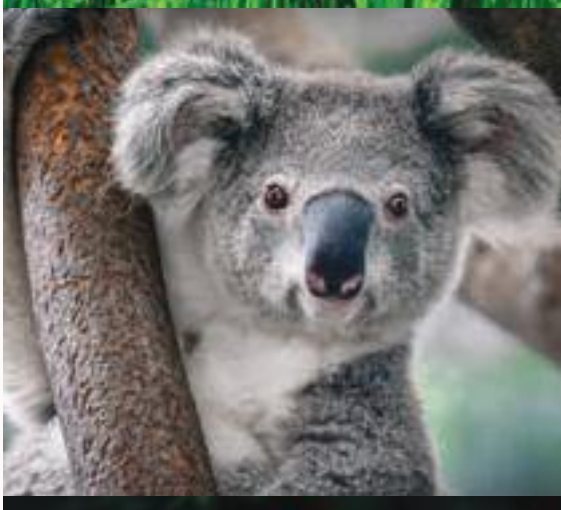

PROGRAMME

GENOME 10K & GENOME SCIENCE

29 AUG - 1 SEPT 2017

NORWICH RESEARCH PARK, NORWICH, UK

GENOME 10K

GENOME SCIENCE 2017

Genome 10K & Genome Science 2017.

Firstly, welcome to Norwich – 'A fine city' – and welcome, of course, to Genome 10K and Genome Science 2017!

These parallel conferences promise to give you a packed programme, with world-renowned researchers who epitomise the prestige and strength of these conferences.

We have organised plenty of networking sessions, including the social mixer, conference dinner and poster sessions, and hope that you make the most of these and the career development opportunities available to you.

GENOME 10K

GENOME SCIENCE 2017

Organisers.

Scientific Organising Committee
Federica Di Palma
Christiane Hertz-Fowler
Mick Watson
Nicholas Loman
Beth Shapiro
Steve O'Brien
Rebecca Johnson

Local Organising Committee
Federica Di Palma
Amanda Chong
Wilfried Haerty
Emily Angiolini
Dawn Turnbull
Helen Tunney
Matt Drew

Genome Science Organising Committee
Christiane Hertz-Fowler
Mick Watson
Nicholas Loman
Konrad Paszkiewicz
Aziz Aboobaker
Michael Quail
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Jenny Graves
Byrappa Venkatesh
Richard Durbin
Oliver Ryder
Harris Lewin
Kerstin Lindblad-Toh
Klaus Koepfli
Benedict Paten
Beth Shapiro
Warren Johnson
Emma Teeling
Tandy Warnow
Federica Di Palma
Guojie Zhang
Elinor Karlsson
Adam Phillippy
Gene Myers
Rebecca Johnson
Olivier Fedrigo

Social media.

We actively encourage you to use social media while attending the conference. However there may be some content speakers may not want to share in public.

We ask all delegates to respect any requests from speakers and refrain from sharing any data or photographs of slides identified as unpublished via social media.

Please use the hashtag

#g10kgs2017

Thank you to our sponsors.

Day 1
Tuesday 29 August

08:30	**Registration starts** **Location:** John Innes Conference Centre
09:30 - 12:30	**Training:** Science communication **Location:** Watson and Crick
12:30 - 13:00	Lunch

Plenary session 1
Location: Main auditorium

13:00 - 13:30	**Welcome:** Federica Di Palma, Earlham Institute, Wendy Thompson, Norfolk County Council & Sally Ann Forsyth, Norwich Research Park
13:30 - 14:15	**Keynote 1:** Adam Phillippy, Computational & Statistics Branch, NHGRI, US **Title:** Towards the gapless assembly of complete vertebrate genomes **Location:** Main auditorium
14:15 - 15:00	**Keynote 2:** Kathy Belov, University of Sydney, AU **Title:** Saving the Tasmanian devil from extinction **Location:** Main auditorium
15:00 - 15:30	Coffee break

Session 1A: Vertebrate Genomics
Chair: Federica Di Palma
Location: Main auditorium

15:30 - 16:00	**Invited Speaker:** Alex Cagan, Wellcome Trust Sanger Institute, UK **Title:** Comparative genomics of animal domestication
16:00 - 16:15	**Name:** Gaik Tamazian **Title:** Comparative whole-genome study of eleven Felidae species from six lineages
16:15 - 16:30	**Name:** Rebecca Jennings **Title:** A Cross-Species Bioinformatics and FISH approach to physical mapping of Mammalian Genomes
16:30 - 16:45	**Name:** Will Nash **Title:** Expansion of gene families and signatures of selection in the Australian marsupials
16:45 - 17:00	**Name:** Neil Gemmell **Title:** The tuatara genome project— Unlocking the genome of a living fossil

G10K | Genome Science | Shared sessions | Training | Breaks

Session 1B: Plant Genomics
Chair: Laura-Jayne Gardiner
Location: Watson and Crick

15:30 - 16:00	**Invited Speaker:** Ksenia Krasileva, Earlham Institute, UK **Title:** Evolution of plant Immune receptors
16:00 - 16:30	**Invited Speaker:** Andrea Harper, University of York, UK **Title:** Using Associative Transcriptomics to predict tolerance to ash dieback disease in European ash trees
16:30 - 16:45	**Name:** Steve Kelly **Title:** The evolution of photosynthetic efficiency
16:45 - 17:00	**Name:** Bernardo Clavijo **Title:** Designing multi-genome graphs for crop genomics and genetics: a wheat-centric view

Session 1C: Microbial Genomics
Chair: Kate Baker
Location: Franklin and Wilkins

15:30 - 16:00	**Invited Speaker:** John Lees, Wellcome Trust Sanger Institute, UK **Title:** Scalable pan-genome-wide association studies in bacteria
16:00 - 16:30	**Invited Speaker:** Gemma Langridge, University of East Anglia, UK **Title:** Contaminant or infective agent? Re-classifying the staphylococci for modern medicine
16:30 - 16:45	**Name:** Susanna Salter **Title:** A novel species of human nasopharyngeal bacteria, distantly related to the avian pathogen *Ornithobacterium rhinotracheale*
16:45 - 17:00	**Name:** Mark McMullan **Title:** The population genetics of the ash dieback invasion of Europe highlights huge adaptive potential of the causal fungus, *Hymenoscyphus fraxineus*
18:00	**Social mixer** **Location:** Earlham Institute

G10K | Genome Science | Shared sessions | Training | Breaks

Session 2A: Evolutionary Genomics
Chair: Beth Shapiro
Location: Main auditorium

09:00 - 09:30	**Invited Speaker:** Emma Teeling, University College Dublin, IRE **Title:** Growing old yet staying young: A genomic perspective on bats' extraordinary longevity
09:30 - 09:45	**Name:** Joel Armstrong **Title:** A reference-free whole-genome alignment of hundreds of mammalian genomes
09:45 - 10:00	**Name:** Elinor Karlsson **Title:** The 200 Mammals Genome Project: Understanding Evolutionary Conservation at Single Base Resolution
10:00 - 10:15	**Name:** Daniel Macqueen **Title:** Whole genome duplication and the evolution of salmonid fish: the state-of the art
10:15 - 10:30	**Name:** Yannick Wurm **Title:** The evolution of social chromosomes in fire ants

