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| Time | **June 24 (Tuesday)** |
| 09:00 – 13:00 | **School SBB-2014.**  **Section “Computational analysis of next-gen sequencing data”** |
| 09:00-09:45 | ***Recommended to attend:***  **D. Liberles**  University of Wyoming, USA  **Lineage-specific processes of genome diversification**  **KEYNOTE TALK** |
| 10:00-11:00 | **Y. Ruan**  The Jackson Laboratory, USA  **Multi-dimensional gene regulation in cancer cells** |
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| 11:00-11:20 | **Coffee break** |
| 11:20-12:10 | **A. Morozov**  BioMaPS Institute for Quantitative Biology, USA  **Thermodynamics in biology: modeling gene regulation** |
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| 13:00-14:00 | **Lunch** |
| 14:00-14:35 | ***Recommended to attend:***  **A. Rzhetsky**  The University of Chicago, USA  **Machine science**  KEYNOTE TALK |
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| 16:00-16:20 | **Coffee break** |
|  | Attending BGRS sections |
| 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** |
| Time | **June 25 (Wednesday)** |
| 09:00 – 13:00 | **School SBB-2014.**  **Section “Evolutionary bioinformatics”** |
| 9:00-9:45 | ***Recommended to attend:***  **L. Kaderali**  University of Technology Dresden, Germany  **Systems biology of host-pathogen interactions**  (Small Hall) |
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| 9:50-10:30 | **C. Mitra**  University of Hyderabad, Hyderabad, India  **Monte Carlo methods for metabolic kinetics** |
| 11:00-11:20 | **Coffee break** |
| 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** |
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| 12:10-13:00 | **D. Liberles**  Department of Molecular Biology, University of Wyoming, Laramie, USA  **The lecture on sequence analysis pipelines to uncover lineage-specific evolution.** |
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| 17:00-18:00 | **School BB-2014. Practical training**  (ICG SB RAS: Lavrentyeva, 10)  **F.V.Kazantsev**  Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia |
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| Time | **June 26 (Thursday)** |
| 09:00 – 13:00 | **School SBB-2014.**  **Section “Gene networks modeling and supercomputing”** |
| 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** |
| 9:35-11:00 | **R. Hofestädt**  Bielefeld University, Germany  **Petri net modeling and simulation of metabolic pathways** |
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| 10:55-11:15 | **Coffee break** |
| 11:15-11:35 | ***Recommended to attend:***  **I. V. Oseledets**  Moscow, Russia  **Numerical methods for high-dimensional problems in biology**  **KEYNOTE TALK** |
| 12:15-12:50 | ***Recommended to attend:***  **A.V. Nedoluzhko** et al.  National Research Center “Kurchatov Institute”, Moscow, Russia  ***De novo* assembly of the mitochondrial genome of ~5000-year-old human from North Caucasus**  **KEYNOTE TALK** |
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| 13:00-14:00 | **Lunch** |
| 14:00-17:40 | **School SBB-2014.**  **Presentations by young scientists** |
| 14:00-14:20 | **А**. **Barlukova**, S. Honoré, F. Hubert, M. Petit  Aix-Marseille University, France  **Dynamic instabilities of microtubules** |
| 14:20-14:40 | **A.A. Igolkina,** M.G. Samsonova  Petersburg State Polytechnical University  **Method to predict thepercentage of cell types in human blood** |
| 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** |
| 15:00-15:20 | **T. Gamilov**  Moscow Institute of Physics and Technology, Dolgoprudnyy, Russia  **1D modelling of different time regimes of enhanced external counterpulsation** |
| 15:20-15:40 | **A**. **Gurkov**, E.M. Kondratyeva, D.S. Bedulina  Institute of Biology at Irkutsk State University, Irkutsk, Russia  **IMAGEJ addon for 2D electrophoresis gel analysis** |
| 15:55-16:15 | Coffee break |
| 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 | **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** |
| 16:40-17:00 | **L.A**. **Krasnobaeva**, L.V. Yakushevich  Siberian State Medical University, Tomsk, Russia  **Rotational dynamics of bases in the gene coding interferon alpha 17 (IFNA17)** |
| 17:00-17:20 | **E. Kulakova**  Novosibirsk State University, Russia  **Computer data analysis of genome sequencing by technology ChIP-seq and Hi-C** |
| 17:20-17:40 | **K. Korla**  School of Life Sciences, University of Hyderabad, India  **Kinetic simulation of mitochondrial shuttles** |
| Time | **June 27 (Friday)** |
| 09:00 – 13:00 | **School SBB-2014.**  **Presentations by young scientists** |
| 9:00-9:20 | **V.V. Lavrekha**, N.A. Omelyanchuk, V.V. Mironova  Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia  **Modeling of cell dynamics in the root apical meristem with dynamical grammar** |
| 9:20-9:40 | **S. Maltseva**, A.P. Chupakhin, А.А. Cherevko, A.K. Khe, E.U. Derevtsov, A.E. Akulov  Institute of Mathematics SB RAS, Novosibirsk, Russia  **Reconstrucrion of the mouse brain vasculature according to the data of high-field MRI scanner** |
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| 9:40-10:00 | **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** |
| 10:00-10:20 | V. Mironova, **D. Novikova**  Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia  **Auxin-induced changes of transcriptome in *Arabidopsis thaliana* l. roots.** |
| 10:20-10:40 | **I. Protsyuk**  UniPro (Новосибирск), Россия  **Shared bioinformatics databases within Unipro UGENE** |
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| 10:40-11:00 | **O**. **Perfilyeva**  ICG SB RAS, Novosibirsk, Russia  **Mathematical modeling of peptidoglycan precursor biosynthesis in the cytoplasm of Esherichia coli cell** |
| 11:00-11:20 | **Coffee break** |
| 11:20-11:40 | **I. Pinskyi**, A. Ivashchenko  Al-Farabi Kazakh National University, Almaty, Kazakhstan  **miRNAs binding to mRNAs of rice Myb genes** |
| 11:40-12:00 | **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** |
| 12:00-12:20 | **N**. **Safronova**, Y.L. Orlov  ICG SB RAS, Novosibirsk, Russia  **Computer analysis of human SNP containing sites by methods of text complexity estimations** |
| 12:20-12:40 | **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** |
| 14:00-17:00 | **School SBB-2014.**  **Presentations by young scientists.**  **Nomination of best presentations** |
| 14:00-14:20 | **V**. **Sokolov**, U.G. Matushkin  ICG SB RAS, Novosibirsk, Russia  **Analysis of bacteria and archaea genomes available in GenBank database by “Eloe” program** |
| 14:20-14:40 | **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** |
| 14:40-15:00 | **T.S**. **Troeglazova**, 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** |
| 15:00-15:20 | **V. Chernova,** A. Doroshkov, V. Mironova, N. Omelyanchuk  ICG SB RAS, Novosibirsk, Russia  **PIN-transporters in the root meristem of Arabidopsis thaliana l- image analysis of expression patterns** |
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| 18:30-19:00 | CLOSING CEREMONY  AWARD FOR THE BEST YOUNG SCIENTISTS REPORTS |