**PRELIMINARY SCIENTIFIC PROGRAM**  
The Multi-conference «Bioinformatics and System Biology»  
(June 13 vs.)

### June 23 (Monday)

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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<tbody>
<tr>
<td>09:00 – 13:00</td>
<td><strong>Registration (House of Scientists, Small Conference Hall Lounge)</strong></td>
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<tr>
<td>13:00 – 13:30</td>
<td>Opening</td>
<td>Great hall, House of Scientists SB RAN</td>
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<tr>
<td>13:30 – 15:00</td>
<td>Plenary lectures</td>
<td>Great hall, House of Scientists SB RAN</td>
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<tr>
<td>15:00 – 15:30</td>
<td>Coffee break</td>
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<tr>
<td>15:30 – 17:50</td>
<td>Plenary lectures</td>
<td>Great hall, House of Scientists SB RAN</td>
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<tr>
<td>18:00 – 20:00</td>
<td>Poster session</td>
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<tr>
<td>20:00 – 23:00</td>
<td>Welcome party</td>
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### June 24 (Tuesday)

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<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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<tbody>
<tr>
<td>08:30 – 09:00</td>
<td>Symposums opening</td>
<td>Exhibition Centre</td>
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<tr>
<td>09:00 – 13:00</td>
<td><strong>BGRS-2014. Evolutionary biology</strong></td>
<td>ISHG-2014. Medical genetics</td>
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<tr>
<td></td>
<td>Prof. D. Liberles</td>
<td>Prof. V.P. Puzyrev, Dr. M.I. Voevoda</td>
</tr>
<tr>
<td>14:00 – 19:00</td>
<td><strong>MM-HPC-2014. Text-mining and intelligent analysis of knowledge in databases</strong></td>
<td>ISHG-2014. Medical genetics</td>
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<td></td>
<td>Prof. Andrey Rzhelsky, Prof. Goncharov S.S, Zagorukho N.G.</td>
<td>Prof. V.P. Puzyrev, Dr. M.I. Voevoda</td>
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<td></td>
<td><strong>School. Practical training</strong></td>
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### June 25 (Wednesday)

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<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>09:00 – 13:00</td>
<td><strong>BGRS-2014. Systems computational biology</strong></td>
<td>ISHG-2014. Translational medicine</td>
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<tr>
<td></td>
<td>Dr. A. Ratushny, Prof. V. P. Golubiatnikov, Prof. L. Kaderali</td>
<td>Prof. M.P. Moshkin, Prof. S. A. Brown</td>
</tr>
<tr>
<td>14:00 – 19:00</td>
<td><strong>BGRS-2014. Plant systems biology</strong></td>
<td>ISHG-2014. Translational medicine</td>
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<td></td>
<td>Prof. E.A. Salina</td>
<td>Prof. M.P. Moshkin, Prof. S. A. Brown</td>
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<td><strong>School. Practical training (ICG)</strong></td>
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<td>Time</td>
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<tr>
<td><strong>June 26 (Thursday)</strong></td>
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</table>
| 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 |
|    | **School.**
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 |
|    | **Open seminar of German/Russian Virtual Network of Bioinformatics "Computational Systems Biology"**
*Prof. R. Hofestaedt* |

**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 |
|    | **School.**
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 |
|    | **School.**
Presentations by young scientists. Nomination of best presentation |

| 19:30 – 23:00 | **Closing of the Conference. Banquet** |

**June 28 (Saturday)**

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>During the day</td>
<td><em>Cultural program: Geological Museum, Sun Museum, Novosibirsk city sight-seeing tour, Novosibirsk Planetarium.</em></td>
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### June 23 (Monday)

<table>
<thead>
<tr>
<th>Time</th>
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<tbody>
<tr>
<td>09:00 – 13:00</td>
<td><strong>Registration</strong> <em>(House of Scientists, Small Conference Hall Lounge)</em></td>
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<tr>
<td>13:00 – 13:30</td>
<td><strong>Opening</strong> <em>Great hall, House of Scientists SB RAN</em></td>
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<tr>
<td>13:30 – 14:15</td>
<td>Y. Ruan</td>
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<tr>
<td></td>
<td>The Jackson Laboratory, USA</td>
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<tr>
<td></td>
<td>FROM 1D INFORMATION TO 3D GENOME STRUCTURE AND FUNCTION</td>
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<tr>
<td>14:15 – 15:00</td>
<td>V.A. Stepanov</td>
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<tr>
<td></td>
<td>FSBI Research Institute of Medical Genetics, Tomsk, Russia</td>
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<tr>
<td></td>
<td>ADAPTIVE EVOLUTION OF GENETIC DIVERSITY AND HUMAN DISEASES</td>
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<tr>
<td>15:00 – 15:30</td>
<td><strong>Coffee break</strong></td>
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<tr>
<td>15:30 – 16:15</td>
<td>A.V. Morozov</td>
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<td>BioMaPS Institute for Quantitative Biology</td>
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<td>EVIDENCE FOR EXTENSIVE NUCLEOSOME CROWDING IN YEAST CHROMATIN</td>
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<tr>
<td>16:15 – 17:00</td>
<td>A. Ratushny</td>
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<td></td>
<td>Institute for Systems Biology, Seattle, USA</td>
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<td>MULTISCALE MODELING AS A FRAMEWORK FOR EXPLORING MOLECULAR MECHANISMS OF BIOLOGICAL SYSTEMS</td>
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<tr>
<td>18:00 – 20:00</td>
<td><strong>Poster session</strong></td>
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<td>20:00 – 23:00</td>
<td><strong>Welcome party</strong></td>
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### June 24 (Tuesday)

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<tr>
<th>Time</th>
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<tbody>
<tr>
<td>09:00 – 13:00</td>
<td><strong>BGRS-2014. Evolutionary biology</strong></td>
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<td>Chairperson:</td>
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<td>Prof. D. Liberles, University of Wyoming, USA</td>
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<tr>
<td>09:00 – 13:00</td>
<td><strong>ISHG-2014. Medical genetics</strong></td>
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<td>Co-chairpersons:</td>
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<tr>
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<td>Dr. V. Puzyrev, FSBI Research Institute of Medical Genetics, Tomsk, Russia</td>
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<td>Dr. M. Voevoda, FSBI Institute of Internal and Preventive Medicine SB RAMS, Novosibirsk, Russia</td>
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<tr>
<td>09:00 – 13:00</td>
<td><strong>School. Computational analysis of next-gen sequencing data</strong></td>
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<td>Time</td>
<td>Speaker/Institution</td>
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| 09:00-09:45| D. Liberles                                                                        | LINEAGE-SPECIFIC PROCESSES OF GENOME DIVERSIFICATION  
**KEYNOTE TALK**                                           |
| 09:45-10:10| K.V. Gunbin, D.A. Afonnikov                                                        | SELECTIVE SHIFTS IN RECENT EVOLUTION OF METAZOA                                           |
| 10:10-10:35| A. I. Klimenko, Yu.G. Matushkin, S.A. Lashin                                      | MODELING EVOLUTION OF SPATIALLY DISTRIBUTED BACTERIAL COMMUNITIES SIMULATION WITH HAPLOID EVOLUTIONARY CONSTRUCTOR |
| 09:00-09:40| A. Polyakov                                                                        | CASES OF AUTOSOMAL RECESSIVE PATHOLOGY IN A GROUP OF MUSCULAR DYSTROPHY X-LINKED TYPE OF INHERITANCE |
| 09:45-10:00| I. Lebedev, A. Kashevarova, N. Skryabin                                           | GENOME ARCHITECTURE AND CHROMOSOMAL DISEASES                                             |
| 10:00-10:20| N. Yudin¹,², T. Mishakova, V. Maksimov, V. Gafarov, S. Malyutina, M. Voevoda         | MODELING EVOLUTION OF SPATIALLY DISTRIBUTED BACTERIAL COMMUNITIES SIMULATION WITH HAPLOID EVOLUTIONARY CONSTRUCTOR |
| 10:35-11:00| V.A. Lyubetsky, A.V. Seliverstov, K.Yu. Gorbunov                                  | 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 | REARRANGEMENT OF CHROMOSOMES: PROBLEMS, ALGORITHMS, DATABASES, AND GENE EXPRESSION REGULATIONS |

