Stanford

Brian Trippe

Assistant Professor of Statistics and, by courtesy, of Computer Science

Bio

BIO

Dr. Brian Trippe is an assistant professor at Stanford in the Department of Statistics, with an affiliation in Stanford Data Science.

In his research, Dr. Trippe develops probabilistic machine learning methods to address challenges in biotechnology and medicine. Recently, his focus has been on generative modeling and inference algorithms for protein engineering.

Before joining Stanford, Dr. Trippe was a postdoctoral fellow at Columbia University in the Department of Statistics, and a visiting researcher at the Institute for Protein Design at the University of Washington.

ACADEMIC APPOINTMENTS

- Assistant Professor, Statistics
- Assistant Professor (By courtesy), Computer Science
- Member, Bio-X
- Member, Stanford Data Science

HONORS AND AWARDS

- Summa cum laude, Columbia College (2016)
- NSF Graduate Research Fellowship, National Science Foundation (2018-2022)
- Euretta J. Kellett Fellowship, Support from Columbia College for study at the University of Cambridge (2016-2017)

PROFESSIONAL EDUCATION

- Ph.D., Massachusetts Institute of Technology , Computational and Systems Biology (2022)
- M.Phil., University of Cambridge , Machine Learning (2017)
- B.A., scl, Columbia College , Biochemistry, Computer Science (2016)

PATENTS

- Brian Trippe. "United States Patent US20230160824A1 Unbiased sorting and sequencing of objects via randomized gating schemes", Microsoft Corporation, May 25, 2023
- Michelle Therese Hoerner Dimon, Marc Berndl, Marc Adlai Coram, Brian Trippe, Patrick F Riley, Philip Charles Nelson. "United States Patent US10546650B2 Neural network for processing aptamer data", Google, Jan 28, 2020

LINKS

- Personal Site: briantrippe.com

Teaching

COURSES

2025-26

- Data Science for Computational Molecular Biology: DATASCI 194B, DATASCI 294B (Spr)
- Literature of Statistics: STATS 319 (Aut)
- Modern Applied Statistics: Learning: STATS 315A (Win)

2024-25

- Topics in Generative Modeling Methods in Protein Modeling and Design: STATS 326 (Spr)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Karsten Householder, Talal Widatalla

Orals Chair

Minkai Xu

Doctoral Dissertation Co-Advisor (AC)

Henry Smith

Doctoral (Program)

Arthur Deng, Nathaniel Diamant

Publications

PUBLICATIONS

- **Predicting mutational effects on protein binding from folding energy**
  Deng, A., Householder, K., Wu, F., Garcia, K., Trippe, B.
  edited by Singh, A., Fazel, M., Hsu, D., Lacoste-Julien, S., Berkenkamp, F., Maharaj, T., Wagstaff, K., Zhu, J.
  JMLR-JOURNAL MACHINE LEARNING RESEARCH.2025: 13129-13151

- **MotifBench: A standardized protein design benchmark for motif-scaffolding problems**
  Zheng, Z., Zhang, B., Didi, K., Yang, K. K., Yim, J., Watson, J., Chen, H., Trippe, B. L.
  arXiv.
  2025

- **Predicting mutational effects on protein binding from folding energy** *International Conference on Machine Learning*
  Arthur, D. L., Householder, K., Wu, F., Thrun, S., Garcia, K. C., Trippe, B. L.
  2025

- **Calibrating Generative Models to Distributional Constraints**
  Smith, H. D., Diamant, N. L., Trippe, B. L.
  arXiv.
  2025

- **De novo design of protein structure and function with RFdiffusion.** *Nature*
  Watson, J. L., Juergens, D., Bennett, N. R., Trippe, B. L., Yim, J., Eisenach, H. E., Ahern, W., Borst, A. J., Ragotte, R. J., Milles, L. F., Wicky, B. I., Hanikel, N., Pellock, et al

2023; 620 (7976): 1089-1100

- **Leveraging polygenic enrichments of gene features to predict genes underlying complex traits and diseases.** *Nature genetics*

  Weeks, E. M., Ulirsch, J. C., Cheng, N. Y., Trippe, B. L., Fine, R. S., Miao, J., Patwardhan, T. A., Kanai, M., Nasser, J., Fulco, C. P., Tashman, K. C., Aguet, F., Li, et al

  2023

- **Confidently Comparing Estimates with the c-value** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*

  Trippe, B. L., Deshpande, S. K., Broderick, T.

