Nam V Nguyen Ph.D.

Computational Biologist | Multi-omics | AI/ML

Ph.D.-trained computational biologist specializing in genomics, transcriptomics, and AI-driven bioinformatics. Focused on advancing precision medicine through multi-omic data integration and machine learning.

CONTACT

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🌐 www.namvietnguyen.bio

EDUCATION

2017 - 2022
UNIVERSITY OF CALIFORNIA IRVINE
Biomedical Sciences **(PhD)**

2014 - 2016
WESTERN UNIVERSITY OF HEALTH SCIENCES
Pharmaceutical Sciences **(MS)**

2009 - 2013
UNIVERSITY OF CALIFORNIA SANTA BARBARA
Biochemistry **(BS)**

ESSENTIAL SKILLS

- **Bioinformatics**
- **Python, R, Bash, Linux**
- **AI/ML**
- **Statistical Methods**
- **NGS**
- **System Biology**
- **Molecular Biology**

WORK EXPERIENCE

Genentech   May 2023 – Dec 2024
Bioinformatic Analyst (Remote)

- Conducted single-cell RNA-seq analysis on pre-clinical models to predict drug responses and model disease progression
- Applied machine learning and statistical methods to large-scale clinical NGS datasets to identify biomarkers in cancer immunology with translational relevance
- Streamlined and documented analysis pipelines to ensure clarity, reproducibility, and effective team collaboration
- Collaborated cross-functionally with reverse translation and computational science teams to support data-driven therapeutic insights

University of California Irvine   Sep 2017 – Nov 2022
Graduate Researcher

- Designed NGS strategies and developed bioinformatics pipelines across multiple research projects
- Applied statistical and genomic analyses to uncover disease mechanisms and biomarkers for FSHD, a rare muscular dystrophy
- Characterized 3D chromatin architecture and epigenetic regulation in cancer cells under DNA damage response

QUALIFICATION

🧬 NGS & Bioinformatics

- Single-cell and bulk RNA-seq, ChIP-seq, ATAC-seq, CUT&RUN, Hi-C, HiChIP
- Proficient in R, Python, Bash, SQL, Linux/UNIX
- Tools & Libraries:
  - R-based: edgeR, limma, ggplot2, Seurat, Dplyr
  - Python-based: Scanpy, pandas, numpy, scikit-learn, TensorFlow, PyTorch
  - NGS Pipelines: CellRanger, STAR, RSEM, macs2, bowtie2
- Pipeline development for NGS and multi-omics: from raw data to analysis, visualization, and interpretation
- HPC & cloud computing: SLURM, SGE; GitHub, Bioconda, Jupyter

🔬 Biology & Research

- Deep knowledge in genomics, transcriptomics, and epigenetics, with domain expertise in cancer immunology and muscle biology
- Applied bioinformatics in target discovery and translational research
- Strong publication record; skilled in scientific writing and presentations
- Excellent documentation and data stewardship

👥 Leadership & Collaboration

- Mentored junior researchers and guided project development
- Strong team communication across interdisciplinary collaborations

PUBLICATION

- Engineered FSHD mutations results in D4Z4 heterochromatin disruption and feedforward DUX4 network activation. iScience (2024)
- Single-nucleus RNA-seq identifies divergent populations of FSHD2 myotube nuclei. PLoS Genet. 16, 1–26 (2020).

For more, visit www.namvietnguyen.bio