

Phu T. Van, PhD

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WORK EXPERIENCE

<i>TwinStrand Biosciences</i>	2021 Jan – Bioinformatics Scientist II → Bfx. Solutions Manager Served as the company's bioinformatics expert for major external clients. Consulted and trained internal departments on bioinformatics. Scaled up the Bioinformatics Solutions group. Reviewed marketing and internal training materials for technical correctness. Performed analyses on duplex sequencing data for numerous mutagenesis and cancer diagnostic projects. Reviewed and 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>	2014–2020 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>	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 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>	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 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