

Curriculum Vitae

Mirela Andronescu

Post-doctoral fellow, Noble Lab

Department of Genome Sciences, University of Washington
Foege Building room S220, 1705 NE Pacific St., Seattle, WA 98195-5065

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EDUCATION

- *Ph.D. in Computer Science (Bioinformatics)*, University of British Columbia (UBC) (2003-2008)
 - *Thesis title*: “Computational approaches for RNA energy parameter estimation”.
 - *Supervisors*: Drs. Anne Condon and Holger Hoos.
 - *Awards*: UBC Governor General’s Gold Medal for the doctorate degree, UBC Faculty of Science Graduate Prize.
- *M.Sc. in Computer Science (Bioinformatics)*, University of British Columbia (2001-2003)
 - *Thesis title*: “Algorithms for predicting the secondary structure of pairs and combinatorial sets of nucleic acid strands”.
 - *Supervisor*: Dr. Anne Condon.
 - *Award*: UBC Governor General’s Gold Medal for the Master’s degree.
- *B.Sc. in Computational Economics*, Academy of Economic Studies, Bucharest, Romania (1994-1999)

AWARDS AND FELLOWSHIPS (selected)

- *NSERC postdoctoral fellowship* (\$40,000 per year for two years), awarded by the Natural Sciences and Engineering Research Council of Canada to exceptional postdoctoral candidates (2009-2010);
- *Governor General’s Gold Medal*, awarded each year to the best Ph.D. graduate university-wide, UBC (2009);
- *Faculty of Science Graduate Prize* (\$1,000), awarded each year to the best Ph.D. thesis in the Faculty of Science at UBC (2009);
- *IBM Ph.D. Fellowship* (\$17,500), awarded by IBM Research to exceptional Ph.D. students worldwide (2007);
- *Li Tze Fong Memorial Fellowship* (\$18,000), awarded to the best graduate students of UBC (2006);
- *Campbell Graduate Fellowship* (\$16,000), awarded to the best graduate students of UBC (2005);
- *Simons Foundation Doctoral Scholarship* (\$7,800), awarded to one outstanding doctoral female student in science or applied science at UBC (2004);
- *University Graduate Fellowship* (\$8,200), awarded to the best graduate students of UBC (2004);
- *Governor General’s Gold Medal*, awarded each year to the best Master’s graduate university-wide, UBC (2004);
- *Merit scholarship* awarded to the students whose GPA was at least 98%, Academy of Economic Studies of Bucharest, Romania (1999).

