

Stanford



Jonathan Pritchard

Professor of Genetics and of Biology

Bio

ACADEMIC APPOINTMENTS

- Professor, Genetics
- Professor, Biology
- Member, Bio-X

LINKS

- Lab web site: <http://pritchardlab.stanford.edu>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

We are interested in a broad range of problems at the interface of genomics and evolutionary biology. One current focus of the lab is in understanding how genetic variation impacts gene regulation and complex traits. We also have long-term interests in using genetic data to learn about population structure, history and adaptation, especially in humans.

FOR UP-TO-DATE DETAILS ON MY LAB AND RESEARCH, PLEASE SEE: <http://pritchardlab.stanford.edu>

Teaching

COURSES

2017-18

- Advanced Genetics: GENE 205 (Win)

2016-17

- Advanced Genetics: GENE 205 (Win)
- Statistical and Machine Learning Methods for Genomics: BIO 268, BIOMEDIN 245, CS 373, GENE 245, STATS 345 (Spr)

2015-16

- Advanced Genetics: GENE 205 (Win)
- Statistical and Machine Learning Methods for Genomics: BIO 268, BIOMEDIN 245, CS 373, GENE 245, STATS 345 (Spr)

2014-15

- Advanced Genetics: GENE 205 (Win)

- Statistical and Machine Learning Methods for Genomics: BIOMEDIN 245, CS 373, GENE 245, STATS 345 (Spr)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Rohan Mehta

Postdoctoral Faculty Sponsor

Harold Pimentel, Eilon Sharon

Doctoral Dissertation Advisor (AC)

Margaret-Mary Antonio, Diego Calderon

Doctoral Dissertation Co-Advisor (AC)

Jessica Ribado

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biology (School of Humanities and Sciences) (Phd Program)
- Biomedical Informatics (Phd Program)
- Genetics (Phd Program)

Publications

PUBLICATIONS

- **Rapid evolution of the human mutation spectrum** *ELIFE*
Harris, K., Pritchard, J. K.
2017; 6
- **Tracing the peopling of the world through genomics.** *Nature*
Nielsen, R., Akey, J. M., Jakobsson, M., Pritchard, J. K., Tishkoff, S., Willerslev, E.
2017; 541 (7637): 302-310
- **Batch effects and the effective design of single-cell gene expression studies** *SCIENTIFIC REPORTS*
Tung, P., Bliischak, J. D., Hsiao, C. J., Knowles, D. A., Burnett, J. E., Pritchard, J. K., Gilad, Y.
2017; 7
- **Mutation Rate Variation is a Primary Determinant of the Distribution of Allele Frequencies in Humans** *PLOS GENETICS*
Harpak, A., Bhaskar, A., Pritchard, J. K.
2016; 12 (12)
- **A Bibliometric History of the Journal GENETICS** *GENETICS*
Telis, N., Lehmann, B. V., Feldman, M. W., Pritchard, J. K.
2016; 204 (4): 1337-1342
- **Detection of human adaptation during the past 2000 years.** *Science*
Field, Y., Boyle, E. A., Telis, N., Gao, Z., Gaulton, K. J., Golan, D., Yengo, L., Rocheleau, G., Froguel, P., McCarthy, M. I., Pritchard, J. K.
2016
- **Lineage-specific and single-cell chromatin accessibility charts human hematopoiesis and leukemia evolution.** *Nature genetics*
Corces, M. R., Buenrostro, J. D., Wu, B., Greenside, P. G., Chan, S. M., Koenig, J. L., Snyder, M. P., Pritchard, J. K., Kundaje, A., Greenleaf, W. J., Majeti, R., Chang, H. Y.
2016; 48 (10): 1193-1203
- **Genetic variation in MHC proteins is associated with T cell receptor expression biases.** *Nature genetics*
Sharon, E., Sibener, L. V., Battle, A., Fraser, H. B., Garcia, K. C., Pritchard, J. K.

