

Hussein A. Hejase

Curriculum Vitae

Michigan State University, East Lansing, MI 48824

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EDUCATION

- Dual Ph.D.
Computer Science
& Quantitative
Biology* January 2014 - Present · Michigan State University, East Lansing, MI
Concentration: *Genomics, Bioinformatics & Computational Biology*
GPA: 3.81
Advisor: Dr. Kevin Liu
- M.S.
Computer Science* August 2011 - December 2013 · Michigan State University, East Lansing, MI
GPA: 3.77
- B.S.
Computer Science* May 2009 - May 2011 · Michigan State University, East Lansing, MI
Minor: *Specialization in Game Design*
GPA: 3.64
- Associates Degree
Mathematics/Physics* January 2008 - May 2011 · Lansing Community College, Lansing, MI
GPA: 3.72

RESEARCH EXPERIENCE

- Graduate Research
Assistant* January 2014 - Present · Michigan State University, East Lansing, MI
Ph.D. Research · Department of Computer Science & Engineering
Advisor: Dr. Kevin Liu
- Scalable phylogenetic analysis and functional interpretation of genomes with complex evolutionary histories.
 - Phylogenomics and comparative genomics
- Graduate Research
Assistant* August 2011 - December 2013 · Michigan State University, East Lansing, MI
M.S. Research · Cellular & Biomolecular Laboratory
Advisor: Dr. Christina Chan
- Developed computational techniques that utilize different types of genomic data to improve drug sensitivity prediction.
 - Developed methods to reconstruct gene regulatory networks and investigated the relationship between different entities in those networks.
 - Developed computational techniques to classify cancer patients using genomic data.
- Undergraduate
Research Assistant* January 2011 - May 2011 · Michigan State University, East Lansing, MI
Undergraduate Research · Protein Structural Analysis & Design Laboratory
Advisor: Dr. Leslie Kuhn
- Worked on SimSite3D protein site comparison & SLIDE ligand docking algorithms to enhance detection of proteins that bind the same molecule.
- Undergraduate
Research Assistant* May 2010 - December 2010 · Michigan State University, East Lansing, MI
Undergraduate Research · Department of Computer Science & Engineering
Advisor: Dr. Yanni Sun

- Worked on algorithms to efficiently detect non-coding RNA in a large sequence dataset based on their structural similarity.

INDUSTRY EXPERIENCE

Genome Analytics Intern

May 2014 - August 2014 · Monsanto, St Louis, MO

- Developed a pipeline to identify pathogens and contaminants in maize using unmapped RNA-seq reads.

IT Assistant System Administrator

May 2011 - May 2013 · Michigan State University, East Lansing, MI
The Graduate School

- Developed and maintained installation and configuration procedures.
- Performed regular security monitoring to identify any possible intrusions.
- Designed and developed new web applications.

TEACHING EXPERIENCE

Lab Instructor

August 2014 - December 2014 · Michigan State University, East Lansing, MI
Introduction to Programming II (CSE 232)

- Course that teaches programming in C++ to computer science students including classes, data structure implementation, templates and generic programming.
- Details:
 - Instructed all labs.
 - Graded computer projects.
 - Provided helproom hours for exam/project preparation.

Teaching Instructor

August 2013 - May 2014 · Michigan State University, East Lansing, MI
Computing Concepts and Competencies (CSE 101)

- Course that teaches introductory computer concepts to non-engineering students including Microsoft word, excel, database and web design.
- Details:
 - Instructed all class lectures.
 - Graded class exams.
 - Provided helproom hours for exam preparation.

AWARDS & ACTIVITIES

- Outstanding Graduate Student Award · Michigan State University, East Lansing, MI · 2017
- Travel award (500\$) from BEACON to attend the Evolution conference · Austin, TX · 2016
- Travel award (500\$) from the National Science Foundation to attend the Phylogenomics Symposium and Software School · Austin, TX · 2016
- 1st place poster award travel grant (600\$) · Engineering Graduate Research Symposium (EGRS) · Michigan State University, East Lansing, MI · 2016

