Marko Djordjevic

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Scientific Interests

Modeling biological systems, Biophysics, Bioinformatics.

Education

- October 2005: PhD in Physics, Columbia University, NY.
- Feb 2004: M. Phil. in Physics, Columbia University, NY.
- May 2002: M. A. in Physics, Columbia University, NY.
- June 2000: Diploma in Physics, Belgrade University, Faculty of Physics, Serbia.

Positions

- Dec 2014: Associate Professor of Biophysics, U. of Belgrade, Faculty of Biology
- Sept 2010: Assistant Professor of Biophysics, Univ. of Belgrade, Faculty of Biology
- Sept 2008: Assistant Professor of Physics, Arkansas State U & The Arkansas Biosciences Institute.
- Apr 2008: Offer of Assistant Professorship at NORDITA (Nordic Institute for Theoretical Physics), Stockholm (declined).
- Oct 2005: Postdoctoral Fellow, Mathematical Biosciences Institute, Ohio State U.
- Jan 2001: Research Assistant, Dept. of Physics, Columbia U.
- Sept 2000: Faculty fellow, Dept. of Physics, Columbia U.
- Jun 1999: Diploma Thesis Research, Institute of Theoretical Physics, Belgrade.

Teaching experience

- *Molecular Biophysics* (Fall 2012, Fall 2013 and Fall 2014), Interdisciplinary PhD Biophysics program, University of Belgrade, Serbia.
- *Neuroinformatics* (Fall 2013), *Computational Immunobiology* (Fall 2013 and Fall 2014), PhD program Faculty of biology, U. of Belgrade, Serbia.
- *Bioinformatics* (Spring 2012, Fall 2012, Fall 2013 and Fall 2014); *Computers in biology* (Spring 2011); *Physics in Biology* (Fall 2010,Fall 2011, Spring 2013, Fall 2013 and Fall 2014); Faculty of Biology, University of Belgrade, Serbia.
- *Electricity and Magnetism* (Spring 2010); *Thermal Physics* (Fall 2009)*; General Physics I* (Spring 2009); *Physics for health science professionals* (Fall 2008); Arkansas State U, AR.
- *Tutorial on ChIP-chip data analysis* (Spring 2007); *VIGRE working group in mathematical biology* (Fall 2006), The Ohio State U, Columbus, Ohio.
- *Introduction to experimental physics laboratory* (Fall 2001); *Introduction to physics laboratory* (Fall 2000 - Spring 2001), Columbia U, New York.

Awards

- March 2011: Marie Curie Fellowship, European Commision - Research Executive Agency, Brussels, Belgium
- Jan 2006: Keystone Symposia scholarship, Taos, New Mexico.
- Feb 2005 Feinberg Postdoctoral Fellowship, Weizmann Institute of Science, Rehovot, Israel (declined).
- Nov 1998: 'Prof. Dr. Djordje Zivanovic' Fellowship, awarded to the best student in generation, Faculty of Physics, Belgrade, Serbia.
- 1995 -2000 'Department of Science' Fellowship (awarded five times), Serbia.
- 1996-1999 'Madlena Jankovic' Fellowship, for success in diploma studies, Belgrade, Serbia.
- July 1995: The bronze medal, XXVI International Physics Olympiad, Canberra, Australia.

Awards to PhD students in the group

- "2016. Young scientist research award", awarded to Jelena Guzina by the Faculty of Biology, University of Belgrade, Serbia, Sept 2016.
- Award for the best oral presentation at the 8th International Young Scientists School of Systems Biology and Bioinformatics, awarded to Andjela Rodic, Novosibirsk, Russia, Sept 2016
- Fellowship for attending the Advanced Lecture Course on Systems Biology, awarded by the organizers of SYSBIO 2016 to Andjela Rodic, Innsbruck, Austria, Jan 2016
- Annual award for the best master thesis in the field of Molecular Biology, awarded to Andjela Rodic by the Foundation "Goran Ljubijankic", Belgrade, Serbia, Dec 2015

Support

- Faculty of Biology coordinator: Swiss National Science Foundation, SCOPES project), IZ73Z0_152297, "Bioinformatics and modeling of bacterial immune systems - understanding control of CRISPR/Cas", from 2014-2017, CHF193.500
- Scientist in charge: *FP7 Marie Curie International Reintegration grant*, PIRG08-GA-2010-276996, "Bioinformatic analysis of transcription regulation: a modeling approach", European Commision - Research Executive Agency, from 2011-2015, EUR 100.000
- Project leader: *Basic Science Research Grant*, OI173052, "Bioinformatic promoter predictions and theoretical modeling of gene circuits in bacteria", Ministry of Science and Technology - Republic of Serbia, from 2011-2014, Support for young scientists to form their groups.

