



## 6th International Moscow Conference on Computational Molecular Biology (MCCMB'13)

**Moscow, Russia, July 25-28, 2013**

**<http://mccmb.belozersky.msu.ru>**

25 <sup>th</sup>	Thursday		
9.00	10.00	<b>Registration and morning coffee</b>	
10.00	10.20	<b>Opening</b>	
10.20	11.40	<b>Chromatin structure</b>	
10.20	11.00	Peter V. Kharchenko*, Artyom A. Alekseyenko, Andrey A. Gorchakov, Mitzi I. Kuroda	Bayesian Analysis of Mass Spec Enrichment in integrative studies of chromatin-associated complexes
11.00	11.20	Dirar Homouz, Gang Chen, Andrzej Kudlicki*	Maximum Parsimony Interpretation of Chromatin Capture Experiments
11.20	11.40	Yuriy L. Orlov*, Dmitri A. Afonnikov, Nariman R. Battulin, Oleg L. Serov, Nikolay A. Kolchanov, Guoliang Li, Yijun Ruan	3D organization of chromosomes mediated by RNAPII complex contacts in human genome
<b>11.40</b>	<b>12.10</b>	<b>Coffee break</b>	
<b>12.10</b>	<b>13.30</b>	<b>Chromatin (and RNA) structure</b>	
12.10	12.50	Maxim Imakaev*, Geoffrey Fudenberg, Leonid Mirny	Chromosomal Architecture Changes Upon Cell Differentiation
12.50	13.10	Malgorzata E. Rowicka*	Landscape of double-stranded DNA breaks in human genome and its correlation with sequence motifs and DNA bendability
13.10	13.30	Leonid Uroshlev*, Vsevolod Makeev, Julie Bernauer	Determination of type and position of ions in RNA-ion complexes using empirical potential method
<b>13.30</b>	<b>15.00</b>	<b>Lunch break</b>	
<b>15.00</b>	<b>16.00</b>	<b>Regulation of transcription</b>	

15.00	15.40	Gary D. Stormo*	Improved methods for determining TF specificity
15.40	16.00	Ivan V. Kulakovskiy*, Victor G. Levitsky, Dmitry G. Oshchepkov, Ilya E. Vorontsov, Vsevolod J. Makeev	From ChIP-Seq data to improved transcription factor binding sites models
<b>16.00</b>	<b>18.00</b>	<b><i>Coffee break and Poster session</i></b>	
<b>18.00</b>	<b>18.30</b>	<b><i>Buses depart for the Conference dinner</i></b>	
<b>26<sup>th</sup></b>	<b>Friday</b>		
<b>9.30</b>	<b>10.00</b>	<b><i>Hangover coffee</i></b>	
<b>10.00</b>	<b>11.40</b>	<b>Functional genomics and genome structure</b>	
10.00	10.40	Serafim Batzoglou*	Genome Evolution During Progression to Breast Cancer
10.40	11.00	Shuai Jiang, Max A. Alekseyev*	Simultaneous Solution to Synteny Blocks Construction and Genome Rearrangements Problems
11.00	11.20	Oleg Gusev*, Elena Shagimardanova, Yoshitaka Suetsugu, Noriaki Satoh, Maria Logacheva, Alexei Penin, Dmitry Alexeev, Vadim Govorun, Georgy Bazykin, Takahiro Kikawada	Drying without dying: multi-omics analysis of mechanisms of anhydrobiosis in the sleeping chironomid <i>Polypedilum vanderplanki</i> (Diptera)
11.20	11.40	Phillip George, Chantal Vaury, Silke Jensen, Igor V. Sharakhov*	Organization and evolution of piRNA clusters in mosquitoes
<b>11.40</b>	<b>12.10</b>	<b><i>Coffee break</i></b>	
<b>12.10</b>	<b>13.30</b>	<b>Genomics and epigenomics</b>	
12.10	12.50	Vadim N. Gladyshev*	Understanding aging and control of lifespan through genome analyses
12.50	13.10	Tatiana Subkhankulova*	Epigenetic profiling of cardiac stem cells from the adult mammalian heart
13.10	13.30	Yulia A. Medvedeva*, Abdullah Khamis, Ivan V. Kulakovskiy, Wail Ba-Alawi, Md. Shariful I. Bhuyan, Hideya Kawaji, FANTOM consortium, Timo Lassmann, Alister R.R. Forrest, Matthias Herbers, Vladimir B. Bajic	Effects of cytosine methylation on transcription factor binding sites
<b>13.30</b>	<b>15.00</b>	<b><i>Lunch break</i></b>	

