

Genome Science

Biology, Technology & Bioinformatics

Day 1: Monday 1st September 2014

Registration: 1.00pm – 6.45pm Zoology

Check-in: 1.00pm – 3.00pm Lady Margaret Hall

Satellite Workshop: Cloud Infrastructure for Microbial Genomics (CLIMB)

The Medical Research Council has recently awarded £8.4m to the CLIMB consortium to support microbial genome bioinformatics and training. The consortium, comprised of Warwick, Birmingham, Cardiff and Swansea, is investing in computer hardware and storage infrastructure in order to provision the world's largest computing 'cloud' dedicated to UK academics engaged in microbial genomics research. This investment will be supported by a busy programme of training activities. Join us before the UK Genome Science meeting officially commences to find out more about what is planned, and help us shape the direction of the project.

Time: Monday 1st September 2014 11.30am – 1.15pm

Location: Lecture theatre B

Chair: Nick Loman (University of Birmingham)

11.30—11.35	Nick Loman <i>University of Birmingham</i>	Chair's introduction
11.35—12.00	Sam Sheppard <i>University of Swansea</i>	Introduction to the CLIMB project
12.00—12.30	Tom Connor <i>University of Cardiff</i>	Microbial bioinformatics in the cloud
12.30—13.00	Daniel Falush <i>Max Planck Institute</i>	Campylobacter genomics
13.00—13.15	Discussion	

Session 1: Opening Remarks & Keynote Lecture

Time: Monday 1st September 2014 3.00pm-4.00pm

Location: Lecture theatre A

Chair: Chris Ponting (MRC Functional Genomics Unit & CGAT, University of Oxford)

15.00—15.15	Chris Ponting <i>MRC FGU & CGAT, Oxford</i>	Opening remarks
15.15—16.00	Jackie Hunter <i>BBSRC</i>	From genome to phenome – the promise of big data

Parallel session 2a: Emerging Technologies

Time: Monday 1st September 2014 4.05pm-6.45pm

Location: Lecture theatre A

Chair: Mike Quail (Wellcome Trust Sanger Institute)

16.05—16.35	Clive Brown <i>Oxford Nanopore</i>	Methods and devices for DNA/RNA sequencing using nanopores
16.35—17.05	Chas André <i>PicoSeq</i>	Single-molecule DNA analysis with SIMDEQ
17.05—17.45	Coffee break	
17.45—18.15	Iain Macaulay <i>WTSI</i>	G&T-Seq: Combined DNA and RNA sequencing from a single cell
18.15—18.45	Gabriele Migliorini <i>ICR</i>	Capture Hi-C (cHi-C) identifies the chromatin interactome of colorectal cancer risk loci

Parallel session 2b: Genome Evolution

Time: Monday 1st September 2014 4.05pm-6.45pm

Location: Lecture theatre B

Chair: Chris Ponting (MRC Functional Genomics Unit & CGAT, University of Oxford)

16.05—16.35	Judith Mank <i>UCL</i>	The evolution of sexual dimorphism: Linking intra-sexual phenotypic and transcriptional variation across the genome
16.35—17.05	Aziz Aboobaker <i>Zoology, Oxford</i>	Understanding the biology of pluripotent stem cells from flatworms
17.05—17.45	Coffee break	
17.45—18.15	Chris Ponting <i>MRC FGU & CGAT, Oxford</i>	Seeking lncRNA function through experimental and computational genomics
18.15—18.30	Christoph Hahn <i>University of Hull</i>	Efficient recovery of complete organelle genomes and nuclear genes from genomic NGS data by baiting and iterative mapping
18.30—18.45	Amir Szitenberg <i>University of Hull</i>	The phylogenetic effect on the abundance of transposable elements in Nematoda

Wine Reception & Poster Session 1: 6.45-8.45pm (Zoology)

Day 2: Tuesday 2nd September 2014

Parallel session 3a: Big Data Analysis

Time: Tuesday 2nd September 2014 9.00am-12.45pm

Location: Lecture theatre A

Chair: Chris Yau (Wellcome Trust Centre for Human Genetics, Oxford)

