Genome Science 2015

University of Birmingham, 7-9th September

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WELCOME

Dear Delegates

Our warmest welcome to the University of Birmingham for the 6th Genome Science meeting. First held in Nottingham in 2010, we have always aimed to showcase the latest developments in genomics and sequencing technology, first-class genome biology (*Is genomics biology?)* and case studies in applied and translational genomics. This meeting, our largest yet, will be no exception. Many thanks to our organisation team: Hannah Eno, Jennie Law and Catherine Wardius and our team of student volunteers. We are also grateful for the generous support of our sponsors who help keep the cost of attendance low. Please ensure you visit all the stands and find out about the products and services on offer. The speaker line-up is incredibly strong, and I know this will be a fantastic meeting. Your feedback on how we can improve in the future is always appreciated. Genome Science 2016 will be held at the University of Liverpool.

I have you have a great meeting. Regards, Nick Loman *on behalf of the Organising Committee*:

Aziz Aboobaker, Holly Bik, Neil Hall, Chris Ponting, Mike Quail and Mick Watson

PROGRAMME

Monday 7 September

1300 – 1400   **Arrival, Registration and Lunch**
                 Great Hall, Aston Webb Building

Keynote speakers
Elgar Concert Hall, Bramall Music Building

Chair: Nick Loman, MRC Independent Research Fellow in Biomedical Informatics, Institute of Microbiology and Infection, University of Birmingham

1400   Daniel MacArthur, Assistant Professor and Group Leader, Analytic and Translational Genetics Unit, Massachusetts General Hospital
            From big data to biology: lessons from 60,000 human exomes

1445   Bill Hanage, Associate Professor, Department of Epidemiology, Harvard School of Public Health
            Is genomics biology?

1530   Coffee - Great Hall

Plenary: New Technologies
Elgar Concert Hall, Bramall Music Building

Chair: Mike Quail, Sequencing R&D Team Leader Wellcome Trust Sanger Institute

1600   **Keynote Speaker:** Mark Akeson, Professor Biomolecular Engineering, Co-Director, UCSC Biophysics Laboratory, University of California Santa Cruz
            Nanopore sequencing for DNA and protein sensing

1645   Daniel Turner, Senior Director of Applications, Oxford Nanopore Technologies
            Oxford Nanopore Updates

1715	Scott Brouilette, Senior Marketing Specialist, Illumina
	Illumina Updates

1730	Michael Schnall-Levin, VP of Computational Biology and Applications, 10X Genomics
	Unlock Powerful Genomics Insights with Linked-Reads: Introducing the GemCode Platform

1745	Cameron Frayling, Base4
	Caution! May contain nudity!

1815 - 1900 Posters and drinks – Great Hall

Followed by a barbecue at the Vale (accommodation location)

Tuesday 8 September

0900   Coffee, Great Hall

Parallel Session 1: Environmental Genomics
Arts Lecture Theatre, Arts Building

Chair: Holly Bik, Birmingham Fellow, School of Biosciences, University of Birmingham

0930	Luisa Orsini, Lecturer in Biosystems and Environmental Change, University of Birmingham
	Only time can tell: studying long-term evolutionary dynamics using biological archives

1000	Douglas Yu, Professor of Ecology, University of East Anglia
	Metabarcoding and mitogenomics for endangered species conservation and management

1030	**Abstract-selected talk:** Martin Ayling, The Genome Analysis Centre
	Metagenomic assembly with viral genomes

1045	**Abstract-selected talk:** Bede Constantinides, University of Manchester
	Characterising highly diverse RNA viromes in geographically distributed Venezuelan bats

Parallel Session 2: Single Cell Genomics
Lecture Theatre 1, Arts Building

Chair: Neil Hall, Professor of Functional and Comparative Genomics, University of Liverpool

0930	Sarah Teichmann, Research Group Leader, European Bioinformatics Institute, European Molecular Biology Laboratory
	Understanding cellular heterogeneity

1000	David Starns (RIKEN/University of Liverpool)
	Gotta Catch 'Em All – using single cell genomics to unravel termite nutritional symbioses