Session 2B: Clinical and Translational Genomics
Chair: Jonathan Coxhead
Location: Watson and Crick

09:00 - 09:30	**Invited Speaker:** Joris Veltmann, Institute of Genetic Medicine, Newcastle University, UK and Department of Human Genetics, Radboud University Medical Centre, Nijmegen, NL **Title:** *De novo* mutations in genetic disease
09:30 - 10:00	**Invited Speaker:** Matthew Hurles, Wellcome Trust Sanger Institute, UK **Title:** Deciphering Developmental Disorders
10:00 - 10:15	**Name:** Vladimir Teif **Title:** Nucleosome positioning as a cell memory in cancer transitions
10:15 - 10:30	**Name:** Weronika Gutowska-Ding **Title:** Good or bad sequencing data? Setting a benchmark for the quality of diagnostic NGS in the lab

Session 2C: Agricultural genomics
Chair: Mick Watson
Location: Franklin and Wilkins

09:00 - 09:30	**Invited Speaker:** Alan Archibald, The Roslin Institute, University of Edinburgh, UK **Title:** Precision engineering for PRRSV resistance in pigs
09:30 - 10:00	**Invited Speaker:** Nicola Patron, Earlham Institute, UK **Title:** Engineering Plant Genomes for Farming and Pharming
10:00 - 10:15	**Name:** Katrina Morris **Title:** Downregulation of immune genes in quail in response to H5N1 infection
10:15 - 10:30	**Name:** Gil Ronen **Title:** Pan-genome assembly of population haplotypes provides a comprehensive solution to common obstacles in modern breeding
10:30 - 11:00	Coffee break

Session 3A: Conservation Genomics

Chair: Emma Teeling
Location: Main auditorium

11:00 - 11:30	**Invited Speaker:** Beth Shapiro, University of California, Santa Cruz, US **Title:** The genomic consequences of inbreeding in mountain lions, *Puma concolor*
11:30 - 11:45	**Name:** Matthew D.Clark **Title:** Conservation genomics of the pink pigeon
11:45 - 12:00	**Name:** Taras K. Oleksyk **Title:** Novel genome assembly approach contributes to natural history and conservation of the Hispaniolan solenodon, *Solenodon paradoxus*
12:00 - 12:15	**Name:** Katrina Morris **Title:** Characterisation of koala lactation genes using a combined transcriptomic, proteomic and genomic approach
12:15 - 12:30	**Name:** Antonia Ford **Title:** Genomic approaches to identification and preservation of wild tilapia species and unique genetic resources

Session 3B: Developmental Biology

Chair: Aziz Aboobaker
Location: Watson and Crick

11:00 - 11:30	**Invited Speaker:** Kristin Tessmar-Raible, Max F. Perutz Laboratories, University of Vienna, AT **Title:** Genomic and transcriptomic approaches for the study of daily, monthly and seasonal timing
11:30 - 12:00	**Invited Speaker:** Andrea Münsterberg, University of East Anglia, UK **Title:** Cellular dynamics and lineage specification in developing somites
12:00 - 12:15	**Name:** Carlos R. Infante **Title:** Enhancers and the convergent evolution of limb reduction in squamates
12:15 - 12:30	**Name:** Dominik Handler **Title:** Using long reads to understand small RNAs

G10K | Genome Science | Shared sessions | Training | Breaks

Session 3C: Microbial communities
Chair: Nick Loman
Location: Franklin and Wilkins

11:00 - 11:30	**Invited Speaker:** Mads Albertsen, Aalborg University, DK **Title:** Towards a fully populated tree of life
11:30 - 12:00	**Invited Speaker:** Lindsay Hall, Quadram Institute, UK **Title:** Early life microbial communities
12:00 - 12:15	**Name:** Christopher Quince **Title:** DESMAN: a new tool for *De novo* Extraction of Strains from MetAgeNomes
12:15 - 12:30	**Name:** Sam Nicholls **Title:** Hansel and Gretel: A fairy tale of recovering haplotypes from metagenomes with a happy ending
12:30 - 13:30	LUNCH and POSTERS (Odd numbers)

Session 4A: Sequencing Technology and Developments
Chair: Mike Quail
Location: Main auditorium

13:30 - 14:00	**Invited Speaker:** Aaron McKenna, University of Washington, US **Title:** Information and storage recovery using the diversity of second-generation sequencing technologies
14:00 - 14:15	**Name:** Deanna Church **Title:** Linked-Reads enable efficient *de novo*, diploid assembly
14:15 - 14:30	**Name:** Rebecca O'Connor **Title:** Novel approach to chromosome-level mapping of avian genomes doubles the number of assemblies
14:30 - 14:45	**Name:** Iliana Bista **Title:** Scaling up the generation of reference quality genomes across a range of vertebrate diversity
14:45 - 15:00	**Name:** Ian Fiddes **Title:** Comparative Annotation Toolkit (CAT) - simultaneous annotation of related genomes using a high quality reference
15:00 - 15:15	**Name:** Lesley Shirely **Title:** High Throughput Genomics Enabled by NEBNext Ultra II FS

Session 4B: Meet the Editors
Location: Watson and Crick

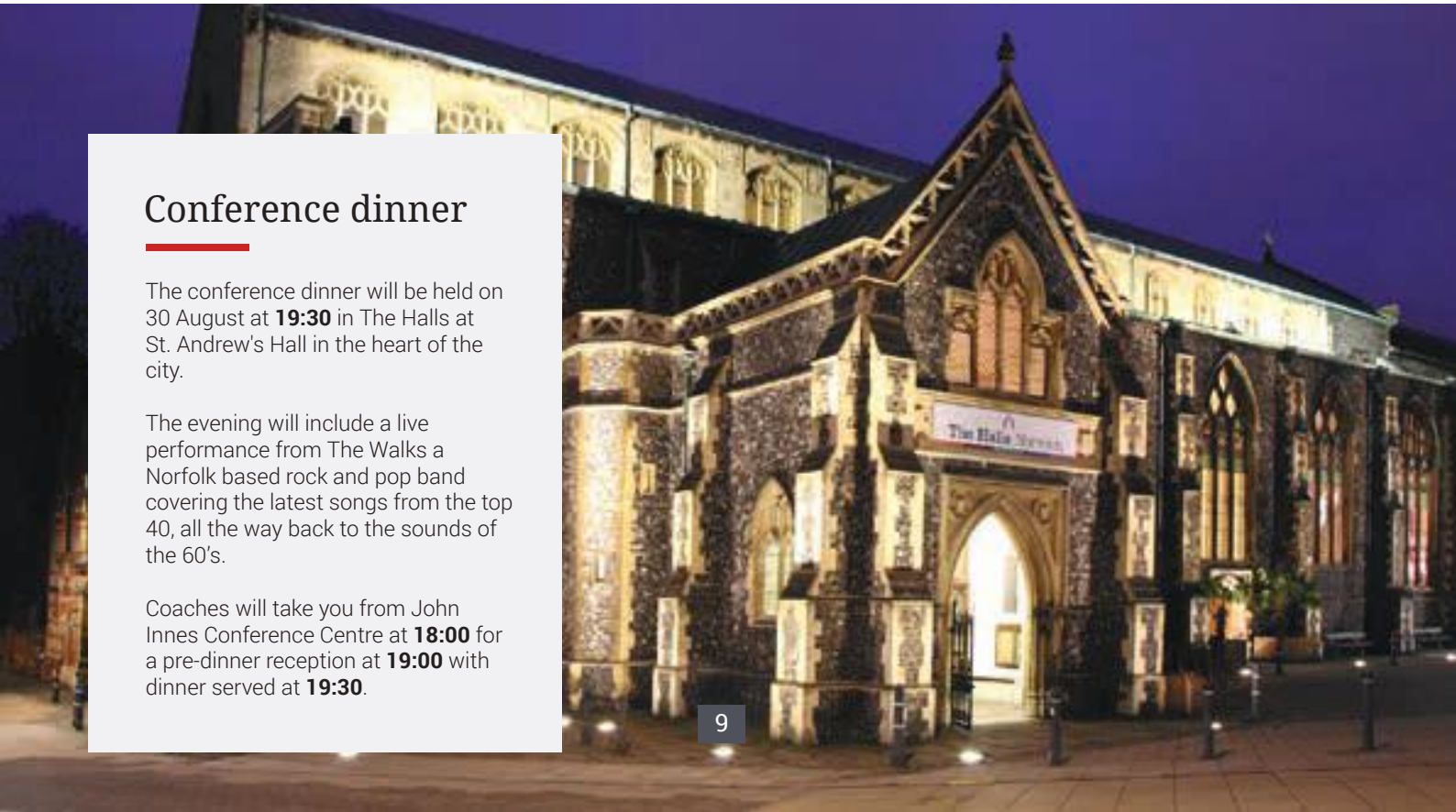
13:30 - 15:15	**Various**
15:15 - 15:45	Coffee break

