

Phu T. Van, PhD

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EDUCATION

Carnegie Mellon University

Ph.D., Biological Sciences

2014

University of Washington

B.S., Biology (Physiology specialization), B.S., Wildlife Sciences

2007

EXPERIENCE

FredHutch

Bioinformatics Analyst, Analyst Group Leader

October 2015 - Present

Seattle, WA

- Led the lab's 3 PhD-level analysts in twice-monthly collaboration meeting and journal club.
- Authored Statistical Analysis Plans, developed analysis pipelines, authored peer-reviewed manuscripts.
- Mentored PhD students and bench scientists on statistics, advised hiring and performed reviews of junior analysts' code.
- Coordinated analyses between FredHutch and University of Cape Town, South Africa on multi-omics Tuberculosis project.
- Performed differential gene expression and geneset enrichment analysis on transcriptomic datasets.
- Performed variable selection and sensitivity analyses on immunology data for HIV vaccine trials.

FredHutch

Postdoctoral Fellow

October 2014 - October 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 enable XML parsing in FlowJo v10.
- Identified correlates of disease in early-stage vaccine candidates in mass cytometry data.

Carnegie Mellon University

PhD Student

August 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.
- Developed processes that improved reduction and alkylation of complex protein samples in preparation for mass spectrometric sequence.
- Developed automated bash and C/C++ workflows to quantify protein abundances and detection biases in 2DE gel images.

Institute for Systems Biology

PhD Student

May 2006 - August 2009

Seattle, WA

- Identified biophysical factors that differentially affect peptide detectability in tandem mass spectra experiments using R.
- Constructed a database with web frontend for exploring mass spectrometric data and planning proteomic experiments.

- Developed a weighted regression algorithm in R for to identify regulators of oxidative stress response in microarray experiments.

TECHNICAL STRENGTHS

Programming	R, Python, Matlab, C/C++, Perl
Data Analysis	dimension reduction, regression/classification, modeling and variable selection
User Interfaces	Shiny, PHP, JavaScript
Databases	MySQL, PostgreSQL, SQLServer
Workflows	Nextflow, Slurm, Docker, GitHub
Markup	LaTeX, Markdown, HTML

PUBLICATIONS AND PATENTS

1. P. Van, W. Jiang, R. Gottardo, and G. Finak. ggCyto: next generation open-source visualization software for cytometry. *Bioinformatics*, 34(22):3951–3953, 11 2018
2. P. T. Van, V. Ganesan, V. Bass, A. Parthasarathy, D. Schlesinger, and J. S. Minden. In-gel equilibration for improved protein retention in 2DE-based proteomic workflows. *Electrophoresis*, 35(20):3012–3017, Oct 2014
3. P. T. Van, V. Bass, D. Shiwarski, F. Lanni, and J. Minden. High dynamic range proteome imaging with the structured illumination gel imager. *Electrophoresis*, 35(18):2642–2655, Sep 2014
4. U. K. Iheagwara, P. L. Beatty, P. T. Van, T. M. Ross, J. S. Minden, and O. J. Finn. Influenza virus infection elicits protective antibodies and T cells specific for host cell antigens also expressed as tumor-associated antigens: a new view of cancer immunosurveillance. *Cancer Immunol Res*, 2(3):263–273, Mar 2014
5. A. Kaur, P. T. Van, C. R. Busch, C. K. Robinson, M. Pan, W. L. Pang, D. J. Reiss, J. DiRuggiero, and N. S. Baliga. Coordination of frontline defense mechanisms under severe oxidative stress. *Mol. Syst. Biol.*, 6:393, Jul 2010
6. T. Koide, D. J. Reiss, J. C. Bare, W. L. Pang, M. T. Facciotti, A. K. Schmid, M. Pan, B. Marzolf, P. T. Van, F. Y. Lo, A. Pratap, E. W. Deutsch, A. Peterson, D. Martin, and N. S. Baliga. Prevalence of transcription promoters within archaeal operons and coding sequences. *Mol. Syst. Biol.*, 5:285, 2009
7. P. T. Van, A. K. Schmid, N. L. King, A. Kaur, M. Pan, K. Whitehead, T. Koide, M. T. Facciotti, Y. A. Goo, E. W. Deutsch, D. J. Reiss, P. Mallick, and N. S. Baliga. Halobacterium salinarum NRC-1 PeptideAtlas: toward strategies for targeted proteomics and improved proteome coverage. *J. Proteome Res.*, 7(9):3755–3764, Sep 2008
8. A. K. Schmid, D. J. Reiss, A. Kaur, M. Pan, N. King, P. T. Van, L. Hohmann, D. B. Martin, and N. S. Baliga. The anatomy of microbial cell state transitions in response to oxygen. *Genome Res.*, 17(10):1399–1413, Oct 2007
9. M. Blundon, V. Ganesan, B. Redler, P. T. Van, and J. S. Minden. Two-Dimensional Difference Gel Electrophoresis. *Methods Mol. Biol.*, 1855:229–247, 2019
10. D. F. E. Ker, S. Eom, S. Sanami, R. Bise, C. Pascale, Z. Yin, S. I. Huh, E. Osuna-Highley, S. N. Junkers, C. J. Helfrich, P. Y. Liang, J. Pan, S. Jeong, S. S. Kang, J. Liu, R. Nicholson, M. F. Sandbothe, P. T. Van, A. Liu, M. Chen, T. Kanade, L. E. Weiss, and P. G. Campbell. Phase contrast time-lapse microscopy datasets with automated and manual cell tracking annotations. *Sci Data*, 5:180237, 11 2018
11. J. S. Minden, F. Lanni, and P. T. Van. Structured illumination system for increased dynamic range in quantitative imaging, July 2019