Community service and Memberships

- **Journal Referee:** *Biochemistry* (American Chemical Society), *Bioinformatics* (Oxford Journals), *BMC Bioinformatics* (BioMed Central), *BMC Biotechnology* (BioMed Central), *BioTechniques* (Informa Life Sciences), *DNA Research* (Oxford Journals), *Bulletin of Mathematical Biology* (The Society for Mathematical Biology), *Nucleic Acids Research* (Oxford University Press), *Pacific Symposium on Biocomputing*, *Physical Biology* (Institute of Physics), *PLoS Computational Biology*, *Proceedings of the National Academy of Sciences of USA*, *Physical Review E* (American Physical Society), *Journal of Bacteriology* (American Society for Microbiology).
- **Editorial Board:** Frontiers in Bioinformatics and Computational Biology, Frontiers Journals.
- **Member of the organizing and the program committee for the conferences:**
  - BELBi 2016 (Belgrade Bioinformatics Conference), Belgrade, Serbia, June 2016
  - TABIS2013 (International Conference on Theoretical Approaches to BioInformation Systems), Belgrade, Serbia, Sept 2013

- 2nd and 3rd Young Researchers Workshop in Mathematical Biology, Columbus, OH, March 2007 and March 2008.

Publications

A. Journal Articles (peer reviewed)

Total number of citations: >800 (per Google Scholar)

Bioinformatics and Computational Biology:

1. Nikolic M, Stankovic T, Djordjevic M, *Contribution of bacterial promoter elements to transcription start site detection accuracy*, Journal of Bioinformatics and Computational Biology, in press, 2016.
2. Guzina J, Djordjevic M, *Promoter recognition by ECF σ factors: analyzing DNA and protein interaction motifs,* Journal of Bacteriology **198**:1927, 2016.
3. Morozova N, Sabantsev A, Bogdanova E, Fedorova Y, Maikova A, Vedyaykin A, Rodic A, Djordjevic M, Khodorkovskii M, Severinov K, *Temporal dynamics of methyltransferase and restriction endonuclease accumulation in individual cells after introducing a restriction-modification system*, Nucleic Acids Research **44**:790, 2016.
4. Guzina J, Djordjevic M, *Bioinformatics as a first-line approach for understanding bacteriophage transcription*, Bacteriophage **5**:e1062588, 2015 (invited review paper).
5. Guzina J, Djordjevic M, *Inferring bacteriophage infection strategies from genome sequence: analysis of bacteriophage 7-11 and related phages*, BMC Evolutionary Biology **15**:S1, 2015.
6. Zukher I, Novikova M, Tikhonov A, Nesterchuk M, Osterman I, Djordjevic M, Sergiev P, Sharma C, Severinov K, *Ribosome-controlled transcription termination is essential for the production of antibiotic microcin C*, Nucleic Acids Research **42**:11891, 2014.
7. Djordjevic M, *Integrating sequence analysis with biophysical modelling for accurate transcription start site prediction.,* Journal of Integrative Bioinformatics **11**(2):240, 2014 (invited review paper).
8. Djordjevic M, *Efficient transcription initiation in bacteria: an interplay of protein-DNA interaction parameters,* Integrative Biology **5**(5):796, 2013.
9. Djordjevic M, *Modeling bacterial immune systems: strategies for expression of toxic - but useful - molecules*, Biosystems **112**(2):139, 2013.
10. Djordjevic M, Djordjevic M, *A simple biosynthetic pathway for large product generation from small substrate amounts*, Physical Biology **9**(5): 056004, 2012.
11. Djordjevic M, Djordjevic M, Severinov K, *CRISPR transcript processing: a mechanism for generating a large number of small interfering RNAs*, Biology Direct **7**(1): 24, 2012.
12. Pavlova O, Lavysh D, Klimik E, Djordjevic M, Ravcheev DA, Gelfand MS, Severinov K, Akulenko N, *Temporal regulation of gene expression of the Escherichia coli bacteriophage phiEco32*, Journal of Molecular Biology, **416**(3): 389, 2012.
13. Djordjevic M, *Redefining Escherichia coli σ^{70} promoter elements: -15 motif as a complement of the -10 motif*, Journal of Bacteriology, **193**(22): 6305, 2011.
14. Pougach K, Semenova E, Bogdanova E, Datsenko KA, Djordjevic M, Wanner BL, and Severinov K, *Transcription, transcripts processing and function of E. coli CRISPR locus*, Molecular Microbiology**, 77**(6): 1367, 2010
15. Djordjevic M, *Inferring protein-DNA interaction parameters from SELEX experiments***.** Methods in Molecular Biology, **674:** 195, 2010 (invited book chapter).
16. Djordjevic M and Bundschuh R, *Open complex formation by bacterial RNA polymerase – a quantitative model*, Biophysical Journal, **94**(11): 4233, 2008.

