

# Phu T. Van, PhD

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## WORK EXPERIENCE

Fred Hutchinson Cancer Research Center	2015–2020	Bioinformatics Analyst, Analyst Group Leader
	Coordinated projects among the lab's 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. Performed reviews of junior analysts' code, mentored PhD students and bench scientists on statistics. Reference: Evan Henrich · <a href="mailto:ehenrich@fredhutch.org">ehenrich@fredhutch.org</a>	
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 parsing of XML-encoded flow cytometry data in FlowJo v10. Performed dimension reduction on mass cytometry data and identified correlates of disease using regression. Reference: Amy Paguirigan, PhD · <a href="mailto:apaguiriri@fredhutch.org">apaguiriri@fredhutch.org</a>	
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 <b>SIGILab</b> , 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 · <a href="mailto:minden@cmu.edu">minden@cmu.edu</a>	
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 weighted regression algorithm in R to predict regulators of stress response in microarray data. Reference: Serdar Turkarslan, PhD · <a href="mailto:serdar.turkarslan@isbscience.org">serdar.turkarslan@isbscience.org</a>	

## 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, WDL, Slurm, Docker, GitHub
Bioinformatics	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>

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| <i>in revision at J. of<br/>Clin. Invest.</i> | <p><i>Jun. 2020</i> Monocyte metabolic programs are associated with resistance to TST/IGRA conversion</p> <p>This manuscript reports a potential link between oleic metabolism and <i>Tuberculosis</i> 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 statistical/machine learning methods. I also assisted in writing the manuscript.<br/>Authors: Jason Simmons, PHU T. VAN, <i>et al.</i></p>         |
| <i>Bioinformatics</i>                         | <p><i>Nov. 2018</i> <b>ggCyto: next generation open-source visualization software for cytometry</b></p> <p>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.<br/>Authors: PHU T. VAN*, Wenxing Jiang*, Raphael Gottardo, Greg Finak (*<i>co-first authors</i>)</p>   |
| <i>Electrophoresis</i>                        | <p><i>Sep. 2014</i> <b>High dynamic range proteome imaging with the structured illumination gel imager</b></p> <p>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.<br/>Authors: PHU T. VAN, Victor Bass, Dan Shiwerski, Frederick Lanni, Jonathan Minden</p> |
| <i>Molecular Systems<br/>Biology</i>          | <p><i>Nov. 2010</i> <b>Coordination of frontline defense mechanisms under severe oxidative stress</b></p> <p>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.<br/>Authors: Amardeep Kaur, PHU T. VAN, <i>et al.</i></p>  |
| <i>United States<br/>Patent</i>               | <p><i>Jul. 2019</i> <b>US10362237: Structured illumination system for increased dynamic range in quantitative imaging</b></p> <p>"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."<br/>Inventors: Jonathan Minden, Frederick Lanni, PHU T. VAN</p>  |