**Recommended to attend:**

D. Liberles  
Department of Molecular Biology, University of Wyoming, Laramie, WY, USA  
LINEAGE-SPECIFIC PROCESSES OF GENOME DIVERSIFICATION  
**KEYNOTE TALK**
<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Title</th>
<th>Speakers</th>
<th>Location</th>
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<tbody>
<tr>
<td>11:00-11:20</td>
<td>Coffee break</td>
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<tr>
<td>11:45-12:10</td>
<td>I.D. Sormacheva, G.A. Smyshlyaev, A.G. Blinov</td>
<td>Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
<td>I. Goncharova, O. Makeeva, N. Tarasenko, A. Markov, S. Buikin1, V. Puzyrev FSBI Research Institute of Medical Genetics, Tomsk, Russia</td>
<td>11:40-12:00</td>
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<td>12:10-12:35</td>
<td>B. Zhong</td>
<td>Institute of Fundamental Sciences, Massey University, New Zealand</td>
<td>L. Bryzgalov, I. Brusentsov, T. Merkulova Institute of Cytology and Genetics SB RAS, Novosibirsk, Russian Federation</td>
<td>12:00-12:20</td>
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<td>12:20-12:40</td>
<td>V.V. Ilinsky1, O.L. Kardymon</td>
<td>Vavilov Institute of General Genetics of</td>
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<td>12:20-12:40</td>
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<td>12:35-14:00</td>
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| 12:40-13:00 | S. Sharapov\textsuperscript{1,2}, Y. Tsepilov, J. Ried, K. Strauch, C. Gieger, Y. Aulchenko  
1\textsuperscript{1}Institute of Cytology and Genetics SD RAS, Novosibirsk, Russia  
2\textsuperscript{2}Novosibirsk State University, Novosibirsk, Russia  
GENOME-WIDE ENVIRONMENTAL SENSITIVITY ANALYSIS OF HUMAN METABOLOMICS DATA |
| 12:35-14:00 | MM-HPC-2014. Text-mining and intelligent analysis of knowledge in databases  
\textit{Chairperson:} |
| 14:00-14:35 | A. Rzhetsky  
The University of Chicago, USA  
\textbf{MACHINE SCIENCE KEYNOTE TALK} |
| 14:00-14:30 | V. Maksimov  
Federal State Budgetary Institution of Internal and Preventive Medicine Siberian Branch under the Russian Academy of Medical Sciences, Novosibirsk, Russia  
PERSOANLIZED GENOMIC MEDICINE: TODAY AND PROSPECTS |
| 14:35-14:55 | Ya.V. Bazaikin, A. P. Chupakhin, A.A. Cherevko, A.K. Khe  
\textsuperscript{1,2}  
\textsuperscript{1}Lavrentyev Institute of Hydrodynamics, Novosibirsk, Russia  
\textsuperscript{2}Novosibirsk State University, Novosibirsk, Russia  
APPLICATION OF THE METHODS OF PERSISTENT HOMOLOGY TO |
| 14:30-14:50 | 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 |
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<tr>
<th>Time</th>
<th>Session</th>
<th>Presenter(s)</th>
<th>Institution(s)</th>
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<tbody>
<tr>
<td>14:55-15:15</td>
<td><strong>CLINICAL DATA ANALYSIS WITH ACUTE CORONARY SYNDROME</strong></td>
<td><strong>V.A. Ivanisenko, O.V. Saik, E.S. Tiys, T.V. Ivanisenko, P.S. Demenkov</strong></td>
<td>Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia; PBSsoft LLC, Novosibirsk, Russia</td>
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<td><strong>ANDSYSTEM: ASSOCIATIVE NETWORK DISCOVERY SYSTEM FOR AUTOMATED LITERATURE MINING IN THE AREA OF BIOLOGY</strong></td>
<td><strong>E. Trifonova¹</strong>, N. Ershov, V. Serebrova, V. Stepanov</td>
<td>Institute for medical genetics SB RAMS, Tomsk, Russia</td>
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<tr>
<td>15:15-15:35</td>
<td><strong>INTEGRATIVE TRANSCRIPTOME-BASED APPROACH FOR ASSOCIATION STUDIES: IDENTIFICATION OF NEW GENETIC MARKERS FOR PREECLAMPSIA</strong></td>
<td><strong>V.B. Berikov</strong></td>
<td>Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia</td>
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<td><strong>RELATIONSHIPS BETWEEN HUMAN GENE SET AND SET OF GENE DISORDERS</strong></td>
<td><strong>S. Lenskiy</strong></td>
<td>Ural Federal University, Ekaterinburg, Russia</td>
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<tr>
<td>15:35-16:00</td>
<td><strong>GENOME-PHENOME RELATIONSHIPS OF POLAR IMMUNOLOGICAL DISEASES</strong></td>
<td><strong>K.V. Gilev¹,², M.A. Yurkin, A.V. Chernyshev, V.P. Mal'tsev</strong></td>
<td>Voevodsky Institute of Chemical Kinetics and Combustion, Novosibirsk, Russia; Novosibirsk State University, Novosibirsk, Russia</td>
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<td><strong>SOLUTION OF THE INVERSE LIGHT-SCATTERING PROBLEM FOR CHARACTERIZATION OF RED BLOOD CELLS</strong></td>
<td><strong>E. Bragina</strong>, M. Freidin, E. Tiys, L. Koneva, V. Ivanisenko, V. Puzyrev</td>
<td>Institute of Medical Genetics, Siberian Branch of Russian Academy of Medical Sciences, Tomsk, Russia</td>
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<tr>
<td>16:00-16:20</td>
<td><strong>Coffee break</strong></td>
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<td>16:20-16:45</td>
<td><strong>COMPUTATION OF DRUG INTERACTIONS AND SIDE EFFECTS</strong></td>
<td><strong>R.M. Hofestaedt, T. Hoppe, A. Shoshi</strong></td>
<td>Bielefeld University, Bielefeld, Germany</td>
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<td><strong>GENE POOL OF THE NATIVE POPULATIONS OF DAGESTAN: TERRITORIAL SUBDIVISION AND CORRELATION WITH LINGUISTIC CLASSIFICATION FROM THE DATA OF Y-CHROMOSOME MARKERS</strong></td>
<td><strong>V. Kharkov</strong>, O. Radzhabov, V. Stepanov</td>
<td>FSBI Research Institute of Medical Genetics, Tomsk, Russia</td>
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<tr>
<td>16:45-18:30</td>
<td><strong>D.V. Antonets</strong>, 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</td>
<td><strong>O. Posukh</strong>&lt;sup&gt;1,2&lt;/sup&gt;, A. Churbanov, T. Karalet, A. Bondar, I. Morozov, V. Mikhal'skaya, M. Zytsar&lt;br&gt;1Institute of Cytology and Genetics, Novosibirsk, Russia; 2Novosibirsk State University, Novosibirsk, Russia; WHOLE EXOME SEQUENCING IN ALTAIAN FAMILIES (THE ALTAI REPUBLIC, SOUTHERN SIBERIA) WITH CONGENITAL HEARING LOSS</td>
<td><strong>Practical training, ICG</strong>&lt;br&gt;E.S. Tiys&lt;br&gt;Institute of Cytology &amp; Genetics SB RAS, Novosibirsk, Russia&lt;br KNOWLEDGE BASE ON HUMAN PROTEOME</td>
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<tr>
<td>17:05-18:00</td>
<td><strong>I.I. Titov</strong>&lt;sup&gt;1,2&lt;/sup&gt;, A.A. Blinov, K.A. Rudnichenko, P.V. Krutov, A.L. Kazantsev, A.I. Kulikov&lt;br&gt;1Institute of Cytology &amp; Genetics SB RAS, Novosibirsk, Russia; 2Novosibirsk State University, Novosibirsk, Russia; NETINFERENCE: THE COMPUTER TOOLS FOR ANALYSIS AND VISUALIZATION OF NETWORKS STRUCTURE, DYNAMICS AND EVOLUTION</td>
<td>M. Ponomarenko, O. Arkova, O. Saik, T. Arshinova, P. Ponomarenko, D. Rasskazov, M. Genaev, E.G Komyshchev, L. Savinkova, N.A. Kolchanov&lt;br&gt;Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia&lt;br ANNOTATIONS IN SILICO OF 388 SNPS OF THE CORE-PROMOTERS OF 68 HUMAN FEEDING BEHAVIOR GENES IN TERMS OF THEIR POTENTIAL ASSOCIATIONS WITH NERVOUS DISORDERS</td>
<td>17:00-18:30 Practical training, ICG</td>
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<td>18:00-19:00</td>
<td>Foyer of Small Hall (House of Scientists SB RAS) Poster session</td>
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<td>Time</td>
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<td><strong>09:00 – 13:00</strong></td>
<td><strong>BGRS-2014. Systems computational biology</strong>&lt;br&gt;Chairpersons: Prof. L. Kaderali, University of Technology Dresden, Germany&lt;br&gt;Dr. A. Ratushny, Institute for Systems Biology, Seattle, USA&lt;br&gt;Prof. V.P. Golubiatnikov, Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia</td>
<td><strong>09:00 – 13:00</strong></td>
<td><strong>ISHG-2014. MICROSYMPOSIUM “TRANSLATIONAL MEDICINE”</strong>&lt;br&gt;Chairpersons: Prof. M. Moshkin, Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia&lt;br&gt;Prof. Y. Iwakura, Center for Animal Disease Models, Research Institute for Biomedical Sciences, Tokyo University of Science, Tokyo, Japan</td>
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<td><strong>09:00-09:45</strong></td>
<td><strong>L. Kaderali</strong>&lt;br&gt;University of Technology Dresden, Germany&lt;br&gt;SYSTEMS BIOLOGY OF HOST-PATHOGEN INTERACTIONS&lt;br&gt;KEYNOTE TALK</td>
<td><strong>09:00-09:10</strong></td>
<td><strong>M. P. Moshkin,</strong> Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Russia&lt;br&gt;Opening remark</td>
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<td><strong>09:45-10:10</strong></td>
<td><strong>M. Djordjevic,</strong> K. Severinov, and M. Djordjevic&lt;br&gt;Institute of Physics, University of Belgrade, Belgrade, Serbia;&lt;br&gt;MODELING BACTERIAL IMMUNE SYSTEMS: CRISPR/CAS REGULATION</td>
<td><strong>10:00-10:20</strong></td>
<td><strong>M. Y. Pakharukova,</strong> N.I. Ershov, D.S. Pirozhkova, V. A. Vavilin, K.S. Zadesenets, T.G. Duzhak, V.A. Mordvinov&lt;br&gt;Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia&lt;br&gt;MOLECULAR MECHANISMS OF METABOLISM, EXCRETION AND DRUG TOLERANCE IN HUMAN LIVER FLUKE OPISTHORCHIS FELINEUS</td>
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<td>Time</td>
<td>Speaker/Institution</td>
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<td>10:35-11:00</td>
<td><strong>MICROTUBULES</strong>&lt;br&gt;M.A. Duk, A.M. Samsonov, M.G. Samsonova&lt;br&gt;A.F. Ioffe Physico-technical Institute of the RAS, St. Petersburg, 194021, Russia</td>
<td>10:40-11:00</td>
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<td><strong>MUCIN2 COMPROMISES ANIMAL SEXUAL BEHAVIOR</strong>&lt;br&gt;P.N. Menshanov, A.E. Akulov, N.N. Dygalo&lt;br&gt;Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
<td>10:40-11:00</td>
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<tr>
<td>11:00-11:20</td>
<td><strong>Coffee break</strong></td>
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<td>11:20-12:05</td>
<td><strong>MECHANISM OF MIRNA ACTION DEFINES THE DYNAMICAL BEHAVIOR OF MIRNA-MEDIATED FEED-FORWARD LOOPS</strong>&lt;br&gt;M. Binder&lt;br&gt;German Cancer Research Center, Division Virus-Associated Carcinogenesis, Heidelberg, Germany</td>
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<td><strong>MODELLING OF THE HEPATITIS C VIRUS LIFE CYCLE</strong>&lt;br&gt;S.P. Medvedev&lt;br&gt;Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
<td>11:20-12:05</td>
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<td><strong>THE USE OF NEW GENOME ENGINEERING TECHNOLOGIES FOR CREATION OF ISOGENIC AMYOTROPHIC LATERAL SCLEROSIS CELL MODEL</strong>&lt;br&gt;A. A. Nemudryi&lt;br&gt;Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
<td>11:20-12:05</td>
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<td>12:05-12:30</td>
<td><strong>N. Ivanisenko, E. Mishchenko, I. Akberdin, P. Demenkov, K. Kozlov, D. Todorov, V.V. Gursky, M.G. Samsonova, A.M. Samsonov, D. Clausznitzer, L. Kaderali, N.A. Kolchanov and V.A. Ivanisenko&lt;br&gt;Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia;</strong>&lt;br&gt;<strong>MATHEMATICAL MODEL FOR SUBGENOMIC HEPATITIS C VIRUS REPLICATION: IMPACT OF DRUG RESISTANCE</strong>&lt;br&gt;N. Ivanisenko&lt;br&gt;Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia; <strong>RESCUE OF BRATTLEBORO RAT STRAIN MUTANT PHENOTYPE USING TALEN AND CRISPR/Cas9 SYSTEMS</strong>&lt;br&gt;A. A. Nemudryi&lt;br&gt;Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
<td>12:10-13:40</td>
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<td>12:30-12:45</td>
<td><strong>N. Egorov&lt;br&gt;InterLabService&lt;br&gt;ADVANCED ACHIEVEMENTS OF ILLUMINA NEXT-GENERATION SEQUENCING</strong>&lt;br&gt;N. A. Stefanova, N.A. Muraleva, A.A. Strunov, E.V. Kiseleva, N.G. Kolosova&lt;br&gt;Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia; Center of neurobiology and neurogenetics, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
<td>12:00-12:20</td>
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<td><strong>THE SENESCENCE-ACCELERATED</strong>&lt;br&gt;N. A. Stefanova, N.A. Muraleva, A.A. Strunov, E.V. Kiseleva, N.G. Kolosova&lt;br&gt;Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia; Center of neurobiology and neurogenetics, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
<td>12:00-12:20</td>
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Recommended to attend:<br>M. Binder<br>German Cancer Research Center, Division Virus-Associated Carcinogenesis, Heidelberg, Germany

