



Julia Salzman

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

Bio

BIO

The Salzman lab views genomic data as a statistical signal processing problem, leveraging tools from statistics, traditional machine learning and deep learning for biological discovery. We have recently introduced a new unifying paradigm, SPLASH (Statistically Primary aLignment Agnostic Sequence Homing), a data-compressive signal extraction that bypasses the historical computational machinery of genomics. Ongoing work extends the scope of this approach, making many problems in genomic sequence analysis easily accessible to computational engineers and statisticians. We are using SPLASH and its sister algorithms to train biological deep learning models at unprecedented scale, and leveraging these models to predict phenotypes and from single cell analyses of human and non-model organisms to drug responses in microbes, and other phenotypes across the tree of life, including in the study of plants, viruses, oceanic systems and their symbioses. The reference-free nature of SPLASH and its sister approaches enable dually the prediction of biological behavior – eg phenotype and attribution of the features responsible for these predictions.

ACADEMIC APPOINTMENTS

- Associate Professor, Department of Biomedical Data Science
- Associate Professor, Biochemistry
- Associate Professor (By courtesy), Statistics
- Associate Professor (By courtesy), Biology
- Member, Bio-X
- Member, Institute for Computational and Mathematical Engineering (ICME)
- Member, Stanford Cancer Institute
- Member, Wu Tsai Neurosciences Institute

HONORS AND AWARDS

- Arc Ignite Investigator, Arc Institute (2023)
- NSF CAREER AWARD, National Science Foundation (2016-2021)
- McCormick-Gabilan Fellowship, Stanford University (2015)
- Alfred P. Sloan Research Fellow, Alfred P. Sloan Foundation (2014)
- Baxter Faculty Scholar Award, Baxter Foundation (2014)
- Pathway to Independence (K99/R00) Award, National Institutes of Health (2012-present)
- Research Grant, National Science Foundation (2009-2012)
- Magna Cum Laude, Princeton University (2002)

PROFESSIONAL EDUCATION

- Ph. D., Stanford University , Statistics (2007)
- A. B., Princeton University , Mathematics (2002)

LINKS

- Lab Website: <http://med.stanford.edu/salzmanlab.html>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

statistical computational biology focusing on splicing, cancer and microbes

Teaching

COURSES

2023-24

- Statistical Genomics for Planetary Health: Oceans, Plants, Microbes and Humans: BIODS 228 (Aut)
- Workshop in Biostatistics: BIODS 260C, STATS 260C (Spr)

2022-23

- Workshop in Biostatistics: BIODS 260A, STATS 260A (Aut)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Isabel Delwel, Yannick Lee-Yow, Julie F. Wang

Postdoctoral Faculty Sponsor

Marie Claire Harrison

Doctoral Dissertation Co-Advisor (AC)

Chester Yu

Doctoral (Program)

Oana Enache, Holly McCann

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biochemistry (Phd Program)
- Biomedical Data Science (Phd Program)
- Biophysics (Phd Program)
- Cancer Biology (Phd Program)

Publications

PUBLICATIONS

- **Cell types of origin of the cell-free transcriptome.** *Nature biotechnology*
Vorperian, S. K., Moufarrej, M. N., Tabula Sapiens Consortium, Quake, S. R., Jones, R. C., Karkaniyas, J., Krasnow, M., Pisco, A. O., Quake, S. R., Salzman, J., Yosef, N., Bulthaupt, B., Brown, P., et al
2022

- **RNA splicing programs define tissue compartments and cell types at single cell resolution.** *eLife*
Olivieri, J. E., Deghannasiri, R., Wang, P. L., Jang, S., de Morree, A., Tan, S. Y., Ming, J., Ruohao Wu, A., Tabula Sapiens Consortium, Quake, S. R., Krasnow, M. A., Salzman, J.
2021; 10
- **Specific splice junction detection in single cells with SICILIAN.** *Genome biology*
Deghannasiri, R., Olivieri, J. E., Damljanovic, A., Salzman, J.
2021; 22 (1): 219
- **Circular RNA Expression: Its Potential Regulation and Function in Abdominal Aortic Aneurysms** *OXIDATIVE MEDICINE AND CELLULAR LONGEVITY*
Han, Y., Zhang, H., Bian, C., Chen, C., Tu, S., Guo, J., Wu, Y., Boeckler, D., Zhang, J.
2021; 2021: 9934951
- **High-throughput SARS-CoV-2 and host genome sequencing from single nasopharyngeal swabs.** *medRxiv : the preprint server for health sciences*
Gorzynski, J. E., De Jong, H. N., Amar, D., Hughes, C. R., Ioannidis, A., Bierman, R., Liu, D., Tanigawa, Y., Kistler, A., Kamm, J., Kim, J., Cappello, L., Neff, et al
2020
- **Molecular sampling at logarithmic rates for next-generation sequencing.** *PLoS computational biology*
Horn, C., Salzman, J.
2019; 15 (12): e1007537
- **Improved detection of gene fusions by applying statistical methods reveals oncogenic RNA cancer drivers.** *Proceedings of the National Academy of Sciences of the United States of America*
Deghannasiri, R., Freeman, D. E., Jordanski, M., Hsieh, G. L., Damljanovic, A., Lehnert, E., Salzman, J.
2019
- **Hyperammonemia after capecitabine associated with occult impairment of the urea cycle.** *Cancer medicine*
Chu, G., Salzman, J.
2019
- **Discovery of gene regulatory elements through a new bioinformatics analysis of haploid genetic screens.** *PLoS one*
Patel, B. B., Lebensohn, A. M., Pusapati, G. V., Carette, J. E., Salzman, J. n., Rohatgi, R. n.
2019; 14 (1): e0198463
- **Ambiguous splice sites distinguish circRNA and linear splicing in the human genome.** *Bioinformatics (Oxford, England)*
Deghannasiri, R., Szabo, L., Salzman, J.
2018
- **ciRS-7 exonic sequence is embedded in a long non-coding RNA locus** *PLOS GENETICS*
Barrett, S. P., Parker, K. R., Horn, C., Mata, M., Salzman, J.
2017; 13 (12): e1007114
- **Statistical algorithms improve accuracy of gene fusion detection.** *Nucleic acids research*
Hsieh, G., Bierman, R., Szabo, L., Lee, A. G., Freeman, D. E., Watson, N., Sweet-Cordero, E. A., Salzman, J.
2017
- **Circular RNA biogenesis can proceed through an exon-containing lariat precursor.** *eLife*
Barrett, S. P., Wang, P. L., Salzman, J.
2015; 4
- **Statistically based splicing detection reveals neural enrichment and tissue-specific induction of circular RNA during human fetal development** *Genome biology*
Szabo1, L.
2015
- **Extensive site-directed mutagenesis reveals interconnected functional units in the alkaline phosphatase active site.** *eLife*
Sunden, F., Peck, A., Salzman, J., Ressler, S., Herschlag, D.

