

Phu T. Van, PhD

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Research Interests

Bioinformatics, analytics, statistical inference, data science

Education

Ph.D. in Biological Sciences, Carnegie Mellon University, 2014

B.S. in Biology (Physiology specialization), University of Washington, 2007

B.S. in Wildlife Sciences, University of Washington, 2007

Research Experience

Bioinformatics Analyst, Analyst Group Leader

FredHutch

Oct. 2015 - present

Seattle, WA

Coordinated 2 analysis teams at FredHutch and University of Cape Town, South Africa. Led Seattle-based team of 3 PhD-level analysts in bi-weekly working meeting and journal club. Performed variable selection and sensitivity analyses for high dimension flow cytometry data from HIV vaccine trials. Created interactive dashboards to help collaborators understand differential gene expression and identify candidate genes for follow-up experiments. Developed analysis pipelines for multiple data types. Authored Statistical Analysis Plans and advised collaborators on research projects.

Postdoctoral Fellow

FredHutch

Aug. 2014 - Oct. 2015

Seattle, WA

Developed R code to normalize mass cytometry experiments using multi-mixture models and identifying outliers for quality control. Developed R code for writing XML representation of cell populations to enable data sharing of flow cytometry experiments. Worked with engineers from FlowJo Inc. (Ashland, OR) to incorporate XML parsing into FlowJo X. Identified correlates of disease in flow cytometry data of early-stage vaccines.

Research Associate

Institute for Systems Biology

May 2006 - Aug. 2009

Seattle, WA

Identified biophysical factors that differentially affect peptide detectability in tandem mass spectra experiments using R. Constructed a database and corresponding web frontend for archaeal proteomic data. Identified genetic regulators of oxidative stress response across different environmental stresses by developing a weighted regression algorithm in R for microarray data.

PhD Student

Carnegie Mellon University

Aug 2009 - May 2014

Pittsburgh, PA

Designed and built a patent-pending 2-dimensional protein gel imager with integrated gel cutting robot for identifying rare proteins. Improved reduction & alkylation of complex protein samples for mass spectrometric sequencing by developing agarose stacking gels to reduce

sample loss between isoelectric focusing and SDS-PAGE. Developed automated workflows to quantify protein abundances and detection biases in 2DE gels using bash shell scripts and C/C++ to process imager output.

Computational Skills

Data Analysis: clustering, regression, variable selection, hypothesis testing

Statistical Computing: R, Python, Matlab

Programming and Scripting: bash, Perl, C

Computing environments: Slurm, Docker, Git/GitHub

Image processing: image registration, segmentation, PSF deconvolution, HDR mapping

Databases: MySQL, postgresSQL, SQLServer

User Interfaces : HTML, JavaScript, PHP, Shiny

Patents & Selected Publications (*co-authors)

Minden, J., Lanni, F. and **Van, P.** “Structured Illumination System for Increased Dynamic Range in Quantitative Imaging”, USPTO 10,362,237 granted July 23, 2019

Simmons, JD, **Van PT**, Stein CM, Velen K, Peterson GJ, Graustein AD, Nguyen FK, Gottardo R, Mayanja-Kizza H, Fielding K, Grant A, Ntshiq T, Wallis RS, Churchyard G, Boom WH, Hawn TR. Resistance to TST/IGRA conversion associates with distinct transcriptional programs related to free fatty acid stimulation. In preparation.

Van PT*, Jiang W*, Gottardo R, Finak G. ggCyto: Next Generation Open-Source Visualization Software for Cytometry. *Bioinformatics* 34(22):3951-3953. 2018

Van PT, Ganesan V, Bass V, Parthasarathy A, Schlesinger D, Minden J. In-gel equilibration for 2DE-based proteomic workflows. *Electrophoresis*. 35(20):3012-7. 2014

Van PT, Bass V, Shiwarski D, Lanni F, Minden J. High dynamic range proteome imaging with the Structured Illumination Gel Imager. *Electrophoresis*. 35(18):2642-55 2014

Van PT, Schmid AK, King NL, Kaur A, Pan M, Whitehead K, Koide T, Facciotti M, Deutsch E, Reiss D, Mallick P and Baliga N. Halobacterium salinarum NRC-1 PeptideAtlas: strategies for targeted proteomics. *Journal of Proteome Research*. 7(9):3755-3764. 2008

Van PT*, Tkaczyk FA*, West SD. Ecology of Myocastor Coypus in the Union Bay area. Bachelor Senior Thesis, College of Forest Resources, University of Washington. 2007