

Organising Committee

Nick Loman

MRC Special Training Fellowship in Biomedical Informatics
University of Birmingham



Nick works as an Independent Research Fellow in the Institute for Microbiology and Infection at the University of Birmingham, sponsored by an MRC Special Training Fellowship in Biomedical Informatics. His research explores the use of cutting-edge genomics and metagenomics approaches to the diagnosis, treatment and surveillance of infectious disease. Nick has so far used high-throughput sequencing to investigate outbreaks of important Gram-negative multi-drug resistant pathogens such as *Pseudomonas aeruginosa*, *Acinetobacter baumannii* and Shiga-toxin producing *Escherichia coli*. His current work focuses on the genetic diversity of *Pseudomonas aeruginosa* infection in chronic lung diseases such as cystic fibrosis as a diagnostic and prognostic marker.

Mick Watson



Mick Watson works at The Roslin Institute and is currently Head of Bioinformatics at Edinburgh Genomics, a next-generation genomics facility at the University of Edinburgh, UK. Mick has over 15 years' experience of bioinformatics research, both in industry and academia. His current research at the University of Edinburgh, UK, uses computational and mathematical techniques to understand genome function, with an emphasis on transcriptomic analysis in systems of relevance to animal health and food security. Mick maintains a popular blog in which he expresses his opinions on all things omics – fittingly named 'opiniomics' – and is a strong supporter of open science.

Mike Quail



Mike Quail is team leader of the Sequencing Research and Development Group at the Sanger Institute which is involved in evaluating new sequencing technologies, ancillary equipment, molecular biology kits and reagents, and in development of new sequencing applications.

Aziz Aboobaker



Dr Aboobaker's research program looks to leverage the planarian model system to study basic questions about how tissue regeneration is orchestrated and the features of stem cell biology that facilitate this. His research focuses on the use of planarians to study the molecular mechanisms related to both aging and cancer. Highly regenerative animals solve the regeneration problem using different cellular solutions, including the use of pluripotent stem cells, lineage committed adult stem cells and dedifferentiation of tissue specific cells that regain potency.



Neil Hall

Neil Hall is Director of The Centre for Genomic Research and Head of the Department of Comparative and Functional Genomics and primarily studies the genomes of protist parasites such as Plasmodia (the causative agent of Malaria) and Trypanosoma (African sleeping sickness, leishmania and chagas disease) to identify the genes that are involved in interaction with the host. By identifying strains and species that have defined phenotypic differences we can use direct genome analysis to identify their genetic basis and study the rate at which genes are evolving. Dr Hall leads the Advanced

Genomics Facility at the School of Biological Sciences which is using high throughput pyrosequencing technology to study genomes and transcriptomes. He likes to be asked about his K-index.



Holly Bik

As an interdisciplinary computational biologist and strong advocate of the Open Access movement, Dr Bik maintains an online lab book and discusses high-throughput sequencing research at Eukaryotic Ebullience (including cross-posts from writing at the Molecular Ecologist). As a scientific contributor at Deep-sea News Dr Bik blogs alongside five other scientists in a quest to “demystify and humanize science in an open conversation that instills passion, awe, and responsibility for the oceans.”



Chris Ponting

Chris' research started with the discovery of many important protein domain families. He then provided leadership in international genome sequencing projects (including those for human and mouse) and, more recently, he forced a reconsideration of the extent and importance of transcribed noncoding DNA in the human genome. Chris is currently Deputy Director of the MRC Functional Genomics Unit. Chris has developed a world-leading expertise in the identification of novel protein domains such as GAF, HAMP, HhH, PDZ, PX, SAM, SPRY, START, Tudor, and ZZ domains. In order to provide access to these domain predictions, Chris teamed up with Peer Bork to launch the SMART domain research tool, which is a mainstay of protein annotation. In 1999, Chris became Programme Leader in the MRC Functional Genomics Unit and, within a year, had been invited to lead the Protein Analysis Section, with Alex Bateman, for the International Human Genome Sequencing Consortium's *Nature* publication. This led to contributions from his group to genome sequencing projects for mouse, rat, chicken, dog, opossum, platypus, zebrafinch, fruit flies, *Anolis* lizard and orangutan. Since then Chris' group has undertaken research on intellectual disability, predicted that over 10 per cent of the human genome is functional, demonstrated the functionality of noncoding RNA genes in mammals and fruitflies, and provided an online atlas of transcription for cortical cell layers in adult male mice.