1030	**Abstract-selected talk:** Harry Noyes, University of Liverpool
	Direct discovery of bovine haplotypes by sequencing from single chromosomes

10:45	**Abstract-selected talk:** Justina Zuraskiene, Wellcome Trust Centre for Human Genetics, University of Oxford
	pcaReduce: combining k-means clustering and principal components analysis for hierarchical clustering of single cell transcriptional profiles

11.00 – 11.30 Coffee – Arts Building

Parallel Session 3: Functional Genomics
Arts Lecture Theatre, Arts Building

Chair: Aziz Aboobaker, Associate Professor in Genetics, University of Oxford

1130	Amy Buck, Wellcome Trust Research Career Development Fellow, Centre for Immunity, Infection and Evolution, University of Edinburgh *RNA and vesicle secretion by helminths: a new mode of parasite-host communication?*
1200	Tatjana Sauka-Spengler, Associate Professor of Genome Biology, Radcliffe Department of Medicine, University of Oxford *Pioneering the chromatin for neural crest specification*
1230	Anura Rambukkana, Professor of Regeneration Biology and Group Leader, Centre for Regenerative Medicine, University of Edinburgh *Bacterial-induced epigenetic reprogramming of adult tissue cell fate*

Parallel Session 4: Bioinformatics Showcase
Arts Lecture Theatre, Arts Building

Chair: Emily Richardson, Research Fellow, MicrobesNG, Institute of Microbiology and Infection, University of Birmingham

1130	**Sponsored Talk:** Dr Tim Bonnert, Associate Director of QIAGEN Advanced Genomics *Sample to Insight with QIAGEN bioinformatics*
1150	**Abstract-selected talk:** Mohammed-Amin Madoui, Genoscope, France *Microbial genome assembly using synthetic error-free reads*
1205	**Abstract-selected talk:** Matt Loose, University of Nottingham *Running and Reading in Real Time: Looking at Squiggles on the Oxford Nanopore minion*
1220	**Abstract-selected talk:** Tom Connor, University of Cardiff T*he Cloud Infrastructure for Microbial Bioinformatics (CLIMB)*
1235	**Abstract-selected talk:** Richard Leggett, TGAC *Flexible, multi-reference software for pre and post-alignment analysis of Nanopore sequencing data, quality and error profiles*

1300 – 1400   Lunch – Great Hall

Parallel Session 5: Plant and Animal Genomics
Lecture Theatre 1, Arts Building

Chair: Mick Watson, Head of Bioinformatics, Edinburgh Genomics, The Roslin Institute, University of Edinburgh

1400	Catherine Kidner, Professor of Plant Evolution and Development; Speciation Genetics, University of Edinburgh/Royal Botanic Gardens Edinburgh *Genetics and genomics of Begonia and understanding diversity*
1430	Paul Flicek, Senior Scientist and Team Leader, Vertebrate Genomics, European Bioinformatics Institute, European Molecular Biology Laboratory *Enhancers and the evolution of mammalian transcriptional regulation*
1500	**Abstract-selected talk:** Paul Bailey, The Genome Analysis Centre, *New Online Resource Provides Millions of Induced Mutations for Gene Function Analysis in Bread Wheat*
1515	**Abstract-selected talk:** Adam Hargreaves, University of Oxford, *Characterisation of snake venom gland transcriptomes using the Oxford Nanopore MinION portable single-molecule nanopore sequencer*

Parallel Session 6: Microbial Genomics

Arts Lecture Theatre, Arts Building

Chair: Dr Nick Loman, MRC Independent Research Fellow in Biomedical Informatics, Institute of Microbiology and Infection, University of Birmingham