**MODELLING OF THE HEPATITIS C VIRUS LIFE CYCLE**

**KEYNOTE TALK**

**THE USE OF NEW GENOME ENGINEERING TECHNOLOGIES FOR CREATION OF ISOGENIC AMYOTROPHIC LATERAL SCLEROSIS CELL MODEL**

**RESCUE OF BRATTLEBORO RAT STRAIN MUTANT PHENOTYPE USING TALEN AND CRISPR/Cas9 SYSTEMS**

**THE SENESCENCE-ACCELERATED**
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<td>12:20-12:40</td>
<td><strong>M.L. Perepechaeva</strong>, N.G. Kolosova, A.Yu. Grishanova Institute of Molecular Biology and Biophysics of SB RAMS, Novosibirsk, Russia <strong>AhR-DEPENDENT GENES CYP1B1 AND CYP2J3 ARE INVOLVE IN CARDIOVASCULAR PATHOLOGY OF SENESCENCE-ACCELERATED OXYS RATS.</strong></td>
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<td>12:40-13:00</td>
<td><strong>A.B. Salmina</strong>, N.A. Malinovskaya, O.L. Lopatina, Y.K. Khomleva Krasnoyarsk State Medical University named after Professor V.F. Voino-Yasenetsky, Krasnoyarsk, Russia <strong>MOLECULAR MARKERS AND TARGETS FOR DIAGNOSTICS AND TREATMENT OF NEURODEGENERATION AND NEURODEVELOPMENTAL DISORDERS</strong></td>
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<td>13.00-14.00</td>
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<td>14:00-17:15</td>
<td><strong>BGRS-2014. Systems computational biology</strong></td>
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<td><strong>Chairpersons:</strong> Prof. L. Kaderali, University of Technology Dresden, Germany</td>
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<td>Dr. A. Ratushny, Institute for Systems Biology, Seattle, USA</td>
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<td>Prof. V.P. Golubyatnikov, Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia</td>
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<td>14:00-17:15</td>
<td><strong>BGRS-2014. Plant systems biology</strong></td>
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<td><strong>Chairperson:</strong> Prof. E. Salina, Institute of Cytology and Genetics SB RAS</td>
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<td>14:00-18:00</td>
<td><strong>School. Practical training</strong></td>
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<td>(ICG SB RAS: Av. Lavrentyeva, 10)</td>
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<td>17:00 – 18:30</td>
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<td><strong>F.V. Kazantsev</strong></td>
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<td>Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
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<td><strong>ISHG-2014. MICROSYMPOSIUM “TRANSLATIONAL MEDICINE”</strong></td>
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<td><strong>Co-chairpersons:</strong> Prof. M. Moshkin, Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia</td>
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<td>Prof. S. A. Brown, Institute of Pharmacology and Toxicology, University of Zurich, Zurich,</td>
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<td>14:00-14:25</td>
<td>K.N. Kozlov, V.V. Gursky, I.V. Kulakovskiy, V.V. Muzhichenko, and M.G. Samsonova</td>
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<td>14:00-14:35</td>
<td>M.V. Kapralov, S.M. Whitney</td>
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<td>14:00-14:40</td>
<td>S.A. Brown</td>
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<td>14:25-14:50</td>
<td>E.V. Kashina, D.Y. Oshchepkov, E.A. Oshchepkova, A.G. Shilov, E.V. Antontseva, D.P. Furman, V.A. Mordvinov</td>
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<td>14:35-14:55</td>
<td>P.M. Ponomarenko, Ponomarenko M.P.</td>
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<td>14:40-15:00</td>
<td>A. Baranova, L.Wang, T. Cui, B.Veitsman, S.Bruskin</td>
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<td>14:50-15:15</td>
<td>I.R. Akberdin, T.V. Ermak, F.V. Kazantsev, T. M. Khlebodarova and V.A. Likhoshvai</td>
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<td>14:55-15:15</td>
<td>F.V. Kazantsev, V.V. Chernova, A.V. Doroshkov, N.A. Omelyanchuk, V.V. Mironova</td>
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<td>15:15-15:40</td>
<td>J. Narula, A. Kuchina, G.M. Süel and O.A. Igoshin</td>
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<td>15:15-15:35</td>
<td>G.I. Karlov, M.G. Divashuk, O.S. Alexandrov, O.V. Rumazova, Khuat T.M.L., P.Yu. Kroupin</td>
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<td>15:40-16:00</td>
<td><strong>Coffee break</strong></td>
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<td>16:00-16:25</td>
<td><strong>O.V. Popik, N.A. Kolchanov, V.A. Ivanisenko</strong> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Center of neurobiology and neurogenetics, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
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<td>16:00-16:20</td>
<td><strong>I.V. Pinsky, A.T. Ivashchenko</strong> Al-Farabi Kazakh National University, Almaty, Kazakhstan miRNAs BINDING TO mRNAs OF RICE MYB GENES</td>
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<td>16:25-16:50</td>
<td><strong>A. Kursanov, O. Solovyova, L. Katsnelson, K. Medvedev, A. Vasilyeva, N. Vikulova, V.S. Markhasin</strong> Institute of Immunology and Physiology UB of RAS, Yekaterinburg, Russia; CARDIAC MECHANICS, CALCIUM OVERLOAD AND ARRHYTHMOGENESIS</td>
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<td>16:20-16:45</td>
<td><strong>Y. Kanayama, H. Ikeda</strong> School of Agricultural Science, Tohoku University, Sendai, Japan METABOLOME AND TRANSCRIPTOME ANALYSES OF A TOMATO INTROGRESSION LINE CONTAINING A SOLANUM PENNELLII CHROMOSOME SEGMENT</td>
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<td>16:50-17:15</td>
<td><strong>P.A. Ryzhkov, N.S. Ryzhkova</strong> Scientific Research Institute of Biology SFEDU, Rostov-on-Don, Russia GRAPH MODEL OF TYPE I DIABETES</td>
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<td>16:45-17:05</td>
<td><strong>D.A. Afonnikov</strong></td>
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<td>17:15-17:50</td>
<td><strong>S.A. Lashin, Yu.G. Matushkin</strong> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia;</td>
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<td>17:05-17:25</td>
<td><strong>A.V. Doroshkov</strong> U.S. Zubairova, M.A. Genaev, S.V. Nikolaev, T.A. Pshenichnikova, D.A. Afonnikov</td>
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<td>17:15-17:50</td>
<td><strong>L.N. Grinkevich</strong> I.P. Pavlov Institute of Physiology of RAS, St. Petersburg, Russia</td>
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| 17:25- 17:45 | Foyer of Small Hall (House of Scientists SB RAS) | **K.N. Sarsenbayev**
Eurasian national university, Astana, Kazakhstan
PROTEOMIC INFORMATION OF SPRING WHEAT VARIETIES DIFFERING IN RESISTANCE TO INFECTION AFTER PUCCINIA RECONDITA INOCULATION |
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
THE PROGRESS IN PHYSICAL MAPPING OF CHROMOSOME 5B OF BREAD WHEAT TRITICUM AESTIVUM |
| 18:00- 19:00 | Foyer of Small Hall (House of Scientists SB RAS) | Poster session                                                                 |

**Novosibirsk State University, Novosibirsk, Russia**
DEC: SOFTWARE TOOLS FOR SIMULATION EVOLUTION IN DIPLOID POPULATIONS

**Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia**
ANALYSIS OF BREAD WHEAT LEAF PUBESCENCE FORMATION AND DIVERSITY USING IMAGE ANALYSIS TECHNIQUE AND MATHEMATICAL MODELING

**EPIGENETIC MECHANISMS OF MEMORY FORMATION: THE ROLE OF THE HISTONE ACETYLATION AND METHYLATION IN AVERSIVE LEARNING**

**ANALYSIS OF BREAD WHEAT LEAF PUBESCENCE FORMATION AND DIVERSITY USING IMAGE ANALYSIS TECHNIQUE AND MATHEMATICAL MODELING**

**THE PROGRESS IN PHYSICAL MAPPING OF CHROMOSOME 5B OF BREAD WHEAT TRITICUM AESTIVUM**
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</table>
| 09:00 – 13:00 | **BGRS-2014. Genomics and epigenetics**  
*Chairpersons:*  
Prof. E. Nikolaev,  
Prof. I. Larina  
| 09:00 – 13:00 | **MM-HPC-2014. High performance computing and software tools for bioinformatics and biomedicine**  
*Chairpersons:*  
| 09:00 – 13:00 | **School. Gene networks modeling and supercomputing**  | 9.00-9.35 | **E. Prokhortouk**  
National Research Center “Kurchatov Institute”, Moscow, Russia;  
Center of Bioengineering, Russian Academy of Sciences, 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  
Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia  
SIBERIAN SUPERCOMPUTER CENTER AS A SERVICE FOR BIOINFORMATICS  
**KEYNOTE TALK**  | 09:00-09:30 | B.G. Mikhailenko, B.M. Glinskiy, N.V. Kuchin, I.G. Chernykh  
Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia  
SIBERIAN SUPERCOMPUTER CENTER AS A SERVICE FOR BIOINFORMATICS  
**KEYNOTE TALK**  | 09:35-11:00 | **Recommended to attend:**  
B.G. Mikhailenko, B.M. Glinskiy, N.V. Kuchin, I.G. Chernykh  
Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia  
SIBERIAN SUPERCOMPUTER CENTER AS A SERVICE FOR BIOINFORMATICS  
**KEYNOTE TALK**  |
| 9.35-9.55 | **V.N. Babenko**  
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia  
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**  
1,2, E.E. Ivashko, Y. Gupta, R. Ludwig, S. Möller  
1University of Lübeck, Department of Dermatology, Germany;  
2Institute of Applied Mathematical Research, Karelian Center of the Russian Academy of Sciences, Petrozavodsk, Russia  
BOINC-BASED DESKTOP GRID INFRASTRUCTURE FOR VIRTUAL DRUG SCREENING  | 9:35-11:00 | **R. Hofestäd**  
Bielefeld University, Germany  
PETRI NET MODELING AND SIMULATION OF METABOLIC PATHWAYS  |
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. Kabankhin, 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  |
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<td>10:15-10:35</td>
<td>C.K. Mitra, A.K. Meena</td>
<td>School of Life Sciences, University of Hyderabad, Hyderabad, India</td>
<td>10:10-10:30</td>
<td>I.V. Protsyuk1, 2, G.A. Grekhov, A.V. Tiunov, M.Y. Fursov</td>
<td>ASSOCIATION BETWEEN MICRORNA AND UTRS FROM HUMAN TLR GENES</td>
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<td>1Novosibirsk State University, Novosibirsk, Russia</td>
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<td>2Center of Information Technologies</td>
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<td>SHARED BIOINFORMATICS DATABASE WITHIN UNIPRO UGENE</td>
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<td>11:15-11:35</td>
<td>P.B. Natalin</td>
<td>Genetic Analysis Team Leader, Genetic Medical &amp; Applied Sciences, Life Sciences Solutions, Thermo Fisher Scientific, Moscow, Russia ION TORRENT™ PLATFORM IN 2014: TECHNOLOGY AND APPLICATIONS</td>
<td>11:15-11:45</td>
<td>I. V. Oseledets1, 2</td>
<td>NUMERICAL METHODS FOR HIGH-DIMENSIONAL PROBLEMS IN BIOLOGY KEYNOTE TALK</td>
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<td>2Institute of Numerical Mathematics RAS, Moscow, Russia</td>
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<td>NUMERICAL METHODS FOR HIGH-DIMENSIONAL PROBLEMS IN BIOLOGY KEYNOTE TALK</td>
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<td>WHOLE GENOME ANALYSIS OF A-TO-I RNA EDITING USING SINGLE</td>
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<td>INTEL® CILK™ PLUS – DATA PARALLELIZATION AND VECTORIZATION IN C/C++ PROGRAMS</td>
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Recommended to attend:

