**SHASHANK NAGARAJA**

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[linkedin.com/in/shashank-nagaraja/](https://www.linkedin.com/in/shashank-nagaraja/) | US Citizen

**EDUCATION**

##### UNIVERSITY OF CALIFORNIA, LOS ANGELES (UCLA) Los Angeles, CA

***B.S. Molecular, Cell, and Developmental Biology***

***Curriculum Highlights*:** Biomedical Research, Molecular Biology, Cell Biology, Genetics, Advanced Biochemistry

##### SYRACUSE UNIVERSITY Syracuse, NY

***M.S. Applied Data Science***

***Curriculum Highlights*:** Statistics, Regression, Machine Learning, Data Mining, NLP, Linear Programming

**SKILLS**

**Programming Skills:**

* **Python, R, SQL, UNIX, Powershell**
* **Machine Learning Algorithm Optimization**
* **Neural Networks Frameworks (TensorFlow & PyTorch)**
* **ETL Pipeline Construction**
* **Batch computing (Amazon EC2, Google Compute)**
* **Model Deployment**
* **Data Visualization (Tableau & Spotfire)**
* **Bioinformatics (NGS Data Analytics)**

**Scientific Skills:**

* NGS Library Preparation
* PCR
* Primer & gRNA Design
* Liquid Chromatography
* Liquid Handling Automation
* Design of Experiment (JMP)

**WORK/RESEARCH EXPERIENCE**

##### Amgen Inc. Thousand Oaks, CA

***Senior Associate Scientist – Process Development June 2019 – Present***

* Executed high throughput formulation screening studies in support of multiple Amgen pipeline molecules
* Implemented performance tuning for machine learning algorithm for viscosity prediction of monoclonal antibody formulations
* Deployed live dashboard for high throughput formulation screening studies to enable real-time process monitoring and decision-making
* Built automation protocols for two liquid handlers (Unchained, Andrews) to increase automation efficiency and decrease lead times and workload for high throughput studies

##### Cedars-Sinai Medical Center West Hollywood, CA

***Research Associate I – Bioinformatics and Functional Genomics Jan 2019 – May 2019***

* Provided end-to-end Computational Biology support on several Bladder, Breast and Ovarian cancer experiments (manuscripts in review)
* Designed NGS analytics pipelines to analyze RNA-Seq, scRNA-seq, CRISPR and ChIP-Seq data to reduce turnaround times and automate data analytics
* Created CRISPR screening libraries by using machine learning methods to classify mutation types

##### Dr. Matteo Pellegrini Lab Westwood, CA

***Research Assistant* *June 2016 – Dec 2018***

* Streamlined algorithm pipeline architecture for proprietary cell classification algorithms from NGS data, significantly reducing required computing power by half and run time by 90%
* Deployed cloud-based solutions in RShiny and AWS to analyze DNA Methylation, WGBS, and microarray data, to enable instant cell type classification
* Developed a novel technique in Differential Methylation site recognition called CEllFi® (technology licensed to Genentech, patent pending)