  2024; 119 (546): 983-994

- **Gaussian Processes at the Helm(holtz): A More Fluid Model for Ocean Currents**

  Berlinghieri, R., Trippe, B. L., Burt, D. R., Giordano, R., Srinivasan, K., Ozgokmen, T., Xia, J., Broderick, T.

  edited by Krause, A., Brunskill, E., Cho, K., Engelhardt, B., Sabato, S., Scarlett, J.

  JMLR-JOURNAL MACHINE LEARNING RESEARCH.2023

- **Diffusion probabilistic modeling of protein backbones in 3D for the motif-scaffolding problem** *International Conference on Learning Representations*

  Trippe, B. L., Yim, J., Tischer, D., Broderick, T., Baker, D., Barzilay, R., Jaakkola, T.

  2023

- **Practical and Asymptotically Exact Conditional Sampling in Diffusion Models**

  Wu, L., Trippe, B. L., Naesseth, C. A., Blei, D. M., Cunningham, J. P.

  edited by Oh, A., Neumann, T., Globerson, A., Saenko, K., Hardt, M., Levine, S.

  NEURAL INFORMATION PROCESSING SYSTEMS (NIPS).2023

- **SE(3) diffusion model with application to protein backbone generation**

  Yim, J., Trippe, B. L., De Bortoli, V., Mathieu, E., Doucet, A., Barzilay, R., Jaakkola, T.

  edited by Krause, A., Brunskill, E., Cho, K., Engelhardt, B., Sabato, S., Scarlett, J.

  JMLR-JOURNAL MACHINE LEARNING RESEARCH.2023

- **Randomized gates eliminate bias in sort-seq assays** *PROTEIN SCIENCE*

  Trippe, B. L., Huang, B., DeBenedictis, E. A., Coventry, B., Bhattacharya, N., Yang, K. K., Baker, D., Crawford, L.

  2022; 31 (9)

- **Many Processors, Little Time: MCMC for Partitions via Optimal Transport Couplings**

  Nguyen, T. D., Trippe, B. L., Broderick, T.

  edited by Camps-Valls, G., Ruiz, F. J., Valera

  JMLR-JOURNAL MACHINE LEARNING RESEARCH.2022

- **For high-dimensional hierarchical models, consider exchangeability of effects across covariates instead of across datasets**

  Trippe, B. L., Finucane, H. K., Broderick, T.

  edited by Ranzato, M., Beygelzimer, A., Dauphin, Y., Liang, P. S., Vaughan, J. W.

  NEURAL INFORMATION PROCESSING SYSTEMS (NIPS).2021

- **LR-GLM: High-Dimensional Bayesian Inference Using Low-Rank Data Approximations**

  Trippe, B. L., Huggins, J. H., Agrawal, R., Broderick, T.

  edited by Chaudhuri, K., Salakhutdinov, R.

  JMLR-JOURNAL MACHINE LEARNING RESEARCH.2019

- **The Kernel Interaction Trick: Fast Bayesian Discovery of Pairwise Interactions in High Dimensions**

  Agrawal, R., Huggins, J. H., Trippe, B., Broderick, T.

  edited by Chaudhuri, K., Salakhutdinov, R.

  JMLR-JOURNAL MACHINE LEARNING RESEARCH.2019

- **Inhibition of cell fate repressors secures the differentiation of the touch receptor neurons of Caenorhabditis elegans.** *Development (Cambridge, England)*

  Zheng, C., Jin, F. Q., Trippe, B. L., Wu, J., Chalfie, M.

  2018; 145 (22)

- **Overpruning in variational Bayesian neural networks** *NeurIPS Workshop on Advances in Approximate Bayesian Inference*
  Trippe, B. L., Turner, R. E.
  2017