otherwise undifferentiated database. Here we propose a mathematical model of such tripartite structures which represents them as random hypergraphs. We show that it is possible to calculate many properties of this model exactly in the limit of large network size and we compare the results against observations of a real folksonomy, that of the on-line photography web site Flickr. We show that in some cases the model matches the properties of the observed network well, while in others there are significant differences, which we find to be attributable to the practice of multiple tagging, i.e., the application by a single user of many tags to one resource, or one tag to many resources.

Pervasive Adaptation

Ben Paechter

Track D - Complexity and Computer Science

The European Commission's Future and Emerging Technologies Proactive Initiative on Pervasive Adaptation targets technologies and design paradigms for pervasive information and communication systems, which are capable of autonomously adapting in dynamic environments. The adaptation of individual components will lead to adaptation of the system as a whole and to the emergence of new system behaviours which will be self-configuring, self-healing, self-optimizing and self-protecting. The prospect of building adapting pervasive systems brings many new trust and security challenges to the complex interactions between people, intelligent devices and computers and will need to take account of the non-deterministic and often non-predictable behaviour of people.

Online clustering with CFinder

Andras Barta, Gergely Palla, Péter Pollner, Tamás Vicsek

Track D - Complexity and Computer Science

In this poster we present the online version of CFinder, which can find overlapping clusters in directed, weighted or undirected networks. Due to the local nature of the clique percolation method, the computation can be distributed among several CPU-s of computers. Our implementation uses an enhanced, grid based computational backend and takes over the CPU and RAM intensive tasks from the user.

The online cfinder will be available from august 2009 on our web site <http://www.cfinder.org> as a free service for fundamental research.

Self Organization and Learning in Cellular Robotics

Michele Sebag

Track D - Complexity and Computer Science

In the perspective of cellular robotics (swarm robotics and multi-cellular robots), self-organization is viewed as a unique way to achieve collective bounded rationality. Robotic entities are interacting with each other subject to limited information, communication and computational resources. Under these constraints, implementing self-organization raises several challenges: 1. Entities must be provided with self-driven rewards, "instincts" enforcing appropriate individual behaviors in a environment- and self-driven fashion. 2. The rules of interaction among entities must be such that the underlying dynamic process converges (emergence of a collective behavior). How to bootstrap the process, avoid trivial solutions (e.g., all entities die) and arrive at interesting collective behaviors? 3. What is a desirable collective behavior? Ideally, the goal could be formalized as the optimization of a computable function. The state of the art in Evolutionary Robotics however suggests that designing such a function remains an art. Should the designer stay in the loop? The talk will discuss some key issues and on-going work done in the SYMBRION framework.

Swarms of Flying Robots for Communication Networks

Sabine Hauert

Track D - Complexity and Computer Science

Swarms of flying robots can be used in disaster areas to autonomously create communication networks for rescuers and victims. Flying robots have the advantage of rapidly overcoming difficult terrain and providing unobstructed wireless communication. To allow for a swarm composed of cheap, transportable and robust robots, we avoid using positioning sensors which typically depend on the environment (GPS, cameras) or are expensive and heavy (lasers, radars). Instead, robot behaviors depend on local communication with robots within transmission range. There currently exists no methodology to design robot controllers resulting in the emergence of desired swarm behaviors. Here, we propose two bio- inspired techniques to overcome this problem. In the first approach, we use artificial evolution as a mean to automatically design simple, efficient and unthought-of controllers for robots. We then reverse-engineer these controllers and reuse the discovered principles in a wide variety of scenarios. In the second approach, we look at the creation, maintenance and evaporation of army-ant pheromone trails during foraging and apply the same principles to the design of robot controllers for the deployment, maintenance and retraction of communication networks.

An allostatic control model for robot behavior regulation

Marti Sanchez, Ulysses Bernardet, Paul Verschure

Track D - Complexity and Computer Science

Behavior of foraging agents is driven by internal variables such as hunger, temperature, security, etc. that have to be maintained within certain limits in order to be stable and predictive over changing environments. We call these variables homeostatic and allostasis the process of achieving this stability through change and self-regulation. We present a novel model for allostatic control, the aim being to generate spontaneous behavior comparable to foraging rats. For this reason the model is used to drive both a real and simulated robot and then compared with behavioral data extracted from tracking rats. Each homeostatic subsystem is a closed feedback loop that equilibrates the difference between an actual value and a desired one via a regulator. The concept of regulator is based on sensing gradients in a vector field, one per homeostatic subsystem. The integration of each sub-system is weighted by the difference in this

equilibrium. We test the model starting from two homeostatic sub-systems: security and arousal. The model is able to generate a rich portfolio of behaviors: from scared behaviors where the robot explores the walls and does occasional traversals of the open field to a more confident exploration where open space is explored as much as walls. Then we are able to extract from behavioral data from tracking rats real values to test against our model. Then we discuss on a biologically plausible neural architecture able to implement each sub-system, the security system being based on path integration. A second part of this paper discusses how the autonomous allostatic control can be included in the well established DAC architecture. At this point, DAC can elicit a limited repertoire of behaviors, mainly driven by its learning mechanisms that associate sensory sequences to actions in order to maximize reward, as in operant conditioning. This translates in the proposed benchmarking tasks in the ability of a DAC driven robot to avoid collisions and learn subsequent chains of actions that will maximize the long term rate of reached targets. This long term reward maximization is interpreted as an Adaptive Layer task when a more classical conditioning view is followed by the learning process and also it is seen as Contextual when higher decision making is required and combined with the usage of short and long term memory. The Reactive layer in the proposed setups is mainly dealing with hardwired reflexes which corresponds to collision avoidance and could go up to path integration capabilities, but still driven by reflexes. We include the introduced model into DAC. Allostatic control, as presented here, is highly related with low-level action selection mechanisms, resolving conflicts between concurrent goals and also the capacity of eliciting the appropriate behavior (from a behavioral repertoire such as defense, attack, escape, homing, feeding, reproductive behaviors, etc.) when exposed to particular situations. Many places in the brain have been shown to be related with action selection: periaqueductal grey, amygdala, basal ganglia, medial hypothalamus and the septo-hippocampal system. The latter describes an elaborated view of action selection in the defense system of animals relating it to the known parts of the brain where such process take place: "More detailed neural analysis, have led to the view of a hierarchical defense system in which the lowest level, the periaqueductal grey, coordinates undirected escape; the medial hypothalamus coordinates directed escape; the amygdala coordinates simple active avoidance; and the anterior cingulate coordinates more complex active avoidance". The same reference supports the fact that it is possible to elicit escape behavior (flight) or defensive aggression (fight) by stimulating points in the medial hypothalamus and the central periaqueductal grey. Regulation can also be achieved through actions in the world and not only by some internal regulatory process. An animal placing itself in an optimal distance to a fire in order to achieve a desired temperature. Other examples support the fact that we can make use of allostasis to control higher level behavior as for example the approach-avoidance conflict which states that when an animal approaches a goal and then oscillates back and forth at a point where the decrease in defensive distance is such that the approach and avoidance tendencies are just in balance. This will be the starting point to make allostatic control available to the other layers of DAC.

Creating Complex Systems by Integrating Desktop and Service Grids

Gábor Terstyánszky

Track D - Complexity and Computer Science

Grid computing offers large pool of resources to run applications. Currently, there are two Grid infrastructures: Desktop Grids (DG) and Service Grids (SG). In Service Grids applications are executed on computing clusters, while Desktop Grids integrate PCs donated by individuals and/or organizations. Service Grids provide guaranteed services contrary to Desktop Grids which do not offer any guarantees on their quality of services. These two types of Grids evolved parallel without interoperation between their resources. The FP7 Enabling Desktop Grids for e- Science (EDGeS) project connected these Grids, particularly BOINC/XtremWeb based DGs and EGEE, by developing and deploying bi-directional bridges

to make these Grids interoperable. The project faced several major challenges, such as data management, resource management and scheduling, security requirements, application porting etc. because DGs and SGs have their own middleware and management policies. The project created the EDGeS infrastructure, which incorporates DGs and SGs. This infrastructure is a complex system itself, which may contain up to a few hundred thousands of computers and data resources. As a result, it may provide almost unlimited resources for researchers to run their applications.

Achieving Consensus Among Agents –opinion-dynamics meets belief revision

Bruce Edmonds

Track D - Complexity and Computer Science

The paper considers the problem of how a distributed system of agents (who communicate only via a localised network) might achieve consensus by copying beliefs (copy) from each other and doing some belief pruning themselves (drop). This is explored using a social simulation model, where beliefs interact with each other via a compatibility function, which assigns a level of compatibility (which is a sort of weak consistency) to a set of beliefs. The probability of copy and drop processes occurring is based on the increase in compatibility this process might result in. This allows for a process of collective consensus building whilst allowing for temporarily incompatible beliefs to be held by an agent. This is an example of socially-inspired computing (by analogy with biologically-inspired). The space of behaviours in a MAS where agents interact with each other at the same time as reasoning/learning themselves is so vast that a "structuring idea" is needed. Here we apply an analogy with human opinion-dynamics as an analogy with which to design, manage and understand a subset of this huge space. Results suggest that a reasonable rate of copy and drop processes and a well connected network are required to achieve consensus, but given that, the approach is effective at producing consensus for many compatibility functions. However, there are some belief structures where this is difficult.

A Formal Language Theoretic Approach to Distributed Computing on Dynamic Networks

Katalin Anna Lázár

Track D - Complexity and Computer Science

In this talk we apply networks of parallel language processors to describe the behaviour of peer-to-peer systems. In our model, the language processors form teams, send and receive information through collective and individual filters. We examine whether the formal language theoretic formalization provides a suitable description of P2P networks. We deal with the dynamics of the string collections.

Can Robots Communicate?

Jürgen Jost, Eckehard Olbrich, Nils Bertschinger

Track D - Complexity and Computer Science

“Communication” is a term used in many different disciplines, including philosophy, psychology, sociology, semiotics, linguistics, ethology, game theory, neurobiology, and information theory. Consequently, this term has different meanings in the different disciplines. The spectrum ranges from a concept that only applies to specific interactions among conscious humans to the transmission of some bit string through some medium like a cable. If one intends to build autonomous artificial systems that are not only able to process information in a pre-specified way but that possess or can develop the capability of acquiring, representing, processing and in particular, sharing knowledge, it is necessary to clarify and formalize the concept of communication. In this sense, the aim of this talk is to develop criteria for and describe and

formalize properties of communication so that we can distinguish between different types of communication and decide whether, or more precisely, in which sense and to which degree interactions between neurons, ants, or robots can be considered as communications. This will include the role of symbols and conventions, of expectations and intentions, and the aspects of double contingency and self-reference.

The Peace Mediator Effect

Andrea Guazzini, Graziano Barnabei, Timoteo Carletti, Franco Bagnoli, Daniele Vilone

Track D - Complexity and Computer Science

Statistical mechanics has proven to be able to capture the fundamental rules underlying phenomena of social aggregation and opinion dynamics, well studied in disciplines like sociology and psychology. This approach is based on the underlying paradigm that the interesting dynamics of multi-agent systems emerge from the correct definition of few parameters governing the evolution of each individual. Into this context, we propose a new model of opinion dynamics based on the psychological construct named "cognitive dissonance". Our system is made of interacting individuals, the agents, each bearing only two dynamical variables (resp. "opinion" and "affinity") self-consistently adjusted during time evolution. We also define two special classes of interacting entities, both acting for a peace mediation process but via different course of action: "diplomats" and "auctoritates". The behavior of the system with and without peace mediators (*PMs*) is investigated and discussed with reference to corresponding psychological and social implications.

Detecting overlapping communities in graphs

Qinna Wang, Eric Fleury

Track D - Complexity and Computer Science

Recently, the area of complex networks has deserved more and more attention for its insights between the properties and functions in real networks. As an important step, the community detection classifies the vertices according to the topology of networks. Multiple methods in community detection have been proposed for finding communities in real networks such as biological networks and social networks, but those traditional approaches build a graph partition in which nodes are selected to only one community. Under this condition, the information about overlapping communities is ignored. However, it's not favourable for network analysis. Many studies indicate that overlapping communities are essential in complex networks because various real networks are covered by mixed communities. Therefore, we introduce a considerable method to uncover overlapping communities and reveal characteristics of networks. We have applied our method on artificial and real networks. The results demonstrate that our method has an excellent performance on uncovering overlapping communities and revealing the characteristics of networks.

Modelling Complexity in Solid Tumours

Helen Byrne

Track E - From Molecules to Living Systems

Like many other biological tissues, solid tumours are highly complex in a number of different ways. For example, interactions at the tissue scale between compliant blood vessels and proliferating tumour cells may generate highly irregular spatio-temporal behaviour, which compromise the response of vascularised tumours to chemotherapy. Equally, when complex interactions between processes occurring at subcellular, cellular and tissue scales are perturbed (as a result of genetic mutations, for example) the well-defined structure of a healthy intestinal crypts may be superseded by irregular or aberrant crypts. In this talk I will present several examples which illustrate the range of mathematical approaches that are being used to study the role of complexity in solid tumour growth and the type of insight that such models can generate.

Autocorrelation function analysis of subcutaneous glucose profiles: an exploratory study

Tim Holt, Luca Sbrano, Frances Griffiths, Simon Gray

Track E - From Molecules to Living Systems

BACKGROUND: Glycaemic stability is important for predicting future blood glucose levels and for avoidance of hypoglycaemia, but is poorly represented by traditional control measures. We derived autocorrelation function (ACF) indices from subcutaneous glucose profiles, to explore the feasibility and possible applications for patient care. **METHODS:** Collection and analysis of fifteen 72- hour time series datasets using a continuous glucose monitoring system (CGMS) from participants with and without diabetes. **RESULTS:** The devices were well tolerated yielding good quality data. The pattern of initial decay of autocorrelation distinguished individuals with and without diabetes more successfully than other autocorrelation indices. A number of potential clinical applications were identified. **CONCLUSIONS:** Autocorrelation analysis is feasible using existing monitoring devices and analytical software. Autocorrelation may be relevant to a number of issues in diabetes management: measuring the ‘smoothness’ of glucose fluctuations; prediction of hypoglycaemia; identifying the minimum frequency of self-monitoring appropriate for the individual; and insulin dose titration in the basal bolus replacement regimen. It may be used to test the performance of glucose monitoring devices by identifying measurement error. Future work may also clarify its role in a dynamical definition of glycaemic stability.

Model human heart or brain signals

Çağlar Tuncay

Track E - From Molecules to Living Systems

A new model is used to mimic various spatial or temporal designs in biological or non biological formations where the focus is on the normal or irregular electrical signals coming from human heart (ECG) or brain (EEG). The electrical activities in several muscles (EMG) or neurons or other organs of human or various animals, such as lobster pyloric neuron, guinea pig inferior olivary neuron, sepia giant axon and mouse neocortical pyramidal neuron and some spatial formations are also considered (in Appendix). In the biological applications, several elements (cells or tissues) in an organ are taken as various entries in a representative lattice (mesh) where the entries are connected to each other (in terms of some molecular diffusions or electrical potential differences). The biological elements evolve in time (with the given tissue or organ) in terms of the mentioned connections (interactions) besides some individual feedings. The anatomical diversity of the species (or organs) is handled in terms of various combinations of the assumptions and parameters for the initial conditions, the connections and the feeding terms and so on. A small number of (iterative) secular equations (coupled map) are solved for the results with few parameters for each case. The same equations may be used for simulation if random parameters are involved. The model, with simple mathematics and easy software, may be followed besides or instead of the known theoretical approaches. The basic aim of the present contribution is to mimic various empirical data for some electrical activities of human heart or brain (or various animals). The mentioned empirical data are available in various experimental literatures and the model results may be considered as in good agreement with them.

Agent Based algorithm for the study of molecular self-organisation

Sara Fortuna, Alessandro Troisi

Track E - From Molecules to Living Systems

Agents based simulations are rule based models traditionally used for the simulations of complex systems. In this paper an algorithm based on the concept of agent based simulations is developed to predict the lowest energy packing of a set of identical rigid molecules. The agents are identified with rigid portions of the system under investigation and they evolve following a set of rules designed to drive the system toward the lowest energy minimum.

The function of communities in protein interaction networks

Anna Lewis, Mason Porter, Nick Jones, Charlotte Deane

Track E - From Molecules to Living Systems

Over recent years a wealth of protein interaction data has become available. Using this data there have been several attempts to identify tightly interconnected groups of proteins that are likely involved in similar processes. Here we establish this connection between modularity and function and give further characterization of these communities.

We employ methods that allow us to identify "communities" in the network at multiple resolutions as, a priori, there is no single scale of interest. We focus on yeast, and investigate functional similarity both through Gene Ontology annotations and through similarity of growth rates under different conditions for gene knockouts. We control for the fact that interacting partners are more similar than a randomly-chosen pair, which is essential for a fair test of functional similarity. We find that many communities are functionally homogeneous, and moreover that there is substantial overlap between the communities that are functionally homogeneous between the two different proxies of gene function (GO annotations and growth rates following gene knockouts).

The viability theory to control complex food processes

Mariette Sicard, Nathalie Perrot, Cedric Baudrit, Romain Reuillon, Paul Bourgine, Isabelle Alvarez, Sophie Martin

Track E - From Molecules to Living Systems

The viability theory developed by Aubin (1991) has been adapted to calculate the optimal monitoring of cheese ripening process. This method was used efficiently in ecology or in finance but never in food process. The aim was to applied viability theory to find the controls allowing to reach a compromise between the quality of the ripened cheeses and the production costs. A viability kernel and the costs simulations of the viable trajectories were computed. Then, the optimal ripening trajectories were validated during pilot ripening trials. The results were finally compared to those obtained for cheeses ripened at 92% of relative humidity and 12°C of temperature, the conditions usually applied in dairy industries for Camembert ripening.

Tag-statistics in complex networks

Gergely Palla, Illés J. Farkas, Péter Pollner, Imre Derenyi, Tamas Tamás

Track E - From Molecules to Living Systems

We study the statistical property of tagged networks, where the further attributes (features, annotations, properties, etc.) provide essential information about the entities represented the nodes. Our main goal is to uncover the relations between the statistical properties of the node tags and those of the graph

topology. We investigate the tag statistics in three large networks representing very different domains of complex systems. A number of the tag related quantities display analogous behaviour, while some other features show variability from network to network. We also find that for each network the topology and the tag distribution are scale invariant, and this self-similar property of the networks can be well characterised by a tag-assortativity exponent, which is specific to each system.

Multiclock discrete models of biological systems

Nolwenn Le Meur, Michel Le Borgne, Jérémy Gruel, Nathalie Th  ret

Track E - From Molecules to Living Systems

Modeling biological systems requires precise temporal concepts. Biological observations are often issued from discrete event measurements, which make discrete modeling especially interesting. However time is absent of these models or defined a priori. In this paper, we propose a new formalism to specify time in discrete logical model and illustrate the power of our approach using a eukaryote cell cycle model.

Timing of molecular processes in a synchronous Boolean model of genetic regulatory network

Alex Graudenzi, Roberto Serra, Marco Villani, Chiara Damiani, Annamaria Colacci, Stuart Kauffman

Track E - From Molecules to Living Systems

A generalization of the model of random Boolean network (RBN) is presented, in which the concept of timing of regulatory processes is explicitly introduced, together with novel types of entity and interaction, directly inspired to real genetic networks. Beyond the attempt of approaching a higher level of faithfulness to the natural world, at the base of the development of the model is the need for a sensible comparison with time-series microarray data-sets, inaccessible to the original RBN model, because of the strict assumptions about the simultaneity of the regulation mechanisms. Preliminary analysis on networks typified by “critical” parameters showed a strong, even though not univocal, influence of a variation in the distribution of the time delays that characterize the entities of the system on the emerging dynamics: the larger the “memory” of the system about its dynamical evolution is, the more ordered the behaviour would tend to be.

The Effect of Spatial Organisation in Response Threshold Models for Social Insects

Konrad Diwold, Alexander Scheidler, Martin Middendorf

Track E - From Molecules to Living Systems

The threshold reinforcement concept has been widely used to explain division of labor in social insects, and has been tested both experimentally and analytically. To date, threshold reinforcement models have not taken spatial extent and distribution of tasks and individuals into account, although these aspects are ubiquitous in social insect colonies. Here, the model was extended to include spatial distribution of tasks and individuals. The results suggest that a colony in this model is able to increase its performance when exposed to an environment in which the different tasks are unequally distributed compared to an environment with equally distributed tasks. This finding could help to explain why some social insects organize their work spatially (e.g., sort their brood). Moreover, it is investigated how beneficial it is for a colony to actively rearrange the work spatially depending on the additional expense the colony has to afford for such a (ongoing) reorganization. We extend the response threshold model to reflect possible strategies for an active spatial rearrangement of the work. Three individual-based mechanisms were tested and compared regarding their adaptivity and efficiency in a dynamic task environment.

A stochastic model of myxobacteria explains several features of motility and development

Antony Holmes, Sara Kalvala, David Whitworth

Track E - From Molecules to Living Systems

Bacterial populations provide interesting examples of how relatively simple signalling mechanisms can result in complex behaviour of the colony. A well studied model is myxobacteria; cells can coordinate themselves to form intricate rippling patterns and fruiting bodies using localised signalling. Our work attempts to understand and model this emergent behaviour. We developed an off-lattice Monte Carlo simulation of cell motility and show it can be used to generate both rippling and fruiting body formations.

Systems Chemistry: Mechanosensitive Self-replication

Sijbren Otto, Jacqui Carnall, Chris Waudby, Jerome Peyralans, Marc Stuart

Track E - From Molecules to Living Systems

How the immense complexity of living organisms has arisen is one of the most intriguing questions in contemporary science. We have started to explore experimentally how organisation can emerge from complex molecular networks. We focus on networks of molecules that can interconvert, to give mixtures that are under thermodynamic control. Molecular recognition between molecules in such mixtures leads to their mutual stabilisation, which drives the synthesis of more of the privileged structures.

We now demonstrate one of the first examples of this behaviour. A simple building block based on a pentapeptide, functionalised with two thiol groups, was allowed to oxidise to form an equilibrium mixture of macrocyclic disulfides, ranging from trimer to heptamer. Over time, the composition of the mixture evolved. Initially the smaller macrocycles (trimer and tetramer) dominated, but after an induction period, exponential growth of the hexamer and heptamer was observed. The shift towards these macrocycles was driven by self-association through the formation of extended beta-sheets. This results in nanoscale aggregates that bear close resemblance to amyloid fibres. This process can be controlled mechanically: different modes of agitation result in the selective formation of macrocycles of different ring sizes.

A mechanism of cancer robustness: the small complex system TE-TA-P [Telomeres-Telomerase-Proliferation]

Jean Deschatrette, Olivier C Martin, Claire Wolfrom

Track E - From Molecules to Living Systems

The robustness of cancer cells relies upon various strategies of adaptation to negative physiological constraints. In particular, the maintenance of telomere length, associated to telomerase activity, allows escape from cell senescence with persistent cell proliferation and phenotype stability overtime. This long-term adaptive behavior is enabled by oscillatory dynamics of the regulatory small complex system [Telomeres-Telomerase-Proliferation]. Robustness of the TE-TA-P system is analyzed in long-term cultured cancer liver cells.

On the Nuclear-Network Dynamics able to convert the Molecular Mechanisms into Biological Information

Walter Riofrio

Track E - From Molecules to Living Systems

The proposal of this study is to contribute with the debate about the usefulness to incorporate in biology and biomedical studies the informational terminology. For instance: what makes genetic information behaves as information? We could ask if these uses are valid and well supported by the current state of the art in biological disciplines or, on the contrary, this vocabulary is only to facilitate the comprehension of the most intricate aspects of biological mechanisms: we do realize exactly what we should have in mind when we observe the use of this concept as part of explanations of some of the experimental evidence on which this biological knowledge is based? And we are not exclusively referring to studies in cognition or perception, but also molecular biology, immune systems, signalling systems, evolution, development, and the like. In this study, we are contending together with the growing conviction that there exists something as computations within biological processes. Moreover, we will argue that discovering the nature of biological computing could produce a radical and profound change in the way we have regarded phenomena such as, for instance, how biological organisms function and evolve.

Keywords: biological computing, biological information, epigenetic phenomena, molecular network, pleiotropy.

Spatially Averaged Microscale Model for quantifying Methemoglobin Anemia

Saikat Chakraborty, Srimoyee Bhattacharya

Track E - From Molecules to Living Systems

Methemoglobin anemia is a disorder of the blood caused by abnormally high levels of methemoglobin (MetHb) resulting from simultaneous reactive uptake of oxygen (O_2) and nitric oxide (NO) by the red blood cell (RBC) of the human lungs. MetHb is produced in the RBC by irreversible NO-induced oxidation of the oxygen carrying ferrous ion (Fe^{2+}) of the heme group of the hemoglobin (Hb) molecule to its non-oxygen binding ferric state (Fe^{3+}). In this work, we study the role of NO in the pathophysiology of methemoglobin anemia and perform quantitative analysis of the relation between levels of NO inhaled by the patient and the severity of the disease. Reactions of NO occurring in the RBC with both Hb and oxyhemoglobin are considered in conjunction with the reaction between oxygen and Hb to form oxyhemoglobin and that for the reduction of MetHb to Hb. Spatially averaged unsteady-state low-dimensional models are obtained from the fundamental three-dimensional diffusion-reaction equations using Liapunov-Schmidt technique of the classical bifurcation theory. Our dynamic simulations of reactive uptake NO and O_2 in the RBC under continuous exposure to both gases reveal that at the end of the pulmonary transit time of 1 s, the oxygen saturation in the RBC equilibrate at 98% while breathing NO-free room air but decreases monotonically to 93% as the concentration of NO increases to 5 ppm and further down to 50% when the NO level in the blood increases to 80ppm. We show that an NO level of 10 ppm or higher while breathing in room air may be considered to be the critical NO concentration for methemoglobin anemia since it causes severe hypoxemia in patients by decreasing the oxygen saturation level to below its critical value of 91%. We simulate the effects of oxygen therapy on MetHb and oxygen saturation levels in the blood and stratify methemoglobin anemia patients who are oxygen responsive from those who fail to respond to pure oxygen. Our dynamic simulations reveal that ventilating patients with pure oxygen serves as an effective therapeutic strategy for NO levels of less than 10ppm in the RBC. For NO levels above 10 ppm, methemoglobin anemia may be treated with methylene blue 1% solution administered intravenously slowly over five minutes. This treatment is affected through the enzyme-inducing effect of methylene blue, which reduces MetHb (Fe^{3+}) back to hemoglobin (Fe^{2+}) by providing an electron. Our kinetic modeling of this metabolic pathway reveals that methylene blue restores the iron in Hb to its oxygen-carrying state

in less than a second of reaching the RBC.

Constraint-based modeling of the *Drosophila* Gap-gene regulatory network

Eric Fanchon, Fabien Corblin, Laurent Trilling

Track E - From Molecules to Living Systems

We present a constraint-based assistant for the modeling of the dynamics of biological networks. The global aim is to automate some modeling tasks by providing high-level functionalities to biologists. Network dynamics is represented by the discrete abstraction of R. Thomas (Thomas and Kaufman (2001)), which is briefly introduced. We explain how this formalism is cast into Constraint Logic Programming (CLP) and boolean Satisfiability (SAT). An originality of this work is that not only the dynamical rules of network evolution are encoded as constraints, but also the available knowledge on network behaviour. The method is flexible and allow to express high-level queries useful in the discovery process: proof of model (in)consistency, automatic model revision, inference of model parameters, etc. The formalization of experimental data and the search for a minimal model is illustrated with the case of the *Drosophila* gap-gene module, which is involved in the first step of embryo segmentation.

Regulatory networks and connected components of the neutral space

Gunnar Boldhaus, Konstantin Klemm

Track E - From Molecules to Living Systems

The functioning of a living cell is largely determined by the structure of its regulatory network, comprising non-linear interactions between regulatory genes. An important factor for the stability and evolvability of such regulatory systems is neutrality - typically a large number of alternative structures give rise to the necessary dynamics. Here we study the discretized regulatory dynamics of the yeast cell cycle [Li et al., PNAS, 2004] and the set of networks capable of reproducing it, which we call functional. Among these, the empirical yeast wildtype network is close to optimal with respect to sparse wiring. Under point mutations which establish or delete single interactions, the neutral space of functional networks is fragmented into $\approx 4.7 \times 10^8$ components. One of the smaller ones contains the wildtype network. On average, functional networks reachable from the wildtype by mutations are sparser, have higher noise resilience and fewer fixed point attractors as compared with networks outside of this wildtype component.

Executing Multicellular Development: Quantitative Predictive Modelling of *C. elegans* Vulva

K. Anton Feenstra, Nicola Bonzanni, Elzbieta Krepska, Wan Fokkink, Thilo Kielmann, Henri Bal, Jaap Heringa

Track E - From Molecules to Living Systems

Understanding the processes involved in multi-cellular pattern formation is a central problem of developmental biology, hopefully leading to many new insights, e.g., in the treatment of various diseases. Defining suitable computational techniques for development modelling, able to perform in silico simulation experiments, is an open and challenging problem. Here we apply the coarse-grained, quantitative approach based on the basic Petri net formalism we introduced previously to mimic the behaviour of the biological processes during multicellular differentiation. We show that for the well-studied process of *C. elegans* vulval development, our model correctly reproduces a large set of in vivo experiments with statistical accuracy. It also generates gene expression time series in accordance with recent biological evidence. Finally, we modelled the role of microRNA mir-61 during vulval development and predict its contribution in stabilising cell pattern formation.

Symmetry in Genomes Reveals Some Features in Their Structure

Michael Sadowsky

Track E - From Molecules to Living Systems

Any genome exhibits a symmetry implemented in frequency dictionary structure. An equivalence (or a close proximity) of information value of two words combining a complementary palindrome (that is a couple of sense and reciprocal antisense strings) makes the symmetry. It should be stressed, that both strings of the palindrome are determined over a single strand. The symmetry is equivalent to the second Chargaff's rule, while various genomes (or genetic entities) exhibit different figures of information value of the strings. The symmetry could be broken down due to a finite sampling effect (i. e., a finiteness of a nucleotide sequence), and peculiarities of a structure of that latter. Both effects were examined, and the statistical semantics structure revealed through the symmetry break resulted from a structure pattern is considered, for a family of genomes.

