

**MINISTRY OF EDUCATION AND SCIENCE OF
THE RUSSIAN FEDERATION**

**PETER THE GREAT ST.PETERSBURG
POLYTECHNIC UNIVERSITY**

The St.Petersburg International Symposium

**«SYSTEMS BIOLOGY AND BIOINFORMATICS»
(SBBI'2016)**

PROGRAMME



**St. Petersburg
June, 30 - July, 2, 2016**

ORGANIZING COMMITTEE

- **Prof. Maria Samsonova**, Peter the Great St-Petersburg Polytechnic University, Russia (*co-chair*)
- **Prof. Dmitrij Frishman**, Peter the Great St-Petersburg Polytechnic University, Russia and Technical University of Munich, Germany (*co-chair*)
- **Prof. Alexander Samsonov**, the Ioffe Physical Technical Institute of The Russian Academy of Sciences, Russia
- **Prof. Sergei Nuzhdin**, University of Southern California, USA

HOST SUPPORTER



PROGRAM AT A GLANCE

The Symposium will be held in the Research and Development building - Main Conference Hall; Peter the Great St.Petersburg Polytechnic University, Polytechnicheskaya st. 29AF, St.Petersburg

June 30, Thursday

08:00 Registration
09:00 **Opening of Symposium**
09:15 Keynote Lecture 1
09:55 Keynote Lecture 2
11:00 Coffee break
11:20 **Session I: Medical systems biology**
13:00 Lunch
14:00 Keynote Lecture 3
14:40 Keynote Lecture 4
15:50 Coffee break
16:10 **Session II: Signalling and cellular regulation & Evolutionary bioinformatics**
18:00 **Welcome party & Sightseeing tour**

July 1, Friday

08:30 Registration
09:00 Keynote Lecture 5
09:40 Keynote Lecture 6
10:40 Coffee break
11:00 **Session III: New methods and algorithms & Signalling and cellular regulation**
12:40 Lunch
14:00 **POSTER SESSION**
16:00 Keynote Lecture 7
16:40 Keynote Lecture 8
19:00 **Symposium dinner**

July 2, Saturday

09:00 Keynote Lecture 9
09:40 **Session IV: Protein structure & Pattern Formation**
10:40 **Closing ceremony**
11:00 **Pushkin and Peterhof bus tour**

June 30, Thursday

08.00 - 09.00	Registration	
	9.00 - 13.00	Morning session
9.00 – 9.15	Opening of Symposium	
9.15 - 9.55	Keynote Lecture 1: Luis Serrano	Whole cell model of a genome reduced bacteria, is it possible?
9.55 – 10.35	Keynote Lecture 2: : Mikhail Gelfand	Spatial, epigenomic, and functional organisation of chromatin
10.35 – 11.00	Igor Zhulin	Establishing the precise evolutionary history of a gene improves prediction of disease-causing missense mutations
11.00 – 11.20	Coffee break	
<i>Session I: Medical systems biology</i>		
11.20 – 11.40	A. Kolodkin, A. Ignatenko, B. Peters, M. Barberis, A. Skupin, R. Balling and Hans V. Westerhoff	The dynamics of reactive oxygen species management: How design principles studies may help to design personalised therapy
11.40 - 12.00	E. Barillot, L. Calzone, M. Kondratova, I. Kuperstein, L. Martignetti and A. Montagud	Exploiting synthetic interactions and signaling
12.00 – 12.20	A.V. Kajava	Predicting risk of amyloidosis by reading proteomes
12.20 – 12.40	D. Vuzman, N.Y. Frank, N. Stitzel, S. Chopra, J. Krier, E. Krieg, S.R. Sunyaev and R.L. Maas	Gene discovery via diagnostics of mendelian diseases
12.40 – 13.00	I. Kuperstein, M. Kondratova, C. Russo, E. Bonnet, E. Viara, HA. Nguyen, D. Cohen, L. Calzone, L. Grieco,	Atlas of cancer signaling network and navicell: systems biology resources for studying cancer