<b>15.00</b>	<b>16.40</b>	<b>Viral genomics</b>	<b>Dmitry Frishman</b>
15.00	15.40	Thomas Rattei*	Comparative genomics and metagenomics of viruses
15.40	16.20	Alexander Goultiaev (Gulyaev)*, René C.L. Olsthoorn	Computational search for functional structures in viral RNA genomes
16.20	16.40	Andrey Chursov*, Dmitrij Frishman, Alexander Shneider	Computational Analysis of Influenza RNA Structures: A New Hypotheses for Old Problems
<b>16.40</b>	<b>17.10</b>	<b><i>Coffe break</i></b>	
<b>17.10</b>	<b>18.10</b>	<b>Viral genomics</b>	<b>Dmitry Frishman</b>
17.10	17.50	Alice McHardy*	Computational methods for studying the phenotypic evolution of human influenza A viruses
17.50	18.10	Irena Artamonova*	CRISPR-systems in microbiomes
<b>27<sup>th</sup></b>	<b>Saturday</b>		
<b>9.30</b>	<b>10.00</b>	<b><i>Morning coffee</i></b>	
<b>10.00</b>	<b>11.40</b>	<b>Genomics, genetics and evolution</b>	
10.00	10.20	Konstantin V. Gunbin, Mikhail P. Ponomarenko, Valentin V. Suslov*, Dmitry A. Afonnikov	Human brain origin and the evolution of TATA-boxes of protein-coding genes expressed in brain
10.20	10.40	Eran Elhaik, Tatiana Tatarinova*	Geographic Population Structure (GPS) of worldwide human populations infers biogeographical origin down to home village
10.40	11.20	Alexey Kondrashov*	Accumulation of deleterious alleles in modern human populations
11.20	11.40	Vladimir Seplyarskiy*, Alexey Kondrashov, Timothy James	High-resolution study of recombination in a highly polymorphic fungus <i>Schizophyllum commune</i>
<b>11.40</b>	<b>12.10</b>	<b><i>Coffee break</i></b>	
<b>12.10</b>	<b>13.30</b>	<b>Genomics, genetics and evolution</b>	
12.10	12.50	Shamil Sunyaev*	Human germ line and somatic mutation rates: evolution, biology and statistical genetics
12.50	13.10	Ekaterina E. Khrameeva*, Mikhail S. Gelfand, Philipp Khaitovich	Association between changes in lipid catabolism and increased gene flow from Neanderthals to Europeans

13.10	13.30	Adam D. Hayward, Virpi Lummaa, Georgii A. Bazykin*	Accumulation of deleterious mutations and fitness in a pre-industrial human population
<b>13.30</b>	<b>15.00</b>	<b>Lunch break</b>	
<b>15.00</b>	<b>16.40</b>	<b>Networks</b>	
15.00	15.40	Olga Troyanskaya*	Tissue-specific understanding of human disease from functional genomic data
15.40	16.00	Andrei Zinovyev*, Inna Kuperstein, Emmanuel Barillot, Wolf-Dietrich Heyer	Mechanisms of genetic interactions and cancer treatment
16.00	16.20	Paola Vera-Licona*, Andrei Zinovyev, Eric Bonnet, Inna Kuperstein, Olga Kel, Alexander Kel, Thierry Dubois, Gordon Tucker, Emmanuel Barillot	A Signaling Pathway Rationale for the Design of Combination Therapies for Cancer
16.20	16.40	Ekaterina Myasnikova*	Identifiability analysis and predictive power of the gene circuit model
<b>16.40</b>	<b>17.10</b>	<b>Coffee break</b>	
<b>17.10</b>	<b>17.50</b>	<b>Protein phosphorylation networks</b>	
17.10	17.50	Andrei V. Karginov, Denis Tsygankov*, Timothy C. Elston, Klaus M. Hahn	Dissecting kinase-mediated downstream pathways with temporal and spatial control of its activation
17.50	18.10	Jonathan Mangion (LifeTechnologies)*	<i>Ion Torrent – Gene Panels and Infectious Disease</i>
<b>28<sup>th</sup></b>	<b>Sunday</b>		
<b>9.30</b>	<b>10.00</b>	<b>Morning coffee</b>	
<b>10.00</b>	<b>11.40</b>	<b>Algorithms</b>	
10.00	10.20	Dmitri Papatsenko*, Henia Darr, Ivan Kulakovskiy, Vsevolod Makeev, Ihor Lemischka	Buffering meta-stable pluripotent states in embryonic stem cells
10.20	10.40	Alexander Artyomenko, Nicholas Mancuso, Pavel Skums, Ion Mandoiu, Alex Zelikovsky*	kGEM: An Expectation Maximization Error Correction Algorithm for Next Generation Sequencing of Amplicon-based Data
10.40	11.00	Anton Korobeynikov*, Alla Lapidus, Pavel Pevzner	SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing
11.00	11.20	Ivan Antonov*, Pavel Baranov, Mark Borodovsky	Detection of frameshifts and improving genome annotation
11.20	11.40	Marina Fridman*, Nina Oparina, Ivan Kulakovskiy,	Origin and expansion of microsatellites is associated

