



About Belarusian State University



The Belarusian State University (BSU) is a leading scientific, educational, innovation and cultural center of the Republic of Belarus. It was founded on October 30, 1921. Today at the BSU near 7400 employees carry out their duties and 2500 of them occupy full-time teaching positions within university's major faculties and institutes. The BSU teaching staff includes 15 academicians and 16 Corresponding Members of the National Academy of Science of Belarus, 400 Doctors of Science and 1840 PhD degree holders. The BSU students' community consists of more than 30,000 undergraduate and graduate students, postgraduate and postdoctoral students. More than 1700 international students from 53 countries of world are pursuing their education at the BSU.

The entire complex of the BSU includes 16 faculties and 6 educational institutes, 10 educational establishments, 10 research and development institutes and centers, 41 research and developments laboratories, 10 innovation and production enterprises. According to major international rankings the BSU is among 2 per cent of world leading universities out of 30 thousand educational institutions. Annually more than 1000 various scientific publications and more than 5000 articles are publishes, more than 100 scientific and practical conferences are held.

Among BSU alumni is a Nobel Prize winner, several prominent scientists, educationalists and political leaders working in many countries of the world.

About United Institute of Informatics Problems



United Institute of Informatics Problems of the National Academy of Sciences of Belarus is the leading organization in Belarus in fundamental and applied research on information technologies: CAD/CAM/CAE systems, applied mathematics, high performance parallel computing, bioinformatics and medical informatics, geoinformation systems, digital cartographic systems, Space informatics, GRID-technologies. The Institute is the provider of scientific and educational Internet networks in Belarus. It takes part in state recommendations on information technologies implementation, scientific support of informatization processes, prognosis in related science and technology fields in Belarus, high skill specialists training.



The staff of the institute is about 390 persons including 148 research workers: 1 Corresponding Member of the National Academy of Science of Belarus, 15 Doctors of Science and 68 – with PhD degree.



Rector's Welcome Message

I am pleased to welcome you at the Belarusian State University, a leading national university in the Republic of Belarus. The BSU is a big educational, scientific and production institution that has a high position in the world. For example, according to QS international ranking in 2015 BSU is among 430 best world universities. The BSU is the only Belarusian university in the list of the prestigious Times Higher Education World University Rankings.

Our university aims at providing students with the best methods and the latest technologies of knowledge acquisition. There are 16 Faculties, 6 Educational institutes and 10 Educational establishments which provide training on undergraduate and post-graduate levels of education. We offer a variety of educational programs at all levels of education. The Higher Education Program is organized at the BSU major Faculties and Educational Institutes through 56 specialties and more than 250 specializations. Training along the Master's Degree Program is conducted through 48 specialties. The PhD Program which is aimed to prepare highly qualified researchers holding a candidate of science (Ph.D.) degree is provided through 142 specialties of different branches of science. In order to equip international students with the Russian Language and learning strategies and skills which enable them to study professional disciplines and be admitted to a degree programs the BSU provides pre-university education program.

The maintenance of research excellence has been a very high priority and all our courses benefit from being taught in an active research environment. Today the BSU includes 10 research and development institutes and centers, 41 research and developments laboratories, 10 innovation and production enterprises. Annually more than 1000 various scientific publications and more than 5000 articles are publishes, more than 100 scientific and practical conferences are held. Belarusian State University is one of the leading universities at the market of development projects. Currently, the university holds 297 assignments (tasks) on 12 state programs of research. BSU is a leading organization and executor in 8 programs.

Our university belongs to a highly internationalized university community and puts a great attention to cooperation with foreign partners both at inter-university level and within international projects framework. About 2500 foreign students study at BSU every year. 25-30 international projects focused on academic exchanges, modernization of university management, design of joint study programs, development of infrastructure, organization of conferences, seminars and other events within such programs as Tempus, Erasmus Mundus, Jean Monnet, EU Cross-Border Cooperation, DAAD, FPB-Belarus, SIDA, VISBY, Baltic University, CIMO, Visegrad Fund, CEI Fund, Eurasia, UNICEF, UNESCO and many others are implemented at BSU annually.

