

TIMOTHY M. FARRELL

28 Haskell St., Allston, MA 02134

<https://tmfarrell.github.io>

(856) 904-6017

tfarrell01@gmail.com

OBJECTIVE

Bioinformatics engineer in biotech industry.

SUMMARY

Biotech engineer with computational/ software engineering skill. Most interested in advancing bioengineering/ biomedicine through automation/ computation.

EDUCATION

Master of Science, Bioinformatics, Boston University, 2014-2016

Project: *Clinical sequencing classifier for highly-polymorphic genes*

Activities: West End Boys and Girls Club STEM Tutor

GPA: 3.02/ 4.0

Bachelor of Science, Biomedical Engineering, Rutgers University, 2008-2012

Project: *Optimization of localizable stem-cell immunotherapeutic*

Activities: Army ROTC, Rutgers Future Scholars Mentorship Program

GPA: 3.31/ 4.0

SKILLS

Laboratory: genomic library prep, PCR, ELISA, confocal microscopy, cell culture (some)

Bioinformatics: standard tools, NGS/ 3GS experiment design/ data analysis, pipeline development/ management

Math/ Stats/ CS: graph theory, linear algebra, machine/ deep learning, stochastic modeling, probabilistic graphs, time series, inference/ statistical modeling

Programming:

Data management: SQL, PostgreSQL, SQLite

Operating systems: Unix-like (preferred), Windows

Languages: Python, shell, Java/ C++, Javascript/ HTML/ CSS (some)

Data analytics: R/ ggplot, pandas/ matplotlib, MATLAB, high-performance computing

RELEVANT EXPERIENCE

Biomedical Informatics Intern, Aug 2015 - May 2016

Dept. of Biomedical Informatics (DBMI), Harvard Medical School (HMS)

Worked to develop a clinical sequencing assay/ classifier for structurally-variant antigens, using both NGS/ 3GS technologies. Supervised by Peter Tonellato, PhD (DBMI, HMS) and collaborated with William Lane, MD PhD (Dept. of Pathology, Brigham Women's Hospital).

Research Assistant, Sept 2015 - May 2016

Dept. of Health Sciences, Boston University

Built preprocessing and preliminary analysis pipeline for dynamic functional connectivity study of Human Connectome Project data (Jason Bohland, PhD). Produced a fast, memory-efficient system that processed 2000 brain images in under 6 hours on a HPC cluster. See [repository](#).

Bioinformatics Intern, May - Aug 2015

Genomic Research Division, New England Biolabs (NEB)

Investigated development of error mitigation applications for emerging third-generation sequencing technologies (3GS). Setup and streamlined sequencing and computational workflows, facilitating future related work at NEB.

Student-Researcher, Aug 2011 - May 2012

Dept. of Biomedical Engineering, Rutgers University

Worked to optimize the immunomodulatory function of a mesenchymal stem cell-based therapeutic, designed to treat localized inflammatory disease.