Session 5A: Genome Informatics
Chair: Rob Davey
Location: Main auditorium

15:45 - 16:15	**Invited Speaker:** Doreen Ware, Cold Spring Harbour, US **Title:** TBC
16:15 - 16:30	**Name:** Colin Dewey **Title:** Genome-wide characterization of RNA processing event dependencies
16:30 - 16:45	**Name:** Daniel Mapleson **Title:** Sequence alignment using optical correlation
16:45 - 17:00	**Name:** John Davey **Title:** Chromosome assemblies with Oxford Nanopore sequencing
17:00 - 17:15	**Name:** William Chow **Title:** gEVAL, a web-based browser to help you evaluate and assess the state of your assembly
17:15 - 17:30	**Name:** Jonas Korlach **Title:** Full-length Transcript (Iso-Seq) Profiling for Improved Genome Annotations

Conference dinner

18:00 - 23:00	**Conference dinner - The Halls, Norwich**



Conference dinner

The conference dinner will be held on 30 August at **19:30** in The Halls at St. Andrew's Hall in the heart of the city.

The evening will include a live performance from The Walks a Norfolk based rock and pop band covering the latest songs from the top 40, all the way back to the sounds of the 60's.

Coaches will take you from John Innes Conference Centre at **18:00** for a pre-dinner reception at **19:00** with dinner served at **19:30**.

Day 3
Thursday 31 August

Session 6A: Population Genomics
Chair: Wilfried Haerty
Location: Main auditorium

09:00 - 09:30	**Invited Speaker:** Richard Durbin, Wellcome Trust Sanger Institute, UK **Title:** Whole genome sequence studies of the Lake Malawi cichlid adaptive radiation
09:30 - 09:45	**Name:** Gemma Murray **Title:** Natural selection shaped the rise and fall of passenger pigeon genomic diversity
09:45 - 10:00	**Name:** Kai Zeng **Title:** Determinants of the efficacy of natural selection on coding and noncoding variability in two passerine species
10:00 - 10:15	**Name:** Alicia C. Bertolotti **Title:** Copy number variation in the Atlantic salmon (*Salm ar*) genome
10:15 - 10:30	**Name:** Maribet Gamboa **Title:** Genome-wide signatures of local adaptation in SNP loci and proteins of stonefly populations along a latitudinal gradient in Japan

Session 6B: Sponsors showcase
Chair: Darren Heavens
Location: Watson and Crick

09:00 - 09:15	**Name:** Sarah Cossey (Earlham Institute) and Spencer Lamb (Verne Global) **Title:** Why Icelandic HPC is Bioinformatics' best friend
09:15 - 09:30	**Name:** Adam Peltan (NEB) **Title:** NEBNext®: Optimised Workflows for NGS Library Preparation
09:30 - 09:45	**Name:** Gaurav Kaul (Intel) **Title:** AI + Precision Medicine + Moore's Law = The 21st Century virtuous cycle
09:45 - 10:00	**Name:** Klaus Hentrich (TTPLabtech) **Title:** Automated low-volume liquid handling for cost-effective NGS library preparation and single cell genomics
10:00 - 10:15	**Name:** Deanna Church (10x Genomics) **Title:** The chromium system for enabling high resolution biology
10:15 - 10:30	**Name:** Kay Körner (Eppendorf) **Title:** Yield, Specificity and Inhibition of PCR: how to get better results!
10:30 - 11:00	Coffee break

G10K | Genome Science | Shared sessions | Training | Breaks

Day 3
Thursday 31 August

Session 7A: Single-Cell Genomics
Chair: Iain Macaulay
Location: Main auditorium

11:00 - 11:30	**Invited Speaker:** Muzlifah Haniffa, Newcastle University, UK **Title:** Deconstructing the immune system using single cell technologies
11:30 - 12:00	**Invited Speaker:** Tamir Chandra, MRC Human Genetics Unit, University of Edinburgh, UK **Title:** Understanding cellular heterogeneity in cellular senescence and ageing through single cell transcriptomics
12:00 - 12:30	**Invited Speaker:** Stephen Sansom, The Kennedy Institute of Rheumatology, University of Oxford, UK **Title:** Transcript structures in the thymus: improvised or rehearsed?

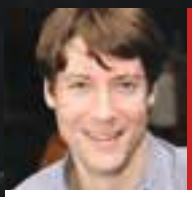
Session 7B: Sponsor showcase
Chair: Chris Watkins
Location: Watson and Crick

11:00 - 11:15	**Name:** Mark Mooney (DNAnexus) **Title:** Creating Community in the Cloud
11:15 - 11:30	**Name:** Thomas Keane (EMBL-EBI rep BioNano) **Title:** Acomys genome project: A comparative genomic framework for evolutionary and biomedical studies
11:30 - 11:45	**Name:** Brad Hehli (Perkin Elmer) **Title:** A Comparison of 16S Amplicons in Microbial Community Standards & Environmental Samples
11:45 - 12:00	**Name:** Michelle Vierra (PacBio) **Title:** PacBio SMRT Sequencing on the Sequel System: higher throughput, lower cost, better science
12:00 - 12:30	**Name:** Cindy Lawley (Illumina) **Title:** Sequencing and Array-based methods for resolving genomic inquiry
12:30 - 13:30	LUNCH and POSTERS (Even numbers)

Plenary session 2
Location: Main auditorium

13:30 - 14:15	**Keynote 3:** Peter Holland, University of Oxford, UK **Title:** Homeobox genes and animal evolution: from duplication to divergence **Location:** Main auditorium
14:15 - 15:00	**Keynote 4:** Hilary Burton, PHG Foundation, Cambridge, UK **Title:** Genomics in healthcare: the challenges of complexity **Location:** Main auditorium
15:00	**Poster prizes, Microbiology Society**
15:15	Coffee break
15:30	**Training:** Career paths **Location:** Darwin Training Suite, Earlham Institute

Keynote speakers.