Academic mobility takes particular importance in the modern world today and is the main component of the inter-university cooperation. More than 1500 teachers, young scientists, undergraduates, master students and postgraduate students of the Belarusian State University travel abroad every year to undergo scientific training, deliver lectures, participate in conferences, as well as to do research and make joint international projects.

As a conclusion, I hope that the discussions and exchanges of ideas at the Symposium held in our university will be valuable for all participants. I wish you successful work and all the very best.

A handwritten signature in blue ink, appearing to read 'S. Ablameyko', written in a cursive style.

Sergey V. Ablameyko, Academician, Rector, Belarusian State University

Message from the General Chairs



We are delighted to welcome you to the 12th International Symposium on Bioinformatics Research and Applications (ISBRA 2016) being held on the campus of Belarusian State University in historic city of Minsk. We are honored to serve the international community by bringing together scholars, scientists and students from academia, laboratories, and industry to this premier meeting.

We would like to thank Program Chairs Anu Bourgeois, Pavel Skums, Xiang Wan and Alex Zelikovsky for putting together a terrific technical program. We thank the program committee and reviewers for their hard work, and also thank all authors who submitted papers and abstracts for their contributions. We believe that you will enjoy all contributed and keynote talks this week!

We are grateful to the Local Organizing Chair Dmitry G. Medvedev and also Yury M. Metelsky for help in coordinating ISBRA 2016. We thank the Finance Chairs Yury Metelsky and Alex Zelikovsky for their outstanding job in managing the bank account and registration system. We also thank the Publicity Chair Erin-Elizabeth A. Durham for her assistance in publicizing the symposium. Finally, we thank the Publications Chair Igor E. Tom for his efforts.

We would like to recognize Belarusian State University for hosting ISBRA 2016. Last but not least, we would like to thank our sponsors: the National Science Foundation, Belarusian State University and United Institute of Informatics Problems of National Academy of Sciences of Belarus. Thanks to their generous support we have been able to award travel fellowships to several graduate students and post-doctoral scholars from different countries of the world.

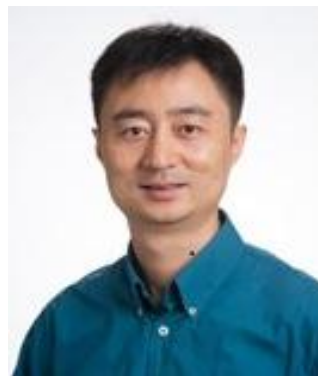
We hope you will have a wonderful time at the symposium and enjoy Belarus - the beautiful country in the heart of Europe

Sergei V. Ablameyko, Belarusian State University

Bernard Moret, École Polytechnique Fédérale de Lausanne

Alexander V. Tuzikov, United Institute of Informatics Problems

Message from the Program Chairs



On behalf of the Program Committee, we would like to welcome you to the 12th edition of the International Symposium on Bioinformatics Research and Applications (ISBRA 2016), held on June 5-8, 2016 at the Belarusian State University in Minsk, Belarus. The symposium provides a forum for the exchange of ideas and results among researchers, developers, and practitioners working on all aspects of bioinformatics and computational biology and their applications.

This year we received 77 submissions in response to the call for extended abstracts. The Program Committee decided to accept 42 of them for publication in the proceedings and oral presentation at the symposium. We have also received 23 submissions in response to the call for short abstracts. The technical program features invited keynote talks by five distinguished speakers. Dr. Teresa M. Przytycka from National Institutes of Health will speak on network perspective on genetic variations: from model organisms to diseases, Prof. Ion Mandoiu from University of Connecticut will speak on challenges and opportunities in single cell genomics, Prof. Alexander Schoenhuth from Centrum Wiskunde and Informatica will speak on dealing with uncertainties in big genome data, Prof. Ilya Vakser from University of Kansas will speak on genome-wide structural modeling of protein-protein interactions and Prof. Max Alekseyev from George Washington University will speak on multi-genome scaffold co-assembly based on the analysis of gene orders and genomic repeats.

