

Phu T. Van, PhD

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WORK EXPERIENCE

	2025Jun -	Bioinformatics Solutions Consultant
Pluto Biosciences	Performed technical onboarding and advised major clients as company's bioinformatics expert. Analyzed scRNASeq data, piloted new scRNASeq analyses in R. Scoped, managed and completed CEO's project to prototype a new data import pipeline. Trained Bioinformatics Solutions Engineer and Marketing staff on bioinformatics. Created bug reports, feature requests and Voice-of-Customer for company Product department. Designed and implemented customer support SLAs with company's Customer Experience Manager.	
	2021Jan - 2024May	Bioinformatics Scientist II → Senior Manager, Bioinformatics Solutions
TwinStrand Biosciences	Served as bioinformatics expert on company panel for approving new projects. Analyzed duplex sequencing data for cancer MRD projects. Trained wetbench scientists on bioinformatics. Spearheaded company's new bioinformatic offerings to customers. Provided analysis guidance to customers, co-authored customer communication SOPs with Field&Technical Support department. Oversaw development of new R data analysis packages. Initiated then supervised data analyses that expanded TwinStrand DuplexSeq™ support to two NGS sequencing platforms. Produced whitepapers, reviewed marketing and customer onboarding materials for technical accuracy.	
	2014 - 2020	Postdoc → Bioinformatics Analyst
Fred Hutch Cancer Center	Coordinated projects among PhD-level analysts, led brainstorming sessions and journal clubs. Performed analyses on flow cytometry and transcriptomic datasets. Created data analysis pipelines & interactive data visualizations. Authored Statistical Analysis Plans & peer-reviewed manuscripts. Reviewed junior analysts' code, mentored PhD students and bench scientists on statistics. Developed R code to normalize mass cytometry data across experiments using multi-mixture models. Performed dimension reduction on mass cytometry data and identified correlates of disease using regression.	
	2009 - 2014	Doctoral Student
Carnegie Mellon University	Designed and built a patented high-dynamic-range protein gel imager with robotic gel cutting arm for capturing rare proteins. Developed SIGILab , a C++ GUI application controlling gel imager's acquisition of high-dynamic-range images. Developed bash scripts to quantify protein abundances in 2DE gel images. Lectured in Modern Biology course and mentored junior students.	

TECHNICAL SKILLS

Programming	R, Python, Matlab, C/C++, bash, JavaScript, Perl
Data Analysis / Statistics	dimension reduction, clustering, regression/classification, linear models, variable selection, hypothesis testing
Databases	MySQL/MariaDB, PostgreSQL, SQLServer
Workflows	Nextflow, Slurm, Docker, GitHub

Cloud Computing

GCP, AWS EC2, S3, ECR

Bioinformatics

BWA, STAR, RSEM, BLAST, SAMtools, BCFtools, bedtools, varscan, delly, limma, edgeR, Seurat

EDUCATION

2009 - 2014

Carnegie Mellon University

PhD, Biological Sciences

2001 - 2007

University of Washington

BS, Biology (Physiology specialization); BS, Wildlife Sciences

SELECTED PUBLICATIONS, SOFTWARE & PATENTS

complete list: <https://scholar.google.com/citations?user=IDadFEkAAAAJ>

2024 Jul

Assessing the genotoxicity of N-nitrosodiethylamine with three in vivo endpoints in male Big Blue® transgenic and wild-type C57BL/6N mice

Environmental &
Molecular
Mutagenesis

This Pfizer collaboration compared DuplexSeq against a gold-standard genotoxic assay in detecting mutations from the carcinogen NDEA in mice, a follow-up to our previous work in rat: [Bercu 2023](#). I analyzed DuplexSeq data and co-wrote both manuscripts.

Authors: Shaofei Zhang, Stephanie Coffing, William Gunther, Michael Homiski, Richard Spellman, PHU T. VAN, *et al.*

2023 Jun

Duplex Sequencing Provides Detailed Characterization of Mutation Frequencies and Spectra in the Bone Marrow of MutaMouse Males Exposed to Procarbazine Hydrochloride

Archives of
Toxicology

This HealthCanada collaboration studied mutations in procarbazine-exposed mice using DuplexSeq compared to the gold-standard LacZ test. I analyzed mutation data and co-wrote the manuscript. We also studied ENU-exposed human cells ([Cho 2023](#)). Authors: Annette Dodge, Danielle LeBlanc, Andrew Williams, PHU T. VAN, *et al.*

2021 Jun

Monocyte metabolic transcriptional programs associate with resistance to tuberculin skin test/interferon- γ release assay conversion

Journal of Clinical
Investigation

This manuscript reports a potential link between oleic metabolism and *Tuberculosis* resistance in humans. I performed alignment, QC and transcript quantification, created data visualizations, made statistical recommendations and co-wrote the manuscript. My analysis code was also used in a follow-up project ([Simmons 2022](#)). Authors: Jason Simmons, PHU T. VAN, *et al.*

2018 Nov

ggCyto: next generation open-source visualization software for cytometry

Bioinformatics

This [R package](#) enables plotting of high-dimensional flow cytometry and mass cytometry data in the grammar-of-graphics style. I contributed to the R codebase, performed testing and co-wrote the manuscript.

Authors: PHU T. VAN*, Wenxing Jiang*, Raphael Gottardo, Greg Finak (*co-first authors)