

Curriculum Vitae

Jeffrey P. Spence, Ph.D.

Contact Information

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Education

Ph.D., 2019	University of California, Berkeley
	Major : Computational Biology
	Thesis Advisor : Yun S. Song
	Thesis Title : <i>Probabilistic models and statistical inference in population genetics</i>
B.A., 2013	Cornell University (<i>with distinction in all subjects</i>)
	Majors : Biological Sciences (<i>cum laude</i>) Mathematics
	Thesis Advisor : Linda K. Nicholson
	Thesis Title : <i>Engineering a mimic of the cis conformation of the amyloid precursor protein cytoplasmic tail using disulfide bonding</i>

Academic Positions

2019 - Present	Postdoctoral Researcher
	Stanford University, Department of Genetics
	Advisor : Jonathan K. Pritchard

Honors and Awards

2019	Early-career Scientist Seminar Series Award, J.F. Crow Institute for the Study of Evolution at the University of Wisconsin–Madison
2018	Outstanding Graduate Student Instructor Award, UC Berkeley
2016	Top poster prize, Probabilistic Models in Genomics Conference, Oxford University

Publications and Reviews (hyperlinked)

* denotes equal contribution

† corresponding author if not last author

& denotes authors listed alphabetically

Preprints and Submitted Manuscripts

- Czech, L., **Spence, J. P.**, and Expósito-Alonso, M. grededalf: population genetic statistics for the next generation of pool sequencing. (*arXiv preprint*).
- Zeng, T.^{*},[†], **Spence, J. P.**^{*},[†], Mostafavi, H., and Pritchard, J. K.[†]. Bayesian estimation of gene constraint from an evolutionary model with gene features. (*bioRxiv preprint*; in review at *Nature Genetics*).
- Expósito-Alonso, M., **Spence, J. P.**, Ruffley, M., Czech, L., Lin, M., Selmoni, O., Gillespie, L., Mualim, K. S., and Hatley, S. Power and limitations of the mutations-area relationship to assess within-species genetic diversity targets for post-2020 Sustainable Development Goals. (*EcoEvoRxiv preprint*).
- Rothschild, D.^{*}, Susanto, T. T.^{*}, **Spence, J. P.**, Genuth, N. R., Sinnott-Armstrong, N., Pritchard, J. K.[†], and Barna, M.[†] A comprehensive rRNA variation atlas in health and disease. (*bioRxiv preprint*).
- Batra, S., S.^{*}, Cabrera, A.^{*}, **Spence, J. P.**^{*}, Hilton, I. B.[†], and Song, Y. S.[†] Predicting the effect of CRISPR-Cas9-based epigenome editing (*bioRxiv preprint*).
- Antonio, M. L.^{*}, Weiß, C. L.^{*}, Gao, Z.^{*}, Sawyer, S.^{*}, Oberreiter, V., Moots, H. M., **Spence, J. P.**, *et al.* Stable population structure in Europe since the Iron Age, despite high mobility. (*bioRxiv preprint*; in revision at *eLife*).
- **Spence, J. P.**[†], Sinnott-Armstrong, N., Assimes, T., and Pritchard, J. K.[†] A flexible modeling and inference framework for estimating variant effect sizes from GWAS summary statistics. (*bioRxiv preprint*; in revision at *eLife*).
- Czech, L.^{*}, Peng, Y.^{*}, **Spence, J. P.**, *et al.* Monitoring rapid evolution of plan populations at scale with pool-sequencing. (*bioRxiv preprint*).
- Aw, A. J., **Spence, J. P.**, and Song, Y. S., A flexible and robust non-parametric test of exchangeability. (*arXiv preprint*; in press at *Annals of Applied Statistics*).

2023

- Mostafavi, H., **Spence, J. P.**, Naqvi, S., and Pritchard, J. K. Systematic differences in discovery of genetic effects on gene expression and complex traits. *Nature Genetics* (2023).

- **Spence, J. P.[†]**, Zeng, T., Mostafavi, H., and Pritchard, J. K. Scaling the Discrete-Time Wright-Fisher model to biobank-scale datasets. *Genetics* (2023). **Selected for November Spotlight.**
- Moots, H. M., Antonio, M. L.* , Sawyer, S.* , **Spence, J. P.***, Weiß, C. L.* , Lucci, M.* , Cherifi, Y. M. S.* , *et al.* A genetic history of continuity and mobility in the Iron Age central Mediterranean. *Nature Ecology & Evolution* (2023).
- Schreiber, J., *et al.*. The ENCODE Imputation Challenge: A critical assessment of methods for cross-cell type imputation of epigenomic profiles. *Genome Biology*, Volume 24 (2023).
- Fan, S.* , **Spence, J. P.***, *et al.*. Whole-genome sequencing reveals a complex African population demographic history and signatures of local adaptation. *Cell*, Volume 186, Issue 5 (2023).
- Lauterbur, M. E., *et al.* Expanding the stdpopsim species catalog, and lessons learned for realistic genome simulations. *eLife*, reviewed preprint.

2022

- Expósito-Alonso, M., Booker, T.R.& , Czech, L.& , Gillespie, L.& , Hately, S.& , Kyriazis, C.& , Lang, P. L.& , Levanthal, L.& , Nogues-Bravo, D.& , Pagowski, V.& , Ruffley, M.& , **Spence, J. P.&**, Toro Arana, S. E.& , Weiß, C. L.& , and Zess, E.& . Genetic diversity loss in the Anthropocene. *Science*, Volume 377, Issue 6613 (2022)
- Patel, R.* , Musharoff, S. A.* , **Spence, J. P.**, *et al.* Genetic interactions drive heterogeneity in causal variant effect sizes for gene expression and complex traits. *American Journal of Human Genetics* (2022).