	E. Barillot and A. Zinovyev	
13.00 – 14.00		Lunch
	14.00 - 18.00	Afternoon session
14.00 - 14.40	Keynote Lecture 3: Nicolaus Rajewsky	Regulatory RNAs
14.40 – 15.20	Keynote Lecture 4: Christine Vogel	The Ups and Downs of Protein Expression Regulation
15.20 – 15.50	Alexander Kel	Modeling of walking pathways in stem cells
15.50 – 16.10		Coffee break
<i>Session II: Signalling and cellular regulation & Evolutionary bioinformatics</i>		
16.10 – 16.30	H. Binder	Function Shapes Content: Gene Signatures and their Impact for Molecular Mechanisms of Cancer
16.30 - 16.50	V.V. Gursky, K.N. Kozlov, A.V. Dmitrenko, S.V. Nuzhdin, M.G. Samsonova	Sequence-based modeling of the Drosophila gap gene network: thermodynamic approach, evolutionary insights, and methods for generalization
16.50 – 17.10	V. Katanaev	Systems biology approaches to G protein-coupled receptor signaling
17.10 – 17.30	Y. Kalaidzidis, R. Villaseñor and M. Zerial	Cell as a computer with mixed analogue-digital architecture
17.30 – 17.50	G. Karev	Principle of minimal information gain in models of prebiological evolution
	18.00	Welcome party & Sightseeing tour

July 1, Friday

08.30 - 09.00		Registration
	9.00 - 13.00	Morning session
9.00 - 9.40	Keynote Lecture 5: Limsoon Wong	Enabling more sophisticated proteomic profile analysis
9.40 - 10.20	Keynote Lecture 6: Werner Mewes	Phenotypes and genotypes from guilt by association to the arrest of the culprit
10.20 - 10.40	A. Samsonova, A. Rana, A. Kanapin, S. Knight and A. Schuh	Towards the development of a genome stability metric for evaluation of cancer genome sequencing data
10.40 - 11.00		Coffee break
<i>Session III: New methods and algorithms & Signalling and cellular regulation</i>		
11.00 - 11.20	E. Korotkov and V. Pugacheva	New mathematical approach for search of multiple alignments of nucleotide and amino acid sequences
11.20 - 11.40	G. Demidov, O. Drechsel, S. Ossowski	ClinCNV: robust statistical method for CNA-detection in wholeexome
11.40 - 12.10	M. Samborskaya, E. Khrameeva and M. Gelfand	Interplay between contact frequency of chromosome regions and their expression levels in drosophila melanogaster and homo sapiens
12.00 - 12.20	Sergey Rukolaine, Igor Gula, Alexander Samsonov	Models of conventional diffusive mass transfer in biological systems
12.20 - 12.40	R. Elkon, G. Korkmaz, R. Lopes, A.P. Ugalde, E. Nevedomskaya, R. Han, K. Myacheva, W. Zwart and R. Agami	Functional genetic screens for enhancer elements in the human genome using CRISPR- CAS9
12.40 - 14.00		Lunch
	14.00 - 18.00	Afternoon session

14.00 - 16.00	<i>Poster session</i>	
16.00 – 16.40	Keynote Lecture 7: Mickey Kosloff	Deciphering and re-designing interaction specificity among signaling proteins
16.40 - 17.20	Keynote Lecture 8: Georgii Bazykin	Changing preferences: deformation of single position amino acid fitness landscapes and evolution of proteins
19.00		Symposium dinner

July 2. Saturday

9.00 - 11.15		Morning session
9.00 – 9.40	Keynote Lectute 9 : Mark Borodovsky	Machine Learning and Gene Finding: A Review of Computational Problems and Solutions for 50,000 Genomes
<i>Session IV: Protein structure & Pattern Formation</i>		
9.40 - 10.00	A.V. Spirov, E.M. Myasnikova, D.M. Holloway	Sequential construction of a model for modular gene expression control, applied to the spatial patterning of the Drosophila gene Hunchback
10.00 – 10.20	D. Suplatov, K. Kopylov, A. Mironov, and V. Švedas	Statistical analysis of linear trends in protein motion to study induced conformational changes in protein structures
10.20 – 10.40	A. Afanasyeva, M. Petukhov and S. Izmailov	Aquabridge – a novel approach for molecular modelling of structural water in protein active sites
10.40– 11.00	Closing ceremony	
	11.00	Pushkin and Peterhof bus tour

