

Program of the MCCMB2017

Thursday, July 27th	
9:00	Registration and morning coffee
10:00	OPENING
Epigenomics	
10:20	Transgenerational transmission of environmental information in animals <i>Tanya Vavouri</i>
11:00	Reconstruction of regulatory pathways from methylation QTL data <i>Matthias Heinig</i>
11:40	COFFEE
Chromatin Structure	
12:10	Understanding genome and chromatin structure by RNA biogenesis and degradation <i>Albin Sandelin</i>
12:50	Factors shaping structural organization of chromatin <i>Ekaterina Khrameeva</i>
13:10	RNA-DNA interactions in chromatin <i>Alexandra Galitsina</i>
13:30	LUNCH
Animal development	
15:00	Generating robustness and precision during embryonic development <i>Eileen Furlong</i>
15:40	Widespread conservation of developmental regulation of alternative splicing in mammals <i>Pavel Mazin</i>

16:00	Single cell transcriptomics reveals sequential fate selection points and mechanism of cell fate commitment of the neural crest <i>Ruslan Soldatov</i>
16:20	Frequency and properties of mosaic somatic mutations in a normal developing brain <i>Alexej Abyzov</i>
16:40	Genes with clonal monoallelic expression contribute disproportionately to expression variation in humans <i>Svetlana Vinogradova</i>
17:00	COFFEE and POSTERS
19:30:00 sharp	LEAVE FOR DINNER

Friday, July 28th	
9:00	Morning coffee
Transcriptomics	
10:00	InfoSigMap: Google Maps of informative gene signatures visualizes their compositional and functional redundancies in transcriptomic studies <i>Andrei Zinovyev</i>
10:40	Global transcriptional network reveals that tocopherols rescue TREM2-driven microglial dysfunction in vivo <i>Alexander Predeus</i>
11:00	InFusion: advancing discovery of fusions genes and chimeric transcripts from RNA-sequencing data <i>Konstantin Okonechnikov</i>
11:20	Expression analysis of human miRNA - mRNA interactome <i>Olga Plotnikova</i>
11:40	COFFEE
Integration and Modeling	
12:10	Understanding key features of CRISPR/Cas system induction through modeling <i>Marko Djordjevic</i>
12:30	Protein synthesis: From the whole translatoome to individual codons and back <i>Pavel Baranov</i>
13:10	Robustness of Hunchback gene pattern formation due to dynamic equilibrium in gap gene system in an early <i>Drosophila</i> embryo <i>Ekaterina Myasnikova</i>
13:30	LUNCH
14:40	Biocad. Sponsored talk
Comparative Genomics	

15:00	Evidence of ancient extreme conservation of genomic regions in animal genomes <i>Dmitry Korkin</i>
15:40	Appearance of new splice sites on human lineage is associated with positive selection and splicing changes <i>Stepan Denisov</i>
16:00	Evolution of brain active gene promoters in human lineage towards the increased plasticity of gene regulation <i>Valentin Suslov</i>
16:20	Using historical collections to understand the evolutionary response of bees to an emergent parasite <i>Alexander Mikheyev</i>
17:00	COFFEE
Cells and Mutations	
17:30	Analysis of clone-specific molecular and phenotypic characteristics <i>Peter Kharchenko</i>
18:10	Error-prone bypass of pre-existing damages during the replication of the lagging strand is substantial source of mutations in cancers and germline <i>Vladimir Seplyarskiy</i>
18:30	Mutational signatures of DNA repair deficiencies and cytotoxin exposures in <i>C. elegans</i> <i>Nadezda Volkova</i>
18:50	LEAVE FOR THE BOAT TRIP

Saturday, July 29th

9:00 Morning coffee

Evolution

10:00 Progress and perspectives in understanding genetic control of complex human traits
Yurii Aulchenko

10:40 Large scale fitness landscape of a protein-coding gene
Fyodor Kondrashov

11:20 Contribution of copy number variants to phenotypic diversity of domestic dog breeds.
Inna Povolotskaya

11:40 COFFEE

Cancer

12:10 Analysis of neuroblastoma super-enhancer landscape identifies two distinct malignant cell types
Valentina Boeva

12:50 A quantitative framework of integrating multi-modal cancer genomic data
Chen-Hsiang Yeang

13:10 Dormant origins initiate short-scale replication forks: an evidence from cancer genomes and Okazaki fragments sequencing
Artem Artemov

13:30 LUNCH

Bacteria

15:00 The Dps nucleoid protein from *E. coli*: is DNA protection accompanied by transcriptional regulation?
Maria Tutukina

15:20 Determinants of spacer choice during naïve and primed CRISPR adaptation by type I-E CRISPR-Cas system of *Escherichia coli*
Ekaterina Savitskaya

15:40	Reconstruction of transcription control networks in Mollicutes by high-throughput identification of promoters <i>Gleb Fisunov</i>
16:00	Comparative genomics analysis of human gut microbiome demonstrated broad distribution of metabolic pathways for mucin glycans foraging <i>Dmitry Ravcheev</i>
16:20	Assessing and integrating the various levels of complexity in plant-microbe interactions <i>Muhammad Naseem</i>
16:40	COFFEE
Botanic Garden	
17:10	Phylotranscriptomic hourglass patterns of embryonic and post-embryonic plant development <i>Ivo Grosse</i>
17:50	TRANSFAC-ing the rice genome <i>Tatiana Tatarinova</i>
18:10	Nicotiana genomes: beyond tobacco <i>Nikolai Ivanov</i>
18:30	Using DNA metabarcoding to identify the composition of herbal teas: comparative analysis of Illumina and ion semiconductor high-throughput sequencing platforms <i>Kamil Khafizov</i>

Sunday, July 30th

9:00	Morning coffee
Protein Structure: Interactions	
10:00	Non-random distribution of homo-repeats in eukaryotic and bacterial proteomes and their impact on biological functions <i>Oxana Galzitskaya</i>
10:20	A view of protein evolution from the perspective of yeast protein-complexes <i>Tapash Ghosh</i>
10:40	Spatial distribution of coding diseases-associated single-nucleotide variants in complexes <i>Olga V. Kalinina</i>
11:20	Molecular modelling and BiFC studies of protein-protein interactions in cytokinin signaling <i>Dmitriy Arkhipov</i>
11:40	COFFEE
TBD	
12:10	TBA <i>Nikolay Dokholyan</i>
12:50	Harnessing the wealth of genomic sequence information: from the detection of novel sequence motifs to the discovery of mobile RNA molecules in plants <i>Dirk Walther</i>
13:30	LUNCH
Protein Structure: Folding and Modeling	
15:00	There and back again: A stereoscopic view on the protein folding puzzle <i>Alexei Finkelstein</i>

15:40	Self-consistency test reveals systematic bias in programs for prediction destabilization upon mutation <i>Dmitry Ivankov</i>
16:00	3D features of proteins and their structural changes related to phosphorylation <i>Boris Sobolev</i>
16:20	Cryo-electron microscopy-based integrative atomic-resolution modeling of the TOM GIP complex <i>Valery Veresov</i>
16:40	COFFEE
Protein Structure: Function	
17:10	Computational structural biology of sodium channels <i>Boris Zhorov</i>
17:50	Bioinformatic analysis of subfamily-specific positions reveals a previously unknown regulatory site in Glyceraldehyde 3-phosphate dehydrogenase family of proteins <i>Dmitry Suplatov</i>
18:10	The impact of human genetic variability on ligand-protein interactions and individual drug response <i>Peter Vlasov</i>
18:30	FAREWELL PARTY