

**RUSSIAN ACADEMY OF SCIENCES  
SIBERIAN BRANCH**

**INSTITUTE OF CYTOLOGY AND GENETICS  
LABORATORY OF THEORETICAL GENETICS**

**PROGRAM  
OF THE FOURTH  
INTERNATIONAL CONFERENCE  
ON BIOINFORMATICS  
OF GENOME REGULATION  
AND STRUCTURE**

**BGRS'2004  
Novosibirsk, Russia  
July 25–30, 2004**

**IC&G, Novosibirsk, 2004**

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**Alexander Vershinin**, Institute of Cytology and Genetics, Novosibirsk, Russia

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**Lev Zhivotovsky**, Institute of General Genetics, Moscow, Russia

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*The information about the Conference BGRS'2004 can be found  
at <http://www.bionet.nsc.ru/meeting/bgrs2004/>*

## Organizers



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Siberian Branch of the Russian Academy of Sciences



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In Silico Biology

# THE FOURTH INTERNATIONAL CONFERENCE ON BIOINFORMATICS OF GENOME REGULATION AND STRUCTURE (BGRS'2004)

## Program at a Glance

The Conference Sessions will be held in the Small Conference Hall  
and in Music Salon (room № 220) of the House of Scientists

### July 25, Sunday, Foyer of the Small Conference Hall

10:00–14:00 Registration of the conference participants\*

\* Participants who come later are welcome for registration in the  
Organizing Committee room (House of Scientists, room № 200)  
on any conference day.

12:30–14:00 Lunch

**14:00** Small Conference Hall  
**Conference Opens:**

*Welcome by*

Academician Vladimir K. Shumny, Director of the Institute  
of Cytology and Genetics SB RAS;

*Greetings of*

Corresponding member of RAS Professor Nikolay A. Kolchanov  
and Professor Ralf Hofestaedt

14:30–17:30 Evening Session

**COMPUTATIONAL      STRUCTURAL      AND      FUNCTIONAL  
GENOMICS**

16:00–16:30 Coffee-break

19:00–23:00 Welcome party

### July 26, Monday, Small Conference Hall

9:00–12:30 Morning Session

**COMPUTATIONAL      STRUCTURAL      AND      FUNCTIONAL  
GENOMICS**

10:30–11:00 Coffee-break

12:30–14:00 Lunch

14:00–16:30 Evening Session

**COMPUTATIONAL STRUCTURAL AND FUNCTIONAL  
GENOMICS**

15:00–15:30 Coffee-break

Computer demos will be available during the entire conference day

**July 27, Tuesday, Small Conference Hall**

9:00–13:00 Morning Session

**COMPUTATIONAL STRUCTURAL AND FUNCTIONAL  
PROTEOMICS**

11:00–11:30 Coffee-break

13:00–14:30 Lunch

14:30–18:00 Evening Session

**COMPUTATIONAL STRUCTURAL AND FUNCTIONAL  
PROTEOMICS**

16:00–16:30 Coffee-break

Computer demos will be available during the entire conference day

**July 28, Wednesday, Foyer of the Small Conference Hall**

9:00–11:30 POSTER SESSION

11:00–11:30 Coffee-break

12:30–14:00 Lunch

**July 29, Thursday, Small Conference Hall**

9:00–13:00 Morning Session

**COMPUTATIONAL EVOLUTIONARY BIOLOGY**

11:00–11:30 Coffee-break

13:00–14:30 Lunch

14:30–17:00 Evening Session

**COMPUTATIONAL EVOLUTIONARY BIOLOGY**

15:30–16:00 Coffee-break

Computer demos will be available during the entire conference day

**July 29, Thursday, Music Salon (room № 220)**

9:00–12:30 Morning Session

**NEW APPROACHES TO ANALYSIS OF BIOMOLECULAR DATA  
AND PROCESSES**

10:30–11:00 Coffee-break

12:30–14:00 Lunch

14:00–17:50 Evening Session

**NEW APPROACHES TO ANALYSIS OF BIOMOLECULAR DATA  
AND PROCESSES**

16:00–16:30 Coffee-break

**July 30, Friday, Conference Hall of the Institute of Cytology  
and Genetics**

**10:00–13:00 TUTORIAL “HIGH PERFORMANCE COMPUTING  
IN BIOINFORMATICS”**

11:00–11:30 Coffee-break

13:00–14:30 Lunch

**July 30, Friday, Small Conference Hall**

9:00–13:00 Morning Session

**COMPUTATIONAL SYSTEM BIOLOGY**

11:00–11:30 Coffee-break

13:00–14:30 Lunch

14:30–17:00 Evening Session

**COMPUTATIONAL SYSTEM BIOLOGY**

15:30–16:00 Coffee-break

Computer demos will be available during the entire conference day

**17:30–18:00 Closing ceremony. Summaries from session chairpersons**

# THE FOURTH INTERNATIONAL CONFERENCE ON BIOINFORMATICS OF GENOME REGULATION AND STRUCTURE (BGRS'2004)

July 25–30, 2004, Novosibirsk, Russia

## Program of oral presentations

The speakers are encouraged to bring their demonstration materials to Room № 200 of the House of Scientists no later than 30 minutes before their session begins.

If you have any questions, please do not hesitate to contact the Organizing Committee in Room № 200 at the House of Scientists.

**July 25, Sunday,** House of Scientists, Small Conference Hall

14:30–17:30 Evening Session

### COMPUTATIONAL STRUCTURAL AND FUNCTIONAL GENOMICS

Chairpersons:

Prof. Ralf Hofestaedt, Bielefeld University, Bielefeld, Germany

Dr. Patrizio Arrigo, CNR ISMAC, Section of Genova, Genova, Italy

Author(s) and Title of Talk	Timeline
Dadashev S.Ya., Grishaeva T.M., <b>Bogdanov Yu.F.</b> N.I. Vavilov Institute of General Genetics RAS, Moscow, Russia DEVELOPMENT OF A METHOD FOR <i>IN SILICO</i> IDENTIFICATION OF DNA SEQUENCES PARTICIPATING IN MEIOTIC CHROMOSOME SYNAPSIS AND RECOMBINATION	14:30–15:00
<b>Sarai A.</b> <sup>1</sup> , Ahmad S. <sup>1</sup> , Gromiha M.M. <sup>2</sup> , Kono H. <sup>3</sup> <sup>1</sup> Dept. Bioscience & Bioinformatics, Kyushu Institute of Technology, Iizuka, Japan <sup>2</sup> Computational Biology Research Center, AIST, Tokyo, Japan <sup>3</sup> Neutron Science Research Center and Center for Promotion of Computational Science and Engineering Japan Atomic Energy Research Institute, Kyoto, Japan GENOME-SCALE PREDICTION OF TRANSCRIPTION FACTORS AND THEIR TARGETS	15:00–15:30

**Makeev V.J.<sup>1</sup>, Lifanov A.P.<sup>2</sup>, Nazina A.G.<sup>3</sup>, Papatsenko D.A.<sup>3</sup>**

<sup>1</sup> Scientific Center "Genetika", Moscow, Russia

<sup>2</sup> Engelhardt Institute of Molecular Biology, Moscow, Russia

<sup>3</sup> Department of Biology, New York University, New York, USA

**15:30–16:00**

**DISTANCE PREFERENCES IN DISTRIBUTION OF BINDING  
MOTIFS AND HIERARCHICAL LEVELS IN ORGANIZATION  
OF TRANSCRIPTION REGULATORY INFORMATION**

***Coffee/tea-break 16:00–16:30***

**Bucher Ph.**

Swiss Institute of Bioinformatics, Epalinges s/Lausann, Switzerland

**16:30–17:00**

**MODELING TRANSCRIPTION FACTOR BINDING SITES  
WITH HIGH-THROUGHPUT SELEX DATA**

**Brok-Volchanski A.S.<sup>1</sup>, Purtov Yu.A.<sup>1</sup>, Lukyanov V.I.<sup>1</sup>,**

**Kostyanicina E.G.<sup>1</sup>, Antipov S.S.<sup>1</sup>, Deev A.A.<sup>2</sup>, **Ozoline O.N.<sup>1</sup>****

<sup>1</sup> Institute of Cell Biophysics RAS, Pushchino, Moscow region, Russia

<sup>2</sup> Institute of Theoretical and Experimental Biophysics RAS, Pushchino, Moscow  
region, Russia

**17:00–17:30**

**GENOME-WIDE MAPPING OF POTENTIALLY TRANSCRIBED  
REGIONS BY NEW PROMOTER-SEARCH ALGORITHM**

## **July 26, Monday, Small Conference Hall**

**9:00–12:30 Morning Session**

### **COMPUTATIONAL STRUCTURAL AND FUNCTIONAL GENOMICS**

#### **Chairpersons:**

Prof. Philipp Bucher, Swiss Institute of Bioinformatics, Epalinges s/Lausann, Switzerland

Prof. Yuri Bogdanov, The Vavilov Institute of General Genetics, Moscow, Russia

Author(s) and Title of Talk	Timeline
<b>Ignatieva E.V.</b> , Oshchepkov D.Yu., Levitsky V.G., Vasiliev G.V., Klimova N.V., Busygina T.V., Merkulova T.I. Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia	
<b>COMPARISON OF THE RESULTS OF SEARCH FOR THE SF-1 BINDING SITES IN THE PROMOTER REGIONS OF THE STEROIDOGENIC GENES, USING THE SITEGA AND SITECON METHODS</b>	<b>9:00–9:30</b>
<b>Levitsky V.G.</b> , Proscura A.P., Podkolodnaya O.A., Ignatieva E.V., Ananko E.A. Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia	
<b>NUCLEOSOME FORMATION POTENTIAL OF THE GENE REGULATORY REGIONS</b>	<b>9:30–10:00</b>