2016; 48 (9): 995-1002

- **Genome-wide association study of behavioral, physiological and gene expression traits in outbred CFW mice.** *Nature genetics*
Parker, C. C., Gopalakrishnan, S., Carbonetto, P., Gonzales, N. M., Leung, E., Park, Y. J., Aryee, E., Davis, J., Blizard, D. A., Ackert-Bicknell, C. L., Lionikas, A., Pritchard, J. K., Palmer, et al
2016; 48 (8): 919-926
- **Thousands of novel translated open reading frames in humans inferred by ribosome footprint profiling.** *eLife*
Raj, A., Wang, S. H., Shim, H., Harpak, A., Li, Y. I., Engelmann, B., Stephens, M., Gilad, Y., Pritchard, J. K.
2016; 5
- **Coregulation of tandem duplicate genes slows evolution of subfunctionalization in mammals** *SCIENCE*
Lan, X., Pritchard, J. K.
2016; 352 (6288): 1009-1013
- **RNA splicing is a primary link between genetic variation and disease** *SCIENCE*
Li, Y. I., van de Geijn, B., Raj, A., Knowles, D. A., Petti, A. A., Golan, D., Gilad, Y., Pritchard, J. K.
2016; 352 (6285): 600-604
- **Genetic Variation, Not Cell Type of Origin, Underlies the Majority of Identifiable Regulatory Differences in iPSCs.** *PLoS genetics*
Burrows, C. K., Banovich, N. E., Pavlovic, B. J., Patterson, K., Gallego Romero, I., Pritchard, J. K., Gilad, Y.
2016; 12 (1)
- **Genetic Variation, Not Cell Type of Origin, Underlies the Majority of Identifiable Regulatory Differences in iPSCs** *PLOS GENETICS*
Burrows, C. K., Banovich, N. E., Pavlovic, B. J., Patterson, K., Romero, I. G., Pritchard, J. K., Gilad, Y.
2016; 12 (1)
- **Abundant contribution of short tandem repeats to gene expression variation in humans** *NATURE GENETICS*
Gymrek, M., Willems, T., Guilmatre, A., Zeng, H., Markus, B., Georgiev, S., Daly, M. J., Price, A. L., Pritchard, J. K., Sharp, A. J., Erlich, Y.
2016; 48 (1): 22-?
- **Whole Genome Sequencing Identifies a Novel Factor Required for Secretory Granule Maturation in Tetrahymena thermophila.** *G3 (Bethesda, Md.)*
Kontur, C., Kumar, S., Lan, X., Pritchard, J. K., Turkewitz, A. P.
2016; 6 (8): 2505-2516
- **WASP: allele-specific software for robust molecular quantitative trait locus discovery** *NATURE METHODS*
van de Geijn, B., McVicker, G., Gila, Y., Pritchard, J. K.
2015; 12 (11): 1061-1063
- **Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions** *CELL*
Grubert, F., Zaugg, J. B., Kasowski, M., Ursu, O., Spacek, D. V., Martin, A. R., Greenside, P., Srivas, R., Phanstiel, D. H., Pekowska, A., Heidari, N., Euskirchen, G., Huber, et al
2015; 162 (5): 1051-1065
- **Genetic Control of Chromatin States in Humans Involves Local and Distal Chromosomal Interactions.** *Cell*
Grubert, F., Zaugg, J. B., Kasowski, M., Ursu, O., Spacek, D. V., Martin, A. R., Greenside, P., Srivas, R., Phanstiel, D. H., Pekowska, A., Heidari, N., Euskirchen, G., Huber, et al
2015; 162 (5): 1051-1065
- **The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans** *SCIENCE*
Ardlie, K. G., DeLuca, D. S., Segre, A. V., Sullivan, T. J., Young, T. R., Gelfand, E. T., Trowbridge, C. A., Maller, J. B., Tukiainen, T., Lek, M., Ward, L. D., Kheradpour, P., Iriarte, et al
2015; 348 (6235): 648-660
- **Reprogramming LCLs to iPSCs Results in Recovery of Donor-Specific Gene Expression Signature** *PLOS GENETICS*
Thomas, S. M., Kagan, C., Pavlovic, B. J., Burnett, J., Patterson, K., Pritchard, J. K., Gilad, Y.
2015; 11 (5)
- **Genomic variation. Impact of regulatory variation from RNA to protein.** *Science*
Battle, A., Khan, Z., Wang, S. H., Mitrano, A., Ford, M. J., Pritchard, J. K., Gilad, Y.
2015; 347 (6222): 664-667