- I. V. Oseledets1, 2
  - 1Skolkovo Institute of Science and Technology,
  - 2Institute of Numerical Mathematics RAS, Moscow, Russia

NUMERICAL METHODS FOR HIGH-DIMENSIONAL PROBLEMS IN BIOLOGY KEYNOTE TALK
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<tr>
<td>11:55-12:15</td>
<td>MOLECULE SEQUENCING IN DROSOPHILA</td>
<td>K.V. Gunbin¹,², K.Y. Popadin</td>
<td>Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
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<td>Center of neurobiology and neurogenetics, Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
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<td>5’ AND 3’ BREAKPOINTS OF MTDNA DELETIONS SHOW DRASTIC DIFFERENCES IN DINUCLEOTIDE PROPERTIES</td>
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<td>12:00-12:20</td>
<td>Z.S.Mustafin¹,², S.A. Lashin¹²</td>
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<td>Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
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<td>HIGH PERFORMANCE COMPUTING COMPUTING SIMULATION OF EVOLUTIONARY PROCESSES IN BACTERIAL COMMUNITIES</td>
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<td>12:15-12:50</td>
<td>HIGH PERFORMANCE COMPUTING COMPUTING SIMULATION OF EVOLUTIONARY PROCESSES IN BACTERIAL COMMUNITIES</td>
<td>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</td>
<td>Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
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<td>HIGH RESOLUTION COMPUTATIONAL MODELS FOR BIOELECTRIC IMPEDANCE ANALYSIS</td>
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<td>A. A. Danilov, V. K. Kramarenko, V. Yu. Salamatova, A. S. Yurova</td>
<td>Institute of Numerical Mathematics RAS, Moscow, Russia</td>
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<td>DE NOVO ASSEMBLY OF THE MITOCHONDRIAL GENOME OF ~5000-YEAR-OLD HUMAN FROM NORTH CAUCASUS</td>
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<td>ON A PARALLEL ALGORITHM FOR MORPHOGENE DIFFUSION-REACTION PROCESSES SIMULATION ON A 2D CELL ENSEMBLE</td>
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<td>13:00-14:00</td>
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<td>Recommended to attend:</td>
<td>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</td>
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<td>14:00-14:05</td>
<td><strong>BGRS-2014. Genomics and epigenetics</strong></td>
<td><strong>Chairpersons:</strong> Prof. E. Nikolaev, Prof. I. Larina</td>
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<tr>
<td>14:00-14:30</td>
<td>R.V. Chereji, T.-W. Kan, V.P. Guryev, A.V. Morozov, <strong>Y.M. Moshkin</strong></td>
<td>1Erasmus Medical Center, Rotterdam, the Netherlands; 2Center of Genetic Resources, Institute of Cytology &amp; Genetics, Novosibirsk, Russia</td>
<td>BIOPHYSICAL PRINCIPLES GUIDING NUCLEOSOME POSITIONING IN VIVO</td>
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<tr>
<td>14:30-14:50</td>
<td>D. Zharkov</td>
<td>SB RAS Institute of Chemical Biology and Fundamental Medicine, Novosibirsk, Russia</td>
<td>5-METHYLcytosine AND DNA OXIDATION: AT THE CROSSROADS OF EPIGENETICS, DNA DAMAGE, AND DNA REPAIR</td>
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<td>14:50-15:10</td>
<td>D.Y. Oschepkov, V.G. Levitsky, I.V. Kulakovskiy, N.I. Ershov, V.J. Makeev, T.I. Merkulova</td>
<td>Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia; EXPERIMENTALLY VERIFIED TRANSCRIPTION FACTOR BINDING SITES MODELS APPLIED FOR COMPUTATIONAL ANALYSIS OF CHIP-SEQ DATA</td>
<td>IS THE SINGLE CELL CHIP-SEQ TECHNIQUE POSSIBLE?</td>
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<tr>
<td>15:10-15:30</td>
<td>T. Subkhankulova, <strong>F. Naumenko</strong></td>
<td>Imperial College, London, UK</td>
<td>IS THE SINGLE CELL CHIP-SEQ TECHNIQUE POSSIBLE?</td>
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<tr>
<td>14:00-14:15</td>
<td><strong>MM-HPC-2014. Hemodynamics and tomography</strong></td>
<td><strong>Chairpersons:</strong></td>
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<td>14:00-14:10</td>
<td>Chupakhin A.P., Cherevko A., Khe A., Chebotnikov A., Krivoshapkin A., Orlov K., Panarin V.</td>
<td>Larentyev Institute of Hydrodynamics SB RAS, Novosibirsk, Russia</td>
<td>COMPREHENSIVE STUDY OF HEMODYNAMICS OF CEREBRAL VESSELS IN THE PRESENCE OF PATHOLOGIES KEYNOTE TALK</td>
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<td>14:00-14:35</td>
<td>A. Barlukova, S. Honoré, F. Hubert, M. Petit</td>
<td>Aix-Marseille University, France</td>
<td>DYNAMIC INSTABILITIES OF MICROTUBULES</td>
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<td>14:35-14:50</td>
<td>Mikhailova A.V., Cherevko A.A., Chupakhin A.P., Krivoshapkin A.L., Orlov K.Y.</td>
<td>Novosibirsk State University, Novosibirsk, Russia</td>
<td>IDENTIFICATION OF BASED ON EXPERIMENTAL CLINICAL DATA HEMODYNAMIC MODEL</td>
</tr>
<tr>
<td>14:50-15:05</td>
<td>A. Borisenko</td>
<td>Irktusk State Medical University, Irktusk, Russia</td>
<td>ANALYSIS OF GENETIC SEQUENCES OF TICK-BORNE ENCEPHALITIS VIRUS IN THE TERRITORY OF THE EURASIAN AREA</td>
</tr>
<tr>
<td>15:00-15:15</td>
<td>A. Vitvitsky</td>
<td>Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia</td>
<td>COMPUTER SIMULATION OF SELF-ORGANIZATION IN THE BACTERIAL MINCDE SYSTEM</td>
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<tr>
<td>15:30-15:45</td>
<td>T. Gamilov</td>
<td>Moscow Institute of Physics and Technology, Dolgoprudny, Russia</td>
<td>1D MODELLING OF DIFFERENT TIME REGIMES OF ENHANCED EXTERNAL</td>
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<tr>
<td>15:45-15:50</td>
<td>T. Gamilov</td>
<td>Moscow Institute of Physics and Technology, Dolgoprudny, Russia</td>
<td>IS THE SINGLE CELL CHIP-SEQ TECHNIQUE POSSIBLE?</td>
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<td>Time</td>
<td>Speaker(s)</td>
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| 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     | Institute of Physiology and Biochemistry, University of Belgrade, Faculty of Biology, Belgrade, Serbia | 15:30-15:50 |
| 16:15-16:35 | S.V. Dzhenin  
Limited Liability Company Eppendorf, Russia | INFLUENCE OF CONSUMABLES ON QUALITY AND PRECISION OF EXPERIMENTS     | Limited Liability Company Eppendorf, Russia | 16:15-16:45 |
Laboratory of Cell Genome Functioning, Institute of Cell Biophysics of RAS, Pushchino MR, Russia | ELECTROSTATIC PROPERTIES OF BACTERIOPHAGE LAMBDA GENOME AND ITS ELEMENTS: VIRUS VS HOST | Laboratory of Cell Genome Functioning, Institute of Cell Biophysics of RAS, Pushchino MR, Russia | 16:30-16:45 |
| 16:55-17:15 | A.A. Ryasik, A.A. Grinevich, L.V. Yakushev  
Institute of Cell Biophysics RAS, | PATIENT SPECIFIC | Institute of Cell Biophysics RAS, | 16:45-17:05 |
| 15:55-16:15 | Coffee break | | | 15:50-16:15 |
| 16:15-16:35 | Coffee break | | | 16:15-16:15 |
| 16:35-16:55 | Gamilov T.M., Simakov S.S.  
Moscow Institute of Physics and Technology, Dolgoprudny, Russia | 1D MODELLING OF DIFFERENT TIME REGIMES OF ENHANCED EXTERNAL COUNTERPULSATION | Moscow Institute of Physics and Technology, Dolgoprudny, Russia | 16:30-16:45 |
| 16:55-17:15 | Y.A. Ivanov, R. Pryamonoosov  
Institute of Numerical Mathematics RAS, Moscow, Russia | PATIENT SPECIFIC | Institute of Numerical Mathematics RAS, Moscow, Russia | 16:45-17:05 |
| 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 | Institute of Numerical Mathematics RAS, Moscow, Russia | 15:20-15:40 |
| 15:20-15:50 | A. Gurkov, E.M. Kondratyeva, D.S. Bedolina  
Institute of Biology at Irkutsk State University, Irkutsk, Russia | IMAGEJ ADDON FOR 2D ELECTROPHORESIS GEL ANALYSIS | Institute of Biology at Irkutsk State University, Irkutsk, Russia | 15:30-15:50 |
| 16:15-16:35 | 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 | Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia | 16:15-16:35 |
| 16:45-17:00 | 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 | Institute of Biochemistry and Physiology of Plants and Microorganisms RAS, Saratov, Russia | 16:45-17:00 |
| 16:35-16:55 | A. Katugina, U.F. Kartavtsev  
Zhirmunsky 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-I GENE | Zhirmunsky Institute of Marine Biology FEB RAS, Vladivostok, Russia | 16:35-16:55 |
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<tr>
<th>Time</th>
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<tr>
<td>17:15-17:35</td>
<td>Pushchino, Russia</td>
<td>Dynamics of nonlinear conformational excitations in functional regions of pttq18 plasmid</td>
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<td>17:05-17:25</td>
<td>RECONSTRUCTION OF VASCULAR NETWORK FOR HEMODYNAMIC MODELING</td>
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<td>Tomsk, Russia</td>
<td>ROTATIONAL DYNAMICS OF BASES IN THE GENE CODING INTERFERON ALPHA 17 (IFNA17)</td>
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<tr>
<td>17:35-17:50</td>
<td>Novosibirsk State University, Russia</td>
<td>COMPUTER DATA ANALYSIS OF GENOME SEQUENCING BY TECHNOLOGY CHIP-SEQ AND HI-C</td>
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<td>17:25-17:45</td>
<td>Verner A.</td>
<td>GETTING SOPHISTICATED: NEW APPROACHES, TRENDS AND DEVELOPMENTS FOR DDPCR</td>
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<td>17.17.35</td>
<td>Medvedev A.Ye., Khrisianovich Institute of Theoretical and Applied Mechanics SB RAS, Novosibirsk, Russia</td>
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<td>17:45</td>
<td>EQUATION OF STATE OF BLOOD FLOWS IN SMALL VESSELS</td>
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<td>18:00-19:00</td>
<td>Foyer of Small Hall</td>
<td>PATIENT SPECIFIC 3D MODELS: SOME GENERATION TECHNIQUES</td>
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<td>(House of Scientists SB RAS)</td>
<td>Poster session</td>
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<td>18:00-19:00</td>
<td>Auditorium near Conference hall in the Exhibition Centre SB RAS</td>
<td>Poster session</td>
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**Institute of Cytology and Genetics SB RAS**

