

"High-throughput Sequencing in Genomics"
Conference Schedule
July 21 – 25, 2013,
Novosibirsk
House of Scientists of the SB RAS

July 21

15:00 Registration

16:00 Opening ceremony

16:15 Musical performance

16:45 Fungal genomics for Energy and Environment.

Igor Grigoryev, DOE Joint Genome Institute, USA

17:30 Sequencing sample prep and data assembly methods: 15 years of accelerated evolution.

Marta Matvienko, CLC Bio, USA

19:00 Welcome Party

July 22

| Section I: Genomics of eukaryotes | | | |
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| | | Moderators - Igor Grigoryev, DOE Joint Genome Institute, USA Vladimir Trifonov, Institute for Molecular and Cellular Biology SB RAS, Novosibirsk | |
| 1 | 9:00 | Yury Orlov Institute of cytology and genetics SB RAS, Novosibirsk | COMPUTER ANALYSIS OF 3D CHROMOSOME CONTACTS IN CELL NUCLEUS REVEALED BY HIGH-THROUGHPUT SEQUENCING: HI-C AND CHIA-PET TECHNOLOGIES |
| 2 | 9:25 | Ancha Baranova George Mason University, USA | WE KNOW IT ALL: WHAT IS NEXT? PROTEIN-CENTRIC ANALYSIS OF PUBLICLY AVAILABLE PPI DATA FOR FUNCTIONALLY DIVERSE KCTD FAMILY AS AN EXAMPLE |
| 3 | 9:50 | Fatima Smagulova European University of Brittany, France | GENOME WIDE MAPPING OF MEIOTIC RECOMBINATION HOTSPOTS IN MICE. |
| 4 | 10:15 | Dmitrii Alexeev Institute of Physico-Chemical Medicine, FMBA, Moscow | GENOME AND TRANSCRIPTOME OF CHIRONOMIDS <i>P. VANDERPLANKI</i> |
| | 10:40 | Coffee break | |
| 5 | 11:05 | Alexey Moskalev Institute of Biology of the Komi Science Centre of the Ural, Syktyvkar) | TRANSCRIPTOME CHANGE OF ADULT DROSOPHILA MELANOGASTER AFTER EXPOSURE TO GAMMA-RADIATION, 2,3,7,8-TETRACHLORODIBENZO-P-DIOXIN, TOLUENE AND FORMALDEHYDE |
| 6 | 11:30 | Viktoria Mironova Institute of Cytology and Genetics, Novosibirsk | AUXIN RESPONSIVE TRANSCRIPTOME IN ARABIDOPSIS THALIANA ROOTS |
| 7 | 11:55 | Konstantin Krutovsky Georg-August-University of Göttingen, Germany; Siberian Federal University, Russia | TARGETED AND COMPLETE GENOME DE NOVO SEQUENCING IN CONIFER TREES WITH GIANT AND COMPLEX GENOMES |
| 8 | 12:20 | Berthold Heinze Federal Research Centre for Forests, Austria | NEXT-GENERATION ALTERNATIVES FOR SEQUENCING MANY GENES IN MANY FOREST TREE INDIVIDUALS |
| | 12:45 | Lunch | |
| 9. | 14:00 | Ekaterina Loseva Institute of Chemical Biology and Fundamental Medicine of SB RAS, Novosibirsk | CHARACTERIZATION OF GENOMIC DNA FRAGMENTS GENERATED DURING APOPTOSIS. |

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| 10. | 14:25 | Alexandr Graphodatsky Institute for Molecular and Cellular Biology SB RAS, Novosibirsk | CHROMOSOMAL ORGANIZATION OF MAMMALIAN GENOMES |
| 11. | 14:50 | Matthias Meyer Max Planck Institute for Evolutionary Anthropology, Germany | ARCHAIC GENOMES |
| 12. | 15:15 | Anna Druzhkova Institute for Molecular and Cellular Biology SB RAS, Novosibirsk | ANALYSIS OF EQUID FOSSIL DNA FROM THE DENISOVA CAVE USING THROUGHPUT SEQUENCING PLATFORMS. |
| 13. | 15:40 | Vladimir Trifonov Institute for Molecular and Cellular Biology SB RAS, Novosibirsk | THE STUDY OF REPTILE SEX CHROMOSOME EVOLUTION BY HIGH-THROUGHPUT SEQUENCING OF CHROMOSOME SPECIFIC LIBRARIES |
| | 16:00 | Coffee break | |