**Kochetov A.V.<sup>1</sup>, Sarai A.<sup>2</sup>, Kolchanov N.A.<sup>1</sup>**

<sup>1</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

<sup>2</sup> Kyushu Institute of Technology, Dept. Biochemical Engineering and Science, Iizuka, Japan **10:00–10:30**

**TRANSLATIONAL POLYMORPHISM AS A POTENTIAL SOURCE  
OF EUKARYOTIC PROTEINS VARIETY**

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***Coffee/tea-break 10:30–11:00***

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**Makunin I.V.<sup>1</sup>, Stephen S.<sup>1</sup>, Pheasant M.<sup>1</sup>, Bejerano G.<sup>2</sup>, Kent J.W.<sup>2</sup>,  
Haussler H.<sup>3</sup>, Mattick J.S.<sup>1</sup>**

<sup>1</sup> ARC Special Research Centre for Functional and Applied Genomics, Institute for  
Molecular Bioscience, University of Queensland, Brisbane, Australia

<sup>2</sup> Department of Biomolecular Engineering, University of California Santa Cruz, Santa  
Cruz, CA, USA **11:00–11:30**

<sup>3</sup> Howard Hughes Medical Institute, University of California Santa Cruz, Santa Cruz,  
CA, USA

**EXTREMELY CONSERVED NON-CODING SEQUENCES IN  
VERTEBRATE GENOMES**

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**Kersey P.J., Morris L., Faruque N., Kulikova T., Whitfield E., Apweiler R.**  
EMBL Outstation, European Bioinformatics Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridge, UK **11:30–12:00**

**GENOME REVIEWS: INTEGRATED VIEWS OF COMPLETE  
GENOMES**

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**Orlov Yu.L.<sup>1</sup>, Potapov V.N.<sup>2</sup>, Poplavsky A.S.<sup>1</sup>**

<sup>1</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

<sup>2</sup> Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia **12:00–12:30**

**COMPUTER ANALYSIS OF GENOMIC SEQUENCE COMPLEXITY:  
NEW APPLICATIONS**

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***Lunch 12:30–14:00***

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**July 26, Monday, Small Conference Hall**

**14:00–16:30 Evening Session**

**COMPUTATIONAL STRUCTURAL AND FUNCTIONAL GENOMICS**

**Chairpersons:**

Prof. Akinori Sarai, Kyushu Institute of Technology, Iizuka, Japan

Dr. Vsevolod Makeev, State Scientific Center “GosNII Genetika”, Moscow, Russia

Author(s) and Title of Talk	Timeline
<b>Abnizova I., te Boekhorts R., Gilks W.</b> MRC-BSU Cambridge, University of Hertfordshire Hatfield, UK <b>SOME WAYS TO INFER A DNA FUNCTION FROM THE SEQUENCE INFORMATION</b>	<b>14:00–14:30</b>

Astakhova T.V.<sup>1</sup>, Petrova S.V.<sup>1</sup>, Tsitovich I.I.<sup>2</sup>, **Roytberg M.A.**<sup>1</sup>

<sup>1</sup> Institute of Mathematical Problems in Biology RAS, Puschino, Moscow region, Russia

<sup>2</sup> Institute of Information Transmission Problems RAS, Moscow, Russia

14:30–15:00

RECOGNITION OF CODING REGIONS IN GENOME ALIGNMENT

*Coffee/tea-break 15:00–15:30*

**Xia X.**

Department of Biology, University of Ottawa, Ottawa, Canada

15:30–16:00

A PECULIAR CODON USAGE PATTERN REVEALED AFTER  
REMOVING THE EFFECT OF DNA METHYLATION

**Alexeevski A.V.**<sup>1</sup>, Lukina E.N.<sup>1</sup>, Salnikov A.N.<sup>2</sup>, Spirin S.A.<sup>1</sup>

<sup>1</sup> Belozersky Institute, Moscow State University, Moscow, Russia

<sup>2</sup> Department of Computational Mathematics and Cybernetic, Moscow State  
University, Moscow, Russia

16:00–16:30

DATABASE OF LONG TERMINAL REPEATS IN HUMAN  
GENOME: STRUCTURE AND SYNCHRONIZATION WITH MAIN  
GENOME ARCHIVES

**July 27, Tuesday, Small Conference Hall**

9:00–13:00 Morning Session

**COMPUTATIONAL STRUCTURAL AND FUNCTIONAL PROTEOMICS**

Chairpersons:

Dr. Luciano Milanesi, Institute of Advanced Biomedical Technologies, CNR,  
Segrate/Milan, Italy

Prof. Sergei Chekmarev, Institute of Thermophysics SB RAS, Novosibirsk, Russia

Author(s) and Title of Talk	Timeline
Turutina V.P., <b>Korotkov E.V.</b> , Laskin A.A. Bioengineering Center RAS, Moscow, Russia LATENT PERIODICITY OF THE PROTEIN FAMILIES	9:00–9:30
Surya pavan Y., <b>Mitra C.K.</b> Department of Biochemistry, University of Hyderabad, Hyderabad, India A MARKOV MODEL FOR PROTEIN SEQUENCES	9:30–10:00
<b>Kalinina O.V.</b> <sup>1</sup> , Novichkov P.S. <sup>1</sup> , Mironov A.A. <sup>1, 2</sup> , Gelfand M.S. <sup>2, 3</sup> , Rakhmaninova A.B. <sup>1</sup> <sup>1</sup> Department of Bioengineering and Bioinformatics, Moscow State University, Moscow, Russia <sup>2</sup> State Scientific Center GosNIIGenetika, Moscow, Russia <sup>3</sup> Institute for Problems of Information Transmission RAS, Moscow, Russia SDPPRED: A METHOD FOR PREDICTION OF AMINO ACID RESIDUES THAT DETERMINE DIFFERENCES IN FUNCTIONAL SPECIFICITY OF HOMOLOGOUS PROTEINS AND ITS APPLICATION TO THE MIP FAMILY OF MEMBRANE TRANSPORTERS	10:00–10:30

**Efremov R.G.**, Volynsky P.E., Nolde D.E., Vereshaga Y.A.,  
 Konshina A.G., Simakov N.A., Arseniev A.S.  
 M.M. Shemyakin and Yu.A. Ovchinnikov Institute of Bioorganic Chemistry RAS,  
 Moscow, Russia **10:30–11:00**  
 MEMBRANE PROTEINS: THE NEW INSIGHTS *VIA*  
 COMPUTATIONAL EXPERIMENTS

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***Coffee/tea-break 11:00–11:30***

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Kuznetsov V.A.<sup>1</sup>, Pickalov V.V.<sup>2</sup>, Knott G.D.<sup>3</sup>, **Kanapin A.A.**<sup>4</sup>  
<sup>1</sup> CIT/NIH & SRA International, Inc. Bethesda, MD, USA  
<sup>2</sup> Institute of Theoretical and Applied Mechanics SB RAS, Novosibirsk, Russia  
<sup>3</sup> Civilized Software, Inc., Silver Spring, MD, USA **11:30–12:00**  
<sup>4</sup> EMBL-EBI Wellcome Trust Genome Campus, Hinxton, UK  
 ANALYSIS OF PROTEOME COMPLEXITY BASED ON COUNTING  
 DOMAIN-TO-PROTEIN LINKS

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**Ramachandran S.**, Jain P., Sachdeva G.  
 G.N. Ramachandran Knowledge Center for Genome Informatics, Institute of  
 Genomics and Integrative Biology, Delhi, India **12:00–12:30**  
 MINING FROM COMPLETE PROTEOMES TO IDENTIFY  
 ADHESINS AND ADHESIN-LIKE PROTEINS: A RAPID AID  
 TO EXPERIMENTAL RESEARCHERS

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**Ivanisenko V.A.**<sup>1</sup>, Pintus S.S.<sup>2</sup>, Krestyanova M.A.<sup>2</sup>, Demenkov P.S.<sup>2</sup>,  
 Znobisheva E.K.<sup>2</sup>, Ivanov E.E.<sup>2</sup>, Grigorovich D.A.<sup>1</sup>  
<sup>1</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia **12:30–13:00**  
<sup>2</sup> Novosibirsk State University, Novosibirsk, Russia  
 PROTEIN FUNCTIONAL SITE PREDICTION AND RELATED  
 PROBLEMS

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***Lunch 13:00–14:30***

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**July 27, Tuesday, Small Conference Hall**

14:30–18:00 Evening Session

**COMPUTATIONAL STRUCTURAL AND FUNCTIONAL PROTEOMICS**

**Chairpersons:**

Prof. Chanchal Mitra, University of Hyderabad, Hyderabad, India

Prof. Eugene Korotkov, Center of Bioengineering RAS, Moscow, Russia

Author(s) and Title of Talk	Timeline
Ko J. <sup>2</sup> , Andre P. <sup>1</sup> , Murga L.F. <sup>1</sup> , <b>Ondrechen M.J.</b> <sup>1</sup> <sup>1</sup> Department of Chemistry and Chemical Biology and Institute for Complex Scientific Software, Northeastern University, Boston, Massachusetts, USA <sup>2</sup> NSF-ROA Awardee on Leave from Department of Chemistry, Indiana University of Pennsylvania, Indiana, Pennsylvania, USA <b>14:30–15:00</b> STATISTICAL METRICS FOR PROTEIN ACTIVE SITE PREDICTION WITH THEMATICS	

**Milanesi L.<sup>1</sup>, Merelli I.<sup>1</sup>, Pattini L.<sup>2</sup>, Cerutti S.<sup>2</sup>**

<sup>1</sup> Institute of Advanced Biomedical Technologies, CNR, Milan, Italy

<sup>2</sup> Department of Biomedical Engineering, Polytechnic University of Milan, Milan, Italy

