22, August Wednesday	
9:00–13:00	**Morning session "Image analysis and mathematical modeling in tomography"** *Chairpersons: Dr. N.V. Denisova*
9:00 – 9:30 *Invited talk*	**Methods of mathematical modeling in modern diagnostic nuclear medicine** <u>N.V. Denisova</u> Institute of Theoretical and Applied Mechanics, Novosibirsk
9:30 – 10:00 *Invited talk*	**Application of Monte Carlo simulations in nuclear medicine imaging** <u>J. Cal-Gonzales</u>, T. Beyer Medizinische Universität Wien, MUW
10:00 – 10:30 *Invited talk*	**An algorithm for tracking c. elegans body movement and muscular activity in Ca2+ dynamics video for tuning and validation of its locomotion simulation** <u>A.Yu. Palyanov</u>[1,2] [1]A.P. Ershov Institute of Informatics Systems SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
10:30 – 10:50	**Simulation and image reconstruction of the combined Siemens PET/CT and PET/MRI systems** <u>H. Kertesz</u> Medizinische Universität Wien, MUW
10:50 – 11:10	Coffee break
11:10 – 11:25	**Mathematical phantoms development for computer simulation of the patient examination procedure by a positron emission tomography method** <u>M. Ondar</u>[1,2], N. Denisova[1] [1] Institute of Theoretical and Applied Mechanics SB RAS, Novosibirsk, Russia [2] Novosibirsk State Technical University, Novosibirsk, Russia
11:25 – 11:40	**The performance improvement of the permutation test algorithm for GSEA** <u>M. Grishchenko</u>[1], A. Yakimenko[1, 2], M. Khairetdinov[1, 2], A. Lazareva[2] [1] 1Institute Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia [2] Novosibirsk State Technical University, Novosibirsk, Russia
11:40 – 11:55	**Inverse problems in tomography: an evolutionary approach** <u>V. Dedok</u> Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia
11:55 – 12:10	**An effective subgradient method for simultaneous restoration and segmentation of blurred images** <u>T. Serezhnikova</u> [1]Krasovsky Institute of Mathematics and Mechanics UB RAS [2]Ural Federal University, Ekaterinburg, Russia
12:10 – 12:25	**Investigation of stopping criterion for OSEM algorithm with application to nuclear medicine** <u>Li Jiyu</u>[1], N.V. Denisova[2], O. Krivorotko[1,3] [1]Novosibirsk State University, Novosibirsk, Russia [2] Khristianovich Institute of Theoretical and Applied Mechanics, Novosibirsk, Russia [3] Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia
12:25 – 12:40	**Single-molecular fluorescence spectroscopy in protein folding: a theoretical modeling of multi-color experiments** V. A. Andryushchenko[1,2], A.Yu. Palyanov[1,3], <u>S.F. Chekmarev</u>[1,2] [1] Novosibirsk State University, Novosibirsk, Russia [2]Institute of Thermophysics, SB RAS, Novosibirsk, Russia [3]Institute of Informatics Systems, SB RAS, Novosibirsk, Russia
12:40 – 12:55	**Intel Software Solutions for Bioinformatics and Life science** <u>Andrianova Olga</u> Director of Software business development in Russia/CEE **Gold Sponsor**
13:10 – 14:00	Poster session
14:00 – 15:00	Lunch
15:00 – 19:00	**Afternoon session "Inverse problems in biology, medicine and social processes"** *Chairperson: Prof. A.I. Ilyin, Dr. O.I. Krivorotko*

15:00 – 15:30 *Invited talk*	**High-performance computing and big data in epidemiology** S. Zhang[1], Yu. Wang[1], S. Kabanikhin[2], O. Krivorotko[2] [1]Tianjin University of Finance and Economics, Tianjin, China [2]Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia
15:30 – 15:50	**Supercomputer analysis of social, epidemiological and economic processes** O. Krivorotko[1,2] [1] Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia
15:50 – 16:10	**Chaos theory as a bioinformatics promissory instrument for a human organism systemic response in-depth study** B.G. Vainer[1, 2], A.V. Shepelin[2] [1] Rzhanov Institute of Semiconductor Physics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia
16:10 – 16:30	**The possibilities of a Universal computer model in the readiness assessment of the Russian regions resource to epidemics of especially dangerous infectious diseases** L. Nizolenko, A. Bachinsky State Research Center of Virology and Biotechnology Vector, Koltsovo, Russia
16:30 – 16:50	**Method of reconstruction of a sequence of non-ribosomal peptides from mass spectra with noise** E. Fomin Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
