

PRELIMINARY SCIENTIFIC PROGRAM

The Multi-conference «Bioinformatics and Systems Biology»

JUNE 23, MONDAY

09:00 – 13:00	Registration (House of Scientists, Small Conference Hall Lounge)	
13:00 – 13:30	Opening	Large Hall, House of Scientists SB RAS
13:30 – 15:45	Plenary lectures	Large Hall, House of Scientists SB RAS
15:45 – 16:15	Coffee break	
16:15 – 18:30	Plenary lectures	Large Hall, House of Scientists SB RAS
18:30 – 20:00	Poster session	
20:00 – 23:00	Welcome party	

9:30-12:00	Institute of Cytology and Genetics SB RAS Workshop of the Center of Neurobiology and Neurogenetics, ICG SB RAS
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JUNE 24, TUESDAY

Time	Small Hall <i>House of Scientists</i>	Exhibition Centre	Music hall <i>House of Scientists</i>
08:30 - 09:00	Symposiums opening		School opening
09:00 - 13:00	BGRS-2014. Evolutionary biology Prof. D. Liberles	ISHG-2014. Medical genetics Prof. V.P. Puzyrev, Prof. M.I. Voevoda	School SBB-2014. Section “Computational analysis of next-gen sequencing data”
14:00 - 19:00	MM-HPC-2014. Text-mining and intelligent analysis of knowledge in databases Prof. A. Rzhetsky, Prof. S.S. Goncharov	ISHG-2014. Medical genetics Prof. V.P. Puzyrev, Prof. M.I. Voevoda	School SBB-2014. Practical training

JUNE 25, WEDNESDAY

09:00 - 13:00	BGRS-2014. Systems computational biology Dr. A. Ratushny Prof. V.P. Golubyatnikov Prof. L. Kaderali	ISHG-2014. Translational medicine Prof. M.P. Moshkin Prof. Y. Iwakura	School SBB-2014. Evolutionary bioinformatics
14:00 - 19:00	BGRS-2014. Systems computational biology Dr. A. Ratushny Prof. V.P. Golubyatnikov Prof. L. Kaderali	BGRS-2014. Plant systems biology Prof. E.A. Salina	ISHG-2014. Translational medicine Prof. M.P. Moshkin, Prof. S.A. Brown School SBB-2014. Practical training (ICG)

JUNE 26, THURSDAY

09:00 - 13:00	BGRS-2014. Genomics and epigenetics Prof. Y. Ruan Prof. E. Prokhortchouk	MM-HPC-2014. High performance computing and software tools for bioinformatics and biomedicine Prof. B.M. Glinskiy D.A. Voronov, Y.L. Orlov	School SBB-2014. Gene networks modeling and supercomputing
14:00 - 19:00	BGRS-2014. Genomics and epigenetics Prof. Y. Ruan Prof. E. Prokhortchouk	MM-HPC-2014. Hemodynamics and tomography Dr. M.A. Shishlenin N.S. Novikov	Open seminar of German/Russian Virtual Network of Bioinformatics “Computational Systems Biology” Prof. R. Hofstaedt

JUNE 27, FRIDAY

09:00 - 13:00	BGRS-2014. Proteomics, metabolomics and computational pharmacology Prof. E. Nikolaev Prof. I. Larina	MM-HPC-2014. Pharmacokinetics and immunology Prof. A.I. Ilyin O.I. Krivorotko	School SBB-2014. Presentations by young scientists
14:00 - 19:00	BGRS-2014. Proteomics, metabolomics and computational pharmacology Prof. E. Nikolaev Prof. I. Larina	MM-HPC-2014. Gene networks Prof. V.P. Golubyatnikov Dr. N.B. Ayupova	School SBB-2014. Presentations by young scientists. Nomination of best presentations. Award ceremony

19:30 - 23:00

Closing of the Conference. Banquet

JUNE 28, SATURDAY

During the day

*Cultural program: Geological Museum, Sun Museum,
Novosibirsk city sight-seeing tour, Novosibirsk Planetarium.*

JUNE 23, MONDAY

09:00 - 13:00 **Registration (House of Scientists, Small Conference Hall Lounge)**

13:00 - 13:30 **Opening** *Large Hall, House of Scientists SB RAS*

13:30 - 17:45 **Plenary session**
Chairpersons: Prof. Nikolay Kolchanov, Prof. Ralf Hofstaedt

13:30 - 14:15 **Y. Ruan**
The Jackson Laboratory, USA
FROM 1D INFORMATION TO 3D GENOME STRUCTURE AND FUNCTION

14:15 - 15:00 **V.A. Stepanov**
FSBI Research Institute of Medical Genetics, Tomsk, Russia
EVOLUTIONARY MEDICINE, GENETIC DIVERSITY AND HUMAN DISEASES

15:00 - 15:45 **A.V. Morozov**
BioMaPS Institute for Quantitative Biology, USA
EVIDENCE FOR EXTENSIVE NUCLEOSOME CROWDING IN YEAST CHROMATIN

15:45 - 16:15 **Coffee break**

16:15 - 17:00 **A. Ratushny**
Institute for Systems Biology, Seattle, USA
MULTISCALE MODELING AS A FRAMEWORK FOR EXPLORING MOLECULAR MECHANISMS OF BIOLOGICAL SYSTEMS

17:00 - 17:45 **E.I. Rogaev**
Department of Psychiatry, Brudnick Neuropsychiatric Research Institute, University of Massachusetts Medical School, USA;
Vavilov Institute of General Genetics RAS, Moscow, Russia;
Center for Brain Neurobiology and Neurogenetics, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University, Moscow, Russia
GENOMIC INVESTIGATION OF THE EVOLUTION AND DISORDER OF THE NERVOUS SYSTEM

17:45 - 18:30 **S.I. Kabanikhin**
Institute of Computational Mathematics and Mathematical Geophysics SB RAS
INVERSE PROBLEMS IN IMMUNOLOGY AND PHARMACOKINETICS

18:30 - 20:00 **Poster session**

20:00 - 23:00 **Welcome party**

9:30-12:00 **Institute of Cytology and Genetics SB RAS**
WORKSHOP of the Center of Neurobiology and Neurogenetics, ICG SB RAS

June 24, Tuesday

Time	Small Hall	Time	Exhibition Centre	Time	Music hall
09:00 - 13:00	BGRS-2014. Evolutionary biology Chairman: <i>Prof. D. Liberles, University of Wyoming, USA</i>	09:00 - 13:00	ISHG-2014. Medical genetics Chairpersons: <i>Prof. V. Puzyrev, FSBI Research Institute of Medical Genetics, Tomsk, Russia</i> <i>Prof. M. Voevoda, FSBI Institute of Internal and Preventive Medicine SB RAMS, Novosibirsk, Russia</i>	09:00 - 13:00	School SBB-2014. Section "Computational analysis of next-gen sequencing data"
09:00-09:45	D. Liberles Department of Molecular Biology, University of Wyoming, Laramie, USA Lineage-specific processes of genome diversification KEYNOTE TALK	09:00-09:40	A. Polyakov Research Centre of Medical Genetics of the RAMS, Moscow, Russia Cases of autosomal recessive pathology in a group of muscular dystrophy X-linked type of inheritance	09:00-09:45	Recommended to attend: D. Liberles University of Wyoming, USA Lineage-specific processes of genome diversification KEYNOTE TALK
09:45-10:10	K.V. Gunbin, D.A. Afonnikov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Selective shifts in recent evolution of Metazoa	09:40-10:00	I. Lebedev, A. Kashevarova, N. Skryabin FSBI Research Institute of Medical Genetics, Tomsk, Russia Genome architecture and chromosomal diseases	10:00-11:20	Y. Ruan The Jackson Laboratory, USA Multi-dimensional gene regulation in cancer cells
10:10-10:35	A. I. Klimenko, Yu.G. Matushkin, S.A. Lashin Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Modeling evolution of spatially distributed bacterial communities simulation with haploid evolutionary constructor	10:00-10:20	N. Yudin, T. Mishakova, V. Maksimov, V. Gafarov, S. Malyutina, M. Voevoda Institute of Internal and Preventive Medicine SB RAMS, Novosibirsk, Russia Association of the dopamine receptor D4 (DRD4) gene polymorphism with cardiovascular disease risk factors		
		10:20-10:40	N. Skryabin, I. Lebedev FSBI Research Institute of Medical Genetics, Tomsk, Russia Somatic genome variability and morphological heterogeneity of breast cancer		