We would like to thank the Program Committee members and external reviewers for volunteering their time to review and discuss symposium papers. We would like to extend special thanks to the Steering and General Chairs of the symposium for their leadership, and to the Finance, Publicity, Workshops, Local Organization, and Publications Chairs for their hard work in making ISBRA 2016 a successful event. Last but not least we would like to thank all authors for presenting their work at the symposium.

Anu Bourgeois, Georgia State University
Pavel Skums, Centers for Disease Control and Prevention
Xiang Wan, Hong Kong Baptist University
Alex Zelikovsky, Georgia State University

Keynote Speakers



Teresa M. Przytycka
Senior Investigator
Computational Biology Branch,
The National Center for Biotechnology Information
National Institutes of Health



Ion Mandoiu
Professor
Computer Science and Engineering Department
University of Connecticut



Alexander Schoenhuth
Senior Researcher
Computational Genomics Research Group
Centrum Wiskunde and Informatica



Ilya Vakser
Professor and Director,
Center for Computational Biology
University of Kansas



Max Alekseyev
Associate Professor
Department of Mathematics and Computational
Biology Institute
George Washington University

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Robert Beiko (Dalhousie University)
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Pavel Skums (Centers for Disease Control and Prevention)
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Georgia State University

ISBRA 2016 Program

Sunday, June 5, 2016

Café “Mensk”, vulica Savieckaja 9 (ул. Советская, 9)

5:00pm-
8:00pm

Registration and Reception

Café “Mensk”,
vulica
Savieckaja 9

Monday, June 6, 2016 Belarusian State University

7:30am-
8:10am

Registration

Rectorate
Building

8:10am-
8:30am

Welcome Remarks

Prof. Dr. Sergey V. Ablameyko

Great Hall of
Rectorate
Building

8:30am-
9:30am

Plenary Session

Chair: *Alex Zelikovsky*

Great Hall of
Rectorate
Building

Keynote talk

Network perspective on genetic variations: from model organisms to diseases

Teresa M. Przytycka, National Institutes of Health

9:30am-
9:50am

Coffee Break

9:50am-
11:55am

Parallel Sessions 1

Session 1A:

Room: Great Hall of Rectorate Building

Chair: *Max Alekseyev*

Sensitive detection of low frequency single nucleotides variants from amplicon and capture sequencing data with Leucippus, *Nikolaos Vasmatzis, Chen Wang, Sarah Kerr, Jamie Bakkum-Gamez, Flora Vaccarino and Alexej Abyzov*

MegaGTA: a sensitive and accurate metagenomic Gene-Targeted Assembler using iterative de Bruijn graphs, *Dinghua*

Session 1B:

Room: Physics Faculty Building, Lecture Hall 213

Chair: *Teresa M. Przytycka*

Consistent visualization of multiple rigid domain decompositions of proteins, *Emily Flynn and Ileana Streinu*

SkipCPP-Pred: Promising Prediction Method for Cell-Penetrating Peptides Using Adaptive k-skip-n-gram Features

Li, Yukun Huang, Chi-Ming Leung, Ruibang Luo, Hing-Fung Ting and Tak-Wah Lam

on a High-quality Dataset, *Wei Leyi and Zou Quan*

HapIso : An Accurate Method for the Haplotype-Specific Isoforms Reconstruction from Long Single-Molecule Reads, *Sergei Mangul, Harry Yang, Farhad Hormozdiari, Elizabeth Tseng, Alex Zelikovsky and Eleazar Eskin.*

HIGHLIGHT: Modeling of Protein Inner-Conformation Dynamics by Solving Mass Transportation Problem, *Sergey Knyazev, Gaik Tamazian, Eugene Stepanov and Yuri Porozov*