16:50– 17:10	Coffee break
17:10 – 17:30	**Inverse modeling of diffusion-reaction processes with image-type measurement data** A. Penenko[1,2], Z. Mukatova[1,2], S. Nikolaev[3], U. Zubairova[3] [1] Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia [3] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
17:30 – 17:45	**Mathematical models of p53–microRNA and their applications** S.D. Senotrusova[1,2], O.F. Voropaeva[1] [1] Institute of Computational Technologies SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia
17:45 – 18:00	**Investigation and numerical solving of a mathematical model of intracellular HIV dynamics: from ODE to PDE** D. Yermolenko[1,2], O. Krivorotko[1,2], S. Kabanikhin[1,2] [1] Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia
18:00 – 18:15	**The optimal control of stochastic differential equations arising in biology, economy and finance** E. Kondakova[1], O. Krivorotko[1,2], S. Kabanikhin[1,2] [1] Novosibirsk State University, Novosibirsk, Russia [2] Institute of Computational Mathematics and Mathematical Geophysics SB RAS, prospect Akademika Lavrentjeva 6, 630090 Novosibirsk, Russia
18:15 – 18:30	**Parameters sensitivity of pharmacokinetics model parameters** V. Lifenko[1], D. Voronov[2], [1]Novosibirsk State University, Novosibirsk, Russia [2] Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia
18:30 – 18:45	**Inverse problem for partial differential equations in social networks** T.Zvonareva[1], S. Kabanikhin[2], O.Krivorotko[2] [1]Novosibirsk State University [2]Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia
18:45 – 19:00	**Identifiability analysis of nonlinear dynamical system** Zh.Bektemessov[1*] [1]al-Farabi Kazakh National University, Almaty, Kazakhstan

23, August Thursday	
9:00 – 13:05	**Morning session "Big data in bioinformatics"** *Chairperson: Dr. E.N. Pavlovskiy, Dr. Yu.L. Orlov*

9:00 – 9:30 *Invited talk*	**Advanced methods in machine learning for bioinformatics** E.N. Pavlovskiy Novosibirsk State University
9:30 – 10:00 *Invited talk*	**Bayesian approach to big data processing: problems and perspectives** M.A. Marchenko Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia
10:00– 10:50	**Complex information system to study common energy metabolic deficiency under neurodegenerative diseases** A. Osypov[1 2], I. Yu. Popova[2] [1] Institute of Higher Nervous Activity and Neurophysiology RAS, Moscow, Russia [2] Institute of Theoretical and Experimental Biophysics RAS, Pushchino MR, Russia **DEPPDB v.3: a portal to study electrostatic and other physical properties of genome DNA and its elements** A. Osypov[1 2], G. Krutinin[3], E. Krutinina[3], P. Beskaravayny[3], S. Kamzolova[3] [1] Institute of Higher Nervous Activity and Neurophysiology RAS, Moscow, Russia [2] Institute of Theoretical and Experimental Biophysics RAS, Pushchino MR, Russia [3] Institute of Cell Biophysics RAS, Pushchino MR, Russia
10:50– 11:10	Coffee break
11:10 – 11:30	**Gene network analysis of complex diseases using GenCoNet** O. Zolotareva[1,2], A. Shoshi[1], R. Hofestädt[1], A. Maier[1], V. Ivanisenko[3],V. Dosenko[4], E. Bragina[5] [1]Bielefeld University, Bioinformatics / Medical Informatics Department, Bielefeld, Germany [2]Bielefeld University, International Research Group "Computational Methods for the Analysis of the Diversity and Dynamics of Genoms", Bielefeld, Germany [3]Institute of Cytology and Genetics, Siberian Branch, Russian Academy of Sciences, Novosibirsk, Russia [4]Bogomoletz Institute of Physiology, Kiev, Ukraine [5]Research Institute of Medical Genetics, Tomsk NRMC, Tomsk, Russia
11:30- 11:50	**Assessment of software for somatic single nucleotide variant identification using simulated whole-genome sequencing data of cancer** W. Kittichotirat[1*], P. Khongthon[1], K. Kusonmano[2], S. Cheevadhanarak[2] [1]Pilot Plant Development and Training Institute, King Mongkut's University of Technology Thonburi, Bangkok 10150, Thailand [2] School of Bioresources and Technology, King Mongkut's University of Technology Thonburi, Bangkok 10150, Thailand