10:35-11:00	V.A. Lyubetsky , A.V. Seliverstov, K.Yu. Gorbunov Institute for Information Transmission Problems, Moscow Rearrangement of chromosomes: problems, algorithms, databases, and gene expression regulations	10:40-11:00	M. Nazarenko , A. Markov, A. Sleptcov, I. Lebedev, N. Skryabin, A. Kashevarova, A. Frolov, O. Barbarash, V. Puzyrev FSBI Research Institute of Medical Genetics, Tomsk, Russia Genome-wide profiling of DNA copy number and methylation in atherosclerosis		
11:00–11:20 Coffee break					
11:20-11:45	O. Reva , I. Korotetskiy, A. Ilyin Bioinformatics and Computational Biology Unit, Biochemistry Department, University of Pretoria, Pretoria, South Africa Discovery of the role of horizontal gene exchange in evolution of pathogenic mycobacteria	11:20-11:40	R. Goncharova , N. Nikitchenko, V. Ramaniuk, N. Savina, T. Kuzhir Institute of Genetics and Cytology, NAS of Belarus, Minsk, Republic of Belarus XPD, XRCC1, OGG1 and ERCC6 polymorphisms and human lifespan	11:20-12:10	A. Morozov BioMaPS Institute for Quantitative Biology, USA Thermodynamics in biology: modeling gene regulation
11:45-12:10	I.D. Sormacheva , G.A. Smyshlyaev, A.G. Blinov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Transposable elements “flying” between Lepidoptera species	11:40-12:00	I. Goncharova , O. Makeeva, N. Tarasenko, A. Markov, S. Buikin, V. Puzyrev Research Institute of Medical Genetics, Tomsk, Russia; Research Institute of Complex Problems of Cardiovascular Diseases, Kemerovo, Russia Molecular genetics peculiarities of fibrogenesis in different pathological traits in humans		
12:10-12:35	B. Zhong Institute of Fundamental Sciences, Massey University, New Zealand Streptophyte algae and the origin of land plants revisited using the chloroplast genomes and nuclear genes	12:00-12:20	L. Bryzgalov , I. Brusentsov, T. Merkulova ICG SB RAS, Novosibirsk, Russia A novel approach to functional SNP discovery from genome-wide data reveals new variants, associated with colon cancer risk		
		12:20-12:40	V.V. Ilinsky , O.L. Kardymon Vavilov Institute of General Genetics RAS; Genotek Inc., Moscow, Russia Fetus whole genome sequence by cell-free DNA from mother’s blood		
		12:40-13:00	S. Sharapov , Y. Tsepilov, J. Ried, K. Strauch, C. Gieger, Y. Aulchenko ICG SB RAS, Novosibirsk, Russia Genome-wide environmental sensitivity analysis of human metabolomics data		

13:00-14:00 Lunch

	<p>MM-HPC-2014. Text-mining and intelligent analysis of knowledge in databases <i>Chairpersons:</i> Prof. A. Rzhetsky, The University of Chicago, USA Prof. S.S. Goncharov, Novosibirsk State University, Russia</p>		<p>ISHG-2014. Medical genetics <i>Chairpersons:</i> Prof. V. Puzyrev, FSBI Research Institute of Medical Genetics, Tomsk, Russia Prof. M. Voevoda, FSBI Institute of Internal and Preventive Medicine SB RAMS, Novosibirsk, Russia</p>		<p>School SBB-2014. Practical training</p>
14:00-14:35	<p>A. Rzhetsky The University of Chicago, USA Machine science KEYNOTE TALK</p>	14:00-14:30	<p>V. Maksimov FSBI Institute of Internal and Preventive Medicine SB RAMS, Novosibirsk, Russia Personalized genomic medicine: today and prospects</p>	14:00-14:35	<p>Recommended to attend: A. Rzhetsky The University of Chicago, USA Machine science KEYNOTE TALK</p>
14:35-14:55	<p>Ya.V. Bazaikin, A. P. Chupakhin , A.A. Cherevko, A.K. Khe Lavrentyev Institute of Hydrodynamics; Novosibirsk State University, Novosibirsk, Russia Application of the methods of persistent homology to clinical data analysis</p>	14:30-14:50	<p>M. Golubenko, R. Salakhov, O. Makeeva, V. Kashtalap, O. Barbarash, V. Puzyrev Institute of Complex Problems of Cardiovascular Diseases, Kemerovo, Russia Analysis of mitochondrial DNA polymorphism in patients with acute coronary syndrome</p>		
14:55-15:15	<p>V.A. Ivanisenko, O.V. Saik, E.S. Tiys, T.V. Ivanisenko, P.S. Demenkov Institute of Cytology and Genetics SB RAS; PBSoft LLC, Novosibirsk, Russia ANDsystem: associative network discovery system for automated literature mining in the area of biology</p>	14:50-15:10	<p>E. Trifonova, N. Ershov, V. Serebrova, V. Stepanov Institute of Medical Genetics SB RAMS, Tomsk, Russia Integrative transcriptome-based approach for association studies: identification of new genetic markers for preeclampsia</p>		
15:15-15:35	<p>V.B. Berikov Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia Centroid-based ensemble of k-means for big data clustering</p>	15:10-15:30	<p>S. Lenskiy, Y. Lenskaya Ural Federal University, Ekaterinburg, Russia Relationships between human gene set and set of gene disorders</p>		

15:35-16:00	R.M. Hofstaedt , T. Hoppe, A. Shoshi Bielefeld University, Bielefeld, Germany Computation of drug interactions and side effects	15:30-15:50	E. Bragina , M. Freidin, E. Tiys, L. Koneva, V. Ivanisenko, V. Puzyrev Institute of Medical Genetics, SB RAMS, Tomsk, Russia Genome-phenome relationships of polar immunological diseases		
16:00-16:20 Coffee break					
16:20-16:45	D.V. Antonets , D.S. Grudin State Research Center of Virology and Biotechnology "Vector", Koltsovo, Russia Using novel generic string kernel to build pan-specific MHC class I peptide binding prediction tool	16:20-16:40	V. Kharkov , O. Radzhabov, V. Stepanov Institute of Medical Genetics SB RAS, Tomsk, Russia Gene pool of the native populations of Dagestan: territorial subdivision and correlation with linguistic classification from the data of Y-chromosome markers		
16:45-17:05	I.I. Titov , A.A. Blinov, K.A. Rudnichenko, P.V. Krutov, A.L. Kazantsev, A.I. Kulikov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Netinference: the computer tools for analysis and visualization of networks structure, dynamics and evolution	16:40-17:00	O. Posukh , A. Churbanov, T. Karafet, A. Bondar, I. Morozov, V. Mikhalskaya, M. Zytsar Institute of Cytology and Genetics, Novosibirsk, Russia Whole exome sequencing in Altaian families (the Altai Republic, Southern Siberia) with congenital hearing loss		
17:05-17:40	L.N. Soldatova , D. Nadis, R.D. King, P.S. Basu, Haddi E., V. Baumlé, N.J. Saunders, W. Marwan, B.B. Rudkin Brunel University, London, UK On Matryoshkas and biomedical protocols KEYNOTE TALK	17:00-17:20	M. Ponomarenko, O. Arkova , O. Saik, T. Arshinova, P. Ponomarenko, D. Rasskazov, M. Genaev, E. Komyshev, L. Savinkova, N.A. Kolchanov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Annotations <i>in silico</i> of 388 SNPs of the core-promoters of 68 human feeding behavior genes in terms of their potential associations with nervous disorders	17:00-18:30	PRACTICAL TRAINING (ICG SB RAS) E.S. Tiys Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Knowledge base on human proteome

		17:20 - 17:40	G.I. Lifshits Institute of Chemical Biology and Fundamental Medicine SB RAS Translational research of pharmacogenetic technologies in the treatment of cardiovascular diseases	
18:00-19:00	Foyer of Small Hall (House of Scientists SB RAS) BGRS POSTER SESSION	18:00-19:00	Auditorium near Conference Hall in the Exhibition Centre SB RAS POSTER SESSION	

June 25, Wednesday

Time	Small Hall	Time	Exhibition Centre	Time	Music hall
09:00 - 13:00	BGRS-2014. Systems computational biology <i>Chairpersons:</i> <i>Prof. L. Kaderali, University of Technology Dresden, Germany</i> <i>Dr. A. Ratushny, Institute for Systems Biology, Seattle, USA</i> <i>Prof. V.P. Golubyatnikov, Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia</i>	09:00 - 13:00	ISHG-2014. MICROSYMPOSIUM "TRANSLATIONAL MEDICINE" <i>Chairpersons:</i> <i>Prof. M. Moshkin, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</i> <i>Prof. Y Iwakura, Research Institute for Biomedical Sciences, Tokyo University of Science, Tokyo, Japan</i>	09:00 - 13:00	School SBB-2014. Section "Evolutionary bioinformatics"
09:00-9:45	L. Kaderali University of Technology Dresden, Germany Systems biology of host-pathogen interactions KEYNOTE TALK	09:00-09:10 09:10-10:00	M.P. Moshkin Opening remark Y. Iwakura Tokyo University of Science, Japan The role of Dectin-1 and Dectin-2 in the host defense against fungi and in intestinal immunity KEYNOTE TALK	09:00-9:45	Recommended to attend: L. Kaderali University of Technology Dresden, Germany Systems biology of host-pathogen interactions (Small Hall)

