

# TIMOTHY M. FARRELL

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## OBJECTIVE

Full-time bioinformatics engineer position in biotech industry.

## SUMMARY

Biotech engineer with computational/ software engineering skill. Most interested in the intersection of bioengineering and automation/ computation.

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## 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

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## SKILLS

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

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

**Bioinformatics:** standard tools (samtools, bedtools, etc.), NGS/ 3GS experiment design/ data analysis, pipeline development/ management

**Programming:**

Data management: SQL, PostgreSQL, SQLite

Operating systems: Unix-like (preferred), Windows

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

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

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## 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 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.