POSTER SESSION

July 1, Friday 14.00 — 16.00

P1. A.V.Gorbunova, I.V.Evsyukov, M.V.Rayko, S.J.O'Brien, O.V.Bajenova

Theodosius Dobzhansky Center for Genome Bioinformatics at St. Petersburg State University, St. Petersburg, Russia

Identification of signal pathways involved in the response to carcinoembryonic antigen in colorectal cancer cells

P2. A.A. Lagunin^{1,2}, S.M. Ivanov^{1,2}, A.V. Rudik²

¹ Pirogov Russian National Research Medical University, Russia

² Institute of Biomedical Chemistry, Russia

In silico prediction of drug-induced changes of gene expression based on structural formulae of drugs

P3. A.A. Anashkina¹, E.N. Kuznetsov², N.G. Esipova¹, V.G. Tumanyan¹

¹ V. A. Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Russia

² V. A. Trapeznikov Institute of Control Sciences, Russian Academy of Sciences, Russia

Overall pattern of interatomic interactions in the structures of protein-dna complexes

P4. S.I. Kabanikhin^{1,2}, D.A. Voronov^{1,2}, **A.Yu.Belonog**², O.I. Krivorotko^{1,2}

¹ Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Russia

² Novosibirsk State University, Russia

Numerical solution of inverse problem for linear pharmacokinetic models

P5. A.S. Pisarev¹, I.A. Pisarev

¹ Peter the Great Saint-Petersburg Polytechnic University, Russia

² Saint Petersburg Electrotechnical University "LETI", Russia

Method and tool for the automated analysis of the hcv trajectories in living cells

P6. A.A Makashov, A.P. Kozlov

The Biomedical Center, Saint-Petersburg, Russia and Peter the Great St.Petersburg Polytechnic University, Russia

Different classes of human genes have different relative evolutionary novelty

P7. A.T. Ivashchenko, A.Yu. Pyrkova, R.E. Niyazova

Al-Farabi Kazakh National University, Kazakhstan

Development of the fragmented algorithm for solving the problem of clustering miRNA sequences and dendrogram construction

P8. S.O. Vechkapova, A.L. Proskura T.A. Zapara, A.S. Ratushnyak

Design Technological Institute of Digital Techniques, Siberian Branch of the Russian Academy of Sciences, Russia

Regulating the nmda-receptors activity by lambertianic acid amide

P9. A.A. Osypov

Institute of Cell Biophysics RAS, Russia

Electrostatics: a new old selection factor in genome

P10. Arthur I. Dergilev¹, Anatoly V. Svichkarev², Evgenii E. Vityaev³, Yuriy L. Orlov^{1,4}

¹Novosibirsk State University, Novosibirsk, Russia

²St.Petersburg Technological Univesity, St.Petersburg, Russia

³Sobolev Institute of Mathematics SB RAS, Russia

⁴Institute of Cytology and Genetics SB RAS, Russia

Knowledge Discovery methods in analysis of genome co-localization of transcription factor binding sites

P11. A.B. Shcherban¹, E. Z. Kochieva², E.A. Salina¹

¹The Federal Research Center "Institute of Cytology and Genetics of Siberian Branch of the Russian Academy of Sciences", Russia

²Federal State Institution «Federal Research Centre «Fundamentals of Biotechnology» of the Russian Academy of Sciences, Russia

Peculiarities of evolution of the ABCG transporter (Lr34) genes in polyploid wheat species and their diploid progenitors

P12. A.I. Lavrova, A.Yu. Zyubin, S.V. Babak

Baltic Federal University, Kaliningrad, Russia

Kinetic modeling of 6-mercaptopurine effects in the individual treatment of childhood acute leukemia