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

**Chairperson:**

**Prof. R. Hofestaedt, Bielefeld University, Germany**
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<th>Time</th>
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<tr>
<td>09:00 – 13:00</td>
<td><strong>BGRS-2014. Proteomics, metabolomics and computational pharmacology</strong></td>
<td>09:00 – 13:00</td>
<td><strong>MM-HPC-2014. Pharmacokinetics and immunology</strong></td>
<td>09:00 – 13:00</td>
<td>School. Presentations by young scientists</td>
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| 09:00 - 09:30| **Chairpersons:**                                                           | 09:00 - 09:30 | **Chairpersons:**                                                                  | 09:00 - 09:20 | **V.V. Lavrekha, N.A.** Omelyanchuk, V.V. Mironova Institute of Cytology and Genes of SB RAS (Novosibirsk), Russia  
<p>| 9.00-9.45 I.M. Larina, V.A. Ivanisenko, E.N. Nikolaev Institute for Biomedical Problems of RAS, Moscow, Russia; PROTEOMICS EXTREME IMPACTS AS A TOOL FOR SYSTEMS | 9.00-9.20 N. Asmanova, G. Koloskov, A.I. Ilin Scientific Center for Anti-Infectious Drugs, Almaty, Kazakhstan ON THE APPLICATION OF EXCRETION DATA AS A CRITERIA OF CHOICE BETWEEN MULTIPLE |</p>
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<tr>
<th>Time</th>
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<th>Speaker(s)</th>
<th>Institution</th>
<th>Description</th>
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| 9:45-10:10 | **KEYNOTE TALK**                                                                                         | **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** | Interdisciplinary Centre for Bioinformatics, Universität Leipzig, Leipzig, Germany; A MACHINE LEARNING ANALYSIS OF URINE PROTEOMICS IN SPACE-FLIGHT SIMULATIONS | **GENOMIC PROTEIMIC PROFILING** RAS, Novosibirsk, Russia **CANCER EXOME DATA BY SHOTGUN PROTEOMICS USING CANCER CELL LINE RECOGNITION** Chemistry RAMS, Moscow, Russia **FLIGHT SIMULATIONS OF URINE PROTEOMICS IN SPACE** A MACHINE LEARNING ANALYSIS OF URINE PROTEOMICS IN SPACE-FLIGHT SIMULATIONS | 09:30-09:50 | SOLUTIONS OF INVERSE PROBLEM IN PHARMACOKINETICS **KEYNOTE TALK** | A.I. Ilyin, S.I. Kabanikhin, O.I. Krivorotko  
1. NSU, Novosibirsk, Russia  
2. ICM&MG, prospect Akademika Lavrentjeva, 6, Novosibirsk, 630090, Russia  
| 10:10-10:35 | **KEYNOTE TALK**                                                                                         | **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** | **IMMUNOLOGY** PHARMAСOKINETICS AND DIFFERENTIAL EQUATIONS OF INVERSE PROBLEMS FOR PHARMACOKINETICS. IDENTIFIABILITY OF COMPARTMENTAL MODELS | 09:50-10:10 | **INVERSE PROBLEM OF PHARMACOKINETICS. IDENTIFIABILITY OF COMPARTMENTAL MODELS** | A.I. Ilyin, S.I. Kabanikhin, D.A. Voronov  
1. NSU, Novosibirsk, Russia  
2. ICM&MG, Novosibirsk, 630090, Russia  
**NUMERICAL SOLUTIONS OF INVERSE PROBLEM OF PHARMACOKINETICS. IDENTIFIABILITY OF COMPARTMENTAL MODELS** | 9:40-10:00 | **VIRTUAL DRUG SCREENING INFRASTRUCTURE FOR VIRTUAL DRUG SCREENING** N. Nikitina, E.E. Ivashko, Y. Gupta, R. Lüdwig, S. Möller. Institute of Applied Mathematical Research, Karelian Research Center RAS, Petrozavodsk, Russia **BOINC:BASED DESKTOP GRID INFRASTRUCTURE FOR VIRTUAL DRUG SCREENING** |  |
| 10:35-11:00 | **APICAL MERISTEM WITH DYNAMICAL GRAMMAR**                                                             | **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 PROTEIMIC PROFILING** | **Solutions of Inverse Problem in Pharmacokinetics** | 10:10-10:30 | **Solutions of Inverse Problem in Pharmacokinetics** | A.I. Ilyin, S.I. Kabanikhin  
1. NSU, Novosibirsk, Russia  
2. ICM&MG, Novosibirsk, 630090, Russia  
**INVERSE PROBLEMS FOR DIFFERENTIAL EQUATIONS OF PHARMACOKINETICS AND IMMUNOLOGY** | 10:00-10:20 | **BOINC:BASED DESKTOP GRID INFRASTRUCTURE FOR VIRTUAL DRUG SCREENING** V. Mironova, D. Novikova. Institute of Cytology and Genetics SB RAS **AUXIN:INDUCED CHANGES OF TRANSCRIPTOME IN ARABIDOPSIS THALIANA L. ROOTS.** |  |
<p>| 10:30-10:50 | <strong>APICAL MERISTEM WITH DYNAMICAL GRAMMAR</strong>                                                             | <strong>Shishlenin M.A.</strong> Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia <strong>CONTINUATION OF THE ACOUSTIC FIELD IN TOMOGRAPHY</strong> | Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia <strong>CONTINUATION OF THE ACOUSTIC FIELD IN TOMOGRAPHY</strong> | <strong>BIOINFORMATICS DETECTION OF POTENTIAL</strong> | 10:30-10:50 | <strong>CONTINUATION OF THE ACOUSTIC FIELD IN TOMOGRAPHY</strong> | Shishlenin M.A. Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia <strong>CONTINUATION OF THE ACOUSTIC FIELD IN TOMOGRAPHY</strong> | 10:20-10:40 | <strong>BIOINFORMATICS DETECTION OF POTENTIAL</strong> A. Paramonov, U.P. Djioev, I.V. Kozlova Research Centre for Family Health and Human Reproduction Problems SB RAMS, Irkutsk, Russia |  |</p>
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<td>11:00-11:20</td>
<td>Coffee break</td>
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<td>11:20-11:45</td>
<td><strong>L.H. Pastushkova,</strong> 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 of RAS; Moscow, Russia; IDENTIFYING OVERREPRESENTED BIOLOGICAL PROCESSES IN COSMONAUTS ON THE FIRST DAY</td>
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<td>11:45-12:10</td>
<td><strong>P.S. Sherin,</strong> 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</td>
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<tr>
<td>12:10-12:35</td>
<td><strong>T. Duzhak,</strong> Yu.P. Tsentalovich International Tomography Center SB RAS, Novosibirsk, Russia LENS CATARACT: EFFECTS OF CRYSTALLINS MODIFICATION</td>
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<tr>
<td>10:40-11:00</td>
<td><strong>O. Perfilyeva</strong> Institute of Cytology and Genetics SB RAS MATHEMATICAL MODELING OF PEPTIDOGLYCAN PRECURSOR BIOSYNTHESIS IN THE CYTOPLASM OF ESHERICHA COLI CELL</td>
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<td>11:15-11:35</td>
<td><strong>A.A. Polshchitsin</strong>¹ ², V.M. Nekrasov, A.V. Chernyshev, and V.P Maltsev ¹Institute of chemical kinetics and combustion, Novosibirsk, Russia; ²Novosibirsk state university, Novosibirsk, Russia. SOLUTION OF INVERSE IMMUNOAGGLUTINATION KINETICS PROBLEM FOR PATCHY PARTICLES WITH A SMALL NUMBER OF BINDING SITES</td>
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<tr>
<td>12:00-12:20</td>
<td><strong>N.V. Sviridova,</strong> K. Sakai Computing Center FEB RAS, Khabarovsk, Russia APPLICATION OF NONLINEAR TIME SERIES ANALYSIS FOR HEMODYNAMIC MODEL VALIDATION ON THE BASE OF PHOTOPLETHYSMOGRAM</td>
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<td>Time</td>
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<td>12:15-12:35</td>
<td><strong>APPLICATION OF A BIEXPONENTIAL FORM OF TWO-COMPARTMENT PHARMACOKINETIC MODELS WITH FIRST-ORDER ABSORPTION IN PHARMACOKINETIC ANALYSIS</strong></td>
<td><strong>G. Koloskov, N. Asmanova, A.I. Ilin</strong>&lt;br&gt;Scientific Center for Anti-Infectious Drugs, Almaty, Kazakhstan</td>
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<td>13:00-14:00</td>
<td>Launch</td>
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<td>14:00-18:15</td>
<td><strong>BGRS-2014. Proteomics, metabolomics and computational pharmacology</strong>&lt;br&gt;<em>Chairpersons:</em></td>
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<td>14:00-14:25</td>
<td><strong>S.F. Chekmarev</strong>&lt;br&gt;Institute of Thermophysics SB RAS, Novosibirsk, Russia; Novosibirsk State University, Novosibirsk, Russia&lt;br&gt;DRIVING FORCE FOR PROTEIN FOLDING: THE TWO-COMPONENT POTENTIAL</td>
<td><strong>N.B. Ayupova, V.P. Golubyatnikov</strong>&lt;br&gt;1 Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia&lt;br&gt;2Novosibirsk State University, Novosibirsk, Russia&lt;br&gt;ON GEOMETRY OF PHASE PORTRAITS OF SOME LOW-DIMENSIONAL GENE NETWORK MODELS&lt;br&gt;KEYNOTE TALK</td>
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<td>14:25-14:50</td>
<td><strong>A.O. Chugunov, P.E. Volinsky, R.G. Efremov</strong>&lt;br&gt;Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry RAS, Moscow, Russia&lt;br&gt;HIGH-COMPUTATIONAL COMPUTING</td>
<td><strong>F.V. Kazantsev, I.R. Akberdin, N.L. Podkolodnyy, V.A. Likhoshvai</strong>&lt;br&gt;Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia&lt;br&gt;GENE NETWORKS MODELING: SPECIFICATION LANGUAGE</td>
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<td>Time</td>
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<td>14:50-15:15</td>
<td>A.Y. Nyporko, Taras Shevchenko National University of Kyiv, Kyiv, Ukraine</td>
<td>PROVIDES INSIGHT INTO THE INNERMOST ORGANIZATION DATABASE BY “ELOE” PROGRAM</td>
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<td>15:40-16:05</td>
<td>E.A. Aksianov, A.V. Alexeevsky, Belozersky Institute of Physico-Chemical Biology, MSU, Moscow, Russia</td>
<td>ALIGNMENT OF “UNALIGNABLE” PROTEIN STRUCTURES</td>
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<td>15:40-16:00</td>
<td>V. Chernova, A. Doroshkov, V. Mironova, N. Omelyanchuk, Institute of Cytology and Genetics, Novosibirsk, Russia</td>
<td>PIN:TRANSPORTERS IN THE ROOT MERISTEM OF ARABIDOPSIS THALIANA L-IMAGE ANALYSIS OF EXPRESSION PATTERNS</td>
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<td>Time</td>
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<td>16:05-16:25</td>
<td>Coffee Break</td>
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<td>16:25-16:50</td>
<td>A.A. Anashkina, N.G. Esipova, E.N. Kuznetsov, V.G. Tumanyan</td>
<td>Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia</td>
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<td>16:50-17:15</td>
<td>A.M. Andrianov, I.A. Kashyn, A.V. Tuzikov</td>
<td>United Institute of Informatics Problems NAS Belarus, Minsk, Belarus</td>
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<td>17:15-17:50</td>
<td>E.N. Nikolaev</td>
<td>Institute for Energy Problems of Chemical Physics RAS, Moscow, Russia</td>
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<td>17:55-18:15</td>
<td>N.V. Pertsev</td>
<td>Sobolev Institute of Mathematics, Omsk</td>
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<td>16:15-16:35</td>
<td>Coffee Break</td>
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<tr>
<td>16:25-16:50</td>
<td>B. Karacaören</td>
<td>Department of Animal Science, Faculty of Agriculture, Akdeniz University, Antalya, Turkey</td>
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<td>16:50-17:15</td>
<td>V.K. Kramarenko, A.Yu. Churikov, P.V. Zavodaev</td>
<td>Moscow Institute of Physics and Technology Russia</td>
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<td>17:15-17:50</td>
<td>E.S. Fomin</td>
<td>Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia</td>
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<td>17:55-18:15</td>
<td>A.A. Vitvitsky</td>
<td>Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia</td>
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<td>16:50-16:55</td>
<td>Discussion</td>
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<td>17:15-17:35</td>
<td>L.A. Krasnobaeva½, L.V. Yakushevich</td>
<td>Siberian State Medical University, Tomsk, Russia</td>
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<td>17:35-17:55</td>
<td>A.A. Vitvitsky</td>
<td>Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia</td>
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THE HIGH-DIMENSIONAL MODELS IN SOME TASKS OF BIOLOGY AND MEDICINE: PROBLEMS OF ANALYTICAL AND NUMERICAL STUDIES