July 23

| Section II: Metagenomics | | | |
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| | | Moderators - Ludmila Chistoserdova, University of Washington, USA Vadim Govorun, Research Institute of Physico-Chemical Medicine FMBA, Moscow | |
| 1 | 9:00 | Ludmila Chistoserdova University of Washington, USA | USING METAGENOMICS FOR UNDERSTANDING FUNCTIONALITY OF COMPLEX MICROBIAL COMMUNITIES |
| 2 | 9:25 | Evgeny Andronov All-Russia Research Institute for Agricultural Microbiology, St.Petersburg | NEW APPROACHES FOR ANALYSES OF SOIL MICROBIOME |
| 3 | 9:50 | Vitaly Kadnikov Center "Bioengineering" RAS, Moscow | METAGENOMIC ANALYSIS OF THE MICROBIAL COMMUNITY IN THE DEEP UNDERGROUND THERMAL HABITAT IN WESTERN SIBERIA |
| 4. | 10:15 | Alexandr Zelenin Research Institute of Physico-Chemical Medicine FMBA, Moscow | THE STRUCTURE OF THE BACTERIAL COMMUNITY FROM DIGESTIVE TRACT OF CRYPTOBIOLOGICAL CHIRONOMIDS <i>POLYPEDILUM VANDERPLANKII</i> BY METAGENOMIC ANALYSIS |
| | 10:40 | Coffee break | |
| 5. | 11:05 | Anna Popenko Research Institute of Physico-Chemical Medicine FMBA, Moscow | SPECIAL TRAITS OF RUSSIAN GUT MICROBIOME: FUNCTIONAL ANALYSIS AND CROSS-NATIONAL COMPARATIVE STUDY |
| 6 | 11:30 | Alexandr Tyacht Research Institute of Physico-Chemical Medicine FMBA, Moscow | TEMPORAL EVOLUTION OF GUT MICROBIOTA COMPOSITION DURING CANCER TREATMENT IN PEDIATRIC PATIENTS AS IDENTIFIED BY METAGENOMIC ANALYSIS |
| 7. | 11:55 | Boris Kovarsky Research Institute of Physical-Chemical Medicine FMBA, Moscow | ANALYSIS OF GENETIC VARIETY OF HUMAN GUT METAGENOME |
| Section III: Genomics of bacteria and viruses | | | |
| | | Moderator - Nikolay Ravin, Center "Bioengineering" RAS, Moscow | |
| | 12:20 | Konstantin Miroshnikov Institute of bioorganic | BACTERIOPHAGE GENOMICS: PROSPECTS OF THE NEXGEN SEQUENCING APPROACH |

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| | | chemistry RAS, Moscow | |
| | 12:45 | Lunch | |
| | 14:00 | Nikolay Ravin Center "Bioengineering" RAS, Moscow | SEQUENCING OF GENOMES OF EXTREMOPHILIC MICROORGANISMS REPRESENTING NEW PHYLOGENETIC LINEAGES |
| 9. | 14:25 | Olga Averina Vavilov Institute of General Genetics RAS, Moscow | COMPLETE GENOME SEQUENCE OF BIFIDOBACTERIUM LONGUM GT15: COMPARATIVE GENOMIC ANALYSIS, GLOBAL REGULATORY GENES, UNIQUE GENES |
| 10. | 14:50 | Alexandr Manolov Research Institute of Physico-Chemical Medicine FMBA, Moscow | DE NOVO ASSEMBLY AND COMPARATIVE ANALYSIS OF THE GENOME OF THE BACTERIA P. STUTZERI KOS6 ISOLATED FROM HYDROCARBON SLUDGE |
| 11. | 15:15 | Ivan Bodoev Research Institute of Physico-Chemical Medicine FMBA, Moscow | SEQUENCING AND DE-NOVO ASSEMBLY OF GENOMIC DNA OF NEISSERIA GONORRHOEAE K51.05 STRAIN |
| 12. | 15:40 | Coffee break | |