P13. I.V. Bizin¹, A.P. Sokolenko², E.Sh. Kuligina², E.N. Imyanitov², D. Frishman¹

¹Department of Bioinformatics, RASA Research Center, Peter the Great St. Petersburg Polytechnic University, Russia

²Department of Tumor Growth Biology, N.N. Petrov Institute of Oncology, Russia

Using exome aggregation consortium database for analyzing germline mutations in human breast cancer by exome sequencing

P14. B.S. Yadav¹, **S. Freilich**², E. Katz¹, A. Finkelshtein¹, and D.A. Chamovitz¹

¹Department of Molecular Biology and Ecology of Plants, Tel Aviv University, Israel

²Newe Ya'ar Research Center, Agricultural Research Organization, Ramat Yishay, Israel

Multidimensional patterns of metabolic response in abiotic stress-induced growth of *Arabidopsis thaliana*

P15. D. B. Roche^{1,2}, L. Chaloin^{3,2}, S. N. Morozkina⁴, A.G. Shavva⁴, A. V. Kajava^{1,2}, V. L. Katanaev⁵

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²Institut de Biologie Computationnelle, Université Montpellier, France;

³Centre d'études d'agents Pathogènes et Biotechnologies pour la Santé, Université Montpellier, France;

⁴Laboratory of Medicinal Chemistry, School of Biomedicine, Far Eastern Federal University, Russia;

⁵Department of Pharmacology and Toxicology, Faculty of Biology and Medicine, University of Lausanne, Switzerland

Rational drug design to target Wnt signaling in triple-negative breast cancer

P16. D.N. Kashirina¹, L.Kh. Pastushkova¹, H. Binder², E.S. Tiys³, V.A. Ivanisenko³, I.M. Larina¹, E.N. Nikolaev⁴, A.G. Brzhozovsky¹

¹State Scientific Center of Russian Federation Institute for Biomedical Problems RAS, Russia

²Leipzig University, Germany

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⁴Emanuel Institute of Biochemical Physics RAS, Russia

Bioinformatics analysis of protein dynamics in urine of healthy volunteers exposed 105-day isolation

P17. S.I. Kabanikhin^{1,2}, **D.A. Voronov**^{1,2}, O.I. Krivorotko^{1,2}, A.Yu. Belonog², A.A. Grodz²

¹Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Russia

²Novosibirsk State University, Russia

Numerical methods for solving inverse problems for sode. Identifiability concepts. Software IPE Pack

P18. A. Sokolkova, S. Surkova, K. Kozlov, M. Samsonova

Mathematical Biology and Bioinformatics Lab, Peter the Great St. Petersburg Polytechnic University, Russia

Quantitative analysis of three-dimensional confocal images obtained with a high-resolution HCR method

P19. S.I. Kabanikhin^{1,2}, O.I. Krivorotko^{1,2}, **D.V. Yermolenko**^{1,2}, D.A. Voronov^{1,2}

¹Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Russia

²Novosibirsk State University, Russia

A variational approach for solving of a parameter identification problem in the mathematical model of HIV dynamics

P20. E.V. Osipova

Kazan Institute of Biochemistry and Biophysics, Kazan Scientific Center, Russian Academy of Science, Russia

Reconstruction of evolution history of lipoxygenase pathway enzymes

P21. E.S. Fomin

Institute of Cytology and Genetics SB RAS, Russia

A new algorithm to the reconstruction of a set of points from the multiset of n^2 pairwise distances in n^2 steps for the *de novo* sequencing problem

P22. T. M. Gorbacheva¹, S. A. Solodskikh¹, V. Yu. Bashmakov¹, A.V. Panevina¹, A. Y. Maslov², V. N. Popov¹

¹ Voronezh State University, Russia

² Albert Einstein College of Medicine of Yeshiva University, USA

Tumor-specific cell free DNA as a biomarker of metastasis

P23. I.V. Sharakhov^{1,3,4}, P. George¹, S. Jensen², R. Pogorelcnik², J. Lee³, Y. Xing³, E. Brassel², C. Vaury²

