Stanford



Mohammad Shahrokh Esfahani

Assistant Professor of Radiation Oncology (Radiation and Cancer Biology)

Radiation Oncology - Radiation and Cancer Biology

CONTACT INFORMATION

- **Administrative Contact**

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Bio

BIO

I lead a computational oncology laboratory that develops machine learning and statistical methods for high-dimensional genomics, with particular expertise in Bayesian and uncertainty-aware modeling to integrate prior biological knowledge with large-scale datasets.

Our research centers on liquid biopsy analytics—especially cell-free DNA (cfDNA)—to noninvasively quantify genetic and epigenetic states relevant to cancer detection, monitoring, and tumor evolution. We developed EPIC-seq, a fragmentomics-based method that uses cfDNA fragmentation patterns to infer regulatory activity and gene expression programs, providing a scalable framework for epigenetic profiling from blood.

A core methodological focus of the lab is enabling reliable inference in extremely low signal-to-noise settings that are typical of cfDNA and early-stage disease. We build robust, interpretable models and benchmarking frameworks that support clinical translation, with the long-term aim of democratizing access to sensitive, minimally invasive cancer diagnostics.

ACADEMIC APPOINTMENTS

- Assistant Professor-Research, Radiation Oncology - Radiation and Cancer Biology
- Member, Bio-X

HONORS AND AWARDS

- Abstract Achievement Award, American Society of Hematology (2019)
- T32 Training Program Fellowship, Stanford Medicine (Department of Radiation Oncology) (2018-2020)
- 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

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

- BSc, University of Tehran, Iran , Electrical Engineering (2007)

PATENTS

- David M. Kurtz, Arash Ash Alizadeh, Maximilian Diehn, Mohammad Shahrokh Esfahani. "United States Patent US17/646,621 Methods to Assess Clinical Outcome Based Upon Updated Probabilities and Treatments Thereof"
- Maximilian Diehn, Arash Ash Alizadeh, Jacob J Chabon, David M Kurtz, Mohammad Shahrokh Esfahani. "United States Patent US17/822,016 Methods of Analyzing Cell Free Nucleic Acids and Applications Thereof"
- Mohammad Shahrokh Esfahani, Maximilian Diehn, Arash Ash Alizadeh, Mahya Mehrmohamadi. "United States Patent US17/980,254 System and method for gene expression and tissue of origin inference from cell-free dna"

LINKS

- Lab Website: https://med.stanford.edu/esfahanilab.html
- Twitter: https://mobile.twitter.com/mohamshah
- Google Scholar: https://scholar.google.com/citations?hl=en&user=3LpGRA8AAAAJ&view_op=list_works&sortby=pubdate

Research & Scholarship

RESEARCH INTERESTS

- Data Sciences

CURRENT RESEARCH AND SCHOLARLY INTERESTS

My laboratory develops computational and statistical methods to extract clinically actionable information from cancer genomic data, particularly circulating cell-free DNA. Our research lies at the intersection of computational oncology, cancer genomics, liquid biopsy, and machine learning, with the goal of enabling earlier diagnosis, more precise risk assessment, and personalized treatment.

A central focus of our work is detecting and characterizing cancer from blood. We develop methods for early cancer detection, minimal residual disease assessment, and longitudinal monitoring of treatment response and resistance. Rather than relying exclusively on tumor mutations, we integrate complementary signals encoded in cell-free DNA, including fragmentation patterns, copy-number alterations, epigenomic organization, inferred gene expression, immune-receptor clonality, and telomere biology. These approaches are designed to recover tumor and host biology even when the fraction of tumor-derived DNA is extremely low.

We also develop machine-learning methods that integrate genomic, transcriptomic, pathological, and clinical data. Current areas of investigation include dynamic modeling of cancer evolution and therapeutic resistance, interpretable classification of hematologic malignancies, cell-type-resolved analysis of tumors and plasma, and teacher-student approaches that transfer information from richly profiled research cohorts to routinely available clinical assays.

Our work spans solid tumors and hematologic malignancies and emphasizes rigorous validation in clinically annotated patient cohorts. The broader objective is to create robust, interpretable, and clinically deployable computational tools that transform routinely generated molecular data into actionable insights for cancer detection and treatment.