2021

- Naqvi, S.* , Slepp, Y.* , Hoskens, H., Indencleef, K., **Spence, J. P.**, *et al.*. Shared heritability of face and brain shape distinct from cognitive traits. *Nature Genetics* (2021).

2020

- **Spence, J.P.** Flexible mean field variational inference using mixtures of non-overlapping exponential families. *Advances in Neural Information Processing Systems 33 (NeurIPS2020)*. **Selected for Spotlight** – top 4% of submissions.

2019

- **Spence, J.P.[†]** and Song, Y.S.[†] Inference and analysis of population-specific fine-scale recombination maps across 26 diverse human populations. *Science Advances*, Vol. 5, No. 10, eaaw9206 (2019).

- Steinrücken, M., Kamm, J.A., **Spence, J.P.**, and Song, Y.S. Inference of complex population histories using whole-genome sequences from multiple populations. *PNAS* Vol. 116, No. 34 (2019) 17115-17120.

2018

- Chan, J., Perrone, V., **Spence, J.P.**, Jenkins, P.A., Mathieson, S., and Song, Y.S. A likelihood-free inference framework for population genetic data using exchangeable neural networks. *Advances in Neural Information Processing Systems 31 (NeurIPS2018)*. **Selected for Spotlight** – top 4% of submissions.
- Moreno-Mayar, J.V.*, Vinner, L.*, de Barros Damgaard, P.*, de la Fuente, C. *, Chan, J. *, **Spence, J.P.***, *et al.* Early human dispersal within the Americas. *Science*, Vol. 362, Issue 6419 (2018) .
- Steinrücken, M., **Spence, J.P.**, Kamm, J.A., Wiczorek, E., and Song, Y.S. Model-based detection and analysis of introgressed Neanderthal ancestry in modern humans. *Molecular Ecology*, Vol. 27 No. 19 (2018) 3873-3888.
- **Spence, J.P.**, Steinrücken, M., Terhorst, J., and Song, Y.S. Inference of population history using coalescent HMMs: review and outlook. *Current Opinion in Genetics and Development*, Vol. 53 (2018) 70-76.

2016

- Mallick, S., *et al.* The Simons genome diversity project: 300 genomes from 142 diverse populations. *Nature*, Vol. 538 (2016) 201-206.
- Kamm, J.A. *, **Spence, J.P.***, Chan, J., and Song, Y.S. Two-locus likelihoods under variable population size and fine-scale recombination rate estimation. *Genetics*, Vol. 203 (2016) 1381-1399.
- **Spence, J.P.***, Kamm, J.A. *, and Song, Y.S. The site-frequency spectrum for general coalescents. *Genetics*, Vol. 202 (2016) 1549-1561.

Service

2022 - present	Member, stdpopsim consortium
2022 - present	Reviewer, Neural Information Processing Systems (NeurIPS)
2021 - present	Program Committee Member, Machine Learning for Computational Biology conference (MLCB)
2021 - present	Reviewer, International Conference on Learning Representations (ICLR). Selected as a “highlighted reviewer” in 2021 (top 10% of reviewers, free registration for the conference)
2017	Student Member, Center for Computational Biology and Department of Molecular and Cellular Biology Faculty Search Committee, UC Berkeley
2016	Student Member, UC Berkeley Computational Biology Retreat Planning Committee
2014 - 2015	Organizer, UC Berkeley Center for Computational Biology Seminar Series

Reviewer, *eLife; Genetics; Molecular Biology and Evolution; PLoS Genetics; Theoretical Population Biology; Molecular Ecology Resources; ...*

Teaching

Fall 2017 *STAT 135: Concepts of Statistics* (Upper division introduction to mathematical statistics),
Graduate Student Instructor, University of California, Berkeley
Recipient of Outstanding Graduate Student Instructor Award

Outreach

Summer 2020 Stanford Summer Research Program Oral Presentation Judge
Judged oral presentations at the end of the Stanford Summer Research Program, a program for undergraduates seeking to enter a Ph.D. program in the sciences.

Summer 2020 SACNAS Travel Grant and Abstract Reviewer
Reviewed Travel Grant applications and abstracts for the 2020 Society for Advancement of Chicanos/Hispanics and Native Americans in Science (SACNAS) conference. Travel grants and abstracts are submitted by undergraduate students interested in attending graduate school in a scientific field.

Spring 2018 Science Fair Judge
Judge and volunteer for two K-12 science fairs run by the Oakland Unified School District.

Spring 2016 *ALIGN* Graduate Student Panelist
Answered questions about graduate school and careers in computational biology for an undergraduate computational biology interest club.

Fall 2015, Fall 2016 *Berkeley Connect* Graduate Student Panelist
Similar to the above, but for students enrolled in a mentoring program interested in performing research in computational biology.

Spring 2015, Spring 2017- Spring 2018 *Bay Area Scientists Inspiring Students*
Perform experiments with elementary school children throughout the San Francisco Bay Area, improving science education and providing role modeling and mentorship for young students.

Spring 2015 *Population Genetics in Berkeley High School*
Helped organize and teach monthly lessons to local first year high school biology students to make research in population genetics accessible to high schoolers and promote interest in STEM careers.