

Phu T. Van, PhD

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SUMMARY

Seeking a scientific or technical position on collaborative teams working to solve data-intensive problems. I am particularly interested in projects that utilize statistical modeling or machine learning.

WORK EXPERIENCE

Fred Hutchinson Cancer Research Center	2015–Present	Systems Analyst, Analyst Group Leader
	Led the lab's PhD-level analysts in collaboration meeting and journal club. Performed analyses on flow cytometry and transcriptomic datasets. Authored Statistical Analysis Plans & peer-reviewed manuscripts. Created bioinformatic analysis pipelines & interactive data visualizations. Mentored PhD students and bench scientists on statistics, performed reviews of junior analysts code. Reference: Evan Henrich · ehenrich@fredhutch.org	
Fred Hutchinson Cancer Research Center	2014–2015	Postdoctoral Research Fellow
	Developed R code to normalize mass cytometry data across experiments using multi-mixture models. Worked with engineers from FlowJo Inc. (Ashland, OR) to enable XML parsing in FlowJo v10. Performed dimension reduction in mass cytometry data and identified correlates of disease progression in early-stage vaccine candidates. Reference: Evan Greene, PhD · palmergreene@gmail.com	
Carnegie Mellon University	2009–2014	Doctoral Student
	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 workflows to quantify protein abundances in 2DE gel images using bash. Reference: Jonathan Minden, PhD · minden@cmu.edu	
Institute for Systems Biology	2006–2009	Research Associate
	Identified factors that affect peptide detectability in mass spectrometry experiments using R. Constructed a SQLServer database with web frontend for exploring mass spectrometry data and planning proteomic experiments. Developed a regression algorithm in R to model regulators of stress response in microarray data. Reference: Serdar Turkarslan, PhD · serdar.turkarslan@isbscience.org	

TECHNICAL SKILLS

Programming	R, Python, Matlab, C/C++, bash, JavaScript, Perl
Data Analysis	dimension reduction, clustering, regression/classification
Statistics	linear models, variable selection, hypothesis testing
Databases	MySQL/MariaDB, PostgreSQL, SQLServer
Workflows	Nextflow, WDL, Slurm, Docker, GitHub
Bioinformatics	STAR, RSEM, BLAST, DEG, GSEA, KEGG, STRING

EDUCATION

2009–2014	Carnegie Mellon University
	PhD, Biological Sciences
2001–2007	University of Washington
	B.S., Biology (Physiology specialization), B.S., Wildlife Sciences

SELECTED PUBLICATIONS & PATENTS

- Mar. 2020* Monocyte metabolic programs are associated with resistance to TST/IGRA conversion
in review This manuscript reports a potential link between oleic metabolism and *Tuberculosis* resistance in humans. I was the primary analyst on this project, responsible for transcriptomic data and also assisted in writing the manuscript.
Authors: Jason Simmon, PHU T. VAN, *et al.*
- Nov. 2018* ggCyto: next generation open-source visualization software for cytometry
Bioinformatics ggCyto enables grammar-of-graphics plotting of high-dimensional flow cytometry and mass cytometry data in a freely accessible R package. I contributed to the R codebase, performed testing and co-wrote the manuscript.
Authors: PHU T. VAN, Wenxing Jiang, Raphael Gottardo, Greg Finak
- Jul. 2019* US10362237: Structured illumination system for increased dynamic range in quantitative imaging
United States Patent The present disclosure provides systems and methods for the measurement of signal intensity across a large dynamic range. The systems disclosed herein employ an iterative image collection strategy that utilizes structured illumination to achieve greater than 1,000,000-fold dynamic range measurements, representing a dramatic improvement over the prior art.
Inventors: Jonathan Minden, Frederick Lanni, PHU T. VAN