CONFERENCE PROGRAM

DAY 1 THURSDAY 27 SEPTEMBER

11:00	Registration and poster hanging
13.40	Introduction Rebecca Furlong, Genome Medicine, UK
	Informatics workshop Chair: David Dooling
13:45	New algorithms and infrastructure for variant detection at population scale Gabor Marth, Boston College, USA
14:15	Network and pathway analysis of somatic mutations in cancer Ben Raphael, Brown University, USA
14:45	Pathway-based analysis of mutation impact Josh Stuart, University of California Santa Cruz, USA
15:15	Sponsored technical presentation – Strand Aishwarya Narayanan, Application Scientist, Strand
15:15–16:00	Coffee
16:00	Illuminating the genetics of complex human diseases Mike Schatz, Cold Spring Harbor Laboratories, USA
16:30	Accessible, transparent, reproducible analysis with Galaxy James Taylor, Emory University, USA
17:00	Informatics challenge David Dooling, Michael Schatz, James Taylor
18:00	Sponsored technical presentation – DNAnexus Andreas Sundquist, CEO and Co-founder of DNAnexus
18:00–19.30	Poster session 1 and welcome reception (odd-numbered posters to be presented)

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DAY 2 FRIDAY 28 SEPTEMBER

08:00–08:55	Coffee/breakfast
	Session 1. Inherited disease: beyond the candidate gene approach Chair: James Lupski
09:00	**Hypothesis-generating clinical genomics research and predictive medicine** Leslie Biesecker, National Human Genome Research Institute, USA
09:30	**Whole-genome sequencing and disease-gene detection** Lynn Jorde, University of Utah, USA
10:00	**Sifting disease-causing signal from genomic noise** Daniel MacArthur, Massachusetts General Hospital, Boston, USA
10:30–11:00	**Coffee** Chair: Leslie Biesecker
11:00	**De novo diagnostics of patients with intellectual disability** Joris Veltman, Radboud University Nijmegen Medical Centre, Netherlands
11:30	**First year experience with the introduction of clinical whole exome sequencing** Sharon Plon, Baylor College of Medicine, USA
12:00	**Selected talk - Clinical diagnostic whole genome sequencing in a paediatric population; experience from our WGS genetics clinic.** Elizabeth Worthey, The Medical College of Wisconsin, USA
12:15	**Selected talk - Characterizing epistatic hotspots of human disease** Tallulah Andrews, MRC Functional Genomics Unit, University of Oxford, UK
12:30	**Sponsored technical presentation – BIOBASE** Jennifer Hogan, VP of Product Management, BIOBASE
12:30–13:45	**Lunch. Posters available**
	Session 2. Ethics: dealing with data Chair: Sharon Plon
13:45	**How to avoid one thousand opportunities to do harm in genomic medicine** Isaac Kohane, Harvard Medical School and Children's Hospital Boston, USA
14.15	**Analyzing Genomes: is there a duty to disclose?** Amy McGuire, Baylor College of Medicine, USA
	Session 3. From discovery sequencing to targeted therapy in cancer
14:45	**Interrogating of cancer genomes: towards more profile-based therapeutics** John Carpten, TGen, USA
15:15	**The implications of clonal genome evolution for cancer medicine** Samuel Aparicio, BC Cancer Research Centre, Canada
15:45–16:15	**Coffee**
16:15	**Selected talk - Surname leakage from personal genomes** Yaniv Erlich, Whitehead Institute for Biomedical Research, USA
16:30	**Selected talk - Multi-level genomic profiling of prostate cancers reveals a landscape spanning ageing and cancer** Johan Lindberg, Karolinska Institutet, Stockholm, Sweden
16:45	**Keynote - Genomics – Catching up to human genetics** Richard Gibbs, Baylor College of Medicine, USA
17:30–19:00	**Poster session 2 with pre-dinner drinks (even-numbered posters to be presented)**
19:30	**Conference dinner at MIT museum (for pre-registered delegates)**

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DAY 3 SATURDAY 29 SEPTEMBER

07:45–08:55	Coffee/breakfast.
	Session 3 continued. From discovery sequencing to targeted therapy in cancer Chair: Peter Laird
09:00	Translating cancer genomes Lynda Chin, MD Anderson Cancer Center, USA
09:30	Genome evolution during progression to breast cancer Arend Sidow, Stanford University, USA
10:00	Selected talk - MutaScope: a high sensitivity variant caller dedicated to high-throughput PCR amplicons sequencing Yost Shawn, University of California San Diego, USA
10:15	Analysis of somatic retrotransposition in human cancers Peter Park, Harvard Medical School, USA
10.30 – 11.00	Coffee
	Session 4. Epigenomics technologies and applications Chair: Oliver Rando
11:00	Exploring the Cancer Methylome Peter Laird, University of Southern California, USA
11:30	The hunt for mammalian epialleles Vardhman Rakyan, Barts and The London School of Medicine and Dentistry, UK
12:00	Folding principles of genomes Job Dekker, University of Massachusetts Medical School, USA
12:30 – 13:45	Lunch. Posters available.
13:45	Ultra-high resolution mapping of protein-genome interactions using ChIP-exo Frank Pugh, Penn State University, USA
14:15	Selected talk - Epigenetic reprogramming in the epithelial-to-mesenchymal transition Stephen Hoang, University of Virginia School of Medicine, USA
14:30	Selected talk - Development of a computational strategy to compare repetitive element enrichment between experimental conditions from high throughput sequencing datasets Steven Criscione, Molecular Biology, Cell Biology, and Biochemistry, Brown University, USA
14:45	Keynote - Towards a patient-based drug discovery Stuart Schreiber, Broad Institute of Harvard and MIT, USA
15.30	Closing remarks