BIOGRAPHICAL SKETCH

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NAME: Irajizad, Ehsan

eRA COMMONS USER NAME (credential, e.g., agency login): EIrajizad

POSITION TITLE: Assistant Professor

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Sharif University of Technology, Iran	BA	09/2014	Industrial Engineering
University of Houston, USA	PhD	12/2018	Computational Biology

A. Personal Statement

I am an Assistant Professor in the Department of Biostatistics at the University of Texas MD Anderson Cancer Center. My current research focuses on the development and application of advanced, computationally intensive artificial intelligence algorithms for integration of highly dimensional multi-omic datasets in order to uncover novel biomarkers for cancer risk assessment and early detection. An additional focus of my work has been on developing novel quantitative methods as well as artificial intelligence techniques that integrate clinical, epidemiological, and multi-platform high-dimensional genetic information to develop personalized risk prediction models for cancer etiology and clinical outcomes. To-date, I have published over 31 peer-reviewed manuscripts including publications in *Nature Communications, Journal of National Cancer Institute, Clinical Cancer Research, Cell Reports Medicine, Gastroenterology*, and the *Journal of Clinical Oncology.* I am also an active collaborator for several funded projects including two NCI-funded Clinical Validation Centers (CVC) for Lung and Pancreas Cancer, for which I am leading efforts related to biomarker modeling and validation and establishment of thresholds for clinical decision making. Additionally, I serve on the Early Detection Research Network (EDRN) statistical working team, working with NCI investigators to generate stable and reproducible artificial intelligence models, design of effective clinical trials, and statistical considerations for an NCI-initiated feasibility study (Vanguard trial) that aims to evaluate the performance of multi-cancer early detection assays for reducing cancer-associated mortality.

Ongoing projects that I would like to highlight include:

1U01CA271888-01
Hanash (PI), Role: Biostatistician/ Artificail intelligence expert
9/1/22-8/31/27
Clinical Validation Center for Lung Cancer Early Detection

U01CA239522
Schmidt (PI) / Zhang (MPI), Role: Biostatistician/ Artificail intelligence expert
4/1/21-3/31/26
Longitudinal Proteomic and Metabolomic Predictors of Pancreatic Cyst Malignant Progression and Early State Pancreatic Cancer

U01CA200468
Maitra (PI), Role: Biostatistician/ Artificail intelligence expert
9/1/22-8/31/27
Clinical Validation Center for Pancreatic Cancer Early Detection

Citations:

1. A four-marker panel (4MP) for pulmonary nodule stratification. Reference #: MDA20-166
2. A plasma polyamine signature in combination with CA125 to predict early-stage ovarian cancer. Reference #: MDA20-130
3. Citrullinated Proteins as Diagnostic Markers, Vaccination Targets, And Therapeutic Targets in Cancer. Reference #: MDA20-088
4. Combination of protein and metabolite biomarkers for the detection of multiple common cancers (PanCancer). Reference #: MDA21-038

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2022 - present	Assistant Professor, The University of Texas M.D. Anderson Cancer Center, Houston, TX
2021 - 2022	Computational scientist, University of Texas MD Anderson
2019 - 2021	Postdoctoral Researcher, University of Texas MD Anderson
2016 - Present	Member, Biophysical Society
2015 - 2018	Teacher Research Assistant, University of Houston, Texas

Honors

2016 - 2017	Scholarship, Houston Endowment Scholarship

Teaching Experiences

2022-Present	*Mentoring 3 PhD students and 1 postdocterol fellow,* University of Texas MD Anderson Cancer Center
2019	*Advanced Machine learning,* Southern Methodist University

C. Contribution to Science

1) **Application of Artificial Intelligence for biomarker discovery:** A major focus has been towards applying advanced statistical modeling and artificial intelligence to discover biomarkers and establish biomarker combination rules that have utility for early detection and risk assessment of cancer. Seminal findings include a neural network blood-based metabolite panel for distinguishing ovarian cancer from benign pelvic masses that improve the positive predictive performance of well-established ovarian malignancy risk algorithm (ROMA), a metabolite-panel for prediciting response to neoadjuvant chemotherapy in triple-negative breast cancer, and a metabolite panel consisting of microbial- and non-microbial metabolites that can identify individuals at high risk of developing pancreatic cancer. I was the lead statistician on all of these studies.
   a. **Irajizad, E**., Han, C.Y., Celestino, J., Wu, R., Murage, E., Spencer, R., Dennison, J.B., Vykoukal, J., Long, J.P., Do, K.A. and Drescher, C., 2022. A blood-based metabolite panel for distinguishing ovarian cancer from benign pelvic masses. Clinical Cancer Research. PMID: 36037307
   b. **Irajizad, E.**, Wu, R., Vykoukal, J., Murage, E., Spencer, R., Dennison, J.B., Moulder, S., Ravenberg, E., Lim, B., Litton, J. and Tripathym, D., 2022. Application of Artificial Intelligence to

Plasma Metabolomics Profiles to Predict Response to Neoadjuvant Chemotherapy in Triple-Negative Breast Cancer. Frontiers in Artificial Intelligence, 5.

c. **Irajizad, E.,** Kenney, A., Tang, T., Vykoukal, J., Wu, R., Murage, E., ... & Fahrmann, J. F. (2023). A blood-based metabolomic signature predictive of risk for pancreatic cancer. Cell Reports Medicine, 4(9).