July 24

| Section III: NGS and data analysis | | | |
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| | | Moderators - Marta Matvienko CLC Bio, USA, Alla Lapidus, Dobzhansky Center for Genome Bioinformatics, Saint Peterburg | |
| 1 | 9:00 | Alla Lapidus Dobzhansky Center for Genome Bioinformatics, SPbU , Russia | GENOME ASSEMBLY AND FINISHING - WHY HIGHT QUALITY REFERENCES ARE NEEDED |
| 2 | 9:25 | Andrey Przhibelskiy St Petersburg Academic University, St.Petersburg | GENOME DRAFT ASSEMBLY ALGORITHMS: FROM THE VERY BEGINNING TILL PRESENT- DAY PROBLEMS |
| 3 | 9:50 | Marie-Theres Gansauge Max Planck Institute for Evolutionary Anthropology, Germany | METHODS FOR ANCIENT DNA SEQUENCING |
| 4 | 10:15 | Elena Kostryukova Research Institute of Physico- Chemical Medicine FMBA, Moscow | EFFECTS OF SAMPLE-PREPARATION STAGE ON RESULTS OF METAGENOMIC ANALYSIS AFTER SHOTGUN SEQUENCING |
| | 10:40 | Coffee break | |
| 5 | 11:05 | Igor Morozov Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk | THE IMPORTANCE OF LIBRARY FRAGMENTS SIZE FOR THE QUALITY OF EMULSION PCR DEPENDENT MPSS DATA |
| 6 | 11:30 | Denis Dmitrienko Dia-M, Moscow | NEW TOOLS FOR THE CREATION OF GENOMIC LIBRARIES |
| 7 | 11:55 | Fedor Kolpakov Design Technological Institute of Digital Techniques of SB RAS, Novosibirsk | BIOUML – SOFTWARE PLATFORM FOR ANALYSIS OF NEXT GENERATION SEQUENCING DATA USING COLLABORATIVE AND REPRODUCIBLE RESEARCH |
| 8 | 12:20 | Olga Golosova NCIT "UNIPRO", Novosibirsk | ANALYSIS OF NEXT-GENERATION SEQUENCING DATA WITH UGENE |
| | 12:45 | Lunch | |
| 9 | 14:00 | Dmitry Shtokalo A.P.Ershov Institute of Informatics Systems SB RAS, Novosibirsk | VERY LONG INTERGENIC NON-CODING RNA (VLINCRNA) DISCOVERY IN NGS DATA |
| 10 | 14:25 | Darya Smirnova Helikon, Moscow | METHODS OF HIGH-PERFORMANCE TARGETED ENRICHMENT OF DNA FOR SUBSEQUENT NGS |
| | 14:40 | Poster session | |

| GENOMICS OF EUKARYOTES | | |
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| 1. | <u>Ivachshenko A.T.</u> , Sagaidak A., Pinsky I. | Binding of microRNA with mRNA of grf genes in completely sequenced plant genomes |
| 2. | <u>Khabudaev K.V.</u> | Comparative molecular phylogenetic analysis of the heavy and light chains of clathrin diatoms and other organisms |
| 3. | <u>Makunin A.</u> , Chernyaeva E., O'Brien S., Trifonov V. | Sequencing of the mammalian b chromosomes on ngs platform |
| 4. | <u>Ovchinnikov V.Y.</u> , Afonnikov D.a., Васильев Г., Katokhin A.V., Kashina E.V., Mordviniv V.A. | Computational and experimental analysis of mirna genes of opisthorchiidae family liver fluke |
| 5. | <u>Petrova E.A.</u> , Kabilov M. | The quest of markers of within species variation in siberian stone pine (Pinus Sibirica du tour) nuclear genome |
| 6. | <u>Semashko T.</u> , Ларин А.К., Popenko A.S., Tyakht A.V., Belogurov A.A., Kostryukova E., Govorun V. | Transcriptome profiling of b-cells of patients with guillain-barre syndrome |
| 7. | <u>Laktionov P.</u> , Maksimov D., Belyakin S. | Damid tissue-specific method for genome-wide mapping of transcription factor binding sites in the male germ-line cells of d. Melanogaster |
| METAGENOMICS | | |
| 8. | <u>Gladkikh A.S.</u> , Belykh O.I., Parfenova V.V., Kalyuzhnaya O. | Pyrosequencing revealed similar species composition of microbial communities associated with two endemic sponges from Lake Baikal |
| 9. | <u>Ilina L.A.</u> , Laptev G., Nagornova K., Bolshakov V., Novikova N. | Using of method of T-RFLP for the metagenomic analisys of rumen microflora of cattle |
| 10. | <u>Karпова I.</u> , Semashko T., Ларин А.К., Ospanova E., Tyakht A.V., Popenko A.S., Zelenin A., Alexeev D., Kostryukova E. | Comparative metagenomic analysis of human intestinal microbiota using various next-generation sequencing systems. |
| 11. | <u>Kurilkina M.</u> , Zakharova Y., Petrova D., Galachyants Y. | The microbial community structure of water column of the deep middle of Lake Baikal |
| 12. | <u>Nagornova K.V.</u> , Laptev G., Nikonov I., Novikov N., LA Ilyina L. | Successful choice of feed additives for poultry depends on the exact knowledge of the intestinal microflora |
| 13. | <u>Ospanova E.</u> , Карпова И.Ю., Ларин А.К., Semashko T., Tyakht A.V., Popenko A.S., Zelenin A., Alexeev D., Kostryukova E. | Comparative analysis of the evaluation of human gut microbial community using sequencing of variable regions of the 16S rRNA genes and shotgun-sequencing |
| 14. | <u>Radnagurueva A.A.</u> , Lavrentieva E.V. | Diversity of microbial communities thermal springs of Baikal rift zone |
| 15. | <u>Serkebaeva Y.</u> , Dedysh S. | Diversity analysis and phylogeny reconstruction of microbial communities in oxic and anoxic peat layers using the 16S pyrosequencing approach |
| 16. | <u>Zaitseva S.V.</u> , Kozyreva L.P., Dagurova O.P. | Using of pyrosequencing for bacterial diversity analysis of microbial communities in Zabaikalye lakes sediments |
| Genomics of bacteria, archaea and viruses | | |
| 17. | <u>Shitikov E.</u> , Ischenko D., Mokrousov I., Narvskaya O., Ilina E., Govorun V. | Russian 'successful' clone B0 of Mycobacterium tuberculosis Beijing genotype: identification of cluster-specific mutations |