Predictive Analysis for Social Dynamics

Richard Colbaugh, Kristin Glass

Track F - Mathematics and Simulation

This paper presents a new approach to predictive analysis for social processes. A key aspect of the proposed methodology is proper characterization of the interplay between the intrinsic aspects of a social process (e.g., the persuasiveness of an argument) and the social dynamics which are its realization (e.g., the way the argument propagates through society). We begin by identifying a class of social processes which are simultaneously important in applications and difficult to predict using existing methods. It is shown that these processes can be modeled within a novel multi-scale framework that is sociologically sensible, expressive, illuminating, and amenable to formal analysis. We then develop a mathematically rigorous, computationally tractable approach to predictive analysis. Among other capabilities, this analytic approach enables assessment of process predictability, identification of measurables which have predictive power, discovery of reliable early indicators for events of interest, and scalable, robust prediction. The potential of the proposed approach is illustrated through case studies taken from economics, politics, and national security.

Studying Lyon's Vélo'V: A Statistical Cyclic Model

Pierre Borgnat, Patrice Abry, Patrick Flandrin, Jean-Baptiste Rouquier

Track F - Mathematics and Simulation

Lyon's community bicycle program called Vélo'v is a major initiative in shared public transportation, in activity since May 2005. It is studied here at a global level, to assess the evolution with time of the number of hired bikes. Based on the entire Vélo'v data set, up to December 2007, a statistical model is proposed to describe the daily and weekly patterns in a cyclostationary manner, jointly with the non-stationary evolutions over larger time-scales larger. Combining this model with linear statistical regression, a procedure is developed for the prediction of the number of bikes hired per hour. This prediction method involves several explanation factors such as the number of subscribed users, the time in the week, the occurrence of holidays or strikes, and weather parameters (temperature, volume of rain). The conclusion is that, for most days, the observation of the number of actually hired bicycles is satisfyingly explained and predicted by the model proposed here.

Analyzing the impact of network clustering on bond percolation and k-core sizes

Sergey Melnik, James Gleeson

Track F - Mathematics and Simulation

An analytical approach to calculating bond percolation thresholds, sizes of k-cores, and sizes of giant connected components on structured random networks with non-zero clustering is presented. The networks are generated using a generalization of Trapman's [P. Trapman, *Theor. Pop. Biol.* 71, 160 (2007)] model of cliques embedded in tree-like random graphs. The resulting networks have arbitrary degree distributions and tunable degree-dependent clustering. The effect of clustering on the bond percolation thresholds for networks of this type is examined and contrasted with some recent results in the literature.

Cluster synchronization in complex networks of coupled non-identical maps

Wenlian Lu, Bo Liu, Tianping Chen

Track F - Mathematics and Simulation

Cluster synchronization in complex networks is considered to be more momentous than complete synchronization in the real world, which is observed as that the oscillators in the network comprise several groups where individuals in the same group synchronize completely but the dynamics in different groups are distinguishing. In this paper, we study cluster synchronization in bi-directed networks of coupled non-identical maps. We present sufficient conditions guaranteeing cluster synchronization and find out that two factors lie in the core position for cluster synchronization: One is that each vertex in the same cluster has the same collection of other clusters linked; the other is that each pair of vertices in the same cluster can access each other. This leads to two cluster synchronization schemes: self-organization and driving, according to whether the edges lie inter-cluster or intra-cluster. Furthermore, we also propose a quantity to measure the cluster synchronizability of a network with respect to the clustering, which is a function of the eigenvalues of the Laplacian corresponding to the eigenspaces transverse to the cluster synchronization manifold. By numerical methods, we discuss the clustering synchronous dynamics and cluster synchronizabilities in four complex network models: (i). p -nearest-neighborhood graph; (ii). Random clustering graph; (iii). Bipartite random graph; (iv). Degree-preferred growing clustering network, to dig how the inter- and intra- cluster couplings affect the cluster synchronizabilities. For the last three models, we find out by numerical examples that when the number of intra-cluster couplings and the inter-cluster couplings reach certain ratio, the clustering synchronizability may be optimal.

Adaptive Dynamics of Realistic Small-World Networks

Olof Mogren, Oskar Sandberg, Vilhelm Verendel, Devdatt Dubhashi

Track F - Mathematics and Simulation

Continuing in the steps of Jon Kleinberg's and others celebrated work on decentralized search, we conduct an experimental analysis of *destination sampling*, a dynamic algorithm that produces small-world networks. We find that the algorithm adapts robustly to a wide variety of situations in realistic geographic networks with synthetic test data and with real world data, even when vertices are unevenly and non-homogeneously distributed.

We investigate the same algorithm in the case where some vertices are more popular destinations for searches than others, for example obeying power-laws. We find that the algorithm adapts and adjusts the networks according to the distributions, leading to improved performance. The ability of the dynamic process to adapt and create small worlds in such diverse settings suggests a possible mechanism by which such networks appear in nature.

The Complex Universe: recent experiments and theoretical challenges

Luciano Pietronero, Francesco Sylos Labini

Track F - Mathematics and Simulation

The field of Cosmology is undergoing a revolution due to the many new data which are becoming available and which are expected in the near future. For several decades this field has been essentially based on conjectures strongly based on the only exactly solvable model available (Friedmann). The observation of large structures in the galaxy distribution has challenged this model already long ago. We pointed out in fact that the correct statistical analysis implied the existence of strong correlation scaling associated to large structures up to the sample boundaries, without evidence for homogeneity. The standard model and analysis assumes instead homogeneity without really testing it. This led to a large debate and one way to try to save the standard model has been to speculate that large structures are real but their amplitude may be very small, so they are essentially irrelevant and are just the remnants of the initial conditions of the early universe. The very recent data from the SDSS project have permitted a test of this point. The result is that the large structures have also a large amplitudes, just like the small ones (1). This result therefore gives new strength to our previous findings. In the meantime other data have challenged the standard model and, for each of these, a new wild hypothesis has been added. Dark matter, inflation and dark energy have been introduced to this purpose. But the newest data provide new and compelling challenges to this picture. The large scale flow of galaxies (2) and the observation (by gravitational lensing) that also dark matter is very clumpy (3) represent important new elements. Our basic point is that the complexity of the universe should be seen as an interesting starting concept and not just as a technical difficulty from which one should try to escape. For example the inhomogeneity and scaling properties could lead to the acceleration effects which led instead to the introduction of dark energy (4). In this perspective also the connection between a highly structured matter distribution with a smooth cosmic background radiation (CMBR) could be seen in a novel framework. It is interesting to note that recently also the interpretation of the statistical properties of the CMBR has been questioned along lines which are conceptually similar to our criticism of the galaxy correlation properties. Also in CMBR the results expected from the standard model have been crucial in the interpretation of observations. A more neutral analysis leads to a radically different result (5). This rapidly evolving situation will lead, in our opinion, to a new picture of the universe in which complex structures should become a central point of its description. In this talk we provide a survey of these points and outline the possible developments. 1. A. Gefter *New Scientist* *New Scientist* March, 2007 and Sylos Labini et al. *Europhysics Letters*, 86 (2009) 49001. (2009) 2. Amanda Gefter, *New Scientist* 21 January 2009, 3. Joyce et al *Europhys.Lett.* 49 (2000) 416-422 and T. Clifton and P. G. Ferreira *Scientific American*, March 2009 5. K.S. Cover arXiv:0905.3971v1 and Li et al., arXiv:0905.0075

Collective observables in repeated experiments. The case of population dynamics.

Timoteo Carletti, Duccio Fanelli

Track F - Mathematics and Simulation

We here discuss the outcome of an hypothetical experiment of populations dynamics, where a set of independent realizations is made available. The importance of ensemble average is clarified with reference to the registered time evolution of key collective indicators. The problem is here tackled for the logistic case study. Theoretical prediction are compared to numerical simulations.

Overlapping Communities, Link Partitions and Line Graphs

Tim Evans, Renaud Lambiotte

Track F - Mathematics and Simulation

In this paper, we use a partition of the links of a network in order to uncover its community structure. This approach allows for communities to overlap at nodes, so that nodes may be in more than one community. We do this by making a node partition of the line graph of the original network. In this way we show that any algorithm which produces a partition of nodes can be used to produce a partition of links. We discuss the role of the degree heterogeneity and propose a weighted version of the line graph in order to account for this.

Self-Organization of Formations and Swarms of Agents

Gilles Labonte, Giovanni Fusina, Gerard Pieris, Bumsoo Kim

Track F - Mathematics and Simulation

Flocks, which comprise formations and swarms, are particularly evocative examples of emergence where complex global behaviours arise from simple local rules that act at the scale of individual agents. We illustrate various self-organized flocking mechanisms with two formations and with a few particular swarms. We demonstrate that, contrary to common belief, swarming can happen without any consensus force acting between the agents. The two formations are such that the agents are equally spaced in either a straight line or in a circle, at a constant altitude. The swarms we produce are a horizontal disk swarm at a specified altitude, a swarm that self-organizes in pursuit of a target, and a swarm that migrates in a specified direction. This study provides a good understanding of flocking mechanisms and a good basis for future work on the applications of flocking.

Critical behaviour in toroidal plasma confinement by 3-D magnetic fields

Mathew McGann, Robert Dewar, Stuart Hudson, Matthew Hole

Track F - Mathematics and Simulation

The existence of pressure-confining plasma equilibria is an article of faith for toroidal fusion reactor designs with no continuous symmetry, but the mathematical theory of such systems is still in its infancy. Such systems have generically non-integrable magnetic-field-line Hamiltonian dynamics, so an equilibrium must be consistent **both** with force balance and magnetic field line chaos. The multi-region relaxed magnetohydrodynamic (MRXMHD) model [1] for toroidal plasma confinement is a combined PDE/Hamiltonian dynamical system model for such equilibria, which postulates the existence of invariant tori (magnetic fields that survive the chaos) in the magnetic field line dynamics across which finite discontinuities in the pressure can be sustained. For small enough deviations from symmetry, such surviving magnetic fields can be found on all length scales, the field profile of the plasma is fractal.

In this paper we investigate the behaviour of a single magnetic surface as the pressure jump approaches a critical value, beyond which the magnetic surface no longer exists, and explore the variation of critical pressure jump with geometric deformation, seeking evidence for universality in the neighbourhood of criticality. The possibility of avalanche behaviour, in which the "break-up" of one magnetic surface can trigger a sequence of such break-ups is conjectured.

Quantifying structure in networks

Eckehard Olbrich, Thomas Kahle, Nils Bertschinger, Nihat Ay, Jürgen Jost

Track F - Mathematics and Simulation

We investigate exponential families of exponential random graph distributions as a framework for quantifying systematically the structure of networks. In this paper we restrict ourselves to undirected unlabeled graphs. For these graphs, the counts of subgraphs with no more than k links are a sufficient statistics for the exponential families of graphs with interactions between at most k links. We investigate in this framework the dependencies between several observables commonly used to quantify structure in networks, such as the degree distribution, cluster and assortativity coefficients.

On the fate of perturbations in critical random Boolean networks

Chiara Damiani, Alex Graudenzi, Marco Villani, Roberto Serra, Annamaria Colacci, Stuart Kauffman

Track F - Mathematics and Simulation

Random Boolean models of genetic regulatory networks, when subject to small noise, may either forget past distinctions or yield divergence in state space trajectories precluding reliable action. With a specific choice of the model parameters, such networks are in a critical regime and optimize capacity to bind past and future. An in-depth study of the response to perturbation of critical random Boolean networks is here presented. It is shown that networks built with critical values of the parameters may, however, frequently show behaviours that are more typical of the ordered or of the disordered regime. A further classification of critical networks is thus proposed with the objective of isolating those networks that exhibit really critical dynamics.

Optimal Control of Electrostatic Self-Assembly of Binary Monolayers

Nickolay Shestopalov, Graeme Henkelman, Travis Powell, Gregory Rodin

Track F - Mathematics and Simulation

In this work, a guided approach to self-assembly of binary monolayers of spheres is considered. An annealing schedule is used to guide the system into a highly ordered state. Optimal annealing schedule based on a single rate-controlling mechanism and derived using classical optimization methods is proposed. The results of molecular dynamics simulations demonstrate that the optimal schedule outperforms commonly used simulated annealing schedules when the rate-controlling mechanism is captured correctly.

Statistical characterisers of transport in a communication network

Neelima Gupte, Satyam Mukherjee, Gautam Mukherjee

Track F - Mathematics and Simulation

We study the statistical characterizers of transport in $2-d$ and $1-d$ communication networks of nodes and randomly distributed hubs. For the case of multiple message transport, a congestion-decongestion transition is seen for high message deposition rates. Signatures of the congested/decongested phase are seen in the travel time distributions of the messages, with the congested phase corresponding to a gaussian distribution, and the decongested phase to a log-normal distribution. These results are robust to different modes of connecting the hubs, and different lattice sizes. Our results may be of relevance in practical contexts.

Toward a knowledge integration for representing food processes

Cedric Baudrit, Mariette Sicard, Pierre-Henri Wuillemin, Nathalie Perrot

Track F - Mathematics and Simulation

It is more and more acknowledged that food processes can be associated with complex systems. They are systems featuring a large number of interacting microbiological and/or physicochemical components, whose aggregate activities are nonlinear and are responsible for the changes of food properties. As a result of time limits, financial constraints and scientific and technological obstacles, knowledge regarding food processes is fragmented and tainted with uncertainty. The pieces of knowledge may arise from various sources of know-how as expert operators, scientific theory, experimental trials *etc.* Faced with this heterogeneous information, it is necessary to develop practical mathematical tools able to integrate and unify the puzzle of knowledge in order to have a better understanding of the whole food process. With this aim, dynamic Bayesian networks provide a practical mathematical formalism that enables to describe dynamical complex systems tainted with uncertainty. It relies on the probabilistic graphical models where the graphical structure of network models highly-interacting sets between variables and probabilities take into account uncertainty pertaining to the system by quantifying dependencies. The aim of this paper is to demonstrate how dynamic Bayesian networks may provide an explicit overview and an objective interpretation of food processes. The ripening process of a soft mold cheese is chosen for demonstration purpose.

Tangled Nature: Co-evolution and the emergence of structure and networks by interacting agents.

Henrik Jeldtoft Jensen

Track F - Mathematics and Simulation

Understanding systems level behaviour of many interacting agents is challenging for example because the interacting components can lead to hierarchical structures with different causations at different levels. We use the Tangled Nature model to discuss the co-evolutionary aspects connecting the microscopic level of the individual to the macroscopic systems level. The inherent properties of all agents are the same, but they differ in the way they are interacting with the community of the other agents. The fundamental microscopic dynamics consists in agents reproducing, mutating and dieing. The micro-dynamics always run at a constant rate. Nevertheless, the systems level dynamics exhibit a completely different type of mode characterised by intermittent abrupt dynamics where major upheavals keep throwing the system between meta-stable configurations of occupancy in type space.

At the macroscopic level the system exhibit collective adaptation. We describe the systems level adaptation in terms of properties of the network of extant types: e.g. degree distribution, connectance, Species Abundance Distributions, Species Area Distributions.

The bulk of the phenomenology is worked out from computer simulations, however a number of aspects can be addressed analytically. We will briefly touch on how mean field, Fokker-Panck equations and field theoretic methods can be used to understand the segregation in type space (species formation) and network properties.

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Geometric Analysis of a Capture Basin Application to cheese ripening process

Mesmoudi Salma, Alvarez Isabelle, Martin Sophie, Sicard Mariette, Wullemin Pierre-Henri
Track F - Mathematics and Simulation

This paper addresses the issue of analysing the results given by viability sets, which represent all the viable states of a dynamical system. Viability sets and capture basin are a relatively new method to study complex dynamical systems, focusing on the preservation of some properties of the system (constraints in the state space) rather than on the possible stable states and equilibria. The viability set delimits the area of the state space where there is always a list of controls that allows the system to verify indefinitely the constraints. A viability set represents a huge amount of information about the system it studies. We propose here a geometric study of viability sets. This study is applied to the viability tube (the sequence of viability set over time) of a food process.

A nonlinear oscillator subject to time-delayed feedback control subject to time-delayed feedback control: analytical results and bifurcation analysis

Wolfram Just, Hartmut Erzgräber
Track F - Mathematics and Simulation

We apply time-delayed feedback control to stabilise unstable periodic orbits of an amplitude-phase oscillator. The control acts on both, the amplitude and the frequency of the oscillator, and we show how the phase of the control signal influences the dynamics of the oscillator. A comprehensive bifurcation analysis in terms of the control phase and the control strength reveals large stability regions of the target periodic orbit, as well as an increasing number of unstable periodic orbits caused by the time delay of the feedback loop. Our results provide insight into the global features of time-delayed control schemes.

Non-linear protocell models: Synchronization and Chaos

Alessandro Filisetti, Roberto Serra, Timoteo Carletti, Marco Villani, Irene Poli
Track F - Mathematics and Simulation

We consider generic protocells models allowing linear and non-linear kinetics for the involved chemical reactions. We are interested in understanding if and how the protocell division and the metabolism do synchronize to give rise to sustainable evolution of the protocell.

Evolutionary Algorithms and Eco-informatics: A myth or reality.

Bonsu Osei, Daniel Bentil, James Hoffmann, Chris Ellingwood

Track F - Mathematics and Simulation

Evolutionary computations and eco-informatics are fast becoming tools for cutting-edge technologies. They have provided insights into the complexity of ecological systems with a view to explaining these processes. This talk focuses on using a combination of both theoretical and data-driven modeling techniques to explain some complexities in ecology. Our approach utilizes Darwin's theory of evolution and information-theoretic model selection techniques as optimization tools to achieve this aim. We first derive a suite of general models for biological invasions and use a modified genetic algorithm to select the 'optimal' model that best describes ground truth data. These models incorporate biologically realistic phenomena such as diffusion, advection, habitat heterogeneity, long and short distance transport and density-dependent growth. The inclusion of the Akaike information criterion within an evolutionary algorithm makes it possible to accomplish both parameter fitting and parsimonious model selection. As a first step we use synthetic data to show the feasibility of this approach. We also carry out further experiments with ground truth data from the Zebra mussel invasion of Lake Champlain (Vermont). We show that our results are in consonance with the known hydrodynamic features of the lake as well as the life-history stage of this invasive species.

Neural network machine learning with a complex intervention for back pain

Martine J. Barons

PhD 'In Progress' Workshop

The data from a complex intervention for lower back pain was subjected to secondary analysis using neural network machine learning techniques. A complex intervention is a treatment regime comprising a number of components that may act both independently and inter-dependently. In this case the treatment for persistent low back pain included written material in the form of The Back Book, physiotherapist consultation and a series of six cognitive behavioural therapy sessions.

A randomised controlled trial of this complex intervention was carried out; from April 2005 to April 2007 patients who met the eligibility criteria were recruited and followed up for one year. The average improvement in the disability and pain measures used were found to be statistically significant, demonstrating the long-term effectiveness of a cognitive behavioural approach to treating low back pain. It was also demonstrated to be cost-effective. In order to address the need to establish if baseline factors are important predictors of treatment response, data mining was undertaken on the extensive dataset collected as part of this trial. Baseline measurements were taken at the beginning of the trial, and repeated at three months, six months and twelve months. The six cognitive behavioural sessions took place within the first three months. The measurements included Modified Von Kor scale, and the Roland and Morris questionnaire (RMQ) score. The Modified Von Kor scale assesses pain and disability associated with back pain in the last four weeks. Three of the six items relate to disability, and three to pain. The RMQ is a widely used measure of lower back pain disability in primary care trials. RMQ contains 24 items relating to patient functions which may be affected by low back pain, and completion is by means of a cross marked by each statement which the patient deems applicable to themselves. The neural network machine learning techniques were applied to the data to classify participants into subgroups of interest: those who attended at least one cognitive behavioural group session, those who attended at least three, and were therefore considered to have complied with the treatment, and those who experienced improvement of at least three points on their RMQ score. The predictors used as inputs to the neural network were all the baseline data except for those items which could not readily be assigned numerical values, such as comments and descriptions. The initial results give success in predicting the three items of interest varied from 65-70%

for compliance with the treatment to 70-74% for significant improvement and 72-76% for attendance at least one session. Further testing was carried out using only RMQ baseline score and Modified Von Kor scores as inputs, and for different sizes and methods of choosing the training set for the neural network.

Developing Sensory Augmentation in Urban Environments for People with Visual Impairment

Anthony Johnston

PhD 'In Progress' Workshop

Finding one's way around a busy town centre or through an unknown village is an ability that is mostly taken for granted. In order to navigate through such an area people with visual impairment make substantial use of familiar and common landmarks, signals and signs. In a new type of urban development, named "Shared Space", many of these sensory aids are being removed (Interreg IIIB, 2003). This is because the aim of Shared Space is to create an area where vehicles, bicycles and pedestrians interact more closely with each other obliging the road users to take more care and be more aware of each other. Consequently they are paradoxically safer. However, this environment presents a problem for people with visual impairment who find they have much fewer navigational aids to help them in their "wayfaring" or navigation from one part of the urban environment to another. The aim of the proposed research is to develop assistive technology to help such people navigate across a Shared Space. The assistive technology that will be investigated includes sensory augmentation: a technology that supplements the sensory clues received by a person with visual impairment. A prototype device will be built that will provide him or her with more information making it easier for them to navigate the new urban environment known as Shared Space. Links to machine vision and complexity science will be discussed.

Competition between sexual and asexual reproduction: a model for geographic parthenogenesis

Yixian Song, Irene Ament, Stefan Scheu, Barbara Drossel

PhD 'In Progress' Workshop

150 years ago Darwin (1859) published his book "On the origin of species". Despite this long time, some central evolutionary questions have not yet found a satisfactory answer, among these is the evolution of sex. Why are most species sexual in spite of the twofold cost due to the production of males? There are a number of hypotheses and models aiming at explaining the enigma of sex, e.g. Muller's ratchet (1964), Williams' Lottery model (1975), Bell's Tangled Bank (1982), and Hamilton's Red Queen (1980). However, a comprehensive theory for explaining sexual reproduction and its variation in space and time, in particular the phenomenon of geographic parthenogenesis (Vandel 1928), is still lacking. Geographic parthenogenesis describes the fact that many species reproduce asexually at the boundaries of their range, i.e. in northern regions, at high elevations, or at the transition to deserts. Our work is based on the observation that the depletion of resources plays an important role for determining the mode of reproduction (Ghiselin 1974). The advantage of sexual individuals lies in the ability to produce offsprings that can exploit new and unutilized resources. The Scheu-Drossel model (2007) was based on limited and structured resources combined with stochastic effects. In this model asexual reproduction wins over sexual reproduction only when mortality is high, when resource diversity is small, when resources regrow fast, or when many different genotypes are allowed to coexist at the same place. By adding spatial structure to this model and a gradient in those parameters that vary between the center and the boundary of a species' range, we obtain a pattern resembling geographic parthenogenesis, with sexuals prevailing in regions of low mortality and high resource diversity, while asexuals prevail at the boundary, where mortality is high or resource diversity low. Based on a single mechanism the model therefore explains both, the enigma of

sex and geographic parthenogenesis.

An agent-based model of immune cell trafficking, inflammation and HIV spread.

Kate Wendelsdorf

PhD 'In Progress' Workshop

My research involves construction of an agent-based model of immune cell trafficking, inflammation, and HIV spread among various organs and tissues. Simulations based on this model have been used to test and generate hypothesis regarding effects of immune responses on HIV spread and evolution in an individual. This short talk will present results from preliminary simulations of inflammation and pathogen spread as a consequence of immune cell traffic and interactions.

Minimizing genome complexity by reductive evolution

Sven Deitz, Sven Panke

PhD 'In Progress' Workshop

Building new functions into cells is the main goal of synthetic biology. To achieve this, circuits encoding for the desired behavior have to be inserted into an existing network of already considerable complexity (including regulatory-, protein-protein-interaction- and transcription-networks among others) where many of the interactions are not completely understood and characterized. The hypothesis is that by reducing the complexity of the target organism, these interdependencies can be reduced and more predictable results can be obtained. Minimizing the genome size of living organisms is a way to reduce this complexity and has been a goal of synthetic biology in recent years. On the one hand it addresses the question of gene essentiality and allows to approach the question of which genes are necessary to support life. On the other hand, it can potentially help to build more deterministic and better characterized platforms for metabolic engineering and synthetic biology by reducing complexity and simplifying the host. We are exploring the possibilities of reductive evolution to reduce the size of the genome and have designed a scheme for a genetic circuit that directly operates on the host's chromosome. We will implement a method to randomly delete fragments of the chromosome and thus reduce the size of the genome. In a second step, a selection mechanism allows selecting for organisms where the genome has effectively been reduced. By applying these two steps iteratively, populations that have successfully reduced the genome size will be selected.

Deriving Neighborhood Properties of Real Networks with Given Degree Distribution

Joydeep Chandra

PhD 'In Progress' Workshop

We derive models to estimate the neighbour distribution of nodes and the component sizes in finite-sized real networks. Based on the models of deriving neighbor distribution in large networks with arbitrary degree distribution, by Newman et. al., our work identifies the limitations of the Newman model in deriving accurate neighbor distribution and component sizes in practical networks that are mostly finite-sized. We observed that the actual average k-hop neighbors of the nodes and the component size in real networks with a given degree distribution is much less than that predicted by the Newman model. This is due to the presence of certain edges that we term as back and cross edges. Thus we refine the Newman model to derive more accurate estimates of neighbour distribution in networks with given degree distribution in the presence of back/cross edges. Further we derive the distribution of back/cross edges of the nodes, with given degree, in Erdos-Renyi networks with given degree distribution and extend the same for networks with any arbitrary degree distribution with certain given properties like clustering coefficient and assortativity. Our models are based on generating function formalism and the results are validated using

extensive simulations.

Stability Analysis of Superpeer Networks in the Framework of Complex Networks

Bivas Mitra

PhD 'In Progress' Workshop

In this work, we propose an analytical framework using percolation theory to assess the stability of complex networks. In face of failure and attack, the structure of a complex network changes due to node removal. We show that the degree distribution of the deformed network after any arbitrary failure/attack can be computed using a simple formula. The formula is further extended to estimate the percolation threshold of the finite size networks for arbitrary node disturbances. We show that for small scale networks, our estimation provides a better approximation of percolation threshold than the available methods and eventually converges to classical theory as network size goes to infinity. We examine the stability of large scale superpeer networks using the developed framework. We formally model the superpeer networks through bimodal degree distribution and failure/attack with the help of node dynamics. Our analysis points to several counter intuitive results and shows that different structural parameters of the network like peer contribution, peer fraction, superpeer degree have profound impact upon the stability of the network. The results obtained from the theoretical analysis are validated through simulation. We show that the simulation results and theoretical predictions are in good agreement. In addition to that, we simulate attack and failure on the real world commercial peer-to-peer networks as Gnutella and show that the proposed theoretical framework provides a reasonable description of the topological changes and stability of the network under attack and failure. We argue that the observed deviation between theory and simulated results is due to the presence of degree-degree correlation in real world networks which has not been considered while modeling the superpeer networks. We show that correlation effects become important for attacks while for random failure they are negligible.

Opinion Formation in Social Systems

Abhishek Mukhopadhyay

PhD 'In Progress' Workshop

We study a simple model to study the opinion formation in a two-party system. The opinion formation process is implemented in a random network of agents in which interactions are not restricted by geographical distance. In addition, we incorporate the rapidly changing nature of the interpersonal relations in the model. At each time step, agents can update their relationships, so that there is no history dependence in the model. This update is determined by their own opinion, and by their preference to make connections with individuals sharing the same opinion and with opponents. Using simulations and analytic arguments, we determine the final steady states and the relaxation into these states for different system sizes. In contrast to earlier studies, the average connectivity (“degree”) of each agent is independent of the system size. This has significant consequences for the long-time behavior of the model.

Opinion Formation in Social Systems

Paul Chapron

PhD 'In Progress' Workshop

A formalization of the Sociology of Organized Action theory has been undertaken, resulting in a model of an organization, its components, and the behaviours of the actors. With such a model, analytical exploration of the different modes and trends of the organisation, and the simulation of the behaviour of social actors allows the sociologist to explore the range of organizational functioning, and the behaviours

that emerge. Yet, nothing is said in this sociological theory about the structural dynamics of these organizations, as the theory only focuses on the mutual influence of human actors' behaviours and the way the organization works. An extension of this model to cover the evolution of organizational structure is a work in progress, as is an extension into the social networks field.

As our model represents how the organization entities (actors and resources) are connected and depend on each other, several networks can be extracted, with various possible weightings, providing a contextualisation of the social actors that are part of what is called a concrete action system. Simple quantities such as centrality have an equivalent in our model that can be interpreted in a sociological way, and the networks may be used by the actors as a new source of informations to deal with the organization. The current model and few ideas towards its evolution will be presented.

Studying the structure and dynamics of organisational networks in the wild

Felix Reed-Tsochas

“Networks: Dynamics and Flows” satellite meeting

This talk will be based on a number of related projects, all grounded in the same empirical data, recording the evolution of an organisational network. Our dataset tracks interactions between manufacturers and suppliers in the New York garment industry over a period of almost 20 years, and provides a unique opportunity to explore the dynamics of a self-organised network. I will start by discussing the dynamics of network contraction, both in terms of the empirically observed behaviour and with respect to a simulation model that we have constructed on this basis. Here, the key findings relate to what mechanisms generate topological robustness in a network that is shrinking. I will then consider what assembly rules, in terms of a stochastic model, are able to generate some of the key structural features observed in our organisational network, if we represent it as a bipartite network. Here, the focus is on the extent to which the proposed bipartite cooperation model may be applied to different contexts. Finally, I consider the propagation of errors in this supplier network, where errors correspond to refund payments. The question here is whether errors appear to propagate through the network, and what mechanisms enable or inhibit contagion.

Mathematical Tools for Studying Collective Behavior in Dynamical Networks

Fatihcan M. Atay

“Networks: Dynamics and Flows” satellite meeting

Mathematical sciences provide some powerful tools for investigating complex networks. Conversely, the latter contributes to the development of new methods by posing novel problems. In this talk I will present ideas from the theory of dynamical systems and graph theory that are useful for studying dynamical networks, that is, networks where either the states of the nodes or the network structure is changing in time. I will mostly focus on collective behavior such as synchronization and consensus, and discuss the emergence of novel behavior through coordination of network action. In addition to undirected, directed, and weighted networks, I will indicate extensions to networks with time delays, networks with time-varying links, and signed networks, i.e. those with both positive and negative weighted links, as in the excitatory and inhibitory connections in the brain.

Detailed Modelling of Gene Regulatory Networks

Markus Kirkilionis

“Networks: Dynamics and Flows” satellite meeting

We discuss new ways of modeling small genetic networks with high resolution of molecular details. The theory is based on an extension of reaction systems where particles can be both unstructured or struc-

tured with discrete state spaces. Genetic regulation is modeled by binding sites along the DNA and the communication of smaller (unstructured) particles (like transcription factors) affecting the state of DNA binding sites.

