ST. PETERSBURG STATE POLYTECHNICAL UNIVERSITY

IOFFE PHYSICAL TECHNICAL INSTITUTE
OF THE RUSSIAN ACADEMY OF SCIENCES

SYSPATHO CONSORTIUM OF THE FP7 FRAMEWORK PROGRAM

SysPatho Workshop

“SYSTEMS BIOLOGY AND MEDICINE”

PROGRAM

St. Petersburg-Tsarskoe Selo, Russia

11 -14 September 2012

INTERNATIONAL PROGRAM COMMITTEE

Prof. Dr. Roland Eils Heidelberg University, Germany

Prof. Dr. Sergei Inge-Vechtomov St. Petersburg State University, Russia

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Russian Academy of Sciences, Russia

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SPONSOR ORGANIZATIONS

SysPatho Project – New Algorithms for Host Pathogen Systems Biology

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St. Petersburg State Polytechnical University

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SysPatho Workshop

“SYSTEMS BIOLOGY AND MEDICINE”

PROGRAM AT A GLANCE

The Conference sessions will be held in the “Prince Kochubey Mansion” – Management Training Centre, Radishcheva st. 4, Tsarskoe Selo - Pushkin

September 11, Tuesday

16:00	Registration
18:00	Opening Workshop
18:15	Keynote Lecture 1
19:00	Classical Music Concert
19:30	Welcome Party

September 12, Wednesday

08:45	Keynote Lecture 2
09:25 – 10:45	**Session I: Host-Pathogen Interactions 1**
10:45 – 11:05	Coffee break
11:05 – 12:15	**Funding Opportunities for Systems Biology**
12:15 – 13:15	Lunch
13:15 – 15:30	Sightseeing Tour to the Catherine Palace, Tsarskoe Selo.
15:30 – 16:50	**Session II: Bioinformatics and Systems Biology of High-Throughput Data**
16:50 – 17:10	Coffee break
17:10 – 18:30	**Session III: Computational and Experimental Systems Approaches**
18:30	Reception and Poster Session

September 13, Thursday

08:45	Keynote Lecture 3
09:25 – 10:45	**Session IV: Medical Systems Biology**
10:45 – 11:05	Coffee break
11:05 – 12:15	**Session IV (continued): Medical Systems Biology**
12:15 – 13:15	Lunch
13:15	St. Petersburg sightseeing bus tour
19:00	Conference dinner

September 14, Friday

08:45	Keynote Lecture 4
09:25 – 10:45	**Session V: Signalling and Cellular Regulation**
10:45 – 11:05	Coffee break
11:05 – 12:15	**Session V (continued): Signalling and Cellular Regulation**
12:15 – 13:15	Lunch
13:15 – 14:25	**Session VI: Host-Pathogen Interactions 2**
14:25	Keynote Lecture 5
15:10	**Discussion of Joint Projects**
15:40	Closing ceremony

September 11, Tuesday ……………………………………………………………**16:30 – 19:30**

	Registration	**16:00 – 18:00**
	Opening of Workshop	**18:00 – 18:15**
1	**Keynote Lecture 1: Mark Biggin** Lawrence Berkeley National Laboratory, CA, USA Modeling Animal Transcription Networks as Highly Connected Quantitative Continua	**18:15 – 19:00**
	Classical Music Concert	**19:00 – 19.30**

Welcome Party 19:30 – 21:00

September 12, Wednesday ……………………………...…Morning session 8:45 – 12:15

Keynote Lecture 2: Albert Goldbeter **08:45 – 09:25**

Unit of Theoretical Chronobiology, Faculty of Sciences
Université Libre de Bruxelles (ULB), Brussels, Belgium

Systems biology of cellular rhythms

Session I: Host-Pathogen Interactions 1

Chair: Vincent Lotteau

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1 **Irene Otero-Muras,** Joerg Stelling **09:25 – 09:45**

Department of Biosystems Science and Engineering, ETH Zürich, Switzerland

Model based analysis of interferon induced apoptosis

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2 **Vitor A.P. Martins dos Santos** **09:45 – 10:05**

Chair for Systems and Synthetic Biology, Wageningen University, The Netherlands

Reverse engineering infection-disease: towards a virtual patient

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3 **Alexei Romanyukha** **10:05 – 10:25**

Institute of Numerical Mathematics of the RAS, Russia

Homeostasis and adaptation. Towards a trade-offs model

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4 **S. Tapilina,** Oleg Demin Jr. **10:25 – 10:35**