09:45-10:10	M. Djordjevic , K. Severinov, M. Djordjevic Institute of Physics, University of Belgrade, Belgrade, Serbia Modeling bacterial immune systems: CRISPR/CAS regulation	10:00-10:20	M.Y. Pakharukova , N.I. Ershov, D.S. Pirozhkova, V.A. Vavilin, K.S. Zadesenets, T.G. Duzhak, V.A. Mordvinov ICG SB RAS, Novosibirsk, Russia Molecular mechanisms of metabolism, excretion and drug tolerance in human liver fluke <i>Opisthorchis felineus</i>	09:50-10:30	C. Mitra University of Hyderabad, Hyderabad, India Monte Carlo methods for metabolic kinetics
10:10-10:35	A. Barlukova , S. Honoré, F. Hubert, M. Petit Aix-Marseille University, France Dynamic instabilities of microtubules	10:20-10:40	E. Kozhevnikova ICG SB RAS, Novosibirsk, Russia Gut mucosal proteoglycan Mucin2 compromises animal sexual behavior		
10:35-11:00	M.A. Duk , A.M. Samsonov, M.G. Samsonova A.F. Ioffe Physical-technical Institute RAS, St.Petersburg, Russia Mechanism of miRNA action defines the dynamical behavior of miRNA-mediated feed-forward loops	10:40-11:00	P.N. Menshanov , A.E. Akulov, N.N. Dygalo ICG SB RAS, Novosibirsk, Russia Hippocampal neurochemical profile in neonatal rats: effects of anesthesia		
11:00-11:20 Coffee break					
11:20-12:05	M. Binder German Cancer Research Center, Division Virus-Associated Carcinogenesis, Heidelberg, Germany Modelling of the hepatitis C virus life cycle KEYNOTE TALK	11:20-11:40	S.P. Medvedev Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia The use of new genome engineering technologies for creation of isogenic amyotrophic lateral sclerosis cell model	11:20-12:05	Recommended to attend: M. Binder German Cancer Research Center, Heidelberg, Germany Modelling of the hepatitis C virus life cycle KEYNOTE TALK
12:05-12:30	N. Ivanisenko , E. Mishchenko, I. Akberdin, P. Demenkov, K. Kozlov, D. Todorov, V.V. Gursky, M.G. Samsonova, A.M. Samsonov, D. Clausnitzer, L. Kaderali, N.A. Kolchanov, V.A. Ivanisenko Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Mathematical model for subgenomic hepatitis C virus replication: impact of drug resistance	11:40-12:00	A.A. Nemudryi Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Rescue of Brattleboro rat strain mutant phenotype using TALEN and CRISPR/Cas systems		
		12:00-12:20	O.S. Kozhevnikova , E.E. Korbolina, N.I. Ershov, N.G. Kolosova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Aging of rat retina: transcriptome study	12:10-12:40	D. Liberles Department of Molecular Biology, University of Wyoming, Laramie, USA The lecture on sequence analysis pipelines to uncover lineage-specific evolution

12:30-12:45	N. Egorov InterLabService Advanced achievements of Illumina next-generation sequencing	12:20-12:40	A.B. Salmina , N.A. Malinovskaya, O.L. Lopatina, Y.K. Khomleva Krasnoyarsk State Medical University, Krasnoyarsk, Russia Molecular markers and targets for diagnostics and treatment of neurodegeneration and neurodevelopmental disorders		
13.00-14.00 Lunch					
14:00-17:15	BGRS-2014. Systems computational biology <i>Chairpersons:</i> Prof. L. Kaderali, University of Technology Dresden, Germany Dr. A. Ratushny, Institute for Systems Biology, Seattle, USA Prof. V.P.Golubyatnikov, Institute of Mathematics SB RAS, Novosibirsk, Russia	14:00-17:15	BGRS-2014. Plant systems biology <i>Chairwoman:</i> Prof. E. Salina, Institute of Cytology and Genetics SB RAS	14:00-17:20	ISHG-2014. MICROSYMPOSIUM "TRANSLATIONAL MEDICINE" <i>Chairpersons:</i> Prof. M. Moshkin, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Prof. S. A. Brown, Institute of Pharmacology and Toxicology, University of Zurich, Switzerland
14:00-14:25	K.N. Kozlov , V.V. Gursky, I.V. Kulakovskiy, V.V. Muzhichenko, M.G. Samsonova St.Petersburg State Polytechnical University, St.Petersburg, Russia Sequence-based model of gap gene regulatory network	14:00-14:35	M.V. Kapralov , S.M. Whitney Plant Science Division, Research School of Biology, The Australian National University, Canberra, Australia Evolution of Rubisco encoding genes in plants and its implications for Rubisco engineering in crops KEYNOTE TALK	14:00-14:40	S.A. Brown Institute of Pharmacology and Toxicology, University of Zurich, Zurich, Switzerland Mechanisms of circadian plasticity KEYNOTE TALK
14:25-14:50	E.V. Kashina , D.Y. Oshchepkov, E.A. Oshchepkova, A.G. Shilov, E.V. Antontseva, D.P. Furman, V.A. Mordvinov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Dioxin-mediated regulation of genes involved in cytokines production by macrophages	14:35-14:55	P.M. Ponomarenko, M.P. Ponomarenko Children's Hospital Los Angeles, Los Angeles, USA An empirical equilibrium equation of a gene response to auxin in plants allows to predict quantitatively the auxin response	14:40-15:00	A. Baranova, L.Wang, T. Cui, B. Veytsman , S. Bruskin School of Systems Biology, George Mason University, Fairfax, USA Attractor based classifiers for prediction of post-treatment survival in cancer and detection of non-malignant diseases

14:50-15:15	I.R. Akberdin , T.V. Ermak, F.V. Kazantsev, T.M. Khlebodarova, V.A. Likhoshvai Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Kinetic modeling of pyrimidine biosynthesis is a first step to <i>in silico</i> bacterial cell	14:55-15:15	F.V. Kazantsev, V.V. Chernova, A.V. Doroshkov, N.A. Omelyanchuk, V.V. Mironova , V.A. Likhoshvai Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Self-organization mechanisms for auxin distribution in the root apical meristem	15:00-15:20	O.E. Redina , S.E. Smolenskaya, T.O. Abramova, L.N. Ivanova, A.L. Markel Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Genetic dissection of inherited hypertensive state in ISIAH rats using kidney gene-expression and genome mapping
15:15-15:40	J. Narula, A. Kuchina, G.M. Süel, O.A. Igoshin Department of Bioengineering, Rice University, Houston, USA Slowdown of cell growth acts as the signal triggering cellular differentiation	15:15-15:35	G.I. Karlov , M.G. Divashuk, O.S. Alexandrov, O.V. Razumova, T.M.L. Khuat, P.Yu. Kroupin Centre for Molecular Biotechnology, Russian State Agrarian University, Moscow, Russia Plant molecular cytogenetics and next-generation sequencing data analysis	15:20-15:40	E. Pozhilenkova Krasnoyarsk State Medical University, Krasnoyarsk, Russia Development of cellular models for translational research in neuropharmacology
15:40-16:00 Coffee break					
16:00-16:25	O.V. Popik , N.A. Kolchanov, V.A. Ivanisenko Center of Neurobiology and Neurogenetics, ICG SB RAS, Novosibirsk, Russia Mathematical modeling of the interactions between molecular genetic systems	16:00-16:20	I.V. Pinsky , A.T. Ivashchenko Al-Farabi Kazakh National University, Almaty, Kazakhstan miRNAs binding to mRNAs of rice Myb genes	16:00-16:20	I.L. Erokhin National Biotechnological Company, LLC, Moscow, Russia Oncogenesis model based on the genome structure of multicellular organisms
16:25-16:50	A. Kursanov , O. Solovyova, L. Katsnelson, K. Medvedev, A. Vasilyeva, N. Vikulova, V.S. Markhasin Institute of Immunology and Physiology UB of RAS, Yekaterinburg, Russia Cardiac mechanics, calcium overload and arrhythmogenesis	16:20-16:45	Y. Kanayama , H. Ikeda School of Agricultural Science, Tohoku University, Sendai, Japan Metabolome and transcriptome analyses of a tomato introgression line containing a <i>Solanum pennellii</i> chromosome segment	16:20-16:40	B. Veytsman , T.Cui, L. Wang, A. Baranova School of Systems Biology, George Mason University, Fairfax, USA Systemic shifts in micro RNA landscape as a diagnostic and prediction tool

16:50-17:15	<p>P.A. Ryzhkov, N.S. Ryzhkova Scientific Research Institute of Biology SFEDU, Rostov-on-Don, Russia</p> <p>Graph model of type I diabetes</p>	<p>16:45-17:05</p> <p>D.A. Afonnikov, M.A. Genaev, E.G. Komyshev, A.V. Doroshkov, T.A. Pshenichnikova, E.V. Morozova, A.V. Simonov ICG SB RAS, Novosibirsk, Russia</p> <p>Computer high-throughput approaches to wheat phenotyping</p>	<p>16:40-17:00</p> <p>L.N. Grinkevich I.P. Pavlov Institute of Physiology RAS, St. Petersburg, Russia</p> <p>Epigenetic mechanisms of memory formation: the role of the histone acetylation and methylation in aversive learning</p>
17:15-17:50	<p>S.A. Lashin, Yu.G. Matushkin Institute of Cytology and Genetics SB RAS; Novosibirsk State University, Novosibirsk, Russia</p> <p>DEC: software tools for simulation evolution in diploid populations</p>	<p>17:05-17:25</p> <p>A.V. Doroshkov, U.S. Zubairova, M.A. Genaev, S.V. Nikolaev, T.A. Pshenichnikova, D.A. Afonnikov ICG SB RAS, Novosibirsk, Russia</p> <p>Analysis of bread wheat leaf pubescence formation and diversity using image analysis technique and mathematical modeling</p>	<p>17:00-18:00</p> <p>School BB-2014. Practical training (ICG SB RAS: Lavrentyeva, 10)</p> <p>F.V. Kazantsev Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</p>
		<p>17:25-17:45</p> <p>K.N. Sarsenbayev Eurasian National University, Astana, Kazakhstan</p> <p>Proteomic information of spring wheat varieties differing in resistance to infection after <i>Puccinia recondita</i> inoculation</p>	
		<p>17.45-18.10</p> <p>E.M. Sergeeva, E.M. Timonova, L.L. Bildanova, M.K. Koltunova, M.A. Nesterov, F. Magni, Z. Frenkel, J. Dolezel, J. Faris, P. Sourdille, C. Feuillet, E.A. Salina ICG SB RAS, Novosibirsk, Russia</p> <p>The progress in physical mapping of chromosome 5b of bread wheat <i>Triticum aestivum</i></p>	