2) Biomarker Validation Efforts: Validation of biomarkers for cancer diagnostics is a pivitol step towards clinical realization. To this end, examples of my validation efforts include a 4-marker protein panel that together with a lung cancer risk prediction model based on subject characteristics ($\text{PLCO}_{\text{m2012}}$) yields improved lung cancer risk assessment compared to current United States Preventive Service Task Force (USPSTF) criteria for lung cancer screening and a 3-marker protein panel for lead-time detection of pancreatic cancer in the pre-clinical setting. I led or co-led statistical efforts for each of these studies.

a. **Irajizad, E.,** Fahrmann, J. F., Marsh, T., Vykoukal, J., Dennison, J. B., Long, J. P., ... & Ostrin, E. J. (2023). Mortality Benefit of a Blood-Based Biomarker Panel for Lung Cancer on the Basis of the Prostate, Lung, Colorectal, and Ovarian Cohort. Journal of Clinical Oncology, 41(27), 4360-4368.
b. Fahrmann JF, Marsh T*, **Irajizad, E***, Patel N, Murage E, Vykoukal J, Dennison JB, Do KA, Ostrin E, Spitz MR, Lam S, Shete S, Meza R, Tammemagi MC, Feng Z, Hanash S. A blood-based panel for personalized lung cancer risk assessment. *J Clin Oncol.* (2022) [Epub ahead of print]. PMID: 34995129. ***co-shared authorship**
c. Fahrmann, J.F., Schmidt, C.M., Mao, X., **Irajizad, E.**, Loftus, M., Zhang, J., Patel, N., Vykoukal, J., Dennison, J.B., Long, J.P., Do, K.A., Hanash, S., 2021. Lead-time trajectory of CA19-9 as an anchor marker for pancreatic cancer early detection. Gastroenterology, 160(4), pp.1373-1383.
d. Fahrmann, J.F., **Irajizad, E.**, Kobayashi, M., Vykoukal, J., Dennison, J.B., Murage, E., Wu, R., Long, J.P., Do, K.A., Celestino, J. and Lu, K.H., 2021. A MYC-driven plasma polyamine signature for early detection of ovarian cancer. Cancers, 13(4), p.913.

3) Generating reliable and reproducible biomarker software: By exploiting the power of parallel computing and artificial intelligence, I have developed various pipelines for biomarker discovery and modeling. Examples include a supercomputer-based pipeline developed to identify frameshifted proteins in lung adenocarcinoma cancer using proteomics output and the association of these frameshifted proteins as sources of neoantigens. Additionally, I have developed a machine learning/artificial intelligence pipeline that generates predictable, computable, and stable biomarker combination rules using omics-level datasets. This pipeline will solve the underlying problems for artificial intelligence especially the instability of the model by exhaustive testing of the model in different permutation forms of the dataset.

a. **Irajizad, E.,** Kenney, A., Tang, T., Vykoukal, J., Wu, R., Murage, E., ... & Fahrmann, J. F. (2023). A blood-based metabolomic signature predictive of risk for pancreatic cancer. Cell Reports Medicine, 4(9).
b. **Irajizad E**, Fahrmann JF, Long JP, Vykoukal J, Kobayashi M, Capello M, Yu CY, Cai Y, Hsiao FC, Patel N, Park S, Peng Q, Dennison JB, Kato T, Tai MC, Taguchi A, Kadara H, Wistuba II, Katayama H, Do KA, Hanash SM, Ostrin EJ. A Comprehensive Search of Non-Canonical Proteins in Non-Small Cell Lung Cancer and Their Impact on the Immune Response. Int J Mol Sci. 2022 Aug 11;23(16):8933. doi: 10.3390/ijms23168933. PMID: 36012199; PMCID: PMC9409146.
c. Huang, L., Long, J. P., **Irajizad, E.**, Doecke, J. D., Do, K. A., & Ha, M. J. (2023). A Unified Mediation Analysis Framework for Integrative Cancer Proteogenomics with Clinical Outcomes. Bioinformatics.

Complete List of Published Work in My Bibliography:
https://www.ncbi.nlm.nih.gov/myncbi/ehsan.irajizad.1/bibliography/public/