# **Nithish Narasimman**

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### Education

#### University of California San Diego, Jacobs School of Engineering

B.S. - Bioengineering: Bioinformatics

June 2023

# Experience

#### **Data Scientist at Octant**

May 2024 - present

- Built computer vision segmentation pipeline to automatically quantify retinal layer thickness from thousands of IHC-stained mouse histological sections
- Applied linear mixed effects modeling in R to account for experimental structure and detect treatment effects in adRP disease models
- Developed population genetics simulations using literature data to model disease progression and treatment response and inform clinical trial design
- Conducted deep mutational scanning analyses on GPCRs, mapping genotype-phenotype relationships to understand protein variant effects

#### **Software Engineering Apprentice at Octant**

June 2023 - May 2024

- Developed React application with a Django backend for chemists to design experiments on Octant's high throughput synthesis platform, speeding up design process from hours to minutes
- Built and benchmarked chemistry machine learning models and prediction pipelines to estimate compound potency, reducing chemical search space and optimizing hit selection

#### Computational Biology Intern at **Zentalis**

June 2022 - August 2022

 Developed computational pipelines to analyze 30GB+ of cancer genomics data, identifying mutational signatures that stratify patient populations by treatment response patterns

#### **Undergraduate Researcher at The Alexandrov Lab**

January 2021 - June 2023

- Implemented HALS optimization in SigProfilerExtractor, reducing mutational signature extraction runtime from tens of hours to under one hour
- Benchmarked SigProfilerAssignment against competing mutational signature tools, demonstrating superior performance and co-authoring published comparative analysis

### **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**

#### <u>MotifFinder</u>

September 2022 - June 2023

- Developed Rust based utility that identifies latent motifs in a given genome
- Utilized tool to discover de novo motifs in P. tricornutum microalgae as candidates for testing inducible promoter functionality in synthetic biology applications