**15:00–15:30**

**REPRESENTATION AND MODELING OF PROTEIN SURFACE DETERMINANTS**

**Ramensky V.E., Tumanyan V.G.**

Engelhardt Institute of Molecular Biology RAS, Moscow, Russia

**15:30–16:00**

**MUTANT PROTEIN STRUCTURES REVEAL MOLECULAR MECHANISMS OF INHERITED DISEASES**

*Coffee/tea-break 16:00–16:30*

**Rahmanov S.V., Makeev V.Yu.**

Laboratory of Bioinformatics, GosNIIGenetika, Moscow, Russia

**16:30–17:00**

**CONSTRUCTING DETAILED KNOWLEDGE-BASED ATOMIC POTENTIALS FOR WATER IN PROTEINS**

**Shaitan K.V.**

M.V. Lomonosov Moscow State University, Moscow, Russia

**17:00–17:30**

**MOLECULAR DYNAMICS SIMULATIONS FOR LARGE SERIES OF PEPTIDES (COMPARATIVE STUDY)**

**Chekmarev S.F.<sup>1,2</sup>, Palyanov A.Yu.<sup>2</sup>, Krivov S.V.<sup>3</sup>, Titov I.I.<sup>2,4</sup>, Karplus M.<sup>3,5</sup>**

<sup>1</sup> Institute of Thermophysics SB RAS, Novosibirsk, Russia

<sup>2</sup> Novosibirsk State University, Novosibirsk, Russia

<sup>3</sup> Laboratoire de Chimie Biophysique, ISIS, Université Louis Pasteur, Strasbourg, France

**17:30–18:00**

<sup>4</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

<sup>5</sup> Department of Chemistry & Chemical Biology, Harvard University, Cambridge, MA, USA

**KINETICS OF PROTEIN FOLDING AND MISFOLDING: LATTICE SIMULATIONS AND ANALYTIC MODEL**

**July 29, Thursday, Small Conference Hall**

**9:00–13:00 Morning Session**

**COMPUTATIONAL EVOLUTIONARY BIOLOGY**

**Chairpersons:**

Prof. Lev Zhivotovsky, N.I. Vavilov Institute of General Genetics RAS, Moscow, Russia

Dr. Mikhail Roitberg, Institute of Mathematical Problems in Biology RAS, Pushchino, Moscow region, Russia

Author(s) and Title of Talk	Timeline
<b>Gelfand M.S.</b> Institute for Information Transmission Problems RAS, Moscow, Russia State Scientific Center GosNIIGenetika, Moscow, Russia Department of Bioengineering and Bioinformatics, Moscow State University, Moscow, Russia	<b>9:00–9:30</b>
<b>EVOLUTION OF BACTERIAL REGULATORY SYSTEMS</b>	

**Nishio Y.**<sup>1</sup>, Nakamura Y.<sup>2</sup>, Usuda Y.<sup>1</sup>, Kawarabayasi Y.<sup>3</sup>, Yamagishi A.<sup>4</sup>, Kimura E.<sup>1</sup>, Matsui K.<sup>1</sup>, Sugimoto S.<sup>5</sup>, Kikuchi H.<sup>6</sup>, Ikeo K.<sup>2</sup>, Gojobori T.<sup>2</sup>

<sup>1</sup> Institute of Life Sciences, Ajinomoto Co., Inc., Kawasaki, Japan

<sup>2</sup> Center for Information Biology and DNA Data Bank of Japan, National Institute of Genetics, Mishima, Japan

<sup>3</sup> Research Center for Glycoscience, National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba, Japan

<sup>4</sup> Department of Molecular Biology, Tokyo University of Pharmacy and Life Science, Hachioji, Japan

<sup>5</sup> Fermentation & Biotechnology Laboratories, Ajinomoto Co., Inc., Kawasaki, Japan

<sup>6</sup> National Institute of Technology and Evaluation, Shibuya, Japan

# COMPARATIVE COMPLETE GENOME SEQUENCE ANALYSIS OF *CORYNEBACTERIA*

9:30–10:00

**Bazykin G.A.**<sup>1</sup>, Ogurtsov A.Y.<sup>2</sup>, Kondrashov A.S.<sup>2</sup>

<sup>1</sup> Dept. of Ecology and Evolutionary Biology, Princeton University, Princeton, NJ, USA

<sup>2</sup> National Center for Biotechnology Information, NIH, Bethesda, Maryland, USA

10:00–10:30

# CHANGE IN CpG CONTEXT IS A LEADING CAUSE OF CORRELATION BETWEEN RATES OF NON-SYNONYMOUS AND SYNONYMOUS SUBSTITUTIONS IN RODENTS

**Stamatakis A.P.**, Ludwig T., Meier H.

Department of Computer Science, Technische Universität München

Department of Computer Science, Ruprecht-Karls Universität Heidelberg

10:30–11:00

# COMPUTING LARGE PHYLOGENIES WITH STATISTICAL METHODS: PROBLEMS AND SOLUTIONS

## *Coffee/tea-break 11:00–11:30*

**Kapitonov V.V.**, Jurka J.

Genetic Information Research Institute, Mountain View, CA, USA

# MOLECULAR PALEONTOLOGY OF DNA TRANSPOSONS IN EUKARYOTIC GENOMES

11:30–12:00

Beresikov E.<sup>3</sup>, Novikova O.<sup>1</sup>, Makarevich I.<sup>2</sup>, Lashina V.<sup>1</sup>, Plasterk R.<sup>3</sup>, **Blinov A.G.**<sup>1</sup>

<sup>1</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

<sup>2</sup> Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, USA

<sup>3</sup> Hubrecht Laboratory, Netherlands Institute for Developmental Biology, Utrecht, The Netherlands

12:00–12:30

# EVOLUTIONARY RELATIONSHIPS AND DISTRIBUTION OF NON-LTR RETROTRANSPOSONS IN EUKARYOTES

**Vershinin A.V.**<sup>1,2</sup>, Allnutt T.R.<sup>2</sup>, Knox M.R.<sup>2</sup>, Ambrose M.J.<sup>2</sup>, Ellis T.H.N.<sup>2</sup>

<sup>1</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

<sup>2</sup> John Innes Centre, Norwich, UK

12:30–13:00

# DOMINANT MODE IN *PISUM* DIVERSITY GENERATION: WHAT IS THE IMPACT OF TRANSPOSABLE ELEMENTS?

## *Lunch 13:00–14:30*

**July 29, Thursday, Small Conference Hall**

14:30–17:00 Evening Session

## COMPUTATIONAL EVOLUTIONARY BIOLOGY

Chairperson:

Dr. Mikhail Gelfand, Institute for Information Transmission Problems, Moscow, Russia

Author(s) and Title of Talk	Timeline
<b>Wyrwicz L.S., Rychlewski L.</b> Bioinformatics Laboratory, BioInfoBank Institute, Poznan, Poland <b>SCANNING THE HUMAN GENOME FOR REGULATORY ISLANDS WITH PHYLOGENETIC FOOTPRINTING ALGORITHM</b>	<b>14:30–15:00</b>
<b>Zhivotovsky L.A.</b> N.I. Vavilov Institute of General Genetics RAS, Moscow, Russia <b>DATING POPULATION EXPANSION BASED ON STR VARIATION WITHIN Y-CHROMOSOME SNP-HAPLOGROUPS</b>	<b>15:00–15:30</b>
<b><i>Coffee/tea-break 15:30–16:00</i></b>	
<b>Zhou Z., Kwoh C.K.</b> Bioinformatics Research Centre, School of CE, Nanyang Technological University, Singapore <b>AN EVOLUTIONARY LINEAGE FOR INTRON LOSS/GAIN IN FIVE EUKARYOTIC GENOMES</b>	<b>16:00–16:30</b>
<b>Sherbakov D.Yu.<sup>1</sup>, Martens K.<sup>2</sup>, Schoen I.<sup>2</sup></b> <sup>1</sup> Limnological Institute SB RAS, Irkutsk, Russia <sup>2</sup> Royal Belgian Institute for Natural Sciences, Brussels, Belgium <b>EXPLAINING APPARENT STALL OF MOLECULAR EVOLUTION IN ASEXUAL OSTRACOD DARWINULA: MODELING APPROACH</b>	<b>16:30–17:00</b>

## July 29, Thursday, Music Salon (room № 220)

9:00–12:30 Morning Session

### NEW APPROACHES TO ANALYSIS OF BIOMOLECULAR DATA AND PROCESSES

Chairpersons:

Dr. Olga Ozoline, Institute of Cell Biophysics RAS, Pushchino, Moscow region, Russia

Author(s) and Title of Talk	Timeline
<b>Binder H.<sup>1</sup>, Kirsten T.<sup>1</sup>, Loeffler M.<sup>1</sup>, Preibisch St.<sup>1</sup>, Stadler P.<sup>1,2</sup></b> <sup>1</sup> Interdisciplinary Centre for Bioinformatics, University of Leipzig, Germany <sup>2</sup> Institute for Informatics, University of Leipzig, Germany <b>SEQUENCE-SPECIFIC SENSITIVITY OF OLIGONUCLEOTIDE PROBES – A MOLECULAR VIEW ON RNA/DNA HYBRIDISATION ON MICROARRAYS AND CONSEQUENCES FOR GENE EXPRESSION ANALYSIS AND CHIP DESIGN</b>	<b>9:00–9:30</b>
<b>Blagov M.S., Poustelnikova E.G., Pisarev A.S., Myasnikova E.M., Samsonova M.G.</b> St.Petersburg State Polytechnical University, St.Petersburg, Russia <b>A SYSTEM FOR ON-LINE PROCESSING OF IMAGES OF GENE EXPRESSION PATTERNS</b>	<b>9:30–10:00</b>
Fattore M., <b>Arrigo P.</b> CNR ISMAC, Section of Genova, Genova, Italy <b>TOPICAL CLUSTERING OF BIOMEDICAL ABSTRACT BY SELF ORGANIZING MAPS</b>	<b>10:00–10:30</b>
<b><i>Coffee/tea-break 10:30–11:00</i></b>	