18:15-19:15 Auditorium near Conference hall in the Exhibition Centre SB RAS
Poster session

Yu.S. Bukin
Limnological Institute, Irkutsk, Russia
PACKAGE OF FUNCTIONS FOR SCRIPT PROGRAMMING LANGUAGE R FOR TESTING THE CONVERGENCE OF POPULATION SAMPLES OF DNA SEQUENCES

K.V. Gunbin*, D.A. Afonnikov, N.A. Kolchanov, E.I. Rogaev, A.P. Derevianko
1Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
2University of Massachusetts Medical School, Worcester, Massachusetts, USA
HOMO SAPIENS DENISOVA CRAFTSMANSHIP CAN BE RELATED WITH EVOLUTION OF THE miRNAS REGULATING mRNAs EXPRESSED IN THE BRAIN REGIONS CRUCIAL FOR CONSCIOUSNESS AND SPEECH

K.V. Gunbin*, D.A. Afonnikov, Y.L. Orlov
1Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
MOLECULAR EVOLUTION OF MAMMALIAN ORTHOLOGOUS PROTEIN GROUPS INVOLVED IN STEM CELL SPECIFICITY

K.V. Gunbin*, D.A. Afonnikov
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
THE RELATION BETWEEN ENVIRONMENTAL CHANGES AND EVOLUTION OF ARCHAEA PROTEIN DOMAINS

K.V. Gunbin*, M.P. Ponomarenko, D.A. Afonnikov, F. Gusev, E.I. Rogaev
1Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
2University of Massachusetts Medical School, Worcester, Massachusetts, USA
WHAT EVOLUTION OF HOMINID TATA-BOXES CAN TELL US ABOUT HUMAN LINEAGE?
K.V. Gunbin*, V.G. Levitsky¹, A.V. Vershinin²
¹Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
²Institute of Molecular and Cellular Biology SB RAS, Novosibirsk, Russia
WHAT EVOLUTION OF RYE SUBTELOMERIC REPEATS CAN TELL US ABOUT CEREALS SPECIATIONS?

A.O. Katugina*, Y.F. Kartavtsev ¹,2
¹A.V. Zhirmunsky Institute of Marine Biology FEB RAS, Vladivostok, Russia
²Far Eastern Federal University, 690091 Vladivostok, 27 Oktyabrskaya st. Russia
COMPARATIVE GENETIC ANALYSIS OF THREE FAR EASTERN SPECIES OF THE GENUS TRIBOLODON ACCORDING TO SEQUENCE DATA OF MITCHONDRIAL DNA CO-1 REGION

S.A. Lashin*, V.V. Suslov, K.V. Gunbin
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
Novosibirsk State University, Novosibirsk, Russia
FORWARD-TIME SIMULATION OF EVOLUTIONARY PROCESSES IN ANCIENT POPULATIONS USING THE DIPLOID EVOLUTIONARY CONSTRUCTOR

S.V. Lenskiy*, T.I. Lenskaya
Ural Federal University, Ekaterinburg, Russia
SEARCH FOR EVOLUTIONAL INVARIANTS BY RANK DISTRIBUTION OF GENE DENSITY IN HOMINIDS

O.O. Maikova*, D.Yu. Sherbakov, S.I. Belikov
Limnological Institute SB RAS, Irkutsk, Russia
THE TWO HYPOTHESES OF BAIKAL ENDEMIC SPONGE (LUBOMIRSKIIDAE) EVOLUTION

Z.S.Mustafin, Yu.G. Matushkin, S.A. Lashin*
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
Novosibirsk State University, Novosibirsk, Russia
ALLELIC COADAPTATION AND FITNESS LANDSCAPE PREDETERMINE THE OPTIMAL EVOLUTIONARY MODE IN PROKARYOTIC COMMUNITIES: A SIMULATION STUDY

D.Yu. Sherbakov¹, R.V. Adelshin, A.S. Anikin², A.Yu. Gornov³
¹Limnological Institute, Irkutsk, Russia
²Irkutsk Antiplague Research Institute of Siberia and Far East, Russia
³Institute for System Dynamics and Control Theory, Irkutsk, Russia
METHODS OF DETECTION AND ESTIMATION OF EVOLUTIONARY CONSERVED ELEMENTS OF RNA SECONDARY STRUCTURE
E.A. Borzov¹, R. Mehta³, A.V. Baranova¹,³, M.Yu. Skoblov*¹,²,⁴
¹ Federal State Budgetary Institution “Research Centre for Medical Genetics” under the Russian Academy of Medical Sciences, Moscow, Russia
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³ School of Systems Biology, College of Science, George Mason University, Fairfax, VA USA
⁴ The Russian National Research Medical University named after N.I. Pirogov (RNRMU).
WHOLE-GENOME COMPARATIVE ANALYSIS OF CpG ISLANDS BETWEEN HUMAN AND CHIMPANZEE

V.S. Sokolov*, K.V. Gunbin, Y.G. Matushkin
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
VARIATION OF ELONGATION EFFICIENCY INDEX OF ARCHAEA GENES DURING EVOLUTION

V.V. Suslov, M.P. Ponomarenko, K.V. Gunbin
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
EVOLUTION OF MODERN HUMAN AND RECOMBINATION OF MEMES

V.V. Suslov
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
INVASION, ADAPTATION AND EVOLUTION: WHEN ALL OUT OF SYNC

V.V. Suslov¹*, N.S. Safronova¹², Y.L. Orlov¹², D.A. Afonnikov¹²
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THE GENOMIC TEXT CHARACTERISTICS AND GC CONTENT ARE RELATED TO THE BACTERIAL GENOME EVOLUTION

¹ I.I. Turnaev¹*, K.V. Gunbin¹, I.R. Akberdin¹, V.V. Mironova¹², N.A. Omelyanchuk¹, D.A. Afonnikov¹².
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² Novosibirsk State University
INCREASING THE NUMBER OF PARALOGS FOR ENZYMES INVOLVED IN TRYPTOPHAN BIOSYNTHESIS DURING THE EVOLUTION OF LAND PLANTS

O.A. Zverkov*, A.V. Seliverstov, V.A. Lyubetsky
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A DATABASE OF RHODOPHYTE PLASTID PROTEIN FAMILIES AND REGULATION OF moeB GENES

BGRS-2014.
Systems computational biology
POSTER SESSION
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
REGULATORY MECHANISMS FOR mESC SELF-RENEWAL: KINETIC AND STOCHASTIC MODELING

Gamaleya Scientific Research Institute for Epidemiology and Microbiology Ministry of Health of Russian Federation, Moscow, Russia
HIDDEN RESERVES OF USED VACCINE SUBSTRAIN

V.A. Likhoshvai1,2, T.M. Khlebodarova1, S.I. Bazhan3,*, I.A. Gainova 4, V.A.Chershnev5, G.A. Bocharov6
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TAT-REV REGULATION OF HIV-1 REPLICATION: MATHEMATICAL MODEL PREDICTS THE EXISTENCE OF OSCILLATORY DYNAMICS

Ermak T.V.1,*, Akberdin I.R.1, Timonov V.S.2,3, Mischenko E.L.1, Oschepkova E.A.1, Perfilyeva O.A.1, Smirnova O.G.1, Khlebodarova T. M1 and Likhoshvai V.A.1,3
1Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
2Siberian State University of Telecommunications and Information Sciences, Novosibirsk, Russia
3Novosibirsk State University, Novosibirsk, Russia
KiNET 1.0 – A NEW WEB DATABASE ON KINETICS DATA AND PARAMETERS FOR E. coli METABOLIC PATHWAYS.

