

Delasa Aghamirzaie

Contact information

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

Summary

A Bioinformatics PhD candidate with more than 5 years of experience in data analysis, programming and machine learning for computational biology and functional genomics. Highly skilled at analyses of next generation sequencing data.

Education

- PhD. Candidate in Genetics, Bioinformatics, and Computational Biology (GBCB), PhD. Expected May 2016, Virginia Polytechnic Institute and State University (Virginia Tech), Blacksburg, Virginia, USA.
 - 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.
 - Thesis: Accelerating Protein Secondary Structure Prediction Using Artificial Neural Networks on GPU (define)
- B.Sc. Computer Engineering, September 2009, Hardware, Department of Computer Engineering and Information Technology, Amirkabir University of Technology (Tehran Polytechnic),
 - Thesis: Suppression of Variation Effects on FPGAs Using Multiple Configurations

Research Interests

- Large-scale data-driven problems in Computational Biology and Bioinformatics
- Developing Computational Tools and Statistical Models for Genomics and Transcriptomics Applications using *Machine Learning* and *Deep Learning*
- Integrative Analysis of Next Generation Sequencing Data
- Single Cell Genomics
- Big Data Analysis
- Functional Genomics
- Gene Regulatory Network Inference
- Long noncoding RNAs
- Genotype-Tissue Expression (GTEx) Analysis

Research Experience

- **Graduate Research Assistant, Group of Dr. Ruth Grene, Co-advised by Dr. Lenwood Heath (Department of Computer Science) Virginia Tech (2012- present)**
 - Analysis of RNA-Seq Data of developing soybean embryos, mutant and wild type Arabidopsis seeds, and seedlings
 - Developed methods for further analysis of RNA-Seq data
 - Co-Expression Network Analysis
 - Bayesian Network Inference of gene expression data incorporating prior knowledge
 - Analysis of Alternative Splicing Events During Embryo Development
 - Analysis of long noncoding RNA
 - Development of CodeWise: A Support Vector Machine (SVM) Classifier for assigning Transcripts Into Coding And Noncoding Classes based both on sequence and on structural features
 - Other methods developed:

- “Expresso”: Exploring transcription factors and their inferred target genes from Arabidopsis ChIP-Seq Data
 - Developing a webserver and DB for integrating and browsing available ChIP-seq data for Arabidopsis
- **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 techniques to gene expression data sets
- **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: Translational Plant Sciences Travel Award
- 2016: Cold Spring Harbor Scholarship Award for Plant Genomics Meeting
- 2015-2016: Genetics, Bioinformatics, and Computational Biology Academic Fellowship
- 2015: Graduate Student Assembly Travel Award
- 2015: Molecular Plant Science Student Grant Proposal Winner
- 2014: Molecular Plant Science 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

Conferences and Workshops

- Biological Data Science meeting, Cold Spring Harbor Laboratories, New York (November 2014)
- 2nd Plant 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 at Virginia Tech

- Deep Learning and Perceptron, Fall 2015
- Computational Biochemistry in Bioinformatics (Spring 2014)
- Bayesian Statistics, Spring 2013
- Introduction to Machine Learning and Perception (Spring 2013)
Modeling and Identifying Regulatory Modules in Soybean Time Series Gene Expression Data using Bayesian Networks

Technical skills

- Next Generation Sequencing:
RNA-seq analysis: Tuxedo Suite Protocol
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
- Version Control:
Github

Invited Talks

- **Delasa Aghamirzaie**, “Fundamentals of Computational Algorithms for Data Analysis of RNA-Seq Data”, Paradigms of Bioinformatics, October 2015
- **Delasa Aghamirzaie**, Erhan Bilal, Takahiko Koyama, Fang Wang, Filippo Utro, Kahn Rhrissorrakrai, 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 Mini-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 ”, 2nd Plant Genomics Congress, St. Louis, USA, September 2014

Publications

- 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”, accepted, The Plant Journal
- **D. Aghamirzaie**, D. Batra, L.S.Heath, A. Schneider, R. Grene, E. Collakova, “Transcriptome-Wide Functional Characterization Reveals Novel Relationships Among Differentially Expressed Transcripts In Developing Soybean Embryos”, BMC Genomics. , November 2015.
- **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.
- Manuscripts in preparation
 - **D. Aghamirzaie**, R. Grene, “An Integrative Analysis of Co-splicing During a Time-Course of Arabidopsis Seed Development.
 - **D. Aghamirzaie**, L.S. Heath, R. Grene, E. Collakova, “CodeWise: Accurate Detection of Noncoding RNAs from Transcriptomics Data”
 - **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.

Poster Presentations at international conferences

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

References:

- Dr. Ruth Grene (Professor of Plant Physiology), grene@vt.edu, 540-231-6761
- Dr. Eva Collakova (Associate Professor of Plant Physiology), collakov@vt.edu, 540-231-7147
- Dr. Lenwood Heath (Professor of Computer Science), heath@vt.edu, 540-231-4352
- Dr. Song Li (Assistant Professor of Plant Genomics and Bioinformatics), songli@vt.edu, 540-231-2756
- Dr. Erhan Bilal, Research Staff Member, IBM T.J Watson Research Center, ebilal@us.ibm.com