NAM VIET NGUYEN, Ph.D.

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Computational biologist with extensive experience in both molecular biology and bioinformatic analysis for NGS data. Worked with multiple DNA sequencing techniques, sequencer platforms, and also hands-on experience on analyzing high-throughput data. Self-motivated and a fast learner with diverse knowledge on system biology. My graduate research focused on determining disease mechanisms and identifying biomarkers of a rare muscular dystrophy. I also worked for Genentech as a computational scientist with a focus on cancer immunology/oncology. My unique experience prepared me to become a well-rounded computational biologist with a strong passion for understanding human diseases. My long-term goal will aim to improve my expertise in computational biology and to contribute to the advancement of genomics and personalized medicine.

EDUCATION

University of California Irvine Sep 2017 – Nov 2022

Doctor of Philosophy (PhD) in Biomedical Sciences

Western University of Health Sciences Aug 2014 – May 2016

Master of Pharmaceutical Sciences (MS)

University of California Santa Barbara Sep 2009 – June 2013

Bachelor of Science in Biochemistry (BS)

WORK EXPERIENCE

Bioinformatic Analyst (Remote) | Genentech May 2022 – Dec 2024

- Conducted single-cell RNA-seq analysis on pre-clinical data to model disease and predict drug responses
    - Bioinformatic skills : Seurat, CellRanger, Scanpy, celltype annotation, DE and clustering analysis
- Applied machine learning and statistical models to analyze large-scale clinical NGS datasets, identifying biomarkers for disease progression in cancer immunology and translating findings to potential therapeutic targets
    - Bioinformatic skills: SummarizedExperiment, MultiAssayExperiment, survival analysis, gene ontology, edgeR, ggplot, limma, linear and logistic regression, neural network
- Organized and documented codes for a large analysis project, ensuring clarity and accessibility for team collaboration and future references
- Collaborated with reverse translation team and computational science team, effectively demonstrating teamwork to achieve project objectives

Graduate Researcher | University of California Irvine Sep 2017 – Nov 2022

- Designed NGS strategies and built bioinformatic pipeline on multiple projects
    - Wet lab NGS preparation: Single-cell RNA-seq, RNA-seq, ChIP-seq, ATAC-seq, HiChIP, Cut&Run
    - Bioinformatic skills: bowtie2, macs2, STAR, RSEM, edgeR, Dplyr, gene ontology, ggplot, gene network analysis, panda, numpy, scikit-learn, TensorFlow
- Applied statistical analysis and genomic approach to determine disease mechanism and biomarkers for FSHD, a rare muscular dystrophy disease
- Determined 3D chromatin architecture and epigenetic regulation by DNA damage response in cancer cells

PUBLICATIONS

***N. V. Nguyen**, *X. Kong, Y. Li, J. S. Sakr, K. Williams, S. Sharifi, J. Chau, A. Bayrakci, S. Mizuno, S. Takahashi, T. Kiyono, R. Tawil, A. Mortazavi, K. Yokomori, Engineered FSHD mutations results in D4Z4 heterochromatin disruption and feedforward DUX4 network activation. iScience (2024). doi: 10.1016/j.isci.2024.1093

Williams, K., Kong, X., **Nguyen, N.**, McGill, C., Tawil, R., Yokomori, K., Mortazavi, A. Muscle group specific transcriptomic and DNA methylation differences related to developmental patterning influence FSHD, bioRxiv.

J. Chau, X. Kong, **N. Viet Nguyen**, K. Williams, M. Ball, R. Tawil, T. Kiyono, A. Mortazavi, K. Yokomori, Relationship of DUX4 and target gene expression in FSHD myocytes. *Hum Mutat*. **42**, 421–433 (2021).

S. Jiang, K. Williams, X. Kong, W. Zeng, **N. V. Nguyen**, X. Ma, R. Tawil, K. Yokomori, A. Mortazavi, Single-nucleus RNA-seq identifies divergent populations of FSHD2 myotube nuclei. *PLoS Genet*. **16**, 1–26 (2020).

Nguyen, N. V., Tran, J. T., & Sanchez, D. J. HIV blocks Type I IFN signaling through disruption of STAT1 phosphorylation. Innate immunity, 24(8), 490–500 (2018).

PRESENTATIONS

Asilomar Chromatin, Chromosomes, and Epigenetics Conference 2019
Oral: The Role of SMCHD1 in FSHD
FSHD International Research Congress 2021
Oral: Genetic engineering and characterization of isogenic FSHD mutant myocytes
FSHD International Research Congress 2022
Poster: Genetic engineering and characterization of isogenic FSHD mutant myocytes

QUALIFICATIONS

NGS Data Processing & Bioinformatic Skills

- Single-cell and bulk RNA-seq, ChIP-seq, ATAC-seq, CUT&RUN, HiC, HiChIP
- Proficient in programming Language R, Bash, SQL, Python and Linux/UNIX environment
- Experienced in statistical and machine learning methods
- Experienced in Version control with GitHub, Jupiter notebook and Bioconda
- Built bioinformatic pipeline to process raw NGS and integrated multi-omic dataset
- Experienced in NGS quality control, alignment, data processing, analysis, visualization, and interpretation
- Experienced in HPC/cloud computing, SLURM and SGE engine
- Experienced in public and proprietary data repositories: TCGA, UCSC, ENCODE, GEO

Areas of Expertise

- Extensive knowledge in genomics and transcriptome, cancer oncology, muscle biology
- Applied bioinformatics for target discovery and translational research

Research and Scientific Skills:

- Strong publication record
- Effective scientific writing and oral presentation
- Excellent documentation and data management

Leadership and Management:

- Trained and mentored junior researchers through guiding their projects
- Effective communication with team and collaborators in interdisciplinary projects

TEACHING & CERTIFICATE

Teaching Associate, COSMOS for high school students, *UC Irvine* 2021
Teaching Associate, Summer Youth Science Fellowship, Cancer Research Institute UC Irvine 2019
Business Concepts for STEM Scientists, *GPS-STEM and Beall Applied Innovation, UC Irvine* 2020