

# Phu T. Van, PhD

*Computational Biologist*

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## SUMMARY

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

## 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>    | BWA, STAR, RSEM, BLAST, SAMtools, BCFtools<br>VardictJava, varscan, delly, limma, edgeR |

## EXPERIENCE

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| <b>TwinStrand Biosciences</b><br><i>Senior Manager, Bioinformatics Solutions</i> | September 2023 - Present<br><i>Seattle, WA</i> |
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- Served as bioinformatics expert on company panel for approving new projects.
- Spearheaded "à la carte" bioinformatics offering to customers to increase revenue.
- Provided bioinformatics guidance to customers
- Trained Field Application Scientists in bioinformatics and co-authored customer communication SOPs with Field&Technical Support department.
- Produced whitepapers and reviewed marketing materials for technical accuracy.

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| <b>TwinStrand Biosciences</b><br><i>Bioinformatics Solutions Manager</i> | November 2021 - August 2023<br><i>Seattle, WA</i> |
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- Served as bioinformatics expert on company panel for approving new projects.
- Mentored Bioinformatics Solutions scientists.
- Oversaw development of new R data analysis packages.
- Initiated and later supervised data analyses that expanded TwinStrand DuplexSeq<sup>TM</sup> support to two new sequencing platforms.

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

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| <b>Fred Hutchinson Cancer Research Center</b><br><i>Bioinformatics Analyst, Analyst Group Leader</i> | October 2015 - December 2020<br><i>Seattle, WA</i> |
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- 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. Eunnara Cho, Carol D Swartz, Andrew Williams, Miriam Rivas, Leslie Recio, Kristine L Witt, Elizabeth K Schmidt, Jeffrey 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, Jeffrey 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<sub>j</sub> t transitions in the bone marrow of mutamouse males exposed to procarbazine. In *Environmental and Molecular Mutagenesis*, volume 62, page 87, 2021
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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
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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
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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
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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

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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