E.V. Ignatieva*
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
THE KNOWLEDGE BASE ON MOLECULAR GENETICS MECHANISMS CONTROLLING HUMAN LIPID METABOLISM

L.I.Kononenko*
1 Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia
2 Novosibirsk State University, Novosibirsk, Russia
DIRECT AND INVERSE PROBLEMS FOR SYSTEMS WITH SMALL PARAMETER IN KINETICS MODELS

K. Korla
School of Life Sciences, University of Hyderabad, India 500046
KINETIC SIMULATION OF MITOCHONDRIAL SHUTTLES
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
Novosibirsk State University, Novosibirsk, Russia
HAPLOID EVOLUTIONARY CONSTRUCTOR 3D: A TOOL FOR SIMULATION OF SPATIALLY DISTRIBUTED PROKARYOTIC COMMUNITIES

I.M. Mikhaelis,* A.V. Chernyshev, M.A. Yurkin, V.M. Nekrasov and V.P Maltsev
Institute of chemical kinetics and combustion, Novosibirsk, Russia;
Novosibirsk state university, Novosibirsk, Russia
APOPTOTIC NUCLEAR VOLUME DECREASE: ANALYSIS OF CONFOCAL IMAGES AND MATHEMATICAL MODEL

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
DATABASE OF QUANTITATIVE CHARACTERS OF PROCESSES IN EMBRYONIC STEM CELLS

O.A. Podkolodnaya*, N.N. Podkolodnaya1, N.L. Podkolodnyy 1,2
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2 Institute of Computational Mathematics and Mathematical Geophysics, SB RAS, 6 Lavrentyeva, Novosibirsk, Russia
THE MAMMALIAN CIRCADIAN CLOCK: COMPUTER ANALYSIS OF GENE NETWORK

O.V. Popik1, O.V. Arkova1, D.A. Rasskazov1, O.V. Saik1, P.M. Ponomarenko2, T.V. Arshinova1, L.K Savinkova1, M.P. Ponomarenko1-*, and N.A. Kolchanov1,3
1 Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
2 Children's Hospital Los Angeles, Los Angeles, CA 90027, USA
3 Novosibirsk State University, Novosibirsk, Russia
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

O.V. Popik*, R. Hofestaedt, V.A. Ivanisenko
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

M.T. Ri1,*, Stefan Wölfl2, M. Zakhartsev2
1 LLC “AcademGene”, Novosibirsk, Russia.
2 Institut für Pharmazie und Molekulare Biotechnologie, Universität Heidelberg, Germany
EXPERIMENTAL DATA FOR TESTING THE ADEQUACY OF EXISTING MATHEMATICAL MODELS
M.T. Ri$^{1,*}$, O.V.Saik$^2$, S.S.Khayrulin$^3$

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$^3$ A.P. Ershov Institute of Informatics Systems, SB RAS, Novosibirsk, Russia

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

A. Ilin$^1$, R. Islamov$^1$, S. Kasenov$^2$, D. Nurseitov$^2$, S. Serovajsky$^{3,*}$

$^1$ Scientific Center for Anti-infectious Drugs, Almaty, Kazakhstan  
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$^3$ Al-Farabi Kazakh National University, Almaty, Kazakhstan

MATHEMATICAL MODELING OF LUNG INFECTION AND ANTIBIOTIC RESISTANCE

M.Y. Shamanina

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

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

A.G. Shlikht$^*$, N.V. Kramorenko

Far-Eastern Federal University, Vladivostok, Russia

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

A.M. Spitsina$^{1,2,*}$, V.M.Efimov$^1$, V.N.Babenko$^1$, Y.L.Orlov$^1$

$^1$ Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia  
$^2$ Novosibirsk State University, Mechanics and Mathematics Department

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

I.L. Stepanenko$^*$, V.A. Ivanisenko

Institute of Cytology & Genetics SB RAS, Novosibirsk, Russia

LOGICAL MODELLING OF NANOG-DEPENDED TRANSCRIPTIONAL GENE NETWORK OF EMBYONIC CARCINOMA STEM CELLS

G.A. Yuldasheva$^1$, A.I. Ilin$^1$, G.M. Zhidomirov$^2$

$^1$ Scientific Centre of Anti Infection Drugs, Kazakhstan  
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LITHIUM HALIDES ENHANCE THE ANTI-CANCER ACTIVITY OF CISPLATIN

A.S. Zhabereva$^{1,2,*}$, M.R. Gainullin$^{1,2}$, M.V. Ivanchenko$^1$, A.E. Kel$^3$

$^1$ Lobachevsky State University of Nizhny Novgorod, Nizhny Novgorod, Russia  
$^2$ Nizhny Novgorod State Medical Academy, Nizhny Novgorod, Russia
GLOBAL MAPPING OF PROTEIN UBIQUITYLATION WITHIN TNF-ALPHA SIGNALING PATHWAY USING GENEXPLAIN PLATFORM

BGRS-2014.
Plant systems biology
POSTER SESSION

Dobrovolskaya O. 1*, Amagai Y. 2, Pont C. 3, Martinek P. 4, Krasnikov A.A. 5, Orlov Y.I. 1, Salina E.A. 1, Salse J. 5, Watanabe N. 2
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3 INRA-UBP UMR-1095, 5 Chemin de Beaulieu, 63100 Clermont –Ferrand, Cedex 2, France.
4 Agrotest Fyto, Ltd., Havlíčkova 2787, 767 01 Kroměříž, Czech Republic
5 Central Siberian Botanical Garden SB RAS, Zolotodolinskaya st., 101, 630090 Novosibirsk, Russia

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

H. Ikeda 1,2*, Y. Kanayama 1
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ANALYSIS OF A TOMATO INTROGRESSION LINE, IL8-3, WITH INCREASED BRIX CONTENT USING THE WHOLE-GENOME SEQUENCE

E.G. Komyshev 1, M.A. Genaev* 2, D.A. Afonnikov 1,2
1 Novosibirsk State University, Novosibirsk, Russia
2 Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

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

Lavrekha VV 1*, Omelyanchuk NA 1, Mironova VV 1,2
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MODELING OF CELL DYNAMICS IN THE ROOT APICAL MERISTEM WITH DYNAMICAL GRAMMAR

Novoselova E.S., Mironova V.V., Kazantsev F.V., Omelyanchuk N.A, Likhoshvai V.A.
Institute of Cytology and Genetics SB RAS, 10 Lavrentyeva, Novosibirsk, Russia

COMPUTATION MODELING OF VASCULAR PATTERNING IN PLANT ROOTS

U.S. Zubairova, S.V. Nikolaev, A.V. Doroshkov, D.A. Afonnikov
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

A MODEL OF TRICHOME SPACING PATTERN FORMATION ON GROWING WHEAT LEAF
U.S. Zubairova*, S.V. Nikolaev
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
A SIMPLE MECHANICAL CELL-BASED MODEL FOR SYMPLASTIC GROWTH OF LINEAR LEAF BLADE

A.Z. Alybaeva*, R.Y. Niyazova, A.T. Ivashchenko
National Nanotechnology Laboratory, Al-Farabi KazNU, Almaty, Kazakhstan
BINDING SITES OF miRNA WITH MYB GENES' mRNA IN B.TAURUS AND B.MUTUS

Barducov N.V., Sipko T.P., Glazko V.I.
Russian State Agrarian University – Moscow Timiryazev Agricultural Academy
APPLICATION OF TERMINAL HELITRON FRAGMENTS AS HIGH POLYMORPHIC MARKERS OF GENOME SCANNING IN UNGULATA

E.F. Baulin*1,2, S.A.Spirin3, M.A. Roytberg1,2,4
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2 Higher School of Economics, Moscow, Russia
3 Belozersky Institute of Moscow State University, Moscow, Russia
4 Moscow Institute of Physics and Technology, Moscow Region, Russia
ANALYSIS AND CLASSIFICATION OF NONSTANDARD RNA MOTIFS

A.G. Bogomolov1*, I.E. Jetybayev 1, N.L. Podkolodnyy1,2, N.B. Rubtsov1,3
1 Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
2 Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia
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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

P.S. Demenkov1,2*, V.A. Ivanisenko1
1 Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
2 Novosibirsk State University, Novosibirsk, Russia
ASSEMBLING GENOMES AND METAGENOMES USING CLUSTER ARCHITECTURE

P. Drozdova*, L. Mironova
Dpt. of Genetics and Biotechnology, St. Petersburg State University, St. Petersburg, Russia
PRIONIZATION OF THE Sfp1 PROTEIN IN YEAST DOES NOT MIMIC ITS INACTIVATION AT WHOLE TRANSCRIPTOME LEVEL
ERKENOV T.
Russian State Agrarian University – Moscow Timiryazev Agricultural Academy
APPLICATION OF MULTILOCUS GENOME SCANNING FOR IDENTIFICATION OF THE KARACHAY HORSE GENETIC STRUCTURE

I. L. Erokhin
National Biotechnological Company, LLC, Moscow, Russia
SINE-MODELING OF GENOME LOOP STEP

N.M. Gruzdeva¹, A.V. Nedoluzhko¹, O.A., Shulga³, E.B. Prokhortchouk², K.G. Skryabin¹.²
¹NRC Kurchatov Institute,
²Centre “Bioengineering” RAS
NOVEL microRNAs PREDICTION IN NON-MODEL ORGANISMS

E.V. Ignatieva*
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CONTROLLED VOCABULARIES AND INFORMATION TABLES FOR THE KNOWLEDGE BASE ON EPIGENETIC CONTROL OF HUMAN EMBRYONIC STEM CELLS

E.V. Ignatieva*, V.G. Levitsky, N.A. Kolchanov
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
FUNCTIONAL CHARACTERISTICS OF HUMAN GENES CONTAINING LOW LEVEL OF PROMOTER POLYMORPHISM REVEALED FROM THE 1000 GENOMES PROJECT DATASET

A.T. Ivaschenko*, O.A. Berillo, A.Y. Pyrkova, R.E. Niyazova
National Nanotechnology Laboratory, Al-Farabi KazNU, Almaty, Kazakhstan
FEATURES OF INTERACTIONS BETWEEN miR-1273 FAMILY AND mRNA OF TARGET GENES

A.M. Korotkova
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
FUNCTIONAL ANALYSIS OF THE PROMOTER REGION OF THE Xist GENE IN MOUSE (Mus musculus)

E.V. Kulakova¹*, L.O. Bryzgalov¹, Y.L. Orlov¹,²,³, G. Li², Y. Ruan³
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²Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
³Genome Institute of Singapore, Singapore
COMPUTER ANALYSIS OF CHROMOSOME CONTACTS REVEALED BY SEQUENCING
E.V. Kulakova\textsuperscript{1}, O.A. Podkolodnaya\textsuperscript{2}, O.L. Serov\textsuperscript{2}, Y.L. Orlov\textsuperscript{1,2*}
\textsuperscript{1}Novosibirsk State University, Novosibirsk, Russia
\textsuperscript{2}Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

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

V.G. Levitsky\textsuperscript{*}, V.V. Mironova
Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

THE PIPELINE FOR COMPOSITE REGULATORY ELEMENTS PREDICTION

Moskalev AA\textsuperscript{1,2,3}, Plyusnina EN\textsuperscript{1,2}, Peregudova DO\textsuperscript{1}, Shaposhnikov MV\textsuperscript{1,2}, Snezhkina A\textsuperscript{4}, Kudryavtseva AV\textsuperscript{4}, Baranova AM\textsuperscript{5}
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TRANSCRIPTOMICS ANALYSIS OF DROSOPHILA MELANOGASTER AGING

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Al-Farabi Kazakh National University, Almaty, Kazakhstan