18:00-19:00	Foyer of Small Hall (House of Scientists SB RAS)	18:10-18:30	A.I. Perflyeva Siberian Institute of Plant Physiology and Biochemistry SB RAS, Irkutsk The statistical analysis of level of an expression of a series of proteins of a plant of <i>Arabidopsis thaliana</i> in the conditions of stressful influence
POSTER SESSION			

June 26, Thursday

Time	Small Hall	Time	Exhibition Centre	Time	Music hall
09:00 - 13:00	BGRS-2014. Genomics and epigenetics <i>Chairpersons:</i> Prof. Y. Ruan, <i>The Jackson Laboratory, USA</i> Prof. E. Prokhortchouk, <i>National Research Center "Kurchatov Institute", Moscow, Russia</i>	09:00 - 13:00	MM-HPC-2014. High performance computing and software tools for bioinformatics and biomedicine <i>Chairpersons:</i> Prof. B.M. Glinskiy, <i>D.A. Voronov, Institute of Computational Mathematics and Mathematical Geophysics SB RAS;</i> Y.L. Orlov, <i>ICG SB RAS, Novosibirsk, Russia</i>	09:00 - 13:00	School SBB-2014. Section "Gene networks modeling and supercomputing"
09:00-9:35	E. Prokhortchouk National Research Center "Kurchatov Institute"; Center of Bioengineering, RAS, Moscow, Russia Ancient DNA: genome and epigenome KEYNOTE TALK	09:00-09:30	B.G. Mikhailenko, B.M. Glinskiy, N.V. Kuchin , I.G. Chernykh ICM&MG SB RAS, Novosibirsk, Russia Siberian Supercomputer Center as a service for bioinformatics KEYNOTE TALK	09:00-09:30	Recommended to attend: B.G. Mikhailenko, B.M. Glinskiy, N.V. Kuchin , I.G. Chernykh Siberian Supercomputer Center as a service for bioinformatics KEYNOTE TALK
09:35-9:55	V.N. Babenko Center of neurobiology and neurogenetics, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Transposons vs genes: survival strategies?	09:30-09:50	N.N. Nikitina , E.E. Ivashko, Y. Gupta, R. Lüdwig, S. Möller University of Lübeck, Department of Dermatology, Germany; Institute of Applied Mathematical Research, Karelian Center of the RAS, Petrozavodsk, Russia BOINC-based desktop GRID infrastructure for virtual drug screening	9:35-11:00	R. Hofestädt Bielefeld University, Germany Petri net modeling and simulation of metabolic pathways

9:55-10:15	I.V. Antonov , A.V. Marakhonov, A. Baranova, M.Y. Skoblov Research Centre for Medical Genetics RAMS, Moscow, Russia Prediction of antisense RNA-RNA interactions in animal cells	09:50- 10:10	I.G. Chernykh , S.I. Kabanikhin, D.A. Voronov Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia CHEMPAK software package: numerical modeling of direct and inverse pharmacokinetics problems		
10:15- 10:35	C.K. Mitra , A.K. Meena School of Life Sciences, University of Hyderabad, Hyderabad, India Association between microRNA and UTRs from human tlr genes	10:10- 10:30	I.V. Protsyuk ^{1,2} , G.A. Grekhov, A.V. Tiunov, M.Y. Fursov ¹ Novosibirsk State University, ² Center of Information Technologies “UniPro”, Novosibirsk, Russia Shared bioinformatics database within UniPro UGENE		
10:35- 10:55	A.T. Ivashchenko , O.A. Berillo, A.Y. Pyrkova, R.E. Niyazova, S.A. Atambayeva National Nanotechnology Laboratory, Al-Farabi KazNU, Almaty, Kazakhstan The features of binding sites of MIR-619- 5P, MIR-5095, MIR-5096 and MIR-5585-3P in the mRNAs of human genes	10:30- 10:50	I.V. Afanasyev Institute of Computational Mathematics and Mathematical Geophysics SB RAS Application of cellular automata for investigation of pollution influence on Macrohectopus and Comephorus population in the lake Baikal		
10:55-11:15	<i>Coffee break</i>				
11:15- 11:35	P.B. Natalin Genetic Analysis Team Leader, Genetic Medical & Applied Sciences, Life Sciences Solutions, Thermo Fisher Scientific, Moscow, Russia ION Torrent™ platform in 2014: technology and applications	11:15- 11:45	I. V. Oseledets Skolkovo Institute of Science and Technology; Institute of Numerical Mathematics RAS, Moscow, Russia Numerical methods for high- dimensional problems in biology KEYNOTE TALK	11:15- 11:35	Recommended to attend: I. V. Oseledets Moscow, Russia Numerical methods for high- dimensional problems in biology KEYNOTE TALK

11:35-11:55	<p>G.St. Laurent, D. Shtokalo, M.R. Tackett, S. Nechkin, D. Antonets, Yu. Vyatkin, Y.A. Savva, P. Kapranov, C.E. Lawrence, R.A. Reenan</p> <p>St.Laurent Institute, Cambridge, USA; AcademGene LLC, Novosibirsk, Russia.</p> <p>Whole genome analysis of A-to-I RNA editing using single molecule sequencing in Drosophila</p>	11:45-12:00	<p>D. Petunin</p> <p>Intel Corp.</p> <p>Intel® Cilk™ plus – data parallelizm and vectorization in C/C++ programs</p>		
11:55-12:15	<p>K.V. Gunbin, K.Y. Popadin</p> <p>Center of neurobiology and neurogenetics, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</p> <p>5' and 3' breakpoints of mtDNA deletions show drastic differences in dinucleotide properties</p>	12:00-12:20	<p>Z.S.Mustafin, S.A. Lashin</p> <p>ICG SB RAS; Novosibirsk State University, Novosibirsk, Russia</p> <p>High performance computing simulation of evolutionary processes in bacterial communities</p>		
12:15-12:50	<p>A.V. Nedoluzhko, E.S. Boulygina, A.S. Sokolov, S.V. Tsygankova, M. Schubert, N.M. Gruzdeva, A.D. Rezepkin, L. Orlando, E.B. Prokhortchouk</p> <p>National Research Center “Kurchatov Institute”, Moscow, Russia</p> <p>De novo assembly of the mitochondrial genome of ~5000-year-old human from North Caucasus</p> <p>KEYNOTE TALK</p>	<p>12:20-12:40</p> <p>12:40-13:00</p>	<p>A.A. Danilov, V.K. Kramarenko, V.Yu. Salamatova, A. S. Yurova</p> <p>Institute of Numerical Mathematics RAS, Moscow, Russia</p> <p>High resolution computational models for bioelectric impedance analysis</p> <p>T.S. Troeglazova, D.Ja. Baishibaev, A.V. Penenko, S.V. Nikolaev, U. Zubairova</p> <p>ICM&MG SB RAS</p> <p>On a parallel algorithm for morpho-gene diffusion-reaction processes simulation on a 2D cell ensemble</p>	12:15-12:50	<p>Recommended to attend:</p> <p>A.V. Nedoluzhko et al.</p> <p>National Research Center “Kurchatov Institute”, Moscow, Russia</p> <p>De novo assembly of the mitochondrial genome of ~5000-year-old human from North Caucasus</p> <p>KEYNOTE TALK</p>
13:00-14:00 Lunch					

14:00-17:50	BGRS-2014. Genomics and epigenetics Chairpersons: Prof. Y. Ruan, The Jackson Laboratory, USA Prof. E. Prokhortchouk, National Research Center "Kurchatov Institute", Moscow, Russia	14:00-18:05	MM-HPC-2014. Hemodynamics and tomography Chairpersons: Dr. M.A. Shishlenin, N.S. Novikov, Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia	14:00-17:40	School SBB-2014. Presentations by young scientists
14:00-14:35	R.V. Chereji, T.-W. Kan, V.P. Guryev, A.V. Morozov, Y.M. Moshkin ^{1,2} Erasmus Medical Center, Rotterdam, the Netherlands; ² Center of Genetic Resources, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Biophysical principles guiding nucleosome positioning in vivo	14:00-14:30	A.P. Chupakhin , A. Cherevko, A. Khe, A.Chebotnikov, A. Krivoschapkin, K. Orlov, V. Panarin Lavrentyev Institute of Hydrodynamics SB RAS, Novosibirsk, Russia Comprehensive study of hemodynamics of cerebral vessels in the presence of pathologies KEYNOTE TALK	14:00-14:20	A. Barlukova , S. Honoré, F. Hubert, M. Petit Aix-Marseille University, France Dynamic instabilities of microtubules
14:35-14:55	D. Zharkov Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk, Russia 5-methylcytosine and DNA oxidation: at the crossroads of epigenetics, DNA damage, and DNA repair	14:30-14:50	A.V. Mikhailova , A.A. Cherevko, A.P. Chupakhin, A.L. Krivoschapkin, K.Y. Orlov Novosibirsk State University, Russia Identification of based on experimental clinical data hemodynamic model	14:20-14:40	A. Borisenko Irkutsk State Medical University, Irkutsk, Russia Analysis of genetic sequences of tick-borne encephalitis virus in the territory of the Eurasian area
14:55-15:15	D.Y. Oschepkov , V.G. Levitsky, I.V. Kulakovskiy, N.I. Ershov, V.J. Makeev, T.I. Merkulova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Experimentally verified transcription factor binding sites models applied for computational analysis of ChIP-seq data	14:50-15:10	A.A. Cherevko, A.P. Chupakhin, A.K. Khe, E.A.Vorontsova, Y.A. Fedorova , A.L. Krivoschapkin, P.A. Seleznev Lavrentyev Institute of Hydrodynamics SB RAS Unsteady hemodynamic simulation of the brain's vascular system with aneurysms	14:40-15:00	A. Vitvitsky Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia Computer simulation of self-organization in the bacterial MinCde system
15:15-15:35	T. Subkhankulova, F. Naumenko Imperial College, London, UK Is the single cell ChIP-seq technique possible?	15:10-15:30	A.I. Konokhova , K.V. Gilev, D.I. Strokotov, M.A. Yurkin, V.P. Maltsev Institute of Chemical Kinetics and Combustion SB RAS, Novosibirsk, Russia The solution of the inverse light-scattering problem for precise morphological characterization of milk fat globules	15:00-15:20	T. Gamilov Moscow Institute of Physics and Technology, Dolgoprudnyy, Russia 1D modelling of different time regimes of enhanced external counterpulsation

