Beyond the Genome: Cancer genomics

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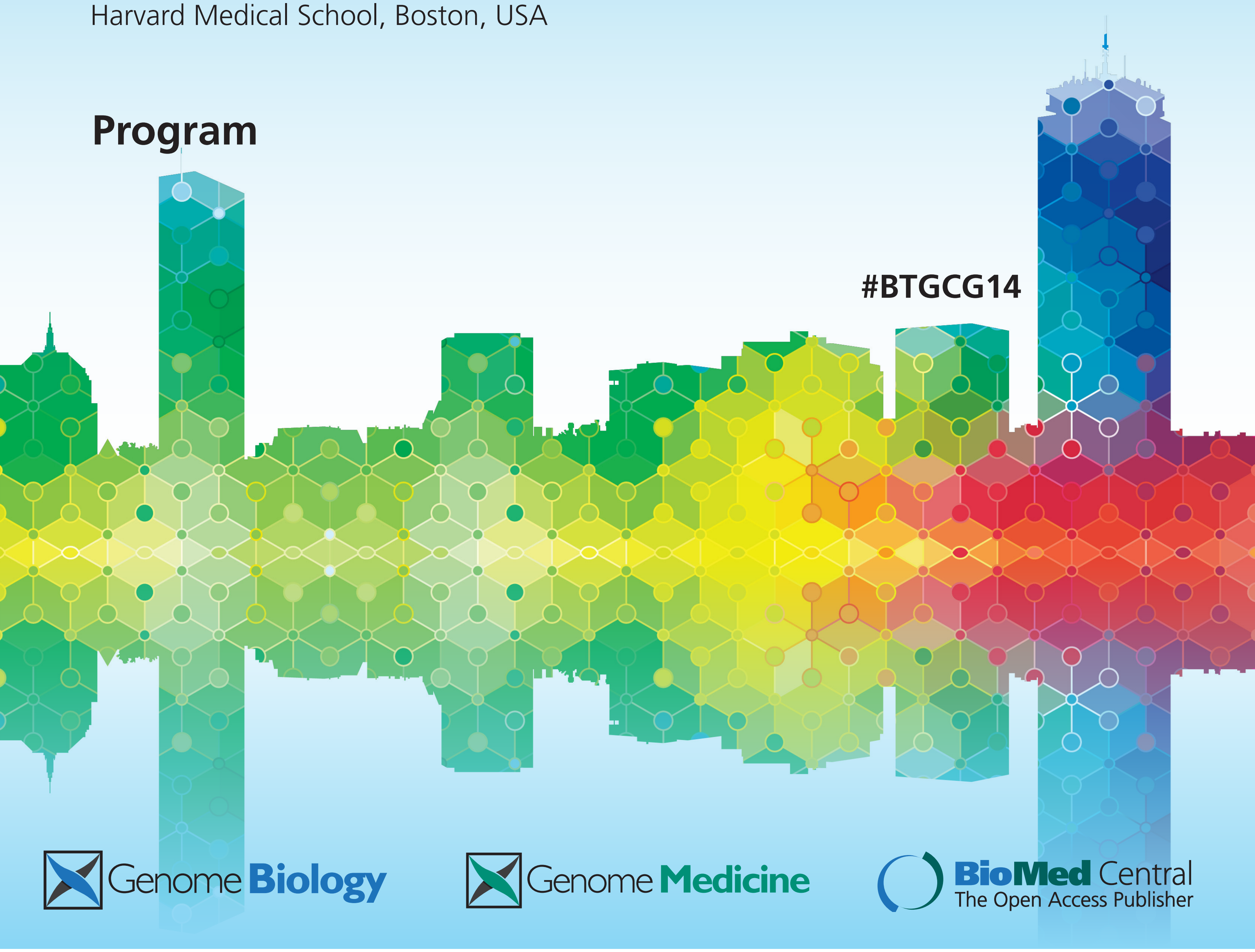
8 - 10 October 2014
Harvard Medical School, Boston, USA

Program



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CONFERENCE PROGRAM

DAY ONE: WEDNESDAY 8 OCTOBER 2014

11:00	Registration/Lunch
12:30	Welcome remarks by the organizers

Session 1: Cancer genomics and epigenomics – large scale discovery. Chair: Gad Getz

12:45	Cancer genomics and evolution Gad Getz, Massachusetts General Hospital and Broad Institute, USA
13:15	Origins and consequences of structural rearrangements Jan Korbel, EMBL, Germany
13:45	Therapeutic landscape of cancer drivers Nuria Lopez-Bigas, University Pompeu Fabra, Spain
14:15	Epigenome alterations drive lethal posterior fossa ependymomas of infancy Michael Taylor, The Hospital for Sick Children, Canada
14:45	*Selected short talk*: Tumor/normal exome sequencing in dogs identifies known and novel lymphoma genes Ingegerd Elvers, Broad Institute, USA & Uppsala University, Sweden
15:00	*Selected short talk*: Pan-cancer gene fusion discovery across 7,470 primary tumor transcriptomes using MOJO Chai Bandlamudi, University of Chicago, USA
15:15	*Sponsored talk*: Enriching nucleic acids for NGS analysis of SNVs, CNVs, gene fusions and more Jonathan Scolnick, NuGEN Technologies
15:30	Coffee break

