

## Delasa Aghamirzaie

### Contact information

- Phone: 540-200-5273, Email: delasa@vt.edu

### Education

- PhD. Candidate in Genetics, Bioinformatics, and Computational Biology (GBCB), May 2016, Virginia Polytechnic Institute and State University (Virginia Tech), Blacksburg, Virginia, USA. GPA: 3.9/4  
Major: **Computer Science**, Minor: *Life Sciences*
- M.Sc. in Computer Engineering, Computer Architecture, October 2011, Department of Computer Engineering and Information Technology, Amirkabir University of Technology (Tehran Polytechnic), Tehran, Iran. GPA: 3.9/4  
Thesis: Accelerating Protein Secondary Structure Prediction Using Artificial Neural Networks on GPU
- B.Sc. Computer Engineering, September 2009, Hardware, Department of Computer Engineering and Information Technology, Amirkabir University of Technology (Tehran Polytechnic), GPA: 3.51/4  
Thesis: Suppression of Variation Effects on FPGAs Using Multiple Configurations

### Research Interests

- Big Data Analysis
- Computational Biology, Computational Genomics, and Bioinformatics
- Machine Learning and Deep Learning
- Developing Computational Tools And Statistical Models for Genomics and Transcriptomics
- Next Generation Sequencing

### Research Experiences

- **Research Intern in Computational Biology Group, IBM T.J Watson Research Center**, Yorktown Heights, NY, May-August 2015
  - Watson Genomics Analytics (WGA) Project
  - Molecular Profile Analysis of Cancer Patients
  - Application of Deep Learning on Gene Expression Data
- **Research Assistant in Dr. Grene's Laboratory**, Department of Plant Pathology, Physiology, and Weed sciences (PPWS), College of Agriculture and Life Sciences, Virginia Tech (2012-2016)
  - Analysis of RNA-Seq Data of Developing Soybean Embryos, Arabidopsis seeds, and Arabidopsis GDU mutants Using Tuxedo Suit Protocol
  - Developed Several Methods For Further Analysis And Understanding Of RNA-Seq Data
  - Analysis Of Alternative Splicing Events During Embryo Development
  - Developed A Support Vector Machine (SVM) Classifier For Classifying Transcripts Into Coding And Noncoding Classes Based On Several Sequential And Structural Features
  - Long Noncoding RNA Investigation In RNA-Seq Data
  - Co-Expression Network Analysis Of RNA-Seq Data
  - Bayesian Network Inference Of Gene Expression Data Using Prior Knowledge Incorporation
  - Expresso: Exploring Arabidopsis' Transcription Factors and Target Genes from ChIP-Seq Data
  - Developing a webserver and DB for integrating and browsing available ChIP-seq data for Arabidopsis
- **Remote Research Scholar in Persepolis Group**, Under Supervision of Dr. Amir H. Assadi, Department of Mathematics, University of Wisconsin-Madison (2010-2011)
  - Gene Expression Data Analysis of Arabidopsis on GPU

- Clustering Gene Expression Data
- Super Structure Artificial Neural Networks on GPU
- **Research Assistant in FPGA Laboratory**, Department of Computer Engineering, Amirkabir University of Technology (9/2009-10/2011)
  - GPU Programming Using Nvidia CUDA Programming Model
  - Protein Secondary Structure Prediction
  - Multi class Pattern Classification
- **Research Assistant in Design Automation laboratory**, Department of Computer Engineering, Amirkabir University of Technology (2008-2009)
  - Variation Effects on FPGAs
  - Effects of Multiple Configurations in Variation Suppression