11:50– 12:05	**The software and database for Vertebrate imperfect mtDNA repeats annotation.** V.A. Shamanskiy[1*], K.Yu. Popadin[1,2], K.V. Gunbin[1,3] [1] School of Life Science, Immanuel Kant Federal Baltic University, Kaliningrad, Russia. [2] Center for Integrative Genomics, University of Lausanne, Lausanne, Switzerland [3] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
12:05 – 12:20	**Deep bioinformatic expert system of analysis, modeling and interpretation of omics BigData of the human genome** A. Shlikht, N. Kramorenko Far Eastern Federal University
12:20 – 12:35	**ARGO_CEL: GPU based approach for potential composite elements discovery in large DNA datasets** O. Vishnevsky[1,2], A. Bocharnikov[1], N. Kolchanov[1,2] [1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia
12:35– 12:50	**Computer system for reconstructing and analyzing random structural models of protein-protein interaction networks** N.L. Podkolodnyy[1,2], D.A. Gavrilov[3], O.A. Podkolodnaya[1] [1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2] Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia [3] Novosibirsk State University, Novosibirsk, Russia
12:50– 13:05	**Developing FoldGO, the tools for multifactorial functional enrichment analysis** A.M. Mukhin[1,2*], D.S. Wiebe[1,2], I. Grosse[2,3], S.A. Lashin[1,2], V.V. Mironova[1,2] [1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia [3] Martin-Luther University, Halle-Wittenberg, Germany
13:05 – 14:00	Poster session
	Algorithm for solving the inverse problem of pharmacokinetics to determine the

	transition coefficients. A. Takuadina L.N. Gumilev Eurasian National University, Astana, Kazakhstan
	Mathematical modeling of medicinal preparations diffusion process in tissues of the person A. Nafikova Sterlitamak branch of the Bashkir state university, Sterlitamak, Russia
	Mathematical model of membrane potential formation at E. coli growth on nitrite N.A. Ree[1], Likhoshvai V.A.[1], T.M. Khlebodarova[1] [1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	Different effects of agroclimatic factors on time to emergence and time to flowering in nine soybean accessions K. Kozlov[1]*, L. Novikova[1, 2], I. Seferova[2], S. Nuzhdin[1,3] and M. Samsonova[1] [1] Peter the Great St.Petersburg Polytechnic University, St.Petersburg, Russia [2] Federal Research Center the N. I. Vavilov All-Russian Institute of Plant Genetic Resources, St.Petersburg, Russia [3] University of Southern California, Los Angeles, CA, USA
	A numerical algorithm of parameter identification in mathematical model of tuberculosis transmission with control programs S.I. Kabanikhin[1,2], O.I. Krivorotko[1,2], V.N. Kashtanova[2,*] [1] Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia
	Inverse and ill-posed problems for nonlinear PDE: applications to life and social sciences M. Shishlenin[1,2,3], D. Lukyanenko[4] [1] Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia [2] Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia [3] Novosibirsk State University, Novosibirsk, Russia [4] Moscow State University, Moscow, Russia
	Identifiability analysis of mathematical models of immunology and epidemiology V.A. Latyshenko[1], O.I. Krivorotko[1,2], S.I. Kabanikhin[1,2] [1] Novosibirsk State University, Novosibirsk, 630090, Russia [2] Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, 630090, Russia
	Principal component analysis for any type sequences (PCA-Seq) V. Efimov[1–4*], K. Efimov[5], V. Kovaleva[2] [1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2] Institute of Systematics and Ecology of Animals SB RAS, Novosibirsk, Russia [3] Novosibirsk State University, Novosibirsk, Russia [4] Tomsk State University, Tomsk, Russia [5] Moscow Institute of Physics and Technology (State University), Moscow, Russia
	Comparison of quality of automated gene network recon-struction using connectivity of random and functional net-works E. Tiys[1, 2*], P. Demenkov[1], V. Ivanisenko[1] [1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia
	Revealing the research institutes and their interactions: a case study of miRNA research A. Firsov[1], I. Titov[2] [1] Novosibirsk State University, Novosibirsk, Russia [2] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia
	FoldGO for functional annotation of transcriptome data to identify fold-change-specific GO categories Wiebe D.S.[1,2], Mukhin A.M.[1,2], Omelyanchuk N.A.[1,2], Mironova V.V.[1,2,*] [1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia
	Pseudo one-compartment models. Methods for assessing the peripheral compartment for them N. Asmanova, A.I. Ilin JSC "Scientific center for anti-infection drugs", Almaty, Kazakhstan
	SNP_TATA_Z-TESTER: unsupervised machine learning web-service to compare alternative sequences in front of a given transcription start in the affinity scale of tata-binding protein binding to promoters P. M. Ponomarenko[a], D. A. Rasskazov[b], V. V. Suslov[b], M. P. Ponomarenko[b,c,*] [a] University of La Verne, La Verne, CA 91750, USA

	[b] Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia [c] Novosibirsk State University, Novosibirsk, Russia
	Genome-scale modeling of carbon assimilation in Geobacillus icigianus M. Kulyashov[1], I. Akberdin[1,2,3], A. Rozanov[2], S. Peltek[2] [1] Novosibirsk National Research University, Novosibirsk, Russia [2] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [3] Biology Department and Viral Information Institute, San Diego State University, San Diego, USA
14:00– 15:00	Lunch
15:00– **19:00**	**Afternoon session "Mathematical modeling of Gene Networks"** *Chairpersons: Prof. V.P. Golubyatnikov, Dr. N.L. Podkolodnyy*
15:00 – 15:30 *Invited talk*	**The multiplex phase interlocker: a novel and robust molecular design synchronizing transcription and cell cycle oscillators** T.D.G.A. Mondeel[1], C. Linke[1], S. Tognetti[2], W. Liebermeister[3], M. Loog[4], H.V. Westerhoff[1], F. Posas[2], M. Barberis[1] [1] Swammerdam Institute for Life Sciences, University of Amsterdam, Amsterdam, The Netherlands [2] Departament de Ciències Experimentals i de la Salut, Universitat Pompeu Fabra, Barcelona, Spain [3] Institut für Biochemie, Charité - Universitätsmedizin Berlin, Berlin, Germany [4] Institute of Technology, University of Tartu, Tartu, Estonia
15:30 – 16:00 *Invited talk*	**Circadian rhythms: data analysis and mathematical modeling** N.L. Podkolodnyy[1,2*], N.N. Tverdohkleb[1,3], O.A. Podkolodnaya[1] [1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2] Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia [3] Novosibirsk State University, Novosibirsk, Russia
16:00 – 16:20	**Population-based mathematical modeling antihypertensive drugs effect using BioUML platform** I.N. Kiselev[1,2], V.I. Baranov[3], F.A. Kolpakov[1,2] [1] Institute of Computational Technologies, SB RAS, Novosibirsk [2] LLC «BIOSOFT.RU» Ltd., Novosibirsk [3] Institute of Physiology and Basic Medicine, Novosibirsk;
16:20 – 16:40	**Estimates from evolutionary algorithms theory applied to gene design** A. Eremeev[1,2], A. Spirov[1,3] [1] The Institute of Scientific Information for Social Sciences RAS, Moscow, Russia [2] Omsk Branch of Sobolev Institute of Mathematics SB RAS, Omsk, Russia [3] The I. M. Sechenov Institute of Evolutionary Physiology and Biochemistry RAS, St. Petersburg, Russia
16:50 – 17:10	Coffee break
17:10 – 17:30	**HEDGE: Highly accurate GPU-powered protein-protein docking pipeline** T. Ermak[1*], A. Shehovtsov[1], P. Yakovlev[1] [1] BIOCAD, Saint Petersburg, Russia
17:30 – 17:50	**Agent-based modelling of genetic deafness propagation under various sociodemographic conditions** S.A. Lashin[1,2*], Yu.G. Matushkin[1,2], A.A. Smirnova[1], G.P. Romanov[3,4], O.L. Posukh[1,2] [1] Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia [3] MK Ammosov North-Eastern Federal University, Yakutsk, Russia [4] Yakut Science Centre of Complex Medical Problems, Yakutsk, Russia
17:50– 18:30	**On existence of a piecewise smooth cycle in one asymmetric gene network model with piecewise linear equations** V. Golubyatnikov [1,2], L. Minushkina[2] [1] Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia **On cycles in models of asymmetric circular gene networks** V. Golubyatnikov [1,2], N. Kirillova [2] [1] Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia
18:30 – 18:50	**An inverse problem in modelling of a symmetric gene network regulated by negative feedbacks** V. Golubyatnikov [1,2], V. Gradov[2] [1] Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Novosibirsk, Russia

24, August Friday	
9:00–13:00	**Morning session "Analysis of dynamical systems."** *Chairpersons: Prof. Sergey Kabanikhin, N. Novikov*
