

## AFP SIG 2014 Schedule

Day 1			
08:30	08:45	Introduction/Welcome	CAFA Organizers
08:45	09:15	<b>Keynote: The Role of Automated Function Prediction in the Era of Big Data and Small Budgets</b>	<b>Philip Bourne, NIH</b>
09:15	09:35	Network-based prediction of protein function: implications for aging	Tijana Milenkovic
09:35	09:55	Predicting protein function with heterogeneous ensembles	Gaurav Pandey
09:55	10:15	Genome-scale Identification and Characterization of Moonlighting Proteins	Daisuke Kihara
10:15	11:00	Coffee Break	
11:00	11:20	Towards the functional annotation of intrinsically disordered regions	Domenico Cozzetto
11:20	11:40	A method for active-site profile based clustering	Janelle Leuthaeuser
11:40	12:00	Functional Characterization of Structural Genomics Proteins in the Crotonase Superfamily	Caitlyn mills
12:00	12:19	Computational prediction of RNA-binding domains in bacterial effectors proteins	Malvika Sharan
12:19	13:39	Lunch	
13:39	14:00	Evaluation and integration of functional annotation flows for non-model organisms: the potato genome as a test case	Tatyana Goldberg
14:00	14:20	How does incomplete data affect the evaluation of protein function prediction?	Yuxiang Jiang
14:20	14:40	GO curation patterns as a reference for performance evaluation of function prediction algorithms	Paul Pavlidis
14:40	15:00	Supervised text mining for functional curation of literature: how the data and performances have evolved in the last ten years	Patrick Ruch
15:00	16:00	Coffee and Posters	
16:00	16:30	<b>Keynote: Function Prediction on a Genome-scale</b>	<b>Mark Gerstein, Yale University</b>
16:30	16:50	UniProt Gene Ontology Annotation and the CAFA challenge	Rachael Huntley
16:50	17:00	concluding remarks for day	Iddo Friedberg / Predrag Radivojac

Day 2			
08:30	08:45	Introduction/Welcome	
		<b>Keynote: Making protein function and subcellular localization predictions – challenges and opportunities</b>	<b>Fiona Brinkman, Simon Fraser University</b>
08:45	09:15		
		Species-centered coevolutionary networks as a source of species-specific functional information	David Juan
09:15	09:35		
09:35	09:55	CAFA talk	TBA
09:55	10:15	CAFA talk	TBA
10:15	10:45	Coffee	
10:45	11:05	CAFA talk	TBA
11:05	11:25	CAFA talk	TBA
11:25	11:45	CAFA talk	TBA
11:45	12:05	CAFA talk	TBA
12:05	12:25	CAFA talk	TBA
12:25	13:30	Lunch	
13:30	13:50	CAFA talk	TBA
13:50	15:50	CAFA Assessment talks	
15:20	15:55	Coffee	
15:55	16:35	Group Discussion: CAFA 2 summary All	
		PHENOstruct: Prediction of human phenotype ontology using heterogeneous data sources	Indika Kahanda
16:35	16:55		
16:55	17:15	Awards	
17:15	17:25	Concluding remarks	