

Agenda

TUESDAY 30TH AUGUST 2016

12noon **Registration Opens**

1.00pm - 2.00pm Lunch

2.00pm - 3.30pm **Conference Open and Opening Keynote**

Session Organiser: Neil Hall

- 14.00 - 14.45 Julian Hiscox (University of Liverpool) Delineating survival from a fatal outcome in Ebola virus disease in humans
- 14.45 - 15.30 Liz Worthey (Hudson Alpha) The clinical utility of whole genome sequencing in the context of rare and common disease

3.30pm - 4.00pm

Break

4.00pm - 6.00pm

Main Plenary Session - Technologies

Session Organiser: Mike Quail

- 16:00 - 16:30 Nick Loman (University of Birmingham) Genomics Goes Mobile: Trains, Planes and Autochthonous Transmission of Zika Virus
- 16:30 - 17:00 Kirsten McLay (Earlham Institute) and Mike Quail (Wellcome Trust Sanger Institute) 10X Genomics: A Tale of Two Cities
- 17:00 - 17:30 Illumina, Application of Illumina technology
- 17:30 - 18:00 Kosuke Yusa (Wellcome Trust Sanger Institute) Application of CRISPR technology

6.00 pm - 8.00pm Welcome Reception

The Courtyard @ The Liverpool Guild of Students

WEDNESDAY 31ST AUGUST 2016

8.00am

Registration Opens

9.00am - 10.45am

Parallel Sessions

Computational Biology

Session Organiser: Chris Ponting

- 9.00 - 9.15 am Thomas Smith (University of Oxford) UMI-Tools: Modelling sequencing errors in Unique Molecular Identifiers improves quantification accuracy in iCLIP and single cell RNA-seq
- 9.15 - 9.40 am - Julian Gough (University of Bristol) tba
- 9.40 - 10.05 am - Julia Steinberg (Wellcome Trust Sanger Institute) tba
- 10.05 - 10.20 am - Frank Dondelinger (University of Lancaster) Efficient High-Dimensional Disease Outcome Prediction in Heterogeneous Populations
- 10.20 - 10.45 am - Mina Ryten (University College London) tba

Microbial Genomics

Session Organiser: Kate Baker

- 9.00 - 9.15 am - Pablo Fuentes-Utrilla (University of Birmingham) Optimisation of the NexteraXT library prep protocol for the production of high quality bacterial genomes for a wide range of GC contents

- 9.15 – 9.40 am - Maria de Toro Hernando (Center for Biomedical Research of La Rioja) - How to reconstruct plasmids from NGS data? PLACNET: advantages and limitations.
- 9.40 – 10.05 am - Nicholas Grayson (Wellcome Trust Sanger Institute) – Sequencing 3000 Bacterial Genomes From Public Health England’s National Collection of Type Cultures
- 10.05 – 10.20 am - Georgia Kapatai (Public Health England) – Novel pneumococcal serotypes: When is a “serotype” a serotype?
- 10.20 – 10.45 am - David Aanensen (Imperial College London) – The Centre for Genomic Pathogen Surveillance

10.45am - 11.15am Break

11.15am - 1.00pm **Parallel Sessions**

Clinical and Translational Genomics

Session Organiser: Christiane Hertz-Fowler

- 11.15 am - 11.45 am Jose Clemente (Icahn School of Medicine at Mount Sinai) The neonatal microbiome: implications for health outcomes and therapeutic interventions
- 11.45 am - 12.15 pm Ana Alfirevic (University of Liverpool) Next generation sequencing and statin-induced muscle damage
- 12.15 pm - 12.30 pm Silvia Argimon (Wellcome Trust Sanger Institute) The Whole Genome Sequence Analysis Network – wgsa.net: a fast and scalable system for genomic surveillance of bacterial and viral pathogens

- 12.30 pm - 12.45 pm Rosie Coates-Brown (Central Manchester University Hospitals NHS Foundation Trust) Detection of low level mosaic variants using next generation sequencing in clinical practice
- 12.45 pm - 1pm Harry Noyes (University of Glasgow) Genomics of the Bantu expansion