1400	Jukka Corander, Professor, Faculty of Mathematics and Natural Sciences, University of Helsinki *Being the clairvoyant: Sequence Element Enrichment (SEER) analysis for deciphering genetic basis of bacterial phenotypes*
1430	Josh Quick, Bioinformatician, School of Biosciences, University of Birmingham *Portable Nanopore sequencing for pathogen sequencing*
1450	Lauren Cowley, PhD student, Public Health England *Sequencing Ebola in the field: a tale of nanopores, mosquitoes and whatsapp*
1510	**Abstract-selected talk:** Tom Connor, Cardiff University *Using genomics to define, explore and expand our understanding of the species Shigella flexneri*
15:20	**Abstract-selected talk:** Andrea Gori, PhD Student, University of Exeter *The distribution and composition of Campylobacter jejuni plasmid pan-genome*
1530	**Coffee – Great Hall**

Vendor sessions

Lecture Theatre 1 Arts Building

Chair: Christiane Hertz-Fowler, Centre Manager, Centre for Genomics Research, University of Liverpool

1600	Dr Herbert van den Berg, KAPA Biosystems *Evolved enzymes for NGS library preparation*
1620	Lynne Apone, Ph.D , New England Biolabs *Novel Solutions for Challenging NGS Samples*
1640	Beckman Coulter
1650	Steve Hughes, Hamilton Robotics *Genomic Automation – Rigid Implementation in a Flexible World*
1700	Thermo Fisher
1710	Sudipto Das, Roche *Exploring the genome and epigenome of metastatic colorectal cancer using a sequence capture strategy*
1720	Cambridge Biosciences *New High Performance Methods for RNA-seq and cfDNA sequencing*

Conference 'Street Food' dinner, Alfie Birds, Custard Factory, Digbeth
Transport provided from Great Hall, coaches at 6pm from outside the Barber Institute

Wednesday 9 September

0900   Coffee, Great Hall

Parallel Session 7: Clinical Genomics
Arts Lecture Theatre, Arts Building

Chair: Andrew Beggs, Clinical Lecturer in General Surgery, School of Cancer Sciences, University of Birmingham

0930   Sarah Ennis, Professor of Genomics, School of Medicine, University of Southampton
                Paediatric exomes: diagnostic and data dilemmas

1000   Pippa Thomson, Lecturer, Centre for Genomic and Experimental Medicine, School of Molecular,
                Genetic and Population Health Sciences, University of Edinburgh
                Using high-throughput sequencing to understand the genetic complexity of psychiatric illness

1030   Anthony Rogers, Congenica
                Why we care about rare diseases

1045   ***Abstract-selected talk:*** *Saskia Sanderson,* Department of Genetics and Genomic Sciences,
                Icahn School of Medicine, New York, NY, *Should everyone have their genomes sequenced?
                Insights from interviews with personal genomics research participants*

1100   Coffee – Great Hall

Parallel Session 8: Computational Genomics
Lecture Theatre 1, Arts Building

Chair: Chris Ponting, Professor of Genomics at the University of Oxford and an
Associate Faculty member at the Wellcome Trust Sanger Institute

0930   Martin Taylor, Group Leader, Biomedical Systems Analysis, Institute of Genetics and Molecular
                Medicine, MRC Human Genetics Unit, University of Edinburgh Western General Hospital
                The frequent evolutionary birth and death of functional promoters

1000   Gosia Trynka, Group Leader, Wellcome Trust Sanger Institute, Immune Genomics
                Using epigenetics for biological interpretation of complex trait associations

1030   ***Abstract-selected talk:*** Nicholas J Harding, Wellcome Trust Centre for Human Genetics,
                University of Oxford
                *Challenges of fine and broad scale diversity in the genome of the malaria vector Anopheles
                gambiae*

10:45   ***Abstract-selected talk:*** Mick Watson, Head of Bioinformatics, Edinburgh Genomics
                Is this the end of RNA-Seq alignment? Benchmarking RNA-Seq quantification tools

Plenary session
Elgar Concert Hall, Bramall Music Building

Chair: Nick Loman, MRC Independent Research Fellow in Biomedical Informatics, Institute of Microbiology and
Infection, University of Birmingham

1130   Inês Barroso Head of Human Genetics at the Wellcome Trust Sanger Institute and leader of the
                Metabolic Disease Group
                Genomics and Metabolic Disease – what have we learned so far?

