Beyond the Genome 2010 – Conference Program

11th October

17:00 - 18:00	Registration and poster setup
18:20 - 18:30	Welcome address *Matthew Cockerill, BioMed Central*
18:30 - 19:15	Keynote: Between a chicken and a grape: estimating the number of human genes *Steven Salzberg, University of Maryland, College Park, USA*
19.30 - 20:00	Keynote: Reading and writing genomes *George Church, Harvard Medical School, Boston, USA*
20:15 - 21:30	Poster viewing
21:30	End of Day 1

12th October

08:00 - 08:30	Registration

Session 1 - Sequencing Cancer and Complex Disease Genomes

Chair: *Elaine Mardis, Washington University School of Medicine, St Louis, USA*

08:30 - 09:15	Keynote: Next-generation cancer genomics *Elaine Mardis, Washington University School of Medicine, St Louis, USA*
09:15 - 09:45	Gene discovery for complex diseases using exomic sequencing: identifying pancreatic cancer susceptibility genes *Alison Klein, Johns Hopkins University, Baltimore, USA*
09:45 - 10:15	Personalized oncogenomics *Steven Jones, Genome Science Centre, Vancouver, Canada*
10:15 - 10:45	TBA *Craig Thompson, University of Pennsylvania, Philadelphia, USA*
10:45 - 11:15	Coffee break
11:15 - 11:45	Large-scale identification of tissue-specific enhancers *in vivo* *Len Pennacchio, Lawrence Berkeley University National Laboratory, USA*

11:45 - 12:15 Deciphering the genetic basis of common diseases by integrated functional annotation of common and rare variants
Olivier Harismendy, The Scripps Research Institute, La Jolla, USA

Selected talks

12:15 - 12:30 BIC-seq: a fast algorithm for detection of copy number alterations based on high-throughput sequencing data
Peter Park, Harvard Medical School, Boston, USA

12:30 - 12:45 Candidate genes and biological processes from autism *de novo* CNVs
Hyun Noh, University of Oxford, UK

12:45 - 13:00 A genomewide ordered-subset linkage analysis for alcohol dependence in African-Americans
Shizhong Han, Yale University, New Haven, USA

13:00 - 13:15 Session sponsor: Avadis NGS – Next-Gen Sequencing analysis for the rest of us
Thon de Boer, Strand Life Sciences

13:15 - 14:00 Lunch

Session 2 - The true gene count. How much of the genome is functional?

Chair: *Michele Clamp, Bioteam, Boston, USA*

14:00 - 14:30 TBA
Michele Clamp, Bioteam, Boston, USA

14:30 - 15:00 Most of the 6.5% - 10% of human DNA bases that are functional now will soon be turned over
Chris Ponting, University of Oxford, UK

15:00 - 15:30 The developmental transcriptome of *Drosophila melanogaster*
Brenton Graveley, University of Connecticut Health Center, Farmington, USA

15:30 - 16:00 Transcriptomics in a high-throughput world
Chad Nusbaum, Broad Institute, Cambridge, USA

16:00 - 16:30 Coffee break

16:30 - 17:00 Synthetic and sequencing-based approaches to high-throughput genetic analysis
Jay Shendure, University of Washington, Seattle, USA

17:00 - 17:15 Session sponsor: From Sample to Sequence: Caliper Solutions for Next Generation Sequencing

Isaac Meek, Caliper Life Sciences

17:15 - 17:30 Helicos single molecule sequencing: unique capabilities and corresponding importance for molecular diagnostics
Patrice Milos, Helicos BioSciences, Cambridge, USA

Selected talks

17:30 - 17:45 Defining the human reference protein-coding gene set
Suganthi Balasubramanian, Yale University, New Haven, USA

17:45 - 18:00 From identification to validation to gene count
Clara Amid, The Wellcome Trust Sanger Institute, Hinxton, UK

18:00 - 18:15 Beyond the FANTOM4
Harukazu Suzuki, RIKEN Omics Science Center, Yokohama, Japan

18:30 - 19:30 Poster viewing

20:00 - 23:00 Conference dinner - Elements at Harvard Medical School

23:00 End of Day 2

13th October

Session 3 - Microbiomes in human and other environments

Chair: *Rob Knight, University of Colorado, Boulder, USA*

08:30 - 09:00 Translational medicine and the human microbiome
Rob Knight, University of Colorado, Boulder, USA

09:00 - 09:30 TBA
Stephan Schuster, Pennsylvania State University, University Park, USA

09:30 - 10:00 Exploring the human gut microbiome
Jun Wang, Beijing Genomics Institute, Shenzhen, China