Developmental Biology

Session Organiser: Matt Loose

- 11.15 am - 11.45 am Gert Jan C. Veenstra (Radboud University) tba
- 11.45 am - 12.15 pm Doug Menke (University of Georgia) Limbs, genitals, and the evolution of enhancer elements in reptilian genomes.
- 12.15 pm - 12.30 John Mulley (University of Bangor) Adaptation to low calorie diets and the genetic basis of diabetes in desert rodents
- 12.30 pm - 12.45 pm Alvina Lai (University of Oxford) The genome of the crustacean *Parhyale hawaiiensis*: a model for animal development, regeneration, immunity and lignocellulose digestion
- 12.45 pm - 1pm Abril Izquierdo (University of Nottingham) Assembly and analysis of transcriptomes of the Octopus: characterisation of transcripts associated with learning and memory

1.00pm - 2.00pm

Lunch and Poster Session

2pm - 3.45pm

Parallel Sessions

Workshops

1. ELIXIR (John Hancock, Earlham Institute), see https://docs.google.com/document/d/1PZc211W_202AalftgJHkujpccuErkZsx7_wJgWiXTFk/edit?usp=sharing for up-to-date agenda
2. Meet the Genome Biology Editor (Andrew Cosgrove)

Vendor Session

Session Organiser: John Kenny

3.45pm - 4.15pm Break

4.15 - 6.00pm **Parallel Sessions**

Microbial Communities and Metagenomics

Session Organiser: Konrad Paszkiewicz (Environmental Genomics)

- 16.15 - 16.45 Sonya Dyhrman (Columbia, NY) tba
- 16.45 - 17.15 Scott Handley (Washington University) Analysis of Viromes in IBD and AIDS
- 17.15 - 17.45 Mick Watson (Roslin Institute) The rumen microbial metagenome associated with high methane production in cattle
- 17.45 - 18.00 tba

4.15 - 6.00pm **Bioinformatics Showcase**

Chair: Nick Loman & Matt Loose

- 16:15 - 16:45 Brian Haas (Broad Institute) Fusion Transcript Discovery Using the Trinity Cancer Transcriptome Analysis Toolkit
- 16:45 - 17:00 David Emms (University of Oxford) OrthoFinder - Accurate gene orthogroup inference for cross-species comparisons of newly sequenced and existing genomes

- 17:00 - 17:15 Luca Venturini (Earlham Institute) Integrating multiple transcript assemblies for improved gene structure annotation with Mikado
- 17:15 - 17:30 Samaneh Kouchaki (University of Manchester) Application of Feature Descriptors to Alignment-free Visualisation of Metagenomic Data
- 17:30 - 17:45 Daniel Mapelson (Earlham Institute) Portcullis - Fast, reliable and accurate splice junction prediction from RNAseq data
- 17.45 - 18.00 tba

7.30pm - 10.00pm

Conference Social Event

PANAM Restaurant and Bar

THURSDAY 1ST SEPTEMBER 2016

8.00am **Registration Opens**

9.00am - 10.45am **Parallel Sessions**

Plant and Animal Genomics

Session Organiser: Mick Watson

- 09.00 - 09.35 Allan Downie (JIC) - Ash dieback: applying 21st century tools to a 21st century disease
- 09.35 - 10.05 Jeff Schoenebeck (Roslin Institute) - A Dog-centric Approach Towards Understanding the Genetics of Craniofacial Anomalies
- 10.05 - 10.25 Laura Kelly (to be confirmed) - Whole Genome Sequencing of 35 Fraxinus (Ash) Species to Identify Genomic Resources Against Tree Pests and Pathogens

- 10.25 - 10.45 Vicky Hunt - The genetic basis of parasitism in the Strongyloides nematodes

Single Cell Genomics

Session Organiser: Alistair Darby

- 09.00 - 09.35 Stefano Pagliara (University of Exeter) Microfluidic single-cell analysis and manipulation
- 09.35 - 10.05 Danielle Goudeau (Joint Genome Institute) tba
- 10.05 - 10.25 Syed Murtuza Baker (Manchester) Bioinformatics pipeline for Single-cell ATACseq
- 10.25 - 10.45 Richard Eccles (University of Liverpool) Implementation of nanolitre robotics for single genomics

10.45am - 11.15am

Break

11.15am - 1.00pm

Closing Plenary

Session Organiser: Nick Loman

- 11.15 - 11.45 Michael Baym (Harvard Medical School) Microbial Evolution Olympics
- 11.45 - 12.15 Jack Gilbert (University of Chicago and Argonne National Laboratory) tba
- 12.15 - 13.00 Ed Yong (author, *The Atlantic* staff writer and journalist) *I Contain Multitudes: The Microbes Within Us and a Grander View of Life*

1.00pm - 2.00pm **Close of meeting and announcement of prizes**

Book signing of *I Contain Multitudes* with Ed Yong