Epigenomics and Morphodynamics

François Képès

“Networks: Dynamics and Flows” satellite meeting

Biologists are fond of wiring diagrams abstracting the system’s components and their interactions. Network-based approaches extend this common viewpoint, while providing a well-paved path to more formal analysis. In particular, a simple topological or dynamical analysis may sometimes allow to reject a biologist’s model with little effort. A deeper analysis may shed light on the plausible mechanisms of a well-described and poorly understood phenomenon. Besides this explanatory capacity, the analysis may in different settings be of predictive value or increase the efficiency of subsequent experimental testing. However, what often appears on the biologist’s cartoons and is not directly amenable to network-based analysis *stricto sensu* is the spatial aspect of the biological process under scrutiny. The spatial development of regulatory networks will be emphasized in this talk.

Complexity-NET

Gavin Salisbury

Complexity-NET is a group of European science and technology funding agencies, research councils and ministries all working together to create an environment that enables the coordination of national activities in Complexity Science and Complex Systems research.

Funded by the European Commission Framework 6 Programme, Complexity-NET is aimed at integrating and strengthening the European Research Area through multinational coordination and cooperation of research programmes.

The Complexity-NET partners issued a first joint call for transnational research projects in complexity science in May this year. Assessment of the Expressions of Interest received, and the invitation to investigators to submit Full Proposals, will take place in September/October 2009.

Agility in Self Care

Mairi Macintyre, Claire Bourne, Amy Grove, Jannis Angelis

Poster (Track A)

Synopsis

The Agility in Self Care project aims to support the national initiative that is “Shifting the focus from a national sick service which treats disease to a national health service which focuses on preventing it” (Wanless, 2007).

Background

Self-care in the community has moved to the top of the political and clinical agenda in recent years in a response to greater pressure on the acute sector and an increased social desire to be involved in and take control of personal healthcare. However it has been recognised that such a paradigm shift will place significant pressure on an already over stretched system that is inherently ‘unlean’ and if transformational changes to the operational environment are not made patients and staff will suffer. Here in though lies the key problem and subsequent focus for this research.

Although numerous attempts have been made to re-design systems and methods of working within the NHS (mainly in the acute sector) few have been sustained and spread throughout the organisation. This

inability to affect long term sustainable changes to ways of working have acted as a serious barrier to effective care improvement and it is the intention of this research to address why sustainability of change is failing and propose a new way forward in future design and implementation strategies and help ensure effective self-care systems are developed among participating primary care case studies.

Aims

The primary aim of the project is to determine the appropriate approach to the emerging area of self-care with recommendations regarding prioritization and implementation to ensure the healthcare needs of the changing UK demographic is met.

The ASC project aims to address why sustainability of change has failed, and then develop a consistent approach to the design and implementation of future self care strategies. This new model for self care would help to ensure effective self care systems are developed, which take both a practical and strategic approach among the participating PCTs. To explore behavioural and operational issues as well as their impact on stakeholders and processes within the context of new operational and behavioural boundaries resulting from Self-care in the community to determine the most effective strategy for implementing effective changes. To investigate the relationship between operations and behavioural models, and to map the connections, networks and processes that exist across organisations and stakeholders. This will enable the project team to assess the degrees of agility to challenge existing Operations/Behavioural thinking and process development. To develop and test an operations model that will help clarify objectives, actions and resources across stakeholders. Therefore improving the quality and effectiveness of collaboration across stakeholder agencies in existing and new conceptualised contexts. To generate generalisable educational material that would disseminate the work across academia and the health, social and other stakeholder care professions. In addition training material will be developed that aims to be used in industry contexts for illustrative and educational purposes or within practical managerial contexts.

Simple picture on analytic network model for R&D feasibility analysis

Sang-Jin Ahn

Poster (Track A)

National R&D expenditure of Korea has been increased noticeably since 2000, and the governmental R&D investment reaches 0.9% of GDP. As many developed countries sustain the level at 0.8% such as U.S.(1.03%), Japan(0.68%), German(0.76%), and France(0.75%), Korea is an outstanding country among developing countries in R&D investment. Annual growth rates(2000-2008) of Korean governmental R&D investment is about 12.8%. As the R&D expenditure has been increasing, the efficient methods to invest R&D have been an important issue. Thus many governmental systems for R&D was applied for the better allocation of limited amount of national resources, determination of national R&D programs with higher priority, and reserving budget for national R&D program with feasibility. The R&D feasibility analysis is one of them. When some R&D program needs budget exceeding about 28 million EURO (37million dollar), its feasibility should be examined before determining investment. Korean ministry of strategy and finance manages the whole system of feasibility study, and Korea Institute of Science and Technology Evaluation and Planning (KISTEP) executes R&D feasibility study. When a governmental financial program is deeply concerned with infrastructure, such feasibility analysis is executed in Korea Development Institute (KDI). R&D feasibility analysis has three main components such as technological feasibility, feasibility in policy, and economical feasibility. Among them, economic feasibility can be usually used to check efficiency of R&D program. When benefits are concerned with market value, cost-benefit analysis should be applied in economic feasibility. However cost-benefit analysis is inappropriate, cost-effectiveness analysis will be substituted. Cost-effectiveness analysis(CEA) is a form of economic analysis that compares the relative expenditure and outcomes of two or more courses of action. The sustaining the existing standards of

services are considered as the effect of infrastructure asset management and the intervention could also be applied in pharmacoeconomics. However there is no common measure of outcomes for R&D investment. Sometimes statistical features of R&D documents could be substitutes for R&D output or outcomes. If statistical features of R&D documents could be effect of some R&D program, recent network-based studies on R&D documents have potential to apply CEA in R&D program. TARL (topics, aging, and recursive linking) model is a general process model to simulate coauthor and citation networks [1]. Innovation network model [2] may explain a universal type of mechanism linking ideas and designs and their evolution. In my study, modified model will be proposed, and it is applied into some topic keywords of R&D program.

Trends and priorities in Human Capital Integration and Modeling for post Bologna Public Policies - a conceptual demarche

Carmen Costea

Poster (Track A)

From the narrowest individual level to the broadest mankind perspective, human development has always been an intricate network of relays, passing on The Heritage: gene and health status, values, artistic talents and crafts, knowledge, technologies, beliefs, discoveries and inventions, and most important, spark awareness to behave robustly and contribute so that anyone become someone. But even if The Heritage emanates its secrets all around the world, from the manuscripts of the Dead Sea to the paintings on chapels' ceilings and the editorials of a gifted writer, nobody can say that reached the bottom of full potential, hibernating trapped in the circumstantial prison of faulty social system. "The Sleep of Reason Breeds Monsters" is not just a bad dream Salvador Dali once had, just as the terrifying "1984", written by Orwell in '48 had spread almost as an epidemic throughout half Europe. We owe it to any of us who has opened the eyes to the truth and handed out their relay to make sure that no Lost Decades will hunt our world again. We owe it to the dream of Europe to repair the half century mistake that lead into the dark millions of people under the communist regime. We owe it to ourselves to build the free society offering alternatives for every kind of human spark, by spreading creativity and progressive values over "viral" mentalities stuck in their own lack of adaptability to the never-ending change we are all experiencing. We owe it to the next generation to still have a world to inherit.

Keeping in mind the main confronting problems: F absolute lack of correlation between workforce demand (skills, qualifications etc) and educational offer; F artificial increase of unemployment because of minimum wage limits; F labour market distortions because of bad policies and union cartels; F fiscal chaos: too many taxes, too high tax levels, too much incertitude in future fiscal policies, the main purpose of this project is to elaborate on how to support each individual attaining its full development potential up to the maximum use of the biological, social and institutional circumstances capacity. In order to pursue the broad scope of the programme the paper is designed to offer alternative solutions for a series of more focused issues: ●Reconversion towards robust development to enlarge the capacity and the adaptability to change and social inclusion of the "lost generation"; ●Create innovative, flexible and dynamic models providing alternatives to workforce system under crisis: age decline, structural misbalances, migration, skill deficit, false cultural achievement or lack of fulfilment in general education; ●Provide suitable open social environments for young people to stimulate innovation and creativity, to develop their professional skills and private persona on a permanent basis in order to implement their ideas and choices; ●Bridge the generations by building up with the experience of the elderly and the youth lightness to create a strong synergy within their common creativity; ●Encourage people to connect for developing platforms to stimulate correlation between human capital demand from businesses and education systems supply and returned the effect of added value as a societal contribution; To identify the problems and design a suitable and sustainable solutions' portfolio the following steps are carried out: 1. Identification of human capital

resources systems insufficiently exploited. Human capital is defined by the sum of competences, skills and informal workgroups that support the societal structures involved in the economy. The human capital is a continuously fluctuant stock of interpersonal relationships inside different micro-systems, frameworks supporting the development of cumulated value of individuals. During the process of the interpersonal relationships there are two important processes that contribute to the self sustaining of the human capital development: a) communication stimulates the inception and consolidation of valuable individual treats, and b) collaborative actions generate a new team level of the value. Therefore, to put the human capital into a good use implies taking into consideration both the individual level, and also the stimulation of effect – the vertical process – and team spirit effect – the horizontal process. There are vectors of interpersonal relations which decisively influence the circuit of the human capital within the system it sustains: -Passing on competences, values, attitudes, experience, knowledge - on a vertical basis, at a generation level: family education, time lasting cultural activities, genetic memory, memory of the humanity, religious education and traditions etc. -Passing on abilities, information, technologies, current values and attitudes - on a horizontal basis, at a community level: public education, real time cultural activity, training, homeschooling, e-learning, knowledge sharing, advertising, PR etc.

2. Human capital is also defined by those elements personally selected from the total human characteristics having utility value for self fulfillment or satisfaction of needs. The robustness of the human capital development refers to modeling portfolios of alternative input abilities)/output(satisfaction of needs) systems and the extraction of functional guidelines to lead individuals to a healthy self developing circuit of need-to-skill-to satisfaction – to higher need – to work out breakthrough processes with reverse feedback vectors as well.

3. The modeling of these alternative systems is to be considered dynamically, as both parts of the yin-yang need-to-skill couple that are also dynamic. The intertwining of the two should be as continuous as possible to minimize deficits (causing workforce crisis, forced migration etc) and leads (causing structural unemployment). Also, the development of skills and the stimulation of synergy effects affect future needs scheme, so forecasting of future demand schemes, based on innovation breakthroughs is mandatory for the good provision of supply schemes. The higher end of the process is the maximization of human potential (based on biological conditions) to achieve a robust and creative free will based on the economic and societal metabolism: a) recover the capacity to develop social inclusion creatively by adaptation to change of the “lost generation” b) boost people development through alternative early and permanent education systems c) create innovative management systems for workforce crisis: age decline, structural misbalances, migration, skill deficit etc. The need-to-skill/skill-to-need context and human capital approach emphasizes the problem of the 40+ generation (especially in former communist block countries):

- psychological gap: they were educated and trained in the spirit of a reactive political and social system and now have to live in a proactive environment
- communication gap: beyond the high skills of communication in foreign languages sometimes spoken at a regional level, the open communication lacks knowledge in telecommunication platforms;
- societal and institutional gap: they were raised in a world that put experience (work years) ahead of results and now they live in a world where these values are reversed – the demand for younger, faster, higher performance leaders and managers;
- financial gap: they were brought up in a world where basic needs were the uniform standard of living and now they live, on the verge of subsistence in a consumerist world where young people gain in their first two-three years of work more than three times their parents’ wages after 20-30 years of work;
- cultural gap: they lived in a time of forced solidarity and cultural censorship, absence of free speech and often absence of free will and now they live in a world of self affirmation and self esteem, where they have to make personal and public choices
- economic gap: they were raised in a world of false social protection and now they see the third way systems (Northern European countries especially) tumbling down in front of a hectic capitalism, where social, healthcare and insurance systems crash under own weight.

PUBLIC Solutions:

- allow home schooling and privately certified early education systems;
- allow autonomy of each school to have their own curricula;
- divert resources from social protection programs (highly flowed

and inefficient) to fiscal incentives for businesses which hire elder people and train them for computer, foreign languages and professional skills; ●eliminate regulations which prevent workers to be hired under qualification positions; ●offer tax exemptions for people who are willing to invest the extra revenues in building SMEs ●eliminate provisions from the Labor Code which create distortions on the labor market – e.g. businesses cannot lay off people with less than three years before retirement age; instead of being a protective measure this only makes companies hire younger people whom they know they won't get stuck with if they are not performing; ●eliminate migration restrictions across the EU and building a civilization of individual and cultural education devoted to national roots values so that the reverse migration flows smoothly as well. PRIVATE Solutions: - establish a new model of understanding life, evolution and co-evolution on the Earth and inside the Society (where the working place is a part); - build up European wide internet database with jobs for experienced workers – blue and white, executive and management; - set up a privately financed training centre for businesses to use for life-long-learning programs for their employees.

Knowing is not enough; we must apply. Willing is not enough; we must do. Goethe

Spatial Diffusion under Control: Transformation of Schooling in 19th Century France

Noël Bonneuil

Poster (Track B)

The transformation over time of level sets has no reason to respond to diffusion processes, especially in social science, where the structure of the level sets of a given variable may be altered by demography or disrupted by unexpected events, and where the actors contribute to shaping their space through investment policies. The pioneering construction of graphic derivatives of set-valued maps by mathematician J-P Aubin (1999) renews understanding of dynamic level sets in social science. The exemplary case of schooling in nineteenth century France shows the velocities of level sets and illustrates how the Franco-Prussian war of 1870-71 disturbed the directions taken in 1867. Comparison of the observed changing space of schooling with the space that would have been observed under rational theoretical policies leads to the conclusion that the actors behaved as though responding to needs and to the gap between boys and girls.

Simple Model of the Elections Based on Lefebvre's Reflexy Theory

Michael Sadosky

Poster (Track B)

A distinction in reasons and motives for choosing a particular political figure makes the key difference between older and young democracy. The former is based on electoral history, while the latter is based on feelings and personal attitude. Besides, a comparatively abundant number of political figures (persons or parties and associations) is specific for young democracies. The problem of a reference votes' distribution is analyzed. Lefebvre's theory of a reflexive control is supposed to make the basis for indifferent choice of political figures. This theory yields a golden section split of votes (or the series of Fibonacci numbers, for the case of multiple choice). A typology of political campaigns based on this theory is proposed. A proximity of ratings of competing persons means the highest electoral tension, a leadership of a person means a high level of mobilization; a neutral situation corresponds to Fibonacci numbers distribution of votes.

Anticipation

Mohammad Ghassem Mahjani, Behrang Mahjani

Poster (Track B)

The modern science has been started starts by Galileo, Copernicus and was followed by Newton. In the Newtonian paradigm, as well as classical physics, future plays no role on the current state of a system. The equations of states in Newtonian systems, as well as quantum states, are described by rules which future has no parameter in them. However, ordinary experiences of life show that in some situations future plays a major role on the present state which this behavior can be considered as an anticipatory behavior. In anticipatory systems causality lies in future. Robert Rosen has discussed anticipatory behavior and has introduced the mechanism of human environment interaction. A brief review of Rosen's modeling is presented followed by a short view on complex systems. Super complex system is taken into account to include anticipation in the paradigm of complex systems.

Simulated synchronisation and emergence of a fishery complex

Jean Le Fur

Poster (Track B)

A multi-agent simulation model of the small-scale fishery sector in Senegal is presented. The aim of the study is to formalise the diversity of interactions and evaluate their effect on the coordination and overall functioning of the fishery sector. Fishermen, traders, boats, trucks, con-sumers, fishing zone, markets, landing sites and fish products are formalised on the basis of observations in the real sector. Simulations show that, given an associated 'selection/creation' process for the working communities, the fishery system reaches a steady state regime optimally organised in terms of production, wealth, working population size and activity (four indicators are presented in this respect). The role of diversity and history in the adaptation and synchronisation of the integrated functional process is highlighted.

Strategy and Knowledge Evolution - Evolutionary Complex Systems in Social Systems?

Carl Henning Reschke

Poster (Track B)

This paper draws together research and perspectives developed by strategists and strategy researchers, economists, sociologists, biologists and physicists to find a common basis for complexity approach to natural and social sciences. Conceptually, it is based upon a 'epistemological-cognitive' interpretation of evolution as learning process that accumulates information and transforms it into 'knowledge' via codification and structural organization of this knowledge (Riedl 2000). Strategy and management as a process of social evolution are about the selection and recombination of new variants in often modular and complex social and material structures, which are in turn influenced by actors' perceptions about these structures. These material elements and their mental representations are selected and recombined during processes of social evolution and in need of be adapted to each other, which may explain the particular paths of social developments in the past.

Children's perception of robots: the use write and draw techniques

Sajida Bhamjee

Poster (Track B)

Children's perception of robots were investigated as part of a wider research project on how humans

interpret robot interaction. The 'Write and Draw' technique was chosen as children may find it easier to express their thoughts through drawing and writing rather than speaking to a researcher.

Ninety one children aged 7-8 from two primary schools participated in the exercise. Literature suggests that children construct theories that are similar to those constructed by scientists (Carey 1985; Drive and Easley 1978). School 1 was asked to draw and write a story about their perception of robots. School 2 was asked to draw a robot, then more specifically asked to write about 2 questions: 'Why have you drawn your chosen robot?' and 'Where did the idea come from?'. The data was compared and examined thematically. Pictures were analysed in terms of the characteristics of the robots, i.e. shapes, colours. Two themes were identified in the stories: anthropomorphism and gender. The stories were then categorized into anthropomorphism or non-anthropomorphism. The theme of gender was categorized by whether the stories were of an 'adventurous' or 'domestic' nature. If there was no mention of adventure or domestic features, the story was classed as 'neutral'. If a story featured both adventure and domestic, the predominant theme was taken.

Children in both schools drew very similar pictures of robots, i.e. Square bodies with arms and legs. Results differed amongst the two schools. 18 out of 24 children anthropomorphised their robots in school 1 but only 11 out of 34 children anthropomorphised their robots in school 2. Examples of anthropomorphism include the robots eating, sleeping or having a family. There was a gender predisposition to type of stories written. In school 1, adventure stories were written by 5 boys and no girls. In addition, domestic stories were written by 5 girls and no boys. The neutral stories were written by 4 boys and 6 girls. In contrast, adventure stories were written by 8 boys and 4 girls in school 2. In addition, domestic stories were written by 4 girls and no boys. Neutral stories were written by 12 boys and 6 girls.

These findings suggest that the difference in questions asked was influential in determining whether the children are more likely to anthropomorphize or construct gender based stories.

The demographic difference between the schools may have also been an underlying influence. The difference in findings could be due to the difference in questions presented to both sets of children. Even though the pictures produced were of a similar nature, the method was still retained in the follow-up sessions. Not only was it useful as a fun introduction but it also gave the children the opportunity to reflect resulting in richer data. The pictures may have been repetitive due to children having a very generalised view about the appearance of robots. The children's limited drawing ability together with the possibility of 'copying' was also taken into consideration.

First Steps Towards an Ontology-based model of recreational (poly)drug use

François Lamy

Poster (Track B)

Recent reports on illicit drugs underscore the necessity of improving public policies concerning substance use and abuse. In particular, the EU Drugs Action Plan (2009-2012) argues for the creation of innovative technologies allowing for a better understanding of decision-making processes among drug users and for the testing of alternative public policies. In this paper, we explore how the combination of an ontology-based behavioural model with interlocked epidemiological and ethnographic surveys could provide a dynamical and trans-disciplinary way to effectively inform drug policy.

Notes on co-evolutionary systems, emergence and habitus.

Steven Martin

Poster (Track B)

The study of co-evolutionary and non-linear systems has started to become popular within the social sciences and related disciplines. While the work of sociologist Pierre Bourdieu has long been influential in

these fields. In this paper I will seek to demonstrate that by combining Stuart Kauffman's NK models, utilising fitness and fitness landscapes, and Bourdieu's conception of the habitus and field, there are potentially new ways of engaging with the understanding of interactions between collective and individual consciousness, and perhaps more importantly, new ways of understanding social inclusion and exclusion.

An improved Lanchester model for market share in a duopoly

Jane Binner, Leslie Fletcher, Vassili Kolokoltsov

Poster (Track B)

Versions of the Lanchester model are widely used to model the evolution of market shares in a duopoly in which each player seeks to win customers from the other by advertising and similar activities. We set out a very general version in which the value of the market and the effectiveness of advertising vary with time and marketing campaigns are time limited, also allowing for a presumption against customer churn – that is, when keeping an existing customer is less costly than gaining a new one. We identify some qualitative properties of the market share trajectory and make a careful examination of the assumptions needed to prove the existence and uniqueness of a Nash equilibrium in the contest for market value.

The mathematics of ordinary language 'complexity' in 'non-mathematical' areas of social life

Gordon Burt

Poster (Track B)

Does mathematics help or hinder our ability to handle complexity? We distinguish two types of use of the word, 'complexity', in two types of context. The word 'complexity' can be used either in a technical sense or in an ordinary language sense. The word can be deployed either in a mathematical context or in a non-mathematical context. Most people most of the time operate in a non-mathematical context and when they use the word 'complexity' they intend an ordinary language meaning. The aim of this paper is to mathematicise the (ordinary language) concept of complexity in non-mathematical contexts. In this way we seek to widen the reach of mathematics, extending its application to the common experience of most people.

Non-mathematical contexts within the academic world are typically found in the humanities, social science and applied social studies faculties, the last of these covering management, education, health and welfare. (Mathematics is not totally absent from these areas, and indeed is quite extensively used in certain areas such as economics, but for the most part discourse is non-mathematical). Outside the academic world, most of social life, most of ordinary language and practice, are held by many people to be beyond the reach of academic theory let alone mathematics.

The weak claim of this paper is that all of these areas are open to mathematical science. Four case studies are offered in illustration of this claim. Mathematical science analysis is carried out on: a letter to the Financial Times about the global financial crisis; a historical novel by Ken Follett; the author's personality as revealed in a role play session; and the religious conversion of William Wilberforce. The strong claim of this paper is that representations of reality which do not have a sound mathematical science foundation are of uncertain validity. The claim reflects a philosophical position which might be referred to as mathematical social science positivism.

How is quality content produced by a mass collaboration?

Katalin Orosz, Illés J. Farkas, Péter Pollner, Tamás Vicsek

Poster (Track B)

We combine editing events, page content, network dynamics, and page discussions to uncover the mechanisms by which the quality of articles on the English Wikipedia may increase.

Multiplicity of equilibria in a model with heterogeneity of social susceptibility of consumers and exogenous price shocks

Paulo Dawid, Vladimir Belitsky

Poster (Track B)

We depart from a Heterogeneous Interacting Agent Model (HIAM) of binary choice, in which, for instance, the agents (consumers) have to decide between to buy or not a determined product at each discrete choice time. The heterogeneity consists in the different intensities the agents react linearly to the majority decision. Those intensities, defined as the consumers' idiosyncratic social susceptibility, are supposed to be a positive random variable distributed independently across the population with a cumulative distribution function (cdf) $\Psi(\cdot)$. Considering then the model in the limit with the number of agents going to infinity, we have that the mean number of agents buying at each time (defined here as demand D_t), due to law of large numbers, behaves deterministically according to a dynamical system characterized by the cdf $\Psi(\cdot)$ and that changes at each time t depending on the actual price of the product P_t . Considering then the sequence of prices as stationary shocks and assuming further conditions on the cdf $\Psi(\cdot)$, mainly that it is continuous and has a strictly positive derivative at $0+$, we obtain a set of necessary and a set of sufficient conditions in order to the resulting dynamical system not present multiplicity of stationary equilibria.

When and how heterogeneity of social susceptibility of consumers implies multiplicity of population relative excess demand

Vladimir Belitsky, Paulo Dawid, Fernando Prado

Poster (Track B)

We consider a model of a duopoly market and analyse possible values of the excess demand – the difference between relative demands for two similar goods competing in the market. In real markets, it is often observed that the excess demand may attain one of two (or more than two) values for the same difference of the goods' prices. This phenomenon, called *multiplicity of the excess demand* (or, alternatively, *social phase transition*), merits attention and explanation due to its social and economic consequences; in particular, in a duopoly market, it causes that the more expensive good may be also constantly more demanded. The source of this phenomenon has been explained: it is the combination of the monetary and the social factors on consumers' decisions. From this explanation arises the question which we answer here: since each of these factors affects different consumers with different intensities, then (a) the heterogeneity of consumers' idiosyncratic perceptions of the fair price difference, and (b) the heterogeneity of consumers' idiosyncratic social susceptibility play a role in the formation of the phenomenon. What is this role? The part (a) of the question has been exhaustively investigated by Heterogeneous Interacting Agent Models (HIAMs, for short) of the social consumption process. The part (b) of the question is answered in our present work. The tools necessary and arguments in our analysis are different from what has been employed by now in the HIAM area. This supports our belief that our results are totally novel.

Predictability and prediction for an experimental music market

Richard Colbaugh, Kristin Glass, Paul Ormerod

Poster (Track B)

Perhaps the most striking characteristic of cultural markets is their simultaneous inequality, in that hit songs, books, and movies are many times more popular than the average, and unpredictability, so that well-informed experts routinely fail to identify these hits beforehand. It is tempting to conclude that the problem is one of insufficient information. Clearly the winners are qualitatively different from the losers or they wouldn't be so dominant, the conventional wisdom goes, so in order to make good predictions we should collect more data and identify these crucial differences. A more nuanced version of this idea admits that the differences between the winning choice and the other options may be small, because the map between option "quality" and success is likely to be a nonlinear one, but the conclusion remains the same: to predict the winners one must learn about the attributes of the various choices. A recent experiment calls into question this conventional wisdom and, indeed, indicates that there may be fundamental limits to what can be predicted about social processes. In the elegant study reported in [Salganik et al. 2006], researchers constructed an online music market and examined the role social influence played in which songs the participants chose to download. The experiment revealed that increasing the extent to which participants were able to observe the selections of others – that is, the strength of the social influence signal – led to an increase (decrease) in the popularity of the most (least) popular songs and a decrease in the predictability of song popularity. This research provides evidence that, for social processes in which individuals pay attention to the behavior of others, it is not possible to obtain useful predictions using standard methods, which focus on the intrinsic characteristics of the candidate process outcomes. We propose that accurate prediction, if it is possible at all, requires careful consideration of the interplay between the intrinsics of a social process and the underlying social dynamics which are its realization. This poster presents a theoretical and empirical examination of the experimental music market of [Salganik 2006]. We begin by deriving a simple model for the market which captures the interplay between market intrinsics and social (influence) dynamics; the model is shown to reproduce the "stylized facts" of the real system, including the observed relationship between social influence and market share inequality / unpredictability. We then conduct a formal assessment of market predictability, finding that market intrinsics (e.g., song quality) possess little predictive power but that very early song download time series is predictive of ultimate market share. These insights regarding market predictability are used to develop a novel prediction algorithm which is able to: 1.) accurately identify market share winners and losers very early in the experiments, and 2.) predict the ultimate market shares of the successful songs. The poster concludes by summarizing the implications of the analysis for other domains in which the events of interest are outcomes of social processes, including political and social movements, fads and fashions, and mobilization/protest events.

Putting Complexity to Work - achieving effective Human-machine Teaming

Patrick Beautement

Poster (Track B)

As people 'put complexity to work' they are increasingly employing machines to help them achieve understanding, make decisions and assist with supporting tasks such as modelling, intervention-monitoring and evaluation. In effect, humans and machines are forming teams - but how effective can these teams be and what are the consequences that follow if they are not? This paper asks the question: what needs to be done to enable machines to make enough sense of complexity so that they can assist people more effectively with this work? This paper first describes a characterisation of complexity which is then used to look at the role of machines in supporting decision-making in these environments. The paper examines

the issues around the formation and sustainment of so-called human-machine teams (HMTs). To this end, the theoretical ranges of collaboration and relationships between machines and people are characterised and the nature of dialogue with machines (about complex issues) is examined. From this, a list of desired machine capabilities is derived. Lastly, implications and conclusions are drawn to answer the initial question and comment on the significant issues which arise and on their potentially serious consequences. The author hopes to stimulate debate on this topic with practitioners (about the degree of contribution that it is realistic to expect from machines in the near future) and with technologists about how machine behaviour can be further augmented.

Homophily and competition: a model of group affiliation

Nicholas Geard, Seth Bullock

Poster (Track B)

Groups are an important social phenomenon, representing an intermediate level of organisation between individuals and society as a whole. The dynamics of groups are an emergent property of decisions made by individuals about both their affiliations and their social contacts. Despite the presence of group level behaviour in a number of different categories of social simulation model, there are few models explicitly of the dynamics of group affiliation and social structure evolve. We present one such model, based upon McPherson's ecological theory of group affiliation.

The Simultaneous Impacts of Social Structure and Personal Characteristics on Spreading Continuous Opinions in Society

Amir Asiaee Taheri, Mohammad Afshar, Masoud Asadpour, Caro Lucas

Poster (Track B)

Continuous opinion dynamics has gained a lot of attention in Sociophysics. Although much research has been done on this issue, many aspects of these phenomena are not explored yet. This research is focused on the simultaneous impacts of social structure and personal characteristics on spreading continuous opinions in society. Considering the uncertainty of beliefs which represent personal characteristics, individuals are softly divided into extremists and moderates. Beside personal attributes, minority party may be cohesive or sparse in comparison to the whole society. These two parameters form four types of society which are examined in this work. Each type is implemented and analyzed in a scale-free (BA model) society. The simulation shows except cohesive-extremist party, cohesive-moderate party has more influence on the society than sparse-extremist one. These results demonstrate the prominence of minority party structure in comparison to personal characteristics of members.

Diffusion of Information Through Private Communication in Realistic Social Networks

Andrea Apolloni, Karthik Channakeshava, Lisa Durbeck, Maleq Khan, Chris Kuhlman, Bryan Lewis, Samarth Swarup

Poster (Track B)

Word of mouth, rumors, and gossip represent non-mainstream forms of communication and their spreading can affect many human affairs: they shape public opinion, impact financial markets, create awareness or panic during disease outbreaks, etc. The diffusion of information through these channels exhibits a resemblance to epidemic processes and is strongly affected by the structure of the social network. Unlike epidemic processes, however, communication flows depend strongly on similarity in social status, personality type, shared opinions or beliefs, etc.

Model of behaviour uncertainty of the economic system

Konsantin Kovalchuk

Poster (Track B)

The model of identification and forecasting of the economic system trajectory states in time is offered in work, which allows complex estimation its conduct from positions of risk (additive distributing), incompleteness (subadditive distributing) and contradiction (superadditive distributing) of information accessible to the manager.