Additional Session Chairs



Dr Andrew Beggs

Andrew Beggs is a Clinical Lecturer in General Surgery in the School of Cancer Sciences, University of Birmingham. He currently holds a Wellcome Trust Postdoctoral Fellowship for Clinician Scientists. His major research interests include colorectal cancer biology and translational medicine. He has published articles in *The Lancet*, *Gut*, *Journal of Pathology* and *PLoS Genetics*. He collaborated in writing the European consensus guidelines for the management of Peutz-Jeghers syndrome. His current research programme is examining the molecular stratification of rectal cancer. He is also carrying out research into soft tissue sarcoma using next generation sequencing technologies, biomarker development technologies and runs a bioinformatics “dry-lab” to search for novel therapeutic targets and stratification markers.

Speaker biographies



Professor Daniel MacArthur

Daniel is a group leader within the Analytic and Translational Genetics Unit (ATGU) at Massachusetts General Hospital. He is also Assistant Professor at Harvard Medical School and the Associate Director of Medical and Population Genetics at the Broad Institute of Harvard and MIT.



Dr Bill Hanage

Dr Hanage employs a mix of theoretical and laboratory work to research the evolution and epidemiology of infectious disease. Dr Hanage has worked extensively developing multilocus sequence typing (MLST; www.mlst.net) and analysis (MLSA) for the study of bacterial pathogens and species, as well as means of analysing data developed using this method. Along with his more theoretical projects he has worked on both bacterial (*Neisseria*, *Streptococci*) and viral pathogens (HIV-1, H1N1 influenza). He is particularly interested in using an evolutionary framework such as methods derived from the population genetics to inform epidemiology. He has acted as an advisor to Glaxo SmithKline and the World Health Organisation.



Professor Mark Akeson

Mark Akeson is a Professor in the Genomics Institute and the Biomolecular Engineering Department at UC Santa Cruz. He has been involved in nanopore sequencing technology development since 1996. His group pioneered the use of enzyme motors to regulate DNA movement through nanopore sensors at Angstrom scale. He is a consultant to Oxford Nanopore Technologies, UK.



Dr Clive Brown

Clive is Chief Technology Officer at Oxford Nanopore. On the Executive team, he is responsible for all of the Company's product-development activities. Clive leads the specification and design of the Company's nanopore-based sensing platform, including strand DNA/RNA sequencing and protein-sensing applications with a strong focus on scientific excellence and successful adoption by the scientific community. Clive joined Oxford Nanopore from the Wellcome Trust Sanger Institute (Cambridge, UK) where he played a key role in the adoption and exploitation of 'next generation' DNA sequencing platforms. This involved helping to set up the world's largest single installation of Illumina (formerly Solexa) Genome Analyzers in a production sequencing environment, initially used to pioneer the 1000 genomes project.

**Dr Luisa Orsini**

Lecturer in Biosystems and Environmental Change at the University of Birmingham whose research interest is understanding how natural populations adapt and evolve in response to environmental changes. The main objective of current research is to identify evolutionary causes and effects of population responses to climatic changes and predict their adaptive potential, and hence survival, to future changes. To meet this goal Dr Orsini studies the keystone species, the waterflea *Daphnia magna*, which is a keystone species in lentic environments and sentinel species for water quality, as well as key model in evolutionary biology and the study of adaptive responses to environmental change. *D. magna*

produces dormant stages which accumulate in sediments of lakes and ponds, resulting in a living history museum of local populations in the form of dormant propagule banks.

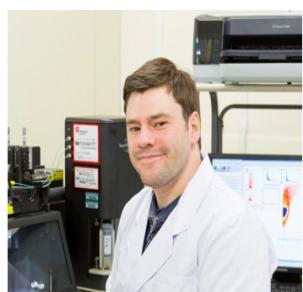
**Professor Douglas W. Yu**

Douglas Yu is a Professor at the University of East Anglia (Norwich, UK) and a Principal Investigator at the Kunming Institute of Zoology (Yunnan, China). His current research interests lie in microbiome evolution and in using genomics tools to improve institutional effectiveness in biodiversity conservation, such as creating DNA-based performance indicators for protected areas.