Name: Dr Adam Phillippy
Affiliation: Computational and Statistics Branch, NHGRI, Maryland, US
Date: 29 August

Towards the gapless assembly of complete vertebrate genomes.

Abstract:
A complete and accurate genome sequence forms the basis of all downstream genomic analyses. However, even the human reference genome remains imperfect, which affects the quality of experiments and can mask true genomic variations. For most other species, quality reference genomes do not exist. Long-read sequencing technologies from Pacific Biosciences and Oxford Nanopore have begun to correct this deficiency and have enabled the automated reconstruction of reference-quality genomes at relatively low cost.

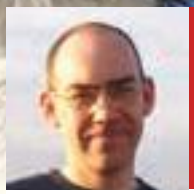
Further combination of these technologies with complementary scaffolding and phasing approaches such as chromatin conformation capture (Hi-C) may soon enable the complete reconstruction vertebrate haplotypes. I will review recent application of these approaches, and present a strategy for the automated assembly of hundreds of high-quality vertebrate reference genomes for the Genome10K project.

Name: Prof Kathy Belov
Affiliation: University of Sydney, AU
Date: 29 August

Saving the Tasmanian devil from extinction.

Abstract:
Kathy's research team have demonstrated that Tasmanian devils have extremely low levels of genetic diversity at the Major Histocompatibility Complex (MHC) providing an opportunity for Tasmanian Devil Facial Tumour Disease (DFTD), a rare contagious cancer, to spread through devil populations without encountering histocompatibility barriers.

They continue this research by studying the relationship between MHC type and disease susceptibility in devil populations, as well as the impact of the emergence and evolution of DFTD strains using genomics technologies.



Name: Prof Peter Holland
Affiliation: University of Oxford, UK
Date: 31 August

Homeobox genes and animal evolution: from duplication to divergence.

Abstract:
To understand the evolution of animals, we must understand genomes and development. One of the most important discoveries in 20th Century biology was the finding that widely different animal species use similar genes, such as homeobox genes, to build their embryos. But if the genes are conserved, why do animal species look so different?

Does evolution subtly change the regulation of key genes, or change the number of genes, or change their protein coding sequences?

Examples of all three routes have been revealed through comparative genomics, including some surprising examples of how evolution changed the number and function of homeobox genes in mammalian evolution.

Name: Dr Hilary Burton
Affiliation: PHG Foundation, UK
Date: 31 August

Genomics in healthcare: the challenges of complexity.

Abstract:
Genomic technologies have greatly enhanced our understanding of health and disease. Sequencing has become cheaper and quicker, whilst our increasing ability to interpret the data using huge computer power and very big databases, means that genomic testing can now influence clinical decisions in many areas of medicine. Whilst new possibilities continue to escalate, moving from scientific research to tried, tested and routine healthcare is not straightforward.

In this presentation I will outline some of the many dimensions of genomics in healthcare including disease prevention, making a precise diagnosis in rare and more common diseases, choosing drug treatments and assessing reproductive risk. I will explore some of the challenges facing health systems, which arise in part from the complexity of genomic information and the fast-moving nature of the technologies, but also include organisational and professional challenges: for example, the regulatory and practical difficulties of sharing personal data in health systems, or the educational programmes required to ensure that all healthcare professionals can use genetic testing appropriately and safely in their practice.

As health systems face the demands of an ageing population, a constant stream of emerging technologies and raised pubic expectations, I will suggest that using genomics effectively can be part of the solution. Together with other biomedical and even digital technologies, it can enable a move towards more personalised healthcare and a shift from end-stage 'rescue' to prevention and earlier diagnosis.

Invited speakers.

Name: Alex Cagan
Affiliation: Wellcome Trust Sanger Institute, UK
Date: 29 August

Comparative genomics of animal domestication.

Abstract:

The domestication of animal species was essential for the emergence of complex human societies. Despite its importance there is much about the domestication process that we still do not know. Domesticated species tend to share a suite of phenotypic traits referred to as the 'domestication syndrome'. However, whether these phenotypic similarities are the result of convergence at the genetic level remains unclear. We generated whole-genome sequences from experimentally domesticated Norway rats and American mink, and identified genes and putatively functional variants that may underlie the phenotypic differences seen in the domesticated animals.

When we combine these data with whole-genome sequences from multiple pairs of domestic animals and their wild sister species we find biological pathways that appear to be recurrently affected by the domestication process across all domesticated animal species. One of these is the ErbB signalling pathway, involved in the development of the reproductive system and neural crest migration.

Name: Ksenia Krasileva
Affiliation: Earlham Institute, UK
Date: 29 August

Evolution of plant Immune receptors.

Abstract:

Understanding evolution of plant immunity is necessary to inform rational approaches for genetic control of plant diseases. The plant immune system is innate, encoded in the germline, yet plants are capable of recognising diverse rapidly evolving pathogens. Availability of plant genomes plant species allowed us to elucidate evolutionary history of plant immune receptors of Nucleotide-Binding Leucine Rich Repeat class (NLRs) that provide genetic diversity to recognize pathogens and induce signaling cascade. We identified the 'core' and highly variable sub-clades of NLRs from across 60 plant species, including previously understudied monocots and uncovered sub-family clade expansions.

A recent paradigm in NLR-based recognition of pathogens involves NLRs with exogenous gene fusions, called integrated domains (NLR-IDs) that can serve as baits for pathogen-derived effectors. We have shown that NLR-IDs are prevalent across flowering plants and identified their ID repertoires. We uncovered a clade of NLRs that is undergoing repeated independent integration events that produces diverse NLR fusions to other genes. This NLR clade is ancestral in grasses with members often found on syntenic chromosomes while integrated domains are exchanged from different genomic locations. Sequence analyses revealed that DNA transposition or ectopic recombination are most likely mechanisms of NLR-ID formation. The identification of a subclass of NLRs that is naturally adapted to new domain integration can inform biotechnological approaches for generating synthetic receptors with novel pathogen 'traps'.

Name: Gemma Langridge
Affiliation: University of East Anglia, UK
Date: 29 August

Contaminant or infective agent? Re-classifying the staphylococci for modern medicine.

Abstract:

In many hospital laboratories, non-*aureus* staphylococci (NAS) are the most common isolates in blood culture. Although *S. aureus* is considered a true pathogen, NAS is often categorised as a contaminant. However, NAS are an important cause of healthcare associated infections, particularly associated with indwelling medical devices, such as prosthetic joints. They are also a reservoir of antimicrobial resistance genes, with resistance to methicillin and other frequently used antibiotics on the rise.