#### Awards and Honors

- 2016: Cold Spring Harbor Scholarship Award for Plant Genomics Meeting
- 2015-2016: GBCB Fellowship
- 2015: Molecular Plant Science (MPS) Student Grant Proposal Winner
- 2014: Molecular Plant Science (MPS) Travel Award Fellowship for 2nd Plant Genomics Conference
- 2013: NIH Fellowship for National Short Course in System Biology, University of California, Irvine
- 2011: Best Master Thesis Award in The Amirkabir University of Technology
- 2011: Ranked 3rd among M.Sc. Students in Computer Engineering
- 2009: Accepted as an Honored/Talented Student to Computer Engineering M.Sc program
- 2005-2009: Ranked 2nd among B.Sc. Students in Computer Hardware Engineering.
- 2007: Cisco Certified Network Associates (CCNA) Degree

#### Selected Conferences, and Workshops

- Biological Data Science meeting, Cold Spring Harbor Laboratories, New York (November 2014)
- 2<sup>nd</sup> Pant Genomics Congress, St. Louis, Missouri (September 2014)
- q-bio conference, Santa Fe, New Mexico (August 2014)
- National Course on System Biology, University of California, Irvine, CA (January 2014)
- Next Generation Sequencing Congress, London, UK (November 2013)
- International Conference on Computational Cell Biology (ICCCB), Blacksburg, VA (August 2013)
- Workshop in Next-Generation Sequence Analysis and Metabolomics (WiNGS), Charlotte, NC (May 2013)

#### Selected Course Projects

- Computational Biochemistry in Bioinformatics (Spring 2014)  
Investigation of Natural Variation Effect In Insulin Resistance Using Normal Mode Analysis For Diabetes Patients
- Introduction to Machine Learning and Perception (Spring 2013)  
Modeling and Identifying Regulatory Modules in Soybean Time Series Gene Expression Data using Bayesian Networks
- Paradigms in Bioinformatics (Fall 2012)  
Review on “ENISI Visual an agent-based simulator for modeling gut immunity”
- Introduction to Bioinformatics (Fall 2010)  
Comprehensive literature review on “Protein Secondary Structure Prediction Using Artificial Neural Networks

#### Technical skills

- Next Generation Sequencing:
  - RNA-seq analysis: Tuxedo Suit Protocol (Tophat, Cufflinks, Cuffmerge, Cuffcompare, Cuffdiff)
  - ChIP-Seq analysis
  - DEXseq, Limma R package (Linear Models for Microarray Data)
  - Gene Set Enrichment Analysis

## Ontologizer for Gene Ontology Enrichment Analysis

- Machine Learning:  
Naïve Bayes Classifiers, Logistic Regression, Support Vector Machines, Artificial Neural Networks, Bayesian Networks, Time-Course Clustering, SplineCluster, k-means
- Deep Learning:  
Restricted Boltzman Machines, Stacked Autoencoders
- Programming languages  
Python, C++: Proficient  
MATLAB, R, Assembly, Pascal, Visual Basic.Net, Java: Intermediate
- Database Programming, and Web Development  
MySQL, SQL Server, HTML, PHP: Intermediate  
Asp.net: Familiar
- Statistics:  
Classical: Hypothesis testing, Classical Regression analysis, ANOVA, One Sample and Two sample t-tests  
Bayesian: Bayesian Regression analysis, MCMC
- GPU programming  
CUDA: Familiar
- Wet Lab Experience:  
RNA Isolation, RT-PCR, Library preparation for RNA-sequencing, Confocal Microscopy: Familiar

