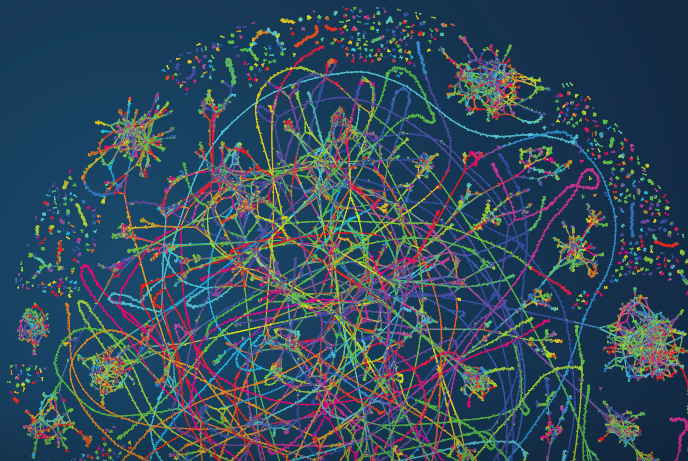# SMRT Informatics Developers Conference

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

PACBIO®

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