

Rosa Aghdam, PhD

Scientist | Wisconsin Institute for Discovery, University of Wisconsin-Madison, Madison, WI, USA

✉: aghdam@wisc.edu; rosaaghdam@gmail.com

🌐 <https://www.linkedin.com/in/rosa-aghdam/>

🌐 <https://scholar.google.com/citations?user=y6uIjXEAAAAJhl=en>

Research Summary

Computational biologist and statistician specializing in statistical and machine learning methods for biological network inference, with a focus on Bayesian networks, microbiome network analysis, and disease biomarker discovery. I develop scalable computational tools and algorithms for high-dimensional omics data and collaborate closely with experimental partners to translate methodological advances into biological insights.

Research Interests

Microbiome network inference and alignment; consensus network construction; Bayesian networks and probabilistic graphical models.

Machine learning for high-dimensional omics data and disease biomarker discovery; gene regulatory network inference and systems biology.

Technical Skills

Programming: R; Python (NumPy, Pandas, scikit-learn, TensorFlow, Keras); MATLAB.

Methods: Bayesian inference; Bayesian networks; hidden Markov models; machine learning; statistical modeling.

Applications: Microbiome data analysis; metagenomics; gene expression and GRNs; cancer genomics.

Current Position

May 2024–Present

Scientist, Wisconsin Institute for Discovery, University of Wisconsin–Madison, Madison, WI, USA

Develop statistical and machine-learning methods for microbiome network analysis and disease prediction using high-dimensional omics data. Lead computational workflows and interdisciplinary collaborations in microbiome research. Mentor graduate and undergraduate students in statistical modeling and biological network analysis.

Academic Appointments

Jul 2022–Apr 2024

Postdoctoral Researcher, Wisconsin Institute for Discovery, University of Wisconsin–Madison, Madison, WI, USA

- Sep 2020–Jun 2022 **Senior Research Fellow**, School of Biological Science, Institute for Research in Fundamental Sciences (IPM), Tehran, Iran
- Feb 2018–Sep 2020 **Research Fellow**, Department of Computer Sciences, Shahid Beheshti University, Tehran, Iran
- Sep 2015–Feb 2018 **Postdoctoral Researcher**, School of Biological Science, IPM, Tehran, Iran
- Sep 2008–Sep 2015 **Research Assistant**, IPM, Tehran, Iran
- Feb 2019–Present **Statistical Advisor**, IRDA startup
- Sep 2015–Present **Member**, Scientific Data Analysis Team (SDAT)

Education

- Sep 2011- Aug 2015 **PhD in Statistics**, Department of Statistics, Faculty of Mathematical Sciences, Shahid Beheshti University, Tehran, Iran
 Advisor: Professor Mojtaba Ganjali, Co-advisor: Professor Changiz Eslahchi
 Thesis: *Improvement of learning Bayesian Network Using Some statistical Criteria*
- Sep 2007 - Feb 2010 **MSc in Statistics**, Department of Statistics, Faculty of Mathematical Sciences, University of Tehran, Tehran, Iran
 Advisor: Professor Hamid Pezeshk
 Thesis: *Parameter Estimation of Profile Hidden Markov Models*
- Sep 2003 - Sep 2007 **BSc in Statistics**, Department of Statistics, Faculty of Mathematical Sciences, Shahid Beheshti University, Tehran, Iran
 Advisor: Professor Mohammad Zokaee
 Thesis: *Determining the Rank of Iran in ESI 2005*

Honors & Awards

- 2025 Earns Science Literacy Award, Title: Decoding Our Inner Universe: The Power of the Microbiome Network Alignment Algorithm
- 2015 Awarded the best M.Sc. Thesis in 21st Research Festival at the University of Tehran
- 2007 Ranked 2nd in Statistics class of 2007 at Shahid Beheshti University

Teaching Experience

- Feb 2021 - Sep 2021 **Tehran University, Tehran, Iran**
 Stochastic process
- Sep 2009 - Feb 2010 **Shahid Beheshti University, Tehran, Iran**
 Statistical software for Statistics students, Statistics and probability I, Statistics and probability II, Descriptive Statistics
- Sep 2008 - Feb 2009 **University of Tehran, Iran**
 Regression Model
- Sep 2011- Jun 2012 **Qazvin Islamic Azad University, Iran**
 Statistics and probability, Applied Statistics, Descriptive Statistics
- Sep 2007 - Sep 2011 **University of Applied Science and Technology, Iran**
 General Math I, General Math II, Applied Statistics, Descriptive Statistics

Software & Computational Tools

CMiNet – R package and Shiny app for constructing consensus microbiome networks.

