

Stanford



Roozbeh Dehghannasiri

Instructor, Biomedical Data Science

Curriculum Vitae available Online

Bio

ACADEMIC APPOINTMENTS

- Instructor, Biomedical Data Science

HONORS AND AWARDS

- Clinical Data Science Fellow, National Library of Medicine - National Institutes of Health (9/2019 - 9/2020)
- Cancer Systems Biology Scholars Fellow, National Institutes of Health - National Cancer Institute (8/2017 - 8/2019)

PATENTS

- Shahram Shirani, Roozbeh Dehghannasiri. "United States Patent 9,294,711 De-interlacing and frame rate upconversion for high definition video", McMaster University, Mar 22, 2016

LINKS

- Google Scholar: https://scholar.google.com/citations?hl=en&user=zqRN1ZEAAAAJ&view_op=list_works&sortby=pubdate

Publications

PUBLICATIONS

- **The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans.** *Science (New York, N.Y.)*
Jones, R. C., Karkanias, J., Krasnow, M. A., Pisco, A. O., Quake, S. R., Salzman, J., Yosef, N., Bulthaup, B., Brown, P., Harper, W., Hemenez, M., Ponnusamy, R., Salehi, et al
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- **The SpliZ generalizes 'percent spliced in' to reveal regulated splicing at single-cell resolution.** *Nature methods*
Olivieri, J. E., Dehghannasiri, R., Salzman, J.
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- **RNA splicing programs define tissue compartments and cell types at single cell resolution.** *eLife*
Olivieri, J. E., Dehghannasiri, 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*
Dehghannasiri, R., Olivieri, J. E., Damjanovic, A., Salzman, J.
2021; 22 (1): 219
- **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., Damjanovic, A., Lehnert, E., Salzman, J.
2019

- **Ambiguous splice sites distinguish circRNA and linear splicing in the human genome** *BIOINFORMATICS*
Dehghannasiri, R., Szabo, L., Salzman, J.
2019; 35 (8): 1263–68
- **Interstitial macrophages are a focus of viral takeover and inflammation in COVID-19 initiation in human lung.** *The Journal of experimental medicine*
Wu, T. T., Travaglini, K. J., Rustagi, A., Xu, D., Zhang, Y., Andronov, L., Jang, S., Gillich, A., Dehghannasiri, R., Martinez-Colon, G. J., Beck, A., Liu, D. D., Wilk, et al
2024; 221 (6)
- **An organism-wide atlas of hormonal signaling based on the mouse lemur single-cell transcriptome.** *Nature communications*
Liu, S., Ezran, C., Wang, M. F., Li, Z., Awayan, K., Long, J. Z., De Vlaminck, I., Wang, S., Epelbaum, J., Kuo, C. S., Terrien, J., Krasnow, M. A., Ferrell, et al
2024; 15 (1): 2188
- **SPLASH2 provides ultra-efficient, scalable, and unsupervised discovery on raw sequencing reads.** *bioRxiv : the preprint server for biology*
Kokot, M., Dehghannasiri, R., Baharav, T., Salzman, J., Deorowicz, S.
2023
- **Large-scale benchmarking of circRNA detection tools reveals large differences in sensitivity but not in precision.** *Nature methods*
Vromman, M., Anckaert, J., Bortoluzzi, S., Buratin, A., Chen, C., Chu, Q., Chuang, T., Dehghannasiri, R., Dieterich, C., Dong, X., Flicek, P., Gaffo, E., Gu, et al
2023
- **TGS1 impacts snRNA 3'-end processing, ameliorates survival motor neuron-dependent neurological phenotypes in vivo and prevents neurodegeneration.** *Nucleic acids research*
Chen, L., Roake, C. M., Maccallini, P., Bavasso, F., Dehghannasiri, R., Santonicola, P., Mendoza-Ferreira, N., Scatolini, L., Rizzuti, L., Esposito, A., Gallotta, I., Francia, S., Cacchione, et al
2022
- **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., Karkanias, J., Krasnow, M., Pisco, A. O., Quake, S. R., Salzman, J., Yosef, N., Bulthaup, B., Brown, P., et al
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- **ReadZS detects cell type-specific and developmentally regulated RNA processing programs in single-cell RNA-seq.** *Genome biology*
Meyer, E., Chaung, K., Dehghannasiri, R., Salzman, J.
2022; 23 (1): 226
- **SICILIAN: Precise and unbiased detection of gene fusions at the resolution of single cells using improved statistical modeling**
Dehghannasiri, R., Olivier, J., Salzman, J.
AMER ASSOC CANCER RESEARCH.2020
- **Towards precise and cost-effective fusion discovery: A landscape of druggable gene fusions across TCGA cancers**
Dehghannasiri, R., Jordanski, M., Freeman, D. E., Hsieh, G. L., Howard, J. M., Lehnert, E., Salzman, J.
AMER ASSOC CANCER RESEARCH.2019
- **An experimental design framework for Markovian gene regulatory networks under stationary control policy.** *BMC systems biology*
Dehghannasiri, R., Shahrokh Esfahani, M., Dougherty, E. R.
2018; 12 (Suppl 8): 137
- **A Bayesian robust Kalman smoothing framework for state-space models with uncertain noise statistics** *EURASIP JOURNAL ON ADVANCES IN SIGNAL PROCESSING*
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2018
- **Sequential Experimental Design for Optimal Structural Intervention in Gene Regulatory Networks Based on the Mean Objective Cost of Uncertainty** *CANCER INFORMATICS*
Imani, M., Dehghannasiri, R., Braga-Neto, U. M., Dougherty, E. R.
2018; 17: 1176935118790247
- **Optimal Bayesian Kalman Filtering With Prior Update** *IEEE TRANSACTIONS ON SIGNAL PROCESSING*
Dehghannasiri, R., Esfahani, M., Qian, X., Dougherty, E. R.

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● **Intrinsically Bayesian robust Karhunen-Loève compression** *Signal Processing*

Dehghannasiri, R., Qian, X., Dougherty, E. R.
2018; 144: 311-322

● **Intrinsically Bayesian Robust Kalman Filter: An Innovation Process Approach** *IEEE TRANSACTIONS ON SIGNAL PROCESSING*

Dehghannasiri, R., Esfahani, M. S., Dougherty, E. R.
2017; 65 (10): 2531-2546

● **Optimal experimental design for materials discovery** *COMPUTATIONAL MATERIALS SCIENCE*

Dehghannasiri, R., Xue, D., Balachandran, P. V., Yousefi, M. R., Dalton, L. A., Lookman, T., Dougherty, E. R.
2017; 129: 311-322

● **Optimal experimental design in the context of canonical expansions** *IET Signal Processing*

Dehghannasiri, R., Qian, X., Dougherty, E. R.
2017; 11 (8): 942-951

● **Optimal Objective-Based Experimental Design for Uncertain Dynamical Gene Networks with Experimental Error.** *IEEE/ACM transactions on computational biology and bioinformatics*

Mohsenizadeh, D., Dehghannasiri, R., Dougherty, E.
2016: -?

● **Efficient experimental design for uncertainty reduction in gene regulatory networks** *BMC BIOINFORMATICS*

Dehghannasiri, R., Yoon, B., Dougherty, E. R.
2015; 16

● **Optimal Experimental Design for Gene Regulatory Networks in the Presence of Uncertainty** *IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS*

Dehghannasiri, R., Yoon, B., Dougherty, E. R.
2015; 12 (4): 938-950