¹ Department of Entomology, Virginia Polytechnic Institute and State University, USA

² Laboratoire Génétique, Reproduction, et Développement, Clermont Université, Université d'Auvergne, Clermont-Ferrand, France

³ The PhD Program in Genomics Bioinformatics and Computational Biology, Virginia Polytechnic Institute and State University, USA

⁴ Laboratory of Evolutionary Cytogenetics, Tomsk State University, Russia

Increased production of piRNAs from euchromatic clusters and genes in *Anopheles gambiae* compared with *Drosophila melanogaster*

P24. I.M. Bizyukov

Siberian state university of telecommunications and information science, Russia

Traversal of an unknown undirected graph using bionics algorithms

P25. I.S. Rusinov¹, A.S. Ershova^{2,3,4}, A.S. Karyagina^{2,3,4}, S.A. Spirin^{1,2,5}, A.V. Alexeevski^{1,2,5}

¹ Faculty of Bioengineering and Bioinformatics, MSU, Russia

² Belozersky Institute of Physical and Chemical Biology, MSU, Russia

³ Gamaleya Institute of Epidemiology and Microbiology, Russia

⁴ Institute of Agricultural Biotechnology, Academy of Agricultural Sciences, Russia

⁵ Scientific Research Institute for System Studies RAS, Russia

Choice of technique for detection of short exceptional words in prokaryotic genomes

P26. I.V. Antonov¹, M.A. Zamkova², A.V. Marakhonov³, M.Y. Skoblov³, Y.A. Medvedeva¹

¹Research Center of Biotechnology RAS, Russia

²Russian N.N.Blokhin Cancer Research Center, Russia

³ Research Centre for Medical Genetics, Russia

Transcriptome wide prediction of lncRNA-RNA interactions by a thermodynamics algorithm

P27. P. O. Fedichev

Gero Limited, Moscow Russia

Target and biomarker identification platform to design new drugs against aging and age-related diseases

P28. Yulia A. Medvedeva¹, Joaquim Custodio², Guerau Fernandez², Miquel A. Peinado², Tanya Vavouri²

¹ Institute of Biotechnology, Research Center of Bioengineering, RAS, Russia

² Institute of Personalized and Predictive Medicine of Cancer, Spain

Chromatin changes induced by treatment with 5-Aza-2-deoxycytidine (Decitabine)

P29. M.Korostishevsky, N.Tarbiy, G.Livshits

Human Population Biology Research Unit, Department of Anatomy and Anthropology, Tel Aviv University, Israel

A simple model of time-to-event expectation for epidemiological analysis of multi-stage age-associated diseases: application to the pain questionnaire family data

P30. A.V. Lioznova¹, A. Khamis², A.V. Artemov¹, V. B. Bajic², **Y. A. Medvedeva¹**

¹ Institute of Biotechnology, Research Centre of Bioengineering, RAS, Russia

² King Abdullah University of Science&Technology, Kingdom of Saudi Arabia

Causal inference search: the relationship between CpG methylation and gene expression

P31. L. Chaloin^{1,2}, L. Ramya^{3,4}, N. Gautham³, A.V. Kajava^{2,5}

¹ Centre d'études d'agents Pathogènes et Biotechnologie pour la Santé, Montpellier, France

² Institut de Biologie Computationnelle, Montpellier, France

³ Centre of Advanced Study in Crystallography and Biophysics, University of Madras, India

⁴ Centre for Nanotechnology and Advanced Biomaterials, SASTRA University, India

⁵ Centre de Recherches de Biochimie Macromoléculaire, Université Montpellier, France

Restricted mobility of side chains on concave surfaces of solenoid proteins may impart heightened potential for intermolecular interactions

P32. L.V. Utkin

Peter the Great Saint-Petersburg Polytechnic University, Russia

A simple genome-wide association study algorithm for estimating the main and epistatic effects with quantitative traits