Teaching

COURSES

2026-27

- Liquid Biopsy: Cell-Free Nucleic Acids and the Future of Precision Oncology: BIOS 428 (Spr)

2025-26

- Liquid Biopsy: Cell-Free Nucleic Acids and the Future of Precision Oncology: BIOS 428 (Spr)

STANFORD ADVISEES

Postdoctoral Faculty Sponsor

Amirsaman Ashtari, Alexander Koepp, Seraphina Shi

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Cancer Biology (PhD Program)

Publications

PUBLICATIONS

- **Distinct Hodgkin lymphoma subtypes defined by noninvasive genomic profiling.** *Nature*
  Alig, S. K., Esfahani, M. S., Garofalo, A., Li, M. Y., Rossi, C., Flerlage, T., Flerlage, J. E., Adams, R., Binkley, M. S., Shukla, N., Jin, M. C., Olsen, M., Telenius, et al
  2023

- **Inferring gene expression from cell-free DNA fragmentation profiles.** *Nature biotechnology*
  Esfahani, M. S., Hamilton, E. G., Mehrmohamadi, M., Nabet, B. Y., Alig, S. K., King, D. A., Steen, C. B., Macaulay, C. W., Schultz, A., Nesselbush, M. C., Soo, J., Schroers-Martin, J. G., Chen, et al
  2022

- **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., Huttmann, A., Casasnovas, O., Westin, J. R., Ritgen, M., Bottcher, 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

- **Clonal hematopoiesis and cytopenias following CAR19 therapy.** *Nature genetics*
  Hamilton, M. P., Phillips, N., Noordenbos, T., Boegeholz, J., Sugio, T., Sworder, B. J., Alig, S. K., Good, Z., Schroers-Martin, J. G., Tamaresis, J., Esfahani, M. S., Lu, Y., Olsen, et al
  2026

- **Enhanced cfDNA methylation profiling by detection and correction of jagged ends.** *Nature methods*
  Wang, R., Hamilton, E. G., Almanza, D., Bonilla, R., Sugio, T., Hui, A., Tian, F., Phillips, N. A., Liu, C. L., Yoo, C. H., Alig, S., Rossi, C., Juul, et al
  2026

- **Urine cell-free RNA for bladder cancer detection and treatment response prediction.** *Nature medicine*
  Liu, K. J., Shi, W. Y., Nesselbush, M. C., Phillips, N. A., Mach, K. E., Luca, B., Bajpai, R. K., Jabara, I., Cheng, J. C., Sugio, T., Shukla, N., Shen, E. C., Koh, et al

2026

- **Multidimensional Characterization of Tumor-Immune Architecture Reveals Clinically Relevant Classic Hodgkin Lymphoma Subtypes.** *Cancer discovery*
  Aoki, T., Duns, G., Rai, S., Jiang, A., Lytle, A., Yin, Y., Kishida, M., Yu Li, M., Lee, C., Smorra, D., Hilton, L. K., Healy, S., Alig, et al
  2026

- **Field-effect-informed urine liquid biopsy for bladder cancer.** *Cell*
  Shi, W. Y., Liu, K. J., Esfahani, M. S., Mach, K. E., Phillips, N. A., Almanza, D., Bajpai, R. K., Schroers-Martin, J. G., Trabanino, L., Lee, T. J., La, V., Rodriguez, G., Holton, et al
  2026

- **Loss of payload sensitivity and other mechanisms of resistance to T-DXd in HER2-mutant NSCLC: implications for subsequent responsiveness to HER2 TKIs.** *Journal of thoracic oncology : official publication of the International Association for the Study of Lung Cancer*
  Nilsson, M. B., Le, X., Poteete, A., Yu, X., He, J., Huang, Q., Shibata, Y., Liu, X., Moran, C., Alizadeh, A. A., Diehn, M., Wakelee, H., Almanza, et al
  2026

- **Integrating ctDNA Analysis and Radiomics for Dynamic Risk Assessment in Localized Lung Cancer.** *Cancer discovery*
  Moding, E. J., Shahrokh Esfahani, M., Jin, C., Hui, A. B., Nabet, B. Y., Liu, Y., Chabon, J. J., Binkley, M. S., Kurtz, D. M., Hamilton, E. G., Chaudhuri, A. A., Liu, C. L., Li, et al
  2025: OF1-OF21

- **Direct Method for Estimating the Fraction of T and B/Plasma Cell-Derived DNA**
  Sugio, T., Esfahani, M., Jun, S., Sworder, B. J., Hamilton, M. P., Hosoya, H., Olsen, M., Kang, X., Liu, C., Tian, F., Miklos, D. B., Kurtz, D., Diehn, et al
  ELSEVIER.2024: 2223-2224

- **Integrating Genomic & Transcriptomic Features for Noninvasive Detection, Characterization, and Monitoring of T-Cell Lymphomas**
  Sugio, T., Nesselbush, M., Shukla, N., Garofalo, A., Mutter, J. A., Esfahani, M., Alig, S. K., Shi, S., Noordenbos, T., Hamilton, M. P., Rossi, C., Tian, F., Liu, et al
  ELSEVIER.2024: 454-455

