

Stanford



Mohammad Shahrokh Esfahani

Instructor, Medicine - Oncology

Bio

BIO

My expertise is in developing machine learning tools for high dimensional data. In particular, I develop Bayesian models, where 'prior knowledge', from external sources or inherent to the data set in hand, can be converted into mathematical terms (i.e. prior probabilities). I have recently focused on analyzing genetic and epigenetic signals in cell-free DNA assays. Traditional (computational) methods in cancer genomics are limited when signal to noise ratio is ultra-low which is often the case in cfDNA analyses. Therefore, there is a growing need to develop novel and more powerful methods to overcome this limitation.

ACADEMIC APPOINTMENTS

- Instructor, Medicine - Oncology

HONORS AND AWARDS

- T32 Training Program Fellowship, Stanford Medicine (Department of Radiation Oncology) (09/2018-)
- Cancer Systems Biology Program Fellowship (NIH-R25), Stanford University (09/2015-08/2017)
- NCI Speaker/Travel Award, NCI (Systems Analysis of Cancer Biology conference) (04/2016)

PROFESSIONAL EDUCATION

- BSc, University of Tehran, Iran, Electrical Engineering (2007)
- MSc, Sharif University of Technology, Iran, Electrical Engineering (2009)
- PhD, Texas A&M University, Electrical Engineering, Machine Learning (2014)

LINKS

- Personal Website: <https://sites.google.com/stanford.edu/shahrokh>
- Twitter: <https://mobile.twitter.com/mohamshah>
- Google Scholar: https://scholar.google.com/citations?hl=en&user=3LpGRA8AAAAJ&view_op=list_works&sortby=pubdate
- CIRI Website: <http://ciri.stanford.edu>
- CLiP Website: <https://clip.stanford.edu/>
- DIREct: <https://direct.stanford.edu/>

