

Phu T. Van, PhD

Machine Learning Specialist

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EDUCATION

Carnegie Mellon University

2014

Ph.D., Biological Sciences

University of Washington

2007

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

OBJECTIVE

Seeking a scientific or technical position on collaborative teams working to solve data-intensive problems. I'm particularly interested in projects that utilize statistical modeling, simulation or machine learning.

EXPERIENCE

FredHutch

October 2015 - Present

Bioinformatics Analyst, Analyst Group Leader

Seattle, WA

- Performed differential gene expression and geneset enrichment analysis on transcriptomic datasets.
- Performed variable selection and sensitivity analyses on flow cytometry datasets.
- Led the lab's 3 PhD-level analysts in twice-monthly collaboration meeting and journal club.
- Coordinated analyses on data integration project with South African Tuberculosis Vaccine Institute.
- Authored Statistical Analysis Plans and peer-reviewed manuscripts.
- Created bioinformatic analysis pipelines and interactive data visualizations.
- Mentored PhD students and bench scientists on statistics, advised hiring and performed reviews of junior analysts code.

FredHutch

October 2014 - October 2015

Postdoctoral Fellow

Seattle, WA

- Developed R code to normalize mass cytometry experiments using multi-mixture models.
- Developed R code for writing XML files 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

August 2009 - May 2014

PhD Student

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 sequencing.
- Developed automated bash and C/C++ workflows to quantify protein abundances and detection biases in 2DE gel images.

Institute for Systems Biology

May 2006 - August 2009

Research Associate

Seattle, WA

- 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 regression algorithm in R to model regulators of stress response in microarray data.

TECHNICAL STRENGTHS

Programming	R, Python, Matlab, C/C++, Perl
Data Analysis	dimension reduction, clustering, regression/classification
Statistics	linear models, variable selection, hypothesis testing
User Interfaces	Shiny, PHP, JavaScript
Databases	MySQL/MariaDB, PostgreSQL, SQLServer
Workflows	Nextflow, Slurm, Docker, GitHub
Markup	LaTeX, Markdown, HTML
Bioinformatics	STAR, RSEM, BLAST, DEG, GSEA, KEGG, STRING

SELECTED PUBLICATIONS & 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. Shiwerski, 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. J. S. Minden, F. Lanni, and P. T. Van. Structured illumination system for increased dynamic range in quantitative imaging, July 2019