17. Bogdanova E, Djordjevic M, Papapanagiotou I, Heyduk T, Kneale G and Severinov K, *Transcription regulation of the type II restriction-modification system AhdI*, Nuclear Acids Research, **36**(5): 1429, 2008.
18. Djordjevic M, *SELEX experiments: novel prospects applications and data analysis for inferring regulatory pathways*, Biomolecular Engineering **24**(2):179, 2007 (invited review paper).
19. Sevostyanova A, Djordjevic M, Kuznedelov K, Naryshkina T, Gelfand M, Severinov K and Minakhin L, *Temporal regulation of viral transcription during development of Thermus thermophilus bacteriophage phiYS40*, Journal of Molecular Biology **366**(2):420, 2007.
20. Djordjevic M, Semenova E, Shraiman B and Severinov K, *Quantitative analysis of transcription strategy by a virulent bacteriophage*, Virology, **354**(2):240, 2006.
21. Djordjevic M, Sengupta A M, *Quantitative modeling and data analysis of SELEX experiments,* Physical Biology **3**:13, 2006.
22. Semenova E, Djordjevic M, Shraiman B and Severinov K, *The tale of two RNA polymerases: transcription profiling and gene expression strategy of bacteriophage Xp10*, Molecular Microbiology **55**:764, 2005.
23. Djordjevic M, Sengupta A M and Shraiman B, *A biophysical approach to transcription factor binding site discovery*, Genome Research **13**(11):2381, 2003.
24. Sengupta A M, Djordjevic M, Shraiman B, *Specificity and robustness in transcription control networks,* Proceedings of the National Academy of Science **99**:2072, 2002.
25. Mendas I, Djordjevic M and Markovic M, *Properties of the nonclassical maximum-entropy states*, Journal of Physics A: Mathematical and General **33**:921, 2000.
26. Mendas I and Djordjevic M, *Boson Bogoliubov group and generalized squeezed states*, Facta Universitatis **1**:173, 1999.

Statistical and High Energy Physics:

27. Djordjevic M and Djordjevic M, *Predictions of heavy-flavor suppression at 5.1 TeV Pb+Pb collisions at the CERN Large Hadron Collider*, Physical Review C **92**:024918, 2015
28. Djordjevic M, Djordjevic M and Blagojevic B, *RHIC and LHC jet suppression in non-central collisions*, Physics Letters B **737**:298, 2014.
29. Djordjevic M and Djordjevic M, *LHC jet suppression of light and heavy flavor observables*, Physics Letters B **734**:286, 2014.
30. Djordjevic M and Djordjevic M, *Heavy flavor puzzle from data measured at the BNL Relativistic Heavy Ion Collider: Analysis of the underlying effects*, Physical Review C **90**:034910, 2014.
31. Djordjevic M and Djordjevic M, Understanding the strong suppression patterns at RHIC and LHC, Modern Physics Letters A **29**: 1430035, 2014 (invited review paper).
32. Djordjevic M, Djordjevic M, *Explaining the fine hierarchy in pion and kaon suppression at LHC: Importance of fragmentation functions,* Journal of Physics G **41**:055104, 2014.
33. Djordjevic M, Djordjevic M, *Generalization of radiative jet energy loss to non-zero magnetic mass*, Physics Letters B **709:**229, 2012.

B. Books

1. Grbic B, Djordjevic M, Popovic-Bozic M and Stosic M, *International physics olympiads 1967-1996, Collected problems and solutions* (in Serbian), Serbian Physical Society Press (2000) [ISBN 86-17-08245-3].
2. Djordjevic M, *Biophysics and bioinformatics of transcription regulation in bacteria and bacteriophages*, PhD Thesis (2005) [ISBN 05-42-23846-2].