P33. A.Yu.Filatova¹, M.Yu. Skoblov^{1,2}

¹ Centre for Medical Genetics, Federal Agency for Scientific Organizations, Russia

² Moscow Institute of Physics and Technology, Russia

Study of the structure and function of human lncRNA LINC00493

P34. Maria V. Sharakhova^{1,2}, Vladimir A. Timoshevskiy¹, David W. Severson², Igor V. Sharakhov^{1,2}

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² Laboratory of Evolutionary Cytogenetics, Tomsk State University, Russia

³ Department of Biological Sciences and Eck Institute of Global Health, University of Notre Dame, South Bend, IN, USA

Genome organization and chromosome evolution of the mosquito *Aedes aegypti*

P35. S.I. Kabanikhin^{1,2}, D.A. Voronov^{1,2}, **A.A. Grodz**², E.I. Vostrikova², O.I. Krivorotko^{1,2}

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² Novosibirsk State University, Russia

Identifiability mathematical systems of physiology

P36. N.Morozova¹, A.Sabantsev¹, E. Bogdanova², Y. Fedorova^{1,3}, A. Maykova^{1,3}, A.Vedyaykin¹, M. Khodorkovskiy¹, K. Severinov^{1,2,3}

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³ Skolkovo Institute of Science and Technology, Russia

Study of effect of gene expression variations on phage infection probability in *E.coli* cells with a Type II restriction-modification system

P37. D.I. Ostromyshenskii, A.S. Komissarov, I.S. Kuznetsova, O.I. Podgornaya

Institute of Cytology RAS, Russia

High-throughput sequencing of mouse chromocenters

P38. A.I. Paramonov¹, Y.P. Dzhioev^{1,2}

¹ FGBU "Scientific Center for family health and human reproduction problems", Russia

² Irkutsk State Medical University, Russia

Some aspects of Zika virus molecular evolution

P39. P. V. Pavlovich^{1,2}, G. P. Arapidi^{1,2}, O. M. Ivanova^{1,2}, P. V. Kapranov^{1,2}, V. M. Govorun^{1,2}

¹ Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry RAS, Russia

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LC-MS/MS identification of peptide fragments of "lncRNAs" in human serum

P40. O.M. Plotnikova¹, D. A. Zubtsov¹, M. Y. Skoblov^{1,2}

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All the truth about miRNA-mRNA prediction tools

P41. N. L. Podkolodnyy^{1,2,3}, N. N. Podkolodnaya^{2,3}, O. A. Podkolodnaya²

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² Institute of Cytology and Genetics SB RAS, Russia

³ Novosibirsk State University, Russia

Computer analysis of biological network

**P42. R.S.Sergeev¹, I.S.Kavaliou², A. Gabrielian³, A. Rosenthal³,
A.V.Tuzikov¹**

¹ United Institute of Informatics Problems NASB, Belarus

² EPAM Systems, Belarus

³ Office of Cyber Infrastructure and Computational Biology, NIAID, Bethesda, USA

Investigation of drug-resistance mutations in MDR/XDR *tuberculosis*

**P43. T.M. Savelieva^{1,2}, G.P. Arapidi^{1,2}, I.A. Fesenko², I.V. Kulakovskiy³,
V.M. Govorun²**

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² Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry RAS, Moscow, Russia

³ Vavilov Institute of General Genetics RAS, Moscow, Russia

Transcription factors regulating gene expression in different cell types of
moss *Physcomitrella Patens*

P44. Y.M. Suvorova, E.V. Korotkov

Research Center of Biotechnology RAS, Moscow, Russia

New measure for protein coding region detection

P45. A. V. Svichkarev, K. N. Kozlov

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University, Russia

DEEP: optimizer with embedded interpreter

**P46. U.S. Zubairova¹, S.V. Nikolaev¹, A.V. Penenko², N.L. Podkolodnyy¹,
S.K. Golushko³, D.A. Afonnikov¹, and N.A. Kolchanov¹**

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³ Design and Technology Institute of Digital Techniques SB RAS, Russia

What a plant cell should detect and control during growth in tissue?

