SNP special interest group

SNP-SIG Meeting

Identification and annotation of SNPs in the context of structure, function, and disease.

ISMB/ECCB 2011
July 15th 2011, Vienna (Austria)

http://snps.uib.es/snp-sig

Highlight Speakers

Atul J. Butte
Stanford University, Stanford (CA), USA

Clinical Assessment Incorporating a Personal Genome.

Mauno Vihinen,
Tampere University, Tampere, Finland.

Genetic variations: origin, effects and prediction.

Keynote Speakers

Steven Brenner
University of California, Berkeley (CA), USA

CAGI Experiments.

Burkhard Rost
Technische Universitat, Munchen, Germany

Trivial step from predicting the effects of SNPs to medicine.

SNP-SIG Organizers

Yana Bromberg, Rutgers University, New Brunswick (NJ), USA
Emidio Capriotti, Stanford University, Stanford (CA), USA

Poster Session

Janita Thusberg, Buck Institute, Novato (CA), USA

Roundtable Discussion

Chris Baker, University of New Brunswick, Saint John (NB), Canada
Maricel Kann, University of Maryland, Baltimore (MD), USA
Sean Mooney, Buck Institute, Novato (CA), USA

SNP-SIG Meeting Programme - July 15th 2011, Vienna (Austria)

08:30 – 08:45 Welcome from the committee

SI: Annotation & prediction of structural/functional impacts of coding SNPs

08:45 – 09:40 **Highlight Speaker: Mauno Vihinen**, Tampere University (Finland)
Genetic variations: origin, effects and prediction.

09:40 – 10:05 **Christian Schaefer**. Technische Universitat Munchen (Germany)
Can we predict structural change upon point mutation?

10:05 – 10:30 **Gilad Wainreb**. Tel Aviv University (Israel)
Protein stability: A single recorded mutation aids in predicting the effects of other mutations in the same amino acid site.

10:30 – 10:45 Coffee Break

10:45 – 11:10 **Piero Fariselli**. University of Bologna (Italy)
Predicting cancer-associated germline variations in proteins.

11:10 – 11:35 **Alain Laederach**. University of North Carolina, Chapel Hill (USA)
Effects of disease-associated SNPs on the structure of the transcriptome.

11:35 – 12:10 **Keynote: Burkhard Rost**, Technische Universitat Munchen (Germany)
Trivial step from predicting the effects of SNPs to medicine.

12:10 – 12:25 **Company Presentation: Frank Schacherer,** BIOBASE GmbH.
Manually curated databases for SNP analysis.

12:25 – 13:30 **Lunch Break and Poster Session with the Authors**

SII: SNPs & Personal Genomics: GWAS, populations and phylogenetic analysis

13:30 – 14:25 **Highlight Speaker: Atul J. Butte,** Stanford University (USA)
Clinical Assessment Incorporating a Personal Genome.

14:25 – 14:50 **Konrad Karczewski**. Stanford University (USA).
Assessing Functional and Clinical Significance of Regulatory Variants.

14:50 – 15:15 **Joel Dudley**. Stanford University (USA).
Evolutionary meta-analysis reveals ancient constraints affecting missing heritability and reproducibility in disease association studies.

15:15 – 15:30 Coffee Break

15:30 – 15:55 **Adam Frankish**. Wellcome Trust Sanger Institute, Hinxton (UK)
Is Understanding Alternative Splicing Important in Interpreting the Potential Functional Effects of SNPs?

15:55 – 16:20 **Sudhir Kumar**. Arizona State University, Tempe (USA).
Comparative Genomics as an Evolutionary Telescope for Genomic Medicine to Peer into the Universe of Human Mutations.

16:20 – 16:55 **Keynote: Steven Brenner,** University of California, Berkeley (USA).
CAGI Experiments

16:55 – 17:45 **Round Table Discussion**

17:45 – 18:00 Closing remarks from the committee