**Favorov A.V.<sup>1</sup>, Gelfand M.S.<sup>1,2,3</sup>, Gerasimova A.V.<sup>1</sup>, Mironov A.A.<sup>1,3</sup>,  
Makeev V.J.<sup>1</sup>**

<sup>1</sup> State Scientific Centre “GosNIIGenetica”, Moscow, Russia

<sup>2</sup> Institute for Problems of Information Transmission RAS, Moscow, Russia

<sup>3</sup> Dept. of Bioengineering and Bioinformatics, Moscow State University, Moscow, Russia

**11:00–11:30**

**GIBBS SAMPLER FOR IDENTIFICATION OF SYMMETRICALLY  
STRUCTURED, SPACED DNA MOTIFS WITH IMPROVED  
ESTIMATION OF THE SIGNAL LENGTH AND ITS VALIDATION ON  
THE ARCA BINDING SITES**

**Frisman E.Ya.<sup>1</sup>, Zhdanova O.L.<sup>2</sup>**

<sup>1</sup> Complex Analysis of Regional Problems Institute FEB RAS, Birobidzhan, Russia

<sup>2</sup> Institute of Automation and Control Processes FEB RAS, Vladivostok, Russia

**11:30–12:00**

**MATHEMATICAL MODELING AND ANALYSIS OF THE  
FIXATION PROCESS OF DISCRETE GENETIC STRUCTURES  
IN A MENDELIAN ONE-LOCUS POPULATION OF DIPLOID  
ORGANISMS**

**Gorban A.N.<sup>1,2</sup>, Popova T.G.<sup>1</sup>, Zinovyev A.Yu.<sup>3</sup>**

<sup>1</sup> Institute of Computational Modeling SB RAS, Krasnoyarsk, Russia

<sup>2</sup> Institute of Polymer Physics, ETH, Zurich, Switzerland

<sup>3</sup> Institut des Hautes Études Scientifiques, Bures-sur-Yvette, France

**12:00–12:30**

**SEVEN CLUSTERS AND UNSUPERVISED GENE PREDICTION**

***Lunch 12:30–14:00***

**July 29, Thursday, Music Salon (room № 220)**

**14:00–17:50 Evening Session**

**NEW APPROACHES TO ANALYSIS OF BIOMOLECULAR  
DATA AND PROCESSES**

**Chairpersons:**

Prof. Andrey Mironov, Moscow State University, Moscow, Russia

Dr. Hans Binder, Interdisciplinary Centre for Bioinformatics, University  
of Leipzig, Germany

Author(s) and Title of Talk	Timeline
Lyubetsky V.A., <b>Gorbunov K.Yu.</b> , V'yugin V.V. Institute for Information Transmission Problems RAS, Moscow, Russia <b>MEASURING THE DISSIMILARITY BETWEEN GENE AND SPECIES TREES, THE QUALITY OF A COG</b>	<b>14:00–14:30</b>
<b>Myasnikova E.M.<sup>1</sup></b> , Reinitz J. <sup>2</sup> <sup>1</sup> St.Petersburg State Polytechnical University, St.Petersburg, Russia <sup>2</sup> University at Stony Brook, New York, USA <b>DETERMINATION OF THE DEVELOPMENTAL AGE OF A DROSOPHILA EMBRYO FROM CONFOCAL IMAGES OF ITS SEGMENTATION GENE EXPRESSION PATTERNS</b>	<b>14:30–15:00</b>
Noe L., <b>Kucherov G.</b> LORIA/INRIA-Lorraine, Villers-les-Nancy, France <b>YASS: ENHANCING THE SENSITIVITY OF DNA SIMILARITY SEARCH</b>	<b>15:00–15:30</b>

**Novichkov P.<sup>1</sup>**, Brudno M.<sup>2</sup>, Mironov A.<sup>1</sup>

<sup>1</sup> Moscow State University, Faculty of Bioengineering & Bioinformatics, Moscow, Russia

<sup>2</sup> Stanford University, Department of Computer Science, Clark Center, Room S260,  
Stanford, CA, USA

**15:30–16:00**

**MAXIMAL INFORMATION CONTENT SEEDS FOR SEQUENCE  
ALIGNMENT**

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***Coffee/tea-break 16:00–16:30***

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**Pozdnyakov M.A.<sup>1</sup>**, Orlov Yu.L.<sup>1</sup>, Vishnevsky O.V.<sup>1</sup>, Proscura A.L.<sup>1</sup>,  
Vityaev E.E.<sup>2</sup>, Arrigo P.<sup>3</sup>

<sup>1</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

<sup>2</sup> Sobolev Institute of Mathematics, Novosibirsk, Russia

<sup>3</sup> ISMAC, Genova, Italy

**16:30–17:00**

**ANALYSIS OF GENE REGULATORY SEQUENCES  
BY KNOWLEDGE DISCOVERY METHODS**

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**Shelenkov A.A.**, Chaley M.B., Korotkov E.V.

Center of Bioengineering RAS, Moscow, Russia

**REVELATION AND CLASSIFICATION OF DINUCLEOTIDE  
PERIODICITY OF BACTERIAL GENOMES USING THE METHODS  
OF INFORMATION DECOMPOSITION AND MODIFIED PROFILE  
ANALYSIS**

**17:00–17:30**

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**Deyneko I.V.<sup>1,2</sup>**, Kel A.E.<sup>3</sup>, Wingender E.<sup>3</sup>, Gössling F.<sup>2</sup>, Blöcker H.<sup>2</sup>,  
Kauer G.<sup>2,4</sup>

<sup>1</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

<sup>2</sup> Department of Genome Analysis, GBF, Braunschweig, Germany

<sup>3</sup> BIOBASE GmbH, Wolfenbuettel, Germany

<sup>4</sup> FH Oldenburg/Ostfriesland/Wilhelmshaven, Germany

**17:30–17:50**

**SIGNAL THEORY – AN ALTERNATIVE PERSPECTIVE  
OF PATTERN SIMILARITY SEARCH**

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**July 30, Friday**, Conference Hall of the Institute of Cytology and Genetics  
**10:00–13:00**

**TUTORIAL “HIGH PERFORMANCE COMPUTING IN  
BIOINFORMATICS”**

**Chairpersons:**

Dr. Dmitry Afonnikov, Institute of Cytology and Genetics SB RAS,  
Novosibirsk, Russia

Dr. Dmitry Sherbakov, Limnological Institute SB RAS, Irkutsk, Russia

Mr. Alexandros Stamatakis, Technische Universitaet Muenchen, Munich, Germany

***Coffee/tea -break 11:00–11:30***

***Lunch 13:00–14:30***



## July 30, Friday, Small Conference Hall

9:00–13:00 Morning Session  
COMPUTATIONAL SYSTEM BIOLOGY

### Chairpersons:

Dr. Vladimir Kapitonov, Genetic Information Research Institute, Mountain View, CA, USA  
Dr. Maria Samsonova, Department of Computational Biology, Center for Advanced Studies, St. Petersburg State Polytechnical University, St. Petersburg, Russia

Author(s) and Title of Talk	Timeline
Chaouiya C. <sup>1</sup> , Sanchez L. <sup>2</sup> , <b>Thieffry D.</b> <sup>1</sup> <sup>1</sup> Laboratory of Developmental Genetics and Physiology, Marseille, France <sup>2</sup> Centro de Investigaciones Biológicas, Madrid, Spain FROM GRADIENTS TO STRIPES: A LOGICAL ANALYSIS OF THE GENETIC NETWORK CONTROLLING EARLY DROSOPHILA SEGMENTATION	9:00–9:30
Gor V. <sup>1</sup> , Shapiro B.E. <sup>1</sup> , Jönsson H. <sup>2</sup> , Heisler M. <sup>1</sup> , Venugopala Reddy G. <sup>1</sup> , Meyerowitz E.M. <sup>1</sup> , <b>Mjolsness E.</b> <sup>3</sup> <sup>1</sup> California Institute of Technology, Pasadena, CA, USA <sup>2</sup> Lund University, Lund, Sweden <sup>3</sup> University of California, Irvine, CA, USA A SOFTWARE ARCHITECTURE FOR DEVELOPMENTAL MODELING IN PLANTS: THE COMPUTABLE PLANT PROJECT	9:30–10:00
<b>Hofstaedt R.</b> , Chen M. Bioinformatics / Medical Informatics, Technische Fakultät, Universitaet Bielefeld, Bielefeld, Germany METABOLIC PATHWAY PREDICTION/ALIGNMENT	10:00–10:30
Likhoshvai V.A. <sup>2,3</sup> , <b>Demidenko G.V.</b> <sup>1</sup> , Fadeev S.I. <sup>1</sup> <sup>1</sup> Sobolev Institute for Mathematics SB RAS, Novosibirsk, Russia <sup>2</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia <sup>3</sup> Ugra Research Institute of Information Technologies, Khanty-Mansyisk, Russia MODELING OF SUBSTANCE SYNTHESIS PROCESS WITHOUT BRANCHING BY THE DELAY EQUATION	10:30–11:00
<b>Coffee/tea-break 11:00–11:30</b>	
<b>Mironov A.A.</b> <sup>1,2</sup> <sup>1</sup> Moscow State University, Department of Bioengineering and Bioinformatics, Moscow, Russia <sup>2</sup> State Scientific Centre "GosNIIGenetika", Moscow, Russia RIBOSWITCHES – A NOVEL TYPE OF REGULATORY SYSTEM	11:30–12:00

**Nutsch T.<sup>1</sup>, Marwan W.<sup>2</sup>, Oesterhelt D.<sup>3</sup>, Gilles E.D.<sup>1</sup>**

<sup>1</sup>Max-Planck-Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany

<sup>2</sup>Science & Technology Research Centre, University of Hertfordshire, U.K.