- **Impact of regulatory variation from RNA to protein** *SCIENCE*
Battle, A., Khan, Z., Wang, S. H., Mitrano, A., Ford, M. J., Pritchard, J. K., Gilad, Y.
2015; 347 (6222): 664-667
- **The Genetic and Mechanistic Basis for Variation in Gene Regulation** *PLOS GENETICS*
Pai, A. A., Pritchard, J. K., Gilad, Y.
2015; 11 (1)
- **msCentipede: Modeling Heterogeneity across Genomic Sites and Replicates Improves Accuracy in the Inference of Transcription Factor Binding.** *PLoS one*
Raj, A., Shim, H., Gilad, Y., Pritchard, J. K., Stephens, M.
2015; 10 (9)
- **msCentipede: Modeling Heterogeneity across Genomic Sites and Replicates Improves Accuracy in the Inference of Transcription Factor Binding.** *PLoS one*
Raj, A., Shim, H., Gilad, Y., Pritchard, J. K., Stephens, M.
2015; 10 (9)
- **Methylation QTLs Are Associated with Coordinated Changes in Transcription Factor Binding, Histone Modifications, and Gene Expression Levels** *PLOS GENETICS*
Banovich, N. E., Lan, X., McVicker, G., van de Geijn, B., Degner, J. F., Blischak, J. D., Roux, J., Pritchard, J. K., Gilad, Y.
2014; 10 (9)
- **fastSTRUCTURE: Variational Inference of Population Structure in Large SNP Data Sets** *GENETICS*
Raj, A., Stephens, M., Pritchard, J. K.
2014; 197 (2): 573-U207
- **The deleterious mutation load is insensitive to recent population history.** *Nature genetics*
Simons, Y. B., Turchin, M. C., Pritchard, J. K., Sella, G.
2014; 46 (3): 220-224
- **The functional consequences of variation in transcription factor binding.** *PLoS genetics*
Cusanovich, D. A., Pavlovic, B., Pritchard, J. K., Gilad, Y.
2014; 10 (3)
- **The chromatin architectural proteins HMGD1 and H1 bind reciprocally and have opposite effects on chromatin structure and gene regulation** *BMC GENOMICS*
Nalabothula, N., McVicker, G., Maiorano, J., Martin, R., Pritchard, J. K., Fondufe-Mittendorf, Y. N.
2014; 15
- **The effect of freeze-thaw cycles on gene expression levels in lymphoblastoid cell lines.** *PLoS one*
Çalışkan, M., Pritchard, J. K., Ober, C., Gilad, Y.
2014; 9 (9)
- **Epigenetic modifications are associated with inter-species gene expression variation in primates** *GENOME BIOLOGY*
Zhou, X., Cain, C. E., Myrthil, M., Lewellen, N., Michelini, K., Davenport, E. R., Stephens, M., Pritchard, J. K., Gilad, Y.
2014; 15 (12)
- **Primate Transcript and Protein Expression Levels Evolve Under Compensatory Selection Pressures** *SCIENCE*
Khan, Z., Ford, M. J., Cusanovich, D. A., Mitrano, A., Pritchard, J. K., Gilad, Y.
2013; 342 (6162): 1100-1104
- **Identification of Genetic Variants That Affect Histone Modifications in Human Cells** *SCIENCE*
McVicker, G., van de Geijn, B., Degner, J. F., Cain, C. E., Banovich, N. E., Raj, A., Lewellen, N., Myrthil, M., Gilad, Y., Pritchard, J. K.
2013; 342 (6159): 747-749