De Novo Assembly of Mitochondrial Genomes from Low Coverage Whole-Genome Sequencing Reads, *Fahad Alqahtani and Ion Mandoiu*

A functional ontology-based score for template-based protein docking, *Anna Hadarovich, Ivan Anishchenko, Petras Kundrotas, Ilya Vakser and Alexander Tuzikov.*

Filling a protein scaffold with a reference, *Letu Qingge, Xiaowen Liu, Farong Zhong and Binhai Zhu*

CPredictor2.0: Effectively Detecting Both Small and Large Complexes from Protein-Protein Interaction Network, *Bin Xu, Jihong Guan, Yang Wang and Shuigeng Zhou*

**12:00p-
1:30pm**

Lunch

**Cafeteria of
Rectorate
Building**

**1:30pm-
2:30pm**

**Plenary Session
Chair: Alexander Tuzikov**

**Great Hall of
Rectorate
Building**

Keynote talk

Genome-wide structural modeling of protein-protein interactions

Ilya Vakser, University of Kansas

**2:30pm-
2:50pm**

Coffee Break

**2:50pm-
4:05pm**

Parallel Sessions 2

Session 2A:

Room: Great Hall of Rectorate Building

Chair: Ion Mandoiu

An improved burden-test pipeline for cancer sequencing data, *Yu Geng, Zhongmeng Zhao, Xuanping Zhang, Wenke Wang, Xiao Xiao and Jiayin Wang*

Progression Reconstruction from Unsynchronized Biological Data using

Session 2B:

Room: Physics Faculty Building, Lecture Hall 213

Chair: Ilya Vakser

NEMo: An Evolutionary Model with Modularity for PPI Networks, *Min Ye, Gabriela Racz, Qijia Jiang, Xiuwei Zhang and Bernard Moret*

Dynamic protein complex identification in uncertain protein-protein interaction

Cluster Spanning Trees, *Rahul Singh and Ryan Eshleman* networks, *Yijia Zhang, Hongfei Lin, Zhihao Yang and Jian Wang*

An Integrative Approach for Identification of Network Biomarkers in Breast Cancer Subtypes, *Forough Firoozbakht, Iman Rezaeian, Alioune Ngom and Luis Rueda* Identifying essential proteins by purifying protein interaction networks, *Min Li, Xiaopei Chen, Jianxin Wang and Yi Pan*

4:05pm-4:25pm
Coffee Break

4:25pm-5:40pm
Parallel Sessions 3

Session 3A:

Room: Great Hall of Rectorate Building

Chair: Rahul Singh

Poisson-Markov Mixture Model and Parallel Algorithm for Binning Massive and Heterogenous DNA Sequencing Reads, *Lu Wang, Dongxiao Zhu, Yan Li and Ming Dong.*

Integrative analysis of combinatorial chromatin interactions using high-throughput sequencing data, *Yevhen Vainshtein, Karsten Rippe and Vladimir Teif*

MitoDel: A Method to Detect and Quantify Mitochondrial DNA Deletions from Next-Generation Sequence Data, *Colleen Bosworth, Sneha Grandhi, Meetha Gould and Thomas Laframboise*

Session 3B:

Room: Physics Faculty Building, Lecture Hall 213

Chair: Victor Krasnoproshin

An Efficient Algorithm for finding all pairs k-mismatch maximal common substrings, *Sharma V. Thankachan, Sriram Chockalingam and Srinivas Aluru*

Client side web based application for search space reduction in approximate circular pattern matching, *Mohammad Samiruzzaman, Costas Iliopoulos, Steven Watts and M Sohel Rahman*

A Gene Family-Free model for Genome Rearrangements with Insertions and Deletions, *Kevin Lamkiewicz and Pedro Feijao*