2015; 4

- **Circular RNA Is Expressed across the Eukaryotic Tree of Life.** *PLoS one*
Wang, P. L., Bao, Y., Yee, M., Barrett, S. P., Hogan, G. J., Olsen, M. N., Dinneny, J. R., Brown, P. O., Salzman, J.
2014; 9 (3)
- **Best permutation analysis** *JOURNAL OF MULTIVARIATE ANALYSIS*
Rajaratnam, B., Salzman, J.
2013; 121: 193-223
- **Association between living environment and human oral viral ecology** *ISME JOURNAL*
Robles-Sikisaka, R., Ly, M., Boehm, T., Naidu, M., Salzman, J., Pride, D. T.
2013; 7 (9): 1710-1724
- **Cell-type specific features of circular RNA expression.** *PLoS genetics*
Salzman, J., Chen, R. E., Olsen, M. N., Wang, P. L., Brown, P. O.
2013; 9 (9)
- **Improved discovery of molecular interactions in genome-scale data with adaptive model-based normalization.** *PLoS one*
Salzman, J., Klass, D. M., Brown, P. O.
2013; 8 (1)
- **A penalized likelihood approach for robust estimation of isoform expression** *eprint arXiv:1310.0379*
Jiang, H., Salzman, .
2013
- **Statistical properties of an early stopping rule for resampling-based multiple testing** *BIOMETRIKA*
Jiang, H., Salzman, J.
2012; 99 (4): 973-980
- **Extensive Gene-Specific Translational Reprogramming in a Model of B Cell Differentiation and Abl-Dependent Transformation** *PLOS ONE*
Bates, J. G., Salzman, J., May, D., Garcia, P. B., Hogan, G. J., McIntosh, M., Schlissel, M. S., Brown, P. O.
2012; 7 (5)
- **Evidence of a robust resident bacteriophage population revealed through analysis of the human salivary virome** *ISME JOURNAL*
Pride, D. T., Salzman, J., Haynes, M., Rohwer, F., Davis-Long, C., White, R. A., Loomer, P., Armitage, G. C., Relman, D. A.
2012; 6 (5): 915-926
- **Widespread mRNA Association with Cytoskeletal Motor Proteins and Identification and Dynamics of Myosin-Associated mRNAs in *S. cerevisiae*** *PLOS ONE*
Casolari, J. M., Thompson, M. A., Salzman, J., Champion, L. M., Moerner, W. E., Brown, P. O.
2012; 7 (2)
- **Circular RNAs Are the Predominant Transcript Isoform from Hundreds of Human Genes in Diverse Cell Types** *PLOS ONE*
Salzman, J., Gawad, C., Wang, P. L., Lacayo, N., Brown, P. O.
2012; 7 (2)
- **Comparisons of CRISPRs and viromes in human saliva reveal bacterial 3 adaptations to salivary viruses** *Environmental Microbiology*
Pride, D.
2012
- **ESRRA-C11orf20 Is a Recurrent Gene Fusion in Serous Ovarian Carcinoma** *PLOS BIOLOGY*
Salzman, J., Marinelli, R. J., Wang, P. L., Green, A. E., Nielsen, J. S., Nelson, B. H., Drescher, C. W., Brown, P. O.
2011; 9 (9)
- **Statistical Modeling of RNA-Seq Data** *STATISTICAL SCIENCE*
Salzman, J., Jiang, H., Wong, W. H.
2011; 26 (1): 62-83
- **Analysis of streptococcal CRISPRs from human saliva reveals substantial sequence diversity within and between subjects over time** *GENOME RESEARCH*

Pride, D. T., Sun, C. L., Salzman, J., Rao, N., Loomer, P., Armitage, G. C., Banfield, J. F., Relman, D. A.
2011; 21 (1): 126-136

- **Proteome-Wide Search Reveals Unexpected RNA-Binding Proteins in *Saccharomyces cerevisiae*** *PLOS ONE*
Tsvetanova, N. G., Klass, D. M., Salzman, J., Brown, P. O.
2010; 5 (9)
- **Reliable concurrent calling of multiple genetic alleles and 24-chromosome ploidy without embryo freezing using parental support™ technology (PS)** *Fertility and Sterility*
Rabinowitz, M.
2008
- **Limits on the ability of quantum states to convey classical messages** *JOURNAL OF THE ACM*
Nayak, A., Salzman, J.
2006; 53 (1): 184-206
- **An improved upper bound for the pebbling threshold of the n-path** *Discrete Mathematics*
Wierman, A.
2004