Phu T. Van, PhD

Computational Biologist

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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 November 2021 - Present
Bioinformatics Solutions Manager *Seattle, WA*

· Served as bioinformatics expert for the company in approving new projects.
· Spearheaded "à la carte" bioinformatics offering to customers to increase revenue.
· Provided bioinformatics guidance to external clients with Field&Technical Support department.
· Assisted Custom Applications department in creating new genomic panels.
· Supervised R&D collaborations between bioinformatic and wetlab technicians.
· Oversaw development of new R data analysis packages.
· Initiated and later supervised data analyses that expanded TwinStrand DuplexSeq(TM) support to two new sequencing platforms.
· Produced whitepapers and reviewed marketing materials for technical accuracy.
· Co-authored customer communication SOPs.

TwinStrand Biosciences January 2021 - October 2021
Bioinformatics Scientist II *Seattle, WA*

· Performed analyses on duplex sequencing data for diverse projects including mutagenesis and cancer MRD.
· Contributed R code to internal bioinformatic pipelines and customer-facing reports.
· Presented findings to commercial and academic clients.
· Performed code reviews of R packages.

Fred Hutchinson Cancer Research Center October 2015 - December 2020
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 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
Postdoctoral Fellow

October 2014 - October 2015
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
PhD Student

August 2009 - May 2014
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
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.

EDUCATION

Carnegie Mellon University
PhD, Biological Sciences

2014

University of Washington
BS, Biology (Physiology specialization), BS, Wildlife Sciences

2007

CONFERENCES, PATENTS AND REPRESENTATIVE PUBLICATIONS

1. 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

2. 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

3. 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

4. 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

5. 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¿ t transitions in the bone marrow of mutamouse males exposed to procarbazine. In *Environmental and Molecular Mutagenesis*, volume 62, page 87, 2021

6. Jason D Simmons, Kimberly A Dill-McFarland, Catherine M Stein, Phu T Van, Violet Chihota, Thobani Ntshiqa, 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

7. 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

8. J. Simmons, P. Van, C. Stein, Chihota V., Velen K., Fielding K., Grant A., Ntshiqa 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

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. *Scientific Data*, 5:180237, 11 2018

11. J. S. Minden, F. Lanni, and P. T. Van. USPTO US10362237: Structured illumination system for increased dynamic range in quantitative imaging, July 2019

12. 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

13. 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

14. 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

15. 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

16. 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

17. 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

18. 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

19. 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