Deep genomic analysis of tumor specimens
Dr. Hossein Khiabanian, Rutgers Cancer Institute of New Jersey

Research Field: Bioinformatics, Cancer Genomics

Project Summary:

Understanding complexity, dynamics, and stochastic patterns in genomic data - concepts native to physics and mathematics - is critical for elucidating how disease states originate and evolve. The main focus of this project is to use statistical, information theoretic approaches to dissect the cellular and molecular heterogeneity that enables cancer cells to evolve. We use high-throughput DNA and RNA sequencing methods, and computationally integrate genetic and clinical data from large cohorts of cancer patients being treated under various precision medicine programs, with the aim to identify markers of Darwinian selection using longitudinal data. Our ultimate goal is to develop novel statistical platforms for fast translation of genomic data into clinical practice.

Applicant GPA and other requirement(s): GPA-not applicable. Required Proficiency in programming and statistical analysis are essential; knowledge of genomics and biology is not required but highly valued.

Applicant responsibilities: please discuss with researcher if invited for interview