

Roozbeh Dehghannasiri

GENERAL INFORMATION *Born:* Oct. 1987, Tehran, Iran.
Citizenship: United States

CONTACT INFORMATION Salzman Lab
Stanford University
Medical School Office Building X325
Stanford, CA 94305
Email: rdehghan@stanford.edu

ACADEMIC EXPERIENCE **Stanford University, Stanford, CA** **Sep. 2017 - present**
Postdoctoral Research Fellow (Cancer Systems Biology and Clinical Data Science Fellow)
Departments of Biomedical Data Science and Biochemistry
Mentor: Professor Julia Salzman
Research Topic: Statistical approaches to study RNA function at scale in the disease and healthy tissue

Texas A&M University, College Station, TX **Sep. 2016 - Jul. 2017**
Postdoctoral Research Associate
Department of Electrical and Computer Engineering, and Center for Bioinformatics and Genomic Systems Engineering
Mentor: Professor Edward R. Dougherty
Research Topic: Optimal Experimental Design and Signal Estimation Under Uncertainty

EDUCATION **Texas A&M University, College Station, TX** **Sep. 2012 - Aug. 2016**
Doctor of Philosophy (GPA: 4/4)
Electrical and Computer Engineering
Advisor: Professor Edward R. Dougherty
Thesis title: Optimal experimental design in the context of objective-based uncertainty quantification

McMaster University, Hamilton, Canada **Sep. 2010 - Aug. 2012**
Master of Applied Science (GPA: A+/A+)
Electrical and Computer Engineering
Advisor: Professor Shahram Shirani
Thesis title: Advanced image and video interpolation techniques based on nonlocal-means filtering

University of Tehran, Tehran, Iran **Sep. 2006 - Aug. 2010**
Bachelor of Applied Science (GPA: 17.72/20)
Electrical and Computer Engineering
Advisor: Professor Ali Olfat
Thesis title: Equalization and detection of the M-PSK modulation order using adaptive and information theoretic approaches

RESEARCH INTERESTS Single-cell RNA-Seq, High-Throughput Sequencing Data Analysis, Machine Learning,

Alternative Splicing, Cancer Systems Biology, Biostatistics, Computational Biology, Bayesian Statistics.

PATENT

Shahram Shirani and **Roozbeh Dehghannasiri**, “De-interlacing and Frame Rate Up-conversion for High Definition Applications”, *US Patent 9,294,711*, Issued March 2016.

MAIN PUBLICATIONS

1– **Tabula Sapiens Consortium**. “The Tabula Sapiens: A multiple-organ, single-cell transcriptomic atlas of humans”, *Science*, Vol. 376, No. 6594, (2022).

2– Olivieri*, J.E., **Dehghannasiri***, **R.** and Salzman, J. “The SpliZ generalizes ‘Percent Spliced In’ to reveal regulated splicing at single-cell resolution”. *Nature methods*, 19(3), pp.307-310 (2022).

3– **Dehghannasiri, R.**, Olivieri, J.E., Damljjanovic, A. and Salzman, J., “Specific splice junction detection in single cells with SICILIAN”. *Genome Biology*, 22(1), pp.1-13 (2021).

4– Olivieri*, J.E., **Dehghannasiri***, **R.**, Wang, P.L., Jang, S., De Morree, A., Tan, S.Y., Ming, J., Wu, A.R., Quake, S.R., Krasnow, M.A. and Salzman, J., “RNA splicing programs define tissue compartments and cell types at single-cell resolution”. *eLife*, 10, p.e70692. (2021).

5– **Dehghannasiri, R.**, Freeman, D.E., Jordanski, M., Hsieh, G.L., Damljjanovic, A., Lehnert, E., and Salzman, J., “Improved Detection of Gene Fusions by Applying Statistical Methods Reveals Oncogenic RNA Cancer Drivers”, *Proceedings of the National Academy of Sciences*, Vol. 116, No. 31, 15524-15533, July 2019.

6– **Dehghannasiri, R.**, Szabo, L. and Salzman, J., “Ambiguous Splice Sites Distinguish CircRNA and Linear Splicing in the Human Genome”, *Bioinformatics*, Vol. 35, No. 8, 1263-1268, 2018.