Algorithms and Practical Applications

- QPMEME – Quadratic Programming Method of Energy Matrix Estimation.
- Kinetic modeling based analysis of bacteriophage gene expression.
- Statistical mechanics based method of SELEX (Systematic Evolution of Ligands by EXponential enrichment) data analysis.
- Biophysically based method for estimate of prokaryotic promoter kinetic parameters.

Attended Programs and Schools

- Evolution of Molecular Networks, Kavli Institute for Theoretical Physics, Santa Barbara, California, January 2007.
- Networks in Growth, Death and Aging, Kavli Institute for Theoretical Physics, Santa Barbara, California, February 2005.
- The 22nd Jerusalem Winter School in Theoretical Physics, Biological Networks and Evolution, Jerusalem, Israel, January 2005.
- Bio-Molecular Networks, Kavli Institute for Theoretical Physics, Santa Barbara, California, January – March 2003.
- Project Lab in Molecular Genetics, Columbia University, New York, Fall 2002.

Talks

A. Conferences and Workshops

1. *Transcription initiation by alternative σ factors: revising the rigidness paradigm, 10th International Multiconference:* BGRS/SB2016 - 10th International Multiconference on Bioinformatics of Genome Regulation and Structure/Systems Biology*, Novosibirisk, Russia,* Sept 2016 (given by PhD student Jelena Guzina).
2. *Modeling CRISPR/Cas system induction: the significance of cooperative transcription regulation,* BGRS/SB2016, Novosibirsk, Russia, Sept 2016 (given by PhD student Andjela Rodic).
3. *Transcription initiation by alternative σ factors,* BELBI2016 - Belgrade Bioinformatics Conference, Belgrade, Serbia, June 2016 (given by PhD student Jelena Guzina).
4. *Examining regulation of restriction-modification systems by quantitative modeling*, BELBI2016 - Belgrade, Serbia, June 2016 (given by PhD student Andjela Rodic).
5. *Achieving a rapid expression of toxic (but useful) molecules within cell*, BELBI2016 - Belgrade, Serbia, June 2016 (given by PhD student Bojana Blagojevic).
6. *From biophysical modeling to bioinformatics*, Belgrade International Molecular Life Science Conference for Students, Belgrade, Serbia, Jan 2015.
7. *Inferring bacteriophage infection strategies from genome sequence: analysis of acteriophage 7-11 and related phages,* Bacteriophages 2015, London, UK, Jan 2016 (given by PhD student Jelena Guzina).
8. *Towards Accurate Transcription Start Site Prediction: a modelling approach*, German Conference on Bioinformatics (GCB2014), Bielefeld, Germany, September 2014.
9. *Modeling bacterial immune systems: CRISPR/CAS regulation*, The 9th international Conference on Bioinformatics of Genome Regulation and Structure\Systems Biology (BGRS\SB-2014), Novosibirsk, Russia, June 2014.
10. *A biophysical approach to bacterial transcription start site prediction*, The 9th international Conference on Bioinformatics of Genome Regulation and Structure\Systems Biology (BGRS\SB-2014), Novosibirsk, Russia, June 2014.