- Best poster award (1st place) · Engineering Graduate Research Symposium (EGRS) · Michigan State University, East Lansing, MI · 2016
- Travel award (1050\$) from Michigan State University to attend the Asia Pacific Bioinformatics Conference · San Francisco, CA · 2016
- Graduate student representative · Graduate Studies and Research Committee · Michigan State University, East Lansing, MI · August 2015 - May 2016
- Best poster award (1st place) · Engineering Graduate Research Symposium (EGRS) · Michigan State University, East Lansing, MI · 2015
- Travel award (500\$) sponsored by the National Science Foundation for the species-tree workshop at the society for systematic biology standalone meeting · University of Michigan, Ann Arbor, MI · 2015
- Travel award (500\$) sponsored by the National Science Foundation for the symposium and software school focusing on new methods for phylogenomics and metagenomics · University of Michigan, Ann Arbor, MI · 2015
- Graduate student representative · Computing Environment Committee · Michigan State University, East Lansing, MI · August 2011 - May 2012
- Global neighbors scholarship (8000\$) · Michigan State University, East Lansing, MI · 2009, 2010 & 2011
- Global spartan scholarship (1000\$) · Michigan State University, East Lansing, MI · 2009 & 2010
- Dean's list · Michigan State University, East Lansing, MI · 2009, 2010 & 2011

TECHNICAL SKILLS

- Programming languages: proficient in C/C++, R, Python & Matlab · competent in JAVA, Perl & C#
- Operating systems: Linux/Unix, Mac OS & MS-Windows
- Development environments: Hadoop, Apache Pig, Apache Hive, ASP.NET, Eclipse, Borland C++ Builder & Visual Studio
- Game engine: Unity 3D
- Database systems : Microsoft SQL Server, MySql & MS Access

PUBLICATIONS

- **Hejase, H.A.**, VandePol, N., Bonito, G.A., Liu, K.J. (2017), FastNet: fast and accurate inference of phylogenetic networks using large-scale genomic sequence data. [doi: [10.1101/132795](https://doi.org/10.1101/132795)]
- **Hejase, H.A.**, VandePol, N., Bonito, G.A., Edger, P.P., Liu, K.J. (2017), Coal-Miner: A statistical method for GWA studies of quantitative traits with complex evolutionary origins. In Proceedings of the 8th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (pp. 107-114). ACM. [doi: [10.1145/3107411.3107490](https://doi.org/10.1145/3107411.3107490)]

- **Hejase, H.A.**, Liu, K.J. (2016), A scalability study of phylogenetic network inference methods using empirical datasets and simulations involving a single reticulation. *BMC Bioinformatics* 17(1):422. [doi: [10.1186/s12859-016-1277-1](https://doi.org/10.1186/s12859-016-1277-1)]
- **Hejase, H.A.**, Liu, K.J. (2016), Mapping the genomic architecture of adaptive traits with interspecific introgressive origin: A coalescent-based approach. *BMC Genomics*. 17(1):8. [doi: [10.1186/s12864-015-2298-2](https://doi.org/10.1186/s12864-015-2298-2)]
- Hejase, A.J., Hejase, H.J., **Hejase, H.A.** (2015), Gender wage gap in Lebanon: explorative analysis. *Journal of Applied Economics and Business Research*. 5(1):1-19. [Link]
- **Hejase, H.A.**, Chan, C. (2015), Improving drug sensitivity prediction using different types of data. *CPT: Pharmacometrics & Systems Pharmacology*. 4:98-105. [doi: [10.1002/psp4.2](https://doi.org/10.1002/psp4.2) / PubMedID: 26225231]
- Bansal, M., **NCI-DREAM consortium**, et al. (2014), A community computational challenge to predict the activity of pairs of compounds. *Nature Biotechnology*. 32(12):1213-1222. [doi: [10.1038/nbt.3052](https://doi.org/10.1038/nbt.3052) / PubMedID: 25419740]
- Costello, J.C., **NCI-DREAM consortium**, et al. (2014), A community effort to assess and improve drug sensitivity prediction algorithms. *Nature Biotechnology*. 32(12):1202-1212. [doi: [10.1038/nbt.2877](https://doi.org/10.1038/nbt.2877) / PubMedID: 24880487]
- **Hijazi, H.**, Chan, C. (2013), A classification framework applied to cancer gene expression profiles. *Journal of Healthcare Engineering*. 4(2):255-283. [doi: [10.1260/2040-2295.4.2.255](https://doi.org/10.1260/2040-2295.4.2.255) / PubMedID: 23778014]
- Wu, M., Liu, L., **Hijazi, H.**, Chan, C. (2013), A multi-layer inference approach to reconstruct condition-specific genes and their regulation. *Bioinformatics*. 29(12):1541-1552. [doi: [10.1093/bioinformatics/btt186](https://doi.org/10.1093/bioinformatics/btt186) / PubMedID: 23610368]
- **Hijazi, H.**, Wu, M., Nath, A., Chan, C. (2012), Ensemble classification of cancer types and biomarker identification. *Drug Development Research*. 73(7):414-419. [doi: [10.1002/ddr.21032](https://doi.org/10.1002/ddr.21032) / PubMedID: 25221378]