9.00—9.30	Chris Yau <i>WTCHG, Oxford</i>	Quantifying the true extent of heterogeneity in the cancer genome: advanced computational methods for characterising uncertainty in tumour heterogeneity deconvolution
9.30—10.00	Oliver Stegle <i>EBI</i>	Modeling gene expression heterogeneity between individuals and single cells
10.00—10.30	Jean-Phillipe Vert <i>Institut Curie</i>	Reconstructing the 3D architecture of the genome
10.30—11.15	Coffee break	
11.15—11.45	Caleb Webber <i>MRC FGU, Oxford</i>	Disease, networks and epistasis
11.45—12.15	Julian Knight <i>WTCHG, Oxford</i>	From genetic association to function: insights from genomic mapping of regulatory variants in immune disease phenotypes
12.15—12.45	Magnus Rattray <i>University of Manchester</i>	Bayesian non-parametric methods for modelling transcription and its regulation

Parallel session 3b: Environmental Genomics

Time: Tuesday 2nd September 2014 9.00am-10.30am

Location: Lecture theatre B

Chair: Peter Kille (University of Cardiff) & Dawn Field (CEH, Wallingford)

9.00—9.30	Dawn Field <i>CEH</i>	Sequencing the Earth: Genomic Observatories and Ocean Sampling Day
9.30—10.00	Mark Blaxter <i>University of Edinburgh</i>	Wolbachia in nematodes: unexpected associations and palaeosymbiology
10.00—10.30	Rob Finn <i>EBI</i>	Towards understanding the functional and taxonomic repertoire of microbial communities using the EBI metagenomics portal

Coffee break: 10.30am-11.15am

Parallel session 3c: Proffered Abstracts

Time: Tuesday 2nd September 2014 11.15am-12.45pm

Location: Lecture theatre B

11.15—11.45	Krzysztof Poterlowicz <i>University of Bradford</i>	Probabilistic modelling of 5C and ChIP-Seq profiles reveal a high-resolution spatial genomic proximity network controlling epidermal keratinocyte differentiation
11.45—12.15	Daniel Wong <i>WTCHG, Oxford</i>	Epigenomic profiling of the MHC transactivator CIITA using an integrated ChIP-seq and genetical genomics approach
12.15—12.45	Stephen Sansom <i>Kennedy Institute, Oxford</i>	Population & single cell transcriptomics reveal the Aire-dependency, composition and relief from Polycomb silencing of self-antigen expression in thymic epithelia

Lunch: 12.45pm-2.30pm

Parallel session 4a: Bioinformatics Infrastructure

Time: Tuesday 2nd September 2014 2.30pm-5.45pm

Location: Lecture theatre A

Chair: Mick Watson (Roslin Institute)

14.30—15.00	Niklas Blomberg <i>ELIXIR</i>	The ELIXIR bioinformatics infrastructure: Data, Computing and Services to Communities
15.00—15.30	Michael Eberle <i>Illumina</i>	Building a Better Medical Genome
15.30—16.00	Geraldine Van der Auwera <i>Broad Institute</i>	Analyzing large cohorts without losing your mind: GATK's new reference model pipeline for variant discovery
16.00—16.45	Coffee break	
16.45—17.15	Matthew Addis <i>Arkivum</i>	Maintaining the long-term value of NGS data
17.15—17.45	Marghoob Mohiyuddin <i>Bina Technologies</i>	Addressing the most challenging variant calling in next generation sequencing and assessing its performance

Parallel session 4b: Plant Genomics

Time: Tuesday 2nd September 2014 2.30pm-5.45pm

Location: Lecture theatre B

Chair: Neil Hall (University of Liverpool)

14.30—15.00	Anthony Hall <i>University of Liverpool</i>	Mutant hunting in complex genomes
15.00—15.30	Richard Buggs <i>QMUL</i>	Can genomics help forestry?
15.30—16.00	Glenn Byran <i>James Hutton Institute</i>	The potato genome: Marker discovery, diversity studies and trait analysis
16.00—16.45	Coffee break	
16.45—17.15	Steven Kelly <i>University of Oxford</i>	Dissecting the regulatory network governing C4 photosynthesis through exploitation of natural variation
17.15—17.45	Darren Heavens <i>TGAC</i>	Back to BACs? A High-Throughput, low cost BAC sequencing pipeline

