BEN TEO

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ACADEMIC POSITIONS

University of Melbourne 2026 – 2028
MACSYS/MIG Research Fellow in Biological Data Science (Accepted)

EDUCATION

University of Wisconsin-Madison Aug 2018 – May 2025
Ph.D. in Statistics (Thesis: *Statistical and Computational Techniques for Continuous Trait Models on Phylogenetic Networks*)

Carnegie Mellon University Aug 2013 – May 2017
B.S. Mathematical Sciences (Statistics Concentration, 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.* Philosophical Transactions of the Royal Society B. https://doi.org/10.1098/rstb.2023.0310.

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.

Teo, B., Bastide, P., and Ané, C. *PhyloGaussianBeliefProp: A Julia package for Gaussian models on phylogenetic networks using belief propagation.* In preparation.

Teo, B. *Adapting cluster graphs for inference of continuous trait evolution on phylogenetic networks.* In preparation.

PRESENTATIONS (T: TALK | P: POSTER | W: WORKSHOP)

(T) *Adapting cluster graphs for inference of continuous trait evolution on phylogenetic networks.* Department of Statistics, National Cheng Kung University. Tainan, Taiwan. Nov 2025.

(T) *Belief Propagation: An Introduction.* Graduate Students & Postdocs Seminar, *Theory, Methods, and Applications of Quantitative Phylogenomics.* ICERM, Brown University. Providence, RI. Fall 2024.

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

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

(T) *Accounting for within-species variation in continuous trait evolution on a phylogenetic network.* Evolution Conference. Cleveland, OH. June 2022

(P) *Leveraging graphical model techniques to study evolution on phylogenetic networks. Theory, Methods, and Applications of Quantitative Phylogenomics.* ICERM, Brown University. Providence, RI. Fall 2024.

(W) *Theory, Methods, and Applications of Quantitative Phylogenomics.* ICERM, Brown University. Providence, RI. Fall 2024

HONORS AND AWARDS (G: GROUP | I: INDIVIDUAL)

(I) SRGC Conference Presentation Award, UW-Madison Graduate School — Summer 2024
(I) Mayr Symposium, Finalist. 3rd Joint Congress on Evolutionary Biology — July 2024
(I) Statistics Poster Competition, 2nd place. CMU Undergraduate Research Symposium — May 2017

(G) Open Hall of Fame Inductee (JuliaPhylo). Inaugural UW-Madison Open Awards — 2025
(G) SORTEE Commendation Award (JuliaPhylo) — 2025

SOFTWARE (M/L: MAJOR/LESSER CONTRIBUTOR)

(M) PhyloGaussianBeliefProp.jl, (L) PhyloTraits.jl

ACADEMIC EXPERIENCE (UW: UW-MADISON | CMU: CARNEGIE MELLON)

(UW) **Teaching Assistant** — Fall 2018 – Fall 2022
Stat 301/324/371: Introductory Applied Statistics
Stat 349: Time Series, Stat 424: Experimental Design, Stat 479: Bayesian Analysis
Stat 850: Regression and Analysis of Variance II

(UW) **Graduate Student Mentor**
Stat 699: Directed Study — Fall 2021

(UW) **Research Assistant**
Statistics Department — Spring 2023 – Spring 2024
Institute for Foundations of Data Science — Summer 2021

(CMU) **Project Assistant, Center for Neural Basis of Cognition (Lee Lab)** — Summer 2017
Modeling/clustering neuron response to parametrized visual stimuli.

(CMU) **Undergraduate Research, Statistics Department** — Summer 2016 – Spring 2017
Hidden Markov Models to determine neuron population structure.

WORK EXPERIENCE

Research Programmer
CMU, Computational Biology Department, Murphy Lab — Oct 2017 – July 2018

- 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.

SKILLS

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