

29 Smith Street — Metuchen, NJ 08840

(732)-318-7702

☑ nikhilkumar516@gmail.com │ ♀ github.com/nikhil │ ♀ kumarcode.com

Education

Rutgers, The State University of New Jersey

Master of Science in Biomedical Engineering

Bachelor of Science in Biomedical Engineering, Minor: Computer Science

Grad GPA: 3.9 / 4.0

• Engineering Honors Program, Dean's List (All Semesters)

Piscataway, NJ May 2017 May 2016

Skills

Programming: Java, Shell, C, Python, R, Elixir, C#, Html, C++, JavaScript, CSS, LaTeX, Matlab, x86 Assembly Environments: Windows, Linux, Gimp, Git, Excel, Word, PowerPoint, Amazon Web Services, OpenCV, SolidWorks

Conferences: AACR 2018, AACR 2019, Open Source Summit 2019, ISMB 2020

Work Experience

Memorial Sloan Kettering Cancer Center

June 2017 - Present

Bioinformatics Engineer

- Developed a robust and portable pipeline for large scale genomic analysis using the Common Workflow language, Singularity containers, and the TOIL executor.
- Full-stack development of pipeline and metadata services using Django, PostgreSQL, Elixir, and Phoenix LiveView
- Dedicated to informative data visualization and contributing back to open source

Harvard Medical School - Department of Biomedical Informatics Summer Intern

Cambridge, MA Summer 2016

New York, NY

- Developed an optimized algorithm for processing 2D genomic data that reduced processing time and storage space by 50% and 35% respectively.
- Used methods such as parallelization, vectorization, and run-length encoding

Merck & Co., Inc.

Intern - Future Leaders Program

Rahway, NJ Summer 2015

- Developed a scientific data platform using Python on Amazon Web Services with scalable and customizable components.
- Implemented a publication recommendation tool on the platform using machine learning and PubMed.

Human Genetics Institute of New Jersey

Computational Research

Piscataway, NJ Spring 2013 - Fall 2014

- Analyzed nucleosome stability on Chip-Seq data resulting in published work.
- Computed expression profile clustering on Rna-Seq data.

Research

Computational Analysis of Gene Expression in Stem Cells

Team Leader - Senior Design

Piscataway, NJ September 2015 - May 2016

- Lead and organized a team to conduct computational analysis on gene expression.
- Designed and tested algorithms to retrieve Chip-Seq differential expression.

Publications

- Chahar et al., (2014). Chromatin Profiling Reveals Regulatory Network Shifts and a Protective Role for HNF4 α during Colitis. Molecular and cellular biology, 17, 3291–3304.
- Kerpedjiev et al., (2018). HiGlass: web-based visual exploration and analysis of genome interaction maps. Genome biology, 19(1), 125.