MiNAA – Microbiome network alignment algorithm.

HighDimMixedModels.jl – High-dimensional mixed-effects modeling across omics data.

Publications (Journal Article)

Number of publications : 30

Number of citations : 375

- 2026 **Rosa Aghdam** and Claudia Solís-Lemus. CMiNet: An R package and user-friendly Shiny app for constructing consensus microbiome networks. *Methods in Ecology and Evolution*, 17(1):52–66, 2026.
- 2026 **Rosa Aghdam**, Shan Shan, Richard Lankau, and Claudia Solís-Lemus. A hybrid framework for disease biomarker discovery in microbiome research combining bayesian networks, machine learning, and network-based methods. *Biology Methods and Protocols*, 11(1):bpaf089, 2026.
- 2026 **Rosa Aghdam**, Qiyao Yang, Patricia Q. Tran, Karthik Anantharaman, and Claudia Solís-Lemus. Activity-informed network analysis reveals keystone microbes shaping freshwater ecosystem function. *Environmental Microbiology Reports*, 18(2):e70245, 2026.
- 2026 **Rosa Aghdam** Qiyao Yang, Reed Nelson, and Claudia Solís-Lemus. Minaa-webapp: A web-based tool for the visualization and analysis of microbiome networks. *SoftwareX*, 34:102578, 2026.
- 2025 Evan Gorstein, **Rosa Aghdam**, and Claudia Solís-Lemus. HighDimMixedModels.jl: Robust high-dimensional mixed-effects models across omics data. *PLOS Computational Biology*, 21(1):e1012143, 2025.
- 2024 **Rosa Aghdam**, Xudong Tang, Shan Shan, Richard Lankau, and Claudia Solís-Lemus. Human limits in machine learning: prediction of potato yield and disease using soil microbiome data. *BMC bioinformatics*, 25(1):366, 2024.
- 2024 Parisa Niloofar, **Rosa Aghdam**, and Changiz Eslahchi. GAEM: Genetic algorithm based expectation-maximization for inferring gene regulatory networks from incomplete data. *Computers in Biology and Medicine*, 183:109238, 2024.
- 2024 Amin Darabi, Sayeh Sobhani, **Rosa Aghdam**, and Changiz Eslahchi. AFITbin: a metagenomic contig binning method using aggregate l-mer frequency based on initial and terminal nucleotides. *BMC bioinformatics*, 25(1):241, 2024.
- 2024 Reed Nelson, **Rosa Aghdam**, and Claudia Solis-Lemus. MiNAA: Microbiome network alignment algorithm. *Journal of Open Source Software*, 9(96):5448, 2024.
- 2023 Negin Sadat Babaiha, **Rosa Aghdam**, Shokoofeh Ghiam, and Changiz Eslahchi. NN-RNALoc: neural network-based model for prediction of mrna sub-cellular localization using distance-based sub-sequence profiles. *Plos one*, 18(9):e0258793, 2023.
- 2023 Maryam Maghsoudi, **Rosa Aghdam**, and Changiz Eslahchi. Removing the association of random gene sets and survival time in cancers with positive random bias using fixed-point gene set. *Scientific Reports*, 13(1):8663, 2023.
- 2023