<sup>3</sup>Max-Planck-Institute for Biochemistry, Martinsried, Germany

**12:00–12:30**

**A COHERENT KINETIC MODEL OF SENSING AND RESPONSE  
IN *HALOBACTERIUM SALINARIUM* PHOTOTAXIS BASED  
ON THE MECHANISM OF FLAGELLAR MOTOR SWITCHING**

**Omelyanchuk L.V., Gunbin K.V.**

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

**12:30–13:00**

**ELEMENTARY MODULE, RECOGNIZING MORPHOGENETIC  
GRADIENTS IN THE TISSUES**

***Lunch 13:00–14:30***

**July 30, Friday, Small Conference Hall**

**14:30–17:00 Evening Session**

**COMPUTATIONAL SYSTEM BIOLOGY**

**Chairpersons:**

Prof. Denis Thieffry, LGPD-IBDM, Marseille, France

Dr. Eric Mjolsness, University of California, Irvine, CA, USA

Author(s) and Title of Talk	Timeline
<b>Omelianchuk N.A., Mironova V.V., Poplavsky A.S., Kukeeva Yu.A., Podkolodny N.L., Kolchanov N.A.</b> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia	<b>14:30–15:00</b>
<b>AGNS: ARABIDOPSIS GENENET SUPPLEMENTARY DATABASE</b>	
<b>Samsonova M.<sup>1</sup>, Surkova S.<sup>1</sup>, Jaeger J.<sup>2</sup>, Reinitz J.<sup>2</sup></b> <sup>1</sup> Department of Computational Biology, Center for Advanced Studies, St. Petersburg State Polytechnical University, St. Petersburg, Russia	
<sup>2</sup> Department of Applied Mathematics and Statistics, and Center for Developmental Genetics, Stony Brook University, Stony Brook, NY, USA	<b>15:00–15:30</b>
<b>QUANTITATIVE APPROACH TO THE FUNCTIONAL GENOMICS OF DEVELOPMENT</b>	
<b><i>Coffee/tea-break 15:30–16:00</i></b>	
<b>Tchuraev R.N.</b> Institute of Biology, Ufa Research Center RAS, Ufa, Russia	
<b>PRINCIPLES OF ORGANIZATION AND LAWS OF FUNCTIONING IN CONTROL GENE NETWORKS</b>	<b>16:00–16:30</b>

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**Zabarovsky E.R.**<sup>1,2</sup>, Kashuba V.I.<sup>1</sup>, Li J.<sup>1</sup>, Kutsenko A.S.<sup>1</sup>, Protopopov A.I.<sup>1</sup>,  
Petrenko L.<sup>1</sup>, Wang F.<sup>1</sup>, Senchenko V.N.<sup>3</sup>, Kadyrova E.<sup>4</sup>, Zabarovska V.I.<sup>1</sup>,  
Muravenko O.V.<sup>2</sup>, Zelenin A.V.<sup>2</sup>, Kisselev L.L.<sup>2</sup>, Winberg G.<sup>1</sup>, Ernberg I.<sup>1</sup>,  
Braga E.<sup>4</sup>, Lerman M.I.<sup>5</sup>, Klein G.<sup>1</sup>

<sup>1</sup> MTC and CGB, Karolinska Institute, Stockholm, Sweden

<sup>2</sup> EIMB RAS, Moscow, Russia

**16:30–17:00**

<sup>3</sup> Bioengineering Center and EIMB RAS, Moscow, Russia

<sup>4</sup> Russian State Genetics Center, Moscow, Russia

<sup>5</sup> FCI-NCI, Frederick, USA

**RESTRICTION SITE TAGGED PASSPORTS AND MICROARRAYS  
FOR ANALYSIS OF COMPLEX BIOLOGICAL SYSTEMS**

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**17:00–17:30 Closing ceremony. Summaries from session chairpersons**

# **THE FOURTH INTERNATIONAL CONFERENCE ON BIOINFORMATICS OF GENOME REGULATION AND STRUCTURE (BGRS'2004)**

July 25–30, 2004, Novosibirsk, Russia

## **POSTER SESSION**

The Poster Session will be held on **July 28** in the Small Conference Hall Foyer. There will be one single Poster Session for all conference sections.

Presentations may be posted starting from 09:00 a.m. July 26 and should be removed no later than 12:00 a.m. July 28.

The Poster presenters are encouraged to be near their poster boards on 28 July from 09:00 a.m. to 11:30 a.m.

If you have any questions, please do not hesitate to contact the Organizing Committee in Room № 200 at the House of Scientists.

## **POSTER PRESENTATIONS**

### **Abdeev R.M.**

Vavilov Institute of General Genetics RAS, Moscow, Russia

Center for Theoretical Problems of Physical-Chemical Bases of Pharmacology RAS, Moscow, Russia

A SYSTEMIC APPROACH TO COMPLEX, MULTI-FACTOR AUTOIMMUNE DISEASES  
AIMED AT CREATION OF ADEQUATE MODELS OF PATHOLOGIES (e.g. PSORIASIS)

### **Afonnikov D.A.**

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

Novosibirsk State University, Novosibirsk, Russia

PREDICTING CONTACT NUMBERS OF AMINO ACID RESIDUES USING A NEURAL  
NETWORK MODEL

**Afonnikov D.A.<sup>1,2</sup>, Ivanisenko V.A.<sup>1</sup>, Ignatieva E.V.<sup>1</sup>, Levitsky V.G.<sup>1</sup>, Likhoshvai V.A.<sup>1</sup>,  
Nikolaev S.V.<sup>1</sup>, Orlov Yu.L.<sup>1</sup>, Titov I.I.<sup>1</sup>, Kolchanov N.A.<sup>1</sup>**

<sup>1</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

<sup>2</sup> Novosibirsk State University, Novosibirsk, Russia

A CURRICULUM FOR BIOINFORMATICS AT THE CHAIR FOR INFORMATIONAL  
BIOLOGY, THE NOVOSIBIRSK STATE UNIVERSITY

**Albini G.<sup>1</sup>, Chetouani F.<sup>1</sup>, Rouillé S.<sup>1</sup>, Karsenty E.<sup>1</sup>, Thomas B.<sup>2</sup>, Legeai F.<sup>1</sup>, Samson D.<sup>1</sup>,  
Pereira L.<sup>5</sup>, Arcade A.<sup>3</sup>, Joets J.<sup>3</sup>, Scala D.<sup>2</sup>, Viara E.<sup>5</sup>, Barillot E.<sup>4</sup>, Duclert A.<sup>1</sup>**

<sup>1</sup> GénoplanteInfo, Unité de Recherche Génomique-Info, INRA, ÉVRY, France

<sup>2</sup> RhoBioInf, Evry Cedex, France

<sup>3</sup> INRA, Ferme du Moulon, Gif-sur-Yvette, France

<sup>4</sup> Institut Curie, Paris, France

<sup>5</sup> SYSRA, ÉVRY, France

GnpMap, AN ENVIRONMENT FOR GENETIC/PHYSICAL MAP DATA MANAGEMENT,  
VISUALIZATION AND COMPARATIVE ANALYSIS

**Amirova S.R., Machavariani M., Filatov I.V., Milchevsky Ju.V., Esipova N.G.,  
Tumanyan V.G.**

Engelhardt Institute of Molecular Biology RAS, Moscow, Russia

COMBINED APPROACH TO PROTEIN SECONDARY STRUCTURE PREDICTION

**Ananko E.A., Nedosekina E.A., Oshchepkov D.Yu., Lokhova I.V., Likhoshvai V.A.**

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

EBV INFECTION AND EBV TRANSFORMATION: RECONSTRUCTION OF GENE  
NETWORKS IN THE GENENET SYSTEM AND SEARCHING FOR REGULATORY  
POINTS

**Andrianov A.M.**

Institute of Bioorganic Chemistry of National Academy of Sciences, Minsk, Republic of Belarus

STRUCTURE AND POLYMORPHISM OF THE HIV-1 PRINCIPAL NEUTRALIZING  
EPITOPE

**Antyufeev V.S.<sup>1</sup>, Nikolaev S.V.<sup>2</sup>**

<sup>1</sup> Institute of Computational Mathematics and Mathematical Geophysics SB RAS, Novosibirsk,  
Russia

<sup>2</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

A FAST PROCEDURE FOR MODELING OF PROTEASOMAL PROTEIN DEGRADATION  
*IN VITRO*

**Babenko V.N.<sup>1,2</sup>, Sverdlov A.<sup>1</sup>, Rogozin I.B.<sup>1,2</sup>, Koonin E.V.<sup>2</sup>**

<sup>1</sup> National Center for Biotechnology Information, National Library of Medicine, National  
Institutes of Health, Bethesda, MD, USA

<sup>2</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

EVOLUTION OF GENE STRUCTURE IN EUKARYOTIC GENOMES

**Bachinsky A.G.<sup>1</sup>, Solovyev V.V.<sup>2</sup>**

<sup>1</sup> Permanent address: State Research Center of Virology and Biotechnology “Vector”, Koltsovo,  
Novosibirsk region, Russia

<sup>2</sup> Softberry Inc., Mount Kisco, NY, USA

NEW APPROACHES TO ANALYSIS OF PROTEIN STRUCTURE AND FUNCTION

**Belenikin M.S.**

Lomonosov Moscow State University, Department of Chemistry, Moscow, Russia

MOLECULAR MODELING AND COMPARATIVE ANALYSIS OF AMINO-TERMINAL  
DOMAIN OF NMDA IONOTROPIC GLUTAMATE RECEPTORS

**Boeva V.A.<sup>1</sup>, Regnier M.<sup>2</sup>, Makeev V.J.<sup>3</sup>**

<sup>1</sup> Moscow State University, Moscow, Russia

<sup>2</sup> INRIA Rocquencourt, Le Chesnay, France

<sup>3</sup> State Center GosNIIGenetika, Moscow, Russia

ALGORITHM FOR SEARCHING FOR HIGHLY DIVERGENT TANDEM  
REPEATS IN DNA SEQUENCES, STATISTICAL TESTS, AND BIOLOGICAL  
APPLICATION IN *DROSOPHILA MELANOGASTER* GENOME