Institute for System Biology SPb, Moscow, Russia

Optimisation of combined treatment (interferon, ribavirin, protease or polymerase inhibitors) for hepatitis C virus

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5 **Sergey Smirnov[1],** Neil Benson[2], Piet Van Der Graa[2], Victoria Flores[2], Ekaterina Goryacheva[1], Oleg Demin[1] **10:35 – 10:45**

[1] Institute for Systems Biology SPb, Moscow, Russia
[2] Pfizer Pharmacometrics, Global Clinical Pharmacology, Walton Oaks, UK

Understanding molecular mechanisms of HCV patients susceptibility to IFN therapy via systems pharmacology modeling

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Coffee break 10:45 – 11:05

Funding Opportunities for Systems Biology **11:05 – 12:15**

Lunch 12:15 – 13:15

Sightseeing Tour to the Catherine Palace, Tsarskoe Selo 13:15 – 15:30

September 12, Wednesday ……………………………………Afternoon session 15:30 – 17:10

Session II: Bioinformatics and Systems Biology of High-Throughput Data

Chair: Mark Biggin

1	**Benno Schwikowski** Institut Pasteur, Paris, France Robust transcriptomic data analysis across individuals	**15:30 – 15:50**
2	**Yuriy L. Orlov[1],** Guoliang Li[2], Kuljeet .S. Sandhu[2], Melissa J. Fullwood[2], Dmitriy A. Afonnikov[1], Chialin Wei[2], Oleg L. Serov[1], Nikolay A. Kolchanov[1], Yijun Ruan[2] [1] Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia [2] Genome Institute of Singapore, Singapore Computer analysis of 3D chromosome contacts mediated by RNA Pol II in human	**15:50 – 16:10**
3	**Miguel Andrade** Computational Biology and Data Mining group Max Delbrück Center for Molecular Medicine, Berlin, Germany Computational study of protein-protein networks	**16:10 – 16:20**
4	**Alexander Kanapin[1],** Anastasia Samsonova[2], Andrey Pisarev[3], Maria Samsonova[3] [1] Wellcome Trust Centre for Human Genetics, University of Oxford, UK [2] Department of Genetics, Harvard Medical School, Boston, USA [3] St. Petersburg State Polytechnical University, St. Petersburg, Russia High-throughput analysis of human transpositional landscape	**16:20 – 16:30**
5	**Alexander Kel** GeneXplain GMBH, Am Exer, Wolfenbüttel, Germany “Walking pathways” and how promoters can help to find new drugs	**16:30 – 16:50**

