

# Phu T. Van, PhD

*Machine Learning Specialist*

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## SUMMARY

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I'm 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 or machine learning.

## TECHNICAL STRENGTHS

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

## EXPERIENCE

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### **Fred Hutchinson Cancer Research Center**

October 2015 - Present

*Systems Analyst, Bioinformatics 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 PhD-level analysts in brainstorming sessions and journal club.
- Coordinated analyses on projects with external collaborators.
- Authored Statistical Analysis Plans and peer-reviewed manuscripts.
- Created bioinformatic analysis pipelines using R, Nextflow and WDL.
- Created interactive data visualizations using RMarkdown, igrph and leaflet.
- Mentored PhD students and bench scientists on statistics, advised hiring and performed reviews of junior analysts' code.

### **Fred Hutchinson Cancer Research Center**

October 2014 - October 2015

*Postdoctoral Fellow*

*Seattle, WA*

- Developed R code to normalize mass cytometry data across experiments using multi-mixture models.
- Worked with engineers from FlowJo Inc. (Ashland, OR) to develop parsing in of XML-encoded flow cytometry data in FlowJo v10.
- Performed dimension reduction on mass cytometry data and identified correlates of disease.

### **Carnegie Mellon University**

August 2009 - May 2014

*PhD Student*

*Pittsburgh, PA*

- 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 processes that improved reduction and alkylation of complex protein samples in preparation for mass spectrometric sequencing.
- Developed workflows to quantify protein abundances in 2DE gel images using bash.

- 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.

## EDUCATION

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**Carnegie Mellon University**  
PhD, Biological Sciences

2014

**University of Washington**

BS, Biology (Physiology specialization), BS, Wildlife Sciences

2007

## CONFERENCES, PATENTS AND REPRESENTATIVE PUBLICATIONS

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1. J. Simmons, P. Van, C. Stein, Chihota V., Velen K., Fielding K., Grant A., Ntshiq T., Peterson G., Graustein A., Nguyen F., Gottard R., Mayanja-Kizza H., Wallis R., Churchyard G., Boom W.H., and Hawn T.R. Resistance to TST/IGRA conversion associates with distinct transcriptional programs. Poster presented at Tuberculosis Research Training Center annual symposia, Seattle, WA, September 2019
2. J. S. Minden, F. Lanni, and P. T. Van. USPTO US10362237: Structured illumination system for increased dynamic range in quantitative imaging, July 2019
3. J. Simmons, P. Van, C. Stein, Chihota V., Velen K., Fielding K., Grant A., Ntshiq T., Peterson G., Graustein A., Nguyen F., Gottard R., Mayanja-Kizza H., Wallis R., Churchyard G., Boom W.H., and Hawn T.R. Monocyte metabolic programs are associated with resistance to tst/igra conversion. in review, March 2020
4. 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
5. 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
6. 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
7. 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
8. 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
9. 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

10. 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
11. 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
12. 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