Modeling Structural Change in Markets

Kun Leng

Poster (Track B)

Today's markets are increasingly dynamic and competitive. To be successful, firms have to be able to learn faster than and learn from their competitors. There is an ever growing need for modeling tools to help policy makers and management teams study a firm's choices and explore phases of industry evolutions. Traditional industry simulation captures dynamic behaviors of system components, only if the current structure remains stationary. To bridge the gap between behavior and structure, we are interested in examining how a single player's behavior can affect the overall structure of a complex system, by employing a modeling methodology called variable structure modeling, introduced by Oeren and Zeigler. Such models entail the possibility of changing the composition of the system as well as the interaction between its components, slightly different from the approach employed in evolutionary economics. Variable structure simulation treats each individual player in an industry as an agent, and investigates the agent's entry and exit strategies as well as the dynamics of his behavior. The consequent modeling framework more accurately describes a wide range of structural changes, as well as evolutions in individual behaviors. It may help us better understand dynamic industries and markets that possess endogenously-varying structures. This poster illustrates the features and power of this methodology and outlines an application to the U.S. housing market.

Cognitive Support for Complex Systems Management: A Microworld Experiment

Daniel Lafond, Jean-François Gagnon, Michel B. DuCharme, Sébastien Tremblay

Poster (Track B)

Introduction

Planners and decision makers in military command and control, designers of complex socio-technical systems and strategic policy makers all depend on their capacity to understand and anticipate the behaviour of complex dynamic systems. There has been significant progress in developing technologies and methods that support human sensemaking and decision making processes in complex domains (e.g., Busemeyer & Pleskac, 2009; Langton & Das, 2007; Lizotte, Bernier, Mokhtari, Boivin, DuCharme & Poussart, 2008). Nonetheless, a better understanding of human cognitive requirements when faced with complex problems is needed to guide the development and evaluation of support technologies and methods. We report an experiment that aimed to study the cognitive functions required for effective decision making in a complex and dynamic environment. We focus on two specific macro-cognitive functions: anticipation and strategy elaboration.

Method

Thirty university students performed a simulated society management task in one of three conditions:

Group 1 was a baseline condition; Group 2 required participants to anticipate the outcomes of their decisions; Group 3 did the same as Group 2, and could then revise their intervention using a decision aid that automated the anticipation function. In all conditions participants were provided with detailed information on the cause-effect relationships between system variables. The anticipation tool used in Group 3 implemented these cause-effect relations and provided the users with an accurate extrapolation of the effects of the participant's decisions for the next game-year. The experiment began with a 15-min tutorial on how to play the game (Groups 1-3), how to generate predictions (Groups 2-3) and how to use the anticipation tool (Group 3). After completing the game, which had no time limit (average completion time: 30-60 min), participants were asked to write down a description of the strategy they used during the task. Anticipation accuracy was measured by asking participants to infer the state of the society for the next year and comparing it to the actual outcome. The degree of strategy elaboration was measured with the post-experimental questionnaire.

Results

An analysis of variance showed no significant difference in goal attainment across the three groups. Participants in Group 2 and Group 3 did not significantly differ in terms of anticipation accuracy. There was no significant correlation between anticipation accuracy and performance. The degree of elaboration of the strategies reported by participants was assessed by two judges (inter-judge correlation, $r = .92$). A significant positive correlation was found between the degree of strategy elaboration and the final score for Group 2, and Group 3, but not Group 1.

Discussion

Focusing on short-term anticipation or providing a tool that yields correct short-term predictions did not help participants succeed in the task. Results highlight a key characteristic of complex systems called policy resistance (Sterman, 2006). Policy resistance means that interventions intended to have a beneficial effect in the short term are not necessarily beneficial in the long term. It appears that long term considerations may be of critical importance in complex systems. The presence of a positive correlation between the degree of strategy elaboration and goal attainment only for the groups that focused on anticipation suggests that the two key cognitive functions studied here, namely anticipation (integration and application of structural knowledge), and strategy elaboration (identification of sub-goals based on system understanding) may be jointly necessary for effective decision making in a complex and dynamic environment. Future work will provide further tests of this conjecture and study strategic planning in more detail.

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Rhythm and Randomness in Human Contact

Mervyn Freeman, Nicholas Watkins, Eiko Yoneki, Jon Crowcroft
Poster (Track B)

There is substantial interest in the effect of human mobility patterns on opportunistic communications. Inspired by recent work revisiting some of the early evidence for a Levy flight foraging strategy in animals,

we analyze datasets on human contact from real world traces. By analyzing the distribution of inter-contact times on different time scales and using different graphical forms, we find not only the highly skewed distributions of waiting times highlighted in previous studies but also clear circadian rhythm. The relative visibility of these two components depends strongly on which graphical form is adopted and the range of time scales. We use a simple model to reconstruct the observed behavior and discuss the implications of this for forwarding efficiency.

A full paper has been submitted to INFOCOM 2010, San Diego.

Origin of stability and auto-organization in an industrial system: Mulhouse 1746-1902

Jean-Luc Mercier, Daniel M. Dubois, Raymond Woessner, Isabelle Bernier, Michel Hau

Poster (Track B)

The small independent Republic of Mulhouse (XVIII-XIX^o century) appears to be an analog to the contemporary Hong Kong or Singapore. Very strict living allows its Calvinist population to accumulate capital. They transform the guild system. A combination of the precepts of law and religion, permits modern capitalism and an incredible level of industrial activity to develop here, which then expands into the region and to Europe more generally. Yet during this time, the city experiences six different political regimes.

The data used comes from the co-authored work of a number of historians (M. Hau, I. Bernier . . .) and from a study [Histoire documentaire de l'industrie de Mulhouse, 1902] edited by the "Industrial Society of Mulhouse (SIM)". From 1746 to 1902, 900 factories are described: we used 264, over 157 years, comprising 57 industrial groups. The method used: Shannon information (Hmax, H, R). Building on this information theory, D. Dubois developed a "D0 fluctuation index", whose time-derivative has the characteristics of a Lyapounov function. The function $dL/dt \leq 0$ indicates stability of the system; $dL/dt = 0$ indicates a weak stability.

The historical approach shows that during the first 14 years, the development of industry was exponential. This positive feedback of "capital-> production-> wages-> benefits -> capital" was described as the first "industrial capitalist" system in the (SIM 1902). This initial system was interrupted in 1760 when the Mulhouse Republic installed a special Court of Justice named "Commission des Fabriques" (Bernier 2009). This Court adjudicated 359 disputes between workers and employers, acting on the industrial system as a negative regulatory feedback. The consequence, during 1760-1798, was that the number of factories now increases linearly. This judicial structure disappears in 1798 with the amalgamation with France, whereupon the companies moved their production to the Vosges Mountains where rivers, and forest, were more abundant, and wages lower (SIM 1902).

The major positive peaks of dL/dt can be correlated with recorded economic problems including: imposition of tariffs (1790), cotton importation (1811), economic speculation on cotton (1833) ... In the same way, some negative peaks (stability peaks) are linked with, for example, the prohibition of foreign limited partnerships (1764), the end of this same prohibition (1795), the first cotton-mule for spinning (1802), or the first foundry (1826). A precise comparison is made between these results and those of earlier historical work over the period 1806-1902 (Hau 1987).

Our consideration of the origin of stability, auto-organization and complexity was based on a particular time window (1764-1790). This short period allows us to fit a quadratic function on H, R, D0, and to calculate the time-derivatives and their components. At first sight, this system is stable ($dL/dt < 0$) with $dH/dt > 0$ and $dR/dt < 0$. More refined analysis reveals instability with $dH/dt < 0$ and $Hmax(-dR/dt) < 0$ or with $dR/dt > 0$ and $Hmax(dH/dt) < 0$.

The words "order – disorder" are polysemic, and have been chosen for other scales of analysis by other scientific investigators. We, however, choose in this text to instead use the words "coherence" (logical,

consistent and orderly) and "incoherence". External Noise (N) and stress and constraints (F) in the system are the source of coherence or incoherence. Because of this double origin, we introduced Exo and Endo-coherence (an endogenous process being one which occurs in constant environmental conditions). "Organization" is the transition from incoherence to coherence.

These definitions allow us to determine an H-organization and an R-organization. H-organization, due to increasing or decreasing of external noise (+N, -N); Stability is obtained by [$dH/dt > 0$ and $H_{max}(-dR/dt) > (1-R)(dH_{max}/dt)$], an increase of Exo-coherence, increase of noise (+N: $H1 > H2$), increase of external activity and decrease of internal stress. Instability is obtained by [$dH/dt < 0$ and $H_{max}(-dR/dt) < (1-R)(dH_{max}/dt)$], Exo-incoherence by decrease in external noise (-N: $H1 < H2$).

R-organization, due to increase or decrease of internal stress (+F, -F); Stability is obtained by [$dR/dt < 0$ and $H(dH_{max}/dt) < H_{max}(dH/dt)$], an increase of Endo-incoherence, increase of internal brakes (-F: $R1 > R2$) which facilitate industrialization during periods of internal depression [Local work * External forcing = 0 & External potential * Local power < 0] or [Local work * External forcing > 0 & External potential * Local power > 0]. Unstability is obtained by [$dR/dt > 0$ and $H(dH_{max}/dt) > H_{max}(dH/dt)$], an increase of Endo-coherence, decrease of internal brakes (+F: $R1 > R2$) by [Local work * External forcing > 0 & External potential * Local power > 0]. The four origins of auto-organizations +N, -N, +F and -F are combined in two terms "NB" and "FB" which synthesize the double equilibrium between the external noise (NB) and the internal constraint (FB). Industrialization and deindustrialization (reduction of industrial capacity or activity in an area / converse to industrialization) are clearly illustrated by the relation between stability and these two terms. Unstability and deindustrialization: $dH/dt < 0$ & $NB < 1$ or $dR/dt > 0$ & $FB < 1$. Stability and industrialization: $dH/dt > 0$ & $NB > 1$ or $dR/dt < 0$ & $FB > 1$.

During the 157 years, the succession of the two modes of auto-organization does not occur randomly but in a very regular way, we note 20 hysteretic cycles crossing the poles: -F-N -> -F+N -> +F+N -> +F-N -> -F-N, or -F-N -> +F+N -> +F-N -> -F-N.

We applied this result to the whole series and obtained 6 classes of stable years and 5 classes of unstable years. Because it was a highly unpredictable system, evolving in space and time, with positive and negative feedback created throughout the period ... Industrial Mulhouse is a complex system.

Relationship between duration and population distribution of municipalities

Hiroto Kuninaka, Mitsugu Matsushita

Poster (Track B)

Population distribution of a given region or a country has been extensively discussed. For example, Zipf suggested that the size distribution of cities obeys the power-law distribution which has the power-law exponent close to unity, which is called Zipf's law.[1] However, some recent studies have revealed that the power exponent changes in time due to various factors such as the distribution of economic activity, population migration, great merger of municipalities, etc.. [2, 3] We investigate the time evolution of the size distribution of municipalities (SDM) in Japan. Our preliminary analysis of the population data of Japan revealed that SDM in Japan obeys the double Pareto distribution, which has the lognormal body and the power-law tail. This distribution can be found in the file size distribution in a computer,[4] the income distribution of U.S.A, [5] etc., and is formed when the distribution of growth time of growing bodies obeys the exponential distribution in which the bodies grow according to Gibrat's process.[4] In this poster presentation, we investigate the time evolution of SDM in Japan from 1980 to 2005, and SDM in Saitama prefecture, which is next to Tokyo. From the analysis based on the data from the ministry of education, culture, sports, science, and technology of Japan,[6] we find the transition from the double Pareto distribution to the lognormal distribution in SDM due to the great merger of municipalities in 2005. In addition, SDM in Saitama prefecture also obeys the double Pareto distribution in 2005. To in-

investigate the origin of the emergence of the distribution, we investigate the duration of each municipality which is strongly affected by the great merger of municipalities from 1955 to 1965 in Japan. In our poster presentation, we will report the time evolution of SDM and the distribution of duration of municipalities.

Bifurcation analysis of geophysical time series

Valerie Livina, Frank Kwasniok, Tim Lenton

Poster (Track C)

We propose a general synthetic framework, combining analytical and experimental techniques, for studying climatic bifurcations and transitions by means of the time series analysis. The method employs three major techniques: (i) derivation of potential from time series using unscented Kalman Filter (UKF); (ii) studying possible bifurcations and transitions of the obtained potential; (iii) projection of the time series according to the estimated perturbation. The method is tested on artificial data and then applied to observed records, in particular, a Greenland temperature proxy. We correctly detect potential changes in artificial series with a varied number of potential wells. In the case of Greenland data, the technique detects a change of the number of system states from two to one (double-well potential transforming into single-well) at about 20 kyr BP.

Can macroevolution emerge in the cellular automaton (eco-)system?

Wojciech Borkowski

Poster (Track C)

On this poster, I will present a simple lattice model of a multi-species ecosystem suitable for the study of emergent properties of macroevolution. Unlike the majority of ecological models, the number of species is not fixed—they emerge by “mutation” of existing species, then survive or go extinct depending on the “energetic” balance between local ecological interactions. The Monte-Carlo numerical simulations show that this model is able to qualitatively reproduce phenomena that have been empirically observed.

Prevention Effects and Cost Efficacies of Intervention Strategies for Novel Influenza

Chung-Yuan Huang, Yu-Shiuan Tsai, Chuen-Tsai Sun, Tzai-Hung Wen

Poster (Track C)

Since April 2009, medical researchers have been committing considerable amounts of time and resources to confirming novel influenza virus structure, developing specific vaccines and antiviral drugs, establishing rapid diagnosis methods, and revising prevention and intervention strategies. Specifically, the efficacies of prevention and intervention strategies are the focus of this paper. To determine the optimal application timing of intervention strategies, we collaborate with public health policy makers to (a) propose two assessment criteria: prevention effect and cost-efficacy, and (b) construct a multi-scale simulation platform to estimate the temporal/spatial transmission dynamics of influenza and compare different impacts of novel influenza resulting from different intervention strategies and/or policy combinations.

Competition between sexual and asexual reproduction: a model for geographic parthenogenesis

Yixian Song, Irene Ament, Stefan Scheu, Barbara Drossel

Poster (Track C)

150 years ago Darwin (1859) published his book "On the origin of species". Despite this long time, some central evolutionary questions have not yet found a satisfactory answer, among these is the evolution

of sex. Why are most species sexual in spite of the twofold cost due to the production of males? There are a number of hypotheses and models aiming at explaining the enigma of sex, e.g. Muller's ratchet (1964), Williams' Lottery model (1975), Bell's Tangled Bank (1982), and Hamilton's Red Queen (1980). However, a comprehensive theory for explaining sexual reproduction and its variation in space and time, in particular the phenomenon of geographic parthenogenesis (Vandel 1928), is still lacking. Geographic parthenogenesis describes the fact that many species reproduce asexually at the boundaries of their range, i.e. in northern regions, at high elevations, or at the transition to deserts. Our work is based on the observation that the depletion of resources plays an important role for determining the mode of reproduction (Ghiselin 1974). The advantage of sexual individuals lies in the ability to produce offsprings that can exploit new and unutilized resources. The Scheu-Drossel model (2007) was based on limited and structured resources combined with stochastic effects. In this model asexual reproduction wins over sexual reproduction only when mortality is high, when resource diversity is small, when resources regrow fast, or when many different genotypes are allowed to coexist at the same place. By adding spatial structure to this model and a gradient in those parameters that vary between the center and the boundary of a species' range, we obtain a pattern resembling geographic parthenogenesis, with sexuals prevailing in regions of low mortality and high resource diversity, while asexuals prevail at the boundary, where mortality is high or resource diversity low. Based on a single mechanism the model therefore explains both, the enigma of sex and geographic parthenogenesis.

Modular Dynamics in Plant Growth and Development

Kun Leng

Poster (Track C)

A large number of plants grow by modular reiteration of structures at three different levels. The central role that modules play in plant growth has been under debate, because only they directly breed daughter units through meristems. Recent studies argue that single plants are merely a medium of integration for modules, which have naturally become a choice of reiteration variable for demographers simulating plant growth.

In this poster, a mathematical model is presented to investigate the modular dynamics of individual plants. This model aims to detect the relative importance of seasonality and reproductive effort on modular growth. Special attention is given to the survival and growth of plants during their crucial development phase which often determines later plant performance.

This model is a logistic system, in which the maximum number of modules per plant (e.g. plant size), M , is a constant, and the instant growth rate, $r(t)$, is a function of demographic processes (e.g. birth and death rates) under optimal conditions influenced by seasonal fluctuations and flowering episodes. Simulations take into account severe seasons at different frequencies, different demographic processes, different flowering occasions and reproductive efforts, different maximum plant sizes, and different plant performances under ideal circumstances.

The function of growth rate, $r(t)$, exhibits regular oscillations, in accordance with seasonal frequencies and breeding occasions. The amplitude of oscillation is jointly determined by climatic severity and reproductive effort. The capacity to multiply, v , drives plant growth substantially, and seems to be the single most important parameter affecting early plant size in this model. The rate of modular accumulation slows down when plant sizes approach M . Therefore, developing daughter modules in the early stage of modular development should be favored, which can lead to greater sizes and enhanced competitive ability later in plant life. The value of v restricts a plant's reproductive effort as well as seasonal severity it can endure. Widely grown plants should show greater reproductive effort during climatically benign periods.

[Key words] Logistic equation, modular dynamics, demographic process, reproductive effort, plant size,

oscillation, seasonality, biological modeling, mathematical modeling.

Self-organized criticality in population outbreaks

Sabrina B. L. Araujo, Gandhi M. Viswanathan, Marcus A. M. de Aguiar

Poster (Track C)

We study the phenomenon of population outbreaks in a spatial predator-prey model. We find that pattern formation and outbreaks occur if the predators have a limited neighborhood of interaction with the preys. The outbreaks can display a scale invariant power law tail, indicating self-organized criticality. We have also studied the system from an evolutionary point of view, where the size of the predation neighborhood is a hereditary trait subjected to mutations. We find that mutation drives the predation neighborhood to an optimal value where pattern formation and outbreaks are still present, but the latter are not scale invariant.

Global Patterns of Speciation and Diversity

Marcus A.M. de Aguiar, Michel Baranger, Elizabeth M. Baptestini, Les Kaufman, Yaneer Bar-Yan

Poster (Track C)

The estimated number of species living in the Earth is between 10 and 100 millions. To understand the process that generates this huge diversity is yet one of the greatest challenges in evolutionary biology. The appearing of new species is called speciation and it can imply in the complete transformation of a species in another one, process known as Anagenesis, or in the division of a species in others, process known as Cladogenesis. In this work we are going to study a particular kind of Cladogenesis where an only ancestor species can split up and give rise to other species. The genetic flow between the groups of individuals in the same specie is the factor that will determine the kind of especiation that will eventually occur (Coyne & Orr, Speciation, Associates, Inc (2004)). For example, if the genetic flow is null we have the Allopatric Speciation, here groups are isolated geographically and the genetic exchange by sexual reproduction cannot occur. It is believed that a great part of species had appeared by Allopatric Speciation. On the other hand we have the Sympatric Speciation, in this case in spite of total genetic flow between the groups of the same specie, differents species appear in the same space of their ancestor, through the process of assortative mating. Speciations where genetic flows occur partially are called peripatric and parapatric speciations. Current models of Sympatric Speciation generally involve the segregation by adaptation to discrete ninches or to a continuous distribution of resources, where the selection associates ecological and mating characters. We have developed a model of speciation that is not based on ecological assumptions, but in the self-organization of the population in sets reproductively isolated due to the assortative mating, a model of neutral speciation that we called of "Topopatric Speciation" (Aguiar, Nature 460, (2009)). We have simulated the evolution of a population of which members, at the beginning, are uniformly distributed in space with identical genomes. The genetic variation increases with the time, due to mutation and to the recombination. The key ingredient of the model involves the introduction of assortative mating based on two critical mating distances: one in physical space S and one in genetic space G . The S parameter restricts the mating to the pairs of individuals whose space distance is lower or equal to the S . Even all the individuals of one same species are able to mate between itself, we make the hypothesis that they prefer to get mate with closer partners. However spatial distance by itself is not able to block the genetic flow, two individuals A and B can exchange genetic material via an individual C located in a distance lower than S between A and B . The physical space is described by a square lattice $L \times L$ with periodic boundary conditions, it is representing a huge space without barriers. The individuals are placed in the lattice. Although each site can support any number of individual, in general the population density in our simulations is low. When the mate occur the new individual will take up the parent space or will spread

with rate D for neighboring sites, the parent dies to give place to the son. The total number of individuals in the population is kept constant. The genetic distance G is the maximum difference allowed between the genomes for that two individuals can get mate. It allows that the individuals recognize themselves as being of the same species and produce fertile offspring. The genetic incompatibility between two individuals can be interpreted as the inefficiency of the male in attracting the female (for being different), differences in the sexual organs, difficulty of the sperm fertilizes the ovule and the production of infertile offspring. We show that this coupling between spatial and genetic distances can take to the spontaneous formation of geographic domain in the population and the sexual isolation of subpopulations in the space of the genomes, in spite of absence of physics barriers, gradients in the resources distribution or natural selection. We identify a species as a group of organisms reproductively separated from all others by the genetic restriction on mating and connected among themselves by the same condition, without requiring all members of the group to be able to mate with each other. An example of the mechanism we have considered in this model occurs with “species in a ring”, in which progressive differences along a chain of individuals result in individuals at one end not being able to mate with those at the other end (Klicka, *Science* 277, (1997)), but we consider this a single species, owing to the ongoing gene flow. Our results show constant rates of new species over long times, species-area relationship in agreement with gotten empirical results in birds, plants, mammals, among others. We also got a behavior of the lognormal type for abundance of species, with abundance of rare species agreeing with results gotten for diverse species in the nature.

Space Debris Networks

Rebecca Newland, Hugh Lewis, Graham Swinerd

Poster (Track C)

There are 3,226 satellites and over 10,000 items of man-made space debris, larger than 10 cm, in orbit around the Earth. Whilst most debris has been generated by explosions, modelling studies suggest that collisions will soon take over as the main debris generating source. Irrespective of its source, debris poses a collision risk to operational satellites and other debris objects. Even a single collision (involving satellites and/or debris) has the potential to create many hundreds of new debris objects which would have long-term negative implications for satellite operators and services.

Space debris mitigation guidelines are currently in place to limit the production of new debris. In addition to these guidelines, Active Debris Removal (ADR) may be needed to reduce the number of debris objects in orbit. However, if debris objects are to be removed by ADR then a robust and quantitative method will be required to identify objects most likely to have a negative impact on the future environment. This requirement arises principally because of the technological challenges and high economic cost of removing these objects.

By treating the space debris environment as a complex system and analysing the data using network and vertex measures, the debris problem can be understood from a new perspective. The aim of the current research is to demonstrate that network theory is an effective approach to analysing space debris environment data. Data from modelling studies are used to represent the space debris environment as networks. Vertices represent debris objects and edges represent the possible future conjunctions between the objects. The networks are analysed using the following measures: degree, strength, assortativity, affinity, clustering, and betweenness centrality.

The results suggest that the space debris environment has a low average degree and is disassortative with hubs. This means that the environment is resilient to random removals as there are only a few vertices, the hubs, which may have a significant effect on the future environment. Furthermore, targeting the vertices with a high degree or betweenness centrality reduces the connectivity of a large space debris network by breaking it into several smaller networks. Therefore, a targeted ADR approach will be necessary if the removal of objects is to have a positive impact on the debris environment.

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Modelling Socio-Environmental Influences in the Spreading of Obesity

Carla Taramasco, Dominique Bicout

Poster (Track C)

This paper deals with the social and/or environmental determinants in the obesity epidemics. Specifically, we underline two critical features of propagation processes: (i) exogenous influences, where individuals may adjust their behaviors due to exposure to common influences as public policies or mass media, and (ii) endogenous effects, where individuals may alter their behaviors as another in their social network change theirs. For this purpose, we propose have developed a theoretical framework and computer simulations allowing us to assess and study the potential impacts of social and/or environmental influences on the propagation of obesity.

Robustness of complex networks to node and cluster damage

Emil Gegov, Mark Atherton, Hamed Al-Raweshidy

Poster (Track D)

The goal of this investigation is to assess the robustness of two popular network structures – random networks and scale-free networks – to node and cluster damage. There is no previous work on the latter. For node damage, we remove nodes iteratively and for cluster damage, we first build a network of clusters and then remove the nodes (clusters).

Toward Understanding the Optimization of Complex Systems

Jiming Liu, Yu-Wang Chen

Poster (Track D)

In response to the increasing demands for solving various optimization problems arisen from complex systems, the paper focuses on the study of a general-purpose distributed/decentralized self-organized computing method, with the help of agent-oriented modeling method. The goal of this paper is to unravel the microscopic characteristics and the hidden complexity of complex computational systems, and furthermore, construct proper mechanisms that will support self-organized computation.

Complexity Profiles: Networks with Ring-Lattice and Small World Relationships

Gerard Pieris, Giovanni Fusina

Poster (Track D)

With the recognition of an increasing number of natural and man made systems as complex systems, there is a greater need for characterizing their complexity. One way to describe the complexity of a system is as a measure of the variety of different options it can execute. The complexity profile is a method for characterizing the complexity of a system at each scale or each size of subsets of entities of the system. Thus it shows the variety of effects the system can produce, where these effects require the coordination of different sizes of subsets of entities. This document investigates the complexity profiles for an abstract system consisting of entities with Gaussian state distribution whose relationship to each other is characterized

by covariance matrices with ring-lattice and simple small-world structures. Small-world relationships have been found to be a characteristic of many complex systems. Understanding the relationship of network structure to their complexity profiles can contribute towards methods for engineering complex systems that have desired complexity profiles.

Emergence of Artificial Culture

Mehmet Erbas

Poster (Track D)

We will research and test hypotheses concerning the design of multi-layer hybrid control architectures for swarm robotic systems. These control architectures will introduce elements of learning planning and deliberation which go well beyond the minimalist controllers currently found in swarm robotic systems, yet at the swarm level we will retain the key characteristics of emergence and self-organisation. Therefore, this project will research the potential for novel emergent interactions between robots with (simple) cognition. A key aim will be the design of necessary architectures and algorithms for robot - robot imitation. This will include the imitation of movement, sound and light among robots. Imitation is believed to be a key factor in the emergence of culture in our robot society as it provides a means of transferring and propagating certain behaviours between robots, while allowing those behaviours to evolve.

Looking for communities in networks: two algorithms, three kinds of noise

Malgorzata Krawczyk

Poster (Track D)

Numerous systems considered in biology, sociology or economy constitute sets of interacting components, with various structure and strength of these interactions. Such a system can be described in a natural way as a network, where components make nodes, and interactions between them - edges. Networks consist of some communities, i.e. standing out groups of nodes, which play particular role in the system. Identification of the communities in a network is often a highly nontrivial task. Methods to be applied should be able to extract essential part of data out from noise. Our task here is to compare two methods of the cluster identification in networks with different kinds of noise.

Statistics of spin avalanches in antiferromagnetic nano-networks

Joanna Tomkowicz, Krzysztof Kułakowski

Poster (Track D)

Networks of nanoparticles with dipolar interactions are of interest for their new magnetic properties. Such networks can be formed of cobalt, iron or ferrihydrite nanoparticles. We consider two types of networks, the scale-free (SC) and the exponential (EX) networks of size N with the number M of nodes to which new nodes are attached. Each node contains a nanoparticle with spin $S_i = \pm 1$. The dipolar interaction is limited to pairs of neighbours in the network. In our numerical experiment we simulate the hysteresis loop in $T = 0$. We investigate compact spin avalanches, using the damage spreading method (DS). The character of obtained avalanches from DS is different than in the conventional methods. The results indicate that the avalanche spectra are characterized by the same statistics as the degree distribution in their home networks. We calculate the range Z of avalanches, i.e. the distance between the damaged node and the furthest changed nodes. We obtained a new scaling relation between the range Z and the size s of avalanches.

$$Z \propto N^\beta f(N^{-\alpha s}) \quad (1)$$

where α and β are growing from 0 (for $M = 1$) to $\alpha = 0.5$ and $\beta = 0.33$ (for $4 < M < 10$). These values are the same for both investigated networks. A check for $M = 25$ confirms α and β values and the independence. Similar behaviour of α and β is found for the avalanche diameter.

Decision Making with Boolean Neural Network: the Emergence of Mental Schemes

Franco Bagnoli, Graziano Barnabei

Poster (Track D)

Human decisional processes result from the employment of selected quantities of relevant information, generally synthesized from environmental incoming data and stored memories. The main goal of these high-level cognitive processes is the production of an appropriate and adaptive response to a cognitive or behavioral task. Different strategies of response production can be adopted, among which the formation of mental schemes, of reasoning and of heuristics. In this paper, we propose a model of Boolean neural network that tries to incorporate these three strategies and accounts for, at moment, the first way of task resolution, namely the creation of mental schemes. The modality with which schemes emerge is given by recurring to global optimization strategies during learning session, and it characterizes the passage from an unconstrained network typical of data-driven processes to an attractor neural network representative of schema-driven processes.

A peer-to-peer protocol in hierarchical navigable small-world network

Wenfeng Feng, Zhibin Zhang, Yongfeng Huang, Xing Li

Poster (Track D)

We improve Kleinberg's hierarchical small world network model to implement a peer-to-peer overlay network. In the overlay, all the nodes are treated as leaves which are uniformly distributed in a complete 2-ary tree, and the node distance is defined as the height of their lowest common ancestor in the tree. Every node in the overlay is linked to at least one d-distance node if the d-distance nodes exist. Through simulation, we demonstrate that, the overlay has average $(\log_2 N)/2$ routing hops, a 100% routing success rate, while the average node degree is $\log_2 N$, the number of messages for node joining is $\log_2 N/2$, the number of message for node leaving is $\log_2 N$.

Arguing the validity of Models and Simulations for Scientific Exploration

Fiona Polack, Paul Andrews, Teodor Ghetiu, Robert Alexander

Poster (Track D)

As a tool for researching complex systems in life sciences, computer simulation must be demonstrably suited to the scientific purpose. Using approaches from traditional computer simulation and critical systems engineering, we propose argumentation techniques to present fitness for purpose arguments. The illustration is a basic argument used to establish and express a basis for understanding between modellers and scientists. The purpose was to establish agreement that an agent-based computer simulation on an extensible platform is adequately equivalent to an earlier, less-efficient, computer simulation used in a trait-based study of ecological abundance.

Extraction of knowledge for complex objects from experimental data using functions of multi-valued logic

Emil Gegov, Boriana Vatchova

Poster (Track D)

Extraction of knowledge from experimental data is accomplished mainly using statistical methods. When the processes are non stationary of the object then statistical characters of data are changed. It is impose to apply methods of theory of random functions i.e to have many realizations of the processes, which are gotten by their reiteration by constant conditions of the experiment. For the purpose of control in real time this circumstance can not be accomplished. There are derived logical conclusions containing of experimental data for knowledge extraction by one realization in real time. This goal is achieved using development of functions of multi-valued logic.

