



Julia Palacios

Associate Professor of Statistics and of Biomedical Data Science

Bio

BIO

Dr. Palacios's research spans Bayesian nonparametrics, probabilistic AI, stochastic processes, and computational statistics. Her group develops stochastic models and efficient inference algorithms for understanding evolutionary dynamics in population genetics, infectious diseases and cancer.

ACADEMIC APPOINTMENTS

- Associate Professor, Statistics
- Associate Professor, Department of Biomedical Data Science
- Member, Bio-X
- Member, Institute for Computational and Mathematical Engineering (ICME)

HONORS AND AWARDS

- Frederick E. Terman Fellow 2017, Stanford University (2017-2019)
- Alfred P. Sloan Research Fellowship 2018, Sloan Foundation (2018-2020)

PROFESSIONAL EDUCATION

- Ph.D, University of Washington , Statistics (2013)

Teaching

COURSES

2025-26

- Introduction to Statistics for Biology: BIO 141, STATS 141 (Spr)
- Introduction to Stochastic Processes I: STATS 217 (Win)
- Workshop in Biomedical Data Science: BMDS 280C, STATS 260C (Spr)

2024-25

- Introduction to Stochastic Processes I: STATS 217 (Win)
- Workshop in Biostatistics: BIODS 260C, STATS 260C (Spr)

2023-24

- Introduction to Statistical Inference: STATS 200 (Aut)
- Introduction to Stochastic Processes I: STATS 217 (Win)
- Workshop in Biostatistics: BIODS 260C, STATS 260C (Spr)

2022-23

- Theory of Statistics II: STATS 300B (Win)
- Workshop in Biostatistics: BIODS 260C, STATS 260C (Spr)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Luis Chumpitaz Diaz, Amber Hu

Postdoctoral Faculty Sponsor

Isaac Goldstein

Doctoral Dissertation Advisor (AC)

Leda Liang, Ivan Specht, Yi-Ting Tsai

Master's Program Advisor

Noemi Reche-Ley, Miko Rimer

Publications

PUBLICATIONS

- **Generalizing matrix representations to fully heterochronous ranked tree shapes.** *ArXiv*
Jennings-Shaffer, C., Chen, C., Palacios, J. A., Matsen Iv, F. A.
2025
- **Efficient Bayesian Phylogenetics under the Infinite Sites Model.** *bioRxiv : the preprint server for biology*
Specht, I., Palacios, J. A.
2025
- **Accounting for reporting delays in real-time phylodynamic analyses with preferential sampling.** *PLoS computational biology*
Medina, C. M., Palacios, J. A., Minin, V. M.
2025; 21 (5): e1012970
- **Curriculum Design in an Evolving Field: Perspectives on Biomedical Data Science from Stanford.** *Annual review of biomedical data science*
Yeh, C. Y., Wall, D. P., Matthys, K., Sabatti, C., Palacios, J.
2025
- **Multiple merger coalescent inference of effective population size.** *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*
Zhang, J., Palacios, J. A.
2025; 380 (1919): 20230306
- **An Efficient Coalescent Model for Heterochronously Sampled Molecular Data** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
Cappello, L., Veber, A., Palacios, J. A.
2024
- **CRP-Tree: a phylogenetic association test for binary traits** *JOURNAL OF THE ROYAL STATISTICAL SOCIETY SERIES C-APPLIED STATISTICS*
Zhang, J., Preising, G. A., Schumer, M., Palacios, J. A.
2024; 73 (2): 340-377
- **Statistical summaries of unlabelled evolutionary trees.** *Biometrika*
Samyak, R., Palacios, J. A.
2024; 111 (1): 171-193
- **Bayesian Change Point Detection with Spike-and-Slab Priors** *JOURNAL OF COMPUTATIONAL AND GRAPHICAL STATISTICS*

