

Automated Function Prediction SIG Meeting

July 20th 2013, Berlin, Germany
ISMB/ECCB 2013

Keynote Speakers



Alex Bateman

European Bioinformatics Institute, UK.

Using protein domains and families for functional prediction



Patricia Babbitt

University of California, San Francisco, USA.

Protein similarity networks: Identification of functional trends from the context of sequence similarity



Anna Tramontano

University of Rome, "La Sapienza", Italy.

CASP: aging or growing up?



Keith Dunker

Indiana University, USA.

Functions of Intrinsically Disordered Proteins

Automated Function Prediction SIG 2013 Programme

- 08:30 Welcome from the organisers
- 08:45 **Keynote – Keith Dunker**, Indiana University, USA.
Functions of Intrinsically Disordered Proteins
- 09:15 **Giorgio Valentini**, Università degli Studi di Milano, Italy.
Scalable Network-based Learning Methods for Automated Function Prediction based on the Neo4j Graph-database
- 09:35 **Joachim Bargsten**, Wageningen University, The Netherlands.
Integrated network- and sequence-based protein function prediction across the plant kingdom
- 09:55 **Christos Ouzounis**, Institute of Applied Biosciences, Greece.
We still haz a job: genome annotashuns
- 10:15 **Coffee break**
- 10:45 **Keynote – Patricia Babbitt**, University of California, San Francisco, USA.
Protein similarity networks: Identification of functional trends from the context of sequence similarity
- 11:15 **Rachael Huntley**, European Bioinformatics Institute, UK.
The Gene Ontology Resource – Common Misconceptions
- 11:35 **Nives Skunca**, ETH Zurich, Switzerland.
Assessing protein function predictions in light of the Open World Assumption
- 11:55 **Noah Youngs**, New York University, USA.
Negative Example Selection in Protein Function Prediction
- 12:15 **Lunch**
- 13:30 **Keynote – Anna Tramontano**, University of Rome “La Sapienza”, Italy.
CASP: aging or growing up?
- 14:00 **Indika Kahanda**, Colorado State University, USA.
Impact of Critical Edges on SVM-based Automated Function Prediction methods
- 14:20 **Jianlin Cheng**, University of Missouri, USA.
Deciphering the association between gene function and spatial gene-gene interactions in 3D genome conformation
- 14:40 **Lightning talks** – Romain Studer, Kimmen Sjolander, Mark Wass
- 15:00 **Coffee and Posters**
- 16:00 **Keynote – Alex Bateman**, European Bioinformatics Institute, UK.
Using protein domains and families for functional prediction
- 16:30 **Gabriel Moreno-Hagelsieb**, Wilfrid Laurier University, Canada.
Operon predictions as the most powerful source of information on the functional association of gene products
- 16:50 **Siew-Yit Yong**, European Bioinformatics Institute, UK.
InterPro - automatic function prediction through high-quality manual annotation
- 17:10 **Iddo Friedberg & Predrag Radivojac**, Miami University & Indiana University, USA.
Introducing CAFA2 and concluding remarks