Machine Vision helping blind people to find their way

Anthony Johnston

Poster (Track D)

Finding one's way around a busy town centre or through an unknown village is an ability that is mostly taken for granted. In order to navigate through such an area people with visual impairment make substantial use of familiar and common landmarks, signals and signs. In a new type of urban development, named "Shared Space", many of these sensory aids are being removed (Interreg IIIB, 2003). This is because the aim of Shared Space is to create an area where vehicles, bicycles and pedestrians interact more closely with each other obliging the road users to take more care and be more aware of each other. Consequently they are paradoxically safer. However, this environment presents a problem for people with visual impairment who find they have much fewer navigational aids to help them in their "wayfaring" or navigation from one part of the urban environment to another. The aim of this research is to develop assistive technology to help such people navigate across a Shared Space. The particular assistive technology being investigated includes sensory augmentation – a technology that supplements the sensory clues received by the user. A prototype device will be built that will provide him or her with more information making it easier for them to navigate the new urban environment. Its efficacy will be tested and discussion with urban planners about the layout of Shared Space and the possibility of introducing a design constraint to take account of the findings may follow.

Cooperative Defensive Strategies for Malware Detection using Artificial Immune Systems

Chris Musselle

Poster (Track D)

Malware, or malicious software, has, and continues to be, an extensive and ever increasing threat to modern society. Though many products have been produced to counter or mitigate this threat in the past (e.g. antivirus, firewalls, intrusion detection systems, email scanners etc.) they rely primarily on searching large databases of previously known threats. This approach is becoming less and less effective with the total number of malware to date, and the rate of generation of new malware dramatically increasing.

An alternative method of detecting malware is based on anomaly detection, and the ability to distinguish between normal and anomalous programs or behaviour patterns on computer systems. This however is by no means a trivial task, and in attempting to solve this problem, much biological inspiration has been gleamed from the immune system, leading, over the years, to the development of the field of Artificial Immune Systems (AIS).

My project aims to incorporate the latest techniques in Artificial Immune Systems and combine them with a network level defensive approach. The main avenue of investigation will be whether cooperation between networked devices will lead to a more efficient response against invading malicious software.

Culture Lab and Lab Culture: how to observe culture emerge in a group of interacting robots.

Carissa Hoareau

Poster (Track D)

It is a given that culture is used as a conceptual tool to distinguish difference between groups of people, but what happens when it is used to highlight similarities and differences in unexpected ways? Not only between people but also between different kinds of subjects and objects which may become redefined in the process of scientific practice. Although there is much discrepancy over what culture actually consists, one can conclude that it is mostly seen to be something of human property, a sort of defining characteristic of what it means to be human. What I would like to do in this poster is to explore the implication of a shift in the framework, from the human to the nonhuman, by looking at the search for culture in a robotic society. I shall do this by considering alternative paradigms of culture and how these are incorporated into a specific case of science in practice – a project titled, ‘The Emergence of Artificial Culture in Robot Societies’ based at the Bristol Robotics Laboratory (UK). Taking leave from data collected through doing an ethnographic study on the project, I shall elaborate on some of the consequences of adopting different understandings of culture for the project, and the implicated subjects and objects. I shall show that culture is constructed by the many attempts to (re)define it in the process of scientific practice. Through this we enter another contribution the project makes to Science and Technology Studies. On the one hand I argue that notions and concepts such as culture get redefined in the process of scientific practice. On the other hand the project works with a predefined notion of culture which suggests that, if only we have a more robust science which dodges the practical difficulties of doing science, away from the mysterious things of meaning and ideology, we are able to build in the facility for robots to create something akin to the chosen notion of culture. I would like to explore how these two different ways of going about looking at the emergence of culture in robot societies actually work together and create an emergent, performative way of doing science and conceptual work.

Computing with Noise - Phase Transitions in Boolean Formulas

Alexander Mozeika, David Saad, Jack Raymond

Poster (Track D)

Computing circuits composed of noisy logical gates and their ability to represent arbitrary Boolean functions with a given level of error are investigated within a statistical mechanics setting. Bounds on their performance, derived in the information theory literature for specific gates, are straightforwardly retrieved, generalized and identified as the corresponding typical-case phase transitions. This framework paves the way for obtaining new results on error-rates, function-depth and sensitivity, and their dependence on the gate-type and noise model used.

Learning, complexity and information density

Joel Ratsaby

Poster (Track D)

What is the relationship between the complexity of a learner and the randomness of his mistakes? This question was posed in [J. Ratsaby 2009] who showed that the more complex the learner the higher the

possibility that his mistakes deviate from a true random sequence. In the current paper we report on an empirical investigation of this problem. We investigate two characteristics of randomness, the stochastic and algorithmic complexity of the binary sequence of mistakes. A learner with a Markov model of order k is trained on a finite binary sequence produced by a Markov source of order k^* and is tested on a different random sequence. As a measure of learner's complexity we define a quantity called the *sysRatio*, denoted by ρ , which is the ratio between the compressed and uncompressed lengths of the binary string whose i^{th} bit represents the maximum *a posteriori* decision made at state i of the learner's model. The quantity ρ is a measure of information density. The main result of the paper shows that this ratio is crucial in answering the above posed question. The result indicates that there is a critical threshold ρ^* such that when $\rho \leq \rho^*$ the sequence of mistakes possesses the following features: (1) low divergence Δ from a random sequence, (2) low variance in algorithmic complexity. When $\rho > \rho^*$, the characteristics of the mistake sequence changes sharply towards a high Δ and high variance in algorithmic complexity. It is also shown that the quantity ρ is inversely proportional to k and the value of ρ^* corresponds to the value k^* . This is the point where the learner's model becomes too simple and is unable to approximate the Bayes optimal decision. Here the characteristics of the mistake sequence change sharply.

Environment orientation; An approach to the simulation of complex systems

Tim Hoverd, Susan Stepney

Poster (Track D)

A naive implementation of a complex system simulation with its plethora of interacting agents would be to represent those interactions as direct communications between the agents themselves. Considerations of the real world that a complex system inhabits shows that agent interactions are actually mediated by the environment within which they are embedded and which embodies facilities used by the agents. This suggests an "environment oriented" simulation architecture.

Low-Density Parity-Check Codes in Multiuser Channels: Statistical Physics Approach

Roberto Alamino, David Saad

Poster (Track D)

In the present work we apply statistical physics techniques developed for the study of disordered systems to study two important classes of multiuser channels, the Multiple-Input Multiple-Output (MIMO) and the Relay channels. Both channels are subjected to Gaussian noise and messages are encoded with low-density parity-check error-correcting codes. These systems can be mapped to finite connected spin systems and the application of the replica method yields information about many important characteristics for the typical case, which includes error thresholds showing the phase transitions from perfect to defective decoding depending on the noise level.

Systemic Processes of Evolutionary Knowledge Organization: The Case of Innovations in Pharmaceuticals?

Carl Henning Reschke

Poster (Track E)

This paper explores how a systemic evolutionary view, which argues that evolution is a knowledge generating process, and conceptually or mathematically related perspectives can contribute to an integrated perspective on the evolution of information organization by linking perspectives from biology and the social sciences. The paper uses the illustrative example of punctuation patterns in pharmaceutical innovations as a starting point for discussing a number of theoretical models and perspectives with respect

to their suitability for such an integrated perspective. These models, if sufficiently correct representations of the characteristics of and tools for research into evolutionary development processes should play a role in explaining the molecular make-up of human organisms. Thus they also must find a reflection in the history and characteristics of pharmaceutical research as well as the more general characteristics of knowledge processes. The implied circularity of scientific concepts used for analysis and processes operating in the evolution of biological organisms and of knowledge indicates the relativity and reflexivity of knowledge, which is seen as expression of evolutionary processes of knowledge growth in the social domain being 'eigenprocesses' of evolutionary development from the building blocks of animate matter to the social domain.

Modeling randomness, irregularities or regularities in the human heart waves

Çağlar Tuncay

Poster (Track E)

The basic aim of this paper is to discuss the physics which may be underlying heart waves (electrocardiogram; ECG, EKG) of humans where the model heart waves for healthy or patient (Bradycardia, Atrial Fibrillation or Tachycardia) subjects are obtained in terms of a coupled map. The secular equations are solved using simple algebra since they contain no differential terms. The map can be used to simulate various irregular signals involving random components (possible in Atrial Fibrillation). The results may be considered as in good agreement with the records and the known biological information. Various predictions are made for the physics of the healthy heart waves or causes for the irregular ones. Presenting theoretical plots similar to ECG time series and making comments about the relevant physics may be of vital importance.

Regularities in the human brain waves

Çağlar Tuncay

Poster (Track E)

Various EEG data of healthy or patient humans for different recording regions or brain states are investigated for characteristic differences. Numerous regularities in them are discussed in terms of statistical distributions (the first time in the literature, up to the author's knowledge). The presented approach and the results may be useful for diagnostic purposes.

Mathematical modeling of the locomotion of amoeba

Ryo Kobayashi, Toshiyuki Nakagaki, Akio Ishiguro

Poster (Track E)

Amoeboid motion is widely observed in the single cell movement of eucaryote. In this paper, we concentrate on the locomotion of the naked amoebae which are crawling around on the substrate. An amoeba extends the part of its body to the direction of movement, which is called pseudopod. During the locomotion, contraction of the actomyosin fibers produce a power, a part of the cell is extended, and also sol-gel transformation is taking place. To guarantee the normal amoeboid locomotion, lots of processes are going simultaneously in the coordinated manner. A mathematical model is presented, in which we adopt the combination of the two models of different type, phase field model and smoothed particle hydrodynamics (SPH). Phase field is used for the expression of cell membrane, and SPH used for the expression of cytoplasm. We will demonstrate simulations of our model which reproduce realistic amoeboid locomotions.

Emergent dynamic of individuals living with diabetes

Frances Griffiths, Jeffrey Borkan, Dave Byrne, Ben Crabtree, Antje Lindenmeyer, Michael Parchman, Shmuel Reis, Jackie Sturt

Poster (Track E)

Aim: To explore a novel approach to understanding individuals as open complex adaptive systems for improving the tailoring of interventions for those living with type 2 diabetes. **Design and methods:** Secondary analysis of interview data from 22 adults living with diabetes and participating in a clinical trial of a behavioural intervention for diabetes. Comparative analysis of cases to identify the emergent dynamics of living with diabetes, that is, current patterns of change resulting from the interaction of many aspects of life past, present and future. Further comparative analysis identified biomedical, behavioural and social attributes and explored how these related to dynamics. **Results:** Individuals could be categorised based on how they live with diabetes (not necessarily blood sugar levels) as follows: calm and steady with not a lot of worry and not a lot of change; steady now in comparison with a chaotic or worried past; uneasy, worried and may be chaotic. The latter category included people who had volatile blood sugar levels and people who were otherwise distressed in relation to diabetes. These categories correlated with attributes such as use of routine to control diabetes, sense of control over diet and confidence about diabetes and its management. For attributes including BMI, HbA1c and perceived social support, no pattern could be found that explained the dynamic categories. **Conclusion:** Individual's living with diabetes can be described in terms of their emergent dynamic. This may provide a way of understanding an individual's potential for adaptation and adjustment in relation to diabetes, capturing aspects of life relevant to diabetes that are missed by other assessments. Further refinement of this approach is needed to evaluate its potential use for patient assessment and tailoring of interventions for improved outcome.

Chronic back pain, complexity and time

Griffiths Frances, Jeffrey Borkan, Dave Byrne, Ben Crabtree, Sarah Lamb, Antje Lindenmeyer, Michael Parchman, Shmuel Reis

Poster (Track E)

Back pain that lasts more than six weeks is common but can be difficult to manage. Evidence suggests a range of treatments are somewhat effective but evidence is lacking about how to tailor treatment plans to individual patients. **Aim:** to find a new approach to classifying back pain that will tailor treatment. **Design and methods:** Secondary analysis of interviews from 15 people living with chronic back pain collected at three time points over 12 months. Analysis based on understanding individuals as open complex systems, constantly adapting but with potential for transformation. Analysis involved identifying each illness trajectory, summarising the emergent present at baseline, 6 months and 12 months and classifying individuals by the pattern of change at each time. Focus groups with physicians and physical therapists validated the analysis. **Results:** At base line 10 interviewees were classified as 'stuck and struggling', 3 as 'pain as reminder' and 2 as 'resigned or becalmed'. By 6 months 8 interviewees remained in the same category, 4 changed category from 'stuck and struggling' to either 'pain as reminder' or 'resigned or becalmed', and 3 were lost to follow up. By 12 months a further 5 were lost to follow up, 1 did not change and 6 changed category: 3 from 'stuck and struggling' to another category – 2 to 'resigned or becalmed' and 1 to 'pain as reminder'; 2 changed from 'resigned or becalmed' to 'pain as reminder' and 1 vice versa. **Conclusions:** It is possible to classify individuals with chronic back pain based on their pattern of change at the present time. These patterns change for individuals over time. Different patterns of change may respond to different management. The approach has potential for classifying patients in clinical practice

prior to tailoring their management plan.

Functional Impact of Membrane Domains: Effects of Receptor Clustering

Bertrand Caré, Hédi Soula

Poster (Track E)

Cellular response to changes on external species concentrations in extracellular medium is induced by ligand binding on dedicated membrane receptors. The classical equations for this kind of binding kinetics assume species dilution to be homogeneous. As there is experimental evidence that receptors tend to group in clusters inside membrane domains, we investigated effects of receptor clustering on cellular response. We implemented a model for cell response using a Monte Carlo algorithm for Brownian motion to simulate ligand diffusion. In some simple cases, analytic solutions for binding kinetics of ligand on clustered receptors are provided, and supported by simulation results. Our simulations show that the dose-response curve is shifted to the right: The so-called "apparent" affinity decreases in conjunction with clustering. However, the actual shape of the response goes from the classical hyperbola (with early saturation) toward a more linear one (with late saturation). A cell could then take advantage of receptor clusterization to change and adapt its affinity/sensitivity by functional adaptation of receptor aggregation. In addition, this mechanism could also provide a functional basis for membrane domains.

Node and link roles in protein-protein interaction networks

Sumeet Agarwal, Charlotte Deane, Nick Jones, Mason Porter

Poster (Track E)

A key question in modern biology is how the complexity of protein-protein interaction networks relates to biological functionality. One way of understanding the set of proteins and their interactions (the interactome) is to look at them as a network of nodes connected by links. By studying the structure of this network, we may hope to learn something about the interactome's organisation. Here we attempt to look at different approaches for using network models to assign structural and functional roles to proteins and protein interactions. It has been proposed that highly connected nodes, or hubs, in the interactome fall into two classes, 'date' and 'party', and that these play a key role in the modular organisation of the yeast interactome. This classification was made on the basis of the extent to which hubs are co-expressed with their interaction partners, but was then used to impute to them specific topological roles. We attempt to use purely topological statistics to examine the extent to which these hubs really fall into the roles thus attributed. We use a community detection approach based on maximising modularity to partition the interaction network into functionally coherent modules. We then assign roles to proteins based on how their interactions are distributed within their own module and across other modules. Based on a study of multiple yeast and human datasets, our results suggest that there is little evidence for a clear date/party distinction, but rather nodes in the protein interaction network seem to perform a variety of roles falling along a continuum, and there is no strong correlation between these roles and co-expression. We also examine alternative approaches to studying topological roles. So far, most work has focused on node-centric measures; here we attempt using a betweenness metric to quantify the centrality of links rather than nodes. We show that this measure relates to protein functional similarity as assessed by annotation overlap in the Gene Ontology, and may also be relevant to understanding how the interactome works as a system.

Time-frequency analysis of the human photoreceptor response

Rosita Barraco, Dominique Persano Adorno, Leonardo Bellomonte, Maria Brai

Poster (Track E)

Understanding the features of biomedical signals is essential for improving our knowledge of the complex systems that generate them. This paper applies the wavelet analysis to the study of the early response (a-wave) of the human photoreceptor system in order to provide a description of the response in terms of the characterizing frequencies and times of occurrence. The peculiarities of the a-wave reflect the functional integrity of the two populations of photoreceptors, rods and cones. They are very numerous and exhibit very complex activation dynamics. The results of the wavelet analysis allow us to determine the time-frequency behavior of the early response under various luminance conditions.

Stochastic dynamics of leukemic cells under an intermittent targeted therapy

Nicola Pizzolato, Dominique Persano Adorno, Davide Valenti, Bernardo Spagnolo

Poster (Track E)

The evolutionary dynamics of a complex system of leukemic cells is investigated by using a Monte Carlo method to simulate the stochastic behavior of reproduction and death in a population of blood cells which can experience genetic mutations. We find several scenarios of the dynamics of cancerous cells as a consequence of the efficacy of the different intermittent modeled therapies.

Multi-level modeling of the stochastic growth dynamics of phototrophic biofilms

João Santos, Sofia Antunes, Andreas Bohn

Poster (Track E)

Phototrophic biofilms are mixed microbial communities composed of autotrophic and heterotrophic organisms. Under certain conditions their biomass-growth dynamics is characterized by the random detachment of large portions of biomass, the so-called sloughing events. In the present work we report on the results of a multi-level modeling approaches to this phenomenon, joining several descriptions on diverse levels of abstraction: i) a data model derived from experimental results, ii) a stochastic description of logistic growth with sloughing, and iii) a detailed kinetic model of phototrophic biofilms. We discuss the effects of environmental factors on growth parameters and sloughing frequency and size, and highlight the role of semantic concepts in the integration of data sources and models.

A Methodological Approach for Modeling Multiscale Complex Systems

Alfons Hoekstra, Eric Lorenz, Alfons Caiazzo, Jean-Luc Falcone, Bastien Chopard

Poster (Track E)

We present a methodology for modelling multiscale complex systems and apply it to the case of in-stent restenosis in coronary arteries.

Executing Multicellular Development: Quantitative Predictive Modelling of *C. elegans* Vulva

K. Anton Feenstra, Nicola Bonzanni, Elzbieta Krepska, Wan Fokkink, Thilo Kielmann, Henri Bal, Jaap Heringa

Poster (Track E)

Understanding the processes involved in multi-cellular pattern formation is a central problem of developmental biology, hopefully leading to many new insights, e.g., in the treatment of various diseases. Defining suitable computational techniques for development modelling, able to perform in silico simulation experiments, is an open and challenging problem. Here we apply the coarse-grained, quantitative approach based on the basic Petri net formalism we introduced previously to mimic the behaviour of the biological processes during multicellular differentiation. We show that for the well-studied process of *C. elegans* vulval development, our model correctly reproduces a large set of in vivo experiments with statistical accuracy. It also generates gene expression time series in accordance with recent biological evidence. Finally, we modelled the role of microRNA mir-61 during vulval development and predict its contribution in stabilising cell pattern formation.

Use of a model biochemical system for lipid peroxidation in phosphatidylcholine liposome suspensions

Anatole Ruslanov, Anton Bashylau

Poster (Track E)

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A significant number of human diseases develop to a large degree via activation of free-lipid peroxidation (LPO). Pharmacological correction of such pathological processes is conducted using natural and synthetic antioxidants (AO). Therapies that include the utilization of AO is a growing application in the treatment of such diseases. Therefore, quantitative assessment of total antioxidant activity (AOA) of complex products and their effective concentrations has become an issue of key importance. Important in this regard is assessment of AOA using modeling systems of lipid peroxidation in vitro. Using these modeling systems, we can detect the presence of AOA in chemical compounds. We conducted a biochemical screening of substances with different chemical nature with the aim of identifying of their AOA and clarifying the features of their AOA; we used a model system based on the phosphatidylcholine liposome suspension under varying duration of the liposome oxidation in vitro. Prolonged oxidation of liposomes (24 hours or more) resulted in finding the AOA features of these substances, which are not detected at small durations of the LPO. Effectiveness of the studied pharmacologically active substances' AOA changed greatly in the long-running process of lipid peroxidation in liposomes. The AOA depended on the chemical nature of the AO, its concentration, and intensity of lipid peroxidation, which was determined by the method of

initiation of the liposome oxidation. The lipophilic AOs more efficiently suppressed the accumulation of carbonyl products of lipid peroxidation in the liposomes under autooxidation than with the Cu²⁺-induced oxidation. The AOA of the lipophilic AOs reached a maximum at the later (24 hours) stages of oxidation. The lipophilic substances that contained unsaturated bonds exhibited maximal efficiency in the early stage of lipid peroxidation (1 hours of oxidation), and their AOA under Cu²⁺-induced oxidation was more pronounced than in autooxidation. The sulfur-containing hydrophilic AOs most efficiently suppressed lipid peroxidation in the early stage of the process (1 hour of oxidation). In the later stages, the AOA of such substances disappears. Carboxylic acids that are capable of forming complexes with metal cations exhibited both antioxidant and prooxidant action—depending on their concentration and the conditions of the lipid peroxidation process. The most effective AOA of the chelating carboxylic acids was recorded at an average duration of oxidation (3 and 6 hours). The inversion of the antioxidant action of the chemical compounds into the prooxidant action was observed in the later phases of lipid peroxidation (oxidation of the duration of 3 hours or more after the initiation of oxidation). The manifestation of such inversion depended on the chemical nature and concentration of AO, the intensity of the lipid peroxidation reactions, and the method of liposome oxidation initiation. In general, the results we obtained indicate that the use of a model biochemical system for lipid peroxidation in phosphatidylcholine liposome suspensions can identify the particular AOA of the AOs of various chemical structures as a function of the intensity and duration of the lipid peroxidation reactions. It was found that substances with a specific mechanism of action also exhibit a specific relation of their AOA on the duration and intensity of the liposome oxidation. We found the phenomenon of transformation of the antioxidant action into prooxidant action as a function of the duration of the period of the lipid peroxidation process. It is important to note that the inversion of antioxidant into prooxidant properties was typical of AOs of different chemical natures and the different mechanism of action. Such an inversion has been identified by us from the lipophilic compounds, substances with saturated C=C-bonds, thiols, and carboxylic acids that form complexes with metal cations of transitional valency. Keywords: antioxidant activity, free-lipid peroxidation, antioxidants.

A virtual cell culture of T-helper lymphocytes

Luis Mendoza

Poster (Track E)

There is a wealth of cellular and molecular information regarding the differentiation of T-helper cells, as well as results of in vitro experimental treatments that modify the normal differentiation process. With the aid of such publicly available information, I inferred the regulatory network that controls the differentiation of T-helper cells. Such network was converted into a continuous dynamical system in the form of a set of coupled ordinary differential equations. The system has a set of fixed point attractors, but the basins of only five of them cover most of the state space. These attractors correspond to the activation states observed experimentally for the precursor (Th0), and effector (Th1, Th2, Th17 and Treg) T-helper cells. Moreover, the model is able to describe the differentiation from a precursor to an effector type due to specific molecular signals. Then, taking a network as a representation of a single cell, I constructed a model of a cell culture where cells respond to and produce different molecular signals. The dynamical behavior of this virtual cell culture was analyzed, showing that it leads to cultures containing subsets of undifferentiated and differentiated cells in appropriate proportions. This model will allow to study the mechanisms leading to imbalances of T-helper populations, which is the cause of several immune disorders.

Dynamics of translating ribosomes: a mean field approach

Luca Ciandrini, Ian Stansfield, Maria Carmen Romano

Poster (Track E)

The translation of the messenger RNA (m-RNA) chain is the final step of protein synthesis. This process, primarily controlled by the dynamics of ribosomes along the m-RNA chain, bears a resemblance to a one-dimensional driven lattice gas. For this reason, the m-RNA translation inspired a statistical-mechanical class of models known under the name of Asymmetric Simple Exclusion Processes (ASEPs) which consider hopping particles or hard rods (the ribosomes) on a lattice (the polynucleotide chain). Although this approach is extremely interesting from a theoretical point of view, it is however not very realistic since it comprises the whole ribosome's biochemical cycle in one single step. In this work we extend this class of models and take account of two fundamental steps of the ribosome's biochemical cycle following a "coarse-grained" perspective. In order to achieve a better understanding of the underlying biological processes and compare the results with experiments, we want to provide a description laying between the minimal ASEP-like models and the (analytically hard to treat) more detailed models,. We use a mean field approach to study the dynamics of particles with associated an internal variable assuming two different value (according to the main biological processes involved). In this framework it is possible to analytically characterize the critical points among different phases of the system (high density, low density or maximal current phase). We underline the differences and the similarities of this model's outcomes to the well known results of previous models. Finally, we propose experiments to compare with and suggest the following direction of this research.

Emergence of complexity in the RNA world

Julien Derr, Michael Manapat, Martin Nowak, Irene Chen

Poster (Track E)

The RNA world hypothesis[1] suggests that life based on DNA molecules arose from a preexistent world where genetic information would have been stored on RNA. How did the RNA world, based only on chemical reactions, achieve the ability to self-replicate? A common belief[2] is that chemical activity in a prebiotic soup composed of single nucleotides would generate a pool of polynucleotides, possibly containing a subset of self-replicating sequences. Nevertheless, estimates of finding catalytic sequences in such a random pool are very low and are spread on a huge range (decades of orders of magnitude[3]).

Here we investigate the emergence of complexity, going from single nucleotide monomers, to a complex polymer exhibiting catalytic activity. Our approach is to analyze the influence of the different basic physical mechanisms on the complexity of the pool of sequences. The mathematical model is inspired from the "prelife" situation[4]. It consists of one bath of nucleotides polymers which undergo three different kinds of reactions. (1) Concatenation: the 5' end of a polymer (head) can bind to the 3' end (tail) of any other polymer. (2) Hydrolysis: Each phosphodiester bond has a probability of hydrolysis expressed by a constant rate. (3) Template directed ligation: The last effect taken into account in this model is the ability of hydrogen bonds to stabilize complementary fragments on a template. If two adjacent fragments are stabilized this way, their binding can occur with a given ligation rate.

The poster discuss our partial analytical understanding of the system as well as results of corresponding stochastic simulations. We also discuss the major results which are the increase of sequence complexity with both concatenation and ligation. We discuss the biological implications or our results, as well as limitations and possible improvement of this model.

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Networks in nuclear dynamics. Nuclear Pore Complexes

Jonás Carmona, Eduardo Ródenas, Peter Askjaer

Poster (Track E)

Nuclear Pore Complexes are highly conserved protein structures that mediate communication between the nucleus and the cytoplasm. Networks provide the infrastructure for communication, production and transportation; and they are a necessary and complementary approach to the traditional point of view (from function to structure) in nuclear dynamics.

We are building three models and plan to perform experiments to understand and predict the distribution of the network (power law or exponential distribution); networks of module regulation with microarray databases; and candidate nuclear pore complex components (nucleoporins) in the nematode *Caenorhabditis elegans* (23 nucleoporins currently known vs 30 in yeast, fruit fly and human).

- Distribution of the network (Error and attack tolerance experiments). For 30 proteins, the nucleoporins, or 100 proteins by including proteins known or predicted to interact with the nucleoporins. Analyze the fraction removed (using RNA interference) vs diameter of the network (analogy with induced embryonic lethality). Our prediction is that the nuclear pore complex has an exponential distribution, and the nuclear pore complex plus interacting proteins a power law distribution with exponential cut off. With these results we are also studying the subcomplexes vs fragmentation process. In one of the silico models we need to know the distribution to infer the links between the nodes and in that way predict new connections for a functional analysis.

- With temporal data from the various life stages of *C. elegans* (from Wormbase and Stanford array databases; in eggs, larval L1, L2, L3, L4 and adults) and also from the different phases of the cell cycle in the larval stage (from microarray experiments in our lab), we are grouping them by similarity in expression pattern, and inferring the regulatory relationships between the groups; creating a network of the entire set of genes in *C. elegans*. The same can be done for the NPC set of genes (NPC + regulators) more specifically. We expect to get a general view of gene expression regulation in the nematode, which will also allow us to make evolutionary comparisons with data published on mouse cells. And at the same time infer the function of unknown genes based on genes with which they are correlated.

- If the structure is conserved the topology must be the same. Even if there are only 23 nucleoporins identified so far and we think there must be 30 proteins in the *C. elegans* nuclear pore complex because it is a highly conserved structure, to predict the missing proteins an important tool is to characterize the network (Density, degree, path length, clustering coefficient, node centrality measures).

Finally our goal is to learn and understand nuclear dynamics from a conceptual, integrated and complex point of view from which we will be able to develop new models, techniques and results.

The CoSMoS Process: Simulations for Scientific Exploration

Paul Andrews, Susan Stepney, Jon Timmis, Fiona Polack, Adam Sampson, Peter Welch, Frederick Barnes

Poster (Track E)

The use of computer simulations to investigate the behaviour of complex systems is an increasingly common discipline. We present here the outline of a process (the CoSMoS process) we are developing to aid and guide the construction of such simulations.

Avoidable emergency admissions - a complex systems problem with IT solutions?