- **Ultrasensitive Circulating Tumor DNA MRD Status Predicts Treatment Failure & Complements PET/CT throughout Treatment for Early and Advanced Stage Classic Hodgkin Lymphoma**
  Boegeholz, J., Rossi, C., Goldstein, J. S., Alig, S. K., Garofalo, A., Esfahani, M., Schroers-Martin, J. G., Liu, C., Olsen, M., Kang, X., Tian, F., Kurtz, D., Andre, et al
  ELSEVIER.2024: 565-566

- **Inferred Gene Expression By Cell-Free DNA Profiling Allows Noninvasive Lymphoma Classification**
  Mutter, J. A., Esfahani, M., Schroers-Martin, J., Alig, S. K., Hamilton, M. P., Sworder, B. J., Tessoulin, B., Boegeholz, J., Flerlage, T., Flerlage, J. E., Binkley, M. S., Sugio, T., Rossi, et al
  AMER SOC HEMATOLOGY.2023

- **Determinants of resistance to engineered T cell therapies targeting CD19 in large B cell lymphomas.** *Cancer cell*
  Sworder, B. J., Kurtz, D. M., Alig, S. K., Frank, M. J., Shukla, N., Garofalo, A., Macaulay, C. W., Shahrokh Esfahani, M., Olsen, M. N., Hamilton, J., Hosoya, H., Hamilton, M., Spiegel, et al
  2022

- **Circulating Tumor DNA Profiling for Detection, Risk Stratification, and Classification of Brain Lymphomas.** *Journal of clinical oncology : official journal of the American Society of Clinical Oncology*
  Mutter, J. A., Alig, S. K., Esfahani, M. S., Lauer, E. M., Mitschke, J., Kurtz, D. M., Kühn, J., Bleul, S., Olsen, M., Liu, C. L., Jin, M. C., Macaulay, C. W., Neidert, et al
  2022: JCO2200826

- **Genomic Profiling of Bronchoalveolar Lavage Fluid in Lung Cancer.** *Cancer research*
  Nair, V. S., Hui, A. B., Chabon, J. J., Shahrokh Esfahani, M., Stehr, H., Nabet, B. Y., Zhou, L., Chaudhuri, A. A., Benson, J. A., Ayers, K., Bedi, H., Ramsey, M. C., Van Wert, et al
  2022

- **Enhanced detection of minimal residual disease by targeted sequencing of phased variants in circulating tumor DNA.** *Nature biotechnology*
  Kurtz, D. M., Soo, J., Co Ting Keh, L., Alig, S., Chabon, J. J., Sworder, B. J., Schultz, A., Jin, M. C., Scherer, F., Garofalo, A., Macaulay, C. W., Hamilton, E. G., Chen, et al
  2021

- **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

- **The landscape of tumor cell states and ecosystems in diffuse large B cell lymphoma.** *Cancer cell*
  Steen, C. B., Luca, B. A., Esfahani, M. S., Azizi, A., Sworder, B. J., Nabet, B. Y., Kurtz, D. M., Liu, C. L., Khameneh, F., Advani, R. H., Natkunam, Y., Myklebust, J. H., Diehn, et al
  2021

- **Chromatin accessibility patterns in cell-free DNA reveal tumor heterogeneity**
  Esfahani, M., Mehrmohamadi, M., Steen, C. B., Hamilton, E. G., King, D. A., Soo, J., Macaulay, C., Jin, M., Kurtz, D. M., Nabet, B., Moding, E., Chabon, J., Newman, et al
  AMER ASSOC CANCER RESEARCH.2020

- **A mid-chemoradiation dynamic risk model integrating tumor features and ctDNA analysis for lung cancer outcome prediction.**
  Moding, E. J., Esfahani, M., Nabet, B., Liu, Y., Chabon, J. J., He, J., Qiao, Y., Xu, T., Yao, L., Gandhi, S., Liao, Z. X., Das, M., Ramchandran, et al
  AMER SOC CLINICAL ONCOLOGY.2020

- **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 Ciloleucel 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. F. 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

- **Constructing Pathway-based Priors Within a Gaussian Mixture Model for Bayesian Regression and Classification.** *IEEE/ACM transactions on computational biology and bioinformatics*

  Boluki, S., Shahrokh Esfahani, M., Qian, X., Dougherty, E. R.

  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. F. 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

- **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., Poultsides, 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** *ZOONOSES 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