To investigate the population structure of NAS, we are establishing a diverse collection, currently just over 400 isolates from clinical samples, healthy volunteers and animals. At the Norfolk and Norwich Hospital, the clinical microbiology laboratory identifies isolates to the nearest species match using the gold standard MALDI-TOF method; we have used both MALDI-TOF and Illumina whole genome sequencing to characterise around 300 isolates from the collection. The lack of a large shared core in NAS directed us to a different approach, but to gain greater resolution over the single gene approach of 16S, we used the concatenated sequence of 16 ribosomal proteins to cluster the strains, resulting in 17 robust cluster (RC) groups. Overlaying the MALDI-TOF species names upon RC groups made it clear that the MALDI-TOF species designations do not necessarily follow the phylogeny. As a test case within NAS, we show that there is a significant phylogenetic distinction between "*S. saprophyticus*" strains isolated from urinary tract disease and those not causing disease.

Clustering of ribosomal protein sequences has revealed robust clades within *Staphylococcus* that provide the opportunity to generate a new, biologically sound definition of NAS.

Name: Andrea Harper
Affiliation: University of York, UK
Date: 29 August

Using Associative Transcriptomics to predict tolerance to ash dieback disease in European ash trees.

Abstract:

Associative Transcriptomics (AT) is a potent method, first developed in the crop plant *Brassica napus*, enabling rapid identification of gene sequence and expression markers associated with trait variation in diversity panels. It can be effective even when advanced genomic resources are unavailable, making it a valuable tool for studying traits in non-model species. Most recently, we applied AT to the problem of ash dieback disease, a fungal disease affecting ash trees which was first discovered in the UK in 2012.

Using a Danish ash diversity panel varying for susceptibility to the disease, we discovered expression-based markers that could be used to identify trees with high levels of tolerance to the disease.

In addition, information about the genes in which the markers are located, is revealing clues to the mechanisms underlying the ability of some trees to tolerate the disease.

Name: Joris Veltman
Affiliation: Institute of Genetic Medicine, Newcastle University, UK and Department of Human Genetics, Radboud University Medical Centre, Nijmegen, NL
Date: 30 August

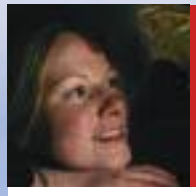
De novo mutations in genetic disease.

Abstract:

How is it possible that severe early-onset disorders are mostly genetic in origin, even though the disorders are not inherited because of their effect on fitness? Genomic studies in patient-parent trios have recently indicated that most of these disorders are caused by *de novo* germline mutations, arising mostly in the paternal lineage.

In this presentation I will discuss our research on the causes and consequences of *de novo* mutations using novel genomic approaches. I will illustrate all of this using severe intellectual disability as a model, for which we are making rapid progress and now have the opportunity to provide medically relevant information to the majority of patients and families involved.

Invited speakers.



Name: Emma Teeling
Affiliation: University College Dublin, IRE
Date: 30 August

Growing old yet staying young: A genomic perspective on bats' extraordinary longevity.

Abstract:

Of all mammals, bat possess the most unique and peculiar adaptations that render them as excellent models to investigate the mechanisms of extended longevity and potentially halted senescence. Indeed, they are the longest-lived mammals relative to their body size, with the oldest bat caught being 41 years old, living approx. 9.8 times longer than expected. Bats defy the 'rate-of-living' theories that propose a positive correlation between body size and longevity as they use twice the energy as other species of considerable size, but live far longer. The mechanisms that bats use to avoid the negative physiological effects of their heightened metabolism and deal with an increased production of deleterious Reactive Oxygen Species (ROS) is not known, however it is suggested that they either prevent or repair ROS damage.

Bats also appear to have resistance to many viral diseases such as rabies, SARS and Ebola and have been shown to be reservoir species for a huge diversity of newly discovered viruses. This suggests that their innate immunity is different to other mammals, perhaps playing a role in their unexpected longevity. Here the potential genomic basis for their rare immunity and exceptional longevity is explored across multiple bat genomes and divergent 'ageing' related markers.

A novel blood based population-level transcriptomics approach is developed to explore the molecular changes that occur in an ageing wild population of bats to uncover how bats 'age' so slowly compared with other mammals. This can provide a deeper understanding of the causal mechanisms of ageing, potentially uncovering the key molecular pathways that can be eventually modified to halt, alleviate and perhaps even reverse this process in man.

Name: Alan Archibald
Affiliation: The Roslin Institute, UK
Date: 30 August

Precision engineering for PRRSV resistance in pigs.

Abstract:

Porcine Reproductive and Respiratory Syndrome (PRRS) is arguably the most important infectious disease for the world-wide pig industry. The effects of PRRS include late-term abortions and stillbirths in sows and respiratory disease in piglets. The causative agent of the disease is the positive-strand RNA PRRS virus (PRRSV). PRRSV has a narrow host cell tropism, targeting cells of the monocyte/macrophage lineage. One of the host proteins involved in facilitating viral entry is CD163 which has been described as a fusion receptor for PRRSV. CD163 is expressed at high levels on the surface of macrophages, particularly in the respiratory system. The scavenger receptor cysteine-rich domain 5 (SRCR5) region of CD163 has been shown to interact with virus in vitro.

We used CRISPR/Cas9 gene editing technology to generate pigs with a deletion of the CD163 exon 7 which encodes the SRCR5 domain. Deletion of SRCR5 showed no adverse effects in pigs maintained under standard husbandry conditions with normal growth rates and complete blood counts observed.

Pulmonary alveolar macrophages (PAMs) and peripheral blood monocytes (PBMCs) were isolated from the animals and assessed in vitro. Both PAMs and macrophages obtained from PBMCs by CSF1 stimulation (PMMs) show the characteristic differentiation and cell surface marker expression of macrophages of the respective origin.

Expression and correct folding of the SRCR5 deletion CD163 on the surface of macrophages and biological activity of the protein as hemoglobin-haptoglobin scavenger was confirmed. Both PAMs and PMMs were challenged with PRRSV genotype 1, subtypes 1, 2, and 3 and PMMs with PRRSV genotype 2. PAMs and PMMs from pigs homozygous for the CD163 exon 7 deletion showed complete resistance to viral infections assessed by replication. Confocal microscopy revealed the absence of replication structures in the SRCR5 CD163 deletion macrophages, indicating an inhibition of infection prior to gene expression, i.e. at entry/fusion or unpacking stages.

Name: Nicola Patron
Affiliation: Earlham Institute, UK
Date: 30 August

Engineering Plant Genomes for Farming and Pharming.

Abstract:

Synthetic biology applies engineering principles to biology for the construction of novel biological systems designed for useful purposes. It advocated for standards and foundational technologies to facilitate biological engineering. Defining standards for plants has enabled us to automate parallel DNA assembly at nanoscales, removing research bottlenecks and providing the international plant community access to reusable, interoperable, characterized, standard DNA parts.

We are applying these principles to programmable genome engineering tools for multiplexed targeted mutagenesis and for the development of tunable, orthologous regulatory elements, synthetic transcription factors and genetic logic gates.