PUBLICATIONS

Peer-reviewed articles published in journals and conferences

- [1]. **M. Andronescu**, A. Condon, H.H. Hoos, D.H. Mathews and K.P. Murphy, “Computational approaches for RNA energy parameter estimation”, *RNA*, in press.
 - *Contribution*: designed, implemented and evaluated all the computational methods, wrote the manuscript.
- [2]. Z. Duan*, **M. Andronescu***, K. Schutz, S. McIlwain, Y.J. Kim, C. Lee, J. Shendure, S. Fields, C.A. Blau, and W.S. Noble, “A three-dimensional model of the yeast genome”, *Nature* 2010, 465:363-7 (* equal contribution).
 - *Contribution*: designed, implemented and tested all the statistical solutions and computational analyses.
 - *Impact*: featured in *Nature* podcast in May 2010, achieved the 5-th place for the most downloaded *Nature* papers, marked as “Must read” on the Faculty of 1000 web site.
- [3]. D. Tulpan, **M. Andronescu**, and S. Leger, “Free energy estimation of short DNA duplex hybridizations”, *BMC Bioinformatics* 2010, 11:105.
 - *Contribution*: co-planned the research, collected and curated part of the data.
- [4]. **M. Andronescu***, C. Pop*, and A. Condon, “Improved free energy parameters for RNA pseudoknotted secondary structure prediction”, *RNA* 2010, 16(1):26-42 (* equal contribution).
 - *Contribution*: designed, implemented and evaluated the RNA parameter estimation algorithms, collected the data, co-supervised the implementation of prediction algorithms, co-wrote the manuscript.
- [5]. **M. Andronescu** and M. Brodie, “Decision tree learning using a Bayesian approach at each node”, *Proceedings of the 22nd Canadian Conference on Artificial Intelligence 2009, Lecture Notes in Artificial Intelligence* 2009, 5549: 4-15.
 - *Contribution*: designed, implemented and evaluated the algorithms, wrote the manuscript.
- [6]. **M. Andronescu**, V. Bereg, H.H. Hoos, and A. Condon, “RNA STRAND: The RNA secondary structure and statistical analysis database”, *BMC Bioinformatics* 2008, 9(1): 340.
 - *Contribution*: collected and curated the data, implemented the MySQL database, performed computational analyses, supervised and extended the implementation of the web interface in PHP, maintained the website <http://www.rnasoft.ca/strand> over five years, co-wrote the manuscript.
 - *Impact*: cited 19 times (Google scholar), marked as “Highly accessed” by BioMed Central.
- [7]. **M. Andronescu**, A. Condon, H.H. Hoos, D.H. Mathews, and K.P. Murphy, “Efficient parameter estimation for RNA secondary structure prediction”, *Bioinformatics* 2007, 23(13): i19-i28, *ISMB/ECCB 2007* (15% acceptance rate).
 - *Contribution*: designed, implemented and evaluated the algorithms, collected and curated the data, wrote the manuscript.
 - *Impact*: cited 37 times (Google scholar).
 - *Award*: one of the three Best Student Papers of 2007 evaluated by MITACS (\$500).
- [8]. **M. Andronescu** and A. Condon, “Finding MFE structures formed by nucleic acid strands in a combinatorial set”, *Nanotechnology: Science and Computing*, J. Chen, N. Jonoska. G. Rozenberg (Eds.), *Natural Computing Series* 2006, Springer, 121-136.
 - *Contribution*: designed, implemented and evaluated the algorithms, wrote the manuscript.
- [9]. D. Tulpan, **M. Andronescu**, S.B. Chang, M.R. Shortreed, A. Condon, H.H. Hoos and L.M. Smith, “Thermodynamically based DNA strand design”, *Nucleic Acids Research* 2005, 33(15): 4951-4964.

- *Contribution*: consulted on the algorithm design, evaluated the algorithms.
 - *Impact*: cited 28 times (Google scholar).
- [10]. M.R. Shortreed, S.B. Chang, D. Hong, M. Phillips, B. Campion, D.C. Tulpan, **M. Andronescu**, A. Condon, H.H. Hoos and L.M. Smith, “A thermodynamic approach to designing structure-free combinatorial DNA word sets”, *Nucleic Acids Research* 2005, 33(15): 4965-4977.
- *Contribution*: consulted on the algorithm design.
 - *Impact*: cited 16 times (Google scholar).
- [11]. **M. Andronescu**, Z.C. Zhang and A. Condon, “Secondary structure prediction of interacting RNA molecules”, *Journal of Molecular Biology* 2005, 345(5): 987-1001.
- *Contribution*: designed, co-implemented and evaluated the algorithm design, supervised the algorithm implementation, wrote the manuscript.
 - *Impact*: cited 76 times (Google scholar).
- [12]. **M. Andronescu**, A.P. Fejes, F. Hutter, H.H. Hoos and A. Condon, “A new algorithm for RNA secondary structure design”, *Journal of Molecular Biology* 2004, 336(3): 607-624.
- *Contribution*: led the design, implementation and evaluation of the algorithms, co-wrote the manuscript.
 - *Impact*: cited 49 times (Google scholar).
- [13]. **M. Andronescu**, R. Aguirre-Hernandez, A. Condon and H. Hoos, “RNAsoft: a suite of RNA secondary structure prediction and design software tools”, *Nucleic Acids Research* 2003, 31: 3416-3422.
- *Contribution*: designed, implemented and evaluated the algorithms, created and maintained the online access to the software at <http://www.rnasoft.ca>.
 - *Impact*: cited 65 times (Google scholar).
- [14]. **M. Andronescu**, D. Dees, L. Slaybaugh, Y. Zhao, A. Condon, B. Cohen and S. Skiena, “Algorithms for testing that sets of DNA words concatenate without secondary structure”, *Natural Computing* 2003, 2(4): 391-415. Also in the *Proceedings of the Eighth International Meeting on DNA Based Computers (DNA 8)* 2002, Sapporo, Japan.
- *Contribution*: implemented and evaluated the algorithms, co-wrote the manuscript.
 - *Impact*: cited 36 times (Google scholar).
 - *Award*: Best Student Paper of the DNA 8 conference (\$1,500).