ORAL PRESENTATIONS

- Fast and accurate algorithms for phylogenomics and systems biology. (May 2017), Cold Spring Harbor Laboratory. Cold Spring Harbor, NY.
- Scalable phylogenetic analysis and functional interpretation of genomes with complex evolutionary histories. (February 2017), Fitch H. Beach award for outstanding graduate research by an engineering PhD student. Michigan State University, East Lansing, MI.
- Coal-Miner: mapping the genomic architecture of adaptive traits with interspecific introgressive origin. (August 2016), BEACON Congress. Michigan State University, East Lansing, MI.

- Coal-Miner: A tool for mapping the genomic architecture of adaptive traits. (June 2016), iEvoBio at Evolution. Austin, TX.
- Coal-Miner: mapping the genomic architecture of adaptive traits with interspecific introgressive origin. (June 2016), Evolution. Austin, TX.
- A scalability study of computational methods for inferring phylogenetic networks using multi-locus sequence data. (April 2016), BEACON Seminar. Michigan State University, East Lansing, MI.
- Mapping the genomic architecture of adaptive traits with interspecific introgressive origin: A coalescent-based approach. (January 2016), The Asia Pacific Bioinformatics Conference. San Francisco, CA.
- Coal-Map: an association mapping method to identify the underlying genetic architecture of complex traits. (November 2015), BEACON Seminar. Michigan State University, East Lansing, MI.
- Coal-Map: an association mapping method to identify the underlying genetic architecture of complex traits. (May 2015), iEvoBio software bazaar at the society for systematic biologists (SSB) standalone meeting. University of Michigan, Ann Arbor, MI.
- A two-step feature selection method for classification of gene expression data. (July 2015), BEACON Seminar. Michigan State University, East Lansing, MI.
- Computational approaches to understand the complex path from genotype to phenotype. (January 2015), Fitch H. Beach award for outstanding graduate research by an engineering PhD student. Michigan State University, East Lansing, MI.
- An exploratory analysis of unmapped RNA-seq reads. (August 2014), Genome Analytics Seminar. Monsanto, St. Louis, MO.
- A multi-layer inference approach to reconstruct condition specific genes and their regulation. (June 2013), Gene Expression in Development and Disease Seminar (GEDDS). Michigan State University, East Lansing, MI.

POSTER PRESENTATIONS

- Coal-Miner: mapping the genomic architecture of quantitative traits with complex evolutionary origins. (May 2017), The 1st Annual Ecology, Evolutionary Biology, & Behavior Research Symposium. Michigan State University, East Lansing, MI.
- FastNet: Fast and accurate inference of phylogenetic networks using large-scale genomic sequence data. (February 2017), Ecology Evolutionary Biology and Behavior (EEBB) seminar for prospective graduate students. Michigan State University, East Lansing, MI.
- Fast and accurate inference of phylogenetic networks using large-scale genomic sequence data. (August 2016), BEACON Congress. Michigan State University, East Lansing, MI.

- Coal-Miner: mapping the genomic architecture of adaptive traits with interspecific introgressive origin. (June 2016), Evolution. Austin, TX.
- Mapping the genomic architecture of adaptive traits with interspecific introgressive origin: A coalescent-based approach. (March 2016), Engineering Graduate Research Symposium (EGRS). Michigan State University, East Lansing, MI.
- Mapping the genomic architecture of adaptive traits with interspecific introgressive origin. (February 2016), Ecology Evolutionary Biology and Behavior (EEBB) seminar for prospective graduate students. Michigan State University, East Lansing, MI.
- A scalability study of computational methods for inferring phylogenetic networks using multi-locus sequence data. (January 2016), The Asia Pacific Bioinformatics Conference. San Francisco, CA.
- Association mapping in the presence of complex sample structure. (August 2015), BEACON Congress. Michigan State University, East Lansing, MI.
- Association mapping in the presence of complex sample structure. (April 2015), Engineering Graduate Research Symposium (EGRS). Michigan State University, East Lansing, MI.
- An exploratory analysis of unmapped RNA-seq reads. (August 2014), Internship Symposium Program. Monsanto, St. Louis, MO.
- A three-layer approach to reconstruct condition specific gene network for *Arabidopsis thaliana*. (October 2012), Inaugural Symposium on Plant Biotechnology for Health and Sustainability. Michigan State University, East Lansing, MI.

REFERENCES

Available upon request.