CV – Yoram Louzoun

A. Education

- B.Sc 1991 Hebrew University – Amirim program, Math, Physics.
- M.Sc 1997 -Tel Aviv University - Astrophysics
- Ph.D. 2000 – Hebrew University – Brain research
- Post-Doc. 2002-Princeton - Immunology

B. Personal Statement

I am a full professor of mathematics and department chair, leading the data science program. My background spans mathematics, immunology, genomics, computer science, and physics. My interdisciplinary lab, with 13–20 students and programmers, focuses on machine learning (ML) and data analysis in immunology, microbiology, and women's health, with a special focus on HLA and transplants. My research is primarily methodological, developing algorithms for diverse applications, including bone marrow transplant optimization, ML for B and T cell repertoire analysis, microbiome analysis, and graph-based ML. Beyond research, my lab excels in creating accessible algorithms and data for the scientific and clinical community.

C. Positions and Employment

2023-	Co-founder of Shela health
2020-2023	Chair of the department of mathematics, Bar Ilan University.
2017-present	Director of Data Science program, department of Mathematics, Bar Ilan University.
2015-present	Consultant for the National Marrow Donor Program bioinformatics group.
2014-present	Full Professor, math department and Gonda brain research center, Bar Ilan University.
2002-2014	Professor, math department, Bar Ilan University.
2000-2002	Postdoctoral fellow in Immunology at Princeton University.
1998-2000	PET, MRI and SPECT data analysis and modeling in the Nuclear Medicine Dept. of the Hadassah Hospital.

D. Honors Juludan Prize for contribution to Medicine, Wolf Foundation Krill prize, Complexity fellowship from Horowitz Foundation, Program in Mathematical and Molecular biology Burroughs Wellcome fellowship, Special Awards for Excellence from the Hadassah Hospital…..

E. Contribution to Science

- In recent years, we have developed models and measures to extract network content from structure, including hierarchy detection, information transfer, and graph-based ML algorithms for entity resolution. These methods integrate novel graph algorithms with advanced deep learning.
- In collaboration with colleagues in physics and biology, I studied the extreme effects of stochastic fluctuations in catalyst-induced growth. I demonstrated that in systems with a negative average growth rate, total reactant populations can still grow indefinitely. This work, now a classic example of rare-event effects in chemical and biological systems, has broad implications in biology and economics, supported by experimental validation.
- I developed advanced algorithms to predict all stages of epitope presentation and TCR-epitope binding (ERGO). My research also explores B and T cell receptor repertoire development using theoretical models, data analysis, and ML methods to infer disease history from immune repertoires.
- We created a suite of ML and analysis tools for microbiome research, including preprocessing (YAMAS, MIPMLP), microbiome-to-image translation for ML (iMic), microbe-metabolite association (LOCATE), optimal microbial transplants, and statistical models for differential analysis (miMic). This work is in collaboration with Omry Koren's microbiome research group at Bar-Ilan University's medical school.
- In partnership with the National Marrow Donor Program, we develop algorithms to improve HLA matching for bone marrow transplants. Our innovations include HLA imputation, matching algorithms, and transplant outcome prediction models.
- We have developed multiple robust tools for early prediction of pregnancy complications, validated across diverse populations.

F. Complete List of Published Work in MyBibliography (over 300 publications):

https://scholar.google.com/citations?user=TE6G3ZcAAAAJ&hl=en&oi=ao