15:35-15:55	M. Djordjevic Institute of Physiology and Biochemistry, University of Belgrade, Faculty of Biology, Belgrade, Serbia A biophysical approach to bacterial transcription start site prediction	15:30-15:50	T.K. Dobroserdova Institute of Numerical Mathematics RAS, Moscow, Russia Numerical simulation of blood flow in the vascular network with pathologies or implants	15:20-15:40	A. Gurkov, E.M. Kondratyeva, D.S. Bedulina Institute of Biology at Irkutsk State University, Irkutsk, Russia IMAGEJ add-on for 2D electrophoresis gel analysis
15:55-16:15 Coffee break					
16:15-16:35	S.V. Dzhenin Limited Liability Company Eppendorf, Russia Influence of consumables on quality and precision of experiments	16:15-16:45	A.V. Kel'manov Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia On some analysis, recognition and classification problems of biometrical sequences in a connection with combinatorial optimization problems KEYNOTE TALK	16:15-16:35	U. Gusev, M.I. Chumakov Institute of Biochemistry and Physiology of Plants and Microorganisms RAS, Saratov, Russia Evaluation of Vire2-complexes by molecular dynamic methods
16:35-16:55	G.G. Krutinin, E.A. Krutinina, S.G. Kamzolova, A.A. Osypov Laboratory of Cell Genome Functioning, Institute of Cell Biophysics RAS, Pushchino MR, Russia Electrostatic properties of bacteriophage Lambda genome and its elements: virus vs host	16:30-16:45	T.M. Gamilov, S.S. Simakov Moscow Institute of Physics and Technology, Dolgoprudny, Russia 1D modelling of different time regimes of enhanced external counterpulsation	16:35-16:55	A. Katugina, U.F. Kartavtsev Institute of Marine Biology FEB RAS, Vladivostok, Russia Comparative genetic analysis of three species of the genus Tribolodon (Cyprinidae, Cypriniformes) based on sequence data of mitochondrial DNA CO-1 gene
16:55-17:15	A.A. Ryasik, A.A. Grinevich, L.V. Yakushevich Institute of Cell Biophysics RAS, Pushchino, Russia Dynamics of nonlinear conformational excitations in functional regions of pttq18 plasmid	16.45-17.05	Y.A. Ivanov, R. Pryamonosov Institute of Numerical Mathematics RAS, Moscow, Russia Patient specific reconstruction of vascular network for hemodynamic modeling	16:40-17:00	L.A. Krasnobaeva, L.V. Yakushevich Siberian State Medical University, Tomsk, Russia Rotational dynamics of bases in the gene coding interferon alpha 17 (IFNA17)
17:15-17:35	M.A. Golyshev, E.V. Korotkov ^{1,2} ¹ Bioinformatics laboratory, Centre of Bioengineering RAS, Moscow, Russia; ² Cybernetics department, National Research Nuclear University "MEPhI", Moscow, Russia. Computer annotation of bacterial genes using phylogenetic profiles	17.05-17.25	A.E. Moskalensky, D.I. Strokotov, M.A. Yurkin, V.P. Maltsev Institute of Chemical Kinetics and Combustion SB RAS, Novosibirsk, Russia Characterization of blood platelets solving the inverse light-scattering problem with pre-computed interpolating set	17:00-17:20	E. Kulakova Novosibirsk State University, Russia Computer data analysis of genome sequencing by technology ChIP-seq and Hi-C

17:35-17:50	A. Verner Bio-Rad Laboratories, Moscow Getting sophisticated: new approaches, trends and developments for DDPCR	17:25-17:45	A.Ye. Medvedev Khristianovich Institute of Theoretical and Applied Mechanics SB RAS, Novosibirsk, Russia Equation of state of blood flows in small vessels	17:20-17:40	K. Korla School of Life Sciences, University of Hyderabad, India Kinetic simulation of mitochondrial shuttles
18:00-19:00	Foyer of Small Hall (House of Scientists SB RAS) POSTER SESSION	17:45-19:00	Auditorium near Conference Hall in the Exhibition Centre SB RAS POSTER SESSION		

Institute of Cytology and Genetics SB RAS

June 26 (Thursday) 14:00-17:30

Open seminar of German/Russian Virtual Network of Bioinformatics "Computational Systems Biology"

Chairman: Prof. R. Hofstaedt, Bielefeld University, Germany

14:00-14:20	R. Hofstaedt Bielefeld University, Germany OPEN SEMINAR OF GERMAN/RUSSIAN VIRTUAL NETWORK OF BIOINFORMATICS "COMPUTATION SYSTEMS BIOLOGY"
14:20-14:40	H. Binder Interdisciplinary Centre for Bioinformatics of Leipzig University (Leipzig), Germany
14:40-15:00	V.A. Ivanisenko Institute of Cytology and Genetics SB RAS (Novosibirsk), Russia
15:15-15:30	O. Popik Institute of Cytology and Genetics SB RAS (Novosibirsk), Russia EVALUATION OF PATHWAYS' EFFICIENCY BASED ON DATA ON PPI AND DISTRIBUTION OF PROTEINS OVER CELLULAR LOCALIZATIONS
15:30-15:45	N. Alemasov Institute of Cytology and Genetics SB RAS (Novosibirsk), Russia STRUCTURAL AND DYNAMICAL PROPERTIES OF SOD1 PROTEIN MUTANTS RELATED TO FAMILIAL AMYOTROPHIC LATERAL SCLEROSIS
15:45-16:00	A. Bragin Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia APPLICATION OF CONFORMATIONAL PEPTIDES FOR ANALYSIS OF ALLERGENIC PROTEINS
16:00-16:15	Coffee break
16:15-16:30	DAAD students talk
16:30-17:30	Discussion

June 27, Friday

Time	Small Hall	Time	Exhibition Centre	Time	Music Hall
09:00 - 12:35	BGRS-2014. Proteomics, metabolomics and computational pharmacology <i>Chairpersons:</i> <i>Prof. E. Nikolaev, Institute for Biomedical Problems RAS, Moscow, Russia</i> <i>Prof. I. Larina, Institute for Biomedical Problems RAS, Moscow, Russia</i>	09:00 - 12:15	MM-HPC-2014. Pharmacokinetics and immunology <i>Chairpersons:</i> <i>Prof. A.I. Ilyin, O.I. Krivorotko</i> <i>Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia</i>	09:00 - 13:00	School SBB-2014. Presentations by young scientists
09:00-9:45	I.M. Larina, V.A. Ivanisenko, E.N. Nikolaev <i>Institute for Biomedical Problems RAS, Moscow, Russia</i> Proteomics extreme impacts as a tool for systems biology KEYNOTE TALK	09:00-09:30	N. Asmanova, G. Koloskov, A.I. Ilyin <i>Scientific Center for Anti-Infectious Drugs, Almaty, Kazakhstan</i> On the application of excretion data as a criteria of choice between multiple solutions of inverse problem in pharmacokinetics KEYNOTE TALK	09:00-9:20	V.V. Lavrekha, N.A. Omelyanchuk, V.V. Mironova <i>Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</i> Modeling of cell dynamics in the root apical meristem with dynamical grammar
		09:30-09:50	A.I. Ilyin, S.I. Kabanikhin, O.I. Krivorotko <i>Institute of Computational Mathematics and Mathematical Geophysics SB RAS</i> The identification and refinement of parameters of mathematical models in immunology	09:20-9:40	S. Maltseva, A.P. Chupakhin, A.A. Cherevko, A.K. Khe, E.U. Derevtsov, A.E. Akulov <i>Institute of Mathematics SB RAS, Novosibirsk, Russia</i> Reconstruction of the mouse brain vasculature according to the data of high-field MRI scanner
09:45-10:10	H. Binder, H. Wirth, A. Arakelyan, K. Lembcke, E.S. Tiys, V. Ivanishenko, N.A. Kolchanov, A. Kononikhin, I. Popov, E.N. Nikolaev, L. Pastushkova, I.M. Larina <i>Interdisciplinary Centre for Bioinformatics, Universität Leipzig, Leipzig, Germany</i> A machine learning analysis of urine proteomics in space-flight simulations	09:50-10:10	A.I. Ilyin, S.I. Kabanikhin, D.A. Voronov <i>Institute of Computational Mathematics and Mathematical Geophysics SB RAS</i> Numerical solutions of inverse problem of pharmacokinetics. Identifiability of compartmental models	09:40-10:00	N. Nikitina, E.E. Ivashko, Y. Gupta, R. Lüdwig, S. Müller <i>Institute of Applied Mathematical Research, Karelian Research Center RAS, Petrozavodsk, Russia</i> Boinc-based desktop GRID infrastructure for virtual drug screening