Name: Matthew Hurles
Affiliation: Wellcome Trust Sanger Institute, UK
Date: 30 August

Deciphering Developmental Disorders.

Abstract:

Children with severe, undiagnosed developmental disorders (DDs), including Intellectual Disabilities as well as multi-system congenital malformations, are enriched for damaging *de novo* mutations (DNMs) in developmentally important genes. Working with the clinical genetic services of the UK and Ireland we have exome sequenced 13,600 families.

We have diagnosed thousands of children, by providing the information back to their clinicians. We've determined that 40-45% of these children have causal *de novo* mutations in protein-coding genes, and we've identified over 30 novel disorders so far. We've also determined that *de novo* mutations are also enriched in highly conserved regulatory elements that are active in fetal brain, but that these only account for a small minority of as yet undiagnosed patients.

Name: Mads Albertsen
Affiliation: Aalborg University, DK
Date: 30 August

Towards a fully populated tree of life.

Abstract:

Small subunit (SSU) ribosomal RNA (rRNA) genes have been the standard phylogenetic markers for the study of microbial evolution and diversity for decades. However, the essential reference databases of full-length rRNA gene sequences are underpopulated, ecosystem skewed, and subject to primer bias; which hampers our ability to study the true diversity. In this talk, I will present out latest method development that combines poly(A)-tailing and reverse transcription of SSU rRNA molecules with synthetic long-read sequencing, to generate millions of high quality, full-length SSU rRNA sequences without primer bias. We applied the approach to complex samples from seven different ecosystems and obtained more than 1,000,000 SSU rRNA sequences from all domains of life.

The novel diversity is overwhelming and include several potentially new archaeal phyla of the deeply branching Asgard Archaea, which are previously suggested to bridge the gap between prokaryotes and eukaryotes. This approach will allow expansion of the rRNA reference databases by orders of magnitude and will enable a comprehensive census of the tree of life. With a fully populated SSU tree of life, it will be possible to prioritize efforts towards making a fully populated genome tree of life. To demonstrate the progress with these efforts, I will also discuss our recent progress on extraction of complete (closed) genomes from metagenomes using high-throughput long-read Nanopore.

Invited speakers.

Name: Kristin Tessmar
Affiliation: Max F. Perutz Laboratories, University of Vienna, AT
Date: 30 August

Genomic and transcriptomic approaches for the study of daily, monthly and seasonal timing.

Abstract:

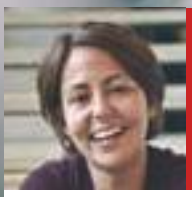
Life is controlled by multiple rhythms. While the interaction of the circadian clock with environmental stimuli is well documented, its relationship to endogenous oscillators with other periods, as well as natural timing variation between individuals of the same species is little understood.

The marine bristle worm *Platynereis dumerilii* harbors a light-entrained circadian, as well as a monthly (circalunar) clock. Our first studies suggest that the circalunar clock persists even when circadian clock function is disrupted as evidenced by the complete absence of molecular and behavioral circadian oscillatory patterns. However, the circalunar clock impacts on the circadian clock on two levels:

a) It regulates the level of a subset of core circadian clock genes.
b) In addition to its molecular input, we furthermore find that the circalunar clock changes the period and power of circadian behavior, although the period length of the daily transcriptional oscillations remains unaltered.
In order to study the molecular and cellular nature of its circalunar clock, as well as its interaction with the circadian clock, we have established transient and stable transgenesis, inducible specific cell ablations, chemical inhibitors, as well as TALEN-mediated genome engineering. We have been investigating the extent of transcript changes in the brain caused by the circalunar clock and compare these changes to other major conditions (sex determination, maturation) occurring during the life of the worm, as well as to the known extent of transcript changes caused by the circadian clock.

The marine midge *Clunio marinus* possesses a circadian clock, and in addition acquired a circalunar clock during the past 20.000 years. Strains of different geographic origins exhibit differences in their circalunar and circadian timing ("chronotypes"), which are genetically encoded and map to 3 quantitative trait loci (QTLs). We sequenced and assembled the 90Mbp genome of the midge and mapped the QTLs to the molecular map. Based on subsequent single nucleotide polymorphism (SNP) analyses differentially fixed in different timing strains, and molecular studies, we suggest that circadian chronotypes in Clunio are caused by activity variants in the enzyme CaMKII.

Given its evolutionary conservation and prominent role in the mammalian brain, it is tempting to speculate, that CaMKII could play a similar role in mammals, and could thus provide a molecular link between extreme chronotypes and frequently co-occurring neuropsychological diseases.



Name: Beth Shapiro
Affiliation: University of California Santa Cruz, US
Date: 30 August

The genomic consequences of inbreeding in mountain lions, *Puma concolor.*

Abstract:

Human land-use changes, including deforestation and establishment of roads and highways, can obstruct natural dispersal and migration corridors, leading to population isolation and inbreeding. Among the most affected species in North America by human land-use changes is the mountain lion, *Puma concolor.* Once distributed across North America, mountain lions are today found only in southern Florida and the western part of the continent.

To explore the genomic consequences of increasing isolation between mountain lion populations, we sequenced and assembled a chromosome-scale *de novo* genome from a mountain lion from the Santa Cruz mountains, 36M, and generate high coverage resequencing data from mountain lions from populations across North America and Brazil.

Using these data, we investigated the relative timing of onset and duration of inbreeding within potentially distinct mountain lion populations. North American mountain lions contain significantly less genomic diversity than Brazilian mountain lions, but show varying levels of inbreeding that does not correspond directly to present-day barriers between them. Finally, we explore the selective consequences of inbreeding on North American mountain lions, and identify genomic changes that may have evolved as a consequence of increased interaction with humans.

Name: Lindsay Hall
Affiliation: Quadram Institute, UK
Date: 30 August

Early life microbial communities.

Abstract:

The gut is home to an astonishingly diverse, dynamic, and populous ecosystem. This complex microbial community, termed the microbiota, is critical for host wellbeing. Disturbances in our microbiota, such as via caesarian sections and antibiotic exposure, can lead to increased susceptibility to pathogens, as well as atopic, and chronic inflammatory diseases. Bifidobacteria constitute a substantial proportion of the gut microbiota, particularly during early life and high-levels are associated with the development of mucosal defence.

Currently there are many bifidobacterial species and strains with claimed health promoting or 'probiotic' attributes, however the mechanisms through which these strains reside within their host and exert benefits is far from complete. In this talk I will discuss the role of the gut microbiota with the host, focusing on the example of bifidobacteria in host colonisation, epithelial cell cross-talk, and pathogen protection.

Name: Andrea Münsterberg
Affiliation: University of East Anglia, UK
Date: 30 August

Cellular dynamics and lineage specification in developing somites.

Abstract:

A fundamental process during both embryo development and stem cell differentiation is the control of cell lineage determination. In developing skeletal muscle, many of the diffusible signalling molecules, transcription factors and non-coding RNAs that contribute to this process have been identified. This has advanced our understanding of the molecular mechanisms underlying the control of cell fate choice. In vertebrate embryos, skeletal muscle is derived from paired somites. These are transient embryonic segments that also contain progenitors for other cell lineages of the musculoskeletal system, such as chondrocytes and axial tendon progenitors.

