AGENDA LIKELY TO CHANGE (EST time zone)
Day 1 – Monday, May 16, 2022

8:30 am – Registration opens

9:15 am – Welcome – Chia-Lin Wei – The Jackson Laboratory

9:30 am – George Weinstock – The Jackson Laboratory

Session 1 – Keynote
10:00 am – Karen Miga – University of California, Santa Cruz

11:00 am – Coffee Break

Session 2 – Long Read Sequencing
11:30 am – Kelvin Liu – Circulomics

12:00 pm – Yi Zhang, Harvard Medical School – “EccDNAs are apoptotic products with high innate immunostimulatory activity”.

12:30 pm – Jianhua Luo, University of Pittsburgh – “Ultra-low error synthetic long-read sequencing to characterize human cancer”.

1:00 pm – Lunch

2:30 pm – Tom Chen, Universal Sequencing – “Generating long read information without long read sequencing”

3:00 pm – Jason Reed, Virginia Commonwealth University – “DNA analysis using high-speed atomic force microscopy”.

3:30 pm - Coffee Break

Session 3 – Epigenomics
4:00 pm – Gang Fang, Icahn School of Medicine – “Mapping different forms of DNA methylation from bacteria, microbiome and human”.

4:30 pm – Winston Timp – Johns Hopkins University

5:00 pm – John Stamatoyannopoulos, Altius Institute for Biomedical Sciences –

5:30 pm – Welcome Reception / Cocktail Hour
Day 2 – Tuesday, May 17, 2022

Session 4 – • Human Genomes
9:00 am– TBD

Session 5 – • Computational Biology
10:00 am – Michael Schatz – Johns Hopkins University

10:30 am – Adam Cribbs, University of Oxford, Oxford, UK – “Single-cell long-read transcript sequencing with scCOLOR-seq”.

11:00 am – Coffee Break

11:30 am – Fritz J Sedlazeck, Baylor College of Medicine – “Comprehensive Structural Variant Detection: From Mosaic to Population-Level”.

12:00 pm – Adam Phillippy – National Human Genome Research Institute

Session 6 – Selected Abstracts talks
12:30 pm – TBD
12:45 pm – TBD
1:00 pm – TBD

1:15 pm – Lunch– 10X talk: Patrick Murphy – “Biology at true resolution: Resolving complex biology at the single cell level”.

Session 7 – • Disease research & clinical applications
2:30 pm –

3:00 pm – Chia-Lin Wei – The Jackson Laboratory

3:30 pm – Wigard Kloosterman, Frame Therapeutics & Cyclomics – “Discovery of cancer neoantigens using long-read transcriptome sequencing”

4:00 pm – Coffee Break

Session 8 – • Technology performance, Benchmark, and Rigor
4:30 pm – Christopher Mason – Weill Cornell Medicine, NY

5:00 pm – Justin Zook – NIST

5:30 pm – Poster Session & sponsor exhibition – Wine and cheese
Day 3 – Wednesday, May 18, 2022

Session 9 – • Microbiome and Infectious Disease
9:00 am – Laura Boykin Okalebo – BioTeam

Session 10 – • Transcriptomics
10:00 am – Jørgen Kjems – Aarhus University
10:30 am – Hagen Tilgner, Weill Cornell Medical School – “Mammalian brain isoforms at single-cell resolution”.
11:00 am – Coffee Break
11:30 pm – Kin Fai Au, Department of Biomedical Informatics at The Ohio State University – “Investigate the complexity of transcriptome and epigenetics by single-molecule long-read sequencing”.
12:00 pm – Olga Anzuków, The Jackson Laboratory – “RNA splicing alterations in breast aging and cancer”.
12:30 pm – Lunch and training session with Carmen Robinett, The Jackson Laboratory – “Specific Aims Page Workshop”.

Session 11 – • Non-human Genomes
2:30 pm – Alex Harkess – Auburn University, Hudson Alpha Institute for Biotechnology
3:00 pm – Matthew Hufford – Iowa State University
3:30 pm – Christine Beck, The Jackson Laboratory – “Long Read Sequencing Reveals Extensive Structural Variation in Diverse Mouse Genomes”.
4:00 pm – Coffee Break

Session 12 – • Closing Keynote
4:30 pm – Evan E. Eichler, University of Washington – “Long-read sequencing, structural variation and disease”.
5:30 pm – Closing Remark
Day 4 – Thursday, May 19, 2022

Computational Biology - Bioinformatics showcase sessions

Session 13 – • Basic Long-read sequencing QC and Analyses (Nanopore and PacBio)
9:00 am – Gabriel E. Rech, Computational Scientist. The Jackson Laboratory for Genomic Medicine.

Session 14 – • Metagenomic
10:00 am – Mikhail Kolmogorov, National Human Genome Research Institute – “Long-read metagenomic assembly with metaFlye”.

11:00 – Coffee Break

Session 15 – • Bionano Access
11:30 am – Benjamin Clifford, Ph.D., Senior Field Application Scientist, Bionano Genomics.

Session 16 – • Transcriptomics
12:30 am – Ana Conesa, Institute for Integrative Systems Biology, Spanish National Research Council – “Tools for transforming long reads into functional insights about isoform expression”.

1:30 pm - Lunch

Session 17 – • Epigenomics
2:30 pm – Sheng Li, Assistant Professor. The Jackson Laboratory.

Session 18– • Genome Assembly
3:30 pm – Sara Simmonds, Genome Assembly Application Scientist at Chan Zuckerberg Initiative – “Shasta: a de novo assembler for long reads”.

4:30 – Coffee Break

Session 19 – • Variants and modifications detection
5:00 pm – Medhat Mahmoud, Baylor College of Medicine - “PRINCESS: A Framework for Comprehensive Detection of Haplotype Resolved SNVs, SVs, and Methylation”
Optional Day 5 (Hands-on wetlab tutorial)- Friday, May 20, 2022

8:30 - Registration opens

9:00 – Introduction to long-read sequencing technologies  
    Rahul Maurya, The Jackson Laboratory

9:30 – Extracting High Molecular Weight DNA from Cells  
    Meihong Li, The Jackson Laboratory

11:30 – Lunch

12:30 – PacBio HiFi SMRTBell Library Prep using Express Template Kit  
    Padmaja Ghospurkar, The Jackson Laboratory

2:45 – Coffee Break

3:15 – Oxford Nanopore Targeted Library Prep and Sequencing  
    Christine Goldfarb, The Jackson Laboratory

5:30 - Wrap Up and Q&A