BENJAMIN KEIJIN TEO

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EDUCATION

University of Wisconsin-Madison   *Aug 2018 – Fall 2024*
Ph.D. Candidate in Statistics

Carnegie Mellon University   *Aug 2013 – May 2017*
B.S. Mathematics (Additional Minor in Computer Science)

RESEARCH INTERESTS

Statistical and computational techniques for scalable inference of trait models on phylogenetic networks.

PUBLICATIONS

Teo, B., Bastide, P., Ané, C. 2024. Leveraging graphical model techniques to study evolution on phylogenetic networks. *arXiv preprint.* https://doi.org/10.48550/arXiv.2405.09327.

Teo, B., Rose, J. P., Bastide, P., and Ané, C. 2023. Accounting for within-species variation in continuous trait evolution on a phylogenetic network. *Bulletin of the Society of Systematic Biologists.* https://doi.org/10.18061/bssb.v2i3.8977.

Tang, S., Lee, T. S., Li, M., Zhang, Y., Xu, Y., Liu, F., **Teo, B.**, and Jiang, H. 2018. Complex pattern selectivity in macaque primary visual cortex revealed by large-scale two-photon imaging. Current Biology, 28(1):38–48. https://doi.org/10.1016/j.cub.2017.11.039.

MANUSCRIPTS

Teo, B., Bacharach, M., Kolb, A., Ané, C., Roch, S., Brandt, C. Capabilities and limitations of explicit network methods for recombinant detection: a case study using Bovine Alphaherpesvirus 1. *In preparation.*

PRESENTATIONS

1. *Leveraging graphical model techniques to study evolution on phylogenetic networks.* 3rd Joint Congress on Evolutionary Biology. Montreal, Canada. July 2024

2. *Belief propagation for continuous trait evolution on phylogenetic networks.* UW-Madison SGSA Student Seminar. Madison, WI. Nov 2022

3. *Accounting for within-species variation in continuous trait evolution on a phylogenetic network.* Evolution conference. Cleveland, OH. June 2022

SOFTWARE

Have contributed or am contributing to: PhyloGaussianBeliefProp.jl, PhyloNetworks.jl

PAST PROJECTS

Sun Prairie Community Schools Data Dashboard (2021)
- Stat 998 project. Built a Shiny app that displays attendance, census, crime-incidence statistics, with an interactive map of Sun Prairie.

Phylogenetic analysis of Algonquian using SNAPP (2021)
- Bot 563 project. Used SNAPP to infer a posterior set of language phylogenies from cognate data while accounting for within-population language variation.

Phylogenetic analysis of Algonquian using BEAST2 (2020)

- Used BEAST2 to infer a posterior set of language phylogenies under various stochastic models of cognate evolution. Performed Bayesian model selection.

PRE-UW RESEARCH EXPERIENCE

Research Assistant at Lee Lab

CMU, Center for the Neural Basis of Cognition (CNBC)   *June – Aug '17*

· Fitted tuning curves/surfaces to V1 neuron firing rate data based on 1D/2D parametrizations of the stimulus space, for each of several classes of visual stimuli. Clustered neurons according to their preferred stimuli class(es) using randomization tests. Visualized the clustering structure of the neurons.

Undergraduate Research Project

CMU, Statistics Department   *June '16 – May '17*

· Used Two-State Hidden Markov Models (HMMs) to model changes in the log inter-spike intervals (ISIs) of V1 neurons. Tested various ad-hoc methods for identifying and clustering synchronously-active neurons based on the estimated latent states.

TEACHING EXPERIENCE @ UW

Teaching Assistant

Stat 301/324/371: Introductory Applied Statistics for Social Sciences/Life Sciences/Engineers
Stat 349: Time Series, Stat 424: Experimental Design, Stat 479: Bayesian Analysis
Stat 850: Theory/Application of Regression and Analysis of Variance II

Graduate Student Mentor

Stat 699: Directed Study

WORK EXPERIENCE

Research Programmer at Murphy Lab

CMU, Computational Biology Department   *Oct '17 – July '18*

· Developer and Tester for CellOrganizer Project, a software package for learning generative models of cell/organelle shape/distribution from 2D/3D fluorescence micrographs.
· Worked with the OME-XML file format for reading and writing micrograph pixel/meta-data.
· Worked variously on segmentation related tasks for basal bodies and white blood cells.
· Compiled CellOrganizer source code for deployment, and built Docker container to export the compiled executables to other Docker-supported platforms.
· Created Bash tool scripts and XML tool definition files to enable CellOrganizer tools to be accessed through Galaxy Project's GUI.
· Linked CellOrganizer Project's GitLab repositories with Jenkins CI to enable automated testing.

TECHNICAL SKILLS

Programming Languages	Julia, R, Python, MATLAB, C, Bash
Markup Languages	Markdown, XML, LaTeX
Software & Tools	Git, Docker, Jenkins CI, Galaxy Project, BEAST2