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

E.A. Krutinina, G.G. Krutinin, S.G. Kamzolova, A.A. Osypov\textsuperscript{*}
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TRANSCRIPTION FACTORS AND ELECTROSTATIC AND OTHER PHYSICAL PROPERTIES OF THEIR BINDING SITES

D.O. Peregudova\textsuperscript{1*}, E.N. Plyusnina\textsuperscript{1,2}, M.V. Shaposhnikov\textsuperscript{1,2}, A.V. Kudryavtseva\textsuperscript{3}, A.V. Snezhkina\textsuperscript{3}, A.A. Moskalev\textsuperscript{1,2,4}
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\textsuperscript{2}Syktyvkar State University, Syktyvkar, Russia
\textsuperscript{3}Engelhardt Institute of Molecular Biology of RAS, Moscow, Russia
\textsuperscript{4}Moscow Institute of Physics and Technology (State University), Dolgoprudny, Russia
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, Pshenichny E.A. Shkurat T.P.
Southern Federal University, Rostov-on-Don, Russia
SCAN ELEMENTS IN THE NON-CODING DNA

E.A. Radchenko*, G.S. Tamazian, P.V. Dobrynin
Saint-Petersburg State University, Saint-Petersburg, Russia
REFERENCE ASSISTED CHROMOSOME ASSEMBLY OF 30 SACCHAROMYCES CEREVISIAE STRAINS FROM SACCHAROMYCES GENOME DATABASE

T.V. Astakhova¹, I.I. Tsitovich², V.V. Yakovlev¹,³, M.A. Roytberg¹,³,⁴*,
¹Institute of Mathematical Problems of Biology, RAS, Moscow Region, Russia
²Institute of Information Transmission Problems, RAS, Moscow, Russia
³Higher School of Economics, Moscow, Russia
⁴Moscow Institute of Physics and Technology, Moscow Region, Russia
INTRON LENGTHS AND PHASES: REGULARITIES AND DATABASE

I.S. Rusinov¹, A.S. Ershova²,³,⁴, A.S. Karyagina²,³,⁴, S.A. Spirin¹,²,⁵, A.V. Alexeevski¹,²,⁵
¹Lomonosov Moscow State University, Faculty of Bioengineering and Bioinformatics, Moscow 119992, Russia;
²Lomonosov Moscow State University, Belyozersky Institute of Physical and Chemical Biology, Moscow 119992, Russia;
³Gamaleya Institute of Epidemiology and Microbiology, Moscow 123098, Russia;
⁴Institute of Agricultural Biotechnology, the Russian Academy of Sciences, Moscow 127550, Russia;
⁵Scientific Research Institute for System Studies, the Russian Academy of Science (NIISI RAS), Moscow 117281, Russia;
RESTRICITION SITES AVOIDANCE IS TRACE OF LOST RESTRICTION MODIFICATION SYSTEMS

A.A. Ryasik*, E.A. Temlyakova, A.A. Sorokin
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BIOLOGICAL GRAPH DATA BASE AND ITS APPLICATIONS

N.S. Safronova¹*, Y.L. Orlov¹,²
¹Novosibirsk State University, Novosibirsk, Russia
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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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ELOE – A WEB-APPLICATION FOR ESTIMATION OF GENE TRANSLATION ELONGATION EFFICIENCY IN VARIOUS ORGANISMS

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SSRFace: ANIDENTIFICATION AND SEARCH TOOL FOR GENOMIC AND TRANSCRIPTOMIC SSR

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GRAPH ANALYSIS OF E.COLI TRANSCRIPTION REGULATION

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COMPUTER AND EXPERIMENTAL ANALYSIS OF MOLECULAR MECHANISMS OF GENE EXPRESSION REGULATION IN BRAIN TUMOR CELLS

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ANALYSIS OF THE DEGENERATE MOTIFS IN REGIONS OF BINDING SITES OF TRANSCRIPTION FACTORS ESSENTIAL FOR EMBRYONIC STEM CELLS MAINTENANCE
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THE mRNA FEATURES IMPORTANT FOR TRANSLATION INITIATION REVEALING USING RIBOSOME PROFILING DATA

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CONTROL OF THE MIRNA PATHWAYS BY THE SECONDARY STRUCTURE AND ITS ACCOUNT IN THE PREDICTION TOOLS

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L-MOLKERN SOFTWARE ALLOWING FOR POLARIZATION EFFECTS IN FREE ENERGY CALCULATION

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COMPUTER ANALYSIS OF EXPRESSION LEVEL OF ALLERGEN-CODING GENES OF PATHOGENIC MICROORGANISMS

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MOLECULAR DYNAMICS STRUCTURE MODELING OF IL-36 CYTOKINES

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SPECTRAL CHARACTERISTICS OF tryptophan IN WATER AND VIBRIO HARVEYI LUCIFERASE

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IMAGEJ ADDON FOR 2D ELECTROPHORESIS GEL ANALYSIS

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METHOD TO PREDICT THE PERCENTAGE OF CELL TYPES IN HUMAN BLOOD

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MOLECULAR MECHANISMS OF INTERACTION OF TUMOR NECROSIS FACTOR WITH TNF-BINDING ORTOPOXVIRAL PROTEINS CrmB

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NEW VERSIONS OF THE PDBSITE DATABASE AND PDBSITESCAN TOOL: PREDICTION OF FUNCTIONAL SITES IN THE PROTEIN 3D STRUCTURE

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BACKBONE ENCODINGS IN PROTEIN STABILITY PREDICTIONS

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SARP: AN ALGORITHM FOR ANNOTATION OF THE COMPOSITIONALLY BIASED REGIONS IN PROTEIN SEQUENCES

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ANALYSIS OF THE BINDING MODE OF ANTIVIRAL PEPTIDES TO THE FLAVIVIRUS ENVELOPE PROTEIN E BASED ON PROTEIN–PROTEIN DOCKING

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IDENTIFICATION OF POTENTIAL INHIBITOR OF PROTEIN KINASE D1 (PKD1) AND 2 (PKD2)

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RECONSTRUCTION OF ASSOCIATIVE GENE NETWORKS SPECIFIC TO TARGET BIOLOGICAL PROCESSES AND PHENOTYPIC TRAITS

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ENHANCING ANTICANCER ACTIVITY OF DOXORUBICIN BY MOLECULAR IODINE COMPLEXES WITH BIOACTIVE ORGANIC LIGANDS AND LITHIUM SALTS

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CONTACT-BASED APPROACH TO STRUCTURAL CLASSIFICATION OF PROTEIN-DNA COMPLEXES

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AN EXTENDED MODEL OF D. MELANOGASTER MACROCHAETE MORPHOGENESIS GENE NETWORK

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DYNAMIC INSTABILITIES OF MICROTBULES

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SOCIAL INTERACTIONS IN COMMUNITIES OF CONFORMISTS AND NON-CONFORMISTS: A CELLULAR AUTOMATON MODEL

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BIOUML: PLUGIN FOR POPULATION-BASED MODELING

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COMPLEX DYNAMICS IN SYSTEMS OF ALTERNATIVE MRNA SPLICING: A MATHEMATICAL MODEL

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INFERRING HYPOTHESES ON PROTEIN-PROTEIN INTERACTIONS DURING EXPERIMENTAL TREATMENT USING PROFILING OF PROTEINS AND PPI DATA FROM PUBLIC DOMAIN

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RECONSTRUCTION OF THE MOUSE BRAIN VASCULAR NET ACCORDING TO THE DATA OF HIGH-FIELD MRI-SCANNER

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COMMUNITY STRUCTURE OF WEB-GRAPHS OF ACADEMIC INSTITUTIONS

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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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SIBERNETIC: NOVEL APPROACH TO REALISTIC MODELING OF INVERTEBRATES BIOMECHANICS

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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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PARALLELIZATION OF ALGORITHM OF PREDICTION OF miRNA BINDING SITES IN mRNA ON THE CLUSTER COMPUTING PLATFORM

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DOTOLOG - DOT PLOT ANALYZATION TOOL

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

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METHODS OF THE INTELLECTUAL ANALYSIS OF DATA IN NATURAL SCIENCES AND ALTERNATIVE ANALYSIS

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INDIVIDUAL MODELLING OF HEMODYNAMIC PROCESSES IN CARDIOVASCULAR SYSTEM BASED ON PERIPHERAL ARTERIAL PULSATION

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UNSTEADY HEMODYNAMIC SIMULATION OF CEREBRAL ANEURYSMS STENTING

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THE COMPELLATION OF HUMAN GENES CONTROLLING FEEDING BEHAVIOR OR ASSOCIATED WITH BODY MASS INDEX AND ITS FUNCTIONAL AND GENOMIC CHARACTERISTICS

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IMPLICATIONS OF HOSTILE ENVIRONMENT AND SOCIAL INSTABILITY IN ADOLESCENT MICE

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AGING OF RAT RETINA: TRANSCRIPTOME STUDY

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COMPUTER ANALYSIS OF HUMAN GENE EXPRESSION DATA IN BRAIN USING MICROARRAYS

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ESTIMATION OF IMPACT OF ALPHA-CRYSTALLIN’S ALTERATIONS ON THE DEVELOPMENT OF AMD-LIKE RETINOPATHY IN OXYS RATS

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MELATONIN IN PREVENTION OF ALZHEIMER’S DISEASE-LIKE PATHOLOGY IN OXYS RATS

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VIRAL EXPRESSION ASSOCIATED WITH GASTROINTESTINAL ADENOCARCINOMAS IN TCGA HIGH-THROUGHPUT SEQUENCING DATA
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CAN OPIOID AND SUBSTANCE P SYSTEM INTERACTION ANTAGONIZE MORPHINE-INDUCED RESPIRATORY DEPRESSION?

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ACTIVATION OF HIPPOCAMPAL CELL PROLIFERATION AND DECREASE OF C-FOS EXPRESSION IN THE AMYGDALA UNDER POSITIVE FIGHTING EXPERIENCE IN MALE MICE

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

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STUDY OF GENES CAUSING ATYPICAL FAMILIAL MYCOBACTERIOSIS IN TOMSK TUBERCULOSIS PATIENTS

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CCR5 AND CXCR4 CORECEPTOR PROFILE IN RESISTANCE HIV EXPOSED BUT SERONEGATIVE INDIVIDUALS OF NIGERIAN ORIGIN

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POSSIBLE ASSOCIATION BETWEEN THE TRPV1 GENE RS222747 POLYMORPHISM AND PRIMARY OPEN ANGLE GLAUCOMA IN WESTERN SIBERIA PATIENTS

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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 SENESCENCE IN OXYS RATS_ RETINAL TRANSCRIPTOME AND CANDIDATE GENE ANALYSIS BY RNASEQ
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THE SNP-MED SYSTEM FOR PERSONAL MEDICINE_ ANALYZE THE EFFECT SNP TO THE FUNCTION OF GENES ASSOCIATED WITH DISEASES

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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 SUPRAMOLECULAR COMPLEXES IN THE PROCESSES OF NEURONAL SYNAPTIC PLASTICITY

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POLYMORPHISM RS1625895 GENE TP53 AND EFFECTIVENESS OF TREATMENT OF DLBCL