## Presentations and Invited Talks

- **Delasa Aghamirzaie**, Erhan Bilal, Takahiko Koyama, Fang Wang, Filippo Utro, Kahn Rhrissorakrai, Raquel Norel, Laxmi Parida, and Ajay Royyuru, "Interpreting Cancer Patient Genomics Data to Assist Clinicians", IBM T.J Watson Research Center, Intern Seminar Series, August 2015
- **Delasa Aghamirzaie**, "Fundamentals of Next Generation Sequencing", Plant Stress Physiology Course, April 2015
- **Delasa Aghamirzaie**, "CodeWise: A Support Vector Machine Classifiers for Accurate detection of Noncoding RNAs", Graduate Student Assembly Symposium, March 2015
- **Delasa Aghamirzaie**, "Comprehensive Functional Characterization Reveals Novel Relationships Among Differentially Expressed Transcripts in Developing Soybean Embryos ", MPS/TPS Min-symposium, Feb, 2015
- **Delasa Aghamirzaie**, "An Accurate Support Vector Machine Classifier For Assessing Coding Potential Of Transcripts Using Several Sequential And Structural Features", Biological Data Science Meeting, Cold Spring Harbor Laboratories, New York, November 2014.
- Ruth Grene, **Delasa Aghamirzaie**, "Toward a Functional Classification of Splice Variants From Soybean Seed Embryos ", 2<sup>nd</sup> Plant Genomics Congress, St. Louis, USA, September 2014.

## Publications

- **D. Aghamirzaie**, Sh. Wu, K. Raja Vulmugran, D. Altarawy, L.S. Heath, R. Grene, "Expresso: Exploring Arabidopsis' Transcription Factors and Target Genes from ChIP-Seq Data", Under Preparation.
- A. Schneider, **D. Aghamirzaie**, H. Elmarakeby, A. Poudel, A.J. Koo, L.S. Heath, R. Grene, E. Collakova, "Potential Targets Of VAL1 Repression In Developing Arabidopsis Thaliana Embryos", Submitted to Plant Cell.
- **D. Aghamirzaie**, L.S.Heath, A. Schneider, R. Grene, E. Collakova, "Transcriptome-Wide Functional Characterization Reveals Novel Relationships Among Differentially Expressed Transcripts In Developing Soybean Embryos", accepted, BMC Genomics.
- **D. Aghamirzaie**, M. Nabiyouni, Y. Fang, C. Klumas, L.S.Heath, R. Grene, E. Collakova, "Changes in RNA Splicing in Developing Soybean (Glycine max) Embryos", Biology 2013, 2, 1311-1337.

- E. Collakova, **D. Aghamirzaie**, Y. Fang, C. Klumas, F. Tabataba, A. Kakumanu, E. Myers, L. Heath, R. Grene, "Metabolic and Transcriptional Reprogramming in Developing Soybean (Glycine max) Embryos", *Metabolites*. May 2013.
- M. Nabiyouni, **D. Aghamirzaie**, "A Highly Parallel Multi-Class Pattern Classification on GPU," 12th IEEE/ACM International Symposium on Cluster, Cloud and Grid Computing (ccgrid), 2012, Best Paper Candidate.
- **D. Aghamirzaie**, A. Razavi, M. Saheb Zamani, M. Nabiyouni, "Reduction of Process Variation Effect on FPGAs Using Multiple Configurations", IEEE/IFIP International Conference on Very Large-Scale Integration (VLSI-SOC'10), September 2010.

#### Selected Poster Presentations

- **D. Aghamirzaie**, Sh. Wu, K. Raja Vulmugran, R. Grene, "Expresso: Exploring Arabidopsis' Transcription Factors and Target Genes from ChIP-Seq Data", *Biological Data Science*, Cold Spring Harbor Laboratory, USA, November 2014.
- **D. Aghamirzaie**, Sh. Wu, K. Raja Vulmugran, R. Grene, "Expresso: Exploring Arabidopsis' Transcription Factors and Target Genes from ChIP-Seq Data", 2<sup>nd</sup> Plant Genomics Congress, St. Louis, USA, September 2014.
- **D. Aghamirzaie**, L. Heath, R. Grene, E. Collakova, "Changes in RNA Splicing in Soybean Seed Embryos", 8<sup>th</sup> q-bio Conference, Santa Fe, NM, August 2014.
- **D. Aghamirzaie**, D. Batra, E. Collakova, L. Heath, R. Grene, "Modeling and Identifying Regulatory Modules in (Glycine max) Soybean Time Series Gene Expression Data using Bayesian Networks". International Conference on Computational Cell Biology (ICCCB 2013), Blacksburg, Virginia, August 2013.