Carmel Martin

Poster (Track E)

Avoidable emergency care for ambulatory care sensitive conditions, particularly hospital admissions and visits to accident and emergency departments, is a major challenge to health care systems, internationally. This poster makes the case for a complex systems perspective on the problem and argues that translation of complexity science theory and research findings with IT solutions are a way forward to address these challenges. A pilot study is in progress. The Problem Ambulatory or primary care sensitive conditions (ACSCs) are those conditions for which hospital admission could be prevented by interventions in primary care. The problem of (ACSCs) is increasing in size, as the population ages, underscores the importance of developing, adopting and implementing innovative programs. The predisposing factors for risk of avoidable admissions have been identified in different practice populations. There is a circumscribed patient group, often older with multiple morbidity, at high risk of avoidable hospital admission, accident and emergency attendance and out of hours home visits irrespective the disease group, however, predicting the timing and triggers for admission have challenged health service planning. Active clinical interventions that have been shown to work to prevent hospitalisation in multiple morbidity patients either prevent the onset of condition, control an acute episodic illness or condition, or manage a chronic condition. Many programs have been designed to improve the care and outcomes of elderly patients with chronic illnesses and psychosocial challenges, yet they have had variable success and are often not cost-effective. Older patients frequently experience chronic illnesses that generally require ongoing, coordinated care from multiple clinical disciplines. In the elderly, chronic illness is often accompanied by psychosocial challenges including loneliness, depression, and isolation. In addition, elderly patients often experience limitations in performing their daily activities. As many of the innovations indicate, the US and most other health care delivery system are not designed to meet these challenges. Intensive levels of medical and social service care and support for the patient and family caregivers are needed from multiple agencies. More research is also needed to guide design decisions to match program features to each target population and delivery setting (given its resources, constraints and structure). Greater emphasis on measuring costs and benefits is also needed to support policy and management decisions regarding program design, implementation and payment. A Complexity Conceptual Framework for the Problem Addressing the multiple dynamics and interdependencies underpinning an individual's decline in health across the physical, psychological, social domains can be approached using a complexity framework. Chronic care must work with individuals and their meanings, and their challenges in adaptability to varied and varying landscapes of internal and external changes. Chronic care is not static, but a dynamic progression among different phases of care and states of health, that are stable, complicated but stable, complex and on the edge of chaos. The inverted u shaped curve appears to reflect underlying processes of homeostasis in human health, and should inform interventions to promote the sustaining of energy (health) and delay or ameliorate the dissipation of resilience to disease and illness (loss of energy). Adaptation, homeostasis ageing, illness and disease Discernible phases or patterns can be identified across longitudinal health states: Simple or stable phases are when the aim is to slow the progress of risk factors, single disease or a disease cluster and optimise quality of life – e.g. raised cholesterol, high blood pressure, pre-diabetes or diabetes. Complicated phases of chronic care occur when there are multiple factors with multiple morbidity, which may be: disease based; or include physical, psychosocial and environmental components; and when the aim is to balance self-care, health and pharmaceutical interventions and health related co-morbidity. Complex phases (dynamic, changing) may move to edge of chaos with acute or sub acute-on-chronic, exacerbations, flares due to potential destabilization in physical and psychosocial environment components; self-care, health and pharmaceutical interventions or health related co-morbidity. They may shift to a pre-terminal phase, frailty, risk of falls, depression, and disease flare. People in this phase of care probably incur 80% of health

care expenditure many through an ACSC. Chaotic phases (out of control) occur when diseases, symptoms or psychosocial or environmental factors ‘blowout’ for example falls, diabetes poor control, severe pain, shortness of breath, diagnosis of cancer, rheumatoid, mental health crisis. When a chaotic health state emerges, an ACSC almost invariably occurs. People in this phase of care generally incur 95% of health care expenditure – often in expensive hospitalization and re-hospitalization and high technology treatment. A complexity and IT enabled solution Because of the unpredictability of the timing of triggers and enablers of decline and the individual trajectory towards an ACSC adverse event, real time intervention around early detection of triggers and enablers of decline must be used. Such an approach has to deal with false positives and rapid progression and thus artificial intelligent agents need to track the presence and absence of monitoring and the progress and intensity of change when monitoring takes place. The starting point for IT-enabled systems design to intervene in complex and chaotic is early detection by the individual, their caregiver of family or the primary care team. User driven smart systems based on smart phone technology would seem a suitable starting point for the identification of early phases of destabilisation, and followed by alerting of real TIME information systems through layered and staged approaches. An IT enabled system with user and care giver 12 hourly or daily self monitoring and narrative recording with feedback to achieve stabilization of self-care, health and pharmaceutical interventions in general worsening health, new symptoms, disease flare-ups, complications such as infections, emotional support needs. The Future Developing and piloting a complex systems intervention to prevent avoidable ACSCs is in progress.

Modelling Emergent Microbial Communities in the Human Gut

Helen Kettle, Harry Flint, Grietje Holtrop, Petra Louis, Glenn Marion

Poster (Track E/EPSRC Showcase)

The growth of hundreds of different strains of bacteria during fermentation in the human gut presents a complex system which plays an important role in human health. For example the production of certain compounds, e.g. butyrate, are thought to protect against cancer of the colon. Recent scientific advances have enabled the identification of the roles played by different groups of bacteria and the subsequent classification of key bacterial functional groups (BFGs). The system maintains high levels of biodiversity since the fermentation products of one BFG may enable the growth of another BFG and so on, leading to a highly connected sustainable network. Here we model the emergent composition of the microbial community by simulating the growth of 200 bacterial strains shared between ten BFGs. Based on expert knowledge, for each BFG we define its metabolic pathways – i.e., which dietary substrates it may grow on and which metabolites (fermentation products) it may consume or produce. However, the values of the parameters controlling the rates of change along these pathways remain largely unknown. Thus these parameter values are generated randomly, from uniform distributions within ranges appropriate to the BFG, for each bacterial strain. The growth of the generated population and nine metabolites on five different dietary substrates is simulated by the numerical solution of ordinary differential equations representing a two compartment model of the human left and right colon. The simulation is run until it reaches steady state and then the process is repeated for another stochastically generated population. In total, 100 different populations, each containing 200 bacterial strains, are generated and their emergent properties compared with characteristic behaviour observed in vitro and in vivo. Using this approach a variety of different model experiments are then undertaken to investigate connections between diet and microbial community composition.

Models of herd behaviour of consumers at a binary choice

Mark Voronovitsky

Poster (Track F)

Abstract We shall consider three models of collective behavior [7]-[9], which are justified logically. These three models of binary choices are connected with three models of herd behavior which was considered by other authors [1]-[4] but differ from them by mathematical approach and results. We consider the mechanism of the choice of a separate participant as a base of the behavior of the collective. We consider also the arising of herd behavior as a process, which flows in sequential moments of time. Therefore we consider the stationary distribution of probability of the choice of participants, if it exists. We gave the mathematical definition of herd behavior of participants and investigated conditions of existence of such behavior. The following models was investigated: the model of the binary choice of the collective in the case of exchange of information between pairs of consumers, the model of the binary choice by queue of Bayes consumers and the model of binary choices of participants when each of them uses the same information. We consider these models with different volumes of information of participant and can see that possibility of herd behavior of participants is more than more is volume of information which each participant receives.

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A Combined Theoretical and Experimental Approach to Goal-Oriented Herds of Internet Crawlers

Katalin Anna Lázár, Erzsébet Csuhaaj-Varjú, András Lörincz

Poster (Track F)

In this paper, we present an approach to the behaviour of the complex system of cooperating and communicating Internet crawlers. We equip a grammar systems theoretic construction with regulated rewriting devices to describe the information harvest of the crawlers. Our aim is to illustrate the wide range of applicability of the regulated rewriting devices in the field of web crawling techniques. We demonstrate that rather simple component grammars suffice to reach universal computational power. We also examine the extent to which communication makes a goal-oriented community efficient in different topologies through simulations.

Mapping Directed Networks

Jonathan J. Crofts, Ernesto Estrada, Desmond J. Higham, Alan Taylor

Poster (Track F)

We develop and test a new mapping that can be applied to directed unweighted networks. Although not a "matrix function" in the classical matrix theory sense, this mapping converts an unsymmetric matrix with entries of zero or one into a symmetric real-valued matrix of the same dimension that generally has both positive and negative entries. The mapping is designed to reveal approximate directed bipartite communities within a complex directed network; each such community is formed by two set of nodes S1 and S2 such that the connections involving these nodes are predominantly from a node in S1 and to a node in S2. The new mapping is motivated via the concept of alternating walks that successively respect and then violate the orientations of the links. Considering the combinatorics of these walks leads us to a matrix that can be neatly expressed via the singular value decomposition of the original adjacency matrix and hyperbolic functions. We argue that this new matrix mapping has advantages over other, exponential-based measures. Its performance is illustrated on synthetic data, and we then show that it is able to reveal meaningful directed bipartite substructure in a network from neuroscience.

Modelling the genetic dynamics of antigenic diversification of trypanosomes using Neyman-Scott cluster processes

Erida Gjini, Daniel T. Haydon, Christina Cobbold, J. David Barry

Poster (Track F)

This paper proposes a mathematical model based on spatial point processes, for the simulation and estimation of parameters involved in the antigenic diversification of trypanosomes. We want to investigate which are the parameter combinations of the constituent processes underlying evolutionary dynamics, like gene conversion and point mutation, that enable a stable and functional distribution of pairwise homologies in the antigenic archive.

Influence of noise and effect of time-delayed interactions on the synchronization of the stochastic Kuramoto model

Karen G. Petrosyan, Bidhan C. Bag, Chin-Kun Hu

Poster (Track F)

We consider the Kuramoto model of globally coupled phase oscillators subject to Ornstein-Uhlenbeck and non-Gaussian colored noise and investigate the influence of noise on the order parameter of the synchronization process [1]. We study numerically the dependence of the threshold as well as the maximum degree of synchronization on the correlation time and the strength of the noise, and find that the threshold of synchronization strongly depends on the nature of the noise. It is found to be lower for both the Ornstein-Uhlenbeck and non-Gaussian processes compared to the case of white noise. A finite correlation time also favors the achievement of the full synchronization of the system, in contrast to the white noise process, which does not allow that. We also consider the stochastic Kuramoto model with time-delayed interactions and study the interplay between the influence of the finite time correlation of noise and the time delay on the synchronization process. Finally, we discuss possible applications of the stochastic Kuramoto model to oscillations taking place in biochemical systems.

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The Laplacian, Stability and Synchronisation in the networked Kuramoto model

Alexander Kalloniatis

Poster (Track F)

The Kuramoto model for one-dimensional phase oscillators connected on a finite network is considered. The problem is presented in terms of the spectrum of the combinatorial Laplacian. Stability is distinguished from synchronisability. The former is seen to occur sequentially, in the vicinity of the synchronised state, from the highest to lowest Laplacian eigenmodes. By going beyond the leading order approximation about the synchronised state in the interaction term we find a critical coupling for synchronisation to be stable, above which appear genuine instabilities and periodic behaviour in the lowest Laplacian mode. Drawing on existing numerical results in the literature and the properties of the Laplacian from the perspective of Laplace-Beltrami theory, we present a conjecture that pictures the onset of synchronization as a sequential de-excitation of structures in the graph corresponding to decreasing eigenvalues of the Laplacian. The structures participating in this process are identified with those probed by the corresponding Laplacian eigenvectors. We explore the consequence of this conjecture for the Kuramoto model on a complete graph and point out a subtlety in extrapolating to an infinite network.

Evolving Sound Communication in a Robot Society

Andrew Guest

Poster (Track F)

The Emergence of Artificial Culture in Robot Societies project explores how cultural behaviour begins, by observing behaviours that emerge from a swarm of evolving, imitating robots. One aspect of this is that each robot should be able to imitate the actions and sounds of the others. Two robots, each taking turns imitating the sounds made by the other, is conceptually easy to visualise. However, when multiple robots are making sounds simultaneously, determining what an imitating robot should do is much more complex.

While imitating the aggregated sound of the swarm is possible, this project requires that a given listening robot be able to distinguish one robot from all others. In effect there is a requirement for one robot to be able to carry on a 'conversation' with another robot even in the cacophony caused by (potentially) dozens of robots making sounds at the same time. Of course, humans possess the remarkable ability to follow a conversation they are having with one person even when there are many other people having many other conversations in the same room. This is known as 'The Cocktail Party Effect'.

This poster describes an approach, which uses advanced signal processing, to provide the robots with a mechanism that counteracts the cacophony of the cocktail party and architecturally allows for the implementation of a learning/evolutionary system that provides the opportunity for the study of the evolution of the same functionality.

Each robot will have a distinct frequency for which it creates sound. Rather than communicating using different sounds the robots will use patterns of sound pulses where the number of pulses, the length of pulses and the length of gaps between pulses can vary. Some patterns will be easier to imitate than others, patterns difficult to imitate will be copied badly leading to them either being dropped from the pool of sound patterns or evolving into a pattern which is more easily imitated. This poster describes the approach taken to implement this system.

Retrieving connectivity in complex networks of long range dependent stochastic processes

Pierre-Olivier Amblard, Sophie Achard, Jérôme Lemoine, Cédric Gouy-Pailler

Poster (Track F)

The paper considers long range dependent processes which are correlated. The structure of correlation is supposed to be described by a complex graph which is unknown. The paper proposes a methodology to retrieve the graph connectivity from the measurements of the stochastic processes. It relies on a joint use of the wavelet decomposition (in order to deal with long range dependence) and the partial correlation coefficients (in order to eliminate ghost links found by correlation analysis). The method is illustrated on some simple toy problems as well as a problem of brain connectivity measured from fMRI data.

Analysis of the Linearised Phase Space Flow using Singular Value Decomposition applied to the Core Model for Ca^{2+} -oscillations.

Tim Johann, Sven Sahle

Poster (Track F)

Similar to the concept of local Lyapunov characteristic exponents, the singular value decomposition (SVD) of the linearised phase space flow (LPSF) will give information of the local deformation of phase space volume. Besides the singular values, SVD also yields the principal axes (PAs) of the deformation imposed by the LPSF matrix, thus providing details of the spacial behaviour of proximate trajectories.

We investigated the orientation of the PAs corresponding to the largest and smallest singular values of the LPSF in the core model for oscillations in calcium signalling with a fixed set of parameter values. This system is a reduced model consisting of only three components (a, b, c), with 8 reactions, involving activation, constant flux, Michaelis-Menten, and Henri-Michaelis-Menten kinetics. With the parameter set used, the system will exhibit a stable limit cycle and one unstable fixed point.

The LPSF, given by the matrix $R = \exp(J\delta t)$, with $J = D_x f(x)$, was decomposed into singular values and corresponding PAs. We call the principal axis of the unit sphere which is mapped to the longest axis of the resulting ellipsoid of the image of R the largest PA and define the smallest PA accordingly.

We found that for most of the phase space volume covered by the limit cycle, the largest and smallest PAs are oriented parallel to the a-c plane, leaving the remaining PA parallel to the b-axis and rendering the change of orientations independent of the b component. Furthermore, an approximately cylindrical symmetry around a parallel of the b-axis is observed, with largest PAs oriented radially.

The feature of a bottleneck coincides with minimal values of either singular values in and around this region, and a limiting surface can be explained by the interplay of velocity vector with largest and smallest PAs.

We want to motivate the application of singular value decomposition of the flow and analysis of the principal axis distribution as means to investigate the dynamics of chemical systems, in particular with larger networks. A general outline of this future work will also be presented.

Bound Electron Waves

Christopher Johns, Anthony Booth, Mark Leeson, Keith Bowden

Poster (Track F)

A closed process cycling through coupled equations is used to model the wave representation of bound electrons. Solutions are approached by iterating through the causal calculation cycle for the respective arrays in turn. The wave solutions (based on a modulated Klein-Gordon equation) appear to offer an

attractor system with spontaneous quantisation properties. It is hoped that this approach to a continuum electron field model will eventually enable improved design calculations such as in the engineering of semiconductors.

Understanding Observed Complex Systems – the hard complexity problem

Bruce Edmonds

Poster (Track F)

Two kinds of problem are distinguished: the first of finding processes which produce complex outcomes from the interaction of simple parts, and the second of finding which process resulted in an observed complex outcome. The former I call the easy complexity problem and the later the hard complexity problem. It is often assumed that progress with the easy problem will aid process with the hard problem. However this assumes that the “reverse engineering” problem, of determining the process from the outcomes is feasible. Taking a couple of simple models of reverse engineering, I show that this task is infeasible in the general case. Hence it cannot be assumed that reverse engineering is possible, and hence that most of the time progress on the easy problem will not help with the hard problem unless there are special properties of a particular set of processes that make it feasible. Assuming that complexity science is not merely an academic “game” and given the analysis of this paper, some criteria for the kinds of paper that have a reasonable chance of being eventually useful for understanding observed complex systems are outlined. Many complexity papers do not fare well against these criteria.

Measuring Complexity in Multi-Agent-Based Simulations

António Fonseca, Jorge Louçã

Poster (Track F)

The quantitative analysis of multi-agent-based simulation results is generally performed through statistical computation. However, statistical measures lack the ability to capture the dynamic nature of simulations. We propose the use of two alternative dynamic measures of complexity, entropy density and excess entropy, to analyse the results of multiagent simulations. The application of these two measures is tested using the minority game model. The test confirms that measuring excess entropy and entropy density for a multiagent-based simulation may complement analytical results. In addition, the use of the two measures allows the detection of emergent behaviours in multi-agent simulations. Finally, the application of complexity measures may prove to be useful in validating simulation models.

Stable Solutions to the Social Choice Problem: Dominant, Weakly Stable, Uncovered Sets and their Extensions

Andrey Subochev

Poster (Track F)

Social Choice problem is defined for a finite number of alternatives, over which a finite number of agents have preferences. Individual preferences of each agent are binary relations on the set of alternatives. Solution to the problem is a rule determining an alternative(s), which is(are) the “best” to the group. The so called Condorcet winner, an alternative that is more preferable for the majority of agents than any other alternative in pairwise comparison, is usually regarded as the best choice. However a Condorcet winner is absent in general case. Numerous attempts were made to extend the set of chosen alternatives up to a certain always non-empty subset of the universal set, defined through majority relation, where alternative a is preferred to an alternative b, if majority of actors prefers so. Being different incarnations of an idea of optimal social choice this solution sets enable one to compare and evaluate social choice procedures. Also,

when there is a connection of a solution set with a particular procedure, this solution helps to reduce the number of potential collective choices, i.e. enables one to make predictions with respect to choice results. In the present report for such class of majority relation as tournaments (i.e. complete and asymmetric relations), three solution concepts are considered: the uncovered set, the minimal weakly stable set and the minimal dominant set (top cycle). The main results presented are the following. 1. A criterion to determine whether an alternative belongs to a minimal weakly stable set is found. It establishes the logical connection between minimal weakly stable sets and covering relation. 2. The concept of stability is employed to generalize the notions of weakly stable and uncovered sets. New concepts of k -stable alternatives and k -stable sets are introduced and their properties and mutual relations are explored. 3. A concept of the minimal dominant set is generalized. It helps to establish that in general case all dominant sets are ordered by strict inclusion. In tournaments the hierarchies of the classes of k -stable alternatives and k -stable sets combined with the system of dominant sets constitute tournament's structure ("microstructure" and "macrostructure" respectively). This internal structure may be treated as a system of reference, which is based on difference in degrees of stability.

Competitive induced resonance

Teresa Vaz Martins, Ana Majtey, Raúl Toral

Poster (Track F)

We study a bistable ϕ^4 model composed by units coupled through both attractive and repulsive links. This system is subjected to a subthreshold signal, and we observe that the response is enhanced for a given fraction of repulsive links. Competitive interactions are taken as a source of disorder, as an alternative to previous studies where response was amplified by disorder induced by noise or diversity. Resorting to numerical simulations and analytical calculations we propose a 'macroscopic mechanism of resonance, considering the effect of disorder on the stationary state distribution, in the absence of signal.

Effects of disease awareness on population structure

Stefan Wieland

Poster (Track F)

The spreading of diseases with the possibility of reinfection, covered by SIS dynamics, can be modelled on adaptive contact networks, where susceptibles try to evade infection by changing their contact patterns depending on the disease status of their neighbours. This interplay of disease dynamics and network alteration adds new phases to the standard SIS model (Blasius et al. 2006, Gross & Kevrekidis 2008) and, in the endemic phase, lets network topology settle down to a characteristic state. This final endemic state does not depend on the initial network topology, but rather on the two essential system parameters. We investigate those final topologies for each relevant phase of the system.

Self-organisation of two-mode stochastic oscillators

Alexander Nikitin, Nigel Stocks

Poster (Track F)

The collective clapping of spectators can be modeled by globally coupled two-mode stochastic pulse oscillators. Every oscillator in the model can oscillate with one of two rhythms. The switching between modes in the individual oscillator happens due to an interaction with other oscillators. For some parameters the global response has almost periodic oscillations. This self-organization in the clapping can be explained by two different phenomena: synchronization and self-modulation. To find the answer to the question: 'Is it synchronization?', we investigate the dynamics of the model and select an appropriate

measure of synchronization. Since the concept of the phase synchronization cannot be applied usefully in our case, we introduce an alternative measure based on the the integral of the coherence function. Since the behavior of the coherence coefficient satisfies our intuitive conception of synchronization, we are incline to the idea the studied self-organization phenomena can be interpreted as a form of synchronization.

Optimal Control of Electrostatic Self-Assembly of Binary Monolayers

Nickolay Shestopalov, Graeme Henkelman, Charles Powell, Gregory Rodin

Poster (Track F)

In this work, a guided approach to self-assembly of binary monolayers of spheres is considered. An annealing schedule is used to guide the system into a highly ordered state. Optimal annealing schedule based on a single rate-controlling mechanism and derived using classical optimization methods is proposed. The results of molecular dynamics simulations demonstrate that the optimal schedule outperforms commonly used simulated annealing schedules when the rate-controlling mechanism is captured correctly.

Modelling burstiness in the complex magnetosphere using Linear Fractional Stable Motion

Nicholas Watkins

Poster (Track F)

The Earth's magnetosphere is quite clearly "complex" in the everyday sense. However, in the last 15 to 20 years there has been a growing thread in magnetospheric physics using and developing some of the emerging science of complex systems. A particularly well-studied set of system properties has been derived from those used in the study of critical phenomena, notably correlation functions, power spectra, distributions of bursts above a threshold, and so on. These have revealed behaviours familiar from many other complex systems, such as burstiness, long range dependence, heavy tailed probability distributions and so forth. The results of these studies are typically interpreted within existing paradigms, most notably self-organised criticality. However, just as in other developing areas of complexity science, it is increasingly being realised that the diagnostics in use have not been extensively studied outside the context in which they were originally proposed. This means that, for example, it is not well established what the expected distribution of bursts above a fixed threshold will be for time series other than Brownian (or fractional Brownian) motion. This poster describes some preliminary investigations into the burst distribution problem, using Linear Fractional Stable Motion as a controllable toy model of a process exhibiting both long-range dependence and heavy tails. A byproduct of the work was a differential equation for LFSM, which we also briefly discuss. My work in this area has been done with many colleagues, but I would particularly like to thank Mervyn Freeman and Sandra Chapman for collaboration over many years, and Dan Credginton, David Riley and Sam Rosenberg for their work while summer students with BAS.

Growth-induced mass flows in fungal networks

Luke Heaton, Nick Jones, Eduardo Lopez, Philip Maini, Mark Fricker

Poster (Track F)

Cord-forming fungi form extensive networks that continuously adapt to maintain an efficient transport system. As osmotically driven water uptake is distal from the tips and aqueous fluids are incompressible, we propose that growth induces mass flows across the mycelium, whether or not there are intrahyphal concentration gradients. To explore this hypothesis we imaged the temporal evolution of networks formed by *Phanerochaete velutina*, and at each stage calculated the unique set of currents that account for the observed changes in cord volume, while minimising the work required to overcome viscous drag. Predicted

speeds were in reasonable agreement with experimental data. Furthermore, cords that were predicted to carry fast moving or large currents were significantly more likely to increase in size than cords with slow moving or small currents. Given the further assumption that *P. velutina* has evolved to reduce the work needed to overcome viscous drag, we should expect to see thickening in the high current cords. This follows because where there is a distribution of currents, significantly greater energy savings can be made by preferentially thickening the high current cords. In conclusion, we note that the incompressibility of the fluids within fungi ensures that there is a rapid global response to local fluid movements. Furthermore, velocity of fluid flow and nutrient concentration are both local signals that can convey quasi-global information about the role of a cord within the mycelium. These observations support our hypothesis that mass flows in fungi can be partly understood as a consequence of fluid incompressibility, osmotic water uptake and growth. We also suggest that local responses to flux density and nutrient concentration might govern the development of these remarkable self-organizing, efficient, adaptive, growing transport networks.

Emergence of local ergodicity from the space-time properties of Lyapunov vectors

Jason R. Green, David J. Wales, R. Stephen Berry

Poster (Track F)

Tangent space basis vector fields, Lyapunov vectors, are fundamental objects of chaotic dynamical systems. Two bases used in numerical calculations, the Gram-Schmidt vectors and the covariant Lyapunov vectors, are propagated with numerical trajectories of a Hamiltonian dynamical system, the Lennard-Jones trimer. Space-time properties measuring stability and localization characterize each vector set and probe the tangent space directions important to the system's evolution. The tangent vector directions and their properties further elucidate the emergence of local ergodicity in this model of an atomic system and an improved estimation of the separate time scales involved.

A multi-agent approach for biological models cooperation

Nadia Abchiche, Fariza Tahi

Poster (Track F)

Several formalisms and approaches exist for mathematically modeling biological processes. The same process can be modelled using different formalisms. Each obtained model could be considered as a "point of view" of the biological model, or an "approach" for studying *in silico* the biological process. It is therefore interesting to be able to make cooperating different mathematical modeling of the same biological process, in order to display behaviors that could not be seen in single model. For this purpose, we propose a multi-agent approach for implementing this cooperation. We have experimented our approach on a well known biological example, the bacteriophage lambda. The bacteriophage lambda is a virus which infects *Escherichia Coli* bacteria. It is considered as a very simple organism and has been greatly studied. In this abstract, we show with a small example, how a deterministic model and a stochastic model of the genetic switch of the phage, cooperate in order to deal with rare chemical reactions and frequent ones according to their relevance.

Experimental and simulation analysis of planar impact brittle material

Filipe Santos, Raul Donangelo, Sergio Souza

Poster (Track F)

In this work we present and discuss experimental results on some observables measured on the fragments created in a well-controlled planar impact experiment. Plates made from two amorphous brittle materials, ceramics and glass, were used as targets. We also present the numerical results of a model for

two-dimensional fragmentation. The simulated results have good agreement with the collected experimental data. We have found that although both materials have similar structural properties, their fracture mechanisms appear to be quite different. The reasons for this diverse behavior are analyzed.

Identification of Qualitative Genetic Regulatory Network Models by a Mathematical Programming Approach

Camilo La Rota, Fabien Tarissan

Poster (Track F)

We propose a method of Genetic Regulatory Network (GRN) model identification using mathematical programming and global optimization techniques. The problem consists in the estimation of the unknown parameters of a GRN model such that the asymptotic dynamics of the model closely match a set of experimental observations. This problem can be naturally cast as an optimization problem that minimizes a given distance between a set of observed expression patterns and estimated values of the parameters, subject to constraints derived from the algebraic equations that describe the dynamics of the biological system. We apply this approach to the inference of regulatory networks controlling lateral organ, meristem and floral organ development in the model plant *Arabidopsis thaliana*.

Limit cycles and update schedules in Boolean networks

Julio Aracena, Luis Gomez, Lilian Salinas

Poster (Track F)

Boolean networks, was introduced by S. Kauffman as a mathematical tool to study the dynamics of gene regulatory networks [Kauffman, 1969; Kauffman and Glass, 1973; Kauffman, 1993]. In this model, a gene expression level is quantified by binary values, 0 or 1, indicating two transcriptional states, either inactive or active, respectively, and this level changes in time according to some local activation function which depends on the states of a set of nodes (genes). This dependence is represented by a directed graph, named interaction graph. The joint effect of the local activation functions defines a global transition function; thus, the other element required in the description of the model is an update schedule which determines when each node has to be updated, and hence, how the local functions combine into the global one. Changes of the update schedule in the model can cause variations in the dynamical behavior of the network. Importantly, they can change the set of attractors, which is of great interest when modeling genetic regulatory networks. Attractors are usually identified with distinct types of cells defined by patterns of gene activity. In particular, the fixed points are often associated with phenomena such as cell proliferation and apoptosis, and the limit cycles with cellular cycle, division, etc. [Huang, 1999; Aracena et al, 2006].

For a long time the synchronous update has been used by default in Boolean network models. One reason for this is the difficulty of really knowing the order (if any) in which the events take place in the cell. However, some non-synchronous updated schedules have appeared in the literature in the last decades [Mendoza and Alvarez-Buylla, 1998; Albert and Othmer, 2003], and are a necessary part of our understanding of Boolean network dynamics. To our knowledge, little analytical work has been done about the differences in the dynamical behavior of a Boolean network when the update schedule is changed. Aracena et al [2009] studied the robustness of the whole dynamical behavior of a Boolean network with respect to different deterministic update schedules (synchronous, block-sequential, sequential). In that article, for a given Boolean network, the authors define equivalence classes of update schedules with the same dynamical behavior, introducing a labeled graph which helps to understand the dependence of the dynamics with respect to the update. In this work, we study the relationship between the labeled graph and the limit cycles of a Boolean network. In particular, we characterize the architecture of the interaction graphs

where for any global transition function, two non-equivalent update schedules yield dynamical behaviors that do not share any limit cycle. Besides, we prove that for any interaction graph and two non-equivalent update schedules, there exists a global transition function such that the corresponding networks do not have the same set of attractors.

Reverse-Engineering Gene Regulatory Networks From Microarray Data with Dynamic Bayesian Networks

Andrea Rau, Florence Jaffrézic, Jean-Louis Foulley, Rebecca Doerge

Poster (GENESYS)

A gene regulatory network is made up of a set of genes that interact, whether directly or indirectly, with one another and with other substances in the cell. Because such interactions regulate the rate and degree to which genes are transcribed into mRNA and translated into proteins, the organization of these gene networks plays an important role in cell behavior. As microarray technology has become increasingly accessible and affordable, the goal of inferring gene regulatory networks from temporal gene expression data has met growing interest in the systems biology community. Although early results have yielded cautiously optimistic results, this problem remains a difficult task for several reasons – biological systems tend to be quite complicated, a large number of genes may be involved in the network, and a limited number of biological replicates and time points are typically available.

A valuable tool that has emerged for inferring gene regulatory networks from temporal microarray expression data is the Dynamic Bayesian Network (DBN), which is a directed graphical model of stochastic processes that can incorporate hidden variables as driving factors (e.g., transcription factors, genes not included on a microarray, or genes not found to be differentially expressed). The current work relies on an approximation to a full hierarchical Bayesian analysis of a DBN, using an iterative empirical Bayes estimation procedure in tandem with Kalman filter/smoothing estimates of the hidden states to estimate the posterior distributions of network parameters. The empirical nature of this method significantly reduces the computation time required for calculation, particularly since the singular value decomposition of a block-Hankel autocovariance matrix can determine the dimension of the hidden state a priori. Significant network edges are chosen based on a z-score calculated from the posterior distribution of the interaction matrix.

Relying on simulated as well as real data, we compare our approach to similar methods on the basis of Area Under the Curve (AUC) of the Receiver Operating Characteristic (ROC) curve, power, specificity, positive predictive value, and computational time. Preliminary work thus far indicates that our proposed method has potential to identify gene networks at a level comparable to existing methods, but with improved computational efficiency.

Causal inference in genome-wide association and linkage studies: a quantitative genetic perspective

Yang Li, Bruno Tesson, Rainer Breitling, Gary Churchill, Ritsert Jansen

Poster (GENESYS)

Recent linkage studies on model organisms have successfully used quantitative trait loci (QTL) for inferring causal networks [1,2,3]. These medium-sized studies typically used 100-400 samples and focused on QTL explaining 5-25% of the total variation. Genome-wide association studies (GWAS) generally require much larger experiments for QTL detection [4]. A recent and still relatively small experiment with 700-1,000 human samples spectacularly connected clinical and molecular traits into causal networks [5]. These studies imply a major breakthrough for causal ‘bottom up’ inference by exhaustively examining all major QTL and pairs of co-mapping traits [6,7]. Initial computer simulations for such major QTLs

have indeed suggested current methods are robust and already sufficiently powerful for several hundreds of samples [8]. However, since the majority of QTL identified in GWAS studies explain much less than 5% of the total variance [4], it is more compelling to explore how the causal inference methods perform with smaller QTL: we need to fully evaluate the relations between sample size, QTL effect size, and false decision rate (FDR). We here show that a population size in the order of 1,000s to 10,000s is sufficient for causal inference with QTL explaining 0.5-30% at 10% FDR in sufficiently accurately measured traits. This heralds a new era for 'old' causal inference concepts [9] in a new field: upcoming large consortia studies allow for causal inference as a promising strategy for identifying QTL and gene networks.