10:10-10:35	M.A. Karpova, D.A. Karpov, M.V. Ivanov, V.G. Zgoda, M.V. Gorshkov, S.A. Moshkovskii Orekhovich Institute of Biomedical Chemistry RAMS, Moscow, Russia Cancer cell line recognition by shotgun proteomics using cancer exome data	10:10-10:30 M.A. Shishlenin Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia Continuation of the acoustic field in tomography	10:00-10:20 V. Mironova, D. Novikova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Auxin-induced changes of transcriptome in <i>Arabidopsis thaliana</i> L. roots
10:35-11:00	I.A. Mescheryakova, E.V. Demidova, E.A. Demidov, T.N. Goryachkovskaya, V.M. Popik, A.I. Semenov, G.N. Kulipanov, N.A. Kolchanov, S.E. Peltek Institute of Cytology and genetics SB RAS, Novosibirsk, Russia Genomic proteomics profiling	10:30-10:50 A.A. Polshchitsin , V.M. Nekrasov, A.V. Chernyshev, V.P. Maltsev Institute of Chemical Kinetics and Combustion; Novosibirsk State University, Novosibirsk, Russia. Solution of inverse immunoagglutination kinetics problem for patchy particles with a small number of binding sites	10:20-10:40 A. Paramonov , U.P. Djioev, I.V. Kozlova Research Centre for Family Health and Human Reproduction Problems SB RAMS, Irkutsk, Russia Bioinformatics detection of potential recombination sites of tick-borne encephalitis virus
			10:40-11:00 O. Perflyeva ICG SB RAS, Novosibirsk, Russia Mathematical modeling of peptidoglycan precursor biosynthesis in the cytoplasm of <i>Esherichia coli</i> cell
11:00-11:20 Coffee break			
11:20-11:45	L.H. Pastushkova , A.S. Kononihin, E.S. Tiys, O.A. Obraztsova, I.V. Dobrohotov, K.S. Kireev, V.A. Ivanisenko, E.N. Nikolaev, I. M. Larina Russian Federation State Scientific Center – Institute for Biomedical Problems RAS; Moscow, Russia Identifying overrepresented biological processes in cosmonauts on the first day	11:15-11:35 A. Leviceh , A. Palyanov Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia On a modification of the theoretical basis of the Penrose-Hameroff model of consciousness	11:20-11:40 I. Pinskyi , A. Ivashchenko Al-Farabi Kazakh National University, Almaty, Kazakhstan miRNAs binding to mRNAs of rice Myb genes
		11:35-11:55 A. Yu. Pyrkova , A.T. Ivashchenko, O.A. Berillo Al-Farabi Kazakh National University, Almaty, Kazakhstan Modelling of the problem of multiple alignment of the nucleotide sequences and dendrogram construction	11:40-12:00 D. Pirozhkova , M.A. Tsyganov ICG SB RAS, Novosibirsk, Russia Species specificity of ATP-dependent efflux in the liver fluke <i>Opisthorchis felineus</i>

11:45-12:10	P.S. Sherin , E.A. Zelentsova, E.D. Sormacheva, T.G. Duzhak, Yu.P. Tsentalovich International Tomography Center SB RAS, Novosibirsk, Russia UVA-induced modifications of lens Alpha-crystallin	11:55-12:15	A.A. Bedelbayev Institute of Mathematics and Mechanics KazNU, Almaty, Kazakhstan Computer mathematical and biochemical modeling and simulation of the life processes in human organs	12:00-12:20	N.V. Sviridova , K. Sakai Computing Center FEB RAS, Khabarovsk, Russia Application of nonlinear time series analysis for hemodynamic model validation on the base of photoplethysmogram signal
12:10-12:35	T.G. Duzhak , Yu.P. Tsentalovich International Tomography Center SB RAS, Novosibirsk, Russia Lens cataract: effects of crystallins modification			12:20-12:40	N. Safronova , Y.L. Orlov ICG SB RAS, Novosibirsk, Russia Computer analysis of human SNP containing sites by methods of text complexity estimations
				12:40-13:00	A. Sergeev Institute of Mathematical Problems of Biology RAS, Puschino, Russia Graph database for molecular biology – advantages of the graph representation of data
13:00-14:00 Lunch					
14:00-17:50	BGRS-2014. Proteomics, metabolomics and computational pharmacology <i>Chairpersons:</i> <i>Prof. E. Nikolaev, Institute for Biomedical Problems RAS, Moscow, Russia</i> <i>Prof. I. Larina, Institute for Biomedical Problems RAS, Moscow, Russia</i>	14:00-17:55	MM-HPC-2014. Gene networks <i>Chairpersons:</i> <i>Prof. V.P. Golubyatnikov,</i> <i>Dr. N.B. Ayupova, Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia</i>	14:00-17:00	School SBB-2014. Presentations by young scientists Nomination of best presentations
14:00-14:25	S.F. Chekmarev Institute of Thermophysics SB RAS; Novosibirsk State University, Novosibirsk, Russia Driving force for protein folding: the two-component potential	14:00-14:30	N.B. Ayupova, V.P. Golubyatnikov Sobolev Institute of Mathematics SB RAS; Novosibirsk State University, Novosibirsk, Russia On geometry of phase portraits of some low-dimensional gene network models KEYNOTE TALK	14:00-14:20	D.S. Vibe ICG SB RAS, Novosibirsk, Russia Computational and functional analysis of auxin response elements TGTCTC dimers in <i>Arabidopsis thaliana</i> L. genes promoters

14:25-14:50	A.O. Chugunov , P.E. Volynsky, R.G. Efremov Shemyakin-Ovchinnikov Institute of Bio-organic Chemistry RAS, Moscow, Russia High-performance computing provides insight into the innermost organization of procaryotic membranes	14:30-14:50	F.V. Kazantsev , I.R. Akberdin, N.L. Podkolodnyy, V.A. Likhoshvai Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Gene networks modeling: specification language	14:20-14:40	V. Sokolov , U.G. Matushkin ICG SB RAS, Novosibirsk, Russia Analysis of bacteria and archaea genomes available in GenBank database by “Eloe” program
				14:40-15:00	A. Spitsina , V.M. Efimov, V.N. Babenko, Y.L. Orlov ICG SB RAS, Novosibirsk, Russia Computer analysis of human gene expression data using BioGPS database of Affymetrix microarrays
14:50-15:15	A.Y. Nyporko Taras Shevchenko National University of Kyiv, Kyiv, Ukraine Features 8-oxo-DGTP behavior in active site of human DNA polymerase	14:50-15:10	S.V. Lenskiy , T.I. Lenskaya Ural Federal University, Ekaterinburg, Russia Power law for rank distribution of gene density in human genome projects	15:00-15:20	T.S. Troglazova , D.Ja. Baishibaev, A.V. Penenko, S.V. Nikolaev, U. Zubairova Novosibirsk State University, Russia On a parallel algorithm for morpho-gene diffusion-reaction processes simulation on a 2D cell ensemble
15:15-15:40	K.E. Medvedev , D.A. Afonnikov Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Computational investigation of high pressure and temperature influence	15:10-15:30	A.A. Akinshin, T.A. Bukharina, D.P. Furman, V.P. Golubyatnikov Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia Modeling of two cells complex in morphogenesis of <i>D. melanogaster</i> mechanoreceptors	15:20-15:40	A. Chekantsev Novosibirsk State University, Russia The system of 3D visualisation for software package “Haploid evolutionary constructor 3D”
15:40-16:05	E.A. Aksianov , A.V. Alexeevsky Belozersky Institute of Physico-Chemical Biology, MSU, Moscow, Russia Alignment of “unalignable” protein structures	15:30-15:50	V.Yu. Salamatova Moscow Institute of Physics and Technology, Moscow, Russia Modelling of soft tissues deformation. Alternative approaches.	15:40-16:00	V. Chernova , A. Doroshkov, V. Mironova, N. Omelyanchuk ICG SB RAS, Novosibirsk, Russia PIN-transporters in the root meristem of <i>Arabidopsis thaliana</i> L.- image analysis of expression patterns
16:05-16:25 Coffee Break					
16:25-16:50	A.A. Anashkina , N.G. Esipova, E.N. Kuznetsov, V.G. Tumanyan Engelhardt Institute of Molecular Biology RAS, Moscow, Russia Native proteins and decoys: subtle structure differences	16:15-16:35	B. Karacaören Department of Animal Science, Akdeniz University, Antalya, Turkey Dynamic association mapping based on random walk model using simulated QTLMAS data set	16:15-16:30	DISCUSSION