Research & Scholarship

RESEARCH INTERESTS

- Data Sciences

Publications

PUBLICATIONS

- **Integrating genomic features for non-invasive early lung cancer detection** *NATURE*
Chabon, J. J., Hamilton, E. G., Kurtz, D. M., Esfahani, M. S., Moding, E. J., Stehr, H., Schroers-Martin, J., Nabet, B. Y., Chen, B., Chaudhuri, A. A., Liu, C., Hui, A. B., Jin, et al
2020
- **Noninvasive Early Identification of Therapeutic Benefit from Immune Checkpoint Inhibition.** *Cell*
Nabet, B. Y., Esfahani, M. S., Moding, E. J., Hamilton, E. G., Chabon, J. J., Rizvi, H. n., Steen, C. B., Chaudhuri, A. A., Liu, C. L., Hui, A. B., Almanza, D. n., Stehr, H. n., Gojenola, et al
2020
- **Dynamic Risk Profiling Using Serial Tumor Biomarkers for Personalized Outcome Prediction.** *Cell*
Kurtz, D. M., Esfahani, M. S., Scherer, F., Soo, J., Jin, M. C., Liu, C. L., Newman, A. M., Duhrsen, U., Huttman, A., Casasnovas, O., Westin, J. R., Ritgen, M., Botcher, et al
2019
- **Functional significance of U2AF1 S34F mutations in lung adenocarcinomas.** *Nature communications*
Esfahani, M. S., Lee, L. J., Jeon, Y. J., Flynn, R. A., Stehr, H. n., Hui, A. B., Ishisoko, N. n., Kildebeck, E. n., Newman, A. M., Bratman, S. V., Porteus, M. H., Chang, H. Y., Alizadeh, et al
2019; 10 (1): 5712
- **Effect of separate sampling on classification accuracy.** *Bioinformatics*
Shahrokh Esfahani, M., Dougherty, E. R.
2014; 30 (2): 242-250
- **Short Diagnosis-to-Treatment Interval Is Associated With Higher Circulating Tumor DNA Levels in Diffuse Large B-Cell Lymphoma.** *Journal of clinical oncology : official journal of the American Society of Clinical Oncology*
Alig, S. n., Macaulay, C. W., Kurtz, D. M., Dührsen, U. n., Hüttmann, A. n., Schmitz, C. n., Jin, M. C., Sworder, B. J., Garofalo, A. n., Shahrokh Esfahani, M. n., Nabet, B. Y., Soo, J. n., Scherer, et al
2021: JCO2002573
- **Evaluating upfront high-dose consolidation after R-CHOP for follicular lymphoma by clinical and genetic risk models.** *Blood advances*
Alig, S. n., Jurinovic, V. n., Shahrokh Esfahani, M. n., Haebe, S. n., Passerini, V. n., Hellmuth, J. C., Gaitzsch, E. n., Keay, W. n., Tahiri, N. n., Zoellner, A. n., Rosenwald, A. n., Klapper, W. n., Stein, et al
2020; 4 (18): 4451-62
- **An Atlas of Clinically-Distinct Tumor Cellular Ecosystems in Diffuse Large B Cell Lymphoma**
Steen, C. B., Luca, B. A., Esfahani, M., Nabet, B. Y., Sworder, B., Farshidfar, F., Shamardani, K., Kurtz, D. M., Liu, C., Advani, R. H., Natkunam, Y., Myklebust, J., Diehn, et al
AMER SOC HEMATOLOGY.2019
- **Broad Genomic Profiling of Bronchoalveolar Lavage Fluid in Lung Cancer**
Nair, V., Hui, A., Chabon, J., Esfahani, M., Stehr, H., Nabet, B., Benson, J., Chaudhuri, A., Zhou, L., Ayers, K., Bedi, H., Ramsey, M., Van Wert, et al
ELSEVIER SCIENCE INC.2019: S747-S748
- **Validated Limited Gene Predictor For Cervical Cancer Lymph Node Metastases**
Bloomstein, J., Von Eyben, R., Rankin, E., Wang-Chiang, J., David, S., Esfahani, M., Kidd, E. A.
ELSEVIER SCIENCE INC.2019: S50
- **Determining cell type abundance and expression from bulk tissues with digital cytometry** *NATURE BIOTECHNOLOGY*
Newman, A. M., Steen, C. B., Liu, C., Gentles, A. J., Chaudhuri, A. A., Scherer, F., Khodadoust, M. S., Esfahani, M. S., Luca, B. A., Steiner, D., Diehn, M., Alizadeh, A. A.
2019; 37 (7): 773-+
- **Detection and Surveillance of Bladder Cancer Using Urine Tumor DNA** *CANCER DISCOVERY*
Dudley, J. C., Schroers-Martin, J., Lazzareschi, D., Shi, W., Chen, S. B., Esfahani, M. S., Trivedi, D., Chabon, J. J., Chaudhuri, A. A., Stehr, H., Liu, C., Lim, H., Costa, et al

