Tarik Jawad Salameh

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github.com/tariks in tariksalameh

Education

Pennsylvania State University	2009—2021
Medical Scientist Training Program	2013—2021
Ph. D., Bioinformatics & Genomics	2020
B.S., Physics	2013
Awards	
B2D2K grant Big Data 2 Knowledge (NIH)	2019, 2020
CTSI grant Clinical / Translational Sciences	2017, 2018
Braddock scholarship Full tuition to College of Science	2009—2013
Elsbach Honors Scholarship Dept. of Physics	2011—2013
Schreyer Honors Scholarship Schreyer Honors College	2009—2013

Experience

Department of Medicine, Division of Pulmonary and Critical Care

Responsible for end-to-end analysis of transcriptome, microbiome, and clinical data for the Intensive Care Unit.

Wrote and implemented best-practice pipelines optimized for the unique challenges presented by critical illness datasets.

First author on two publications currently under review.

Discovered biomarker for mortality based on stool samples on day of admission to ICU.

Characterized immunophenotype differences of patients who develop chronic critical illness.

Curated -omics and clinical datasets from multiple sources for collaborations with other labs investigating critical illnesses.

Institute of Personalized Medicine June 2015—Feb 2020

Milton S. Hershey Medical Center, Hershey, PA 17033

Graduate Research Assistant

Received Bioinformatics training under co-mentors Feng Yue and James Broach.

Responsible for processing next-gen sequencing data from patients across a wide range of disease states and experiment types.

Specialized in machine learning for predictive modeling of outcomes and interpretation of molecular pathophysiology.

Wrote Peakachu, a ML framework for training chromatin-loop detection models from arbitrary experiments with high efficiency.

University Park, State College, PA 16802

Undergraduate Research Assistant

Responsible for simulation and analysis of proposed expansions of the IceCube detector array in Antarctica.

Contributed to first-ever detection of extra-solar neutrinos, published in *Science*.

Skills

Computation

 $\label{eq:python} Python \cdot \text{NumPy} \cdot \text{Pandas} \cdot \text{scikit-learn} \cdot \text{APACHE Arrow} \cdot \text{QIIME2} \cdot \text{Mothur} \cdot \text{matplotlib} \cdot \text{altair} \cdot \text{Vega} \cdot \text{AutoML} \cdot \text{mljar} \cdot \text{interpretML} \cdot \text{R} \cdot \text{ggplot} \cdot \text{WGCNA} \cdot \text{limma-voom} \cdot \text{DESeq2} \cdot \text{dplyr} \cdot \text{Unix} \cdot \text{Bash} \cdot \text{Lua} \cdot \text{Rust} \cdot \text{quarto} \cdot \text{SQL} \cdot \text{NLP} \cdot \text{Neural Networks} \cdot \text{HPC} \cdot \text{Docker} \cdot \text{Singularity} \cdot \text{Data Science}$

Statistics

 $\label{eq:GLM-Mixed-effects} GLM \cdot Mixed-effects \ models \cdot Cox \ survival \ analysis \cdot Key \ driver \ analysis \cdot Bayesian \ methods \cdot Multinomial \ regression \cdot Clinical \ statistics \cdot Compositional \ data \ analysis$

Biology

 $\label{eq:pathophysiology} \begin{array}{l} \text{Pathophysiology} \cdot \text{Microbiology} \cdot \text{Pharmacology} \cdot \text{Immunology} \cdot \text{Oncology} \cdot \text{Biochemistry} \cdot \\ \text{Epigenomics} \cdot \text{Transcriptomics} \cdot \text{Proteomics} \cdot \text{Metabalomics} \cdot \text{Genomics} \cdot \text{Infectious diseases} \end{array}$

Misc.

Academic writing · Arabic · Communication · HTML/Markdown

Publications

Salameh, T, Roth, K, Schultz, L, Ma, Z, Bonavia, A, Broach, J, Hu, B, Howrylak, J. "Chronic Critical Illness in the MICU is Linked with Myeloid-derived Suppressor Cells". In preparation.

Salameh, T, Roth, K, Schultz, L, Ma, Z, Bonavia, A, Broach, J, Hu, B, Howrylak, J. "Gut Microbiome Dynamics and Associations with Mortality in Critically III Patients". Under review. Preprint doi.org/jtd5 2022.

Mockus, T, Lauver, M, Ren, H, Netherby, C, **Salameh**, T, Kawasawa, Y, Yue, F, Broach, J, Lukacher, A, others. "CD4 T cells control development and maintenance of brain-resident CD8 T cells during polyomavirus infection". PLoS pathogens 2018; 14(10):e1007365.

Lopez, C, Tucker, S, **Salameh**, T, Tucker, C. "An unsupervised machine learning method for discovering patient clusters based on genetic signatures". Journal of biomedical informatics 2018; 85:30–39.

Coble, J, Sheldon, K, Yue, F, **Salameh**, T, Harris, L, Deiling, S, Ruggiero, F, Eshelman, M, Yochum, G, Koltun, W, others. "Identification of a rare LAMB4 variant associated with familial diverticulitis through exome sequencing". Human molecular genetics 2017; 26(16):3212–3220.

Yang, H, Luan, Y, Liu, T, Lee, H, Fang, L, Wang, Y, Wang, X, Zhang, B, Jin, Q, Ang, K, **others**. "A map of cis-regulatory elements and 3D genome structures in zebrafish". Nature 2020; 588(7837):337–343.

Salameh, T, Wang, X, Song, F, Zhang, B, Wright, S, Khunsriraksakul, C, Ruan, Y, Yue, F. "A supervised learning framework for chromatin loop detection in genome-wide contact maps". Nature communications 2020; 11(1):1–12.

IceCube Collaboration. "Evidence for high-energy extraterrestrial neutrinos at the IceCube detector". Science 2013; 342(6161):1242856.

Coble, J, Sheldon, K, Yue, F, Schneper, L, Choi, C, Poirier, K, **Salameh**, T, Harris, L, Deiling, S, Ruggiero, F, others. "Genomics of Gastrointestinal Disorders: a Familial Based Approach". The FASEB Journal 2016; 30:832–1.

Salameh, T. Chromatin Loop Detection via Machine Learning on Genome-Wide Contact Data (Doctoral dissertation, The Pennsylvania State University).