Manuscripts in preparation

- [15]. **M. Andronescu**, Y. Wang, M. Mathews, C. Dale, W.S. Noble and E. Rubel, “Proteomics of brain cells responsible for hearing in mice and chickens”.
- *Contribution*: co-designed the mass spectrometry data analysis, supervised its implementation.
- [16]. **M. Andronescu** and A. Brown, “A dynamic programming algorithm to compute the gradient of the RNA partition function”.
- *Contribution*: designed, implemented and evaluated the algorithms, wrote the manuscript.

Peer-reviewed abstracts and posters (selected)

- [17]. **M. Andronescu**, Z. Duan, K. Schutz, S. McIlwain, Y.J. Kim, C. Lee, J. Shendure, S. Fields, C.A. Blau and W.S. Noble, “A three-dimensional model of the yeast genome”, 1-page abstract and platform presentation, *Yeast Genetics and Molecular Biology Meeting* 2010, Vancouver, BC.

- [18]. **M. Andronescu**, Z. Duan, K. Schutz, J. Shendure, S. Fields, C.A. Blau and W.S. Noble, “Genome-wide chromosomal interactions in yeast”, poster presentation, *Annual retreat of the Dept. of Genome Sciences* 2009, University of Washington.
- Award: Best Poster of the Genome Sciences department (\$1,250).
- [19]. **M. Andronescu**, M.H. Hoffman and W.S. Noble, “Exploratory data analysis of genomic segmentations”, 1-page abstract and poster presentation, *Annual ENCODE Meeting* 2009, Bethesda, MD, USA.
- [20]. **M. Andronescu** and A. Condon, “Secondary structure prediction of RNA pairs”, 2-page abstract in the *Proceedings of the Eighth Annual International Conference on Research in Computational Molecular Biology (RECOMB) 2004*, San Diego, CA.
- [21]. **M. Andronescu**, H. H. Hoos and A. Condon, “RNA Designer: A computational method for designing RNA molecules with a specific secondary structure”, 1-page abstract in the *Proceedings of the Eighth Annual Meeting of the RNA Society (RNA) 2003*, Vienna, Austria.

RESEARCH EXPERIENCE

- *Post-doctoral fellow*, Noble Lab, Dept. of Genome Sciences, University of Washington (2009-2010)
Supervisor: Dr. William Stafford Noble. Completed work and work in progress include:
 - Computational algorithms and statistical analysis of high-throughput genome-wide sequencing data for the discovery of functional chromatin interactions with applications to the genomes of yeast (ref. [2]), mouse and human (collaboration with Drs. C. Anthony Blau, Stanley Fields, Jay Shendure and Christine Disteche);
 - Analysis of mass spectrometry and gene expression data of specific regions of the brain in order to discover new insights into the molecular mechanisms of hearing in mammals (mouse) and birds (chicken) (ref. [15], collaboration with Drs. Edwin Rubel and Michael MacCoss);
 - Computational algorithms for peptide and protein identification and quantification from (tandem) mass spectrometry data, as well as mass spectrometry data denoising (ref. [15], collaboration with Dr. Michael MacCoss);
 - Computational and machine learning algorithms for the identification of tumor cell types from high-throughput data from leukemia (collaboration with Dr. C. Anthony Blau);
 - Statistical analysis of RNA-seq data from three developmental stages of mouse embryonic stem cells (collaboration with Drs. C. Anthony Blau and Larry Ruzzo);
 - Statistical analysis of quantitative PCR data to identify differentially expressed genes in chickens with and without induced hearing loss (collaboration with Drs. Jennifer Stone and Robin Gibson);
 - Machine learning algorithms to predict immune response to HIV/SIV vaccines (collaboration with Dr. Daniel Zak, Institute for Systems Biology).
- *Graduate Research Assistant*, Dept. of Computer Science, University of British Columbia (2002-2008)
Supervisors: Drs. Anne Condon and Holger Hoos. Designed efficient machine learning algorithms for estimating the energy parameters used in energy-based RNA secondary structure prediction; created algorithms that use large amounts of training data efficiently and accurately; developed and implemented stochastic local search and dynamic programming algorithms for RNA secondary structure design and prediction. I am the main author of the following software tools and database:
 - The Constraint Generation (CG) and Boltzmann Likelihood (BL) packages, implementing machine learning algorithms for RNA free energy parameter estimation from large amounts of structural and thermodynamic RNA data (refs. [1,4,7], collaboration with Drs. Kevin Murphy, UBC, and David Mathews, University of Rochester);
 - RNA STRAND, a comprehensive online RNA secondary structure and statistical analysis database: <http://www.rnasoft.ca/strand> (ref. [6]).