In addition, some endothelial cells, adipocytes and brown fat cells are somite derived. We are developing approaches to examine the full complexity and molecular profiles of progenitor cells that are present in early and later stage somites. This will allow us to delineate molecularly distinct cell types, to define progenitors and lineage relationships, and to identify crucial pathways, hubs and markers for the lineages of the musculoskeletal system. In parallel, we use imaging approaches to assess cellular behaviours during somite maturation, a highly dynamic process that involves significant morphogenetic changes. A more detailed understanding of the key mechanisms and factors involved will be important for stem cell science, regenerative medicine and tissue engineering.

Invited speakers.

Name: Aaron McKenna
Affiliation: University of Washington, US
Date: 30 August

Information storage and recovery using the diversity of second-generation sequencing technologies.

Abstract:

Second-generation sequencing has been traditionally seen in terms of a key trade-off: a huge increase in information recovery at the cost of information fragmentation. Here we show that such weaknesses can be overcome by leveraging a series of inventive techniques developed by the field at large. First, we demonstrate that second-generation sequencing can be used to recover chromosomal level contiguity in the *de novo* genome assembly of a previously unsequenced Muridae species.

In addition, we demonstrate it's utility in recovering the 'orthogonal genome': human engineered information storage within the genomes of single living cells, and its application to tracing whole-organism lineage.

Name: Doreen Ware
Affiliation: Cold Spring Harbour, US
Date: 30 August

Biog:

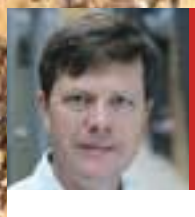
Using multidisciplinary approaches that combine computational analysis, modeling, and prediction with experimental verification, Doreen Ware's lab seeks a deeper understanding of the evolution of genome sequences in plants and their implications for agricultural improvement.

By looking comparatively across the genomes of plants in the same lineage, they seek answers to the following questions: How are genes conserved and lost over time? What are the fates of duplicated genes? What is the impact of structural variation on phenotypic variation? Ware's team also studies gene regulation in plants, focusing on gene regulatory networks, targeting transcription factors and microRNA genes with the objective of understanding how these parts of the plant genome work together in determining spatial and temporal expression of genes.

The lab had an important role in the project to produce a haplotype map reference genome of maize, spearheading the most comprehensive analysis of the crop yet. This has provided important information on the variation of the reference genome, as well as comparative data showing changes in the genome acquired through domestication and breeding. They have devoted special attention to examining diversity within maize, grape, and tomato, aiming to accelerate the development of strategies to introduce new germplasm that is needed to meet demands of increasing population and a changing environment.

The lab also has brought fully sequenced genomes into an integrated data framework, to enhance the power of their comparative studies. This past year, Ware was named as its principal investigator for the National Science Foundation-funded Gramene project, a comparative genomics resource for agriculturally important crops and models to support sustainable food and fuel production.

Ware, as principal investigator for plants, has also helped lead an effort funded by the Department of Energy to create—out of many separate streams of biological information—a single, integrated cyber-"knowledgebase" for plants and microbial life.



Name: Richard Durbin
Affiliation: Wellcome Trust Sanger Institute, UK
Date: 31 August

Whole genome sequence studies of the Lake Malawi cichlid adaptive radiation.

Abstract:

The adaptive radiations of haplochromine cichlid fish in the East African great lakes provide paradigmatic systems to study the dynamics of species formation, and of natural and sexual selection. The most extensive radiation is in Lake Malawi, where in the last million years or so one or a few ancestral populations have given rise to a flock of more than 500 species, filling almost all piscine ecological niches in the lake.

Over the past few years we have collected with collaborators over 2500 samples and sequenced the whole genomes of over 300 fish from over 100 species of Lake Malawi cichlids. All species are genetically close, with pairwise divergence typically between 0.1 and 0.25%, compared to heterozygosity between 0.05 and 0.15%. In addition to extensive incomplete lineage sorting, we see strong signals of gene flow between clades at different levels in the radiation, based on PCA, F statistics and related methods.

There appear to be several long chromosomal regions exhibiting unusual phylogeny, perhaps indicative of a role for large inversions in species separation. At a finer scale, although for close species pairs Fst can be under 20%, we also see local spikes or "islands" of high differentiation that are statistically significant under simple models of population separation, suggestive of loci under selection. Finally, at a functional level, we see higher non-synonymous to synonymous differences between species in genes involved in retinal processing, the innate immune system, oxygen transport, and a number of other pathways.

Name: Muzlifah Haniffa
Affiliation: Newcastle University, UK
Date: 31 August

Deconstructing the immune system using single cell technologies.

Abstract:

Muzlifah has used functional genomics, comparative biology and more recently single cell RNA sequencing to study human mononuclear phagocytes. In this seminar, she will discuss the power and utility of single cell RNA sequencing to identify new dendritic cells, monocytes and progenitor cells relevant for immunotherapy.

Invited speakers.

Name: Tamir Chandra
Affiliation: MRC Human Genetics Unit, University of Edinburgh, UK
Date: 31 August

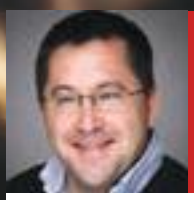
Understanding cellular heterogeneity in cellular senescence and ageing through single cell transcriptomics.

Abstract:

A key event in a healthy cell turning into a cancer cell is the activation of an oncogene. To prevent transforming to a cancer cell, the cell harbouring the oncogene activates a tumour suppressive programme, pushing itself into an irreversible growth arrest, called oncogene induced senescence (OIS). Everyone carries OIS cells, for example in the benign lesions (such as moles) that never progress to malignant cancer. Most of the time these lesions stably exist over decades, but sometimes individual cells escape and progress to cancer. What enables individual cells to turn malignant and how are they different from the cells around them?

Here we present single cell transcriptomes of a time-course of human fibroblasts on their way to senescence after oncogene activation. Applying machine learning to order cells along a senescence trajectory, we find an unexpected bifurcation, leading to two distinct senescence endpoints. Each of these endpoints exclusively expresses sets of canonical senescence genes.

Most importantly, one population failed to regulate key genes thought essential for the stability of the senescent state, leading to a scenario where the heterogeneity of the benign state might enable escape to malignancy.



Name: Stephen Sansom
Affiliation: The Kennedy Institute of Rheumatology, University of Oxford, UK
Date: 31 August

Transcript structures in the thymus: improvised or rehearsed?

Abstract:

Epithelial cells of the thymus are remarkable for their ability to promiscuously express nearly all protein coding genes in order to assess the self-reactivity of developing T-cells. Such T-cells must also be able to tolerate the isoform specific epitopes that they will encounter as they monitor the various tissues of the body.

Currently, the extent and fidelity of peripheral isoform representation in thymic epithelial cells is only poorly understood. We therefore used population and single-cell transcriptomics to compare transcript architectures between the thymus and peripheral tissues. These data also provide insights into the process by which the isoform repertoire of thymic epithelial cells is generated.