- Seyed Amir Malekpour, **Rosa Aghdam**, Maryam Shahdoust, and Mehdi Sadeghi. wp-logicnet: logic gate and structure inference in gene regulatory networks. *Bioinformatics*, 39(2):btad072, 2023.
- 2021 **Rosa Aghdam**, Mahnaz Habibi, and Golnaz Taheri. Using informative features in machine learning based method for covid-19 drug repurposing. *Journal of Cheminformatics*, 13(70), 2021.
- 2021 Raziye Masumshah, **Rosa Aghdam**, and Changiz Eslahchi. A neural network-based method for polypharmacy side effects prediction. *BMC bioinformatics*, 22(1):1–17, 2021.
- 2021 Sayyed Hadi Mahmoodi, **Rosa Aghdam**, and Changiz Eslahchi. An order independent algorithm for inferring gene regulatory network using quantile value for conditional independence tests. *Scientific Reports*, 11(1):1–15, 2021.
- 2021 Mahnaz Habibi, Golnaz Taheri, and **Rosa Aghdam**. A SARS-CoV-2 (COVID-19) biological network to find targets for drug repurposing. *Scientific Reports*, 11(1):1–15, 2021.
- 2019 Elnaz Saberi Ansari, Changiz Eslahchi, Mahsa Rahimi, Lobat Geranpayeh, Marzieh Ebrahimi, **Rosa Aghdam**, and Gweneg Kerdivel. Significant random signatures reveals new biomarker for breast cancer. *BMC Medical Genomics*, 12(1):160, 2019.
- 2019 **Rosa Aghdam**, Vahid Rezaei Tabar, and Hamid Pezeshk. Some node ordering methods for the K2 algorithm. *Computational Intelligence*, 35(1):42–58, 2019.
- 2017 **Rosa Aghdam**, Taban Baghfalaki, Pegah Khosravi, and Elnaz Saberi Ansari. The Ability of Different Imputation Methods to Preserve the Significant Genes and Pathways in Cancer. *Genomics, proteomics & bioinformatics*, 15(6):396–404, 2017.
- 2016 **Rosa Aghdam**, Mojtaba Ganjali, Parisa Niloufar, and Changiz Eslahchi. Inferring gene regulatory networks by an order independent algorithm using incomplete data sets. *Journal of Applied Statistics*, 43(5):893–913, 2016.
- 2016 **Rosa Aghdam**, Taban Baghfalaki, Pegah Khosravi, and Elnaz Saberi Ansari. Comparative Analysis of Gene Regulatory Networks Concepts in Normal and Cancer Groups. *Bioinformatics & Biocomputational Research*, 1(1), 2016.
- 2016 **Rosa Aghdam**, Mohsen Alijanpour, Mehrdad Azadi, Ali Ebrahimi, Changiz Eslahchi, and Abolfazl Rezvan. Inferring gene regulatory networks by PCA-CMI using Hill climbing algorithm based on MIT score and SORDER method. *International Journal of Biomathematics*, 9(03):1650040, 2016.
- 2015 Mahnaz Habibi, Pooneh Khoda Bakhshi, and **Rosa Aghdam**. LRC: A new algorithm for prediction of conformational B-cell epitopes using statistical approach and clustering method. *Journal of immunological methods*, 427:51–57, 2015.
- 2015 **Rosa Aghdam**, Mojtaba Ganjali, Xiujun Zhang, and Changiz Eslahchi. CN: a consensus algorithm for inferring gene regulatory networks using the SORDER algorithm and conditional mutual information test. *Molecular BioSystems*, 11(3):942–949, 2015.
- 2014 **Rosa Aghdam**, Mojtaba Ganjali, and Changiz Eslahchi. IPCA-CMI: an algorithm for inferring gene regulatory networks based on a combination of PCA-CMI and MIT score. *PloS one*, 9(4):e92600, 2014.
- 2014 Sattar Soltani, Hossein Askari, Nasim Ejlali, and **Rosa Aghdam**. The structural properties of DNA regulate gene expression. *Molecular BioSystems*, 10(2):273–280, 2014.
- 2013 **Rosa Aghdam**, Hamid Pezeshk, Seyed Amir Malekpour, Soudabeh Shemehsavar, and Changiz Eslahchi. A clustering approach for estimating parameters of a profile hidden Markov model. *International journal of data mining and bioinformatics*, 8(1):66–82, 2013.

- 2012 Ali Ebrahimi, **Rosa Aghdam**, Parisa Niloofar, Mojtaba Ganjali, and Changiz Eslahchi. LSPC: An algorithm for inference of gene networks using Bayesian network. *Journal of Emerging Trends in Computing and Information Sciences*, 3(5), 2012.
- 2011 **Rosa Aghdam**, Hamid Pezeshk, Seyed Amir Malekpour, Mehdi Sadeghi Shemehsavar, Soudabeh, and Changiz Eslahchi. A Bidirectional Bayesian Monte Carlo Approach for Estimating Parameters of A Profile Hidden Markov Model. *Applied Science Segment*, 1(2):1–10, 2011.
- 2010 **Rosa Aghdam**, Nasim Ejlali, and Hamid Pezeshk. A New Method for Estimating Parameters of a Profile Hidden Markov Model. *Biostatistics, Bioinformatics and Biomathematics*, 2(1):33–42, 2010.

Research Grants

- 2018-2020 PI for project no. 97009558 "Learning Gene Regulatory Networks Based on Bayesian Networks" in Iran National Science Foundation (INSF).