-
- Cappello, L., Padilla, O., Palacios, J. A.
2023
- **adaPop: Bayesian inference of dependent population dynamics in coalescent models.** *PLoS computational biology*
Cappello, L., Kim, J., Palacios, J. A.
2023; 19 (3): e1010897
 - **Adaptive Preferential Sampling in Phylodynamics With an Application to SARS-CoV-2.** *Journal of computational and graphical statistics : a joint publication of American Statistical Association, Institute of Mathematical Statistics, Interface Foundation of North America*
Cappello, L., Palacios, J. A.
2022; 31 (2): 541-552
 - **AN ADJACENT-SWAP MARKOV CHAIN ON COALESCENT TREES** *JOURNAL OF APPLIED PROBABILITY*
Simper, M., Palacios, J. A.
2022
 - **Deconvoluting complex correlates of COVID-19 severity with a multi-omic pandemic tracking strategy.** *Nature communications*
Parikh, V. N., Ioannidis, A. G., Jimenez-Morales, D., Gorzynski, J. E., De Jong, H. N., Liu, X., Roque, J., Cepeda-Espinoza, V. P., Osoegawa, K., Hughes, C., Sutton, S. C., Youlton, N., Joshi, et al
2022; 13 (1): 5107
 - **Enumeration of binary trees compatible with a perfect phylogeny.** *Journal of mathematical biology*
Palacios, J. A., Bhaskar, A., Disanto, F., Rosenberg, N. A.
2022; 84 (6): 54
 - **Statistical Challenges in Tracking the Evolution of SARS-CoV-2** *STATISTICAL SCIENCE*
Cappello, L., Kim, J., Liu, S., Palacios, J. A.
2022; 37 (2): 162-182
 - **The impact of the COVID-19 preventive measures on influenza transmission: molecular and epidemiological evidence.** *International journal of infectious diseases : IJID : official publication of the International Society for Infectious Diseases*
Tran, L. K., Huang, D., Li, N., Li, L. M., Palacios, J. A., Chang, H.
1800
 - **Adaptive Preferential Sampling in Phylodynamics With an Application to SARS-CoV-2** *JOURNAL OF COMPUTATIONAL AND GRAPHICAL STATISTICS*
Cappello, L., Palacios, J. A.
2021
 - **Distance metrics for ranked evolutionary trees.** *Proceedings of the National Academy of Sciences of the United States of America*
Kim, J., Rosenberg, N. A., Palacios, J. A.
2020
 - **SEQUENTIAL IMPORTANCE SAMPLING FOR MULTIREOLUTION KINGMAN-TAJIMA COALESCENT COUNTING** *ANNALS OF APPLIED STATISTICS*
Cappello, L., Palacios, J. A.
2020; 14 (2): 727-51
 - **SEQUENTIAL IMPORTANCE SAMPLING FOR MULTIREOLUTION KINGMAN-TAJIMA COALESCENT COUNTING.** *The annals of applied statistics*
Cappello, L., Palacios, J. A.
2020; 14 (2): 727-751
 - **Discussion on "Horseshoe-based Bayesian nonparametric estimation of effective population size trajectories" by James R. Faulkner, Andrew F. Magee, Beth Shapiro, and Vladimir N. Minin.** *Biometrics*
Cappello, L., Ghosh, S., Palacios, J. A.
2020
 - **Bayesian Estimation of Population Size Changes by Sampling Tajima's Trees.** *Genetics*
Palacios, J. A., Véber, A., Cappello, L., Wang, Z., Wakeley, J., Ramachandran, S.
2019; 213 (3): 967-986

- **Bayesian Estimation of Population Size Changes by Sampling Tajima's Trees.** *Genetics*
Palacios, J. A., Véber, A., Cappello, L., Wang, Z., Wakeley, J., Ramachandran, S.
2019; 213 (3): 967-986
- **Bayesian Estimation of Population Size Changes by Sampling Tajima's Trees.** *Genetics*
Palacios, J. A., Véber, A. n., Cappello, L. n., Wang, Z. n., Wakeley, J. n., Ramachandran, S. n.
2019
- **Exact limits of inference in coalescent models.** *Theoretical population biology*
Johndrow, J. E., Palacios, J. A.
2018
- **No Evidence for Recent Selection at FOXP2 among Diverse Human Populations** *CELL*
Atkinson, E., Audesse, A., Palacios, J., Bobo, D., Webb, A., Ramachandran, S., Henn, B.
2018; 174 (6): 1424-+
- **PHYLODYN: an R package for phylodynamic simulation and inference** *MOLECULAR ECOLOGY RESOURCES*
Karcher, M. D., Palacios, J. A., Lan, S., Minin, V. N.
2017; 17 (1): 96-100
- **phylodyn: an R package for phylodynamic simulation and inference.** *Molecular ecology resources*
Karcher, M. D., Palacios, J. A., Lan, S., Minin, V. N.
2016
- **Quantifying and Mitigating the Effect of Preferential Sampling on Phylodynamic Inference.** *PLoS computational biology*
Karcher, M. D., Palacios, J. A., Bedford, T., Suchard, M. A., Minin, V. N.
2016; 12 (3)
- **An efficient Bayesian inference framework for coalescent-based nonparametric phylodynamics** *BIOINFORMATICS*
Lan, S., Palacios, J. A., Karcher, M., Minin, V. N., Shahbaba, B.
2015; 31 (20): 3282-3289
- **Bayesian Nonparametric Inference of Population Size Changes from Sequential Genealogies** *GENETICS*
Palacios, J. A., Wakeley, J., Ramachandran, S.
2015; 201 (1): 281-?
- **Phylogeography of the Trans-Volcanic bunchgrass lizard (*Sceloporus bicanthalis*) across the highlands of south-eastern Mexico** *BIOLOGICAL JOURNAL OF THE LINNEAN SOCIETY*
Leache, A. D., Palacios, J. A., Minin, V. N., Bryson, R. W.
2013; 110 (4): 852-865
- **Gaussian Process-Based Bayesian Nonparametric Inference of Population Size Trajectories from Gene Genealogies** *BIOMETRICS*
Palacios, J. A., Minin, V. N.
2013; 69 (1): 8-18