16:50-17:15	<p>A.M. Andrianov, I.A. Kashyn, A.V. Tuzikov United Institute of Informatics Problems NAS Belarus, Minsk, Belarus</p> <p>Computational prediction of novel anti-HIV-1 agents based on potent and broad neutralizing antibody VRC01</p>	16:35-16:55	<p>L.A. Krasnobaeva, L.V. Yakushevich Siberian State Medical University; Tomsk State University, Tomsk, Russia</p> <p>Rotational dynamics of bases in the gene coding Interferon alpha 17 (IFNA17)</p>	16:30-17:00	AWARD FOR THE BEST YOUNG SCIENTISTS REPORTS
17:15-17:50	<p>E.N. Nikolaev Institute for Energy Problems of Chemical Physics RAS, Moscow, Russia TO BE ANNOUNCED</p>	16:55-17:15	<p>E.S. Fomin ICG SB RAS, Novosibirsk, Russia</p> <p>Reconstruction cyclic sequences from their circular distances multiset</p>		
		17:15-17:35	<p>A.A. Vitvitsky ICM&MG SB RAS, Novosibirsk, Russia</p> <p>Computer simulation of self-organization in the bacterial MINCDE system</p>		
		17:35-17:55	<p>N.V. Pertsev Sobolev Institute of Mathematics, Omsk Branch, Omsk, Russia</p> <p>The high-dimensional models in some tasks of biology and medicine: problems of analytical and numerical studies</p>		
		18:00-19:00	Auditorium near Conference hall in the Exhibition Centre SB RAS POSTER SESSION		

BGRS-2014.
EVOLUTIONARY BIOLOGY
POSTER SESSION

E.A. Borzov¹, R. Mehta³, A.V. Baranova^{1,3}, M.Yu. Skoblov^{*,1,2,4}

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WHOLE-GENOME COMPARATIVE ANALYSIS OF CpG ISLANDS BETWEEN HUMAN AND CHIMPANZEE

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PACKAGE OF FUNCTIONS FOR SCRIPT PROGRAMMING LANGUAGE R FOR TESTING THE CONVERGENCE OF POPULATION SAMPLES OF DNA SEQUENCES

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HOMO SAPIENS DENISOVA CRAFTSMANSHIP CAN BE RELATED WITH EVOLUTION OF THE miRNAs REGULATING mRNAs EXPRESSED IN THE BRAIN REGIONS CRUCIAL FOR CONSCIOUSNESS AND SPEECH

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MOLECULAR EVOLUTION OF MAMMALIAN ORTHOLOGOUS PROTEIN GROUPS INVOLVED IN STEM CELL SPECIFICITY

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THE RELATION BETWEEN ENVIRONMENTAL CHANGES AND EVOLUTION OF ARCHAEA PROTEIN DOMAINS

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WHAT EVOLUTION OF HOMINID TATA-BOXES CAN TELL US ABOUT HUMAN LINEAGE?

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WHAT EVOLUTION OF RYE SUBTELOMERIC REPEATS CAN TELL US ABOUT CEREALS SPECIATIONS?

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COMPARATIVE GENETIC ANALYSIS OF THREE FAR EASTERN SPECIES OF THE GENUS TRIBOLODON ACCORDING TO SEQUENCE DATA OF MITOCHONDRIAL DNA CO-1 REGION

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FORWARD-TIME SIMULATION OF EVOLUTIONARY PROCESSES IN ANCIENT POPULATIONS USING THE DIPLOID EVOLUTIONARY CONSTRUCTOR

S.V. Lenskiy^{*}, T.I. Lenskaya

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SEARCH FOR EVOLUTIONAL INVARIANTS BY RANK DISTRIBUTION OF GENE DENSITY IN HOMINIDS

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THE TWO HYPOTHESES OF BAIKAL ENDEMIC SPONGE (LUBOMIRSKIIDAE) EVOLUTION

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ALLELIC COADAPTATION AND FITNESS LANDSCAPE PREDETERMINE THE OPTIMAL EVOLUTIONARY MODE IN PROKARYOTIC COMMUNITIES: A SIMULATION STUDY

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METHODS OF DETECTION AND ESTIMATION OF EVOLUTIONARY CONSERVED ELEMENTS OF RNA SECONDARY STRUCTURE

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VARIATION OF ELONGATION EFFICIENCY INDEX OF ARCHAEA GENES DURING EVOLUTION

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EVOLUTION OF MODERN HUMAN AND RECOMBINATION OF MEMES

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INVASION, ADAPTATION AND EVOLUTION: WHEN ALL OUT OF SYNC

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THE GENOMIC TEXT CHARACTERISTICS AND GC CONTENT ARE RELATED TO THE BACTERIAL GENOME EVOLUTION

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INCREASING THE NUMBER OF PARALOGS FOR ENZYMES INVOLVED IN TRYPTOPHAN BIOSYNTHESIS DURING THE EVOLUTION OF LAND PLANTS

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A DATABASE OF RHODOPHYTE PLASTID PROTEIN FAMILIES AND REGULATION OF *moeB* GENES

BGRS-2014. SYSTEMS COMPUTATIONAL BIOLOGY POSTER SESSION

I.R. Akberdin*, **N.V. Ivanisenko**, **E.A. Oschepkova**, **N.A. Omelyanchuk**, **Yu.G. Matushkin**, **D.A. Afonnikov**, **N.A. Kolchanov**

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REGULATORY MECHANISMS FOR mESC SELF-RENEWAL: KINETIC AND STOCHASTIC MODELING

E.I. Aksenova*, **O.L. Voronina**, **M.S. Kunda**, **A.N. Semenov**, **A.A. Zamyatnin**, **V.G. Lunin**, **A.L. Gintsburg**

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HIDDEN RESERVES OF USED VACCINE SUBSTRAIN

V.A. Likhoshvai^{1,2}, **T.M. Khlebodarova**¹, **S.I. Bazhan**^{3*}, **I.A. Gainova**⁴, **V.A. Chereshnev**⁵, **G.A. Bocharov**⁶

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TAT-REV REGULATION OF HIV-1 REPLICATION: MATHEMATICAL MODEL PREDICTS THE EXISTENCE OF OSCILLATORY DYNAMICS

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KiNET 1.0 – A NEW WEB DATABASE ON KINETICS DATA AND PARAMETERS FOR *E. COLI* METABOLIC PATHWAYS.

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THE KNOWLEDGE BASE ON MOLECULAR GENETICS MECHANISMS CONTROLLING HUMAN LIPID METABOLISM

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DIRECT AND INVERSE PROBLEMS FOR SYSTEMS WITH SMALL PARAMETER IN KINETICS MODELS

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KINETIC SIMULATION OF MITOCHONDRIAL SHUTTLES

S.A. Lashin*, **A.I. Klímenko**, **Z.S. Mustafin**, **A.D. Chekantsev**, **R.K. Zudin**, **Yu.G. Matushkin**
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HAPLOID EVOLUTIONARY CONSTRUCTOR 3D: A TOOL FOR SIMULATION OF SPATIALLY DISTRIBUTED PROKARYOTIC COMMUNITIES

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APOPTIC NUCLEAR VOLUME DECREASE: ANALYSIS OF CONFOCAL IMAGES AND MATHEMATICAL MODEL

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DATABASE OF QUANTITATIVE CHARACTERS OF PROCESSES IN EMBRYONIC STEM CELLS

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THE MAMMALIAN CIRCADIAN CLOCK: COMPUTER ANALYSIS OF GENE NETWORK

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ANNOTATIONS OF SNPs IN PROMOTERS OF HUMAN ONCOGENES VEGFA, EGFR, ERBB2, IGF1R, VEGFR1(2) AND HGFR IN TERMS OF POTENTIAL RESISTANCES TO MONOCLONAL ANTIBODY DRUGS

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EVALUATION OF PATHWAYS' EFFICIENCY BASED ON DATA ON PPI AND DISTRIBUTION OF PROTEINS OVER CELLULAR LOCALIZATIONS

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EXPERIMENTAL DATA FOR TESTING THE ADEQUACY OF EXISTING MATHEMATICAL MODELS

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THE MATHEMATICAL MODEL OF Rob, MarR, MarA REGULATORY CIRCUIT OF ESCHERICHIA COLI GENE NETWORK

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MATHEMATICAL MODELING OF LUNG INFECTION AND ANTIBIOTIC RESISTANCE

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PUTATIVE CANDIDATE GENES TRANSCRIPTIONALLY UPREGULATED BOTH IN ACUTE AND CHRONIC PHASE OF RESPONSE DURING INFESTATION OF MICE AND SYRIAN GOLDEN HAMSTERS WITH LIVER FLUKES OF OPISTHORCHIIDAE FAMILY

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INTEGRATED GENOME-ORIENTED INFORMATION SYSTEM FOR MONITORING AND CONTROL OF BIOLOGICAL SYSTEMS

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COMPUTER ANALYSIS OF HUMAN GENE EXPRESSION DATA USING BioGPS DATABASE OF MICROARRAY AFFYMETRIX U133

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LOGICAL MODELLING OF NANOG-DEPENDENT TRANSCRIPTIONAL GENE NETWORK OF EMBRYONIC CARCINOMA STEM CELLS

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LITHIUM HALIDES ENHANCE THE ANTICANCER ACTIVITY OF CISPLATIN

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GLOBAL MAPPING OF PROTEIN UBIQUITYLATION WITHIN TNF-ALPHA SIGNALING PATHWAY USING GENEXPLAIN PLATFORM

BGRS-2014.
PLANT SYSTEMS BIOLOGY
POSTER SESSION

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GENETIC DISSECTION OF THE INFLORESCENCE BRANCHING TRAIT IN DIPLOID, TETRAPLOID AND HEXAPLOID WHEATS

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ANALYSIS OF A TOMATO INTROGRESSION LINE, IL8-3, WITH INCREASED BRIX CONTENT USING THE WHOLE-GENOME SEQUENCE