Session 5: Keynote lecture

Time: Tuesday 2nd September 2014 5.45pm-6.30pm

Location: Lecture theatre A

Chair: Rory Bowden (Wellcome Trust Centre for Human Genetics, Oxford)

17.45—18.30	George Weinstock <i>The Jackson Laboratory,</i>	Genomic studies of the human microbiome and disease
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Conference Dinner

Time: Tuesday 2nd September 2014 7.30pm-11.00pm

Location: Lady Margaret Hall

Day 3: Wednesday 3rd September 2014

Session 6: Sponsors Session

Time: Wednesday 3rd September 2014 9.00-10.30am

Location: Lecture theatre A

Chair: David Buck (Oxford Genomics Centre, WTCHG, University of Oxford)

9.00—9.20	Scott Brouillette <i>Illumina</i>	Accelerating the validation of genomic variants with CRISPR/Cas9 genome editing
9.20—9.40	Mike Lelivelt <i>Life Technologies</i>	Ion Torrent semiconductor sequencing update
9.40—10.00	Sudipto Das <i>Roche</i>	Tailoring approaches for whole exome & epigenome analysis from a FFPE sample perspective
10.00—10.10	Michelle Hiscutt <i>Beckman Coulter</i>	Automated solutions for NGS sample preparation
10.10—10.20	Paul Butler <i>Perkin Elmer</i>	Automation of NGS sample preparation: from benchtop NGS to genome centres
10.20—10.30	Dalia Daujotyte <i>Lexogen</i>	RNA-Seq sample prep does not need to be complicated

Coffee break: 10.30-11.15am

Parallel session 7a: Clinical Genomics

Time: Wednesday 3rd September 2014 11.15am-3.15pm

Location: Lecture theatre A

Chair: Nazneen Rahman (Institute of Cancer Research)

11.15—11.45	Nazneen Rahman <i>ICR</i>	Implementing genomic medicine – cancer predisposition as an exemplar
11.45—12.15	Ultan McDermott <i>WTSI</i>	Personalised cancer medicine in the era of genome sequencing
12.15—12.45	Sian Ellard <i>University of Exeter</i>	Genomic testing leads clinical care in neonatal diabetes: a new paradigm
12.45—14.00	Lunch and poster session 2	
14.00—14.30	Mark Pallen <i>University of Warwick</i>	Clinical microbial genomics and metagenomics: overview and applications
14.30—14.45	Hang Phan <i>WTCHG, Oxford</i>	Accurate and high resolution HLA typing from targeted exome sequencing data
14.45—15.00	Susanne Weller <i>University of Oxford</i>	“From bench to bedside” via bioinformatics: Advances in cancer research and diagnostic
15.00—15.15	Organisers	Closing remarks