1215   Matthew Cobb, University of Manchester
                Life's greatest secret: the story of the race to crack the genetic code

1300   Conference close

**Dr Matthew Cobb will be signing copies of his new book in the coffee area of the Bramall Building after his
talk.**

Posters

1. Laura Oikkonen, University of Oxford
   Making the most of RNA-seq: Pre-processing sequencing data for reliable SNP variant detection
2. Stefan Bagby, University of Bath
   Use of MinION data to assemble the 67% GC genome sequence of Bordetella pertussis
3. Dagmar Frisch, University of Oklahoma
   Paleogenetic records of Daphnia pulicaria in two North American lakes reveal the impact of cultural eutrophication
4. M.W.Wojewodzic, University of Birmingham
   Seeking for Transgenerational Effects of Diet Quality in Clones –Ecophysiological and RNA-seq approaches.
5. Tamsin M. O. Majerus, University of Nottingham
   Investigation of the genetic control of colour-pattern in the 2- and 10-spot ladybirds
6. Lisa Crossman, University of East Anglia
   Marine Streptomyces genomes from Illumina and Nanopore sequences
7. Gloria Despacio-Reyes, Wellcome Trust Sanger Institute
   Using new transcriptomic data to improve the annotation of long non-coding RNA genes
8. Bhavana Harsha, Wellcome Trust Sanger Institute
   Comparative genomics of Onchocerca volvulus
9. Katherine Fawcett, University of Oxford
   De novo point mutations in patients diagnosed with ataxic cerebral palsy
10. Deepa Manthravadi, Wellcome Trust Sanger Institute
    The HAVANA Manual Annotation of Vertebrate Genomes: creating comprehensive gene sets for human and mouse
11. Georgia Kapatai , Public Health England
    Molecular pneumococcal capsular typing using whole genome sequencing: moving the Streptococcus pneumoniae reference service into the genomic era.
12. Michael Clark, University of Oxford
    Quantitative gene expression profiling with targeted RNA sequencing
13. Matthew Gemmell, University of Aberdeen
    Comparison of 16S rRNA v1-2 and v3-4 regions for bacterial community analysis in stool samples using Illumina MiSeq V3 chemistry
14. Reema Singh, University of Dundee
    Refined Transcriptome Annotation via de novo Assembly in Two Social Amoeba Species
15. Adam Peltan, New England Biolabs
    Repair of challenging FFPE DNA improves library success rate and sequencing quality
16. Chris Lounds, New England Biolabs
    Hemoglobin Depletion Increases Sensitivity of Next Generation Sequencing-based Profiling
17. Lynne Apone, New England Biolabs
    High Quality Library Construction and Reliable Quantitation with NEBNext Reagents
18. Fiona Stewart, New England Biolabs
    NGS Library Preparation Method for Transcriptome Profiling With Enhanced Sensitivity of Transcript Detection
19. Ian Sudbery, University of Sheffield
    The trouble with UMIs
20. Avraam Tapinos , University of Manchester
    Alignment by numbers: Sequence assembly using compressed numerical representations
21. Nicole Gruenheit, University of Manchester
    REMI-seq – a step change in Dictyostelium functional genomics
22. Dave Baker, The Genome Analysis Centre
    High Throughput Development of Pacbio 20kb Template Preparation
23. Judith E. Risse, University of Edinburgh
    Catching shufflons in the act: Using nanopore reads to study Bacteroides fragilis
24. Oliver Deusch, Waltham Petcare
    The adolescent feline faecal microbiome: a longitudinal study into the effects of age,
25. Neil Pearson, The Genome Analysis Centre
    3D printing for rapid laboratory prototyping
26. Darren Heavens, University of Edinburgh
    A method to simultaneously construct up to 12 different sized Illumina Nextera long mate pair libraries with reduced DNA, time and costs
27. Teri Evans, University of Nottingham
    The genome of the salamander Ambystoma mexicanum
28. Bert Overduin, University of Edinburgh
    Bioinformatics Training for Genomics – One year on