Grafting gene networks.
Supervisor: Nigel Burroughs (WSBC).

Introduction: Inferring gene regulatory networks has been an area of intense research for decades with the development of a number of statistical and machine learning methods, these all being primarily based on correlation or information frameworks. However, utilising multiple experiments to infer a global network remains highly problematic, particularly for causal network inference from time-series data. This is because network inference requires simple models to be used because of low data complexity, models that can be considered a linearization of the dynamics about one point in phase space. Different experiments are linearised about different points; hence for widely separated points the linearised models do not cover more than one experimental data set.

Data: 3 microarray time series data, 20-40 time points per time series. 8000 genes, of which about 1000 are differentially expressed in each time-series.

Project:

1. You will learn about Bayesian network inference using Markov chain Monte Carlo (MCMC) algorithms for sparse network models and information based network inference.

2. You will generate causal networks using our R package GRENITS, generating networks for each experiment. These networks will be compared for commonality and differences, both between data sets and to an information based network. A consistency network will be constructed.

3. A grafted network will be constructed incorporating both evidence for links, but also differential expression. This will require a probabilistic model to be constructed and implemented in MatLab, R or C++.

Skills: Knowledge of MCMC. Programming in MatLab, R or C++.

Potential for a PhD. The PhD project would involve inference of root nodulation regulatory networks in plants where we have extensive time series data for 2 plants, 2 tissues over 3 conditions, (20 time points). The idea is to integrate the data to construct a global network, possibly using the grafting ideas above, and compare across species. The biological supervisor would be Miriam Gifford.