**Chaley M.B., Frenkel F.E., Korotkov E.V., Skryabin K.G.**

Centre "Bioengineering" RAS, Moscow, Russia

RELATIONSHIPS BETWEEN GENERAL CLASSIFICATION OF GENES' LATENT  
TRIPLET PERIODICITY AND THE UNIVERSAL PHYLOGENETIC TREE

**Chelobanov B.P., Ivanisenko V.A.<sup>1</sup>, Kharkova M.V., Laktionov P.P., Rykova E.Yu.,  
Vlassov V.V.**

Institute of Chemical Biology and Fundamental Medicine SB RAS, Russia

<sup>1</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

IDENTIFICATION AND ANALYSIS OF CELL SURFACE NUCLEIC ACIDS-BINDING  
PROTEINS

**Chumakov M.I., Burmatov A.V., Bogdanov V.I., Volohina I.V.**

Institute of Biochemistry and Physiology of Plants and Microorganisms RAS, Saratov, Russia

EXPERIMENTAL AND COMPUTER EVALUATION OF AGROBACTERIAL SST-DNA  
BINDING VIRE2 PROTEIN ABILITY TO INTERACT WITH LIPID MEMBRANES

**Denisov S.V.<sup>1</sup>, Gelfand M.S.<sup>1, 2, 3</sup>**

<sup>1</sup> M.V. Lomonosov Moscow State University, Moscow, Russia

<sup>2</sup> Institute for Information Transmission Problems RAS, Moscow, Russia

<sup>3</sup> State Scientific Center GosNII Genetika, Moscow, Russia

CONSERVATION OF ALTERNATIVE SPLICING REGULATORY SIGNAL UGCAUG IN  
MOUSE AND HUMAN GENOMES

**Ershova A.S., Alexeevski A.V.<sup>1</sup>, Spirin S.A.<sup>1</sup>, Karyagina A.S.**

Institute of Agricultural Biotechnology, Russian Academy of Agricultural Sciences, Moscow,  
Russia

<sup>1</sup> Belozersky Institute, Moscow State University, Moscow, Russia

COMMON STRUCTURAL FEATURES OF HOMEODOMAINS AND HOMEODOMAIN-  
DNA COMPLEXES

**Fadeev S.I.<sup>1</sup>, Gainova I.A.<sup>1</sup>, Berezin A.Yu.<sup>1</sup>, Ratushny A.V.<sup>2</sup>, Matushkin Yu.G.<sup>2</sup>,  
Likhoshvai V.A.<sup>2, 3</sup>**

<sup>1</sup> Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia

<sup>2</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

<sup>3</sup> Ugra Research Institute of Information Technologies, Khanty-Mansyisk, Russia

DETERMINATION OF STATIONARY SOLUTIONS IN GENE NETWORK MODELS BY  
HOMOTOPY METHOD

**Fadeev S.I.<sup>1</sup>, Osokina V.A.<sup>2</sup>, Likhoshvai V.A.<sup>3, 4</sup>**

<sup>1</sup> Sobolev Institute of Mathematics SB RAS, Novosibirsk, Russia

<sup>2</sup> Novosibirsk State University, Novosibirsk, Russia

<sup>3</sup> Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

<sup>4</sup> Ugra Research Institute of Information Technologies, Khanty-Mansyisk, Russia

ABOUT COMPUTATIONAL RESEARCH OF MATHEMATICAL MODELS OF  
HYPOTHETICAL GENE NETWORKS BY PARAMETER CONTINUATION.

**Favorov A.V.<sup>1</sup>, Favorova O.O.<sup>2</sup>, Andreewski T.V.<sup>2</sup>, Sudomoina M.A.<sup>2</sup>, Alekseenkov A.D.<sup>2</sup>,  
Kulakova O.G.<sup>2</sup>, Boiko A.N.<sup>2</sup>, Gusev E.I.<sup>2</sup>, Parmigiani G.<sup>3</sup>, Ochs M.F.<sup>4</sup>**

<sup>1</sup> State Scientific Centre “GosNIIGenetika”, Moscow, Russia

<sup>2</sup> Russian State Medical University, Moscow, Russia

<sup>3</sup> Johns Hopkins University, Baltimore, MD, USA

<sup>4</sup> Fox Chase Cancer Center, Philadelphia, PA, USA

MCMC METHOD HAS FOUND THAT MULTIPLE SCLEROSIS IS ASSOCIATED WITH TWO-THREE GENES COMBINATIONS

**Filatov I.V., Milchevsky Ju.V., Esipova N.G., Tumanyan V.G.**

Engelhardt Institute of Molecular Biology RAS, Moscow, Russia

COMPUTATION OF THE THREE DIMENSIONAL STRUCTURE OF THE HUMAN TYPE (III) COLLAGEN

**Frenkel F.E., Chaley M.B., Korotkov E.V., Skryabin K.G.**

Centre "Bioengineering" RAS, Moscow, Russia

INFORMATIONAL ASPECTS OF THE LATENT TRIPLET PERIODICITY ANALYSIS

**Fursov M.Yu.<sup>1</sup>, Baksheyev D.G.<sup>1</sup>, Rodionov K.V.<sup>1</sup>, Golubitskii A.A.<sup>1</sup>, Saraev D.V.<sup>2</sup>, Denisov S.I.<sup>2</sup>, Blinov V.M.<sup>2</sup>**

<sup>1</sup> Novosibirsk Center of Information Technologies “UniPro”, Novosibirsk, Russia

<sup>2</sup> State Research Center of Virology and Biotechnology “Vector”, Koltsovo, Russia

A PRACTICAL METHOD FOR MAXIMUM EXACT MATCHES IN LARGE GENOMES

**Galimzyanov A.V.**

Institute of Biology, Ufa Research Center RAS, Ufa, Russia

ON ONE ALGORITHM FOR MODELING PASSIVE TRANSPORT IN CELL SETS OF ARBITRARY CONFIGURATION

**Gariev I.A., Uporov I.V., Varfolomeev S.D.**

Moscow State University, Moscow, Russia

SEARCHING STRUCTURAL PROTEIN DATABASES FOR ENZYMATIC ACTIVE SITES BY 3D PATTERNS

**Gerasimova A.V.<sup>1</sup>, Ravcheyev D.A.<sup>2,3</sup>, Gelfand M.S.<sup>1,2,3</sup>, Rakhmaninova A.B.<sup>2</sup>**

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COMPARATIVE GENOMIC ANALYSIS OF RESPIRATION SWITCH IN GAMMA-PROTEOBACTERIA

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CLOSED TRAJECTORIES IN THE GENE NETWORKS

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HOPF BIFURCATION AND CLOSED TRAJECTORIES IN THE GENE NETWORKS

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A MODEL OF TRYPTOPHAN BIOSYNTHESIS REGULATION

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TWO GENE NETWORKS UNDERLYING THE FORMATION OF THE ANTERIOR-  
POSTERIOR AND DORSO-VENTRAL WING IMAGINAL DISC COMPARTMENT  
BOUNDARIES IN DROSOPHILA MELANOGASTER

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COMBINED OPTIMIZATION TECHNIQUE FOR BIOLOGICAL DATA FITTING

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MATHEMATICAL MODEL OF THE GENE NETWORK OF TNF $\alpha$ -INDUCED NF-kappaB  
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THE DISTANCE FUNCTION FOR COMPUTING THE CONTINUOUS DISTANCE OF  
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**Ignatieva E.V., Ananko E.A., Podkolodnaya O.A., Stepanenko I.L., Khlebodarova T.M.,  
Merkulova T.I., Podkolodny N.L., Grigorovich D.A., Poplavsky A.S., Naumochkin A.N.,  
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TRANSCRIPTION REGULATORY REGIONS DATABASE (TRRD): ITS STATUS IN 2004

**Ignatieva E.V., Levitsky V.G., Vasiliev G.V., Klimova N.V., Busygina, T.V., Merkulova T.I.**  
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DISTRIBUTION OF THE SF-1 SITES IN THE GENOMIC SEQUENCES PREDICTED BY  
THE SITEGA METHOD AND THEIR EXPERIMENTAL VERIFICATION

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A NEW ALGORITHM FOR RECOGNIZING THE OPERON STRUCTURE OF  
PROKARYOTES

**Kamzolova S.G., Sorokin A.A., Dzhelyadin T.R., Beskaravainy P.M., Osypov A.A.**

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ELECTROSTATIC PROPERTIES OF E. COLI GENOME DNA

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ANALYSIS OF OLIGONUCLEOTIDE COMPOSITION IN DNA OF *E. COLI* GENOME AND  
PROMOTER SITES



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SYMMETRY AND SPATIAL STRUCTURE OF THE CANONICAL SET OF AMINO ACIDS

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ANALYSIS OF NUCLEOSOME FORMATION POTENTIAL AND CONFORMATIONAL PROPERTIES OF HUMAN J1-J2 TYPE ALPHA SATELLITE DNA

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GENOME-WIDE IDENTIFICATION OF MITOCHONDRIAL DNA TOPOISOMERASE I IN ARABIDOPSIS

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BACTERIAL METAL RESISTANCE SYSTEMS REGULATED BY TRANSCRIPTION REGULATORS OF THE MERR FAMILY

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TRRD\_ARTSITE DATABASE: STRUCTURES OF TRANSCRIPTION FACTOR BINDING SITES

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COMPARISON OF THE STRUCTURES OF *IN VITRO* SELECTED AND NATURAL BINDING SITES OF TRANSCRIPTION FACTORS

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ABOUT NUMERICAL INVESTIGATION OF AUTO-OSCILLATIONS IN HYPOTHETICAL GENE NETWORKS

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FROM PROTEIN SEQUENCE TO PROTEIN SPECIFICITY: COMPLETELY AUTOMATED DISCOVERY AND MAPPING OF SPECIFICITY DETERMINING RESIDUES