Parallel session 7b: Microbial Genomics

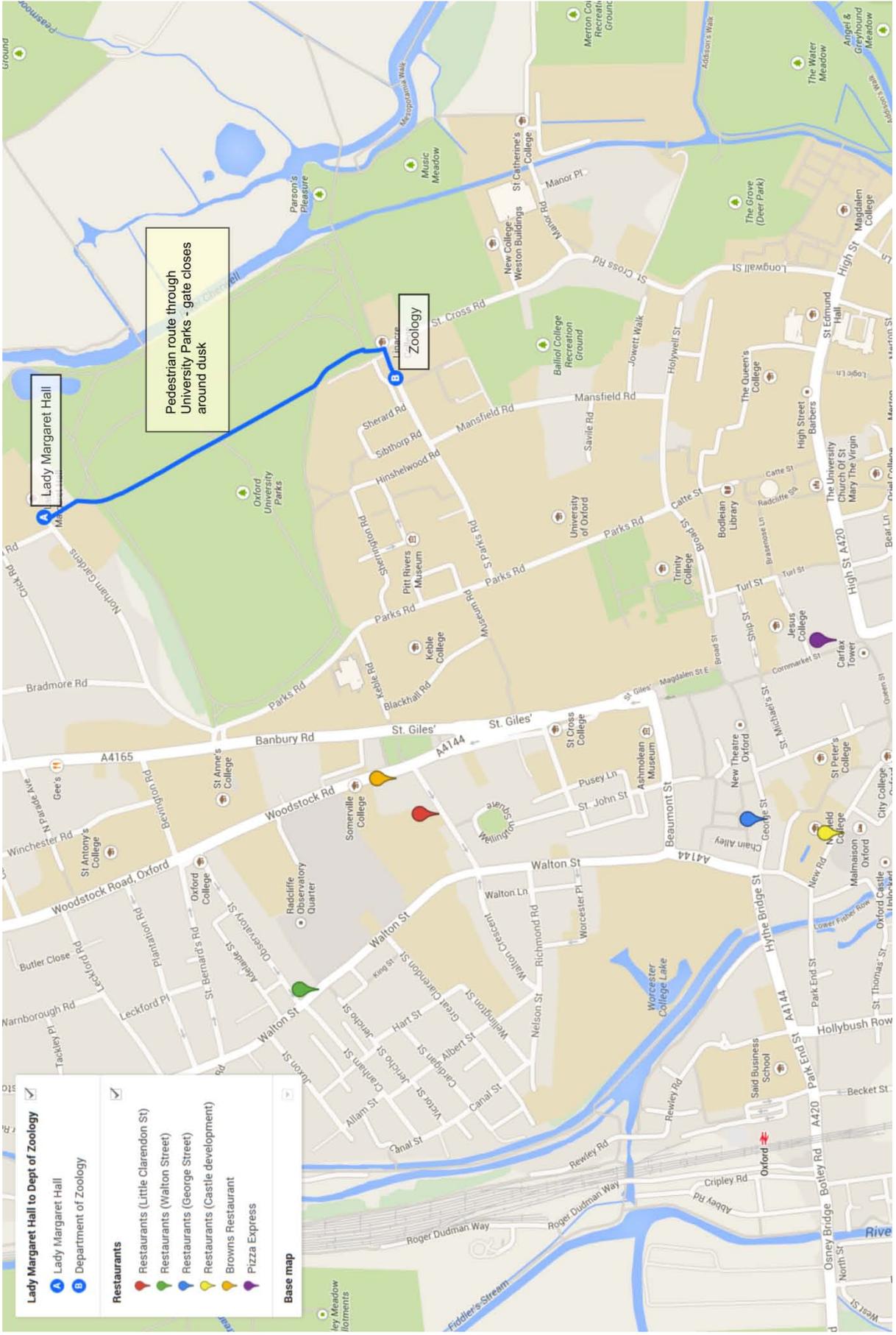
Time: Wednesday 3rd September 2014 11.15am-3.15pm

Location: Lecture theatre B

Chair: Nick Loman (University of Birmingham)

11.15—11.45	Nick Loman <i>University of Birmingham</i>	Nanopore sequencing in clinical microbiology
11.45—12.15	Zam Iqbal <i>WTCHG, Oxford</i>	Translation of sequencing from research to the clinic: an example
12.15—12.45	Holly Bik <i>UC Davis</i>	The genome deficit for microbial eukaryotes
12.45—14.00	Lunch and poster session 2	
14.00—14.30	Torsten Seemann <i>Monash, Melbourne</i>	Rapid bacterial outbreak characterization from high-throughput sequencing data
14.30—14.45	Camilla Ip <i>WTCHG, Oxford</i>	A pipeline for inferring the diversity of intra-host quasi-species of Hepatitis C virus genomes sequenced with a new probe-capture viral RNA-Seq (Illumina) protocol
14.45—15.00	Sebastian van Hal <i>University of Western Sydney</i>	Molecular epidemiology of Vancomycin Resistance <i>Enterococcus faecium</i> bacteraemia
15.00—15.15	Organisers	Closing remarks

Close: 3.15pm



- Lady Margaret Hall to Dept of Zoology**
- Lady Margaret Hall
 - Department of Zoology
- Restaurants**
- Restaurants (Little Clarendon St)
 - Restaurants (Walton Street)
 - Restaurants (George Street)
 - Restaurants (Castle development)
 - Browns Restaurant
 - Pizza Express
- Base map**

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