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From gene clustering to genetical genomics: using or reconstructing biological networks

Matthieu Vignes, Jimmy Vandel, Nathalie Keussayan, Juliette Blanchet, Simon de Givry, Brigitte Mangin
Poster (GENESYS)

We retrace here our work in understanding of mechanisms underlying a biological process that evolved from models for gene clustering towards genetical genomics. The former topic focused on an integrated study of available data to produce biological knowledge resulting from the grouping of genes. The latter project deals with the inference of graphs that encode relationships within a biological complex system. Both approaches use a measure of gene activity (e.g. transcript level) to decipher the network encompassing associated relationships (e.g. regulations). Genetical genomics includes the genetic variation in the population to reconstruct the very biological processes from carried out measures. We present in this paper some developments regarding statistical gene clustering that could be useful to genetical genomics. We also present some results for network reconstruction combining genetic and genomics data.

Natural variation of the dynamics of global gene transcription regulation in aging worms

Ana Viñuela, L. Basten Snoek, Joost A.G. Riksen, Jan E. Kammenga
Poster (GENESYS)

Over the past decades the study of induced mutants has revealed major genes affecting lifespan and aging in the fly *Drosophila melanogaster* and the worm *Caenorhabditis elegans*. But so far it is unclear if and how gene regulation changes with age and how this is affected by natural variation. High-throughput gene transcription profiling in mutant and wildtype worms and flies showed that gene transcription variation did not decrease with age, suggesting that gene regulation remains constant throughout life. But currently detailed insight into genome-wide regulatory patterns in aging organisms is lacking. Here we present the first study of the temporal dynamics of global gene transcription regulation in a recombinant inbred line population of aging worms. These SNP genotyped recombinant inbred lines (RILs) were derived from a cross between two of the most genetically divergent wildtypes N2 and CB4856. We extracted mRNA from juvenile, reproductive and old worms and measured genome-wide gene expression in all RILs using 60 mer microarrays. In addition we measured average lifespan for all RILs. Genetic mapping of gene transcription (eQTL) revealed age specific as well as age independent eQTLs. The number of eQTL and their effect decreased with age. But the effect of a few eQTL increased with age indicating "old-age" specific transcription regulation. These age dependent transcripts have a different temporal expression

depending on which parental allele harboring the age eQTL is present. Research is ongoing to see if these time-dependent eQTLs can explain the genetic variation in lifespan across the CB4856 x N2 RILs.

Integrative methods to support phenotype-genotype research in bioenergy crops

Keywan Hassani-Pak, Shao Chih Kuo, Jan Taubert, Steve Hanley, Chris Rawlings

Poster (GENESYS)

The phenotype-genotype problem starts with phenotypic variation and tries to determine which genes are involved. This problem is challenging because most phenotypes of agricultural interest are complex with many genes contributing to expression of the phenotype. Quantitative trait loci (QTL) are chromosomal regions identified through linkage analysis that assign variation observed in a phenotype to a region on a genetic map. Even well-defined QTL, however, may encompass many potential candidate genes, perhaps hundreds. It is therefore hard to objectively choose underlying candidate(s) that drive the phenotype. We are developing means to support systematic analysis of QTL regions and prioritise genes for experimental analyses. Our methods will be used to identify genes controlling biomass production in willow (a second generation bioenergy crop). As the willow genome is not yet sequenced, we are working on the closely related poplar genome (first sequenced tree) and experimental resources from Arabidopsis. As for many other sequenced genomes, the poplar genome is currently lacking comprehensive and up-to-date annotations. However, resolving the functional annotation of over 45000 predicted genes in poplar and understanding the way they link to phenotypes still remains a major challenge and requires an integrative as well as large-scale approach. Therefore, we are developing a functional genome annotation pipeline using data integration methods from the freely available Ondex system (<http://ondex.org>). The pipeline exploits comparative genomics, data integration and text mining to predict the protein function of open reading frames (ORFs) identified from the poplar genome. The outcome is an integrated heterogeneous network, where genes contain positional information and proteins are enriched with Gene Ontology, pathways and publications. Additionally, some recently published poplar and willow QTL were examined and mapped to genomic positions and consequently linked to underlying genes within the integrated dataset. We are also mapping the trait descriptions to controlled vocabularies including Trait Ontology and Phenotype Ontology. The combination of positional information, functional annotation and phenotype information offers a variety of ways to approach the problem of identifying candidate genes underlying a QTL. This integrated data set along with network-based query and visualization tools for the Ondex system will facilitate the job of narrowing down a QTL region, selecting and validating candidate genes that contribute to complex phenotypes.

Sparse Bayesian Instrumental Variable Analysis with Genetic Instruments

Felix Agakov, Paul McKeigue, Jon Krohn, Jonathan Flint

Poster (GENESYS)

One of the key goals of observational epidemiology is to be able to distinguish causal and non-causal explanations of observed associations between phenotypic biomarkers and outcomes, which is difficult due to possible confounding or reverse causation. One approach to the problem is by exploiting the instrumental variable (IV) analysis method with genetic instruments. However, the classical IV argument is severely limited by the assumption that effects of the instrument (genotype) on outcome are mediated only through the phenotypic biomarker (i.e. there is no pleiotropy). We discuss a general framework for IV analysis with genetic instruments, which extends the classic IV argument by relaxing the assumption of no pleiotropy. Our method is based on Bayesian inference in a sparse linear model with a rich structure, which allows for pleiotropic links and conditionally coupled biomarkers. Our approach can be widely applied to validate biomarkers as causal risk factors or as possible proxy endpoints for early-stage clinical

trials. We demonstrate it by examining effects of gene expressions in the liver on the HDL levels in the blood for heterogeneous stock mice.

Multivariate genetic and genomic analyses of boar taint in pigs

Burak Karacaören, Dirk-Jan de Koning, Ingela Velander, Steen Petersen, Chris S. Haley, Alan L. Archibald
Poster (GENESYS)

Boar taint (BT) is an undesirable odour that may occur when cooking meat of male pigs that has been associated with high levels of androstenone and/or skatole in the tissue. Variation in both skatole and androstenone has a heritable component. In this study we explore relationships of genetic markers significantly associated with skatole in previous investigations with other response/ explanatory variables in order to better understand the biology underlying boar taint.

Aim: The main aim of this study was to apply genome wide explanatory analyses on boar taint to investigate the effects of significant markers to other production and explanatory variables using principal component regression, clustering analyses with different linkage methods and Bayesian Network.

Material. From a population of 6000 pigs, we selected 500 full sib pairs that had divergent skatole levels (one pig with high and one with low skatole). These pigs also had data on production traits and were tested for androstenone levels. For genome wide analysis, 6178 markers were genotyped. After quality control we retained 2635 SNPs and 829 individuals for the analysis.

Methods. First, a multivariate step-wise regression was carried out to determine the important fixed effects and covariates. Subsequently, principal component analysis was used to find the loadings that explain the highest variation over the response variables. The principal components analysis is useful for reduction of the dimensions of the dataset and breaking possible dependency among explanatory variables. Clustering analyses can be used to classify the variables based on different linkage methods when classes are initially not known and could also be used to reduce the dimension of the dataset. Variables within the same cluster are regarded as more related to each other. We explored relations within significant markers and with other response/ explanatory variables to better understand the biology underlying boar taint. Finally, we applied a Bayesian network model to the phenotypic and marker data. A Bayesian Network is a directed acyclic graph in which nodes represent random variables and arcs define directed stochastic dependencies quantified by probability distributions (Sebastiani et al, 2005). The Bayesian Network was constructed by B-course (Myllymaki et al, 2002) web based software using response and explanatory variables and significant markers from the association study. In order to decide the significant markers to be used in the network we used GRAMMAR and DSP test approaches (Karacaören et al, submitted) and used the top 4 markers in the analyses. In addition, we also used other production traits and fixed effects in the Bayesian Network. We have created joint posterior distributions using both probabilistic and classification models. For inferring causality we constructed the Bayesian network with and without latent variables to explain completely or partially non-observed variation (Myllymaki et al, 2002).

Results. In the stepwise regression model fixed effects were: herd at birth, year of birth, age in days, litter size total born, litter size alive at day 5 and slaughter week. The determination coefficients (with adjustment for number of explanatory terms in the model), using stepwise regression varied between 9% for skatole levels and 72% for daily gain between 30-100 kg. It must be noted that some of the production traits in the model were highly interconnected (e.g. 'weight' and 'age' are closely connected to 'daily gain') The first four principal components explained at least 75% of the total variation. Instead of using 14 explanatory variables we used 4 principal components in regression models and we obtained similar adjusted explanatory coefficients. For the clustering analyses, different methods clustered skatole and androstenone levels into same clusters albeit with different similarity levels. This cluster was found in relation with the cluster that includes weight end of the test, slaughter weight and daily gain (30-100)

kg. We constructed the naïve estimate of the Bayesian network while assuming all latent variables were observed. ‘Disease’ status (high boar taint or low boar taint) was found to be related to daily gain (30-100) kg, and various markers and other production traits. We also created the Supervised Bayesian Network conditional on the disease status. It was found that marker 1 (*cyp2e_1*) was associated with disease status as well as androstenone levels and some other production traits.

Although stepwise regression, clustering and the Bayesian Network showed partially consistent results, there were also discordant results from the various analyses. The Bayesian Network could be considered as a complementary analysis to association mapping possibly with principal component analyses and clustering analyses. Although the learned network does not have to show causal relationships, it can be informative and generate additional hypotheses.

Exploring the genetics underlying hypertension using radiotelemetric blood pressure measurements in the BXH/HXB rat recombinant inbred lines

Sarah Langley, Josef Zicha, Theodore Kurtz, Michal Pravenec, Sylvia Richardson, Timothy Aitman, Enrico Petretto

Poster (GENESYS)

Hypertension is a risk factor for several cardiovascular diseases, including heart failure and stroke, and the underlying genetic factors can be explored using the heritability of blood pressure variation. In this study, we utilized radiotelemetric blood pressure data in the BXH/HXB Recombinant Inbred (RI) lines of rats to investigate blood pressure regulation and regulatory systems by means of new methods for integrated physiological time series analysis and linkage analysis. Time series blood pressure was collected from 28 BXH/HXB RI Lines and the two parental strains, Brown Norway and Spontaneously Hypertensive Rat. 500 measurements per second were collected over a period of 30 minutes in each animal; there are between two and eleven animals per strain. After outlier removal and processing, eight blood pressure and heart rate phenotypes were extracted from the time series data using both parametric and spectral methods and were subsequently mapped to the genome using a genome-wide genetic map comprised of 1,400 single nucleotide polymorphisms. The high frequency nature of the time series data should allow for a more detailed analysis, as the inclusion of spectral with parametric phenotypes will better capture the variations in blood pressure and heart rate and the combined analysis of multiple related phenotypes from the same data set should aid in finding genomic locations and interactions associated with hypertension. By performing spectral time series analysis, secondary patterns and trends present within these blood pressure measurements, which relate to physiological traits and are often discarded, can be extracted and mapped to give further insight into blood pressure regulation. We found genomic loci associated with six of the eight phenotypes we analyzed, at different FDR levels ($< 25\%$), and three phenotypes had multiple loci associated with them. Loci for blood pressure were found on chromosomes 10, 17 and 19 and all fell within preciously known loci regions; a novel heart rate locus was found on chromosome 14. Further phenotypes are to be extracted and mapped to the genome, in conjunction with gene expression profiles from seven tissues to explore the relationship between blood pressure regulation, gene expression and genetic marker data. We expect to find multiple genetic control points, and identify functional pathways and networks.

Extending KEGG Pathways for a Better Understanding of Prostate Cancer Using Graphical Models

Adel Aloraini, James Cussens, Richard Birnie

Poster (GENESYS)

In this ongoing work, partial information about WNT-signaling pathway found in KEGG has been used

as prior knowledge to guide a machine learning algorithm, based on linear regression, to show how cellular system works in WNT-signaling pathway. We are using a set of graphical models called dependency networks to give bigger picture of how genes in different components in the pathway affect each other. The search space is constructed exhaustively based on the prior knowledge extracted from WNT-signaling pathway (inhibition, direct effect, indirect cause, etc). After all candidates are found in the search space that restricted by background knowledge, Akaike information criteria score function (AIC) is used to score each model by balancing between the accuracy and the complexity of each model. Beside AIC score function, for each family in the networks in the search space, the set of parents are examined by Residual Sum of Squares (RSS). Since if a set of parents in the regression model leads RSS to be zero, this means that AIC will go to infinite value, which in turn gives nonsense result. Therefore, each resultant model from the exhaustive search is further examined to see if RSS is non-zero. If RSS equals to zero the correlation coefficient is used to drop parents (independent variables) with small correlation with the child gene (dependent variable) until RSS has non-zero value. The initial result that we have obtained basically looks at which genes from one component cause or react with which in another component. However, the result also shows how genes in each component react with each other. Although this needs further study, we observed that some genes in each component either dependent on each other, where undirected arrow is concluded, or one causes another, where directed arrow is used. In the future work we will examine the accuracy of each model, and examine a new set of graphical models called Chain Graphs (CGs) in which every component corresponds to undirected/directed or both graph and the joining between different blocks is directed graph.

Constructing and comparing networks of drought stress response across Durum wheat cultivars

Michael Defoin-Platel, Matthew Hindle, Marcela Baudo, Stephen Powers, Rowan Mitchel, Mansoor Saqi, Dimah Z Habash

Poster (GENESYS)

Wheat in general is a grass species of great importance but durum wheat in particular is widely grown agriculturally and used in the production of pasta and bread. Drought is one of the major abiotic limitations to crop yield with significant agricultural, economic, political and social impact, especially for durum wheat since it is mainly farmed in rain-fed environments. Recently, an experiment has been conducted at Rothamsted Research (UK), where the transcriptomics responses to water stress imposed under controlled environment conditions of three cultivars of durum wheat were studied at a genome scale using Affymetrix microarrays. The first cultivar, called Cham1, is a drought resistant variety widely grown in the Mediterranean basin and the second one, called Lahn, is a high yielding variety from Syria, which performs well under well-watered conditions but is susceptible to changes in temperature and water availability. The third cultivar, named RIL2219, is one of the 114 Recombinant Inbred Lines (RIL) originating from the cross between Cham1 and Lahn. Understanding the mechanisms and conditions by which these three wheat cultivars respond to water stress is very challenging and require the integration and comparative analysis of data spanning multiple domains. In this work, we have created a co-expression network to study units of regulation (regulons) across the three cultivars. Firstly, we have identified potential transcription factors (TFs) using BLAST for sequence comparisons using three TF databases (Grassius, PlntDB, AGRIS). This was then followed by a search for possible regulated genes for each TF by looking at the level of co-expression (unsigned correlation) in a drought time course experiment. Regulons were merged when they had genes in common and resulting networks were then analysed and compared among the cultivars, both in terms of topology and biological functions. Particular attention has been given to the regulons significantly expressed after one day of stress in the three cultivars. This analysis uncovered a massive regulon, specific to Lahn the drought susceptible parent, revealing an early but co-ordinated

response to water stress in this cultivar.

Developing an Adaptive and Interoperable MetaSystem for Assuring Information Security within a Highly Complex Networking Environment

Elena Irina Neaga, Michael Henshaw

Poster (Satellite Meeting)

The new security challenges of the 21st century are different than in the past. Security and protection of critical infrastructures (transportation system, public utilities etc.) enabled through networking should require sophisticated socio-technical systems defined as a metasystem and new deployment strategies. The complexity of the contemporary world embedded several critical issues such as terrorism, potentially unknown or hidden attacks/threats and natural disasters also need strategies and advanced systems or a metasystem for supporting quick responses or crisis management. New networked organizational infrastructure of threatening parties-with many groups being leaderless-and their quickness in coming together in swarming attacks requires dynamic and effective collaborative approaches to counteracting measures which include adaptive security systems. The metasystems should support reducing risk as well as emergency and consequence management tools. Generally for responding to new types of conflicts, threats and attacks, the future security systems shall encompass harmonious inter-organizational coordination as a holistic security metasystem and risk management intelligent applications in order to achieve a total effect greater than the sum of the individual components. The types of integration, interoperability, responsiveness, and adaptability needed to meet these requirements are best achievable through Network Enablement such as applying the concept of Network Enabled Capability(NEC).

The following main categories of security systems will be presented:

1. Interoperable and Adaptive Security Systems applying Comprehensive Knowledge Models human and computer-based as well as bio-inspired methods and techniques
2. Self Organising Security Systems bio-inspired “borrowing” the properties characterizing the living organisms: multicellular architecture, cellular division, and cellular differentiation. Implemented in silicon according to these properties, a self-organizing system is able to grow, to self-replicate, and to self-repair. The growth and branching processes, performed by the so-called Tom Thumb algorithm, lead thus to the configuration and cloning mechanisms of the systems. The repair processes allow its “cicatization” and regeneration mechanisms.

The poster will present the main features of a cybersecurity metasystem that unfolds into an emergency response management infrastructure capable to react in due time to unknown and new kinds of attacks/threats. The system can adapt to its changing environment through its self organizing properties. Attempting to transfer the way immunity works in living organisms the system can dynamically adapt to embrace new risk situations and can dynamically create and learn new comprehensive knowledge models as it encounters new critical situations.

This intended project will be focused on a development methodology of using bio-inspired architectural patterns and/or natural computing principles in order to support the management of risk and complexity for assuring critical infrastructure protection and information security within a highly networking environment. Generally, networking enables several developments in the society such as industrial/business collaboration, value co-creation and success of critical intervention in case of natural disasters, threats and military operations. Information and risk management are at the core of security systems. The main innovative aspects of this project are as follows: • a holistic approach of risk management and information security. • investigation of self organising capabilities to provide security, adaptability and interoperability features for risk management systems. • investigation and application of bio-inspiration theories for information security systems. • applying natural computing principles.

The final aim of this project is to develop an adaptive risk management meta system in order to support the prevention, forecasting, identification and respond in critical time to threats or natural disasters as well as risk evaluation and mitigate the consequences.

The novelty of this project will arise from using the concept of self-organizing systems as a resilient architectural foundation on which the operational mechanism for deploying dynamic, short living emergency response organizations capable to react quickly to emerging crisis situations can be evolved. Therefore the the main innovation will be embedded within an architecture that has the capabilities to identify/unfold into an emergency response management infrastructure capable to react in due time to unknown and new types of attacks/threats. The architecture will incorporate self organising capabilities that can also be used for assessing and minimising risks. The metasystem will include an implementation of resilience in order to adapt to changing environments through its self-organizing ability. Mimicking the way immunity works in biological organisms the system can dynamically adapt to embrace new risk situations and can dynamically create and learn new risk models as it encounters new risk situations.

Scale-free critical Boolean networks

Florian Greil, Barbara Drossel

Poster (Satellite Meeting)

Boolean networks form a simple discrete dynamics on a directed graph. The structure of real-world networks is, of course, not random, however, random Boolean networks are an important first step on the way to understanding general features of more complex networks and their dynamics.

We explain why networks with power-law in-degree distributions exhibit qualitatively different dynamics compared to the usual Poissonian networks. Scale-free in-degree distributions are more realistic as a huge amount of networks occurring in nature are known to have a broad degree distribution.

The key concept for statistical understanding of the system behavior is to classify the nodes of the network according to their relevance for the dynamics. A recently developed stochastic process is used to determine the relevant nodes of the network by determining stepwise the frozen nodes which are not relevant. If the exponent of the in-degree distribution is larger than 3, the dynamics equals the classical case. When the exponent is between 2 and 3, the number of the non-frozen nodes increases as a power law with the system size with an exponent between 0 and 2/3. [F. Greil, B. Drossel; PRE 80, 026102 (2009)]

Boolean networks with reliable dynamics

Tiago Peixoto, Barbara Drossel

Poster (Satellite Meeting)

Gene regulation of evolved organisms is marked by a high degree of reliability. In order to further understand this, we investigated the properties of Boolean networks that follow a given reliable trajectory in state space. We consider reliability from two perspectives: According to temporal fluctuations of the update time, and to fluctuations of the expression level (boolean value) due to a temperature parameter. The first reliability criterion allows for the direct creation of sequences of states which is independent of the order in which the nodes are updated (i.e. with maximum fitness), as well as the minimal networks which are capable of realizing them. The second reliability criterion is obtained by maximizing a corresponding fitness function and mutating the underlying network. We explored numerically the topology, the update functions, and the state space structure of these reliable networks.

References:

Noise in random Boolean networks, Tiago P. Peixoto and Barbara Drossel, Phys. Rev. E 79, 036108
Boolean networks with reliable dynamics, Tiago P. Peixoto and Barbara Drossel, arXiv:0905.0925v1

Characterization of phospholipase D localisation in relation to small G-proteins and a novel fluorescent substrate

Mina-Olga Aletrari, Matthew Hodgkin

Poster (Satellite Meeting)

Extracellular stimuli increase the activity of phospholipase D (PLD) to hydrolyse phosphatidylcholine (PC), yielding phosphatidic acid (PA) and choline. PA production is stimulated in a variety of cells (such as fibroblasts, white cells, and epithelial cells) by a range of agonists, e.g. hormones, growth factors, antibodies. Although the role of PA in different signalling cascades is not fully understood, the inhibition of PA production by transphosphatidylation halts complex cellular process such as cell movement, secretion and proliferation. For example, PLD is considered essential to IgE-dependent secretion in mast cells and, in epithelial cells, regulates proliferation and epidermal growth factor (EGF) receptor internalisation. This project involves the development of real-time assays for PLD activation and PC hydrolysis using both mast cell and epithelial cell models.

The two most commonly expressed PLD isoforms – PLD1 and PLD2 – are found at low levels in most cells and so our work used fluorescent versions of PLD, its activators and its substrate PC. A novel fluorescent version of the PLD-substrate PC (DBPC) has been characterised in live RBL-2H3 cells. DBPC is an analogue of PC containing a fluorescent BODIPY group and Dabcyl quenching groups. RBL-2H3 cells treated with 1 μ g DBPC (2hrs at 37°C/5% CO₂) exhibited punctate labelling which was stable for up to 24 hours. DBPC had approximately 50% localisation with the lysosomal marker LysoTracker Red. Oscillatory changes were evident in both stimulated and unstimulated cells, suggesting a change in the actions of the punctiform structures upon stimulation.

The aromatic Dabcyl groups quench the BODIPY fluorescence when the lipid is intact. However, once DBPC is hydrolysed, the BODIPY is no longer quenched and its fluorescence increases. This permitted the design of real-time fluorescence in vitro PLD assays in which PLD activity can be monitored by periodic increases in fluorescence. The objective is to characterise the role of small G-proteins as PLD1b activators and the function of potential co-factors such as calcium ions.

Further to real-time in vitro assays, localisation between Cherry-PLD1b and -2a (red) and the small G-protein GFP-Rac1 (green) were observed using transient transfections, in an epidermal cell line originating from cervical carcinoma (HeLa). Localisation between wildtype, constitutively active and dominant negative eGFP-Rac1 (green) and PLD have been analysed with and without stimulation with 20 μ M EGF (10mins at 37°C/5% CO₂). PLD1b localises with wildtype Rac1 upon EGF stimulation, although this does not occur prior to stimulation. PLD2a appears unaffected by EGF stimulation and does not localise with Rac1 wildtype or either Rac1 mutant. Future experiments will include transfection of Cherry-PLD into HeLa cells and mast cells with DBPC to create a live in vivo PLD assay.

The Risk Centre

Frank Schiller, George Prpich, Gill Drew, Sophie Rocks, Simon Pollard

EPSRC Showcase Poster Session

The Collaborative Centre of Excellence for Managing and Understanding Natural and Environmental Risks (the Risk Centre) provides leading research, training, education and consultancy on environmental risk management at Cranfield University.

The Risk Centre has multidisciplinary approach and is made up of a core team (with expertise in risk assessment, modelling, knowledge transfer and organisational maturity) as well as wider expertise of Cranfield University colleagues. The Centre's aim is to develop and communicate best practice across organisations involved in environmental risk management.

The Risk Centre is jointly funded by the Department for Environment, Food and Rural Affairs (Defra), the Engineering and Physical Sciences Research Council (EPSRC), the Economic and Social Research Council (ESRC), and the Natural Environment Research Council (NERC).

The Risk Centre's activities cover four main themes; • Strategic risk appraisal – comparing diverse risks in an organisation • Risk and evidence – the development and use of information in a risk assessment • Organisational maturity – the assessment and influencing of organisational culture to diverse risks • Knowledge exchange – communication of risks to strategic bodies.

The Risk Centre remit, work plan, expected outputs and impacts will be discussed along with initial findings from this work.

This work is jointly funded by EPSRC, ESRC, NERC, and Defra.

Improving the risk maturity of a social network

Frank Schiller, George Prpich, Gill Drew, Sophie Rocks, Simon Pollard

EPSRC Showcase Poster Session

Within a network of organisations, 'governance' can be interpreted as addressing the delegation of risk, assigning accountabilities and responsibilities, and how the organisation draws in advice from advisers to inform decisions. Risk governance considers how relevant risk information is collected, analysed and internally communicated as well as how management decisions are taken. It is recognised that it is crucial to understand the particular cultures working within a network. These are brought about by different legislations, use of different scientific methods, disciplinary affiliations etc.

The work presented in this poster builds upon the prior art of risk governance and considers the different risk cultures in organisations in order to govern risks more coherently and to improve performance. Indeed, it is essential that when improving the overall risk maturity of a network there is an awareness of these different cultures so as not to alienate groups during implementation. Whereas existing maturity models focus on organisations the challenge is to adapt these models to a network of several organisations with different risk cultures.

The poster will show a map of the network developed in the early stages of the project and introduce to the social research methods (organisational maturity, cultural web, expert interviews etc.) that will be used to carry out the project.

This work is jointly funded by EPSRC, ESRC, NERC, and Defra.

Evolution of Cellular Automata with Memory

Christopher Stone, Larry Bull

EPSRC Showcase Poster Session

The Density Classification Task (DCT) is a well known test problem for cellular automata (CAs). In this task a one-dimensional binary CA is initialized with a random initial configuration and iterated for a maximum number of steps or until a fixed point is reached. If the initial configuration contains more ones than zeros, the CA is deemed to have solved the task if a fixed point of all ones is reached and vice versa. This is a difficult task for a CA as a solution requires coordination of the global state of the CA using only the local communication between cells provided by the CA neighbourhood.

A variety of evolutionary computation approaches have been used to evolve solutions to this problem. Typically, a Genetic Algorithm (GA) is used to search the space of binary CAs with radius $r=3$. Each GA individual comprises a string of length 128 bits representing the transition rule for a particular CA. However, a binary string representation is not able to exploit the symmetries inherent in the DCT. There are two types of such symmetry arising from the interchange of zeros and ones and left and right position in the solution.

To address this problem we use a new representation inspired by the ternary representation used by Learning Classifier Systems. Our template representation is based upon the format of the CA neighbourhood. In this representation, each GA individual consists of a variable-length list of templates, each corresponding to one or more particular CA neighbourhood configurations.

In this work, we investigate the evolvability of DCT solutions when the underlying CA is augmented with memory. We implement a form of memory using the well-known Least Mean Square (LMS) algorithm with learning rate β . This provides an exponentially-weighted moving average memory with no CA transition function overhead. The learning rate β controls the amount of memory with $\beta = 0$ providing infinite memory and $\beta \geq 0.5$ corresponding to no memory. The CA transition function operates on the thresholded memory value and not the previous state information used by a standard CA. Memory provides a type of inertial effect and excessive memory inhibits the spatio-temporal development of the CA. Selecting an appropriate amount of memory is thus important for effective problem solving.

Initial results using a sample of fixed memory settings suggest that the template representation supports a more efficient genetic search compared to the bit string representation and that when a moderate ($0.3 < \beta < 0.5$) amount of memory is present the GA is able to find better solutions compared to the no memory case ($\beta = 0.5$).

In order to explore further the hypothesis that memory aids evolutionary search we extend the GA so that each individual in the population carries its own memory setting controlling the amount of memory that it uses. Upon creation of offspring, the parent's memory setting is copied to the child and perturbed with a simple self-adaptation mechanism to allow variation of the memory setting value. We find that the best performing individuals have evolved memory settings of $\beta = [0.3, 0.5]$. To ensure that the results were directly attributable to the inclusion of memory in the CA, we rerun the experiment with no memory enabled. Without memory only five high performance solutions are found, unlike the case with memory enabled, which produces 36 runs with a performance of 0.7 or greater.

Thus, memory is shown to improve evolvability of solutions and appropriate memory settings are able to be evolved as a component part of these solutions. Comparison of evolved rules shows that the presence of memory has enabled independent runs of the GA to evolve families of rules close in Hamming space which possess similar performance characteristics.

This work was supported under EPSRC grant number EP/E049281/1.

Advanced Protocols via Emergence for Ad hoc Networks

Jennifer Jackson, Mark Leeson

EPSRC Showcase Poster Session

As technology advances and the need for mobile ad hoc services increases, networks and systems depending upon them will become more complex leading to the necessity of such systems to be self-organised and display characteristics of emergence, robustness, adaptability and scalability. A protocol is therefore needed for ad hoc networks of the future, falling outside the capacity of current protocol designs and produced via emergence. Such a design needs to offer solutions to communication scenarios which cannot be premeditated prior to deployment. The proposed methodology not only creates, but also dynamically adapts the communication protocol via emergence based upon an alphabet of characteristics and performance metrics using simple protocol mapping techniques and minimisation of a fitness function via a genetic selection process.

Compartmental Modelling of Virus Propagation Behaviour in Bluetooth Networks

Jennifer Jackson, Sadie Creese

EPSRC Showcase Poster Session

As mobile wireless communications become ubiquitous, the networks and systems that depend upon them will become more complex. In parallel to this, the spread of digital viruses and malicious content will be an ever increasing threat within this interconnected paradigm requiring counteracting mechanisms to continuously adapt. Modelling virus propagation behaviour in mobile wireless and peer-to-peer communications devices is still immature. A compartmental-based virus propagation model has been developed for Bluetooth communication networks incorporating wireless technological traits and factors that are known to affect virus propagation including human interaction, heterogeneous devices and anti-virus measures.