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| 18. | <u>Smetanina M.A.</u> , Dymova M.A., Курильщикова А.М., Filipenko M.L. | Successful applying of the method of whole genome sequencing of barcoded DNA libraries to identify the genotypes of Mycobacterium tuberculosis associated with drug resistance |
| NGS AND DATA ANALYSIS | | |
| 19. | <u>Altukhov I.</u> , Ishchenko D., Ilina E., Alexeev D. | Comparative genome analysis of Helicobacter pylori and Neisseria gonorrhoeae |
| 20. | <u>Proskura A.L.</u> , Zapara T., Ratushnyak A. | Macrocomplexes ionotropic glutamate receptors, their function and relationship with cognitive impairment |
| MEDICAL GENOMICS | | |
| 21. | <u>Fedorova S.</u> , Reidla M., Alekseev A.N., Khusnutdinova E.K., VILLEMS R. | Genetic portraits of native populations of Sakha (Yakutia) |
| 22. | Soloviev A.V., Dzhemileva L., Posukh O., Teryutin F., Pshennikova V. Rafailov A., Ushnitskaya V. Alekseev A., Khusnutdinova E., <u>Fedorova S.</u> | The architecture of ancestral haplotype associated with the splice site mutation IVS1+1G>A in GJB2 (Cx26) gene in Yakut population isolate in Eastern Siberia (according to the data 7 SNP-markers) |
| 23. | <u>Stepanov G.A.</u> , Semenov D., Kuligina E., Koval O., Rabinov I., Richter V. | Changes in the RNA profile of human cells under the influence of small nucleolar box C/D RNA analogues |
| 24. | <u>Denisov E.</u> , Gerashchenko T., Zavyalova M., Litvyakov N., Vtorushin S., Cherdyntseva N., Perel'muter V. | Intratumoral morphological heterogeneity of breast cancer as an attractive model for applying high-throughput genome and transcriptome analysis, for an understanding of tumor phylogenetics, and for the identification of disease markers |
| 15:30 | Coffee break | |

July 25

| Section IV: Medical genomics | | | |
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| | | Moderator - Vadim Stepanov, Research Institute of Medical Genetics SB RAMS, Tomsk | |
| 1 | 9:00 | Vadim Stepanov Research Institute of Medical Genetics SB RAMS, Tomsk | HIGH-THROUGHPUT SNP GENOTYPING: DECANALIZATION OF IMMUNE RESPONSE DURING HUMAN DISPERSAL |
| 2 | 9:25 | Florian Graedler Illumina, Netherlands | FROM CANCER TO NIPT - NGS TECHNOLOGY IN CLINICAL APPLICATIONS |
| 3 | 9:50 | Marya Nazarenko Research Institute of Medical Genetics SB RAMS, Tomsk | MICROARRAY ANALYSIS OF THE DNA METHYLATION PROFILE OF VASCULAR TISSUES AND WHOLE BLOOD FROM PATIENTS WITH ATHEROSCLEROSIS |
| 4 | 10:15 | Ekaterina Trifonova Research Institute of Medical Genetics SB RAMS, Tomsk | IDENTIFICATION OF THE PATHOPHYSIOLOGICAL MECHANISMS OF PREECLAMPSIA BY GENOME-WIDE EXPRESSION ANALYSIS |
| | 10:40 | Coffee break | |
| 5 | 11:05 | Olga Saik Institute of Cytology and Genetics of SB RAS, Novosibirsk | ANALYSIS OF RNASEQ DIGITAL GENE EXPRESSION FOR EXPANDING DISEASE “ASSOCIOME” RECONSTRUCTED BASED ON INFORMATION STORED IN DATABASES |
| 6 | 11:30 | Dmitry Baryakin Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk | SMALL NON-CODING RNAS OF HUMAN BLOOD PLASMA |
| 7 | 11:55 | Anna Savelyeva Institute of Chemical Biology and Fundamental Medicine SB RAS, Novosibirsk | RIBONUCLEIC ACID COMPOSITION OF EXTRACELLULAR VESICLES FROM HEALTHY DONOR'S BLOOD |
| 8 | 12:20 | Pavel Natalyin Life Technologies, Moscow | HIGH-THROUGHPUT SEQUENCING FOR BASIC SCIENCE AND MEDICINE |
| | 12:35 | Closing ceremony | |
| | 12:45 | Lunch | |