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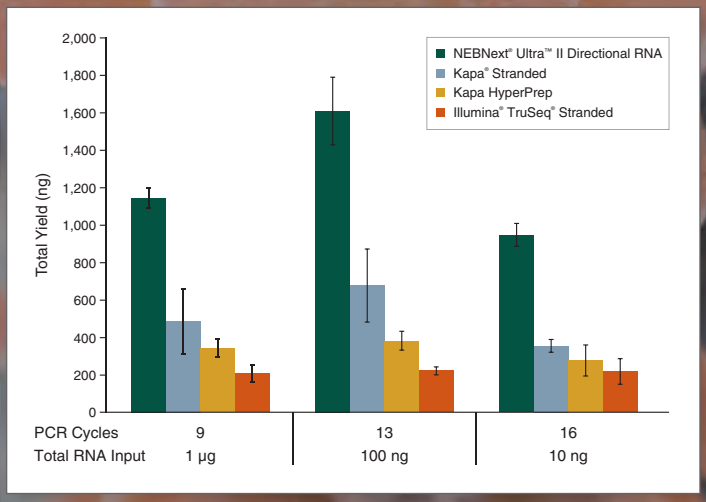

Poly(A)-containing mRNA was isolated from 10 ng, 100 ng and 1 µg of Universal Human Reference RNA (Agilent® #740000) and libraries were made using the NEBNext Ultra II Directional RNA Kit (plus the NEBNext poly(A) mRNA Magnetic Isolation Kit), Kapa Stranded mRNA-Seq Kit, Kapa mRNA HyperPrep Kit and Illumina TruSeq Stranded mRNA Kit. The input RNA amount and number of PCR cycles are indicated.

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THE CLIENT

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THE CHALLENGE

Cutting-edge, high-throughput DNA sequencing instruments generate large amounts of data, from a few hundred gigabytes to several terabytes per run. This output requires significant computing effort, making the storage, processing, analysis and sharing of the data extremely challenging.

Like any research institute that is governed by large data-driven science, EI is constantly dealing with large volumes of data arriving at very high velocity. This puts significant strain on their computing storage infrastructure, requiring increased storage space and data center hosting capability, as well as increased operational cost to cool the infrastructure.

In addition to the volume of data, EI faces challenges from a security and privacy perspective. A reluctance to put all data in the cloud and the need to know where data is at all times, meant searching for a solution elsewhere.

THE SOLUTION

As the trend for HPC in scientific research continues to rise, EI needed a strategic data center partner that could improve efficiencies by distributing large-scale genomics and computing biology data analysis.

EI selected Verne Global's data center campus in Iceland based on its previous expertise providing long-term, low-cost, sustainable power for computing as well as, experience working with private and public organisations.

EI also needed a provider that could directly connect customers in each country, and Verne Global's access to the National Research Education Networks allowed them to connect to EI's campus in the Norwich Research Park, England, and Verne Global's campus in Iceland.

BENEFITS

Verne Global provides flexible, scalable, secure and highly optimised data center solutions, as well as access to one of the world's most modern and reliable power grids, utilising 100% renewable energy.

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I hope the impact of our collaboration with Verne Global will be the catalyst for many more academic institutions in the UK and Europe to consider migrating their computing infrastructures to Iceland and benefit from one of the world's most reliable and cost-effective green energy resources. I'm very proud that Earlham Institute is at the forefront of this shift.

Dr Timothy Stitt, Head of Scientific Computing
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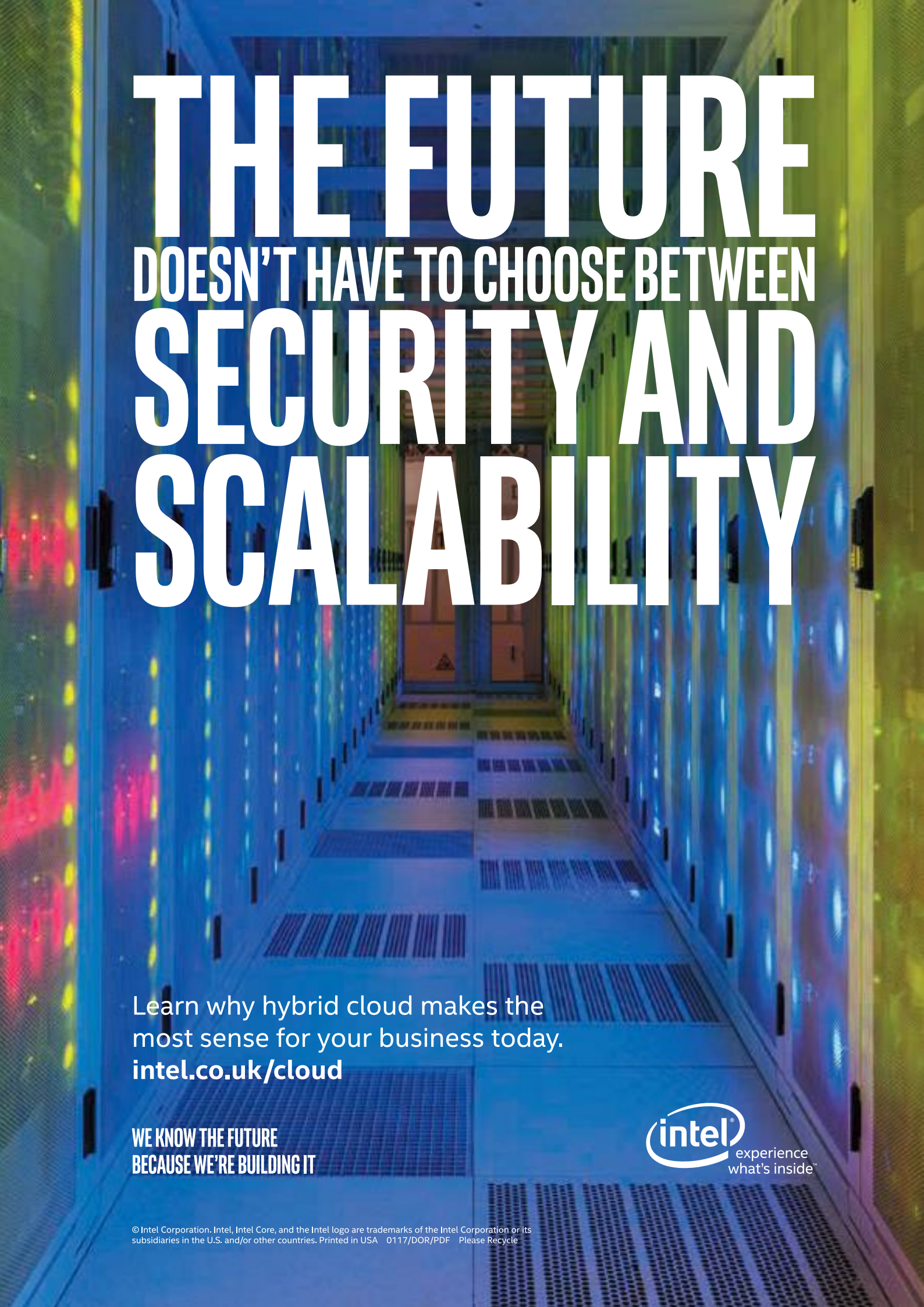
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