Nithish Narasimman

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Education

University of California San Diego, Jacobs School of Engineering
B.S. - Bioengineering: Bioinformatics - Major GPA: 3.84
Relevant coursework: Algorithms, Data Structures, Bioinformatics Algorithms

Experience

Data Scientist at Octant May 2024 - present

- *Analyzed in vivo mouse data for autosomal dominant retinitis pigmentosa (adRP)*
- *Ran deep mutational scanning analyses on various gPCRs such as GLP1R, GIPR to elucidate structure-function relationships*

Software Engineering Apprentice at Octant June 2023 - May 2024

- *Developed **React** application with a **Django** backend for chemists to design chemical synthesis experiments on Octant's high throughput synthesis platform*
- *Gathered requirements from users, created design documentation, and iterated over 6 weeks to develop and test application culminating in a presentation to 30+ Octant scientists*

Computational Biology Intern at Zentalis June 2022 - August 2022

- *Developed and validated pipelines with upwards of 30GB of in-house cancer genomics data to correlate mutational signatures with drug efficacy*
- *Utilized **Python** packages such as **pandas** and **seaborn** to generate data visualizations and correlations between datasets*

Undergraduate Researcher at The Alexandrov Lab January 2021 - June 2023

- *Contributed to SigProfilerExtractor and SigProfilerAssignment, tools for deriving somatic mutational signatures from cancer samples using nonnegative matrix factorization (NMF)*
- *Benchmarked different optimization strategies in **Python** to identify rate of convergence of various initialization methods of the NMF engine*

Publications

- Marcos Díaz-Gay, Raviteja Vangara, Mark Barnes, Xi Wang, S M Ashiqul Islam, Ian Vermes, Stephen Duke, **Nithish Bharadhwaj Narasimman**, Ting Yang, Zichen Jiang, Sarah Moody, Sergey Senkin, Paul Brennan, Michael R Stratton, Ludmil B Alexandrov, *Assigning mutational signatures to individual samples and individual somatic mutations with SigProfilerAssignment,* Bioinformatics, Volume 39, Issue 12, December 2023, btad756, https://doi.org/10.1093/bioinformatics/btad756

Projects

MotifFinder - ***Find de novo motifs using motif search algorithms*** September 2022 - June 2023

- *Developed **Rust** based CLI that identifies latent motifs in a given genome using Gibbs Sampling, Randomized Motif Search, and Median String search algorithms with parallel data loading and processing*
- *Utilized tool to discover **de novo motifs** in P. tricornutum, a microalgae, and presented results to Department of Bioengineering*