

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, May2016-August2016
 - 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

- ≡ 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)
- ≡ 2nd 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 Enrichement Analysis

- ≡ Machine Learning:
Naïve Bayes Classifiers, Logistic Regression, Support Vector Machines, Artificial Neural Networks, Bayesian Networks, Time-Course Clustering, SplineCluster, k-means
- ≡ 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

- ≡ **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 ”, 2nd Plant Genomics Congress, St. Louis, USA, September 2014.

Publications

- ≡ **D. Aghamirzaie**, L.S.Heath, A. Schneider, R. Grene, E. Collakova, Comprehensive functional characterization reveals novel relationships among differentially expressed transcripts in developing soybean embryos. Submitted to Plant Cell.
- ≡ **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. (2013). 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“, Espresso: 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“, Espresso: Exploring Arabidopsis’ Transcription Factors and Target Genes from ChIP-Seq Data”, 2nd Plant Genomics Congress, St. Louis, USA, September 2014.

- IR **D. Aghamirzaie**, L. Heath, R. Grene, E. Collakova, "Changes in RNA Splicing in Soybean Seed Embryos", 8th q-bio Conference, Santa Fe, NM, August 2014.
- IR **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.