Erfan Sayyari

Contact Information

Department of Electrical and Computer Engineering
UC, San Diego
Phone: 301 747 5505
email: esayyari@ucsd.edu
google scholar: goo.gl/sk5hJY

Education

UC San Diego, La Jolla, CA

Sep. 2013 – **June 2019** (expected)

- \bullet Ph.D candidate in Electrical and Computer Engineering Department GPA: 3.83
- Advisor: Prof. Siavash Mirarab
- Thesis Topic: New methods to estimate and assess phylogenetic trees from genome-wide data.

Sharif University of Technology, Tehran, Iran

Sep. 2008 – July 2013

• Bachelor of Science in Department of Electrical Engineering

Skills

Computational Biology, Phylogenomics, Metagenomics, Variant Calling, Machine Learning, Algorithms, Statistics, Optimization, Deep Learning

Programming Languages and Tools

- **Programming languages**: C/C++, Bash, Python (Pandas, NumPy, SciPy, scikit-learn, TensorFlow, Keras, Dendropy, Qiime2), R, MATLAB, LATEX
- Applications/Tools: Vi/Vim, Eclipse, PyCharm, Git, Marcdown, Docker, InkScape
- Operating Systems: Linux, Mac OSX, Windows.

Research Experience

- Research Assistant, UC, San Dieg, CA
- June 2015 present

- Advisor: Siavash Mirarab
- Member of Center for Microbiome Innovation, UC San Diego, CA Jan. 2018—present
- Member of Artificial Intelligence for Healthy Living Center (AIHL),
 UC San Diego, CA
 Jan. 2018—present
 - part of the IBM Cognitive Horizons Network

Selected Software

- ASTRAL (https://github.com/smirarab/ASTRAL) I routinely contribute to ASTRAL, a tool that is well known for estimating species trees from gene trees. More particularly, I implemented a statistical method to assess the reliability of inferred species trees from gene trees (local posterior probability) in ASTRAL.
- \bullet DISTIQUE (https://github.com/esayyari/DISTIQUE) Coalescent-based species tree estimation algorithm from gene trees
- **DiscoVista** (https://github.com/esayyari/DiscoVista) Command-line software package for visualizing phylogenetic discordance.
- Gene tree estimation pipeline (https://github.com/esayyari/bootstrap) Bash command-line pipeline of automatic inferring and bootstrapping gene trees

Selected Course Projects

- Gesture/Sign Recognition (in C/C++ and MATLAB) A cross modal algorithm to do gesture/sign recognition based on depth and motion information using linear dynamic systems trained by PCA and CCA.
- Conditional Random Fields for Punctuation Prediction (Python) Implementing a Conditional Random Fields model for prediction punctuation tags for English language text. Two different techniques are used for training the model: Gibbs sampling and Collins Perceptron.

- Latent Dirichlet Allocation for Document Topic Discovery (Python) Using Latent Dirichlet Allocation (LDA) to discover the underlying topics of a set of documents in an un-supervised scheme based on frequency of words in docu-
- Recursive Auto Encoder (RAE) Method of Learning Meanings for Sentences Reconstructing a recursive auto encoder neural network for recognizing sentence level sentiment using a dynamic representation for sentences.

Publication

- 1. Rabiee, M., Sayyari, E. and Mirarab, S., 2018. Multi-allele species reconstruction using ASTRAL. Molecular phylogenetics and evolution.
- 2. Zhang, C., Rabiee, M., Sayyari, E. and Mirarab, S., 2018. ASTRAL-III: polynomial time species tree reconstruction from partially resolved gene trees. BMC bioinformatics, 19(6), p.153.
- 3. Sayyari, E. and Mirarab, S., 2018. Testing for Polytomies in Phylogenetic Species Trees Using Quartet Frequencies. Genes, 9(3), p.132.
- 4. Sayyari, E., Whitfield, J. and Mirarab, S., DiscoVista: Interpretable visualizations of gene tree discordance, Molecular Phylogenetics and Evolution, Volume 122, 2018, Pages 110-115
- 5. Sayyari, E., James Whitfield, and Siavash Mirarab. Fragmentary gene sequences negatively impact gene tree and species tree reconstruction. Molecular Biology and Evolution (in press) (2017).
- 6. Zhang, C., Sayyari, E. and Mirarab, S., 2017, October. ASTRAL-III: Increased Scalability and Impacts of Contracting Low Support Branches. In RECOMB International Workshop on Comparative Genomics (pp. 53-75). Springer, Cham.
- 7. Mai, U., Sayyari, E. and Mirarab, S., 2017. 11Minimum variance rooting of phylogenetic trees and implications for species tree reconstruction. PloS one, 12(8), p.e0182238. (Best paper award at GLBIO 2017)
- 8. Sayyari, E. and Mirarab, S., 2016. Anchoring quartet-based phylogenetic distances and applications to species tree reconstruction. BMC genomics, 17(10),
- 9. Sayyari, E. and Mirarab, S., 2016. Fast coalescent-based computation of local branch sup- port from quartet frequencies. Molecular biology and evolution, 33(7), pp.1654-1668.
- 10. Weibel, N., Hwang, S.O., Rick, S., Sayyari, E., Lenzen, D. and Hollan, J., 2016, January. Hands that Speak: An Integrated Approach to Studying Complex Human Communicative Body Movements. In System Sciences (HICSS), 2016 49th Hawaii International Conference on (pp. 610-619). IEEE
- 11. Sayyari, E., Farzi, M., Estakhrooeieh, R.R., Samiee, F. and Shamsollahi, M.B., 2012, July. Migraine analysis through EEG signals with classification approach. In Information Science, Signal Processing and their Applications (ISSPA), 2012 11th International Conference on (pp. 859-863). IEEE.

Teaching Experience

UC San Diego, La Jolla, California USA

Spring, 2014 - present

- Undergraduate courses: Engineering Probability and Stats, Circuits and Systems, Probability and Random Processes
- Graduate courses: Algorithms for biological data analysis, Random Processes

Workshops and Tutorials

Summer 2016

Phylogenomics Symposium and Software School on ASTRAL, PASTA, and ASTRID

Other Experience Cluster maintenance, UC San Diego

Fall 2016 - present

• Includes updating and maintenance of lab cluster, and training students