- The MultiRNAFold package, containing software for secondary structure prediction of one, two, and many interacting RNA or DNA molecules (ref. [11]);
- CombFold, predicting which strand, out of a combinatorial set formed from DNA or RNA input strands, folds to a secondary structure with the lowest minimum free energy (refs. [8,14]);
- RNA Designer, designing an RNA sequence that folds to a given secondary structure (ref. [12]);
- RNAsoft web page, offering web services to the above tools: <http://www.rnasoft.ca> (ref. [13]);

These tools have been used by researchers at various institutes, including California Institute of Technology, Scripps Research Institute, University of Toronto, Columbia University, and they are accessible online or upon request.

- *Summer Intern*, IBM T.J. Watson Research Center, Hawthorne, NY (2006)
Supervisor: Dr. Mark Brodie. Pursued research in machine learning; designed and implemented a decision tree algorithm which can effectively combine prior expert knowledge and training data by using a probabilistic iterative approach (ref. [5]).

TEACHING EXPERIENCE

- *Lecturer* for several classes of the graduate Machine Learning course and graduate Bioinformatics course, Dept. of Computer Science, University of British Columbia (2003-2007)
- *Graduate Teaching Assistant*, Dept. of Computer Science, University of British Columbia (2001-2007)
Conducted tutorials, laboratories, office hours and grading, as outlined below. Obtained excellent teaching evaluations.
 - CPSC 540 Machine Learning (Spring 2007), teaching evaluation average (TEA) 4.71 out of a maximum of 5;
 - CPSC 219 Software Development (Fall 2003), TEA 4.20;
 - CPSC 405 Modeling and Simulation (Spring 2003), TEA 4.07;
 - CPSC 219 Software Development (Fall 2002), TEA 4.73;
 - CPSC 216 Data Structures (Spring 2002), TEA 4.85 (departmental teaching award);
 - CPSC 216 Data Structures (Fall 2001), TEA 3.57.
- *Bioinformatics Instructor*, Canadian Bioinformatics Workshop, Vancouver, BC (Feb 2005)
Instructor for the RNA Laboratory; teaching assistant for the two weeks of the workshop.
- *Instructor* for the GIRLsmarts Workshop for sixth grade girls, Vancouver, BC (Jun 2004)
Designed and taught the “Computer Assembly and Disassembly” activity.
- *Graduate Teaching Assistant*, Academy of Economic Studies, Bucharest, Romania (1999-2000)
Teaching assistant for the course Computer and Operating Systems. Conducted tutorials, laboratories and grading; developed an introductory Assembly manual.

SUPERVISORY AND MENTORING EXPERIENCE

- *Co-supervisor* of four undergraduate students, two graduate students and one research scientist on projects related to the analysis of mass spectrometry data and tumor subclonal identification, University of Washington (UW), and RNA secondary structure prediction at the University of British Columbia (UBC):
 - Michael Mathews, undergraduate research assistant, UW (Sep 2009 - Sep 2010)
 - * *Main advisor*: William Stafford Noble
 - * *Project*: Mass spectrometry data analysis, peptide identification and quantification
 - Kris Weber, graduate summer intern, UW (Jun 2010 - Sep 2010)
 - * *Main advisors*: William Stafford Noble, Anthony Blau
 - * *Project*: Tumor subclonal identification
 - Mitchell Watrous, research scientist, UW (Jan 2010 - Aug 2010)

