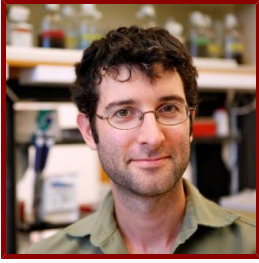


Stanford



Hunter Fraser

Professor of Biology

 Curriculum Vitae available Online

Bio

ACADEMIC APPOINTMENTS

- Professor, Biology
- Member, Bio-X
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

LINKS

- Fraser Lab: <https://web.stanford.edu/group/fraserlab/>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

We study the evolution of complex traits by developing new experimental and computational methods.

Our work brings together quantitative genetics, genomics, epigenetics, and evolutionary biology to achieve a deeper understanding of how genetic variation shapes the phenotypic diversity of life. Our main focus is on the evolution of gene expression, which is the primary fuel for natural selection. Our long-term goal is to be able to introduce complex traits into new species via genome editing.

Teaching

COURSES

2021-22

- The Science and Ethics of Personalized Genomic Medicine: BIO 4N (Win)

2020-21

- Evolutionary Genomics: BIO 332 (Spr)
- Problem solving in infectious disease: BIO 60 (Sum)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Cheyenne Payne

Postdoctoral Faculty Sponsor

Katya Mack, Ban Wang

Doctoral Dissertation Advisor (AC)

Alex Starr

Master's Program Advisor

Adam Behrendt

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

Publications

PUBLICATIONS

- **Primate cell fusion disentangles gene regulatory divergence in neurodevelopment.** *Nature*
Agolia, R. M., Sun, D. n., Birey, F. n., Yoon, S. J., Miura, Y. n., Sabatini, K. n., Pa#ca, S. P., Fraser, H. B.
2021
- **Human-chimpanzee fused cells reveal cis-regulatory divergence underlying skeletal evolution.** *Nature genetics*
Gokhman, D. n., Agolia, R. M., Kinnebrew, M. n., Gordon, W. n., Sun, D. n., Bajpai, V. K., Naqvi, S. n., Chen, C. n., Chan, A. n., Chen, C. n., Petrov, D. A., Ahituv, N. n., Zhang, et al
2021
- **Detecting selection with a genetic cross.** *Proceedings of the National Academy of Sciences of the United States of America*
Fraser, H. B.
2020
- **The somatic mutation landscape of the human body.** *Genome biology*
Garcia-Nieto, P. E., Morrison, A. J., Fraser, H. B.
2019; 20 (1): 298
- **Fine-mapping cis-regulatory variants in diverse human populations.** *eLife*
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2019; 8
- **Tissue-Specific cis-Regulatory Divergence Implicates *eloF* in Inhibiting Interspecies Mating in *Drosophila*.** *Current biology : CB*
Combs, P. A., Krupp, J. J., Khosla, N. M., Bua, D., Petrov, D. A., Levine, J. D., Fraser, H. B.
2018
- **Functional Genetic Variants Revealed by Massively Parallel Precise Genome Editing** *CELL*
Sharon, E., Chen, S. A., Khosla, N. M., Smith, J. D., Pritchard, J. K., Fraser, H. B.
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- **Functional Genetic Variants Revealed by Massively Parallel Precise Genome Editing.** *Cell*
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- **Pooled ChIP-Seq Links Variation in Transcription Factor Binding to Complex Disease Risk** *CELL*
Tehranchi, A. K., Myrthil, M., Martin, T., Hie, B. L., Golan, D., Fraser, H. B.
2016; 165 (3): 730-741
- **Dissecting the Genetic Basis of a Complex cis-Regulatory Adaptation.** *PLoS genetics*
Naranjo, S., Smith, J. D., Artieri, C. G., Zhang, M., Zhou, Y., Palmer, M. E., Fraser, H. B.
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- **Genetic conflict reflected in tissue-specific maps of genomic imprinting in human and mouse.** *Nature genetics*
Babak, T., Deveale, B., Tsang, E. K., Zhou, Y., Li, X., Smith, K. S., Kukurba, K. R., Zhang, R., Li, J. B., van der Kooy, D., Montgomery, S. B., Fraser, H. B.
2015; 47 (5): 544-549
- **Gene expression drives local adaptation in humans** *GENOME RESEARCH*
Fraser, H. B.
2013; 23 (7): 1089-1096
- **Polygenic cis-regulatory adaptaion in the evolution of yeast pathogenicity** *GENOME RESEARCH*
Fraser, H. B., Levy, S., Chavan, A., Shah, H. B., Perez, J. C., Zhou, Y., Siegal, M. L., Sinha, H.
2012; 22 (10): 1930-1939
- **Existing methods are effective at measuring natural selection on gene expression.** *Nature ecology & evolution*
Fraser, H. B.
2022
- **Bacterial Retrons Enable Precise Gene Editing in Human Cells**
Zhao, B.
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- **Transcriptome diversity is a systematic source of variation in RNA-sequencing data.** *PLoS computational biology*
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- **Bacterial Retrons Enable Precise Gene Editing in Human Cells.** *The CRISPR journal*
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- **cis-Regulatory changes in locomotor genes are associated with the evolution of burrowing behavior.** *Cell reports*
Hu, C. K., York, R. A., Metz, H. C., Bedford, N. L., Fraser, H. B., Hoekstra, H. E.
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- **Divergent patterns of selection on metabolite levels and gene expression.** *BMC ecology and evolution*
Kern, A. F., Yang, G. X., Khosla, N. M., Ang, R. M., Snyder, M. P., Fraser, H. B.
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- **GRINS: Genetic elements that recode assembly-line polyketide synthases and accelerate their diversification.** *Proceedings of the National Academy of Sciences of the United States of America*
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- **Lineage-specific selection and the evolution of virulence in the Candida clade.** *Proceedings of the National Academy of Sciences of the United States of America*
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- Tehranchi, A., Hie, B., Dacre, M., Kaplow, I., Pettie, K., Combs, P., Fraser, H. B.
2019; 8
- **Improving Estimates of Compensatory cis-trans Regulatory Divergence** *TRENDS IN GENETICS*
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 - **Tissue-Specific cis-Regulatory Divergence Implicates eIF in Inhibiting Interspecies Mating in Drosophila** *CURRENT BIOLOGY*
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 - **Comparative expression profiling reveals widespread coordinated evolution of gene expression across eukaryotes** *NATURE COMMUNICATIONS*
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- **Discordance of DNA Methylation Variance Between two Accessible Human Tissues.** *Scientific reports*
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