**Dr Sarah Teichmann**

Dr Teichmann is a research group leader at EMBL-EBI and senior group leader at the Wellcome Trust Sanger Institute. She is also a Principal Research Associate in the Department of Physics/Cavendish Laboratory and a fellow of Trinity College, Cambridge. She is a leader in systems biology, which aims to explain how individual molecules within a cell cooperate to produce the cell's overall behaviour. Her research also offers new insights into how proteins behave. After receiving her PhD in computational biology from the UK's MRC

Laboratory of Molecular Biology, where she returned to set up her own group in 2001, focusing on transcription factors, proteins that help control the activity of genes. This included building a database (www.transcriptionfactor.org) that allows researchers to search for genes predicted to encode transcription factors. Seminal work has shown how proteins club together to form larger 'machines', or complexes, by assembling via ordered pathways, and part of this is a further database, 3DComplex.org. Sarah is a co-founder of the state of the art Single Cell Genomics Centre, a joint EMBL-EBI/Sanger initiative to clarify how gene activity is controlled throughout single cells of different types. Her work has been recognised by a number of awards, including the Biochemical Society's Colworth Medal, the Lister Prize, the Royal Society Crick Lecture and membership of the European Molecular Biology Organisation

**Dr David Starns**

David started his PhD after graduating with a BSc in Biomedical science from the University of Essex in 2013. He is now completing a joint graduate studentship program at the University of Liverpool in collaboration with RIKEN, Japan with supervisors Alistair Darby, Neil Hall and Moriya Ohkuma. His current work is on the diversity of treponemes in the gut of termites and their roles in the degradation of recalcitrant wood.

**Dr Amy Buck**

Amy Buck earned her PhD in Biochemistry at the University of Colorado, Boulder, where she studied RNA-protein dynamics in the RNase P ribozyme in the lab of Professor Norman Pace. Wanting to apply her RNA background to the field of virology, she joined the Division of Pathway Medicine and the Centre for Infectious Diseases at the University of Edinburgh in 2005. She worked for 1.5 years as postdoctoral researcher to develop nucleic acid biosensors while writing an Incoming Marie Curie Fellowship to focus on the biology and functions of microRNAs

in viral infection. In 2009, she was awarded a BBSRC New Investigator award and an Advanced Fellowship at the University of Edinburgh to build her research group within the Centre for Immunity, Infection and Evolution and to initiate new lines of research on small RNA function and secretion in helminth models.

**Associate Professor Tatjana Sauka-Spengler**

Tatjana Sauka-Spengler is Associate Professor of Genome Biology at the Radcliffe Department of Medicine at the University of Oxford and runs a research group at the Weatherall Institute of Molecular Medicine. Professor Sauka-Spengler has interdisciplinary background and training in both physics and biology and her research is guided by a profound interest in understanding network organisation of gene regulatory programmes underlying developmental processes. One of the main focuses of her lab is on deciphering gene regulatory circuitry that orchestrates early specification steps in

the development of vertebrate neural crest cells.

**Professor Anura Rambukkana**

Professor Rambukkana's group at the University of Edinburgh studies a pioneering approach from a natural bacterial infection process with cellular reprogramming capacity to address the basic biology of stem cells and cell fate changes in adult tissues. Our recent discovery that human bacterial pathogens like *Mycobacterium leprae* hijacks the notable plasticity of its adult host tissue niche Schwann cells and reprogrammes them to stem cell-like

cells opens new premise of investigations not only for developing safer strategies for cell fate changes *in vivo* for tissue regeneration but also for targeting key host-encoded functions of cell reprogramming for combating bacterial infections, particularly the emerging global threat by drug/antibiotic resistant bacteria.

**Dr Catherine Kidner**

Dr Kidner's work looks at determining the genetics underlying differences between species, in particular understanding how many genetic changes and what type of changes cause variation in plant growth and form. A combination of classical genetics and new sequencing technologies is being used to link the variation in form to variation in the sequence and expression of genes. The research group is particularly interested applying these techniques to tropical species, as the tropics contain most of the world's diversity but have been

genetically understudied. As a study system the group is working on Begonia, a species rich genus (1500+ species) found in wet rainforests throughout the world, with a focus on Section Gireoudia. This is a group of about 66 Central American Begonia species, very variable in form and including many examples of convergent evolution, which makes it an excellent system to study the evolution of development.