Session 2: Biology from cancer genomics. Chair: Jan Korbel

16:00	Human genome analysis Mark Gerstein, Yale University, USA
16:30	Delivering large-scale clinical testing of cancer predisposition genes – what does it take? Nazneen Rahman, The Institute of Cancer Research & Royal Marsden NHS Foundation Trust, London, UK
17:00	Clonal evolution in breast cancer revealed by single nucleus genome sequencing Nicholas Navin, MD Anderson Cancer Center & University of Texas, USA
17:30	*Selected short talk*: Exome sequencing identifies highly recurrent *MED12* somatic mutations in breast fibroadenoma Weng Khong Lim, National Cancer Centre Singapore & Duke-NUS Graduate Medical School, Singapore
17:45	*Selected short talk*: Drastic genomic divergence of recurrent medulloblastoma invalidates targeted therapies discovered at diagnosis Sorana Morrissy, The Hospital for Sick Children, Canada

Keynote Lecture. Chair: Jan Korbel

18:00	Convergent sense/antisense transcription at intragenic super-enhancers targets AID-initiated genomic instability Frederick Alt, Howard Hughes Medical Institute, Boston Children's Hospital & Harvard Medical School, USA
18:45	Drinks reception

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DAY TWO: THURSDAY 9 OCTOBER

Session 3: Integrated, systems and network approaches. Chair: Michael Taylor

09:00	*Sponsored talk*: Precision molecular profiling of cancer using ddPCR Jen Berman, PhD, Senior Scientist, Digital Biology Center, Bio-Rad Laboratories
09:15	Epigenetic reprogramming in cancer Christoph Plass, German Cancer Research Center (DKFZ), Germany
09:45	Interrogating regulatory networks to discover master regulators of tumor initiation, progression, and drug resistance Andrea Califano, Columbia University, USA
10:15	*Selected short talk*: Uncovering master regulators of oncogenic transformation by network analysis of the LINCS library of transcriptional signatures of cellular perturbations Mario Medvedovic, University of Cincinnati, USA
10:30	*Selected short talk*: Genomic, epigenomic and transcriptional analyses in a Tet-Myc driven mouse model of liver cancer Valerio Bianchi, Center for Genomic Science of IIT@SEMM, Istituto Italiano di Tecnologia, Italy
10:45	Coffee break

Session 4: Translation and clinical application. Chair: Nicholas Navin

11:15	Drugging the cancer interactome: rational target selection for drug discovery Bissan Al-Lazikani, The Institute of Cancer Research, London
11:45	Liquid biopsies as non-invasive tool to monitor tumor genomes Michael Speicher, Medical University of Graz, Austria
12:15	Lessons from the study of extraordinary responders David Solit, Memorial Sloan Kettering Cancer Center, USA
12:45	*Selected short talk*: Bioinformatic analyses approaches for personalized oncogenomics Katayoon Kasaian, British Columbia Cancer Agency Genome Sciences Centre, Canada
13:00	Lunch

Session 5. Beyond the cancer genome. Chair: Michael Schatz

14:00	Spatial systems biomedicine – linking the ome to multiscale structure Rosalie C Sears, Oregon Health & Science University & Knight Cancer Institute, USA
14:30	The human microbiome – cancer link Sarah Highlander, J. Craig Venter Institute, USA
15:00	Genomic medicine – transforming cancer research and care Lynda Chin, MD Anderson Cancer Center, USA
15:30	*Selected short talk*: Genetic similarity between cancers and comorbid Mendelian diseases identifies candidate driver genes Rachel Melamed, Department of Biomedical Informatics, Columbia University, USA
15:45	*Selected short talk*: Bacteria-human somatic cell lateral gene transfer is enriched in cancer samples Julie Dunning Hotopp, University of Maryland Baltimore, USA
16:00	Coffee break
16:30	*Sponsored talk*: The Cancer Pan-Genome in the Cloud Deniz Kural, Seven Bridges Genomics

Keynote Lecture. Chair: Michael Schatz

16:45	Applying cognitive computing in clinical decision support Rob High, IBM, USA
17:30-19:30	Poster reception & evening buffet

CONFERENCE PROGRAM

DAY THREE: FRIDAY 10 OCTOBER

Session 6: Data visualization and big data challenges. Chair: Jan Aerts

09:00	*Sponsored talk*: Detection of multi-allelic and structural variants in tumor normal data Becky Drees , Spiral Genetics
09:15	Informatics challenge
09:30	Re-inserting human interaction into cancer genome interpretation Cydney Nielsen, University of British Columbia, Canada
10:00	Genomic media and clinical cancer medicine Eliezer Van Allen, Dana-Farber Cancer Institute & Broad Institute, USA
10:30	Coffee break
10:45	Visual exploration of genomic data Helga Thorvalsdottir, Broad Institute, USA
11:15	Guided visual exploration of patient stratifications in cancer genomics Nils Gehlenborg, Harvard Medical School, USA
11:45	*Selected short talk*: Allele-specific quantification of structural variations in cancer genomes Jian Ma, University of Illinois at Urbana-Champaign, USA
12:00	*Selected short talk*: Clustering tumors based on patterns in alternative splicing Elizabeth Purdom, University of California Berkeley, USA
12:15	Lunch

Session 7: Bioinformatic analysis of cancer genomes. Chair: Nuria Lopez-Bigas

13:15	Informatics challenge results
13:30	Pan-cancer network analysis of combinations of somatic mutations Ben Raphael, Brown University, USA
14:00	Interactive analysis and quality assessment of single-cell copy number variations Michael Schatz, Cold Spring Harbor Laboratory, USA
14:30	Coffee break
14:45	Mapping intra-tumor heterogeneity using multidimensional single cell data Dana Pe'er, Columbia University, USA
15:15	Structural variation analysis of tumor genomes Peter Park, Harvard Medical School, USA
15:45	*Selected short talk*: Using *de novo* assembly to exhaustively catalog tumor mutations David Jaffe, Broad Institute, USA
16:00	*Selected short talk*: Moduli spaces of phylogenetic trees describing tumor evolutionary patterns Hossein Khiabanian, Columbia University, USA
16:15	Closing remarks