Coffee break 16:50 – 17:10

September 12, Wednesday ……………………………………...Evening session 17:10 – 18:30

Session III: Computational and Experimental Systems Approaches

Chair: Mikhail Gelfand

1	**N.V. Ivanisenko**[1, 2], E.L. Mishchenko[1], I.R. Akberdin[1], P. S. Demenkov[1], V.A. Likhoshvai[1, 2], M.G. Samsonova[3], D. Clausznitzer[4], L. Kaderali[4], N.A. Kolchanov[1, 2], V.A. Ivanisenko[1, 5] [1] The Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia [2] The Novosibirsk State University, Russia [3] St. Petersburg State Polytechnical University, Russia [4] Institute for Medical Informatics and Biometry, Medical Faculty Carl Gustav Carus, University of Technology Dresden, Germany [5] PB-soft LLC, Novosibirsk, Russia A stochastic model for suppression of subgenomic hepatitis C virus replication in Huh-7 cells	**17:10 – 17:20**
2	L.Mariani[1], E.Chiroli[1], L.Nezi[2], H.Muller[3], S.Piatti[4], A.Musacchio[5, 6], **A.Ciliberto[1]** [1] IFOM - The FIRC Institute of Molecular Oncology, Milan, Italy [2] Luigi Nezi, Department of Genomic Medicine, MD Anderson Cancer Center, Houston, USA [3] Instituto Italiano di Tecnologia, Center for Genomic Science of IIT@SEMM c/o IFOM-IEO-CAMPUS, Milan, Italy [4] Centre de Recherche de Biochimie macromoléculaire, Montpellier, France [5] MPI für molekulare Physiologie, Dortmund, Germany [6] Centre for medical biotechnology, Faculty of Biology, University of Duisburg-Essen, Germany Role of the Mad2 dimerization interface in supporting the Spindle Assembly Checkpoint independently from kinetochores	**17:20 – 17:30**
3	**Igor Goryanin** Computational Systems Biology, University of Edinburgh, Edinburgh, UK Microbial Fuel Cells	**17:30 – 17:50**
4	**Inna N. Lavrik[1, 2, 4, 5]**, Kolja Schleich[1, 2], Uwe Warnken[3], Nicolai Fricker[1, 2], Martina Schnölzer[3], Peter H. Krammer[1] [1] Division of Immunogenetics, German Cancer Research Center (DKFZ), Heidelberg, Germany [2] BIOQUANT, Heidelberg, Germany [3] Functional Proteome Analysis, German Cancer Research Center (DKFZ), Heidelberg, Germany [4] Division of Theoretical Bioinformatics, German Cancer Research Center (DKFZ), Heidelberg, Germany [5] Department of Translational Inflammation Research, Institute of Experimental Internal Medicine, Otto von Guericke University, Magdeburg, Germany Towards understanding of apoptosis regulation by systems biology	**17:50 – 18:10**
5	**V.G. Levitsky[1],** D.Y. Oshchepkov[1], G.V. Vasiliev[1], N.I. Ershov[1], T.I. Merkulova[1], I.V. Kulakovskiy[2, 3], V.J. Makeev[2, 3] [1] Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia [2] Engelhardt Institute of Molecular Biology of the RAS, Moscow, Russia [3] Vavilov Institute of General Genetics of the RAS, Moscow, Russia *In silico* verification of transcription factor binding sites in ChiP-Seq data	**18:10 – 18:20**

6	**Alvaro Köhn-Luque** Department for Innovative Methods of Computing, Technishe Universität Dresden, Germany Modelling Vascular Morphogenesis	**18:20 – 18:30**

Reception and Poster session 18:30

September 13, Thursday ………………………………………Morning session 8:45 – 12:15

Keynote Lecture 3: Nikolay Kolchanov

Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia
Novosibirsk State University, Russia

Human brain origin and the evolution of regulatory and coding regions of protein-coding genes expressed in brain

08:45 – 09:25

Session IV: Medical Systems Biology

Chairs: Niels Grabe and Igor Goryanin

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1 **Matthias Machacek**

Novartis Pharma AG, Switzerland

From targets to human: Engineering of biotherapeutics

09:25 – 09:45

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2 **Oleg Demin**

Institute for Systems Biology SPb, Moscow, Russia

Application of systems pharmacology modeling in drug development

09:45 – 10:05

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3 **V. Sokolov**[1], O. Demin Jr.[1], S. Smirnov[1], L. Cucurull-Sanchez[2], C. Pichardo-Almarza[2], V. Flores[2], N. Benson[2], O. Demin[1]

[1] Institute for System Biology, Moscow, Russia
[2] Pfizer Global R&D, Sandwich, UK

PK properties optimization for transglutaminase-2 inhibitor as potential drug for celiac disease treatment

10:05 – 10:15

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4 **Michal Or-Guil**

Department of Biology, Humboldt University, Berlin, Germany
Research Center ImmunoSciences, Charité, Berlin, Germany

Exploring ensemble properties of serum antibody binding: Mathematical modeling and data analysis of antibody reactivity data

10:15 – 10:25

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5 **O. Demin Jr.**[1], S. Smirnov[1], V. Sokolov[1], L. Cucurull-Sanchez[2], C. Pichardo-Almarza[2], V. Flores[2], N. Benson[2], O. Demin[1]

[1] Institute for System Biology, Moscow, Russia
[2] Pfizer Global R&D, Sandwich, UK

Modeling of celiac disease immune response and therapeutic effect of potential drugs

10:25 – 10:35

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6 K. Peskov, **Yuri Kosinsky**

Modeling & Simulation, Novartis Pharma LLC, Moscow, Russia

Mechanistic modeling approach relating human gut microbial community to physiologically-relevant biomarkers