6:00pm **Minsk excursion**

Rectorate Building

Tuesday, June 7, 2016

Belarusian State University

8:30am-9:30am **Plenary Session**

Physics Faculty Building,

Chair: Ion Mandoiu

Lecture Hall 418

Keynote talk

Multi-genome scaffold co-assembly based on the analysis of gene orders and genomic repeats

Max Alekseyev, George Washington University

9:30am-9:50am
Coffee Break

9:50am-
11:55am

Parallel Sessions 4

Session 4A:

**Room: Physics Faculty Building,
Lecture Hall 418**

Chair: Alex Zelikovsky

Path-Difference Median Trees, *Alexey Markin and Oliver Eulenstein.*

The SCJ small parsimony problem for weighted gene adjacencies, *Nina Luhmann, Annelise Thévenin, Aida Ouangraoua, Roland Wittler and Cedric Chauve*

Accurate reconstruction of epidemic history using analysis of intra-host microbial populations, *Pavel Skums, Olga Glebova, June Zhang, Zoya Dimitrova, David S. Campo, Alex Zelikovsky and Yury Khudyakov*

Phylogeny Reconstruction from Whole-Genome Data using Variable Length Binary Encoding, *Lingxi Zhou, Yu Lin, Bing Feng and Jijun Tang*

Mean values of gene duplication and loss cost function, *Pawel Gorecki, Jarosław Paszek and Agnieszka Mykowiecka*

Session 4B:

**Room: Physics Faculty Building,
Lecture Hall 213**

Chair: Ileana Streinu

Tractable Kinetics of RNA-Ligand Interaction, *Felix Kuehnl, Peter F. Stadler and Sebastian Will.*

Structural Insights into Antiapoptotic Activation of Bcl-2 and Bcl-xL Mediated by FKBP38 and tBid, *Valery Veresov and Alexander Davidovskii*

Integrative Atomic-Level Structure Modeling of the General Import Pore Complex, *Anna Dudko, Alexander Davidovskii and Valery Veresov*

Computer Modeling Of Gene-Gene And Gene-Environment Interaction In Essential Hypertension, *Olga Pavlova, Vladimir Malugin, Svetlana Ogurtsova, Alexander Novopolcev, Tatjana Gorbat, Maria Liventseva and Alexander Mrochek*

Predicting lncRNA-Protein Interactions Based on Protein-Protein Similarity Network Fusion, *Xiaoxiong Zheng, Zhanzhan Cheng, Yang Wang, Jihong Guan and Shuigeng Zhou*

12:00pm-
1:30pm

Lunch

**Café “Mensk”, vulica
Savieckaja 9**

1:30pm-
2:30pm

Plenary Session

Chair: Alex Zelikovsky

**Physics Faculty Building,
Lecture Hall 418**

Keynote talk

Dealing with uncertainties in big genome data

Alexander Schoenhuth, Centrum Wiskunde & Informatica

2:30pm-
2:50pm

Coffee Break

2:50pm-
4:05pm

Parallel Sessions 5

Session 5A:

**Room: Physics Faculty Building,
Lecture Hall 418**

Chair: *Alexander Schoenhuth*

Improve Short Read Homology Search using Paired-End Read Information, *Prapaporn Techa-Angkoon, Yanni Sun and Jikai Lei.*

OVarCall: Bayesian Mutation Calling Method Utilizing Overlapping Paired-End Reads, *Takuya Moriyama, Seiya Imoto, Rui Yamaguchi, Yuichi Shiraishi, Kenichi Chiba and Satoru Miyano*

Studying the error for HCV amplicon sequencing with the Illumina MiSeq platform, *Zoya Dimitrova, Lilia Ganova-Raeva, Amanda Sue, Pavel Skums, Natalia Saveleva and Yury Khudyakov.*

Session 5B:

**Room: Physics Faculty Building,
Lecture Hall 213**

Chair: *Sergei Bosiakov*

Improved detection of 2D gel electrophoresis spots by using Gaussian mixture model, *Michal Marczyk*