10:00 - 10:30 Skin microbiome in health and disease
Julie Segre, National Human Genome Research Institute, NIH, Bethesda, USA

10:30 - 11:00 Coffee break

11:00 - 11:30 The rare biosphere: sorting out fact from fiction
Mitchell Sogin, Josephine Bay Paul Center, Woods Hole, USA

Selected talks

11:30 - 11:45 A data analysis and coordination center for the Human Microbiome Project
Jennifer Wortman, University of Maryland School of Medicine, Baltimore, USA

11:45 - 12:00 Statistical methods for comparing the abundances of metabolic pathways in metagenomics
Bo Liu, University of Maryland Institute for Advanced Computer Studies, College Park, Baltimore, USA

12:00 - 12:15 Beyond the genome (BTG) is a (PGDB) pathway genome database: HumanCyc
Miles Trupp, SRI International, Menlo Park, USA

12:15 - 13:00 Lunch

Session 4 - Insights from genomic analyses into evolution

Chair: *Sarah Tishkoff, University of Pennsylvania, Philadelphia, USA*

13:00 - 13:30 Genomic variation and adaptation in Africa: implications for human evolutionary history and disease
Sarah Tishkoff, University of Pennsylvania, Philadelphia, USA

13:30 - 14:00 Reconstructing sex chromosome evolution
David Page, Whitehead Institute for Biomedical Research, Cambridge, USA

14:00 - 14:30 Mining 1000 Genomes data to identify the causal variant in regions under positive selection
Shari Grossman, Broad Institute, Cambridge, USA

14:30 - 15:00 Tracking for Genes and Finding Mutations: Finding Genes for Complex Traits in the Domestic Dog (*Canis familiaris*)
Elaine Ostrander, National Human Genome Research Institute, NIH, Bethesda, USA

15:00 - 15:30 Coffee break

Selected talks

15:30 - 15:45 Genome sequencing and analysis of admixed genomes of African and Mexican ancestry: implications for personal ancestry reconstruction and multi-ethnic medical genomics
Francisco De La Vega, Life Technologies, Foster City, USA

15:45 - 16:00 Genome wide association study SNPs in the human genome diversity project samples: Does selection affect unlinked SNPs with shared trait associations?
Amanda Casto, Stanford University, USA

16:00 - 16:15 The genetic structure of South Asian populations as revealed by 650 000 SNPs

Mait Metspalu, University of Tartu, Estonia

16:15 - 16:30 Next-generation sequencing and the era of personal Y genomes
Qasim Ayub, The Wellcome Trust Sanger Centre, Hinxton, UK

Session 5 - Workshop: Cloud computing in genomics and bioinformatics

Chair: *Folker Meyer, Argonne National Lab, University of Chicago, USA*

16:45 - 17:00 Welcome and Overview
Folker Meyer, Argonne National Lab, University of Chicago, and Vivien Bonazzi, National Human Genome Institute, Bethesda, USA

The novel cloud platform

17:00 - 17:20 The cloud platform - a purely technical perspective. Paradigm, security, data transfer, limitations
Narayan Desai, Argonne National Laboratory, University of Chicago, USA

17:20 - 17:40 Using commercial clouds for bioinformatics
Chris Dagdigian, Bioteam, Boston, USA

17:40 - 18:00 Private clouds
Bob Grossmann, Open Cloud Consortium / Bionimbus, USA

18:00 - 18:20 Coffee break

Three parallel sessions with different foci

18:20 - 19:20 Session I: Getting on to the cloud and sequence analysis in the cloud
Titus Brown, Michigan State University, USA

18:20 - 19:20 Session II: Using CLOVR for bioinformatics purposes
Florian Fricke and Sam Angiuoli, University of Maryland School of Medicine,
Antonio González Peña and Nigel Cook, University of Colorado, USA

18:20 - 19:20 Session III: Real technical challenges and limitations of the cloud platform
Narayan Desai, Argonne National Laboratory, and Michael Schatz, Cold Spring Harbor Laboratory, USA

Real-world examples

19:20 - 19:40 Assembly in the cloud
Michael Schatz, Cold Spring Harbor Laboratory, USA

19:40 - 20:00 The Galaxy workflow system

	James Taylor, Galaxy, Emory University, USA
20:00 - 20:20	The Argonne Workflow Engine (AWE): scaling applications inside the cloud *Narayan Desai, Argonne National Laboratory, USA*
20:20 - 20:40	Applying Cloud Computing to Community Genome Analysis & Distribution *Lincoln Stein, Cold Spring Harbor Laboratory, USA*
20:20 - 20:40	Closing remarks
20:50	End of Day 3