10:35 – 10:45

Coffee break 10:45 – 11:05

7	**Lodewyk F. A. Wessels** Bioinformatics and Statistics, The Netherlands Cancer Institute, Amsterdam, The Netherlands Complex molecular interactions as determinants of disease outcome and therapy response	**11:05 – 11:25**
8	**Niels Grabe** National Center for Tumor Diseases, University Hospital Heidelberg, Germany Novel insights into epidermal tissue repair using 3D tissue cultures	**11:25 – 11:35**
9	**Ingmar Glauche** Institute for Medical Informatics and Biometry (IMB), Faculty of Medicine Carl Gustav Carus, Dresden University of Technology, Germany Therapy of chronic myeloid leukemia: simulation studies of different treatment combinations and patient-specific risk estimation	**11:35 – 11:55**
10	**Janine Roy,** Christof Winter, Zerrin Isik, Michael Schroeder Biotechnology Center, Dresden University of Technology, Germany Google goes cancer: improving outcome for cancer patients by network-based ranking of marker genes	**11:55 – 12:05**
11	**Florian Markowetz** Cancer Research UK, Cambridge Research Institute, Li Ka Shing Centre, Cambridge, UK Dissecting cancer heterogeneity	**12:05 – 12:15**
	Lunch 12:15 – 13:15	
	St. Petersburg sightseeing bus tour 13:15	
	Conference dinner 19:00	

September 14, Friday ……………………………………………………Morning session 8:45 – 12:15

Keynote Lecture 4: Mikhail Gelfand

A. A. Kharkevich Institute for Information Transmission Problems of the RAS, Moscow, Russia **08:45 – 09:25**

Evolution of regulatory interactions in bacteria

Session V: Signaling and Cellular Regulation

Chairs: Roland Eils and Nikolay Kolchanov

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1 **Alexander Hoffmann** **09:25 – 09:55**

UC San Diego, San Diego Systems Biology Center, USA

Combinatorial and dynamic control logic within pathogen-responsive gene regulatory networks

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2 **Simon B. Eickhoff** **09:55 – 10:15**

Cognitive Neuroscience Group, Department of Clinical Neuroscience and Medical Psychology, Heinrich-Heine University, Düsseldorf, Germany
Brain Network Modeling Group, Institute for Neuroscience and Medicine (INM-1), Research Center Jülich, Germany

Systems biology approaches to understanding network functions of the human brain

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3 **L.V. Beloussov** **10:15 – 10:35**

Faculty of Biology, Lomonosov Moscow State University, Russia

Formalizing and exploring top-down causation in morphogenesis and cell differentiation

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4 **Alexander Samsonov [1],** M. A. Duk [2], M.G. Samsonova [2] **10:35 – 10:45**

[1] The A.F. Ioffe Physical-Technical Institute of the RAS, St. Petersburg, Russia
[2] State Polytechnical University, Russia

The microRNA determine the early stage dynamics of the regulation network

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Coffee break 10:45 – 11:05

8	**D.Y. Oshchepkov[1],** E.A. Oshchepkova[1], E.V. Kashina[1], E.V. Antontseva[1], D.P. Furman[1, 2], V.A. Mordvinov[1] [1] Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia [2] Novosibirsk State University, Russia Dioxin in regulation of genes involved in cytokinine synthesis by macrophages: a possible pathway underlying dioxin immunotoxicity and cancer	**11:05 – 11:25**
9	**Nils Bluethgen** Humboldt University zu Berlin, Institute for Theoretical Biology, Berlin, Germany Using data-driven models of feedback regulation in EGFR signal transduction to predict optimal targeted therapy in colon cancer	**11:25 – 11:45**
10	**Valerii Sukhorukov [1, 2]**, Daniel Dikov [3, 4], Andreas S. Reichert [3, 4], Michael Meyer-Hermann [1,5] [1] Helmholtz Centre for Infection Research, Braunschweig, Germany [2] Frankfurt Institute for Advanced Studies, Frankfurt am Main, Germany [3] Frankfurt Institute for Molecular Life Sciences, Frankfurt am Main, Germany [4] Goethe University of Frankfurt am Main, Germany [5] Technical University Braunschweig, Germany Architecture and dynamics of the mitochondrial reticulum in healthy systems and in age-related disorders	**11:45 – 11:55**
11	**Ovidiu Radulescu** DIMNP, Université de Montpellier 2, Montpellier, France Specificity and flexibility of RAS-ERK signalling by slow and fast loops	**11:55 – 12:05**
12	**Ilka Maria Axmann** Institute for Theoretical Biology (ITB), Charité-Universitätsmedizin, Berlin, Germany Designing biocomputing devices based on RNA-RNA interactions	**12:05 – 12:15**
	Lunch 12:15 – 13:15	

