

Phu T. Van, PhD

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WORK EXPERIENCE

<i>TwinStrand Biosciences</i>	<i>2021 Jan –</i> Bioinformatics Scientist II → Bfx. Solutions Manager Advised internal departments on computational tools and procedures. Performed analyses on duplex sequencing data for numerous mutagenesis and cancer diagnostic projects. Contributed R code to internal bioinformatic pipelines and customer-facing reports. Prepared data products and presented findings to industry and academic clients. Reference: Clint Valentine III, MS · clint@twinstrandbio.com
<i>Fred Hutchinson Cancer Research Center</i>	<i>2014–2020</i> Postdoc → Bioinformatics Analyst 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. Reference: Amy Paguirigan, PhD · apaguiriri@fredhutch.org
<i>Carnegie Mellon University</i>	<i>2009–2014</i> 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 bash scripts to quantify protein abundances in 2DE gel images. Lectured in Modern Biology course and mentored junior students. Reference: Jonathan Minden, PhD · minden@cmu.edu
<i>Institute for Systems Biology</i>	<i>2006–2009</i> 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 weighted regression algorithm in R to predict regulators of stress response in microarray data. Reference: Serdar Turkarslan, PhD · serdar.turkarslan@isbscience.org

TECHNICAL SKILLS

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

EDUCATION

2009-2014 Carnegie Mellon University

PhD, Biological Sciences

2001-2007 University of Washington

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

SELECTED PUBLICATIONS & PATENTS

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

- Journal of Clinical Investigations* Jun. 2021 **Monocyte metabolic transcriptional programs associate with resistance to tuberculin skin test/interferon- release assay conversion**
This manuscript reports a potential link between oleic metabolism and *Tuberculosis* resistance in humans. As the primary analyst on the project, I aligned the raw transcriptomic data to the genome, quantified gene expression, created data visualizations and made recommendations on downstream statistical/machine learning methods. I also wrote the computational parts of the manuscript.
Authors: Jason Simmons, PHU T. VAN, *et al.*
- Bioinformatics* Nov. 2018 **ggCyto: next generation open-source visualization software for cytometry**
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)
- Electrophoresis* Sep. 2014 **High dynamic range proteome imaging with the structured illumination gel imager**
I built the Structured Illumination Gel Imager (SIGI), which enabled a 1000-fold increase in dynamic range over then-current methods while imaging 2D electrophoretic gels. I wrote the prototype imager software in Matlab, the production software in C/C++ and this manuscript, which informed the subsequent patent application for the imager.
Authors: PHU T. VAN, Victor Bass, Dan Shiwerski, Frederick Lanni, Jonathan Minden
- Molecular Systems Biology* Nov. 2010 **Coordination of frontline defense mechanisms under severe oxidative stress**
This manuscript reports a previously-undiscovered gene network that regulates cellular response to oxidative stress in microbes. I analyzed microarray data, wrote the R code for predicting the gene network, and co-wrote the manuscript.
Authors: Amardeep Kaur, PHU T. VAN, *et al.*
- United States Patent* Jul. 2019 **US10362237: Structured illumination system for increased dynamic range in quantitative imaging**
"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