

# Phu T. Van, PhD

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## EDUCATION

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### Carnegie Mellon University

Ph.D., Biological Sciences

2014

### University of Washington

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

2007

## OBJECTIVE

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Seeking a scientifically-oriented position on collaborative teams working on difficult problems. I'm particularly interested in data-intensive projects requiring statistical modeling or machine learning.

## EXPERIENCE

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### FredHutch

*Bioinformatics Analyst, Analyst Group Leader*

October 2015 - Present

*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

*Postdoctoral Fellow*

October 2014 - October 2015

*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

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

### Institute for Systems Biology

*Research Associate*

May 2006 - August 2009

*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

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

## SELECTED PUBLICATIONS & PATENTS

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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