7– **Dehghannasiri, R.**, Esfahani, M.S., and Dougherty, E.R., “An Experimental Design Framework for Markovian Gene Regulatory Networks Under Stationary Control Policy”, *BMC Systems Biology*, 12 (Suppl 8):137 2018.

8– **Dehghannasiri, R.**, Qian, X., and Dougherty, E.R., “A Bayesian Robust Kalman Smoothing Framework for State-Space Models with Uncertain Noise Statistics”, *EURASIP Journal on Advances in Signal Processing*, Vol. 2018, No. 1, 55, 2018.

9– **Dehghannasiri, R.**, Esfahani, M.S., Qian, X., and Dougherty, E.R., “Optimal Bayesian Kalman Filtering with Prior Update”, *IEEE Transactions on Signal Processing*, Vol. 66, No. 8, 1982-1996, 2018.

10– **Dehghannasiri, R.**, Qian, X., and Dougherty, E.R., “Intrinsically Bayesian Robust Karhunen-Löve Compression”, *Signal Processing*, Vol. 144, 311-322, 2018.

11– Mohsenizadeh, D. N.*, **Dehghannasiri, R.***, and Dougherty, E.R., “Optimal Objective-Based Experimental Design for Uncertain Dynamical Gene Networks with Experimental Error”, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, Vol. 15, No. 1, 218-230, 2018.

12– **Dehghannasiri, R.**, Qian, X., and Dougherty, E.R., “Optimal Experimental Design in the Context of Canonical Expansions”, *IET Signal Processing*, Vol. 11, No. 8, 942-951, 2017.

13– **Dehghannasiri, R.**, Esfahani, M.S., and Dougherty, E.R., “Intrinsically Bayesian Robust Kalman Filter: An Innovation Process Approach”, *IEEE Transactions on Signal Processing*, Vol. 65, No. 10, 2531-2546, 2017.

14– **Dehghannasiri, R.**, Xue, D., Balachandran, P.V., Yousefi, M.R., Dalton, L.A., Lookman, T. and Dougherty, E.R., “Optimal Experimental Design for Materials Discovery”, *Computational Materials Science*, Vol. 129, 311-322, 2017.

15– **Dehghannasiri, R.**, Yoon, B.-J., and Dougherty, E.R., “Efficient Experimental Design for Uncertainty Reduction in Gene Regulatory Networks”, *BMC Bioinformatics*, 16(Suppl 13):S2, 2015.

16– **Dehghannasiri, R.**, Yoon, B.-J., and Dougherty, E.R., “Optimal Experimental Design for Gene Regulatory Networks in the Presence of Uncertainty”, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, Vol. 12, No. 4, 938-950, 2015.

OTHER PUBLICATIONS

1–Meyer, E., Chaung, K., **Dehghannasiri, R.** and Salzman, J., 2022. “ReadZS detects cell type-specific and developmentally regulated RNA processing programs in single-cell RNA-seq”. *Genome Biology*, 23(1), pp.1-28, (2022).

2– Chen, L., Roake, C.M., Maccallini, P., Bavasso, F., **Dehghannasiri, R.**, Santonicola, P., *et. al.*, “TGS1 controls snRNA 3’end processing, prevents neurodegeneration and ameliorates SMN-dependent neurological phenotypes in vivo”, *Nucleic Acids Research*, Vol. 50, No. 21, pp. 12400-12424, (2022).

3– Zhao, J., Wang, G., Ming, J., Lin, Z., Wang, Y., **The Tabula Microcebus Consortium**, Wu, A.R. and Yang, C., “Adversarial domain translation networks for integrating large-scale atlas-level single-cell datasets”. *Nature Computational Science*, 2(5), pp.317-330, (2022).

4– Vorperian, S.K., Moufarrej, M.N., **The Tabula Sapiens Consortium**, and Quake, S.R., “Cell types of origin of the cell-free transcriptome”. *Nature Biotechnology*, pp.1-7 (2022).

5– Imani, M., **Dehghannasiri, R.**, Braga-Neto, U., and Dougherty, E.R., “Sequential Experimental Design for Optimal Structural Intervention in Gene Regulatory Networks Based on the Mean Objective Cost of Uncertainty”, *Cancer Informatics*, Vol. 17, 1-10, Jan. 2018.