2019; 9 (4): 500–509

- **Circulating DNA for Molecular Response Prediction, Characterization of Resistance Mechanisms and Quantification of CAR T-Cells during Axicabtagene Ciloleucef Therapy** *American Society of Hematology*
Sworder, B., Kurtz, D. M., Macaulay, C., Frank, M. J., Alig, S., Garofalo, A., Sahaf, B., Esfahani, M. S., Spiegel, J. Y., Oak, J., Beygi, S., Jin, M. C., Chabon, et al
2019
- **Circulating tumor DNA analysis for detection of minimal residual disease after chemoradiotherapy for localized esophageal cancer.** *Gastroenterology*
Azad, T. D., Chaudhuri, A. A., Fang, P. n., Qiao, Y. n., Esfahani, M. S., Chabon, J. J., Hamilton, E. G., Yang, Y. D., Lovejoy, A. n., Newman, A. M., Kurtz, D. M., Jin, M. n., Schroers-Martin, et al
2019
- **Towards Non-Invasive Classification of DLBCL Genetic Subtypes By Ctdna Profiling** *American Society of Hematology*
Esfahani, M. S., Alig, S., Kurtz, D. M., Soo, J., Jin, M. C., Macaulay, C., Craig, A., Garofalo, A., Steen, C. B., Scherer, F., Sworder, B., Diehn, M., Alizadeh, et al
2019
- **An experimental design framework for Markovian gene regulatory networks under stationary control policy**
Dehghannasiri, R., Esfahani, M., Dougherty, E. R.
BMC.2018
- **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
- **Distinct Chromatin Accessibility Profiles of Lymphoma Subtypes Revealed By Targeted Cell Free DNA Profiling**
Mehrmohamadi, M., Esfahani, M. S., Soo, J., Scherer, F., Schroers-Martin, J. G., Chen, B., Kurtz, D. M., Hamilton, E., Liu, C., Diehn, M., Alizadeh, A. A.
AMER SOC HEMATOLOGY.2018
- **Noninvasive Genotyping and Monitoring of Classical Hodgkin Lymphoma**
Jin, M. C., Schroers-Martin, J. G., Kurtz, D. M., Buedts, L., Esfahani, M. S., Macaulay, C., Sworder, B., Soo, J., Glover, C., Roschewski, M., Wilson, W. H., Duhrsen, U., Huettmann, et al
AMER SOC HEMATOLOGY.2018
- **Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma** *JOURNAL OF CLINICAL ONCOLOGY*
Kurtz, D. M., Scherer, F., Jin, M. C., Soo, J., Craig, A. M., Esfahani, M., Chabon, J. J., Stehr, H., Liu, C., Tibshirani, R., Maeda, L. S., Gupta, N. K., Khodadoust, et al
2018; 36 (28): 2845–+
- **Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma.** *Journal of clinical oncology : official journal of the American Society of Clinical Oncology*
Kurtz, D. M., Scherer, F., Jin, M. C., Soo, J., Craig, A. F., Esfahani, M. S., Chabon, J. J., Stehr, H., Liu, C. L., Tibshirani, R., Maeda, L. S., Gupta, N. K., Khodadoust, et al
2018: JCO2018785246
- **Optimal Bayesian Kalman Filtering With Prior Update** *IEEE TRANSACTIONS ON SIGNAL PROCESSING*
Dehghannasiri, R., Esfahani, M., Qian, X., Dougherty, E. R.
2018; 66 (8): 1982–96
- **Detection and surveillance of bladder cancer using urine tumor DNA.** *Cancer discovery*
Dudley, J. C., Schroers-Martin, J. n., Lazzareschi, D. V., Shi, W. Y., Chen, S. B., Esfahani, M. S., Trivedi, D. n., Chabon, J. J., Chaudhuri, A. A., Stehr, H. n., Liu, C. L., Lim, H. n., Costa, et al
2018
- **Clinical Impact of Somatic Copy Number Alterations in Circulating Tumor DNA from Diverse Lymphoma Subtypes**
Jin, M., Kurtz, D. M., Esfahani, M. S., Soo, J., Craig, A., Scherer, F., Stehr, H., Schroers-Martin, J. G., Bangs, C., Cherry, A., Natkunam, Y., Roschewski, M., Wilson, et al
AMER SOC HEMATOLOGY.2017
- **Noninvasive detection of clinically relevant copy number alterations in diffuse large B-cell lymphoma.**
Jin, M. C., Kurtz, D., Esfahani, M., Scherer, F., Craig, A. M., Soo, J., Khodadoust, M., Saganty, R., Chabon, J. J., Schroers-Martin, J., Stehr, H., Advani, R. H., Rossi, et al

