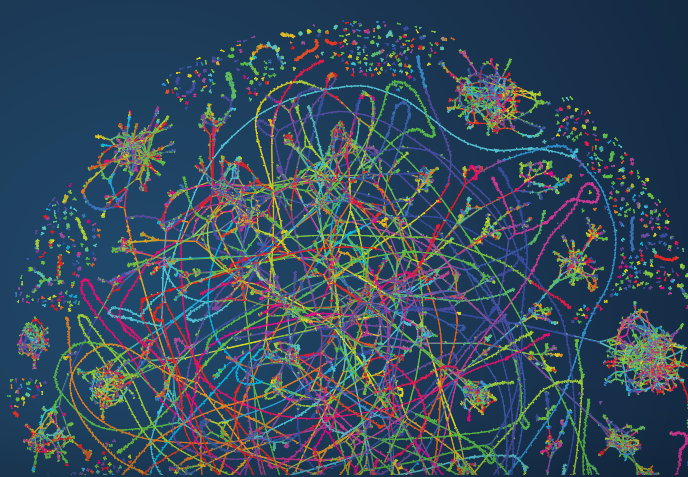


# SMRT Informatics Developers Conference

Town and Country Hotel, San Diego, CA  
Wednesday, January 16, 2019



## 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 Speaker: The Magical World of PacBio® Genome Sequencing

Jeremy Schmutz, Faculty Investigator, HudsonAlpha Institute of Biotechnology and Plant Program Lead, DOE Joint Genome Institute

1:10 - 1:40 p.m. SMRT® Analysis @ Scale - Including Highly Accurate Long Reads

James Drake, Director, Algorithms, PacBio

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

Genome Assembly Using Highly Accurate Long Reads

Richard Hall, Ph.D., Director, Bioinformatics Applications, PacBio

PRINCESS: Framework for Comprehensive Detection and Phasing of SNP and SVs

Fritz Sedlazeck, Ph.D., Assistant Professor, Baylor College of Medicine

Detecting and Phasing Small Variants with Highly Accurate Long Reads

William Rowell, Senior Scientist, Bioinformatics Applications, PacBio

TAMA: Tools for Genome-based Iso-Seq Annotation

Richard Kuo, Bioinformatician, The Roslin Institute, The University of Edinburgh

Haplotyping Using Full-length Transcript Sequencing in a F1 Maize Hybrid Reveals Allele-specific Expression

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

De Novo Assembly of Haplotype-Resolved Human Genomes

Arang Rhie, Ph.D., Postdoctoral Fellow, National Human Genome Research Institute, National Institutes of Health

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

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

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

Tzvetana Kerelska, Director, Product Management, Informatics, PacBio