SUBMITTED PAPERS

1– Kokot*, M., **Dehghannasiri*, R.**, Baharav, T. Z., Salzman, J., and Deorowicz, S. “NOMAD2 provides ultra-efficient, scalable, and unsupervised discovery on raw sequencing reads”. *bioRxiv*, (2023).

2– **Dehghannasiri, R.**, Henderson, G., Bierman, R., Chaung, K., Baharav, T. Z., Wang, P. L., and Salzman, J. (2022). Unsupervised reference-free inference reveals unrecognized regulated transcriptomic complexity in human single cells. *bioRxiv*, (2022).

3– Vromman, M., Anckaert, J., Bortoluzzi, S., Buratin, A., Chen, C.Y., Chu, Q., Chuang, T.J., **Dehghannasiri, R.**, *et. al.*, “Large-scale benchmarking of circRNA detection tools reveals large differences in sensitivity but not in precision”, *bioRxiv*, (2022).

- 4– Tabula Microcebus Consortium, Ezran, C., Liu, S., Ming, J., Guethlein, L.A., Wang, M.F., **Dehghannasiri, R.**, *et. al.*, “Mouse lemur transcriptomic atlas elucidates primate genes, physiology, disease, and evolution”, *bioRxiv*, (2022).
- 5– Wu, T.T.H., Travaglini, K.J., Rustagi, A., Xu, D., Zhang, Y., Jang, S.K., Gillich, A., **Dehghannasiri, R.**, *et. al.*, “Activated interstitial macrophages are a predominant target of viral takeover and focus of inflammation in COVID-19 initiation in human lung”, *bioRxiv*, (2022).
- 6– **Tabula Microcebus Consortium**, “Tabula Microcebus: a transcriptomic cell atlas of mouse lemur, an emerging primate model organism,” *bioRxiv*, (2021).

**REFEREED
CONFERENCE
PUBLICATIONS**

- 1– **R. Dehghannasiri**, J. Olivieri, and J. Salzman, “SICILIAN: Precise and unbiased detection of gene fusions at the resolution of single cells using improved statistical modeling”, *AACR Annual Meeting*, June. 2020.
- 2– **R. Dehghannasiri**, M. Jordanski, and J. Salzman, “DEEPEST-Fusion: Pan-cancer statistical gene fusion discovery and characterization”, *RNA Society Annual Conference*, June 2019, Krakow, Poland.
- 3– **R. Dehghannasiri**, M. Jordanski, D. E. Freeman, G. L. Hsieh, J. M. Howard, E. Lehnert, and J. Salzman, “Towards precise and cost-effective fusion discovery: A landscape of druggable gene fusions across TCGA cancers”, *AACR Annual Meeting*, Apr. 2019, Atlanta, GA.
- 4– **R. Dehghannasiri**, X. Qian, and E.R. Dougherty, “Robust smoothing for state-space models with unknown noise statistics”, *IEEE Asilomar Conference on Signals, Systems, and Computers*, Nov. 2018, Pacific Grove, CA.
- 5– **R. Dehghannasiri**, M.S. Esfahani, X. Qian, and E.R. Dougherty, “Bayesian Kalman filtering in the presence of unknown noise statistics using factor graphs”, *IEEE Asilomar Conference on Signals, Systems, and Computers*, Nov. 2017, Pacific Grove, CA.
- 6– **R. Dehghannasiri**, X. Qian, and E.R. Dougherty, “An objective-based experimental design framework for signal processing in the context of canonical expansions”, *IEEE Asilomar Conference on Signals, Systems, and Computers*, Nov. 2017, Pacific Grove, CA.
- 7– **R. Dehghannasiri**, X. Qian, and E.R. Dougherty, “Optimal experimental design in canonical expansions with applications to signal compression”, *IEEE Global Conference on Signal and Information Processing (GlobalSIP)*, Dec. 2016, Washington, D.C.
- 8– **R. Dehghannasiri**, M.S. Esfahani, and E.R. Dougherty, “A Bayesian framework for robust Kalman filtering under uncertain noise statistics”, *IEEE Asilomar Conference on Signals, Systems, and Computers*, Nov. 2016, Pacific Grove, CA.
- 9– **R. Dehghannasiri**, M.S. Esfahani, and E.R. Dougherty, “Inference of nonlinear ODE-based gene regulatory networks via intrinsically Bayesian robust Kalman filtering”, *ACM International Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB)*, Oct. 2016, Seattle, WA.
- 10– D. N. Mohsenizadeh*, **R. Dehghannasiri***, and E.R. Dougherty, “Optimal dynamics uncertainty reduction in gene networks in the presence of experimental error”, *IEEE-EMBS International Conference on Biomedical and Health Informatics (BHI)*,

Feb. 2016, Las Vegas, NV.

