CONFERENCE PROGRAM

DAY 1: TUESDAY 1 OCTOBER

08:00–09:30	Registration
09:30–09:40	Welcome remarks by the organizers
DAY 1 THEME : SINGLE CELL ANALYSES. Chairperson: Nicholas Navin	
09:40–11:20	Session 1: Single cell analyses
	Single cell sequencing: an overview of the field Nicholas Navin, The University of Texas MD Anderson Cancer Center, USA
	Preimplantation genetic diagnosis by single cell genome sequencing Fuchou Tang, Peking University, China
	Single-cell analysis reveals unique transcription program in human metastatic breast cancer cells Devon A Lawson, UCSF, USA
11:20–11:40	Coffee break
11:40–13:10	Session 2: Cancer sequencing and evolution
	Single-cell genomics: life at the single molecule level Sunney Xie, Harvard University, USA
	The development of NGS clinical testing in prenatal diagnosis and reproductive medicine Xu Xun, BGI-Shenzhen, China
	Profiling cancer, one cell at a time James Hicks, Cold Spring Harbor Laboratory, USA
13:10–14:20	Lunch
14:20–14:40	Sponsored talk – How droplet digital PCR is transforming genome analysis Yann Jouvenot, Bio-Rad Laboratories, USA
14:40–15:40	Session 3: Human variation and disease
	Single-cell genomics to study DNA mutation, genetic heterogeneity and disease Thierry Voet, Sanger Institute, UK
	Genome sequencing from cell-free DNA Jacob Kitzman, University of Washington, USA
15:40–16:25	Short talks 1
	High-throughput single cell RNA-Seq to define stem cell population heterogeneity Magali Soumillon, Harvard University, USA
	One strand is better than two: sequencing only template strands expands the scope of single cell genomics Ester Falconer, British Columbia Cancer Agency, Canada
	Extensive variation in chromatin states across humans Maya Kasowski, Stanford University, USA
16:25–16:45	Coffee break
16:45–16:55	Sponsored talk
16:55–17:45	Keynote Speaker–Day 1
	Single cell genomics Stephen Quake, Stanford University and Howard Hughes Medical Institute, USA
17:45–19:45	Poster Session 1 & Welcome Reception/Open Data Award Presentation For more details see page xxvii

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DAY 2: WEDNESDAY 2 OCTOBER

DAY 2 THEME: PLANT GENOMICS, Chairperson: Mario Caccamo

9:30–11:10	Session 4: Plant epigenomics
	Crop genomics comes of age Mario Caccamo, The Genome Analysis Centre, UK
	Inheritance and reprogramming of heterochromatin with small RNA Rob Martienssen, Cold Spring Harbor Laboratory, USA
	Cell type resolution DNA methylomes of the *Arabidopsis* root Ryan Lister, University of Western Australia, Australia
11:10–11:30	Coffee break
11:30–12:30	Session 5: Crop genomics
	Reducing ligation bias of small RNAs during library preparation for NGS and its impact on plant small RNA sequencing Tamas Dalmay University of East Anglia, UK
	Functional genomic tools for wheat Jorge Dubcovsky, UC Davis, USA
12:30-13:00	Session 6: *Arabidopsis* 1001 genomes project
	Population epigenomics and mechanisms of epigenetic inheritance Robert Schmitz, Salk Institute, USA
13:00–14:10	Lunch
14:10–14:20	Sponsored talk
14:20–14:50	Session 7: Small RNA regulation of plant development
	A high resolution gene expression atlas of the maize shoot apex reveals complex regulation in small RNA networks Marja Timmermans, Cold Spring Harbor Laboratory, USA
14:50–15:35	Short talks 2
	Bioinformatics approaches to discover Presence-Absence Variants in maize Aude Darracq, URM de Génétique Végétale, France
	Next-generation mapping of *Arabidopsis* genes Behnaz Saatian, Western University, Canada
	Using exome-capture technology to develop functional genomics tools for wheat Ksenia Krasileva, University of California, Davis, USA
15:35–15:55	Coffee break
15:55–16:05	Sponsored talk
16:05–16:55	Keynote Speaker–Day 2
	The genotype-phenotype map in *Arabidopsis* Magnus Nordborg, Gregor Mendel Institute of Molecular Plant Biology, Austria
16:55–18:55	Poster Session 2 & Reception
20:00–22:00	Conference dinner

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DAY 3: THURSDAY 3 OCTOBER

DAY 3 THEME: INFORMATICS, Chairpersons: Michael Schatz, Alicia Oshlack, Yingrui Li

9:10–10:40	Session 8: Making assemblies
	Hybrid *de novo* assembly of eukaryotic genomes Michael Schatz, Cold Spring Harbor Laboratory, USA
	Differential gene expression analysis for *de novo* assembled transcriptomes Alicia Oshlack, Murdoch Children's Research Institute Royal Children's Hospital, Australia
	An attempt to fill the bioinformatics gap between genomics and applications Yingrui Li, BGI-Shenzhen, China
10:40-11:00	Commercial Presentation – Panasas
11:00–11:20	Coffee break
11:20–11:50	Session 9: Bioinformatics challenge
	Bioinformatics challenge Michael Schatz, Cold Spring Harbor Laboratory, USA
11:50–12:50	Session 10: Cloud-based analyses
	Galaxy as a platform for high-throughput genomics Jeremy Goecks, Emory University, USA
	Bio-IT & cloud sobriety Chris Dagdigian, BioTeam, USA
12:50–13:20	Session 11: Evolutionary genetics from a computational viewpoint
	Sequencing ancient human genomes Janet Kelso, Max Planck Institute for Evolutionary Anthropology, Germany
13:20–14:30	Lunch
14:30–14:50	Sponsored / technical talks
14:50–15:35	Short talks 3
	Development of a genomic region database and analysis tool for the Galaxy platform Matloob Khushi, The University of Sydney, Australia
	Exploring kmer spectra to assess and validate next generation sequencing datasets and assemblies Bernardo J Clavijo, The Genome Analysis Centre, UK
	Disease variant interpretation and prioritization with GEMINI. Aaron R Quinlan, University of Virginia, USA
15:35–15:55	Coffee break
15:55–16:15	Results of 'Bioinformatics challenge'
16:15–17:05	Keynote Speaker–Day 3
	A global alliance for sharing genomic and clinical data David Haussler, UC Santa Cruz, USA
17:05	Closing remarks