

Phu T. Van, PhD

Computational Biologist

pvan@alumni.cmu.edu , <https://ptvan.github.io>

SUMMARY

I'm interested in scientific or technical positions on collaborative teams working to solve complex problems in computational biology.

TECHNICAL STRENGTHS

Programming	R, Python, Matlab, C/C++, bash, JavaScript, Perl
Data Analysis	dimension reduction, clustering, regression/classification
Statistics	linear models, variable selection, hypothesis testing
Databases	MySQL/MariaDB, PostgreSQL, SQLServer
Workflows	Nextflow, WDL, Slurm, Docker, GitHub
Markup/Interfaces	LaTeX, Markdown, Shiny, HTML
Bioinformatics	BWA, STAR, RSEM, BLAST, SAMtools, BCFtools VardictJava, varscan, delly, limma, edgeR

EXPERIENCE

TwinStrand Biosciences <i>Senior Manager, Bioinformatics Solutions</i>	September 2023 - Present <i>Seattle, WA</i>
--	--

- Served as bioinformatics expert on company panel for approving new projects.
- Spearheaded company's new bioinformatic offerings to customers.
- Trained wetbench scientists on bioinformatics.
- Provided bioinformatics guidance to Commercial department and major external customers.
- Collected Voice of Customers from major commercial and academic clients.
- Authored customer-facing whitepapers and marketing collateral for Commercial department.
- Co-authored data retention and acceptable use policy for customer-facing cloud platform.

TwinStrand Biosciences <i>Bioinformatics Solutions Manager</i>	November 2021 - August 2023 <i>Seattle, WA</i>
--	---

- Served as bioinformatics expert on company panel for approving new projects.
- Provided bioinformatics guidance to customers and co-authored customer communication SOPs with Field&Technical Support department.
- Mentored Bioinformatics Solutions scientists.
- Oversaw development of new R data analysis packages.
- Initiated and later supervised data analyses that expanded TwinStrand DuplexSeqTM support to two new sequencing platforms.

TwinStrand Biosciences <i>Bioinformatics Scientist II</i>	January 2021 - October 2021 <i>Seattle, WA</i>
---	---

- Performed analyses on duplex sequencing data for diverse projects including mutagenesis and cancer MRD.
- Reviewed and contributed R code to internal bioinformatic pipelines and customer-facing reports.
- Prepared data products and presented findings to industry and academic clients.

Fred Hutchinson Cancer Research Center <i>Bioinformatics Analyst, Analyst Group Leader</i>	October 2015 - December 2020 <i>Seattle, WA</i>
--	--

- 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, igraph 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.

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.

EDUCATION

Carnegie Mellon University

2014

PhD, Biological Sciences

University of Washington

2007

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

CONFERENCES, PATENTS AND PUBLICATIONS

1. Joel P Bercu, Shaofei Zhang, Zhanna Sobol, Patricia A Escobar, Phu Van, and Maik Schuler. Comparison of the transgenic rodent mutation assay, error corrected next generation duplex sequencing, and the alkaline comet assay to detect dose-related mutations following exposure to n-nitrosodiethylamine. *Mutation Research/Genetic Toxicology and Environmental Mutagenesis*, 891:503685, 2023

2. Annette E Dodge, Danielle PM LeBlanc, Gu Zhou, Andrew Williams, Matthew J Meier, Phu Van, Fang Yin Lo, Charles C Valentine III, Jesse J Salk, Carole L Yauk, et al. Duplex sequencing provides detailed characterization of mutation frequencies and spectra in the bone marrow of mutamouse males exposed to procarbazine hydrochloride. *Archives of Toxicology*, pages 1–15, 2023
3. Eunnara Cho, Carol D Swartz, Andrew Williams, Miriam Rivas, Leslie Recio, Kristine L Witt, Elizabeth K Schmidt, Jeffry Yaplee, Thomas H Smith, Phu Van, et al. Error-corrected duplex sequencing enables direct detection and quantification of mutations in human tk6 cells with strong inter-laboratory consistency. *Mutation Research/Genetic Toxicology and Environmental Mutagenesis*, page 503649, 2023
4. Annette E Dodge, Danielle LeBlanc, Andrew Williams, Phu Van, Jake Higgins, Fang Yin Lo, Jeffry Yaplee, Clint C Valentine, Jesse J Salk, Carole L Yauk, et al. Characterisation of procarbazine-induced mutation spectrum in the bone marrow of mutamouse males using duplex sequencing. In *ENVIRONMENTAL AND MOLECULAR MUTAGENESIS*, volume 63, pages 92–93. WILEY 111 RIVER ST, HOBOKEN 07030-5774, NJ USA, 2022
5. E Cho, F Marchetti, P Van, J Higgins, FY Lo, J Yaplee, CC Valentine III, J Salk, and CL Yauk. Optimal methodological design for duplex sequencing (tm) in tk6 cells determined through a time and concentration response analysis following enu treatment. In *Environmental and Molecular Mutagenesis*, volume 62, page 36, 2021
6. D LeBlanc, M Meier, A Williams, J Buick, J Higgins, J Yaplee, P Van, FY Lo, CC Valentine, JJ Salk, et al. Duplex sequencing reveals an attenuated mutation frequency increase in the germ cells of mutamouse males exposed to n-ethyl-n-nitrosourea and benzo [a] pyrene relative to the tgr lacz assay. In *Environmental and Molecular Mutagenesis*, volume 62, page 87, 2021
7. AE Dodge, D LeBlanc, A Williams, P Van, J Higgins, FY Lo, J Yaplee, CC Valentine, JJ Salk, and CL Yauk. Duplex sequencing (tm) reveals increases in mutation frequencies and c_i t transitions in the bone marrow of mutamouse males exposed to procarbazine. In *Environmental and Molecular Mutagenesis*, volume 62, page 87, 2021
8. Jason D Simmons, Kimberly A Dill-McFarland, Catherine M Stein, Phu T Van, Violet Chihota, Thobani Ntshiqha, Pholo Maenetje, Glenna J Peterson, Penelope Benchek, Mary Nsereko, et al. Monocyte transcriptional responses to mycobacterium tuberculosis associate with resistance to tuberculin skin test and interferon gamma release assay conversion. *Msphere*, 7(3):e00159–22, 2022
9. Gemma Moncunill, Jason Carnes, William Chad Young, Lindsay Carpp, Stephen De Rosa, Joseph J Campo, Augusto Nhabomba, Maxmillian Mpina, Chenjerai Jairoce, Greg Finak, et al. Transcriptional correlates of malaria in rts, s/as01-vaccinated african children: a matched case–control study. *Elife*, 11:e70393, 2022
10. J. Simmons, P. Van, C. Stein, Chihota V., Velen K., Fielding K., Grant A., Ntshiqha 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 transcriptional programs associate with resistance to tuberculin skin test/interferon- release assay conversion. *Journal of Clinical Investigations*, June 2021
11. 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
12. 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. *Scientific Data*, 5:180237, 11 2018

13. J. S. Minden, F. Lanni, and P. T. Van. USPTO US10362237: Structured illumination system for increased dynamic range in quantitative imaging, July 2019
14. 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
15. 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
16. 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
17. 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 Immunology Research*, 2(3):263–273, Mar 2014
18. 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. *Molecular Systems Biology*, 6:393, Jul 2010
19. 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. *Molecular Systems Biology*, 5:285, 2009
20. 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. *Journal of Proteome Research*, 7(9):3755–3764, Sep 2008
21. 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 Research*, 17(10):1399–1413, Oct 2007