11– D. N. Mohsenizadeh, **R. Dehghannasiri**, and E.R. Dougherty, “An experimental design to reduce dynamics uncertainty in genomic networks”, *ACM International Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB)*, Sep. 2015, Atlanta, GA.

12– **R. Dehghannasiri**, B.-J. Yoon, and E.R. Dougherty, “Computationally efficient experimental design strategy for reducing gene network uncertainty”, *IEEE Global Conference on Signal and Information Processing (GlobalSIP)*, Dec. 2014, Atlanta, GA.

13– **R. Dehghannasiri**, “Video de-interlacing using asymmetric nonlocal-means filtering”, *IEEE Asilomar Conference on Signals, Systems, and Computers*, Nov. 2014, Pacific Grove, CA.

14– **R. Dehghannasiri**, S. M. Reza Soroushmehr, and S. Shirani, “Frame rate up-conversion using nonparametric estimator”, *IEEE International Conference on Image Processing (ICIP)*, Oct. 2014, Paris, France.

15– **R. Dehghannasiri**, B.-J. Yoon, and E.R. Dougherty, “Designing experiments for optimal reduction of uncertainty in gene regulatory networks”, *IEEE International Workshop on Genomics and Signal Processing and Statistics (GENSIPS)*, Nov. 2013, Houston, TX.

16– **R. Dehghannasiri** and S. Shirani, “A view interpolation method without explicit disparity estimation”, *IEEE International Conference on Multimedia and Expo Workshops (ICMEW)*, Jul. 2013, San Jose, CA.

17– **R. Dehghannasiri** and S. Shirani, “A novel de-interlacing method based on locally-adaptive nonlocal-means”, *IEEE Asilomar Conference on Signals, Systems, and Computers*, Nov. 2012, Pacific Grove, CA.

POSTERS

R. Dehghannasiri, J. Olivieri, and J. Salzman, “Statistical algorithms reveal regulated alternative splicing at single-cell resolution”, *GRC Single-Cell Genomics*, Les Diablerets, Switzerland, May 2022.

R. Dehghannasiri, J. Olivieri, and J. Salzman, “Statistical detection of splice sites that drive differential alternative splicing in single cells”, *Bay Area RNA Club*, Virtual, Dec. 2020.

R. Dehghannasiri, M. Jordanski, and J. Salzman, “Towards precise and cost-effective fusion discovery: A landscape of druggable gene fusions across TCGA cancers”, *Systems Approaches to Cancer Biology*, Portland, OR, May 2019.

R. Dehghannasiri, M. Jordanski and J. Salzman, “Towards precise and cost-effective Fusion Discovery: A Landscape of Druggable Gene Fusions Across TCGA Cancers”, *Stanford Biochemistry Retreat*, Santa Cruz, CA, October 2018.

R. Dehghannasiri and J. Salzman, “Highly sensitive and specific statistical approach for accurate detection of gene fusions and cryptic splicing events using RNA-seq”, *International Conference on Intelligent Biology and Medicine (ICIBM 2018)*, Los Angeles, CA, June 2018.

R. Dehghannasiri, M. Jordanski, R. Bierman, E. Lehnert, G. Hsieh, and J. Salzman, “Towards precise and cost-effective fusion discovery: A statistical fusion detection algorithm with a cloud-based implementation”, *6th Annual Stanford Cancer Systems Biology Symposium*, Stanford, CA, May 2018.

R. Dehghannasiri, B.-J. Yoon, and E.R. Dougherty, “Efficient experimental design for uncertainty reduction in gene regulatory networks”, *12th Annual Conference of the MidSouth Computational Biology and Bioinformatics Society (MCBIOS)*, Little Rock, AR, March 2015.

