Bioinformatics Workshop Agenda – June 27, 2017

Hosted by the Genomics Resource Center, University of Maryland School of Medicine



THE LEADER IN LONG-READ SEQUENCING



8:30 - 8:55 a.m.	Registration and Continental Breakfast
9:00 - 9:10 a.m.	Welcome and Introduction Roberto Lleras, Manager, Field Applications Scientist, Bioinformatics, PacBio
9:10 - 9:55 a.m.	Introduction to SMRTLink 5.0
	Minor Variant Detection with Juliet Roberto Lleras, Manager, Field Applications Scientist, Bioinformatics, PacBio Structural Variant Detection with PBSV Aaron Wenger, Ph.D., Staff Scientist, PacBio
10:00 - 11:15 a.m.	Concurrent Breakout Sessions

SESSION	I: So, I Have a	Diploid	Assembly	.Now What?

10:00 - 10:30 a.m.	Understanding, Curating, and Analyzing Your Diploid Genome Assembly
	Sarah Kingan, Ph.D., Senior Scientist, Bioinformatics, PacBio
10:30 - 10:45 a.m.	Chromosome-scale De Novo Assembly of Mammalian Genomes Using Chromatin Interaction Data
	lay Ghurve Ph.D. Candidate Department of Computer Science University of Maryland

10:45 - 11:15 a.m.	SESSION I	Discussion
10.10 11.10 4.111.	020010111	Discussion

SESSION II: Mini-training Session: Best Practices in Multiplexing with PacBio

10:00 - 10:30 a.m.	Best Practice for Interpreting Demultiplexed Output
	Carmen Guarco, Ph.D., Scientist, Field Applications Support, Bioinformatics, PacBio
10:30 – 10:50 a.m.	Downstream Applications: Minor Variant Calling, Microbial Assembly, CCS2, and Iso-Seq
	Roberto Lleras, Manager, Field Applications Scientist, Bioinformatics, PacBio
10:50 - 11:15 a.m.	SESSION II Discussion

11:15 - 11:30 a.m.	Coffee Break
11:30 - 11:45 a.m.	Breakout Sessions Wrap-up
11:45 - 12:30 p.m.	Keynote: Accurate Detection of Complex Structural Variation
	Fritz J. Sedlazeck, Ph.D., Lead Scientific Programmer, Human Genome Sequencing Cente Baylor College of Medicine
12:30 - 12:45 p.m.	Open Forum for User Questions, Comments and Feedback on SMRTLink
12:45 - 12:55 p.m.	Closing Remarks

1:00 p.m. Lunch

Thanks to our Partners:







