

CURRICULUM VITÆ

Personal Data

Name: **Dumitru Brinza**
Ph.D in Computer Science and Bioinformatics

Current affiliation: Department of Computer Science and Engineering
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Education

06/2007 Ph.D. in Computer Science (Bioinformatics), advisor Dr. Alexander Zelikovsky
Dept. of Computer Science, Georgia State University, USA

06/2002 B.S. in Applied Mathematics, Specializing in Computer Science and Optimization Methods
Dept. of Mathematics and Cybernetics, Moldova State University

Research Interests

Discrete Algorithms and Combinatorial Optimization, Bioinformatics
Computational Biology, Proteomics, Computational Mass Spectrometry
Ad Hoc and Sensor Networks

Honors and Awards

11/2006 Genetic Analysis Workshop 15 Scholarship \$1,600, by Illumina, St. Pete Beach, Florida

10/2006 Computational Genomics Conf. Travel and Registr. Awards \$1,500, VBI at Virginia Tech

07/2006 Molecular Basis of Disease Fellowship \$22,000, Georgia State University, Atlanta

04/2006 **Outstanding Graduate Research Award**, Georgia State University, Atlanta

11/2005 Best Poster Award, Fifth Georgia Tech Intl Conf on Bioinformatics, Georgia Tech

07/2005 Molecular Basis of Disease Fellowship \$22,000, Georgia State University, Atlanta

01/2004 Georgia State University Scholarship \$14,000, Georgia State University, Atlanta

Professional Experience

2007–0000 post-doctoral fellow, advisor Dr. Pavel Pevzner
Department Computer Science and Engineering, University of California at San Diego

2004–2007 research assistant
Department Computer Science, Georgia State University, Atlanta, USA

2002–2004 software engineer
Unisim-Soft S.R.L Copmany, Chisinau, Moldova

2001–2002 senior software engineer
National Bank of Moldova, Chisinau, Moldova

2000–2001 senior software engineer
Republican Center of Informatics and Calculus, Chisinau, Moldova

Teaching Experience

Spring 2006 CSc 4520/6520 “Algorithms: Design and Analysis”, Georgia State University

Professional Service

- 2007 PC member, IEEE International Conference on Bioinformatics and Biomedicine (BIBM)
- 2007 Poster-Chair on International Symposium on Bioinformatics Research and Applications (ISBRA)
- 2006 Co-Chair on International Workshop on Bioinformatics Research and Applications (IWBRA)
- 2006 Conference Assistant IEEE Intl Conf on Granular Computing (GRC)
- 2005 Technical Committee Second SECABC Fall Workshop on Biocomputing

Refereeing

IEEE International Conference on Bioinformatics and Biomedicine (BIBM)
International Conference on Combinatorial Optimization and Applications (COCOA)
International Computing and Combinatorics Conference (COCOON)
International Symposium Bioinformatics Research and Applications
IEEE Transactions on NanoBioscience
IEEE IEEE/ACM Transactions on Computational Biology and Bioinformatics
International Journal Bioinformatics Research and Applications
International Workshop Bioinformatics Research and Applications
First International Workshop on Mobile Ad-hoc and Ubiquitous Sensor Networks
IEEE Journal Systems, Man and Cybernetics
IEEE Journal on Selected Areas in Communications

Software Packages

1. **2SNP**: fast and scalable phasing software for trios and unrelated individuals, based on 2-SNP haplotypes, <http://alla.cs.gsu.edu/~software/2SNP>.
2. **DACS**: software for searching statistically significant multi-SNP combinations associated with a disease, <http://alla.cs.gsu.edu/~software/DACS>.
3. **TrioPhasing**: integer linear programming based software for phasing Trio data, requires LP solver, <http://alla.cs.gsu.edu/~software/trioPhasing.html>.
4. **DEEPS**: Deterministic Energy-Efficient Protocol for Sensor networks, NS2 implementation requires LEACH protocol, <http://alla.cs.gsu.edu/~software/DEEPS>.

Refereed Journal Articles and Book Chapters

1. Brinza, D., He, J., and Zelikovsky, A. (2006) ‘Optimization Methods for Genotype Data Analysis in Epidemiological Studies’, book chapter in *Bioinformatics Algorithms: Techniques and Applications*.
2. Brinza, D. and Zelikovsky, A. (2006) ‘2SNP: Scalable Phasing Method for Trios and Unrelated Individuals’, *Journal of IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*.

3. Brinza, D. and Zelikovsky, A. (2006) ‘2SNP: Scalable Phasing Based on 2-SNP Haplotypes’, *BIOINFORMATICS*, Pub 2006 Feb 1; **22(3)**:371–373. Epub 2005 Nov 15.
4. Brinza, D., He, J., Mao, W. and Zelikovsky, A. (2005) ‘Family Trio Phasing and Missing Data Recovery’, *International Journal Bioinformatics Research and Applications*, IJBRA’05 **Vol. 1**, No.2 pp. 221–229.

Refereed Conference Articles

5. Brinza, D. and Zelikovsky, A. (2007) ‘Risk Factor Searching Heuristics for SNP Case-Control Studies’, *Proc. of IEEE International conference on Bioinformatics and Biomedicine (BIBM 2007)*.
6. Brinza, D. and Zelikovsky, A. (2007) ‘Discrete Methods for Association Search and Status Prediction in Genotype Case-Control Studies’, *Proc. of IEEE 7-th International Symposium on Bioinformatics and BioEngineering (BIBE’07)*.
7. Brinza, D. and Zelikovsky, A. (2006) ‘Combinatorial Analysis of Disease Association and Susceptibility for Rheumatoid Arthritis SNP Data’, **Travel Award**, *Proc. of Genetic Analysis Workshop (GAW15)*, **13**:6–11.
8. Andre R. de Vries, Ilja M. Nolte, Geert T. Spijker, Dumitru Brinza, Alexander Zelikovsky, and Gerard J. te Meerman (2006) ‘Cross Haplotype Sharing Statistic: Haplotype length based method for whole genome association testing’, **Travel Award**, *Proc. of Genetic Analysis Workshop (GAW15)*, **13**:16–21.
9. Brinza, D., He, J. and Zelikovsky, A. (2006) ‘Combinatorial Search Methods for Multi-SNP Disease Association’, *Proc. International Conf. of the IEEE Engineering in Medicine and Biology (EMBC’06)*, pp. 5802–5805.
10. Brinza, D. and Zelikovsky, A. (2006) ‘Combinatorial Methods for Disease Association Search and Susceptibility Prediction’, 6th Workshop on Algorithms in Bioinformatics (WABI 2006), *Lecture Notes in Bioinformatics* **4175**, pp. 286–297.
11. Brinza, D., Perelygin, A., Brinton, M. and Zelikovsky, A. (2006) ‘Search for multi-SNP Disease Association’, *The Fifth International Conference on Bioinformatics of Genome Regulation and Structure (BGRS’06)*, pp. 122–125.
12. Brinza, D. and Zelikovsky, A. (2006) ‘DEEPS: Deterministic Energy-Efficient Protocol for Sensor networks’, ACIS International Workshop on Self-Assembling Wireless Networks (SAWN’06), *Proc. of SNPD 2006*, pp. 261–266.
13. Brinza, D. and Zelikovsky, A. (2006) ‘Phasing of 2-SNP Genotypes based on Non-Random Mating Model’, International Workshop on Bioinformatics Research and Applications (IWBRA’06), *Proc. of ICCS 2006*, LNCS **3992**, pp. 767–774.
14. Mao, W., Brinza, D., Hundewale, N., Gremalschi, S. and Zelikovsky, A. (2006) ‘Genotype Susceptibility and Integrated Risk Factors for Complex Diseases’, *Proc. IEEE Intl Conf on Granular Computing (GRC 2006)*, pp. 754–757.
15. Altun, G., Hu, H.-J., Brinza, D., Harrison, R.W., Zelikovsky, A. and Pan, Y. (2006) ‘Hybrid SVM kernels for protein secondary structure prediction’, *Proc. IEEE Intl Conf on Granular Computing (GRC 2006)*, pp. 762–765.
16. Brinza, D., Calinescu, G., Tongngam, S. and Zelikovsky, A. (2005) ‘Energy-Efficient Continuous and Event-Driven Monitoring’, *2nd IEEE International Conference on Mobile Ad-Hoc and Sensor Systems (MASS’05)*, 10.1109/MAHSS.2005.1542792.

17. Mao, W., He, J., Brinza, D. and Zelikovsky, A. (2005) ‘A Combinatorial Method for Predicting Genetic Susceptibility to Complex Diseases’, *International Conference of the IEEE Engineering In Medicine and Biology Society (EMBC’05)*, pp. 224–227.
18. Brinza, D., He, J., Mao, W. and Zelikovsky, A. (2005) ‘Phasing and Missing Data Recovery in Family Trios’, *International Workshop on Bioinformatics Research and Applications (IWBRA’05), Proc. of ICCS 2005 LNCS 3515*, pp. 1011–1019.
19. Brinza, D., Hincu, G., (2002) ‘Design of multithread algorithm for Simplex method’, *Moldova State University Journal*, pp. 17–32.
20. Brinza, D., Savcenco, V., Bercu, I. and Magariu, N. (1998) ‘Developing of an Algorithms Builder’, *Publication in Moldova State University Journal*, pp. 9–11.

Poster and Oral Presentations

1. Banderia, N., Brinza, D., Hixson, K., Smith, R., and Pevzner, P. (2007) ‘High-throughput spectral networks reconstruction of whole proteome’, *Human Proteome Organisation’s (HUPO 2007)*.
2. Brinza, D. and Zelikovsky, A. (November 2006) ‘Case(Control)-Free Multi-SNP Combinations in Case-Control Studies’, *Algorithmic Biology 2006, at University of California, San Diego*.
3. Brinza, D. and Zelikovsky, A. (November 2006) ‘Combinatorial Analysis of Disease Association and Susceptibility for Rheumatoid Arthritis SNP Data’, *Genetic Analysis Workshop 15, St Pete Beach, FL*.
4. Brinza, D., He, J. and Zelikovsky, A. (September 2006) ‘Combinatorial Search Methods for Multi-SNP Disease Association’, *International Conf. of the IEEE Engineering in Medicine and Biology (EMBC’06), New-York, NY*.
5. Barkhash, A., Perelygin, A., Brinza, D., Pilipenko, P., Bogdanova, YU., Romaschenko, A., Voevoda, M. and Brinton, M. (July 2006) ‘GENETIC RESISTANCE TO FLAVIVIRUSES’, *Genomics Proteomics Bioinformatics and Nanotechnologies for Medicine (GPBM’06), Novosibirsk, RU*.
6. Brinza, D. and Zelikovsky, A. (Jun 2006) ‘Combinatorial Search Methods for Genotypes Associated with Lung Cancer’, *Molecular Basis of Disease Symposium (MBD’06), Atlanta, GA*.
7. Barkhash, A., Perelygin, A., Brinza, D., Pilipenko, P., Bogdanova, YU., Romaschenko, A., Voevoda, M. and Brinton, M. (May 2006) ‘VARIABILITY IN THE 2-5 OLIGOADENYLATE SYNTHETASE (OAS) GENE CLUSTER IS ASSOCIATED WITH SEVERITY OF TICK-BORNE ENCEPHALITIS VIRUS-INDUCED DISEASE IN RUSSIAN PATIENTS’, *9-th Southeastern Regional Virology Conference 2006, Atlanta, GA*.
8. Brinza, D. and Zelikovsky, A. (May 2006) ‘Phasing of 2-SNP Genotypes based on Non-Random Mating Model’, *International Workshop on Bioinformatics Research and Applications (IWBRA’06), Reading, UK*.
9. Mao, W., Brinza, D., Hundewale, N., Gremalschi, S. and Zelikovsky, A. (May 2006) ‘Genotype Susceptibility and Integrated Risk Factors for Complex Diseases’, *IEEE Intl Conf on Granular Computing (GRC 2006), Atlanta, GA*.
10. Brinza, D. and Zelikovsky, A. (November 2005) ‘2SNP: New Scalable Phasing Method’, *The Fifth Georgia TECH International Conference on Bioinformatics (GTICB’05), Atlanta, GA, best poster award*.
11. Brinza, D. and Zelikovsky, A. (October 2005) ‘2SNP: New Scalable Phasing Method’, *The Second SECABC Fall Workshop ON Biocomputing (SECABC’05), Atlanta, GA*.

12. Brinza, D. and Zelikovsky, A. (August 2005) 'New 2-SNP Statistics method for Phasing and Missing data recovery', *Georgia State Biotech Symposium, Atlanta, GA*.
13. Brinza, D., He, J., Mao, W. and Zelikovsky, A. (May 2005) 'Family Trio Phasing and Missing Data Recovery', *Research in Computational Molecular Biology (RECOMB'05), Boston, MA*.
14. Brinza, D., Calinescu, G. and Zelikovsky, A. (October 2004) 'Energy-Efficient Continuous and Event-Driven Monitoring', *Georgia Electronic Design Center Industry Advisory Board (GEDC IAB'04), Atlanta*.
15. Brinza, D., Derado, G., Aznita, R., Li, Y. and Zelikovsky, A. (May 2004) 'Energy efficient protocols for ad-hoc static networks', *Georgia Electronic Design Center Industry Advisory Board (GEDC IAB'04), Atlanta, GA*.

Expertise

Applications: Oracle 8i/10i, JBuilder, C++Builder, Delphi, MS Office, Microsoft Visual Basic, Adobe Photoshop, CorelDraw, 3D MAX, Apache, Toad, AutoCad, Macromedia Flash, MathLab, MySQL, MSSQL, Eclipse, PyMOL, BLAST.

Programming Languages: C/C++, Java, Assembler, PSP, JSP, PL/SQL, XML/XSL, HTML, JavaScript, DHTML, Delphi(Pascal), VB, COM, ActiveX, ASP, Perl, OODB, MPI, TCL/OTCL.

Operating Systems: Dos/Windows 98/NT/2000/XP, UNIX, Linux, Solaris.

Statement of Research

Currently my research is focused on the rapidly developing part of bioinformatics devoted to open problems in analysis of genetic variation across human population. It is widely believed that haplotype/genotype structure carries information on susceptibility to most of common hereditary diseases. I apply my extensive background in optimization, AI, linear algebra, statistics and discrete mathematics to practical and theoretical problems arising in protein structure analysis, computational genomics, and genetic epidemiology.

My research is mainly focused on analysis of genetic variation across population. I have proposed and implemented a novel and extremely fast scalable algorithm for haplotype inference (2SNP). This algorithm uses concepts from graph theory and statistics. The software implementation of 2SNP has been favorably compared with all known phasing algorithms including PHASE, HAPLOTYPER, HAP and others. This work has been published in *Bioninformatics* and received the Best Poster Award at the Fifth Georgia Tech International Conference on Bioinformatics. The developed software packages are made publicly available for the benefit of biomedical community - 2SNP software package can be downloaded from (<http://alla.cs.gsu.edu/~software/2SNP>). Many researchers all over the world have already applied my package to phase large datasets with chromosome- and genome-wide genotypes.