Infection Subgraphs of Dynamic Sexual Contact Networks

Katy Robinson, Caroline Colijn, Ted Cohen

EPSRC Showcase Poster Session

Numerous sexually transmitted infections are highly prevalent throughout the world, many of which (such as HIV) remain incurable. However, by studying their spreading patterns, it can be possible to prevent new infections or at least to decrease the rate at which they appear. Using survey data that includes ego-centric information (e.g. number of sexual partners & concurrency), and known disease dynamics, complex epidemic network models can be produced.

Sub-graphs can be extracted from these which show the part of the network available to an infection starting at a particular point in the network at a particular time, providing information on the structure of the available sub-network on which a particular pathogen can spread and so on the behaviour of the most at-risk sections of the population. In order to study which factors most affect the structure of these D-graphs, we created 700 different graphs, using fourteen different D-values (ranging from three to 100 weeks) and 50 start-nodes, chosen according to their degree in the behavioural network (five of each degree between one and ten). From these D-graphs we have found several interesting results relating to degree distribution, concurrency and duration of infectiousness.

CoSMoS: Complex Systems Modelling and Simulation Infrastructure

Susan Stepney, Peter H. Welch

EPSRC Showcase Poster Session

CoSMoS is a four year EPSRC-funded project to develop a modelling and simulation process and infrastructure specifically designed to allow complex systems to be explored, analysed, and designed within a uniform framework. Here we outline the components of CoSMoS, and report on the current state of the process and infrastructure.

Analysis of a Robot Arm with Exoskeleton for Coordinate Measurement in Complex Environments

John Thornby, Redland Sanders

EPSRC Showcase Poster Session

In partnership with Metris UK we present the modelling and development of a revolutionary Robot Coordinate-measuring Arm (RCA). The RCA combines the automation capability of traditional Coordinate Measurement Machine (CMM) methods with the mobility and part accessibility of an articulated

arm, resulting in a versatile and powerful tool for coordinate measuring applications with a target accuracy of sub-100 μm .

The RCA exploits novel, patented technology to accelerate repetitive 3D inspection jobs. A highly accurate 7-axis articulated arm is housed within a robotized exoskeleton driven by electromotors. We utilise Denavit-Hartenberg parameters to model the robot links and investigate the accessible configurations of the exoskeleton under the effects of arbitrary offsets and twists. We further examine the configuration space of a 2-axis version of the system, its singular points and the singularities of the mapping to the space of controls.

We demonstrate the compliance of the RCA to accepted engineering standards and discuss improvements in the calibration and error-correction of the unit, which have reduced residuals by a factor of two. We identify singular poses as a large cause of uncertainty and propose solutions to circumvent them.

This work is supported by the UK Technology Strategy Board under the EPSRC-managed scheme “Gathering Data in Complex Environments”.

Intercellular Ca^{2+} wave propagation: a mathematical study in the Fire-Diffuse-Fire framework

Jamie Harris, Yulia Timofeeva

EPSRC Showcase Poster Session

Calcium is a highly versatile cellular medium that is known to regulate many different physiological processes, from cell division and differentiation to cell death. Calcium oscillations within the cytosol represent the most widespread oscillatory behaviour at the cellular level and are often associated with the propagation of Ca^{2+} waves within and between cells. Intercellular propagation appears to be mediated by the passage of Ca^{2+} or IP_3 (a second messenger known to raise the level of cytosolic Ca^{2+}) through gap junctions.

Here we introduce a theoretical framework for studying calcium wave propagation through a cell culture based upon a generalisation of the Fire-Diffuse-Fire model which uses a threshold process to mimic the nonlinear properties of Ca^{2+} channels. We demonstrate how the travelling wave solutions can be constructed using the so-called ‘sum-over-trips’ formalism. The introduced framework allows us to obtain calcium wave speeds as a function of important system parameters and to identify the parameter conditions for wave propagation failure.

Dendritic democracy: the role of hyperpolarisation-activated current

Anthony Woolcock, Yulia Timofeeva

EPSRC Showcase Poster Session

Neurons receive synaptic inputs primarily onto their dendrites, which filter synaptic potentials as they spread toward the soma. There is experimental evidence that synaptic efficacy increases as a function of distance from the soma. Distance dependent synaptic scaling is just one of several mechanisms for achieving so-called “dendritic democracy” whereby the spatially extended single neuron can compensate for dendritic attenuation. Other mechanisms for boosting somatic response to distal inputs include sub-threshold resonance (via active currents such as I_h), local dendritic spikelets, and global dendritic spikes. Although well studied experimentally, to date this phenomenon has not been thoroughly explored from a theoretical perspective. Recently a number of key measures of democracy using a passive model of a dendritic tree with distributed excitatory synaptic conductances have been analysed [Timofeeva, Cox, Coombes, Josic, *J. Comput. Neurosci.*, 2008, Vol 25, 228-244]. Here we investigate dendritic democracy in the presence of hyperpolarisation-activated (I_h) current in dendrites. The focus of this particular study will be on a measure of equalising the first depolarising response at the soma. We demonstrate how the

synaptic scaling laws can be found for the cases of treating the synapse as either a direct current injection or a conductance change (i.e. a shunting current injection).

Computation Evolution of Dynamical Complex Networks

Thomas Gorochofski, Mario di Bernardo, Claire Grierson

EPSRC Showcase Poster Session

Networks in some form underpin virtually all complex systems making their study a fundamental tool for understanding system level behaviours. Much existing work considers networks in a static context, neglecting the fact that in many real-world systems structure changes over time, evolving due to new requirements. In some cases rules exist governing this process and can be used to efficiently evolve complex networks for our own purpose, or to reliably control existing systems.

This work introduces methods for incorporating dynamic attributes into complex networks, with the aim of providing a coherent framework to investigate and model evolving structures. This will be based on a computation-based optimisation approach where systems are described as networks of coupled ordinary differential equations with node and coupling dynamics that can vary. We introduce the idea of a network "supervisor" whose task it is to re-wire the network such that a chosen cost function is minimised. To illustrate some of these methods a new simulation tool called NetEvo will be presented to analyse how differing constraints and performance measures can effect the types of network produced. Finally, we outline the future directions of this work and some possible applications.

Network Reordering Through Matrix Factorization

Clare Lee, Desmond J. Higham, Keith Vass

EPSRC Showcase Poster Session

Many large, complex networks contain hidden substructures that can be revealed using a range of post-processing algorithms. In particular, reordering the network nodes appropriately may help to summarize key properties by exposing significant clusters, or more generally sets of neighbours with similar features. This work focuses on the use of matrix factorisation methods to derive useful network reorderings. Algorithms in this category have the advantage that they can typically be motivated from first principle modelling arguments [Higham et al (2007)]. They have also been shown to have close connections with other, more *ad hoc*, approaches [Ding and He (2004)].

Our results have been tested on real data concerning the behaviour of genes and proteins in cells. Microarray data produces large non square matrices of information recording the behaviour of a large number of genes across a small number of samples. This data is by its very nature non-negative. One aim is to cluster or order the genes/samples into groups where members behave similarly to each other and differently to those in other groups. This allows us to find sets of genes whose behaviour distinguishes different sample types. We have focused on two approaches, based on the singular value decomposition (SVD) [Higham et al (2005)] [Higham et al(2007)] and various types of non-negative matrix factorization (NMF) [Berry et al (2007)] [Ding et al (2005)] [Ding et al (2008)].

Inferring the Network of Influence in the Global Media System

Nicholas Fyson, Nello Cristianini, Tjil De Bie

EPSRC Showcase Poster Session

At any given moment, news outlets around the world make individual decisions on what stories to cover and which to ignore, but these decisions are not independent of one another. Tracking the locations of statistically significant 'markers' (aka memes), we aim to reconstruct the directed network that dictates

how the output of a given outlet influences that of another. We take a constraint-based approach, using tests of conditional independence and a heuristic to render the problem computationally tractable. In contrast to the existing literature, the nature of our data allows us to use to define a measure of directional conditional independence (DCI), meaning we can learn the orientation of edges locally, and not simply the skeleton of the network. We use an adapted version of the Max-Min Parents-Children (MMPC) algorithm to reduce the search space, theoretically allowing us to scale our approach to large networks containing hundreds of nodes. We demonstrate initial tests of the approach, using synthetic data generated by a model similar to that of an SIR epidemic.

Finite size effects in a stochastic condensation model

Paul Chleboun, Stefan Grosskinsky

EPSRC Showcase Poster Session

We study finite size effects on the condensation transition in a driven diffusive system known as the zero-range process. The condensation transition is already well understood in the thermodynamic limit, however this is at best an idealisation of real finite systems. Even for relatively large system sizes these effects can be significant and counterintuitive. We observe a large overshoot of the stationary current above the limiting critical value and an abrupt change between putative fluid and condensed phases. This is reminiscent of a first order transition although the phase transition is known to be continuous in the thermodynamic limit. Close to the abrupt transition we also observe metastable type switching between the two ‘phases’. We derive an effective free energy landscape and predict the scaling of the lifetime of the two phases. Approximations for the fluid and condensed ‘phases’ are used to derive the leading order finite size effects.

Detecting Hidden Structure - Natural Computation in Biomolecules

David Kelly, Karoline Wiesner, Mark Dillingham

EPSRC Showcase Poster Session

Analysing the conformational dynamics of biomolecules through the medium of Fluorescence Resonance Energy Transfer (FRET) spectra presents significant statistical challenges. Selecting the correct model class can be problematic. It is proposed to use the information theoretic techniques of computational mechanics to construct minimal, optimal models of the system, thereby not only circumventing the issue of model class selection but also allowing insight into the computational capabilities of biomolecules. In order to use these techniques, methods of symbolising continuous signals and interpreting the models in a physical context must be devised. Here we present the results of some preliminary attempts to extend the techniques of computational mechanics to continuous signals and identify directions future work will take.

EPSRC funding activities in complexity science

Gavin Salisbury

EPSRC Showcase Poster Session

Complexity science has been supported by EPSRC for a number of years, and is a current priority area for the Cross-disciplinary Interfaces Programme. Our initial strategy was aimed at building UK research capacity in this exciting, cross-disciplinary field. More recently we have encouraged researchers to develop and apply the tools and techniques of complexity science in order to tackle real-world complex systems, such as energy provision.

EPSRC also coordinates Complexity-NET, a group of European science and technology funding agencies, research councils and ministries all working together to create an environment that enables the coordination of national activities in complexity science and complex systems. This year Complexity-NET issued a call for exploratory transnational research projects, which closed in July. For more information see our website, www.complexitynet.eu.

EPSRC's specific research and training activities in complexity science over the last five years have included:

- Novel computation: coping with complexity
- Taught courses in complexity science and complex systems
- Large Scale Complex IT Systems Research Centre
- Three Doctoral Training Centres in complexity science - at the Universities of Bristol and Warwick (from 2007) and Southampton (from 2009)
- Fundamentals of complexity science
- Energy challenges for complexity science

Our total investment in complexity science through these activities alone has exceeded £40M.

A new call for large-scale programmes of research, Complexity science for the real world, closed recently; the announcement of the successful grants will be made in December 2009 and will represent a further investment of up to £10M.

Unsolicited proposals in this cross-disciplinary field which focus primarily on underpinning mathematics, physics and modelling methodologies for the design, control and understanding of complex systems are also welcome from UK academics through EPSRC responsive mode at any time. Please contact Gavin Salisbury, gavin.salisbury@epsrc.ac.uk, before applying for advice on eligibility and remit.

Communication Strategies for Self-regulated Division of Labour in Robot Society

Md Omar Faruque Sarker, Torbjorn Dahl

EPSRC Showcase Poster Session

Within the context of EPSRC project, "Defying the Rules: How Self-regulatory Systems Work", we have been conducting collaborative research to identify a set of general rules and conditions for emergent self-regulation of division of labour (DoL). We have studied multiple diverse instances of self-regulatory social systems in humans, ants and robots. Along with our research partners, we have developed a model of self-regulated DoL termed the attractive field model (AFM). The model describes the basic properties of self-regulated DoL, i.e., continuous flow of task information, variable sensitization of individuals to tasks, concurrency and flexibility of individuals in selecting tasks. We have, particularly, been exploring the self-regulatory bottom-up control mechanisms for social robotic systems (SRS). Multi-agent task allocation or DoL is a challenging research issue in the field of multi-agent and multi-robot systems e.g., swarm robotics. Existing researchers have approached DoL using predefined (off-line) and emergent (real-time) task-allocation, typically in the swarm robotics paradigm. Unlike the swarm robotic approach, which is inspired by biological systems alone and commonly aims for minimal intelligence agents, we propose to solve DoL using the AFM. In order to demonstrate the validity of the AFM and to evaluate it a mechanism for DoL, we have implemented the generic rules in a system of intelligent, communicating and interacting robots. Within this work, we want to explore the performance of three different communication strategies for information dissemination among the robots: global, local and stigmergic. We report on early experiments in this evaluation. SwisTrack, a state of the art open-source, multi-agent tracking system, along with a 16-megapixel GigE camera has been set-up to perform three sets of experiments to evaluate each communication strategy. The initial results from the global mode experiment with a few robots (3-6) shows us that our model can satisfy the criteria of self-regulated DoL based on our proposed generic rules.

The ongoing work focuses on implementing the different communication strategies among a large number of robots (about 40) and optimizing various experiment parameters' for self-regulated DoL for the different communication strategies.

Complex Flows in Granular Media

Samuel Brand

EPSRC Showcase Poster Session

By detailed Molecular Dynamics we investigate the rheology of granular suspensions driven through a fixed plate channel by a pressure gradient in the suspending fluid. We aim to understand the various possible flow states, disordered flow, ordered flow (granular crystallization) and jammed. In particular we locate a melting transition between ordered and disordered flow and a freezing transition to jamming as well as making close connections to colloidal suspensions.

Genetic Sensors

Jamie Luo, Matthew Turner, Jonathan Millar

EPSRC Showcase Poster Session

Cells are able to adapt to changes in their environment and their own internal state. It is natural to then hypothesize that the GRNs (genetic regulatory networks) of cells possess network structures which operate as sensors that detect the cell's environment or internal state and initiating an appropriate response. This project aims to use insilico simulations to investigate the design principles of such genetic sensors. A boolean idealisation is employed to model the GRNs coupled with evolutionary techniques to find network structures capable of performing certain detection tasks. We focus here primarily on simulating *Arabidopsis thaliana*'s light sensory network. Priliminary results are presented below using BDEs (Boolean Delay Equations).

Cross-frequency coupling of oscillatory neuronal activity between brain regions

Angela Onslow, Matt Jones, Rafal Bogacz

EPSRC Showcase Poster Session

The mechanisms by which distinct brain regions bind different sources and types of information - such as associating colour, shape and use with a perceived object, or using memories to plan future actions, are currently unknown. However, one phenomenon which presumably reflects coordination of activity across neuronal networks during such cognitive processing is the cross-frequency coupling of oscillatory activity between brain regions.

We present a detailed analysis of three proposed methods for determining the strength and significance of coupled activity across a range of frequencies in local field potential recordings. Comparison of Cross-Frequency Modulation Index [1], Cross-Frequency Coherence [2] and Envelope-to-Signal Correlation [3] performance on simulated data revealed that whilst the Modulation Index gave the most reliable results, it was adversely affected by the use of short data windows, a desirable feature if the methods are to detect rapid, behaviour-related changes in cross-frequency coupling. The performance of all three methods was found to be greatly influenced by the choice of filter design, which has become a focus of current work.

Future work will use these methods to analyse data recorded from the hippocampus and prefrontal cortex of rats performing a T-maze task, relating changes in coupling with dynamic behavioural demands on learning, memory and decision-making. Results will be incorporated into computational models of hippocampal-cortical interactions, with a view to shedding light on the mechanisms and functional consequences of network coordination during cognition.

[1] High gamma power is phase-locked to theta oscillations in human neocortex, R. T. Canolty, E. Edwards, S. S. Dalal, M. Soltani, S. S. Nagarajan, H. E. Kirsch, M. S. Berger, N. M. Barbaro & R. T. Knight – *Science* 313 (2006) 1626-1628

[2] Gamma power is phase-locked to posterior alpha activity, D. Osipova, D. Hermes & O. Jensen – *PloS ONE* 3(12) (2008) e3990

[3] Task-related coupling from high- to low-frequency signals among visual cortical areas in human subdural recordings, A. Bruns & R. Eckhorn – *International Journal of Psychophysiology* 51 (2004) 97-116

The Evolution of Calcium Cell Signalling

Matt Oates, Julian Gough, Alistair Hetherington

EPSRC Showcase Poster Session

A good measure of complexity in higher organisms is the number of different cell types, from 3 in some fungi up to 170 in humans. The abundance of many protein domains that are involved in extracellular processes correlate with the number of cell types. One such extracellular process is the complex system by which cells communicate between each other via signalling pathways. The aim of this project is to understand how the complexity of calcium signalling pathways has emerged in higher organisms over evolution.

A survey of known calcium signalling protein domains is given, based on the defined "Calcium Toolkit" found in the literature. Comprehensive predictions of proteins containing these domains in all completely sequenced genomes are given. Such a database is likely, as a byproduct, to be of great utility to the molecular biology community working on cell-signalling. However, its purpose in the context of this project is to provide an annotation of the building blocks of intracellular signalling in all genomes, which can be mapped onto a phylogenetic tree of life to reveal how they have emerged over evolution. This will begin to address the more profound question of how cellular complexity has evolved.

Quantifying Distortion in the Drosophila Eye Phenotype

Quentin Caudron, John Aston, Bruno Frenguelli, Kevin Moffat

EPSRC Showcase Poster Session

The presence of hyperphosphorylated tau protein in nerve cells leads to the self-assembly of insoluble neurofibrillary tangles, which results in cell death. When tau is expressed in the eye of the common fruit fly, these tangles accumulate and a degradation of the structure of the eye becomes apparent. In this study, we create quantitative descriptors for the appearance of the *Drosophila melanogaster* eye phenotype using methods from stereology and image processing. We use scanning electron microscopy images as a data set, from which relevant structural information related to individual ommatidia is extracted. Using edge detection and boundary-walk algorithms, we analyse the distributions of areas and area-to-perimeter ratios of ommatidia in an attempt to measure their regularity of shape, and locate geometric centroids for each ommatidia to calculate distances to nearest neighbours. This information is used as a robust measure of disorder in the *Drosophila* eye phenotype, allowing direct comparison between different strains of fly, and providing insight into the nature of protein-protein interactions.

Engineered Bacterial Outer Membrane Vesicles (iGEM 2009)

Stephen Reid, Petros Mina, Panayiotis Sterghides, Mattia Fazzini, Antos Matyjaszkiewicz, Emily Nicoli

EPSRC Showcase Poster Session

The International Genetically Engineered Machine competition (iGEM) is the premiere undergraduate Synthetic Biology competition. Student teams are given a kit of biological parts at the beginning of the

summer from the Registry of Standard Biological Parts. Working at their own schools over the summer, they use these parts and new parts of their own design to build biological systems and operate them in living cells.

This year, the Bristol team aims to construct a system for directed delivery of proteins into cells by outer membrane vesicle (OMV) protein secretion. Lab work will be informed by an enhanced version of the BSim agent-based modelling framework, with a greatly expanded feature set and increased biological realism.

Gram-negative bacteria naturally produce outer membrane vesicles (OMVs): spherical, bilayered proteolipids from 20-200nm in diameter. OMVs can carry outer membrane, periplasmic and cytoplasmic proteins, DNA, RNA and other factors associated with virulence. They have been implicated in the delivery of toxins to host cells, in the transfer of proteins and genetic materials between bacterial cells and in cell-to-cell signalling. Synthetic biology offers the potential to engineer these mechanisms for human benefit, for example, the injection of toxic cocktails of proteins into cancerous cells or the replacement of proteins missing as a result of genetic defects. These systems may be further enhanced by localised delivery of OMVs, for example, via the control of magnetotactic bacteria using external magnetic fields.

We intend to design Biobricks allowing the secretion of any protein in OMVs via fusion with novel, non-toxic partners known to be enhanced in OMVs. We hope that the Biobricks will become widely used as a simple and effective means of protein secretion, whilst also conveying the unique engineering advantages of vesicular encapsulation.

The mechanisms of magnetotaxis and OMV secretion will be implemented into BSim, the award-winning modelling framework developed by last year's Bristol team, to assist in experimental design and to test speculative ideas. Another key new feature will allow users to 'plug in' gene regulatory network models and see their effect at the population level.

Waving goodbye to traffic jams

Martine J. Barons

EPSRC Showcase Poster Session

Traffic flow can be modelled as a density of microscopic particles like a fluid, or as individual cars with drivers making decisions based on the information they have. The aim of this study was to further the understanding of the connection between these two descriptions by comparing traffic flow described by a scalar conservation law model and by a cellular automata model. The simulations based on cellular automata support the conclusion that the corresponding conservation law describes the large scale microscopic description correctly using just standard entropy conditions. This discovery was partly unexpected. The cellular automata model showed stationary patterns producing spatially separate high and low density phases which existed in all sizes and for which no typical size can be identified, in correspondence with observations of real traffic flow. The cellular automata model was also induced to produce stable stop and go wave behaviour over a many-run aggregation, and an attempt was made to scale this up to physically realistic spatiotemporal size with partial success. The purpose of this study was to identify whether the Lighthill, Whitham and Richards PDE model can be made to predict the behaviour of the microscopic cellular automata model, whether new entropy conditions are needed, and if there is any relation between these and observed real data. The flow of road traffic can be modelled on a microscopic level, for example by cellular automata, and on a macroscopic level by partial differential equations (PDE). There is not full agreement between these two descriptions, particularly in the fact that simple Markov chain models are capable of predicting all the basic space-time patterns of real traffic whilst the macroscopic models are not. A simple Markov model is used to demonstrate the successes and limits of reproducing physically realistic traffic behaviour with a microscopic model. The connection with the macroscopic model described by the

classic Lighthill, Whitham and Richards (LWR) PDE model is shown through the analysis of the flux / density diagram, called the Fundamental Diagram. Data samples from the M42 motorway were used to compare with the output of both models to assess their accuracy in predicting the behaviour of real traffic. In the 1950s James Lighthill and Gerald Whitham, two experts in fluid dynamics, (and independently P. Richards) thought that the Navier-Stokes equations describing the flow of water could be used to describe the flow of vehicular traffic. Treating vehicles as small particles and their density as the main quantity to be considered, the assumption is made that the number of cars is conserved, making this a conservation law. Since traffic jams display sharp discontinuities, there is a correspondence between traffic jams and shock waves. As solutions to fluid dynamic models can develop discontinuities in finite time, even starting from smooth initial data, such models for traffic flow seem appropriate. This conservation law is well described by an extensive and mature PDE theory which includes consideration of characteristics of the equation, weak solutions and admissibility criteria. Cellular automata models are similarly well studied in many applications, and special cases have been identified. In relation to traffic, they have been used with various rules for driver behaviour. None of the approaches taken so far has been entirely satisfactory in predicting real traffic, particularly spatiotemporal patterns like stop and go waves, and there is some disagreement within the traffic modelling community as to the best approach. The simulation example of the density bump was analysed by examining density profiles at representative intervals. This revealed that the behaviour of the simulation was the behaviour predicted by the Lighthill, Whitham and Richards PDE model with standard entropy conditions. The conclusion drawn is that the connection between the microscopic and macroscopic descriptions of traffic have been shown to exist through the Fundamental Diagram. The macroscopic model is, somewhat unexpectedly, able to describe correctly the microscopic model on large scale without the need to derive some new entropy solutions. The conclusion can be drawn that the microscopic model is able to connect with real data, despite its simplicity, in producing Fundamental Diagrams which are a fairly good fit using parameter values which have a reasonable physical interpretation. Stop and go waves are a feature of particular interest, since in real traffic they are a cause of so much wasted resources. A successful model of these would pave the way to their reduction and perhaps elimination. This simple microscopic model is capable of producing stop and go wave behaviour which corresponds to the physical system in important ways. Future work may include investigation into the stability of simulated stop and go waves on physical scales. This is known to be hard, as it usually leads into parts of the model parameter space which produce non-physical traffic behaviour. The discovery of a functional form for the Fundamental Diagrams produced by the simulations or by real data could be connected to the macroscopic description via examination of the function's characteristics.

A pain in the back!

Martine J. Barons

EPSRC Showcase Poster Session

The data from a complex intervention for lower back pain was subjected to secondary analysis using neural network machine learning techniques. A complex intervention is a treatment regime comprising a number of components that may act both independently and inter-dependently. In this case the treatment for persistent low back pain included written material in the form of The Back Book, physiotherapist consultation and a series of six cognitive behavioural therapy sessions. The proportion of the population with low back pain over a year, its annual period prevalence, is approximately 37%. A 1998 UK study found that 75% of those with low back pain who consulted their general practitioner still had symptoms one year later, and 30% of them had developed persistent, disabling low back pain. The direct health care costs associated with low back pain were 32 million in 1998, the majority spent on physiotherapy and general practice. A randomised controlled trial of this complex intervention was carried out; from April 2005 to April 2007 patients who met the eligibility criteria were recruited and followed up for one year. The average improvement in the disability and pain measures used were found to be statistically

significant, demonstrating the long-term effectiveness of a cognitive behavioural approach to treating low back pain. It was also demonstrated to be cost-effective. However, an individual experiencing an average improvement would not perceive any change, and a different definition for improvement is required when considering an individual. There is a need to establish if baseline factors are important predictors of treatment response. Low back pain is defined as pain of a musculo-skeletal origin in the area bounded above by the 12th rib, and below by the gluteal folds. The comparative adjectives acute, sub-acute and chronic are counterintuitively defined as follows: Acute pain is defined as that lasting six weeks or less, sub-acute as lasting six to twelve weeks, and chronic pain as lasting more than three months. The Recruitment of participants to the trial was limited to those with sub-acute and chronic pain, and excluded those whose pain was caused by a serious disorder. Catastrophic beliefs are a patient's belief that they are disabled and that increased pain signifies harm and the need to restrict activity. Pain behaviours are suboptimal behaviours engaged in because of the experience or fear of pain, such as holding oneself stiffly, or poor posture. Typically these exacerbate the back pain situation. In contrast, increased patient confidence that they are not disabled and that pain is not an indicator of serious problems leads to fewer pain behaviours, reduced incidence of depression, and fewer long term problems. Fear avoidance is the avoidance of a feared activity or pain, and has been consistently and strongly associated with the progression of acute low back pain to disability. The Back Book, given to all participants, was designed principally to challenge negative beliefs and behaviours, rather than to impart factual information. Those randomised to the cognitive behavioural approach arm of the study were, in addition, given the opportunity to attend six, weekly group sessions led by a health professionals (nurse, psychologist, occupational therapist or physiotherapist) who had received a two-day training course in leading cognitive behavioural training sessions. As well as receiving messages relating to challenging catastrophic beliefs and pain behaviours, the participants were able to give and receive feedback on how these had been implemented in practice during the treatment phase. Some participants reported that the interaction with others in the same (or worse) situations as themselves was the most beneficial element of attending these sessions. Pain self-efficacy is a measure of the patient's confidence to carry out activities despite the back pain. The intervention is aimed primarily at increasing pain self-efficacy and so to reduce fear avoidance and avert progression towards disability. Pain self-efficacy is not prima facie the only indicator of the outcomes of interest, namely attendance at cognitive behavioural training sessions, compliance with the treatment, or appreciable improvement in the patient's condition. In order to address the need to need to establish if baseline factors are important predictors of treatment response, data mining was undertaken on the extensive dataset collected as part of this trial. Baseline measurements were taken at the beginning of the trial, and repeated at three months, six months and twelve months. The six cognitive behavioural sessions took place within the first three months. The data records for those patients who were not randomised to the cognitive behavioural approach trial were excluded, as were those for those for whom either input data or outcome information was missing. This left a usable dataset of 291 participants (from the initial 705) for whom all desired information was available. The neural network machine learning techniques were applied to the data to classify participants into subgroups of interest: those who attended at least one cognitive behavioural group session, those who attended at least three, and were therefore considered to have complied with the treatment, and those who experienced improvement of at least three points on their RMQ score. The predictors used as inputs to the neural network were all the baseline data except for those items which could not readily be assigned numerical values, such as comments and descriptions. The initial results give success in predicting the three items of interest varied from 65-70% for compliance with the treatment to 70-74% for significant improvement and 72-76% for attendance at at least one session. Further testing was carried out using only RMQ baseline score and Modified Von Korff scores as inputs, and for different sizes and methods of choosing the training set for the neural network.

Inferring protein signalling networks in cancer using dynamic Bayesian networks

Steven Hill, Yiling Lu, Gordon Mills, Sach Mukherjee

EPSRC Showcase Poster Session

Intracellular protein signalling plays an important role in the control of cell function. Aberrations in signalling behaviour play a key role in the biology of cancer. We utilise dynamic Bayesian networks (DBNs) to infer protein signalling networks from noisy, continuous time series data. Employing DBNs (as opposed to static Bayesian networks) allows for the inference of regulatory feedback. Also, our Bayesian approach enables the incorporation of existing biological knowledge into inference. We propose a method for generating realistic noisy simulated data from a published ODE simulation. This data is then used to test our inference methods and probe questions of experimental design. We also apply the method to proteomic time series data from breast cancer cell lines.

Out-of-Equilibrium Economic Dynamics

James Porter, Sayantan Ghosal

EPSRC Showcase Poster Session

Common Economic approaches make strong assumptions; typically to ensure that there is a unique, stable equilibrium which will be reached in negligible time if indeed the question of reaching an equilibrium is dealt with at all. Our work looks at what happens when we strip away some of these assumptions. We draw on analytical and computational techniques to analyse the case study of an exchange economy. Dramatically limiting the amount of information agents are assumed to have we show, analytically, that we do still get convergence to a (Pareto) optimal outcome, the limit is non-unique. Furthermore when examined numerically we find that convergence is a very slow yet unstable process. We extend this work by introducing some “imperfections” in trading: agents are willing to make “bad” trades.

Inference and Complexity in Complex Composite Systems

David Saad, David Lowe, Roberto Alamino, Jack Raymond, Etienne Mallard

EPSRC Showcase Poster Session

This project tackles a particularly demanding area of composite systems: complex systems of interacting subcomponents where there is a combination of local interactions between subcomponents together with a different scale of longer range interactions. We employ a framework based on inherently distributive and approximative probabilistic approaches for studying composite networks. The methods we use to describe uncertainty, information transfer and emergent properties in complex systems are based on complex connected graphs, that in conjunction with methods of statistical physics, facilitate the decomposition of high dimensional joint distributions into simpler, computable quantities. The novelty of the project stems from the focus on systems which exhibit this composite character: a combination of localised and long range, sparse and dense, weak and strong interactions between subcomponents in such graphs. Here we present all the results and achievements related to this project so far.

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