AMER SOC CLINICAL ONCOLOGY.2017

- **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
- **Early detection of molecular residual disease in localized lung cancer by circulating tumor DNA profiling.** *Cancer discovery*
Chaudhuri, A. A., Chabon, J. J., Lovejoy, A. F., Newman, A. M., Stehr, H. n., Azad, T. D., Khodadoust, M. S., Esfahani, M. S., Liu, C. L., Zhou, L. n., Scherer, F. n., Kurtz, D. M., Say, et al
2017
- **Constructing Pathway-based Priors Within a Gaussian Mixture Model for Bayesian Regression and Classification.** *IEEE/ACM transactions on computational biology and bioinformatics*
Boluki, S. n., Shahrokh Esfahani, M. n., Qian, X. n., Dougherty, E. R.
2017
- **Incorporating biological prior knowledge for Bayesian learning via maximal knowledge-driven information priors.** *BMC bioinformatics*
Boluki, S. n., Esfahani, M. S., Qian, X. n., Dougherty, E. R.
2017; 18 (Suppl 14): 552
- **Development and Validation of Biopsy-Free Genotyping for Molecular Subtyping of Diffuse Large B-Cell Lymphoma** *58th Annual Meeting and Exposition of the American-Society-of-Hematology*
Scherer, F., Kurtz, D. M., Newman, A. M., Esfahani, M. S., Craig, A., Stehr, H., Lovejoy, A. F., Chabon, J. J., Liu, C. L., Zhou, L., Glover, C., Visser, B. C., Poultides, et al
AMER SOC HEMATOLOGY.2016
- **Distinct biological subtypes and patterns of genome evolution in lymphoma revealed by circulating tumor DNA** *SCIENCE TRANSLATIONAL MEDICINE*
Scherer, F., Kurtz, D. M., Newman, A. M., Stehr, H., Craig, A. F., Esfahani, M. S., Lovejoy, A. F., Chabon, J. J., Klass, D. M., Liu, C. L., Zhou, L., Glover, C., Visser, et al
2016; 8 (364)
- **Circulating tumour DNA profiling reveals heterogeneity of EGFR inhibitor resistance mechanisms in lung cancer patients** *NATURE COMMUNICATIONS*
Chabon, J. J., Simmons, A. D., Lovejoy, A. F., Esfahani, M. S., Newman, A. M., Haringsma, H. J., Kurtz, D. M., Stehr, H., Scherer, F., Karlovich, C. A., Harding, T. C., Durkin, K. A., Otterson, et al
2016; 7
- **Noninvasive Cancer Classification Using Diverse Genomic Features in Circulating Tumor DNA**
Esfahani, M., Newman, A. M., Scherer, F., Tibshirani, R., Diehn, M., Alizadeh, A. A., ACM
ASSOC COMPUTING MACHINERY.2016: 516
- **An Optimization-Based Framework for the Transformation of Incomplete Biological Knowledge into a Probabilistic Structure and Its Application to the Utilization of Gene/Protein Signaling Pathways in Discrete Phenotype Classification** *IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS*
Esfahani, M. S., Dougherty, E. R.
2015; 12 (6): 1304-1321
- **Discrete optimal Bayesian classification with error-conditioned sequential sampling** *PATTERN RECOGNITION*
Broumand, A., Esfahani, M. S., Yoon, B., Dougherty, E. R.
2015; 48 (11): 3766-3782
- **Incorporation of Biological Pathway Knowledge in the Construction of Priors for Optimal Bayesian Classification** *IEEE-ACM TRANSACTIONS ON COMPUTATIONAL BIOLOGY AND BIOINFORMATICS*
Esfahani, M. S., Dougherty, E. R.
2014; 11 (1): 202-218
- **Classifier design given an uncertainty class of feature distributions via regularized maximum likelihood and the incorporation of biological pathway knowledge in steady-state phenotype classification** *PATTERN RECOGNITION*
Esfahani, M. S., Knight, J., Zollanvari, A., Yoon, B., Dougherty, E. R.
2013; 46 (10): 2783-2797
- **Identification and Analysis of the First 2009 Pandemic H1N1 Influenza Virus from US Feral Swine** *ZOOZOSES AND PUBLIC HEALTH*

Clavijo, A., Nikooienejad, A., Esfahani, M. S., Metz, R. P., Schwartz, S., Atashpaz-Gargari, E., DeLiberto, T. J., Lutman, M. W., Pedersen, K., Bazan, L. R., KOSTER, L. G., Jenkins-Moore, M., Swenson, et al
2013; 60 (5): 327-335

- **Effect of Separate Sampling on Classification and the Minimax Criterion**

Esfahani, M., Dougherty, E. R., IEEE
IEEE.2013: 72–73

- **Probabilistic reconstruction of the tumor progression process in gene regulatory networks in the presence of uncertainty** *8th Annual Conference of the MidSouth-Computational-Biology-and-Bioinformatics-Society (MCBIOS)*

Esfahani, M. S., Yoon, B., Dougherty, E. R.
BIOMED CENTRAL LTD.2011