

Programme of the Annual Scientific Conference Monday 22nd and Tuesday 23rd April 2024 UKHSA, COLINDALE

DAY 1 Monday 22nd April 2024

12:00 pm Registration and Lunch

1:00 pm Welcome – Marie Chattaway & Paolo Ribeca, UK Health Security Agency

SESSION 1, Chaired by Xavier Didelot, University of Warwick

1:10 pm Microbiome response to antibiotics across multiple scales

Chris Quince (Earlham)

1:30 pm Diversity and distribution of mobile genetic elements in foodborne pathogens

Clare Barker (UKHSA)

1:50 pm A phylogenetic approach for estimating rates of gene gain/loss and selection

Caitlin Collins (Cambridge)

2:10 pm Classifying microbial species in contaminated disease-outbreak isolates using kmer

spectra-based multidimensional clustering

Ryan Morrison (UKHSA)

2:30 pm Knowledge mobilization

Noel McCarthy (Trinity College Dublin)

2:50 pm From research to routine - building the public health genomics programme in Wales

Tom Connor (Cardiff)

3:10 pm Coffee break/poster viewing

SESSION 2, Chaired by Noel McCarthy, Trinity College Dublin

3:40 pm KEYNOTE SPEAKER

Genomic platforms for surveillance of enteric fever and AMR

Kat Holt (LSHTM)

4:10 pm LineageCapture: Phylogenetic identification of bacterial clade members excluded by

SNP clustering

Matt Moore (Warwick)

4:30 pm Projections for COVID-19, a tale of two problems

Matt Keeling (Warwick)

4:50 pm Microevolution during the emergence of pandemic monophasic Salmonella

Typhimurium ST34

Robert Kingsley (Quadram)

5:10 pm KPop: An assembly-free and scalable method for the comparative analysis of

microbial genomes

Paolo Ribeca (UKHSA)











DAY 2 Tuesday 23rd April 2024

09:00 am Registration, Coffee and Networking

SESSION 3, Chaired by Marie Chattaway, UK Health Security Agency

10:00 am KEYNOTE SPEAKER

Applying innovative genomic approaches to the prevention and control of infectious

diseases

Deborah Williamson (UKHSA)

10:30 am EnteroBase in 2024

Sascha Ott (Warwick)

10:50 am Fresh perspectives on bacterial variation: at genome scale and within patients

Gemma Langridge (Quadram)

11:10 am Detection and characterisation of Salmonella enterica serovar Infantis (eBG31)

harbouring blaCTX-M-1 causing clinical disease in humans in England.

Matt Bird (UKHSA)

11:30 am Distinguishing imported cases from locally acquired cases within a geographically

limited genomic sample of an infectious disease

Xavier Didelot (Warwick)

11:50 am An integrated approach for academic training and professional registration,

addressing inequalities for healthcare scientists

Marie Chattaway (UKHSA)

12:00 pm Group Photo, followed by Poster Viewing and Lunch

SESSION 4, Chaired by Paolo Ribeca, UK Health Security Agency

1:00 pm Harnessing Genomics for a One Health Approach: Insights from Salmonella Pathogen

Lead

Marie Chattaway (UKHSA)

1:20 pm Inference of infectious disease transmission through a relaxed bottleneck using

multiple genomes per host Jake Carson (Warwick)

1:40 pm Signatures of Pathogen Emergence

Julian Parkhill (Cambridge)

2:00 pm Cóimeáil: A Nanopore-based bioinformatics pipeline for the rapid typing and

characterisation of gastrointestinal pathogens

David Greig (UKHSA)

2:20 pm Exploring Black Perspectives on the Impacts of Patient and Public Involvement and its

Evaluation (The ELEVATE Study)

Jade Jordan (Warwick)

2:40 pm Deducing clonal complex population structure from gene content

Emily Fotopoulou (UKHSA)

3:00 pm Closing Remarks - Xavier Didelot







