

Phu T. Van, PhD

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WORK EXPERIENCE

TwinStrand Biosciences	2021/11–	Bioinformatics Solutions Manager	Served as bioinformatics expert for the company in approving new projects. Provided bioinformatics guidance to external clients through Field&Technical Support departments. Supported Custom Applications department in creating new genomic panels. Supervised Advanced Sequencing Technology projects in collaboration with Laboratory Sciences department. Oversaw production of new R software packages in collaboration with Bioinformatics Development department. Spearheaded data mining collaborations with the Data Engineering department and co-led joint Machine Learning Interest Group. Reviewed company marketing and training materials for technical accuracy. Initiated and later supervised data analyses that expanded DuplexSeq(TM) support to two new sequencing platforms. Reference: Clint Valentine III, MS · clint@twinstrandbio.com
	2021/01-10	Bioinformatics Scientist II	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: Fang Yin Lo, PhD · mailto:fangyinlo@gmail.com
Fred Hutchinson Cancer Research Center	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 · apagui@fredhutch.org
	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
Carnegie Mellon University			

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
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>

Journal of Clinical Investigations	<p>Jun. 2021 Monocyte metabolic transcriptional programs associate with resistance to tuberculin skin test/interferon- release assay 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 downstream statistical/machine learning methods. I also wrote the computational parts of the manuscript. Authors: Jason Simmons, PHU T. VAN, <i>et al.</i></p>
Bioinformatics	<p>Nov. 2018 ggCyto: next generation open-source visualization software for cytometry</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. Authors: PHU T. VAN*, Wenxing Jiang*, Raphael Gottardo, Greg Finak (*co-first authors)</p>
Electrophoresis	<p>Sep. 2014 High dynamic range proteome imaging with the structured illumination gel imager</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. Authors: PHU T. VAN, Victor Bass, Dan Shiwarski, Frederick Lanni, Jonathan Minden</p>
United States Patent	<p>Jul. 2019 US10362237: Structured illumination system for increased dynamic range in quantitative imaging</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." Inventors: Jonathan Minden, Frederick Lanni, PHU T. VAN</p>