Function SIG 2016

Start	Finish	Talk	Speaker
9:00 AM	9:10 AM	Introduction/Welcome	Casey Greene/Mark Wass
9:10 AM	9:25 AM	Using PSAMM for integrating functional annotations into phenotypic simulations	Ying Zhang
9:25 AM	9:40 AM	Rule Mining and Selection for Protein Functional Annotation	Rabie Saidi
9:40 AM	9:55 AM	Hunting Human Mendelian Disease-Associated Genes Using Matrix Completion with Side information	Pooya Zakeri
9:55 AM	10:10 AM	System-wide automatic extraction of functional features using eADAGE	Jie Tan
10:10 AM	10:45 AM	Coffee Break	
10:45 AM	11:25 AM	Keynote: Modeling the Cell as a Hierarchy of Subsystems	Trey Ideker
11:25 AM	11:40 AM	The search for functional specificity	Jesse Gillis
11:40 AM	11:55 AM	GOstruct 2.0: Automated Protein Function Prediction for Annotated Proteins	Asa Ben-Hur
11:55 AM	12:10 PM	Explicit Site-specific Function Prediction: automatically inferring function labels for protein regions	Richard Bonneau
12:10 PM	12:25 PM	Predicting Functional Relationships In Osteoblasts	Jacob Luber
12:25 PM	1:40 PM	Lunch	
1:40 PM	2:20 PM	Keynote: The Multiple Lives of Moonlighting Proteins	Constance Jeffery
2:20 PM	2:35 PM	Utilizing computed chemical properties to characterize the functions of Structural Genomics proteins	Caitlyn Mills
2:35 PM	2:50 PM	Genome-scale prediction of moonlighting proteins using diverse protein association information	Daisuke Kihara
2:50 PM	3:05 PM	The Bologna Annotation Resource (BAR 3.0): improving the functional annotation of protein sequences	Giuseppe Profiti
3:05 PM	3:20 PM	Tribe: a version-control server for user-created gene sets	Rene Zelaya
3:20 PM	4:05 PM	Coffee and Posters	
4:05 PM	4:20 PM	Computational prediction of bacterial type III effector proteins	Tatyana Goldberg
4:05 PM	4:50 PM	CAFA3: The Road Ahead	Iddo Friedberg/Casey Greene
4:50 PM	5:00 PM	Concluding remarks and awards	Casey Greene/Mark Wass

NOTE: 5:30pm opening reception for ISMB