P47. Sergei Vakulenko^{1,2}, Ovidiu Radulescu³, Ivan Morozov⁴

¹ Institute for Mech. Engineering Problems, Russia

² Saint Petersburg National Research University of Information Technologies, Mechanics and
Optics, Russia

³ Université Montpellier, France

⁴ University of Technology and Design, Russia

Maximal switchability of gene networks

P48. S.I. Kabanikhin^{1,2}, O.I. Krivorotko^{1,2}, **V.N. Kashtanova**², D.A. Voronov^{1,2}

¹Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Russia

²Novosibirsk State University, Russia

A numerical algorithm of parameter identification in mathematical model of tuberculosis epidemiology with treatment

P49. A.P. Yakimov^{1,2}, M.A. Khodorkovskii², D. Baitin^{1,2}, M.G. Petukhov^{1,2}

¹Petersburg Nuclear Physics Institute, NRC Kurchatov Institute, Russia

²Peter the Great St.Petersburg Polytechnic University, Russia

Improved version of SeqOPT, the method for *de novo* design of stable alpha-helices

P50. S.I. Tarnovskaya¹, A.M. Kiselev², A.A. Kostareva², D.I. Frishman^{1,3,4}

¹Department of Bioinformatics, RASA Research Center, Peter the Great St. Petersburg Polytechnic University, Russia

²Almazov Federal Medical Research Centre, Russia

³Department of Bioinformatics, Technische Universität München, Wissenschaftszentrum Weihenstephan, Freising, Germany;

⁴Institute for Bioinformatics and Systems Biology, HMGU German Research Center for Environmental Health, Germany

Structural analysis of mutations in Ig-like domain causing restrictive cardiomyopathy

P51. A.I. Klimenko, Yu.G. Matushkin, Z.S. Mustafin, A.D. Chekantsev, R.K. Zudin, S.A. Lashin

Institute of Cytology and Genetics SB RAS, Russia

Novosibirsk State University, Russia

HEC 3D: a tool for multilayer modeling of spatially distributed microbial communities

P52. A.M. Spitsina

Institute of Cytology and Genetics SB RAS, Russia

Mechanics and Mathematics Department, Novosibirsk State University, Russia

EXPGENE - software for analysis and processing of gene expression data

P53. I. L. Erokhin

"NBC" LLC, Russia

On the Nature of Stem Cells

P54. M.Yu. Skoblov^{1,2}, I.A. Krivosheeva¹, J.V. Vyakhireva¹, A.V. Marakhonov^{1,2}

¹Research Centre for Medical Genetics, Federal Agency for Scientific Organizations, Russia

²Moscow Institute of Physics and Technology, Russia

Antisense regulation of human genes RIC8A, S100A13, AFAP1-AS1

P55. Dunarel Badescu¹, Abdoulaye Baniré Diallo², Vladimir Makarevich²

¹McGill University, Faculty of Medicine, Canada

²Department of Computer Science, Université du Québec à Montréal, Canada

Estimating the role of horizontal gene transfer in the evolution of prokaryotes

P56. Ya.A. Sharapova, V.K. Švedas

Faculty of Bioengineering and Bioinformatics, Lomonosov Moscow State University, Russia

Homologous bacterial and viral sialidases have different organization of their catalytic sites

P.57 A.A. Chertkova¹, J. Schiffman², M.G. Samsonova¹, S.V. Nuzhdin^{1,2}, V.V. Gursky^{1,3}

¹ Peter the Great St. Petersburg Polytechnic University, St. Petersburg, Russia

² University of Southern California, Los Angeles, U.S.A.

³ Ioffe Institute, St. Petersburg, Russia

Evolution simulation in the regulatory regions of the segmentation genes in Drosophila

P58. A.A.Ageeva

Mechanics and Mathematics Department, Novosibirsk State University, Russia

Development and research neural deep belief network learning algorithms for face recognition tasks in difficult conditions

List of Participants

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