

Program BioRegSIG 2011

7:30 a.m.		Registration
8:30 a.m.	10 min	Welcome: Lonnie Welch
8:40 a.m.	45 min	Chair: Isidore Rigoutsos Keynote: Alexander Stark Research Institute of Molecular Pathology (IMP), Vienna, Austria <i>Regulatory genomics in Drosophila</i>
9:25 a.m.	25 min	Invited: Benoit Ballester European Bioinformatics Institute, Hinxton, UK <i>Five-vertebrate ChIP-seq reveals the evolutionary dynamics of transcription factor binding</i>
	25 min	Invited: Kjetil Klepper Dept. of Cancer Research and Molecular Medicine, Norwegian University of Science and Technology, Trondheim, Norway <i>MotifLab: A tools and data integration workbench for motif discovery and regulatory sequence analysis</i>
10:15 a.m.	30 min	Coffee break
10:45 a.m.	25 min	Chair: Saurabh Sinha Invited: Ana Teresa Freitas Department of Electrical and Computer Engineering, Technical University of Lisbon, Portugal <i>Identification of regulatory signals using graph modularity analysis</i>
	20 min	Contributed: Kathleen Marchal <i>Unveiling combinatorial regulation through the combination of ChIP information and in silico cis-regulatory module detection</i>
	20 min	Contributed: Ivan V. Kulakovskiy <i>Preferred pair distance templates reveal functional transcription factor binding sites</i>
	20 min	Contributed: Bram Van de Sande <i>Discovery of regulators for co-expressed human genes using large sequence search spaces</i>
	20 min	Contributed: Pieter Monsieurs <i>Transcriptional cross-regulation as survival mechanism in bacteria</i>
12:30 p.m.	60 min	Lunch

1:30 p.m.	45 min	Chair: Kathleen Marchal Keynote: Martin Vingron Max Planck Institute for Molecular Genetics, Berlin, Germany <i>Transcription factor binding sites, histone modifications, and two promoter classes</i>
2:15 p.m.	25 min	Invited: Esko Ukkonen Department of Computer Science, University of Helsinki, Finland <i>Modeling regulatory complexes using both TF-DNA and TF-TF interactions</i>
	25 min	Invited: Virginie Bernard Centre for Molecular Medicine and Therapeutics, Child and Family Research Institute, Department of Medical Genetics - University of British Columbia, Vancouver BC, Canada <i>The functional importance and detection of regulatory sequence variants</i>
	25 min	Invited: Roderic Guigo Center for Genomic Regulation, Barcelona, Catalonia, Spain <i>Alternative splicing variability in human populations</i>
3:30 p.m.	30 min	Coffee break
4:00 p.m.	25 min	Chair: Ana Teresa Freitas Invited: Tim Hubbard Wellcome Trust Sanger Institute, Hinxton, UK <i>TBA</i>
	25 min	Invited: Ivo L. Hofacker Institut für Theoretische Chemie, Universität Wien, Austria <i>Prediction of bacterial small RNA targets</i>
	25 min	Invited: Pål Sætrom Dept. of Computer and Information Science and Dept. of Cancer Research and Molecular Medicine, Norwegian University of Science and Technology, Trondheim, Norway <i>Analyzing and designing small RNA-mediated gene regulation</i>
	20 min	Contributed: Pieter Meysman <i>Use of structural DNA properties for the prediction of regulator binding sites with conditional random fields</i>
20 min	Contributed: Heike Sichtig <i>A computational paradigm for more specific TFBS detection</i>	
5:55 p.m. 6:00 p.m.	5 min	Concluding remarks: Finn Drabløs End