Designing the platform for phenotyping stem cuttings and clones of ornamental woody plants, *Vadim Demidchik, Alexander Mikhalchenko, Alexander Valvachev, Dmitriy Kolbanov, Anatoliy Sokolik, Vladimir Krasnoproshin and Sergey Ablameyko*

Significance of Reduced Features for Subcellular Bioimage Classification, *Babu Baniya, Carol Lushbough and Etienne Gnimpieba*

4:05pm-
4:25pm

Coffee Break

4:25pm-
5:40pm

Parallel Sessions 6

Session 6A:

**Room: Physics Faculty Building,
Lecture Hall 418**

Chair: *Zoya Dimitrova*

A Method to Detect Large Deletions at Base Pair Level using Next-Generation Sequencing Data, *Matthew Hayes and Jeremy Pearson.*

FSG: Fast String Graph Construction for De Novo Assembly of reads data, *Paola Bonizzoni, Gianluca Della Vedova, Yuri Pirola, Marco Previtali and Raffaella Rizzi.*

Framework for integration of genome and exome data to improve the identification of somatic variants, *Vinaya Vijayan, Siu Ming Yiu and Liqing Zhang.*

Session 6B:

**Room: Physics Faculty Building,
Lecture Hall 213**

Chair: *Vladimir Malugin*

NemoProfile: effective representation for network motifs and their instances, *Wooyoung Kim and Lynnette Haukap*

Differential functional analysis and change motifs in gene networks to explore the role of anti-sense transcription, *Marc Legeay, Beatrice Duval and Jean-Pierre Renou*

Predicting MicroRNA-disease associations by random walking on multiple networks, *Wei Peng, Wei Lan, Zeng Yu, Jianxin Wang and Yi Pan*

7:00pm **Banquet**

Café “Mensk”,

Wednesday, June 8, 2016 Belarusian State University

8:30am-9:30am **Plenary Session** **Great Hall of Rectorate building**
Chair: Pavel Skums

Keynote talk

Challenges and opportunities in single cell genomics

Ion Mandoiu, University of Connecticut

9:30am-9:50am **Coffee Break**

9:50am-11:55am **Parallel Sessions 7**

Session 7A:

Room: Great Hall of Rectorate Building

Chair: Ion Mandoiu

Predicting Combinative Drug Pairs via Integrating Heterogeneous Features for both Known and New Drugs, *Jia-Xin Li, Jian-Yu Shi, Ke Gao and Siu Ming Yiu*

Epistasis Analysis of microRNAs in Colon Cancer Using Empirical Bayesian Elastic Nets, *Jia Wen, Andrew Quitadamo, Benika Hall and Xinghua Shi*

EnhancerDBN: An Enhancer Prediction Method Based on Deep Belief Network, *Hongda Bu, Yanglan Gan, Yang Wang, Jihong Guan and Shuigeng Zhou*

Pattern Recognition of Chemical Fingerprints from Large-Scale Databases of Molecules and Reactions, *Neo Christopher Chung and Anna Gambin*

TRANScendence: transposable elements database and de-novo mining tool allows inferring TEs activity chronology, *Michał Startek, Jakub Nogły, Dariusz Grzebelus and Anna Gambin*

Session 7B:

Room: Physics Faculty Building, Lecture Hall 213

Chair: Alex Zelikovskiy

Pharmacophore-based virtual screening of novel HIV-1 fusion inhibitors mimicking potent and broad neutralizing antibody 10e8, *Ivan Kashyn, Alexander Tuzikov and Alexander Andrianov*

Computational design of entry inhibitor scaffolds targeting the third variable loop of HIV-1 gp120, *Yuri Kornoushenko, Ivan Kashyn, Alexander Tuzikov and Alexander Andrianov*