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TFBS ANALYZER: A WEB TOOLKIT FOR ANALYSIS AND PREDICTION OF  
TRANSCRIPTION FACTOR BINDING SITES

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STATISTICAL ANALYSIS OF MICROARRAY DATA: IDENTIFICATION AND  
CLASSIFICATION OF HUMAN CELL CYCLE GENES

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ANALYSIS OF PLANT MITOCHONDRIAL GENOME ORGANIZATION:  
CHARACTERISTICS OF REPEATS AND SEQUENCE COMPLEXITY

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A SIMPLE TEST FOR LINKAGE DISEQUILIBRIUM BETWEEN A MARKER ALLELE  
AND A GENE MUTATION IN HETEROZYGOTE CARRIERS

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EVOLUTIONARY TREE RECONSTRUCTION AND TRAVELING SALESMAN  
PROBLEM: A POWERFUL ALGORITHM FOR SHAGGY TREES

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MOLECULAR MODELING OF THE NUCLEOTIDE-BINDING DOMAIN OF THE WILSON'  
DISEASE PROTEIN: THE ATP-BINDING SITE AND DOMAIN DYNAMICS

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MANUAL CURATION OF EST LIBRARIES BY TISSUE SPECIFICITY AND CELL ORIGIN

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THE CONSERVATION OF TRANSCRIPTION FACTOR-BINDING SITES IN  
SACCHAROMYCES GENOMES

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VALIDATION OF RANDOM BIRTH-DEATH MODEL OF EVOLUTION OF PROTEOME  
COMPLEXITY

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EVOLUTIONARY ALGORITHMS FOR MATHEMATICAL MODELS OF GENE  
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EXPLICIT INTEGRAL METHOD FOR NONLINEAR DYNAMIC MATHEMATICAL  
MODELS IDENTIFICATION

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DETECTION OF CLASSICAL ATTENUATION IN BACTERIAL GENOMES

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ANALYSIS OF PERIODICITIES IN THE DINUCLEOTIDE CONTEXT OF NUCLEOSOMAL  
DNA USING THE METHOD PHASE

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ANALYSIS OF THE CONTEXT FEATURES OF SF-1 BINDING SITE AND  
DEVELOPMENT OF A CRITERION FOR SF-1 REGULATED GENE RECOGNITION BY  
THE SITEGA METHOD

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DNA NUCLEOSOME ORGANIZATION OF THE FUNCTIONAL GENES REGIONS AND  
ITS RELATION TO GENE EXPRESSION LEVEL

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ON THE STATIONARY POINTS OF REGULATORY CONTOURS OF GENE NETWORKS

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INFORMATION ABOUT SECONDARY STRUCTURE IMPROVES QUALITY OF PROTEIN ALIGNMENT

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AMINO ACID BIOSYNTHESIS ATTENUATION IN BACTERIA

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GENE NETWORK OF THE ARABIDOPSIS DEVELOPING SHOOT MERISTEM AND ITS DESCRIPTION IN THE GENENET COMPUTER SYSTEM

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COMPUTER ANALYSIS AND PREDICTION OF POTENTIAL IRON-RESPONSIVE ELEMENTS IN 5' AND 3' UTR OF EUKARYOTE GENES TRANSCRIPTS

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THE ALPHA-GALACTOSIDASE SUPERFAMILY: SEQUENCE BASED CLASSIFICATION OF ALPHA-GALACTOSIDASES AND RELATED GLYCOSIDASES

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COMPUTER MODELING OF THE FUNCTION OF TRANSCRIPTION FACTORS DURING MACROPHAGE ACTIVATION

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INTER-SUBUNIT CONTACTS OF THE PROTEASOMAL ALPHA-SUBUNITS AS DETERMINANTS OF PARALOG GROUPS

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PROTEIN FAMILY PATTERNS BANK PROF\_PAT. CURRENT STATUS

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NEW LTR RETROTRANSPOSABLE ELEMENTS FROM EUKARYOTIC GENOMES

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THE NEW APPROACH OF BOTH NEW AND OLD SEGMENTAL DUPLICATIONS SEARCH: REPETITIVE DNA AS A MOLECULAR ARCHAEOLOGY TOOL

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NUCLEOSOME POSITIONING SIGNAL ANALYSIS

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CONTEXT FEATURES OF TRANSCRIPTION FACTOR BINDING SITE SEQUENCES:  
RELATION TO DNA-BINDING DOMAIN CLASSIFICATION

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SITECON: A TOOL FOR DETECTING CONSERVATIVE CONFORMATIONAL AND  
PHYSICOCHEMICAL PROPERTIES IN TRANSCRIPTION FACTOR BINDING SITES  
ALIGNMENTS AND FOR SITE RECOGNITION

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PROTEIN FOLDING AND MISFOLDING: A BIFURCATION STUDY OF A LATTICE  
MODEL

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STRUCTURAL MEMORY OF A LATTICE PROTEIN

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ON RESEARCH INTO HYPOTHETICAL NETWORKS OF ECOLOGICAL NATURE

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METHOD FOR INTEGRATION OF DATABASES WITH COMMON SUBJECT DOMAINS

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GENENET: VISUAL MODELING AND ANALYSIS OF GENE NETWORKS

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A DATABASE ON DNA SEQUENCE/ACTIVITY RELATIONSHIPS: APPLICATION TO PHYLOGENETIC FOOTPRINTING

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SREBP BINDING SITES: CONTEXT FEATURES AND ANALYSIS OF GENOME DISTRIBUTION BY THE SITECON METHOD

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ON ENERGY DISTRIBUTION OF RANDOM WALKS WITH CONSTRAINTS AND GEOMETRICAL COMPLEXITY OF POLYMERS

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A MOLECULAR MECHANISM FOR THE STRUCTURE-FUNCTIONAL ALTERATIONS IN MUTANT FORMS OF HUMAN P53 PROTEIN

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COMPUTER SIMULATIONS OF ANIONIC UNSATURATED LIPID BILAYER: A BASE SYSTEM TO STUDY PEPTIDE-MEMBRANE INTERACTIONS

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PERIODICAL PATTERNS IN SEQUENCES OF SPIDROINS 1 AND 2 AND SECONDARY STRUCTURE PREDICTION

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TOWARDS COMPUTER DYNAMIC MODELING OF WHOLE CELL

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BENCHMARKING OF TRANSMEMBRANE HELIX PREDICTION SERVERS

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EVOLUTION OF DIPLOID PROGENITORS OF COMMON WHEAT ON THE BASE OF  
RAPD AND SUBTELOMERIC REREATS ANALYSIS

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SEARCH FOR REGULATORY MOTIFS IN *DROSOPHILA MELANOGASTER* GENOME

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LONG SEGMENTAL REPEATS IN HUMAN GENOME: DENSITY, DISTRIBUTION,  
STRUCTURE

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STRUCTURAL AND FUNCTIONAL ANALYSIS OF POORLY CHARACTERIZED  
PROTEIN FAMILIES AT THE ONTARIO CENTRE FOR STRUCTURAL PROTEOMICS

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BINARY TREE FOR CLUSTERING OF REGULATORY SIGNALS

**Surkova S.Yu., Samsonova M.G.**

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TEMPORAL AND SPATIAL PRECISION IN FORMATION OF SEGMENTATION GENE  
EXPRESSION DOMAINS IN *DROSOPHILA*

**Tchugunov A.O.<sup>1,2</sup>, Chavatte P.<sup>3</sup>, Efremov R.G.<sup>1</sup>**

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Moscow, Russia

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MOLECULAR MODELING OF HUMAN MT<sub>1</sub> AND MT<sub>2</sub> MELATONIN RECEPTORS

**Titov I.I.<sup>1,2</sup>, Vorobiev D.G.<sup>2</sup>, Palyanov A.Yu.<sup>1</sup>**

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WEB-SERVER GARNA FOR RNA STRUCTURE ANALYSIS: ITS STATE IN 2004

**Triboy T.I., Sherbakov D.Yu.**

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COUNTERING COORDINATED AMINO ACID SUBSTITUTIONS IN PHYLOGENETIC ANALYSIS

**Turnaev I.I., Ananko E.A., Podkolodnaya O.A.**

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CENTRAL REGULATION OF THE GENE NETWORK OF THE CELL CYCLE IN MAMMALS: AN ANALYSIS OF CLOSED REGULATORY LOOPS

**Varlamova E.S.<sup>1</sup>, Afonnikov D.A.<sup>1,2</sup>**

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IMPROVED PREDICTION OF PROTEIN CONTACT MAPS USING INFORMATION ON RESIDUE CONTACT NUMBERS

**Vasilenko N.L.<sup>1</sup>, Balueva K.E.<sup>2,4</sup>, Likhoshvai V.A.<sup>1,3</sup>, Nevinsky G.A.<sup>2</sup>, Matushkin Yu.G.<sup>1</sup>**

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CONSTRUCTION OF MOLECULAR TRIGGER IN *E. COLI*

**Vasyunina E.A.<sup>1</sup>, Rogozin I.B.<sup>1,2</sup>, Sinitsina O.I.<sup>1</sup>, Plaksina A.S.<sup>1</sup>**

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THEORETICAL AND EXPERIMENTAL STUDY OF MUTATIONS INDUCED BY 8-OXOGUANINE

**Vishnevsky O.V.<sup>1</sup>, Ignatieva E.V.<sup>1</sup>, Arrigo P.<sup>2</sup>**

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THE ARGO\_SITES: AN ANALYSIS AND RECOGNITION OF THE TRANSCRIPTION FACTOR BINDING SITES BASED ON SETS OF DEGENERATE OLIGONUCLEOTIDE MOTIFS