R. Dehghannasiri, B.-J. Yoon, and E.R. Dougherty, “Designing experiments for optimal reduction of uncertainty in gene regulatory networks”, *1st Texas A&M ENG-LIFE Workshop*, College Station, TX, November 2013.

RESEARCH EXPERIENCE

Postdoctoral Research Associate, Salzman Lab, Department of Biochemistry, Stanford University

Advisor: Professor Julia Salzman

Sep. 2017 - Present

Statistical approaches to elucidate RNA function in healthy tissues and cancer:

- Unsupervised and reference-free study of transcriptomic complexity in human single cells
- Developed statistical methods for accurate detection of RNA splice junctions, regulated alternative splicing, and RNA processing in single cells
- Built the first catalog of regulated RNA splicing across the human body
- Developed statistical methods for gene fusion detection and quantification in tumors
- Systematic and pan-cancer analysis of gene fusions with new discoveries for cancer driving signatures
- Statistical quantification of splice site degeneracy in eukaryotic transcriptomes
- Developed computational methods for *de novo* detection of cryptic splice site

Research Assistant, Genomic Signal Processing Lab, Texas A&M University

Advisor: Professor Edward R. Dougherty

Aug. 2012 - Aug. 2017

Worked on uncertainty analysis in dynamical models under a Bayesian framework:

- Uncertainty quantification and optimal experimental design for gene regulatory networks
- Bayesian robust filtering and signal compression for uncertain signal models

Bioinformatics Analyst, Institute for Plant Genomics and Biotechnology, Texas A&M Agrilife

Advisor: Professor Patricia Klein

Sep. 2012 - Aug. 2013

Studied next gene sequencing and wrote scripts used for bioinformatic analysis.

Research Assistant, Multimedia Signal Processing Lab, McMaster University

Advisor: Professor Shahram Shirani

Sep. 2010 - Aug. 2012

Worked on different high definition image and video processing applications

HONORS AND AWARDS	Clinical Data Science Fellowship, Department of Biomedical Data Science, Stanford University	August 2019
	NCI Invited Speaker, Mathematical Oncology Meeting, Portland, OR	May 2019
	Best Paper Award at the International Conference on Intelligent Biology and Medicine (ICIBM), Los Angeles, CA	June 2018
	Second Best Poster Presentation Award at the 6th Annual Stanford CCSB Symposium	May 2018
	Stanford Cancer Systems Biology Scholars Program Fellowship, Center for Cancer Systems Biology, Stanford University	Mar. 2017
	NSF Student Travel Award	Dec. 2014, Mar. 2016, Oct. 2016
	Dwight Look College of Engineering Graduate Climate Travel Grant	Sep. 2015
	Best Paper Award at the 12th Annual MCBIOS Conference	Mar. 2015
	Dwight Look College of Engineering Travel Grant	Nov. 2013, Mar. 2015
	McMaster Outstanding Thesis Research Award	Aug. 2012
	Faculty of Engineering Scholarship as an exceptional student in term, University of Tehran	Fall 2006-Spring 2010
	Ranked 3rd among Electrical and Computer Engineering students, with focus on Telecommunications Engineering, University of Tehran	Spring 2008-Spring 2010
	Iranian Ministry of Energy Award, honored and awarded by the Iran's Minister of Energy	Sep. 2006
TEACHING EXPERIENCE	Ranked 168th among approximately 500000 participants in the nationwide Iranian university entrance exam in Mathematics and Physics field for B.Sc. degree	Summer 2006
	Teaching Assistant, Computer Aided Engineering, Professor Dongmei Zhao, McMaster University	Winter 2012
	Teaching Assistant, Signals & Systems, Professor Terry Todd, McMaster University	Fall 2011
	Teaching Assistant, Calculus I, Professor Shahriar Heshmati, University of Tehran	Fall 2009
PROFESSIONAL AFFILIATIONS	Teaching Assistant, Calculus I, Professor Shahriar Heshmati, University of Tehran	Fall 2008
	American Association of Cancer Research (Associate Member) IEEE	

ACM SIGBio
McMaster Alumni Association
The Association of Former Students of Texas A&M