NGS evaluation of HCV strains from individuals co-infected with HIV, *Zoya Dimitrova, Lilia Ganova-Raeva, Ivailo Alexiev, Lili Punkova, Amanda Sue, Pavel Teoharov, Pavel Skums and Yury Khudyakov*

Methods for Genome-wide Analysis of MDR and XDR Tuberculosis from Belarus, *Roman Sergeev, Ivan Kavaliou, Andrei Gabrielian, Alex Rosenthal and Alexander Tuzikov*

QUASIM: SIMulating Viral QUASpecies evolution under immune response, *Alexander Artyomenko, Igor Mandric, Pavel Skums, Yury Khudyakov and Alex Zelikovskiy*

12:00pm- Lunch

Cafeteria of

1:30pm

Rectorate Building

1:30pm-
2:45pm

Parallel Sessions 8

Session 8A:

Room: Great Hall of Rectorate Building

Chair: Vladimir Teif

Semantic Biclustering: a New Way to Analyze and Interpret Gene Expression Data, *Jiri Klema, Frantisek Malinka and Filip Zelezny*

An in silico automated pipeline to identify tumor specific neoantigens from whole genome and exome sequencing data, *Takanori Hasegawa, Shuto Hayashi, Eigo Shimizu, Shinichi Mizuno, Rui Yamaguchi, Satoru Miyano, Hidewaki Nakagawa and Seiya Imoto*

Session 8B:

Room: Physics Faculty Building, Lecture Hall 213

Chair: Sebastian Will

DNAStructProfiler: An automated pipeline for reconstruction of DNA/RNA secondary structures conservation profiles, *Daria Grechishnikova and Maria Poptsova*

A Multiagent Ab Initio Protein Structure Prediction Tool for Novices and Experts, *Thiago Lipinski-Paes, Michele Dos Santos Silva, José Fernando Ruggiero Bachea and Osmar Norberto de Souza*

DCJ-RNA: Double Cut and Join for RNA Secondary Structures Using a Component-Based Representation, *Ghada Badr and Haifa Al-Aqel*

2:45pm-
3:05pm

Coffee Break

3:05pm-
4:20pm

Parallel Sessions 9

Session 9A:

Room: Great Hall of Rectorate Building

Chair: Alexander Tuzikov

High-performance sensing of DNA hybridization on surface of self-organized MWCNT-arrays decorated by organometallic complexes, *Valentina Egorova, Halina Grushevskaya, Nina Krylova, Igor Lipnevich, Taisija Orekhovskaja, Boris Shulitski and Vladimir Krot.*

Haplotype Inference for Pedigrees with Few Recombinations, *Bonnie Kirkpatrick*

Session 9B:

Room: Physics Faculty Building, Lecture Hall 213

Chair: Pavel Skums

Selectoscope: a modern web-app for positive selection analysis of genomic data, *Andrey Zaika, Iakov Davydov and Mikhail Gelfand*

Web-application for assessment of load-bearing capacity of human tubular bones with surgical defect, *Sergei Bosiakov, Ihar Shpileuski, Denis Alekseev and*

Kirill Yurkevich

Towards a more accurate error model for BioNano optical maps, *Menglu Li, Angel C.Y. Mak, Ernest T. Lam, Pui-Yan Kwok, Kevin Y. Yip, Ting Fung Chan and Siu Ming Yiu.* VALiBS: a visual aligner for bisulfite sequences, *Xiaodong Yan, Min Li, Jianxin Wang, Fang-Xiang Wu and Yi Pan*

4:30pm Closing Remarks

**Great Hall of
Rectorate Building**

Important addresses

Rectorate Building	vulica Babrujskaja 5a (ул. Бобруйская 5a)	Registration (Monday-Wednesday), Plenary and Parallel Sessions
Physics Faculty Building	vulica Babrujskaja 5 (ул. Бобруйская 5)	Parallel Sessions
Café “Mensk”	vulica Savieckaja 9 (ул. Советская, 9)	Registration and Reception (Sunday), Lunch and Banquet (Tuesday)