Dr Paul Flicek



Paul Flicek is a Team Leader and Senior Scientist of the European Molecular Biology Laboratory and leads the Vertebrate Genomics Team at the European Bioinformatics Institute (EMBL's Hinxton Outstation) near Cambridge, England. He has strategic responsibility over the seven faculty groups that together deliver the collection of EBI resources for Genes, Genomes and Variation. He is head of the Ensembl project and also has leadership roles in data management activities for several international consortia. Paul's research is focused on genome annotation, comparative regulatory genomics and the evolution of transcriptional regulation. He is also interested in the large-scale infrastructure required for modern bioinformatics including storage and access methods for high throughput sequencing data. He has played a role in a number of major international efforts including the 1000 Genomes Project, ENCODE and the mouse, chicken, and various primate genome projects.

Professor Jukka Corander



Jukka Corander is a Professor of Statistics at University of Helsinki. He is the vice-director of the COIN Centre of Excellence in computational inference research, funded by the national research council of Finland. Corander has published over 140 scientific articles and he received the ERC starting grant in 2009 for development of intelligent inference algorithms in Bayesian statistics. The statistical methods introduced by the group of Corander have led to numerous discoveries on the evolution, virulence and transmission of pathogenic bacteria and viruses.

Josh Quick



Josh is currently undertaking a PhD in Bioinformatics with Nick Loman at the University of Birmingham and this follows a previous role as Systems Integration Engineer at Illumina. Josh has been involved in establishing genome surveillance in Guinea, West Africa.

Dr Lauren Cowley



Lauren Cowley is a PhD student at Public Health England working in the Gastrointestinal Bacterial Reference Unit. Her PhD is on the use of whole genome sequencing to understand the genetic basis for bacteriophage resistance and susceptibility in *Escherichia coli* O157. So far this has included sequencing the typing phages, analysing *E. coli* O157 long and short read sequencing data for gene association with phage type and building a TraDIS library of *E. coli* O157. Previous bioinformatics experience has included sequencing analysis of various strains of *E. coli* O157 and the typing phages and publications based on this. Lauren has also been involved in the

Ebola response and worked in Sierra Leone in PHE's diagnostic labs during December 2014 and in Guinea in the European Mobile Lab during June 2015. Her work in Guinea involved sequencing new positive cases of Ebola on the MinION and working closely with epidemiologists to intercept transmission chains. Lauren enjoys twitter and can be found with the handle @LaurenCowley4



Dr Sarah Ennis

Sarah Ennis leads the [Genomic Informatics](#) Group and works closely with Professor Andy Collins in Genetic Epidemiology. Her group specialises in the analysis of next generation sequencing data with numerous projects studying detailed genomic sequence with reference to human disease causality. Her work benefits from strong collaborative links with clinical staff at Southampton University Hospital Trust. She is based in the Duthie building on the hospital site and attracts postgraduate and postdoctoral staff with strengths in human biology, programming and statistics.



Dr Pippa Thomson

Lecturer and Psychiatric Genetics and Biology Group Leader at the Centre for Genomic and Experimental Medicine (CGEM) within the Institute of Genetics and Molecular Medicine (IGMM). Working in the laboratory of Professor David Porteous, and alongside colleagues from the Royal Edinburgh Hospital's Division of Psychiatry, Dr Thomson is using genetics to understand how the brain controls behaviour through studying genetic susceptibility to psychiatric illness (depression, bipolar disorder and schizophrenia). Dr Thomson was awarded an RCUK Fellowship in Translational Medicine (Genetics, Genomic and Pathway Biology), combining both genetic, statistical and molecular approaches to understand the genetic basis of major mental illness, and continues this work, using linkage, association and whole genome sequence analysis to

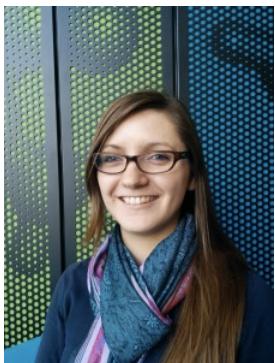
identify risk variants for mental illness and related quantitative traits such as cognition and mood, in both clinical and population-based cohorts. Key to this is using bioinformatics to understand the biological processes affected and integrating our understanding of the interaction between genetic and environmental effects acting on these complex phenotypes. In parallel, Dr Thomson uses molecular cell biology to investigate the functional effects of a risk variant in GPR50 a candidate gene for affective disorder. This has identified a potential role for GPR50 in neurodevelopment through the activation of the WAVE complex.