9:00 – 9:30 *Invited talk*	**On the construction of the cerebral hemodynamics model based on clinical data** <u>A.A. Cherevko</u>[1,4], M.A. Shishlenin[2,3,4], A.K. Khe[1,4], E.E. Bord[4], V.V. Berestov[5], K.Y. Orlov[5], V.A. Panarin[5] [1]Lavrentyev Institute of Hydrodynamics of SB RAS (Novosibirsk), Russia [2]Sobolev Institute of Mathematics of SB RAS (Novosibirsk), Russia [3]Institute of Computational Mathematics and Mathematical Geophysics (Novosibirsk), Russia [4]Novosibirsk State University (Novosibirsk), Russia [5]Meshalkin national medical research center (Novosibirsk), Russia
9:30–9:50	**Spatial heterogeneity influences evolutionary scenarios in microbial communities explained by ecological stratification: a simulation study** <u>A.I. Klimenko</u>, Yu.G. Matushkin, S.A. Lashin Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia Novosibirsk State University, Novosibirsk, Russia
9:50–10:10	**The optimal feedbacks in the mathematical model of chemo-therapy for a nonmonotonic therapy function** <u>N. Novoselova</u>[1,2] [1]Krasovskii Institute of Mathematics and Mechanics, Ural Branch of the Russian Academy of Sciences, Yekaterinburg, Russia [2]Ural Federal University, Yekaterinburg, Russia
10:10 – 10:30	**Fighting celiac disease: improvement of pH-stability of cathepsin L by computational design** <u>A. Chugunov</u>[1,2], D. Nolde[2], V.F. Tereshchenkova[3], E.A. Dvoryakova[4], I.Yu. Filippova[3], E.N. Elpidina[4], R. Efremov[1,2] [1]National Research University Higher School of Economics, Moscow 101000, Russia [2]M.M. Shemyakin & Yu.A. Ovchinnikov Institute of Bioorganic Chemistry, Russian Academy of Sciences, Moscow 117997, Russia [3]Chemical Faculty and [4]A.N. Belozersky Institute of Physico-Chemical Biology of M.V. Lomonosov Moscow State University, Moscow 119234, Russia
10:30–10:50	**The uniqueness of the solution of the two-dimensional direct problem is the propagation of the action potential along the nerve fiber.** <u>A.J. Satybaev</u>[1*], G.S. Kurmanalieva[1] [1]Osh Technological University, Osh, Kyrgyzstan
10:50 – 11:10	Coffee break
11:10–11:25	**Creation of a modular model of metabolic processes in skeletal muscles during moderate physical load using BioUML platform** <u>I.N. Kiselev</u>[1,2], V.I. Baranov[3], F.A. Kolpakov[1,2] [1]Institute of Computational Technologies, SB RAS, Novosibirsk [2]LLC «BIOSOFT.RU» Ltd., Novosibirsk [3]Institute of Physiology and Basic Medicine, Novosibirsk
11:25 - 11:40	**Asymptotic stability of solutions in one model of disease** <u>M.A. Skvortsova</u>[1,2] [1]Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia [2]Novosibirsk State University, Novosibirsk, Russia
11:40 – 11:55	**The 2D coefficient inverse problem of the ultrasound waves propagation** <u>N. Novikov</u>[1,3*], M. Shishlenin[1,2,3] [1]Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia [2]Institute of Mathematics SB RAS, Novosibirsk, Russia [3]Novosibirsk State University, Novosibirsk, Russia
11:55 – 12:10	**Digital heart: personalized medicine and inverse problems** <u>A. Prikhodko</u>[3*], M. Shishlenin[1,2,3] [1]Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia [2]Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia [3]Novosibirsk State University, Novosibirsk, Russia
12:10 – 12:25	**Siberian supercomputer center as a service for bioinformatics research** <u>I. Chernykh</u>, B. Glinskiy, N. Kuchin, S. Lomakin Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, Russia
12:25 – 12:40	**Finding epistasis in high-throughput experimental data** L.A. Esteban[1], N.S. Bogatyreva[1,2,3], F.A. Kondrashov[4], <u>D.N. Ivankov</u>[3,4*] [1]Universitat Pompeu Fabra (UPF), 08003 Barcelona, Spain

	[2] Bioinformatics and Genomics Programme, Centre for Genomic Regulation (CRG), 88 Dr. Aiguader, 08003 Barcelona, Spain [3] Laboratory of Protein Physics, Institute of Protein Research of the Russian Academy of Sciences, 4 Institutskaya str., 142290, Pushchino, Moscow region, Russia [4] Institute of Science and Technology, Am Campus 1, 3400 Klosterneuburg, Austria
12:40 – 12:55	**High performance computing in astrophysics. The organic formation in protostellar disc.** I.M. Kulikov[1] [1]Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk, 630090, Russia
13:00– 14:00	Poster session
14:00– 15:00	Lunch