

Stanford



Julia Salzman

Assistant Professor of Biochemistry and of Biomedical Data Science

Bio

ACADEMIC APPOINTMENTS

- Assistant Professor, Biochemistry
- Assistant Professor, Biomedical Data Science
- Member, Bio-X
- Member, Stanford Cancer Institute
- Faculty Fellow, Stanford ChEM-H
- Member, Wu Tsai Neurosciences Institute

HONORS AND AWARDS

- 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

Circular RNA regulation and function; computational and experimental approaches

Teaching

COURSES

2019-20

- Topics in Biomedical Data Science: Large-scale inference: BIODS 215 (Win)

2018-19

- Developing an Original Research Proposal: BIOC 360 (Sum)
- Introduction to Analysis of RNA Sequence Data: BIOC 239 (Sum)

2017-18

- Biochemistry Bootcamp: BIOC 202 (Aut)
- Biological Macromolecules: BIOC 241, BIOE 241, BIOPHYS 241, SBIO 241 (Win)
- Topics in Biomedical Data Science: Large-scale inference: BIODS 215 (Win)

2016-17

- Topics in Biomedical Data Science: Large-scale inference: BIODS 215 (Spr)

STANFORD ADVISEES

Med Scholar Project Advisor

Ramon Lorenzo Labitigan

Doctoral Dissertation Reader (AC)

Scott Longwell, Chris Ritchie

Orals Chair

Caitlin Roake

Postdoctoral Faculty Sponsor

Roosbeh Dehghannasiri

Doctoral Dissertation Advisor (AC)

Rob Bierman, Elisabeth Meyer, Julia Olivieri

Doctoral Dissertation Co-Advisor (AC)

Jason Qin

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biochemistry (Phd Program)
- Biomedical Informatics (Phd Program)
- Biophysics (Phd Program)
- Cancer Biology (Phd Program)

Publications

PUBLICATIONS

- **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*
Dehghannasiri, 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., Rohatgi, R.
2019; 14 (1): e0198463
- **Ambiguous splice sites distinguish circRNA and linear splicing in the human genome.** *Bioinformatics (Oxford, England)*
Dehghannasiri, 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*
Szabo, 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., Dinnyen, 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, J.
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