		Vsevolod Makeev	with conversion more than with replication
<b>11.40</b>	<b>12.10</b>	<b><i>Coffee break</i></b>	
<b>12.10</b>	<b>13.30</b>	<b>Systems biology and evolution</b>	
12.10	12.50	Philipp Khaitovich*	Insights into human evolution from metabolome studies
12.50	13.10	Olga Ozoline*, Konstantin Shavkunov, Olga Glazunova, Eugeny Fesenko, Maria Tutukina, Sergey Kiselev, Sergey Antipov, Victoria Pokusaeva, Valeriy Panyukov	Promoter islands as instruments of bacterial evolution
13.10	13.30	Valentina Boeva*, Tatiana Popova, Kevin Bleakley, Andrei Zinovyev, Jean-Philippe Vert, Isabelle Janoueix-Lerosey, Olivier Delattre, Emmanuel Barillot	Predicting copy number alterations and allelic status in cancer genomes with Control-FREEC using whole genome or exome sequencing data
<b>13.30</b>	<b>15.00</b>	<b><i>Lunch break</i></b>	
<b>15.00</b>	<b>16.40</b>	<b>Functional bioinformatics and systems biology</b>	
15.00	15.20	Dmitry N. Ivankov*, Samuel Payne, Stefano Bonissone, Si Wu, Roslyn Brown, Ljiljana Paša-Tolić, Matthias Birschenk, Iris Antes, Richard Smith, Michael Y. Galperin, Pavel A. Pevzner, Dmitrij Frishman	Proteogenomic analysis of bacterial signal peptides
15.20	15.40	Audrey M. Michel, Pavel V. Baranov*	Computational model of translation initiation leaky scanning and its application to ribo-seq data
15.40	16.00	Sulbha Choudhari, Ruchi Lohia, Andrey Grigoriev*	How to sequence a glacier: a computational biologist's rough guide
16.00	16.20	Inna Kuperstein* , David P. A. Cohen, Laurence Calzone, Maia Chanrion, Daniel Louvard, Sylvie Robine, Andrei Zinovyev, Emmanuel Barillot	Modelling signalling networks for explaining synthetic gene interactions leading to invasive phenotype in colon cancer mouse model
16.20	16.40	Charles Cantor*	Detection of RNA sequences in living cells by RNA mediated protein complementation
<b>16.40</b>	<b>17.10</b>	<b><i>Coffee break</i></b>	
<b>17.10</b>	<b>18.10</b>	<b>Alternative splicing</b>	

17.10	17.30	Pavel Mazin*, Philipp Khaitovich	Conserved age-related splicing regulation in primate brains.
17.30	17.50	Dmitri Pervouchine*, Sarah Djebali, Alessandra Breschi, Julien Lagarde, Thomas Gingeras, Roderic Guigó	Comparative deep sequencing survey of alternative splicing in human and mouse
17.50	18.10	Ivan P. Gorlov*, Alexei N. Fedorov, Christopher Logothetis, Olga Y. Gorlova, Christopher Amos	Genes with a large intronic burden show a higher evolutionary conservation on protein level
<b>18.10</b>	<b>18.20</b>	<b>Closing</b>	
<b>18.20</b>	<b>21.30</b>	<b><i>Farewell party</i></b>	