**Vitreschak A., Noe L., Kucherov G.**

INRIA-Lorraine/LORIA, Villers-lès-Nancy, France

COMPUTER ANALYSIS OF MULTIPLE REPEATS IN BACTERIA

**Vladimirov N.V.<sup>1</sup>, Likhoshvai V.A.<sup>1,2</sup>**

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STOCHASTIC MODEL OF TRANSLATION ELONGATION BASED ON CONTINUOUS TIME MONTE CARLO METHOD

**Vorobjev Y.N., Emelianov D.Y.**

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## MODELING OF CONTEXT-DEPENDENT CONFORMATIONAL PARAMETERS OF DNA DUPLEXES

**Watanabe M.<sup>1</sup>, Goto N.<sup>2</sup>, Watanabe Y.<sup>1</sup>, Nishiguchi S.<sup>1</sup>, Shimada K.<sup>1</sup>, Yasunaga T.<sup>2</sup>,  
Yamanishi H.<sup>1</sup>**

<sup>1</sup> Hirakata Ryoikuen, Osaka, Japan

<sup>2</sup> Department of Human Genome Research, Genome Information Research Center, Osaka  
University, Osaka, Japan

## EVOLUTION OF INTERLEUKIN-18 BINDING PROTEIN FAMILY

**Walker N.J.<sup>1,2</sup>, Sharrocks A.D.<sup>1</sup>, Attwood T.K.<sup>1,2</sup>**

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## USE OF AN INTEGRATED RULE SYSTEM FOR IDENTIFICATION OF THE TRANSCRIPTION FACTOR BINDING SITES MCM1 AND FKH2 IN *S. CEREVISIAE*

**THE FOURTH INTERNATIONAL CONFERENCE  
ON BIOINFORMATICS OF GENOME REGULATION AND STRUCTURE  
(BGRS'2004)**

July 25-30, 2004, Novosibirsk, Russia

**COMPUTER DEMONSTRATIONS**

For installation, please do not hesitate to contact the Organizing Committee in Room №200 at the House of Scientists.

July 26, Monday

**<sup>1</sup>Ananko E.A.\***, <sup>1</sup>Rasskazov D.A., <sup>1</sup>Miginsky D.S., <sup>1,2</sup>**Podkolodny N.L.\***

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**GENENET: RECONSTRUCTION AND ANALYSIS OF GENE NETWORKS**

**Gunbin K.V.\***, Omelyanchuk L.V., Ananko E.A.

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**TWO GENE NETWORKS UNDERLYING THE FORMATION OF THE ANTERIOR-POSTERIOR AND DORSO-VENTRAL WING IMAGINAL DISC COMPARTMENT BOUNDARIES IN DROSOPHILA MELANOGASTER**

**<sup>1</sup>Tarasov D.S.**, <sup>2</sup>Leontiev A.Yu., <sup>1</sup>Akberova N.I

Kazan State University, Kazan, Russia

Kazan State Academy of Veterinary Medicine, Kazan, Russia

**A LANGUAGE FOR MODELING GENETIC REGULATION IN PROCARYOTES**

**<sup>1</sup>Fadeev S.I.\***, <sup>1</sup>Korolev V.K., <sup>2</sup>Likhoshvai V.A.

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**PROGRAM PACKAGE HGNET FOR COMPUTATIONAL INVESTIGATION OF HYPOTHETICAL GENE NETWORKS**

**<sup>1</sup>Fadeev S.I.\***, <sup>1</sup>Gainova I.A., <sup>1</sup>Berezin A.Yu., <sup>2</sup>Ratushny A.V., <sup>2</sup>Matushkin Yu.G., <sup>2</sup>Likhoshvai V.A.

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**DETERMINATION OF STATIONARY SOLUTIONS IN GENE NETWORK MODELS BY HOMOTOPY METHOD**

**Vladimirov N.V.\***, Likhoshvai V.A.

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**STOCHASTIC MODEL OF TRANSLATION ELONGATION BASED ON CONTINUOUS TIME MONTE CARLO METHOD**

July 27, Tuesday

**Golubitskii A.A.**

Novosibirsk Center of Information Technologies "UniPro", Novosibirsk, Russia

**A PRACTICAL METHOD FOR MAXIMUM EXACT MATCHES IN LARGE GENOMES: UNIPRO GENOME BROWSER – TOOL FOR VISUAL ANALYSIS AND ANNOTATION OF LARGE GENOMES**

**Levitsky V.G.**

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia

RECON: A PROGRAM FOR PREDICTION OF NUCLEOSOME FORMATION POTENTIAL

**Levitsky V.G.\***, Katokhin A., Khlebodarova T.M., Podkolodnaya O.A., Podkolodny N.L., Furman D.P.

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NUCLEOSOME POSITIONING REGION DATABASE - COMPILATION OF EXPERIMENTAL

DATA ON LOCATIONS AND CHARACTERISTICS OF NUCLEOSOME FORMATION SITES

**Orlov Yu.L.\***, Potapov V.N., Poplavsky A.S.

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COMPUTER ANALYSIS OF GENOMIC SEQUENCE COMPLEXITY: NEW APPLICATIONS

**Orlov Yu.L.\***, Levitsky V.G.

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NUCLEOSOME POSITIONING SIGNAL ANALYSIS

**Oshchepkov D.Yu.\***, Grigorovich D.A., Ignatieva E.V., Khlebodarova T.M.

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SITECON: A TOOL FOR TRANSCRIPTION FACTOR BINDING SITE RECOGNITION.

Podkolodnaya O.A., **Ananko E.A.\***, **Ignatieva E.V.\***, Stepanenko I.L., Khlebodarova T.M., Merkulova T.I., **Podkolodny N.L.\***, Grigorovich D.A., Poplavsky A.S., Naumochkin A.N., Pozdnyakov M.A., Romashchenko A.G. Kolchanov N.A.

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TRRD: SYSTEM OF COMPUTER-ASSISTED SUPPORT OF EXPERIMENTAL AND THEORETICAL RESEARCH OF TRANSCRIPTION REGULATION MECHANISMS

**Rodionov K.V.**

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A PRACTICAL METHOD FOR MAXIMUM EXACT MATCHES IN LARGE GENOMES: UNIPRO DPVIEW – A TOOL FOR FINDING AND ANALYZING MATCHES BETWEEN GENOMES

**July 29, Thursday**

**Afonnikov D.A. \***, N.A.Kolchanov

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CRASP: THE PROGRAM FOR ANALYSIS OF COORDINATED SUBSTITUTIONS IN MULTIPLE ALIGNMENTS OF PROTEIN SEQUENCES

**Gribkov M.A.**, Korotkova M.A.

Moscow Engineering-Physics Institute (State University), Moscow, Russia

A SYSTEM FOR COMPLEX ANALYSIS OF PROTEIN MACROMOLECULES SPATIAL STRUCTURES

**Ivanisenko V.A.\***, Pintus S.S., Grigorovich D.A.

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PDBSITE: A DATABASE OF THE 3D STRUCTURE OF PROTEIN FUNCTIONAL SITES.

**Kolpakov F.A.**

Biosoft.Ru/DevelopmentOnTheEdge.com, Novosibirsk, Russia  
Design Technological Institute of Digital Techniques SB RAS, Novosibirsk, Russia  
BIOUML – OPEN SOURCE EXTENSIBLE WORKBENCH FOR SYSTEMS BIOLOGY

**Pintus S.S., Ivanisenko V.A.**

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia  
GAIN OF NEW FUNCTIONS IN PROTEINS AS A RESULT OF MUTATIONS. COMPUTER ANALYSIS OF THE P53 PROTEIN

**<sup>1</sup>Podkolodnaya N.N.\*, <sup>3</sup>Paramonova N.V., <sup>2,3</sup>Podkolodny N.L., <sup>3</sup>Likhoshvai V.A.**

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THE EDITOR OF GENENET MODELS

**Vishnevsky O.V.\*, E.V.Ignatjeva, T.Busygina, O.A.Podkolodnaya**

Institute of Cytology and Genetics SB RAS, Novosibirsk, Russia  
ARGO: WEB SYSTEM FOR DETECTION OF DEGENERATE MOTIFS AND RECOGNITION OF REGULATORY REGIONS OF EUKARYOTIC GENES.

**July 30, Friday**

Khlebodarova T.M., Podkolodnaya O.A., Ananko E.A., Stepanenko I.L., Ignatieva E.V.,

**Oshchepkov D.Y.\*, Miginski D.S., Kolchanov N.A.**

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ARTSITE DATABASE: STRUCTURE OF IN VITRO SELECTED AND NATURAL TRANSCRIPTION FACTOR BINDING SITES

**<sup>1</sup>Korostishevsky M., <sup>2</sup>Burd A., <sup>2</sup>Mester D., <sup>1</sup>Bonne-Tamir B., <sup>2</sup>Nevo E., <sup>2</sup>Korol A.**

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<sup>2</sup>Institute of Evolution, University of Haifa, Haifa, Israel

EVOLUTIONARY TREE RECONSTRUCTION AND TRAVELING SALESMAN PROBLEM: A POWERFUL ALGORITHM FOR SHAGGY TREES

**Omelianchuk N.A.\*, Mironova V.V.\*, Poplavsky A.S., Kukeeva Yu.A., Podkolodny N.L.,**

Kolchanov N.A

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AGNS: ARABIDOPSIS GENENET SUPPLEMENTARY DATABASE

**<sup>1</sup>Titov I.I.\*, <sup>1</sup>Vorobjev D.G., <sup>2</sup>Palyanov A.Yu.**

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GARNA-SERVER FOR RNA SECONDARY STRUCTURE ANALYSIS

<sup>1</sup>Zykovich A.S., <sup>2</sup>**Axenovich T.I.**

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**DEVELOPMENT OF METHOD FOR IN SILICO MAPPING OF QUANTITATIVE  
TRAIT LOCI**

**Xia X.**

Department of Biology, University of Ottawa, Ottawa, Canada

**DAMBE: AN INTEGRATED ENVIRONMENT FOR DATA ANALYSIS IN MOLECULAR  
BIOLOGY AND EVOLUTION**