Phu T. Van, PhD

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Objective

A technical or scientific position in a collaborative team. Opportunities addressing data-intensive problems using modelling, visualization and prediction are particularly welcome.

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
Led the lab's 3 PhD-level analysts in bi-weekly working meeting and journal club. Coordinated analysis between FredHutch and University of Cape Town (South Africa) on multi-site multi-omics data integration project. Performed variable selection and sensitivity analyses for HIV vaccine trial data. Created interactive dashboards to help collaborators identify candidate genes for follow-up experiments. Developed analysis pipelines for multiple data types. Authored Statistical Analysis Plans and advised collaborators on research projects. Co-authored peer-reviewed manuscripts, talks and posters. Mentored PhD students and non-scientific staff on statistics and experimental design. Performed reviews of junior analysts' code.

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.

PhD Student
Carnegie Mellon University   Aug 2009 - May 2014   Pittsburgh, PA
Designed and built a patented high-dynamic-range protein gel imager with integrated gel cutting robot for identifying and capturing rare proteins. Improved reduction & alkylation of complex protein samples for mass spectrometric sequencing by developing agarose stacking gels that reduced sample loss during processing. Developed automated bash and C/C++ workflows to quantify protein abundances and detection biases in 2DE gel images.

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 accompanying 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.

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, Ntshiqa 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