September 14, Friday ………………….………………………………..Afternoon session 13:15 – 16:00

Session VI: Host-Pathogen Interactions 2

Chair: Alexander Hoffmann

6	Ulfert Rand[1], Melanie Rinas[2], Johannes Schwerk[1], Mario Köster[1], Thomas Höfer[2], **Hansjörg Hauser[1]** [1] Department of Gene Regulation and Differentiation, Helmholtz Centre for Infection Research, Braunschweig, Germany [2] Division of Theoretical Systems Biology, German Cancer Research Center (DKFZ) and BioQuant Center, Heidelberg, Germany Type-I Interferon response is controlled by multi-layered stochasticity	**13:15 – 13:35**
7	**Lars Kaderali** Institute for Medical Informatics and Biometry (IMB), Dresden University of Technology, Germany SysPatho: Systems biology of Host-Pathogen Interactions	**13:35 – 13:55**
8	**TBA**	**13:55 – 14:05**
9	**Karl Rohr** University of Heidelberg, BIOQUANT, IPMB, German Cancer Research Center (DKFZ) Department of Bioinformatics and Functional Genomics, Biomedical Computer Vision Group (BMCV), Heidelberg, Germany Tracking and Registration for Live Cell Image Analysis	**14:05 – 14:25**
	Keynote Lecture 5: Luis Serrano Center for Genomic Regulation, Barcelona, Spain A quantitative systems biology study on a model bacterium	**14:25 – 15:10**
	Discussion of Joint Projects Chair: Roland Eils	**15:10 – 15:40**
	Closing ceremony	**15:40**

POSTER SESSION

September 12, Wednesday …………………………………………………........................... **18:30**

P1. I.R.Akberdin [1], F.V.Kazantsev[1], N.A.Ree [1], V.S.Timonov[3, 4], E.A.Oshchepkova [1], A.V.Ratushny[5], T.M.Khlebodarova[1], S.I.Fadeev [2, 3], N.A. Kolchanov[1, 3], V.A.Likhoshvai [1, 3]

[1] Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia
[2] Sobolev Institute of Mathematics, SB RAS, Novosibirsk, Russia
[3] Novosibirsk State University, Russia
[4] Siberian State University of Telecommunications and Information Sciences, Novosibirsk, Russia
[5] Institute for Systems Biology, Seattle, USA

Modeling and analysis of dynamics of the gene networks: automatic generation and storage in a new database

P2. J.Arens[1,2], T.Mazel, A.Biesemann and **L.Dehmelt**[1,2]

[1] Fachbereich Chemische Biologie, Dortmund University of Technology, Germany
[2] Department of Systemic Cell Biology, Max Planck Institute of Molekular Physiology, Dortmund, Germany

Comprehensive analysis and computational modeling of microtubule regulation in neuromorphogenesis

P3. I.I. Artamonova[1,2], A. Mushegian[3]

[1]Vavilov Institute of General Genetics RAS, Moscow, Russia
[2]Lomonosov Moscow State University, Faculty of Bioengineering and Bioinformatics, Moscow, Russia
[3]Stowers Institute for Medical Research, Kansas City Missouri, USA

Bacterial genes in eukaryotic genomes: horizontal gene transfer or sample contamination? Lessons from the *Nematostella vectensis* genome

P4. J.Bausch, A.M. Henney

Virtual Liver Network, University Heidelberg, Germany

The Virtual Liver Network – an overview

P5. S.Depner, L.Velten, R.Merkle, A.Mathur, F.Matthaeus, U.Klingmüller
Group Systems Biology of Signal Transduction, German Cancer Research Center (DKFZ), Heidelberg, Germany

Systems Biology of Lung Cancer – Linking Dynamic Properties of Signaling Networks to Migratory Behavior of Lung Carcinoma Cells in Monolayer Culture

P6. A.S.Glotov_[1, 2], O.S.Glotov [1, 2], E.S.Vashukova [1, 2], E.U.Marochkina [2], I.V.Tarkovskaya [2], I.A.Makchrova [2], I.V. Pugacheva [2], R.V.Kurilov[2], M.V.Aseev [1, 2], T.E.Ivashchenko [1, 2], V.S.Baranov [1]

[1] Laboratory of prenatal diagnostic, The D.O. Ott Research Institute of Obstetrics and Gynecology, Saint-Petersburg, Russia
[2] Genetic Laboratory, Ltd BioGlot, Saint-Petersburg, Russia

Genetic based method for discrimination of lipoproteins level in citizens of North-West region of Russia

P7. I. A. Gula, A.M. Samsonov

The A.F. Ioffe Physical-Technical Institute of the RAS, St. Petersburg, Russia

Model of gap gene expression in *Drosophila* embryo based on telegraph equation

P8. V.V. Gursky[1], M.G. Samsonova[2], J.Reinitz[3]

[1] The A.F. Ioffe Physical-Technical Institute of the RAS, St. Petersburg, Russia
[2] St. Petersburg State Polytechnical University, St. Petersburg, Russia
[3] University of Chicago, Chicago, U.S.A.