Mentoring & Student Supervision

PhD Students

- May 2024–Present **Mason Garza**, University of Wisconsin–Madison
Thesis: Disease Prediction Based on Microbiome Data
- Jan 2021–Present **Zahra Ghaeli**, Shahid Beheshti University, Tehran, Iran
Thesis: Constructing Microbiome Networks
- May 2023–Jan 2025 **Evan Gorstein**, University of Wisconsin–Madison
Thesis: Robust High-Dimensional Mixed-Effects Models Across Omics Data

Master Students

- Sep 2025–Present **Jiayi Gao**, University of Wisconsin–Madison
Thesis: Constructing Consensus Microbiome Networks
- Jul 2022–Jun 2024 **Xudong Tang**, University of Wisconsin–Madison
Thesis: Human Limits in Machine Learning: Prediction of Potato Yield and Disease Using Soil Microbiome Data
- Jan 2021–Jun 2022 **Amin Darabi**, Shahid Beheshti University, Tehran, Iran
Thesis: Metagenomic Binning Using Assembly Graphs
- Feb 2019–Jun 2022 **Maryam Maghsoudi**, Shahid Beheshti University, Tehran, Iran
Thesis: Statistical Methods for Identifying Cancer Biomarkers from Significant Gene Sets
- Feb 2019–Jun 2022 **Amir Hossein Aliakbari**, University of Tehran, Iran
Thesis: Predicting the Role of Multiple Stroke Diseases in Mortality Risk Using Machine Learning and Deep Learning
- Feb 2019–Feb 2021 **Negin Sadat Babaiha**, Shahid Beheshti University, Tehran, Iran
Thesis: Improving Prediction of RNA Sub-Cellular Localization Using Artificial Neural Networks
- Feb 2019–Feb 2021 **Raziyeh Masumshah**, Shahid Beheshti University, Tehran, Iran
Thesis: Neural Network-Based Model for Polypharmacy Side Effects Prediction
- Feb 2017–Feb 2019

Sayed Hadi Mahmoodi, University of Tehran, Iran
Thesis: Improving Bayesian Network Learning Algorithms for Gene Regulatory Networks

Undergraduate Students

- May 2024–Present **Sophia Yang**, University of Wisconsin–Madison
Project: Keystone Taxa Interactions in Microbial Networks and Environmental Dynamics in Lake Mendota
- Jul 2022–Jun 2024 **Reed Nelson**, University of Wisconsin–Madison
Project: Microbiome Network Alignment Algorithm
- Feb 2021–Jun 2022 Supervision of **4 Undergraduate Students**, Shahid Beheshti University, Tehran, Iran

Journal Reviewing

Reviewer for 40+ manuscripts since 2018 for journals including:

Bioinformatics; Briefings in Bioinformatics; IEEE Access; Methods in Ecology and Evolution; Wiley Interdisciplinary Reviews: Systems Biology and Medicine; BMC Bioinformatics; BMC Genomics; Pattern Recognition; Pattern Recognition Letters; Journal of Computational Biology; Computational and Mathematical Methods in Medicine; Iranian Journal of Biotechnology Journal; Journal of Statistical Computation and Simulation

Conference Papers

- 2014 **Rosa Aghdam**, Mojtaba Ganjali, and Changiz Eslahchi. A Hybrid Algorithm for Inferring Gene Regulatory Networks. Twelfth Iranian Statistical Conference. Kermanshah, Iran, 2014.
- 2013 **Rosa Aghdam**, Mohsen Alijanpour, Mehrdad Azadi, and Ali Ebrahimim. Applying a Hybrid Method based on PC algorithm-based approach and MIT Score to Infer Gene Regulatory Networks. 5th Iranian Conference on Bioinformatics. Tehran, Iran, 2013.
- 2012 **Rosa Aghdam**, Hamid Pezeshk, and Mojtaba Ganjali. A new method for estimating parameters of a profile hidden Markov model based on phylogenetic tree. 11th conference of Statistics. Tehran, Iran, 2012.

Oral Presentations

- 2025 ENAR 2025 Spring Meeting, New Orleans, LA, USA. Title: Microbiome Analysis in Action: A Suite of Packages for Constructing Networks and Predicting Diseases.
- 2024 Invited talk at Creighton University, Omaha, Nebraska, USA. Title: Biological Networks and Models.
- 2023 Invited talk at Friday@4 Plant Pathology, University of Wisconsin-Madison, Madison, WI, USA. Title: Unlocking the predictive power of soil microbiome data on disease and yield outcomes using Machine learning models.