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SeedCounter - MOBILE AND DESKTOP APPLICATION FOR HIGH-THROUGHPUT PHENOTYPING SEEDS IN WHEAT

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MODELING OF CELL DYNAMICS IN THE ROOT APICAL MERISTEM WITH DYNAMICAL GRAMMAR

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COMPUTATION MODELING OF VASCULAR PATTERNING IN PLANT ROOTS

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A MODEL OF TRICHOME SPACING PATTERN FORMATION ON GROWING WHEAT LEAF

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A SIMPLE MECHANICAL CELL-BASED MODEL FOR SYMPASTIC GROWTH OF LINEAR LEAF BLADE

BGRS-2014.
GENOMICS AND EPIGENETICS
POSTER SESSION

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BINDING SITES OF miRNA WITH MYB GENES' mRNA IN *B. TAURUS* AND *B. MUTUS*

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APPLICATION OF TERMINAL HELITRON FRAGMENTS AS HIGH POLYMORPHIC MARKERS OF GENOME SCANNING IN UNGULATA

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ANALYSIS AND CLASSIFICATION OF NONSTANDARD RNA MOTIFS

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FLUORESCENCE *IN SITU* HYBRIDIZATION WITH MICRODISSECTED DNA PROBES ON CHROMOSOMES OF SPECIES WITH LARGE GENOME SIZE WITHOUT SUPPRESSION OF REPETITIVE DNA SEQUENCES

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ASSEMBLING GENOMES AND METAGENOMES USING CLUSTER ARCHITECTURE

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PRIONIZATION OF THE Sfp1 PROTEIN IN YEAST DOES NOT MIMIC ITS INACTIVATION AT WHOLE TRANSCRIPTOME LEVEL

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APPLICATION OF MULTILOCI GENOME SCANNING FOR IDENTIFICATION OF THE KARACHAY HORSE GENETIC STRUCTURE

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SINE-MODELING OF GENOME LOOP STEP

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NOVEL microRNAs PREDICTION IN NON-MODEL ORGANISMS

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CONTROLLED VOCABULARIES AND INFORMATION TABLES FOR THE KNOWLEDGE BASE ON EPIGENETIC CONTROL OF HUMAN EMBRYONIC STEM CELLS

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FUNCTIONAL CHARACTERISTICS OF HUMAN GENES CONTAINING LOW LEVEL OF PROMOTER POLYMORPHISM REVEALED FROM THE 1000 GENOMES PROJECT DATASET

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FEATURES OF INTERACTIONS BETWEEN miR-1273 FAMILY AND mRNA OF TARGET GENES

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FUNCTIONAL ANALYSIS OF THE PROMOTER REGION OF THE *Xist* GENE IN MOUSE (*MUS MUSCULUS*)

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COMPUTER ANALYSIS OF CHROMOSOME CONTACTS REVEALED BY SEQUENCING

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COMPUTER DATA ANALYSIS OF GENOME SEQUENCING BY TECHNOLOGY ChIP-seq AND Hi-C

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THE PIPELINE FOR COMPOSITE REGULATORY ELEMENTS PREDICTION

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TRANSCRIPTOMICS ANALYSIS OF *DROSOPHILA MELANOGASTER* AGING

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INTERACTION BETWEEN miRNA AND mRNA OF MYB TRANSCRIPTIONAL FACTORS FAMILY GENES OF MAIZE

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DEPPDB – A PORTAL FOR ELECTROSTATIC AND OTHER PHYSICAL PROPERTIES OF GENOME DNA

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DNA PHENOTYPE AND BIOPHYSICAL BIOINFORMATICS OF TRANSCRIPTION REGULATION IN PROKARYOTES: THE ROLE OF ELECTROSTATICS AS A NATURAL SELECTION FACTOR

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TRANSCRIPTION FACTORS AND ELECTROSTATIC AND OTHER PHYSICAL PROPERTIES OF THEIR BINDING SITES

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IDENTIFICATION OF *DROSOPHILA MELANOGASTER* GENES AS BIOSENSORS OF CHEMICAL POLLUTANTS (FORMALDEHYDE, DIOXIN, TOLUENE) AND GAMMA-IRRADIATION IN LOW DOSES

N.S. Ponomareva*, D.E. Romanov, E.A. Pshenichny, T.P. Shkurat

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SCAN ELEMENTS IN THE NON-CODING DNA

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REFERENCE ASSISTED CHROMOSOME ASSEMBLY OF 30 *SACCHAROMYCES CEREVISIAE* STRAINS FROM *SACCHAROMYCES* GENOME DATABASE

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INTRON LENGTHS AND PHASES: REGULARITIES AND DATABASE

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RESTRICTION SITES AVOIDANCE IS TRACE OF LOST RESTRICTION MODIFICATION SYSTEMS

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BIOLOGICAL GRAPH DATA BASE AND ITS APPLICATIONS

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COMPUTER ANALYSIS OF HUMAN SNP CONTAINING SITES BY METHODS OF TEXT COMPLEXITY ESTIMATIONS

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GRAPH DATABASE FOR MOLECULAR BIOLOGY: ADVANTAGES OF THE GRAPH REPRESENTATION OF DATA

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THE STRUCTURAL ORGANIZATION AND EVOLUTION OF 5S rDNA OF WHEAT CHROMOSOME 5BS BY DATA OF PARTIAL SEQUENCING

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TOOLKIT FOR CHIP-seq BASED COMPARATIVE ANALYSIS OF THE PWM METHODS FOR PREDICTION OF TRANSCRIPTION FACTOR BINDING SITES

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OF TRANSCRIPTION FACTORS ESSENTIAL FOR EMBRYONIC STEM CELLS MAINTENANCE

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OF MYCOBACTERIUM TUBERCULOSIS

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of Digital Techniques SB RAS, Novosibirsk, Russia
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AND ITS ACCOUNT IN THE PREDICTION TOOLS

BGRS-2014.

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POSTER SESSION**

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CALCULATION

A.O. Bragin, V.S. Sokolov, P.S. Demenkov, Yu.G. Matushkin, V.A. Ivanisenko

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T.V. Ivanisenko*, P.S. Demenkov, N.V. Ivanisenko, V.A. Ivanisenko

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of General Genetics of the RAS, St.Petersburg Russia
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E.S. Tiys, P.S. Demenkov, O.V. Saik, O.V. Popik, V.A. Ivanisenko*

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A STRUCTURAL MECHANICS MODEL FOR ATOMIC FORCE MICROSCOPY-BASED INDENTATION TEST OF EPIDERMAL PLANT CELLS

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A UNIVERSAL MODEL OF THE EPIDEMICS CAUSED BY SPECIAL PATHOGENS: A TOOL FOR EPIDEMIOLOGIST

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LOGICAL-AND-PROBABILITY SIMULATION MODEL OF DATE ANALYSES

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LOGICAL-AND-PROBABILITY SIMULATION MODEL OF INFLUENCE OF THE CLIMATIC FACTORS IN TICK-BORN ENCEPHALITIS DISEASE'S INDICES

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DATABASE OF FRAME MODELS OF GENETIC REGULATION OF THE METABOLIC PROCESSES ASSOCIATED WITH DISEASES

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MICROSATELLITE VARIATION TO COMPARE MIGRATION SCENARIOS AND DEMOGRAPHIC PROCESSES IN POPULATIONS CHUM SALMON NORTHERN RANGE

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IMPLICATIONS OF HOSTILE ENVIRONMENT AND SOCIAL INSTABILITY IN ADOLESCENT MICE

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THE SENESCENCE-ACCELERATED OXYS RATS AS A MODEL OF ALZHEIMER DISEASE

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CAN OPIOID AND SUBSTANCE P SYSTEM INTERACTION ANTOGONIZE MORPHINE-INDUCED RESPIRATORY DEPRESSION?

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CONSERVATIVE mTOR SIGNALING PATHWAY AS A TARGET FOR PROPHYLAXIS OF ACCELERATED BRAIN AGING

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PRACTICAL APPROACH FOR DNA EXTRACTION OF *LINGUATULA SERRATA* NYMPHS: AN ANALYTICAL METHOD

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ASSOCIATION OF THE GENETIC MARKERS FOR MYOCARDIAL INFARCTION WITH SUDDEN CARDIAC DEATH IN A RUSSIAN POPULATION

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MODELING GENETIC INFLUENCES ON TWO DISEASES THAT ARE UNUSUALLY RARE IN CO-OCCURRENCE - BRONCHIAL ASTHMA AND PULMONARY TUBERCULOSIS

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CONGENIC STRAINS FOR STUDYING ACCELERATED SENEESCENCE IN OXYS RATS. RETI-
NAL TRANSCRIPTOME AND CANDIDATE GENE ANALYSIS BY RNAseq

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THE SNP-MED SYSTEM FOR PERSONAL MEDICINE: RISK ASSESSMENT
OF DISEASES ASSOCIATED WITH SINGLE-NUCLEOTIDE POLYMORPHISMS

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MUTATION ANALYSIS OF MYCOBACTERIUM TUBERCULOSIS GENOME
AND ASSOCIATION WITH DRUG RESISTANCE

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INTERMOLECULAR INTERACTIONS IN THE IONOTROPIC GLUTAMATE RECEPTOR
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PLASTICITY

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POLYMORPHISM RS1625895 GENE *TP53* AND EFFECTIVENESS OF TREATMENT OF DLBCL

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