

# Stanford

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## Julia Palacios

Associate Professor of Statistics, of Biomedical Data Science and, by courtesy, of Biology

### Bio

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#### BIO

Dr. Palacios seek to provide statistically rigorous answers to concrete, data driven questions in evolutionary genetics and public health . My research involves probabilistic modeling of evolutionary forces and the development of computationally tractable methods that are applicable to big data problems. Past and current research relies heavily on the theory of stochastic processes, Bayesian nonparametrics and recent developments in machine learning and statistical theory for big data.

#### ACADEMIC APPOINTMENTS

- Associate Professor, Statistics
- Associate Professor, Biomedical Data Science
- Associate Professor (By courtesy), Biology
- 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

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#### COURSES

##### 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)

##### 2021-22

- Theory of Probability: STATS 116 (Aut)

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

#### 2020-21

- Workshop in Biostatistics: BIODS 260C, STATS 260C (Spr)

### STANFORD ADVISEES

#### Doctoral Dissertation Reader (AC)

Paula Gablenz, Amber Hu, Jimmy Smith

#### Postdoctoral Faculty Sponsor

Bingjing Tang

#### Doctoral Dissertation Advisor (AC)

Julie Zhang

## Publications

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### PUBLICATIONS

- **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
- **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