Method for derivation of connectionist gene circuit equations from a sequence-level theory of transcriptional control

P9. S. Hashemikhabir, **T.Can**

Department of Computer Engineering, Middle East Technical University, Ankara, Turkey

Integration of protein-protein interactions and RNAI screens for reconstruction of signaling networks

P10. R. Hassanpour, **O.Gazi**

Cankaya University, Ankara – Turkey

Automatic Segmentation of Liver from Computed Tomography Examinations

P11. Z.Isik [1], J.Roy [1], C.Winter [1], R.Cetin-Atalay [2], V.Atalay [3], and M.Schroeder [1]

[1] Biotechnology Center, Technische Universität Dresden, Dresden, Germany
[2] Department of Molecular Biology and Genetics, Bilkent University, Ankara, Turkey
[3] Department of Computer Engineering, Middle East Technical University, Ankara, Turkey

Assessment of network data on outcome prediction of cancer patients

P12. T.V. Ivanisenko[1, 2], P.S. Demenkov[1, 2], **V.A. Ivanisenko**[1, 2]

[1] Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia
[2] PBSoft LLC, Novosibirsk, Russia

Reconstruction of the associative genetic networks based on integration of automated text-mining methods and protein-ligand interactions prediction

P13. V.A. Ivanisenko[1, 2], P.S. Demenkov [1, 2], T.V. Ivanisenko [1, 2]

[1] Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia
[2] PBSoft LLC, Novosibirsk, Russia

Associative network discovery system (ANDSYSTEM): automated literature mining tool for extracting relationships between diseases, pathways, proteins, genes, micrornas and metabolites

P14. K.N. Kozlov[1], A.M. Samsonov[2], M.G. Samsonova[1]

[1] St. Petersburg State Polytechnical University, Russia
[2] The A.F. Ioffe Physical-Technical Institute of the RAS, St. Petersburg, Russia

Improved differential evolution entirely parallel method

P15. K. Kozlov, S.Surkova, E.Myasnikova, M. Samsonova

St. Petersburg State Polytechnical University, Russia

Modeling of gap gene expression in Drosophila Kruppel mutants

P16. N. Levtov[1], S. S. Amberkar[2], L.Kaderali[2], **Z.Volkovich**[1]

[1] Department of Software Engineering, Ort Braude College, Karmiel, Israel
[2] University of Heidelber, Bioquant, Heidelberg, Germany

Detecting Non-Uniform Clusters in Large Scale Interaction Graphs

P17. E.M. Myasnikova
St. Petersburg State Polytechnical University, Russia

Identifiability analysis and predictive power of the gene circuit model

P18. A S. Pisarev

St. Petersburg State Polytechnical University, Russia

Heuristic optimization method for inverse problem solving

P19. S.A. Rukolaine, A.M. Samsonov

The A.F. Ioffe Physical-Technical Institute of the RAS, St. Petersburg, Russia

Different models of diffusion, related to the equation of the Jeffreys type

P20. T.E. Sannikova [1], V.N. Anisimov[2]

[1]Institute of Numerical Mathematics RAS, Moscow, Russia
[2]Department of Carcinogenesis and Oncogerontology, NN Petrov Research Institute of Oncology, St.Petersburg, Russia

Mathematical modeling of metformin influence on oncogenesis in SHR mice

P21. D.S. Simushkin, I.N. Volodin

Kazan Federal University, Russia

FDR is the d-risk

P22. S.Surkova[1], E.Golubkova[2], Manu[3], L.Panok[3], L.Mamon[2], J.Reinitz[3], M.Samsonova[1]

[1] St. Petersburg State Polytechnical University, Russia
[2] St. Petersburg State University, Russia
[3] The University of Chicago, Chicago, USA

Quantitative characterization of the segmentation gene expression in Drosophila gap mutants