I have applied other combinatorial optimization techniques such as integer linear programming and discrete optimization on graphs to search for disease-associated multi-SNP combinations and to estimate risk factor for attaining hereditary diseases. The developed methods have been able to find statistically significant disease association for datasets where all previously known search methods failed. Disease-association based methods have been utilized for disease susceptibility prediction. The prediction accuracy of the algorithms is shown to be significantly high for several diseases and conditions. This work has been presented at the 6th Workshop on Algorithms in Bioinformatics *WABI'06*. The software package can be downloaded from (<http://alla.cs.gsu.edu/~software/DACS>). I have successfully applied these methods in cooperation with Professor T. Dragani (Italian National Cancer Institute) to lung cancer, with Professor M. Brinton (GSU Biology Dept.) to tick-born encephalitis, and with Professor K. Grant (GSU Chemistry Dept.) to resistance to anti-depression drugs.

I also participated in the development of a novel linear algebraic approach (MLR-Tagging) applicable to one of the central problems of computational population genetics such as tagging (finding minimum number of tags accurately representing the entire genotype). The latest results have been published in *Bioninformatics*. The software package can be downloaded from (<http://alla.cs.gsu.edu/~software/tagging/tagging.html>). The summary of my work in optimization methods for genotype data analysis in epidemiological studies will be published in a book chapter that can be downloaded from (<http://cs.ucsd.edu/~dbrinza/cv/pub/book6.pdf>).

I have also been involved in predicting of secondary protein structure based on sequential data. I have modified several well known AI techniques by introducing linear programming modules for solving internal subproblems and have successfully applied them for the protein secondary structure prediction. This work has been presented at the Conference on Granular Computing (GRC'06).

Currently, I am involved in several projects devoted to disease association study, susceptibility prediction, macro-arrays expression study, mass-spectrometry data and protein structure modeling. In my professional work I would like to develop new algorithms in the area of bioinformatics applying my accumulated knowledge and training. Majority of my publications can be downloaded from the web site (<http://cs.ucsd.edu/~dbrinza/cv>).

Teaching Statement

There are two main goals when teaching students which I set to myself. First, to provide students with the knowledge necessary for their future studies and career. And second, not less important, to interest them in research in computer science in general and analysis of algorithms in particular. To achieve those goals I try to base my teaching on the following principles. The first is providing the intuition and motivation for any problem or methodology which I teach. After grasping the general idea from a simplified model or an example it is much easier to understand the more complex concept. One of the reasons I personally was attracted to algorithms was the ability to formalize the problems and the solutions. I try to provide many visual aids and explanations for the material I teach. Intuition is the first step in understanding a problem. However, deep understanding often requires a formal theoretical foundation. When explaining key algorithms and techniques I like to provide the formal arguments behind the algorithmic choices and properties. Even a relatively dry subject can be spiced up by providing historical references and trivia. References I use when the introductory material is taught. Finally, I believe a teacher's enthusiasm for a subject is contagious, and am glad when it passes on in class or in one-on-one conversations. After a lecture on combinatorial methods in disease association and disease susceptibility prediction which I gave this fall, I was told by a student that I really love my work. I think this love for research topics should be evident to students, as it will encourage them to follow the research path. Recently I was very encouraged by the student feedback, when my teaching of programming course was ranked in the top 10% in student evaluation, in the category of advanced graduate courses.

Teaching Experience: During my PhD studies I taught "Algorithms: Design and Analysis" for graduate and senior undergraduate students. I also served as a TA for "Advanced Algorithms in Bioinformatics", "Parallel and Distributed Computing", "High Performance Computing", "Networks", "Advanced Algorithms for VLSI CAD and Communication Networks".

References

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Georgia State University
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Atlanta, GA 30303
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Ph.: (404) 651-0649

Prof. Pavel Pevzner

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Dr. Teresa Przytycka

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Computational Biology Branch
Building 38A 8S812
Bethesda, MD 20894
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Dr. Ion Mandoiu

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Prof. Daniel M. Gusfield

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University of California Davis
2125 Kemper Hall, 1 Shields Avenue
Davis, CA 95616
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