11. *Integrating Sequence Analysis with Biophysical Modelling for Accurate Transcription Start Site Prediction*, 10th International Symposium on Integrative Bioinformatics (IB2014), Newcastle, UK, May 2014.
12. *Bioinformatic analysis of bacterial promoters*, TABIS 2013 - Theoretical Approaches to BioInformation Systems 2013, Belgrade, Serbia, September 2013.
13. *Bioinformatics analysis of gene expression strategies of bacterial viruses,* TABIS 2013, Belgrade, Serbia, September 2013 (given by PhD student Jelena Guzina).
14. *CRISPR transcript processing: an unusual mechanism for rapid production of small RNAs,* ICSB 2012 - The 13th International Conference on Systems Biology, Toronto, CA, Aug 2012.
15. *Predictions of bacterial transcription start sites - a biophysical approach,* RBC 2012 - The 5th Regional biophysics conference, Kladovo, Serbia, Sept 2012.
16. *Transcription Start Site Prediction in Bacteria*, DMBI 2012 - International Meeting on Data Mining in Bioinformatics, Belgrade, Serbia, Jun 2012.
17. *CRISPR transcript processing: an unusual mechanism for rapid production of desired molecules,* IPCAT 2012 - 9th International Conference on Information Processing in Cells and Tissues, Trinity College, Cambridge, UK, Apr 2012.
18. *A Genome-wide Analysis of Poised Promoters in Bacteria*, 7th Annual Rocky Mountains Bioinformatics Conference, Snowmass Village, Colorado, Dec 2009.
19. *Biophysical modeling of transcription initiation in bacteria*, 8th International conf. on Information Processing in Cells and Tissues (IPCAT 2009), Franscini Ascona, Switzerland, Apr 2009.
20. *Quantitative modeling of transcription initiation in bacteria*, BioSysBio Conference 2009, Cambridge, UK, Mar 2009.
21. *Using biophysics to investigate engineering principles behind transcription initiation*, Engineering principles in Biological Systems, Cold Spring Harbor, NY, Dec 2008.
22. *Biophysical modeling of transcription initiation*, 2008 APS March Meeting, New Orleans, Louisiana, Mar 2008.
23. *Theoretical modeling of transcription initiation by bacterial RNA polymerase*, Partners Meeting, OSU MBI, Columbus, Ohio, Nov 2007.
24. *The open complex formation by bacterial RNA polymerase*, poster spotlight at Q-bio Conference on Cellular Information Processing, Santa Fe, Aug 2007.
25. *Using in vitro selection to infer transcription regulatory networks*, Evolution of Molecular Networks, KITP, Santa Barbara, California, Feb 2007.
26. *Computational analysis of gene regulation*, Partners Meeting, OSU, Columbus, Ohio, Nov 2006.
27. *Computational search for transcription factor binding sites*, 9th Annual Conference on Computational Genomics, Baltimore, Maryland, Oct 2006.
28. *Quantitative modeling and data analysis of SELEX experiments*, 2006 APS March Meeting, Baltimore, Maryland, Mar 2006.
29. *Biophysics and bioinformatics of transcription*, Partners Meeting, OSU, Columbus, OH, Nov 2005.
30. *Quantitative modeling and analysis of data for SELEX experiments*, 91st Statistical Mechanics Conference, Piscataway, New Jersey, May 2004.
31. *Biophysical approach to identification of transcription factor binding sites*, 5th General Conference of the Balkan Physical Union, Vrnjacka Banja, Serbia, Aug 2003.
32. *A biophysical approach to transcription factor binding site discovery*, 88th Statistical Mechanics Conference, Piscataway, New Jersey, Dec 2002.

B. Colloquia and Seminars

1. *Biophysical Modeling and Bioinformatics,* International Biophysics Week, Kolarac Foundation, Belgrade, Belgrade, March 2016 (given by PhD student Jelena Guzina).

2. *Modeling bacterial immune systems,* Seminar of Bioinformatics, Faculty of Mathematics, University of Belgrade, Belgrade, Nov 2015 (given by PhD student Andjela Rodic).
3. *Bioinformatics analysis of transcription regulation in bacteria and bacteriophages,* Bioinformatics seminar, Faculty of Mathematics, University of Belgrade, March 2015, Belgrade (given by PhD student Jelena Guzina).
4. *Biophysical Modeling and Bioinformatics of Gene Expression Regulation,* Colloquium at Faculty of Physics, University of Belgrade, Belgrade, Serbia, June 2014.
5. *Bioinformatics and Biological System Modeling*, Lecture Series in Honor of 150 Years of Faculty of Biology, University of Belgrade, Belgrade, Serbia, Nov 2013.
6. *Modeling the open complex formation by bacterial RNA polymerase*, NORDITA (Nordic Institute for Theoretical Physics) Seminar, Stockholm, Sweden, Mar 2008.
7. *Theoretical modeling of Gene Regulation*, ISU Mathematics Colloquium, Iowa State University, Ames, Iowa, Feb 2008.
8. *Modeling and Bioinformatics of Gene Transcription*, Frontiers in Systems and Integrative Biology, UCLA, Los Angeles, California, Feb 2008.
9. *Gene Regulation: Biophysical Modeling and Bioinformatics Applications*, Biophysics Seminar, Brown University, Providence, Rhode Island, Feb 2008.
10. *Biophysics and Bioinformatics of Gene Regulation*, Physics Colloquium, Western Kentucky University, Bowling Green, Kentucky, Feb 2008.
11. *Quantitative Modeling of Gene Regulation*, Mathematics Colloquium, West Virginia University, Morgantown, West Virginia, Feb 2008.
12. *Biophysical modeling of the open complex formation by bacterial RNA polymerase*, Physics Colloquium, National Central University, Taipei, Taiwan, Jan 2008.
13. *Theoretical modeling of transcription initiation in bacteria*, Center for Nonlinear Studies Seminar, LANL, Los Alamos, Dec 2007.
14. *Biophysics and bioinformatics approaches to gene expression regulation,* Iowa State University Mathematics Colloquium, Iowa State University, Ames, Nov 2007.
15. *Theoretical modeling of the open complex formation in bacteria,* Computational and Applied Mathematics Seminar, Iowa State University, Ames, Iowa, Nov 2007.
16. *Quantitative modeling of transcription initiation by bacterial RNA polymerase*, Applied Mathematics Colloquium, Columbia University, New York, Oct 2007.
17. *Quantitative modeling of transcription initiation in bacteria,* Brookhaven National Laboratory, Upton, New York, Oct 2007.
18. *Theoretical modeling of the open complex formation in bacteria,* Lunch Seminar, University of California at San Francisco, San Francisco, Oct 2007.
19. *Biophysics and bioinformatics of gene transcription*, Department of Biology Colloquium, Institute for Physiology and Biochemistry, Belgrade, Serbia, Sept 2007.
20. *Biophysics and bioinformatics of gene transcription*, Physics Colloquium, Faculty of Natural Sciences and Mathematics, Novi Sad, Serbia, Sept 2007.
21. *Quantitative modeling of transcription initiation in bacteria,* Theoretical Physics Seminar, Jozef Stefan Institute, Ljubljana, Slovenia, Aug 2007.
22. *Transcription factor binding energy vs. biological function*, Plant Biotechnology Seminar, Columbus, Ohio, Jan 2007.
23. *Search for transcription factor binding sites in eukaryotes: a principal limit and a novel method*, Plant Biotechnology Seminar, Columbus, Ohio, Jan 2006.
24. *Biophysics and bioinformatics of transcription regulation in bacteria and bacteriophages*, Postdoctoral Seminar, OSU MBI, Columbus, Ohio, Oct 2005.