- * *Main advisors:* Anthony Blau, William Stafford Noble
- * *Project:* Analysis of genome interaction data
- Daniel Chee, undergraduate summer intern, UW (Jun 2009 - Sep 2009)
 - * *Main advisor:* William Stafford Noble
 - * *Project:* Denoising tandem mass spectrometry data
- Cristina Pop, graduate summer student, UBC (May 2008 - Aug 2008)
 - * *Main advisor:* Anne Condon
 - * *Project:* RNA free energy parameter estimation for pseudoknots (ref. [4])
- Vera Bereg, undergraduate summer student, UBC (May 2004 - Aug 2004)
 - * *Main advisors:* Holger Hoos, Anne Condon
 - * *Project:* RNA secondary structure analysis and online database (ref. [6])
- Zhi Chuan Zhang, undergraduate research assistant, UBC (Sep 2002 - Aug 2003)
 - * *Main advisor:* Anne Condon
 - * *Project:* Prediction of RNA suboptimal secondary structures (ref. [11])

INDUSTRY EXPERIENCE (selected)

- *Analyst Programmer*, Starom Invest Ltd., Bucharest, Romania (2001)
Contributed to the development of a distributed system offering virtual machines and networks for rental through the Internet; developed a custom Linux installation kit using Python.
- *System Administrator*, Romanian Academy, Centre for Mathematical Statistics, Romania (2000-2001)
Administered and maintained the computer network, servers, and secure connection to the Internet.
- *Programmer*, Net Concept Ltd., Bucharest, Romania (1999-2001)
Developed web pages using Java Servlets and Oracle; administered the servers and network.
- *Web Programmer*, Media Net Publishing Ltd., Bucharest, Romania (1999)
Developed dynamic web pages using Perl, and multimedia applications using Macromedia tools.

SERVICE

- *Reviewer* of research articles for various conferences and journals, including:
 - the *RNA Journal* (2009);
 - the *Bioinformatics Journal* (2008-2009);
 - the *BioMed Central (BMC) Bioinformatics Journal* (2006-2009);
 - the *International Journal of Data Mining and Bioinformatics (IJDMB)* (2009);
 - the *International Journal of Integrative Biology (IJIB)* (2008);
 - the *International Joint Conference on Artificial Intelligence (IJCAI)* (2009);
 - the *Learning and Intelligent OptimizatioN Workshop (LION)* (2009);
 - the *Congress on Evolutionary Computation (CEC)* (2009).
- *Bioinformatics Reading Group Coordinator*, Dept. of Computer Science, UBC (2006-2008)
Organized reading group talks, developed new connections with speakers outside of the department or university and invited them to give talks.
- *Member of the Graduate Affairs Committee*, Dept. of Computer Science, UBC (2006-2007)
Evaluated and ranked scholarship applications; advised students on how to write a winning scholarship application; participated in the selection of graduate degree requirements and comprehensive course requirements for specific cases.
- *Teaching Assistant Coordinator*, Dept. of Computer Science, UBC (2003-2005)
Assisted teaching assistants during tutorials upon request; assisted, advised and represented teaching assistants on teaching-related problems; maintained the teaching evaluation records; nominated best teaching assistants for departmental and university awards; suggested allocations of teaching assistants to courses.

INVITED TALKS AND PRESENTATIONS (selected)

- “A three-dimensional model of the yeast genome”, platform (oral) presentation at the *Yeast Genetics and Molecular Biology Meeting*, Jul 2010, Vancouver, BC.
- “Computational approaches for RNA energy parameter estimation”, invited talks to the Gentleman Lab, Fred Hutchinson Cancer Research Center, and to the Noble Lab, Dept. of Genome Sciences, University of Washington, May 2008.
- “Efficient parameter estimation for RNA secondary structure prediction”, paper presentation at the *International Conference On Intelligent Systems For Molecular Biology (ISMB) 2007*. Also invited talk to the Eddy Group, HHMI Janelia Farm Research Center, VA, Jul 2007.
- “Improving RNA energy models computationally”, two Ph.D. work presentations to the bioinformatics and machine learning reading groups, IBM T.J. Watson Research Center, NY, Jul 2006.
- “Towards a better thermodynamic model for RNA secondary structure formation”, invited talk to the Mathews Lab, Dept. of Biochemistry and Biophysics, University of Rochester Medical Center, Rochester, NY, Jul 2005.
- “Algorithms for secondary structure prediction and design”, invited talk, School of Computer Science, University of Waterloo, ON, Apr 2004.
- “Algorithms for testing that DNA word designs avoid unwanted secondary structures”, paper presentation at the *Eighth International Meeting on DNA Based Computers DNA 8* conference, Sapporo, Japan. Also invited talk to the Winfree Group, Computer Science Dept., California Institute of Technology, CA, Jul 2002.