ROBERT J. SEAGER, JR.

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EDUCATION

Boston University *Boston, MA*
Ph.D., M.S., Biomedical Engineering *May 2020*
Awards: NIH Quantitative Biology and Physiology Trainee

Texas A&M University *College Station, TX*
B.S., Nuclear Engineering, Minor: Mathematics, *Summa Cum Laude* *May 2014*

EXPERIENCE

Labcorp/OmniSeq March 2020-Present
Senior Bioinformatics Scientist (2023-Present), Bioinformatics Scientist (2020-2023) *Buffalo, NY*

- Assisted in development of bioinformatics platforms for genomic and immune profiling of solid tumors for precision treatment of cancer patients
- Analyzed large-scale sequencing, biomarker, and medical record datasets using artificial intelligence, machine learning, and data science techniques
- Developed biomarkers and gene signatures for the prediction of treatment outcomes for various cancer therapies
- Built software tools for automated quality monitoring and process control of next generation sequencing workflows
- Published 16 peer-reviewed articles (5 as first author), made 7 first author conference poster presentations at clinical oncology conferences, and was listed as inventor on one patent

Boston University May 2015 - May 2020
Ph.D. Researcher *Boston, MA*

- Developed computational models of how the tumor microenvironment affects intracellular and intercellular signaling to quantitatively analyze how this interplay affects gross tumor development
- Published 3 peer-reviewed publications

RESEARCH

Cancer Biomarker Development 2020 - Present

- Identified biomarkers associated with treatment outcomes for cancer patients, including markers of tumor immunogenicity, cell proliferation, and antigen expression
- Applied machine learning and data analysis techniques to large-scale clinical and next-generation DNA and RNA sequencing datasets to integrate multi-modal, high-dimensional data
- Collaborated with interdisciplinary teams including clinical, academic, and industry researchers

Tumor Genomic and Immune Profiling Data Analysis 2020 - Present

- Profiled the distributions of clinically relevant factors, including potential treatment targets and markers of tumor immune escape, in both specific cancer type and pan-cancer contexts
- Applied data analysis and machine learning techniques to large-scale clinical and next-generation DNA and RNA sequencing datasets.
- Collaborated with clinical, academic, and pharmaceutical industry researchers

Computational Modeling of Cancer Cell Signaling 2017 - 2020

- Developed computational models of cell signaling, information processing, gene expression, and motility in tumor cells
- Combined large-scale signaling pathway, gene expression, transcription factor binding arrays data to inform and fit model and parameters
- Developed hypothetical pharmaceutical strategies to force tumor-suppressive signaling by cross-referencing signaling model with drug target data

SKILLS

Skills: Machine Learning, AI-Assisted Coding and Development, Data Science, High-Dimensional Data Analysis, Medical Data Cleaning and Analysis, Publication-Oriented Research, Written Communication, Public Speaking and Presentation

Programming Languages: Python, R, C++, FORTRAN