

MONDAY, JULY 24

- 10:00 AM **Function SIG organizers**
Welcome, Day 1
- 10:10 AM **Maria Brbic**, IRB
The landscape of microbial phenotypic traits and associated genes
- 10:30 AM **Yannick Mahlich**, TUM Munich
fusionDB: assessing microbial diversity and environmental preference via functional similarity networks
- 10:50 AM **Da Chen Emily Koo**, New York University
Region-specific Function Prediction: automatically inferring function labels for protein regions
- 11:10 AM **Ahmet Süreyya Rifaioğlu**, Middle East Technical University
Investigation of Multi-task Deep Neural Networks in Automated Protein Function Prediction
- 11:40 AM **Dmitry Korkin**, Worcester Polytechnic Institute (WPI)
Determining Rewiring Functional Effects of Alternative Splicing Variants on Protein-Protein Interactions
- 12:00 PM **John Moutl**, University of Maryland
Keynote: Community Driven Critical Assessment: how well does it work, what have we learned, and what next?
- 2:00 PM **Ilya Novikov**, Baylor College of Medicine
Reasoning on Gene Ontology Networks Predicts Novel Protein Annotations
- 2:20 PM **Cen Wan**, University College London
Predicting Protein Function Directly from STRING Network Topology using Deep Learning Techniques
- 2:40 PM **Christophe Dessimoz**, University of Lausanne
Proceedings Talk: Orthologous Matrix (OMA) algorithm 2.0: more robust to asymmetric evolutionary rates and more scalable hierarchical orthologous group inference
- 3:10 PM **Matthieu David**, University of Nantes
All-to-all spectra comparisons within minutes for peptides identification in tandem mass spectrometry
- 3:30 PM **Christina Marino-Buslje**, Fundación Instituto Leloir
Comparing residue-coevolution networks across protein families
- 4:30 PM **Seyed Ziaeddin Alborzi**, INRIA Nancy Grand-Est
Automatic Generation of Functional Annotation Rules Using Inferred GO-Domain Associations
- 4:50 PM **Peter Freddolino**, University of Michigan
Protein Function Prediction by COFACTOR in CAFA3
- 5:10 PM **Jonathan G. Lees**, UCL
A Domain-Based Machine Learning Approach for Function Prediction using CATH FunFams
- 5:15 PM **Itamar Borukhov**, Compugen Ltd.
Computational Functional Annotation: The Predictive Power of Different Data Sources
- 5:20 PM **Maxat Kulmanov**, King Abdullah University of Science and Technology
Predicting protein functions from sequence using a neuro-symbolic deep learning model

- 5:25 PM **Matt Jeffryes**, European Bioinformatics Institute
Crowdsourcing Protein Family Database Curation
- 5:40 PM **Jasmin Coulombe-Huntington**, Université de Montreal
Proteome-wide chemical-genetic interaction map in human cells reveals drug mechanisms and novel gene functions

TUESDAY, JULY 25

- 8:30 AM **Function SIG organizers**
Welcome, Day 2
- 8:40 AM **Hagit Shatkay**, University of Delaware
Keynote: Tell Us where You are Going: Pondering Literature, Locations, Life and Proteins
- 9:10 AM **Daisuke Kihara**, Purdue University
Proceedings Talk: DextMP: Deep dive into Text for predicting Moonlighting Proteins
- 10:00 AM **Iddo Friedberg and Naihui Zhou**, Iowa State University
The third Critical Assessment of Function Annotation: Lessons Learned and Preliminary Results
- 11:00 AM *CAFA Predictor 1*
- 11:30 AM *CAFA Predictor 2*
- 11:50 AM **Huaiyu Mi**, University of Southern California
Phylogenetic- based gene function prediction in the Gene Ontology Consortium
- 12:10 PM **Rabie Saidie**, European Bioinformatics Institute
A Self-training Approach for Functional Annotation of UniProtKB Proteins
- 12:15 PM **Giuseppe Profiti**, Università di Bologna
BAR 3.0: going beyond protein function annotation
- 12:20 PM **Liisa Holm**, University of Helsinki
PANNZER 2: Annotate a complete proteome in minutes!
- 12:25 PM **Mary Jo Ondrechen**, Northeastern University
Thinking outside the informatics box: Computed chemical properties for protein function annotation
- 2:00 PM **Petri Törönen**, University of Helsinki
Artificial Dilution Series: A General Framework for Benchmarking Classifier Evaluation Metrics
- 2:20 PM **Yuxiang Jiang**, Indiana University
Elucidating the Function Space of Proteins Defined by Ontologies
- 2:40 PM **Stavros Makrodimitris**, Delft University of Technology
Label-Space Dimensionality Reduction and a Similarity-Based Representation for Protein Function Prediction
- 3:00 PM **John Williams**, MRC Harwell Institute
Predicting Novel Abnormal Circadian Phenotypes in Mouse
- 3:30 PM **Ghazaleh Taherzadeh**, Griffith University
Structure-based prediction of protein-peptide binding regions using Random Forest
- 3:50 PM **Jeffrey Yunes**, UCSF
Automating Genomic Context Analysis with a Probabilistic Model of Protein Function and Relatedness
- 4:00 PM *Awards and Close*