SMRT Informatics Developers Conference

Town and Country Hotel, San Diego, CA January 17, 2018



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12:00 - 12:30 p.m. Registration and Lunch

12:30 - 12:40 p.m. Introduction and Opening Remarks

Tzvetana Kerelska, Director, Product Management, Informatics, PacBio

12:40 - 1:10 p.m. Keynote: The Evolution of Reference Assembly: Improving Animal

Genomes Using Long Reads and High Heterozygosity

Tim Smith, Ph.D., Genetics, Breeding and Animal Health Unit,

USDA Agricultural Research Service, U.S. Meat Animal Research Center

1:10 - 1:40 p.m. SMRT Link and Analysis Tools for PacBio Data

James Drake, Director, Algorithms, PacBio

1:40 - 2:40 p.m. Lightning Presentations:

From Contigs to Chromosomes with Proximo Hi-C

Zev Kronenberg, Ph.D., Senior Computational Biologist, Phase Genomics

Towards Haplotype-Resolved Genomes with Canu

Sergey Koren, Ph.D., National Human Genome Research Institute, National Institutes of Health

Isoform Phasing Using Iso-Seq Data

Elizabeth Tseng, Ph.D., Principal Scientist, Bioinformatics, PacBio

SQANTI and TAPPAS: Making Sense of Iso-Seq Data

Ana Conesa, Ph.D., Genomics of Gene Expression, University of Florida, Gainesville

Repeat Expansion Genotyping with NoAmp and RepeatAnalysis

Brett Bowman, Staff Scientist, PacBio

Identifying Structural Variants in Individuals and Populations with PacBio Long Reads

Aaron Wenger, Ph.D., Principal Scientist, Bioinformatics, PacBio

2:40 - 3:05 p.m. Afternoon Break

3:05 - 4:25 p.m. Open Discussion: *De Novo* Assembly, Annotation, and Variant Analysis

of Large Genomes

Moderated by: Roberto Lleras, Manager, Field Applications Scientist,

Bioinformatics, PacBio

4:25 - 4:30 p.m. Closing Remarks

Tzvetana Kerelska, Director, Product Management, Informatics, PacBio

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