- 2022 7th Annual UW–Madison Postdoctoral Research Symposium, University of Wisconsin-Madison, Madison, WI, USA
- 2020 9th Iranian Conference on Bioinformatics. Tehran, Iran
- 2019 Third Frontiers in Biological Sciences symposium at School of Biological Sciences, part of the Institute for research in fundamental sciences (IPM) in Iran
- 2017 Workshop on Advanced Statistical Methods (SDAT Team)
- 2018 Workshop on Advanced Statistical Methods in Cognitive Science (SDAT Team)
- 2014 Twelfth Iranian Statistical Conference. Kermanshah, Iran
- 2013 5th Iranian Conference on Bioinformatics. Tehran, Iran
- 2012 11th conference of Statistics. Tehran, Iran
- 2009 Fifth Workshop on Applied Stochastic Process. Tehran, Iran

Posters

- 2024 **Rosa Aghdam**, Xudong Tang, Shan Sha, Richard Lankau, and Claudia Solis-Lemus. Unlocking human limits in the microbial realm for enhanced plant phenotype prediction with soil microbiome data and machine learning. Research in Computational Molecular Biology (RECOMB), Cambridge, MA, USA, 2024.
- 2023 **Rosa Aghdam**, Xudong Tang, Shan Sha, Richard Lankau, and Claudia Solis-Lemus. Using neural network and machine learning approaches to analyze soil microbiome data sets. The Midwest Machine Learning Symposium, Chicago, USA, 2023.
- 2022 Maryam Maghsoudi, **Rosa Aghdam**, and Changiz Eslahchi. Nominal p-value: An inaccurate predictor of the gene significance. First international and 10th Iranian Conference on Bioinformatics. Kish, Iran, 2022.
- 2020 Parisa Niloofer, **Rosa Aghdam**, and Changiz Eslahchi. An order-independent algorithm for inferring directed gene regulatory networks from incomplete data. 9th Iranian Conference on Bioinformatics. Tehran, Iran, 2020.
- 2020 **Rosa Aghdam** and Changiz Eslahchi. Robustness study of order-independent pc-based algorithm using quantile value for conditional independent tests. 9th Iranian Conference on Bioinformatics. Tehran, Iran, 2020.
- 2020 Negin Babaiha, **Rosa Aghdam**, and Changiz Eslahchi. Improvement of prediction of rna's location in the cell by taking advantage of common neural network methods and architectures. 9th Iranian Conference on Bioinformatics. Tehran, Iran, 2020.
- 2020 Raziye Masumshah, **Rosa Aghdam**, and Changiz Eslahchi. Neural network based method for polypharmacy side effects prediction. 9th Iranian Conference on Bioinformatics. Tehran, Iran, 2020.
- 2017 **Rosa Aghdam**, Taban Baghfalaki, Pegah Khosravi, and Elnaz Saberi Ansari. Preserving Significant Genes and Pathways via different Imputation Methods. Great Lakes Bioinformatics Conference, ISCB. Chicago, USA, 2017.

References

Prof. Claudia Solís-Lemus

Mailing Address: Wisconsin Institute for Discovery, University of Wisconsin-Madison,
Madison, WI, USA
Email: solislemus@wisc.edu
Phone: +16082633615
<https://stat.wisc.edu/staff/solis-lemus-claudia>

Prof. Jo Handelsman

Mailing Address: Wisconsin Institute for Discovery, University of Wisconsin-Madison,
Madison, WI, USA
Email: jo.handelsman@wisc.edu
Phone: +16083164339
<https://wid.wisc.edu/people/jo-handelsman>

Prof. Golnaz Taheri

Mailing Address: School of Electrical Engineering and Computer Science, Digital Fu-
tures, KTH Royal Institute of Technology, Stockholm, Sweden
Email: golnazt@kth.se
Phone: +46 8 790 62 05
<https://www.kth.se/profile/golnazt>

Dr. Pegah Khosravi

Mailing Address: UCF Institute for Artificial Intelligence, University of Central Florida,
Orlando, FL, USA
Email: pegah.khosravi@ucf.edu
Phone: +19293937074
<https://med.ucf.edu/person/pegah-khosravi-ph-d/>

Prof. Changiz Eslahchi

Mailing Address: Department of Computer Science, Faculty of Mathematical, Shahid
Beheshti, Tehran, Iran.
Email: ch-eslahchi@sbu.ac.ir
Phone: +98 912 2125787
<http://en.sbu.ac.ir/Pages/Profiles.aspx?proffID=375515>

Prof. Hamid Pezeshk

Mailing Address: School of Mathematics, Statistics and Computer Sciences and Center
of Excellence in Biomathematics, College of Science, University of Tehran, Tehran, Iran.
Email: pezeshk@khayam.ut.ac.ir
Phone: +98 912 3054045
<https://profile.ut.ac.ir/en/pezeshk/publications>

Prof. Mehdi Sadeghi

Mailing Address: School of Biological Science, Institute for Research in Fundamental
Sciences (IPM), Tehran, Iran.
Email: sadeghi@nigeb.ac.ir
Phone: +98 21 22293639
<http://www.ipm.ac.ir/personalinfo.jsp?PeopleCode=IP1400010>