25. *Bioinformatics of transcription regulation in bacteria and bacteriophages*, Computational Biology & Medical Informatics Seminar, IBM T. J. Watson Res. Center, Yorktown Heights, NY, Jan 2005.
26. *Quantitative analysis of gene expression regulation: a biophysical approach*, Rockefeller University, New York, New York, Jan 2005.
27. *Quantitative analysis of gene expression regulation: a biophysical approach*, Princeton University, Princeton, New Jersey, Jan 2005.
28. *Biophysics and bioinformatics of transcription regulation*, Computational Physics and Bioinformatics Group Seminar, Weizmann Institute of Science, Rehovot, Israel, Dec 2004.
29. *Computational analysis of gene expression regulation in bacteria and bacteriophages*, Brookhaven National Laboratory, Upton, New York, Dec 2004.
30. *Computational analysis of gene expression regulation in bacteria and bacteriophages*, Columbia University, New York, New York, Dec 2004.
31. *Computational approaches to transcription regulation,* Colloquium at Faculty of Physics, Belgrade, Serbia, Sept 2004.

C. Posters

1. *Modeling transcription initiation in bacteria*, ICSB 2007: The eight international conference on systems biology, Long Beach, California, Oct 2007.
2. *The Open Complex Formation by Bacterial RNA Polymerase*, Q-bio Conference on Cellular Information Processing, Santa Fe, Aug 2007.
3. *Quantitative Modeling of a Restriction-modification Gene Switch in Bacteria*, Q-bio Conference on Cellular Information Processing, Santa Fe, Aug 2007
4. *Binding energy vs. biological function*, Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor Laboratory, New York, Mar 2007.
5. *Quantitative analysis of virulent bacteriophage transcription strategies*, 9th Annual Conference on Computational Genomics, Baltimore, Maryland, Oct2006.
6. *Computational Analysis of Transcription Regulation: Some Principal Limits and a Novel Method*, Regulation of Eukaryotic Transcription: from Chromatin to mRNA, Taos, New Mexico, Apr 2006.
7. *A principal Limit in Search for Transcription Factor Binding Sites*, Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor Laboratory, New York, Mar 2006.
8. *SELEX experiments: Modeling and Data Analysis*, The 22nd Jerusalem Winter School in Theoretical Physics, Biological Networks and Evolution, Jerusalem, Israel, Jan 2005.
9. *Search for transcription factor binding sites - biophysics approach*, XVI National Symposium on Condensed Matter Physics - SFKM, Sokobanja, Serbia, Sept 2004.
10. *Optimal design of SELEX experiments, Systems Biology: Genomic Approaches to Transcriptional Regulation*, Cold Spring Harbor Laboratory, New York, Mar 2004.