Dr Martin Taylor

Martin is interested in understanding how new DNA sequence changes arise and the consequences of those changes for human health. Many of the insights come from investigating the record of past evolution, using "the light of evolution" to explore the human genome. His main aims are centred around three interlinked themes: of Understanding mutational

processes, interpretation of genetic variation and the evolution of gene regulation. Prior to establishing the group in Edinburgh, Martin worked at the EMBL, European Bioinformatics Institute (EBI), with Dr Nick Goldman on the application of evolutionary models to understand genome evolution. Before this he was at the Wellcome Trust Centre for Human Genetics, at the University of Oxford, with Professor Richard Mott providing bioinformatics support to multiple research groups and pursuing his own research interests in evolutionary genomics. Martin maintained active participation in the international FANTOM consortium through each of these positions. During his PhD studies, Martin worked with Professor David Porteous on the characterisation of a chromosomal translocation that segregated with major mental illness, contributing to the discovery of the DISC1 gene. He obtained a BSc (Hons, 1st) in Genetics from the University of Liverpool.



Dr Gosia Trynka

Gosia Trynka is a group leader at the Wellcome Trust Sanger Institute where her group uses integrative approaches to identify and understand the role of genetic variants in modulating the immune system and in predisposing individuals to autoimmunity. She co-led international efforts to analyse the genetics of celiac disease, including conducting a genome-wide association study (GWAS) and an Immunochip-based study which together identified 57 non-HLA risk variants. More recently she developed statistical methods to integrate disease associated variants with epigenetic marks in order to identify pathogenic cell types and implicate plausible molecular mechanisms underlying association signals.



Professor Inês Barroso

Inês is Head of Human Genetics at the Wellcome Trust Sanger Institute and leader of the Metabolic Disease Group, which uses genetic and genomic approaches to understand the aetiology of common and rare forms of metabolic disease, as well as host genetics of infection. She joined the Wellcome Trust Sanger Institute in 2002, where she established the Metabolic Disease Group. Her team uses genetic and genomic approaches to understand the causes and mechanisms of common and rare forms of metabolic disease, with a focus on type 2 diabetes and obesity. More recently, her group has also been studying host genetics of infection. Her group uses genome-wide association approaches to identify genes with a role in obesity and quantitative traits related to type 2 diabetes. They have been leaders in large consortia, such as MAGIC and GIANT, that aim to increase power by performing meta-analyses across many different studies. Her team also uses re-sequencing approaches to identify rare variants (mutations) that may underlie disease in affected individuals with extreme forms of disease, (for example, severe early onset obesity). Lastly, to understand gene function her team are also using mouse models, such as classical knockouts and CRISPR/Cas9 engineered mutants, to gain insights into disease mechanism. Inês's work has to date led to the identification of hundreds of loci implicated in monogenic syndromes of insulin resistance, severe obesity or other cardiometabolic quantitative traits



Matthew Cobb

I am Professor of Zoology and am a member of three Faculty of Life Science research themes: Computational and Evolutionary Biology, Sensory and Computational Neuroscience and History of Science, Technology and Medicine. He earned his PhD in Psychology and Genetics from the University of Sheffield in 1984, and spent most of his career in France. He specialises in insect behaviour, with a focus on chemical communication and the olfactory responses

of *Drosophila* larvae. He recently co-edited *Insect Taste* and has translated a number of books on the history and philosophy of science. As well as writing for publications such as the *Times Literary Supplement*, the *Los Angeles Times* and *Permanent Revolution*, his book on the 17th century discovery of egg and sperm appeared in 2006 (*The Egg & Sperm Race*, published in the US as *Generation*). His history of the French Resistance in the Second World War will appear in June 2009 (*The Resistance: The French Fight Against the Nazis*).