

WILLIAM S. DEWITT, PHD

Department of Genome Sciences, University of Washington
Foege Building S130C, 3720 15th Ave NE, Seattle WA 98195-5065
[wsdewitt\[at\]uw.edu](mailto:wsdewitt@uw.edu) | wsdewitt.github.io

EDUCATION

PhD 2022	University of Washington Genome Sciences	advisors: Dr. Erick Matsen, Dr. Kelley Harris dissertation: <i>Some problems in probabilistic modeling of germline and somatic evolutionary processes</i>
MS, BA 2011	University of Vermont Physics	advisor: Dr. Kelvin Chu thesis: <i>Imaging protein statistical substate occupancy in a spectrum-function phase space</i>

ACADEMIC APPOINTMENTS

Sept 2024 – present	University of Washington, Seattle Genome Sciences	Assistant Professor
May 2022 – June 2024	University of California, Berkeley Electrical Engineering & Computer Sciences	McDonnell Foundation Fellow host: Dr. Yun S. Song

ACADEMIC AFFILIATIONS

Dec 2024 – present	Computational Biology Program Fred Hutchinson Cancer Center, Seattle	Affiliate Investigator
Oct 2024 – present	Computational Molecular Biology Program University of Washington, Seattle	Training Faculty
Sept 2024 – present	NIH/NHGRI Genome Training Grant University of Washington, Seattle	Training Faculty
April 2022 – April 2024	Santa Fe Institute, Santa Fe, NM	JSMF-SFI Postdocs in Complexity

PUBLICATIONS AND PREPRINTS (* = co-first authorship, † = co-senior authorship)

J Pae, N Schwan, B Ottino-Loffler, **WS DeWitt**, A Garg, J Bortolatto, AA Vora, J Shen, A Hobbs, TBR Castro, L Mesin, FA Matsen IV, M Meyer-Hermann, GD Victora. *Transient silencing of hypermutation preserves B cell affinity during clonal bursting*. [Nature \(2025\): 1-9](#)

W Dumm, D Ralph, **WS DeWitt**, A Vora, T Araki, GD Victora, FA Matsen IV. *Leveraging DAGs to improve context-sensitive and abundance-aware tree estimation*. [Phil. Trans. R. Soc. B 380: 20230315 \(2025\)](#)

HK Haddox, G Angehrn, L Sesta, C Jennings-Shaffer, SD Temple, JG Galloway, **WS DeWitt**, JD Bloom, FA Matsen IV, RA Neher. *The mutation rate of SARS-CoV-2 is highly variable between sites and is influenced by sequence context, genomic region, and RNA structure*. [bioRxiv 2025.01.07.631013 \(2025\)](#)

M Jagota, C Hsu, T Mazumder, K Sung, **WS DeWitt**, J Listgarten, FA Matsen IV, CJ Ye, YS Song. *Learning antibody sequence constraints from allelic inclusion*. [bioRxiv 2024.10.22.619760 \(2024\)](#)

GE Boyle, KA Sitko, JG Galloway, HK Haddox, AH Bianchi, A Dixon, MK Wheelock, AJ Vandt, ZR Wang, RES Thomson, RK Garge, AE Rettie, AF Rubin, RC Geck, EMJ Gillam, **WS DeWitt**, FA Matsen IV, DM Fowler. *Deep mutational scanning of CYP2C19 reveals a substrate specificity-abundance tradeoff*. [Genetics, Volume 228, Issue 3, November 2024, iyae156. \(2023\)](#)

WS DeWitt, SN Evans, E Hiesmayr, S Hummel. *Mean-field interacting multi-type birth-death processes with a view to applications in phylodynamics*. [Theoretical Population Biology](#) Volume 159 (2024)

M Celentano, **WS DeWitt**, S Prillo, YS Song. *Exact and efficient phylodynamic simulation from arbitrarily large populations*. [arXiv:2402.17153 \[q-bio.PE\]](#) (2024)

W Dumm, M Barker, W Howard-Snyder, **WS DeWitt**, FA Matsen IV. *Representing and extending ensembles of parsimonious evolutionary histories with a directed acyclic graph*. [J. Math. Biol.](#) **87**, 75 (2023).

HK Haddox, JG Galloway, B Dadonaite, JD Bloom[†], FA Matsen IV[†], **WS DeWitt**[†]. *Jointly modeling deep mutational scans identifies shifted mutational effects among SARS-CoV-2 spike homologs*. [bioRxiv 2023.07.31.551037](#) (2023)

WS DeWitt, L Zhu, MR Vollger, ME Goldberg, A Talenti, AC Beichman, K Harris. *mutyper: assigning and summarizing mutation types for analyzing germline mutation spectra*. [JOSS](#) **8(85)**, 5227 (2023)

MR Vollger, PC Dishuck, WT Harvey, **WS DeWitt**, X Guitart, ME Goldberg, A Rozanski, J Lucas, M Asri, KM Munson, AP Lewis, K Hoekzema, GA Logsdon, D Porubsky, B Paten, K Harris, P Hsieh, EE Eichler, Human Pangenome Reference Consortium, *Increased mutation and gene conversion within human segmental duplications*. [Nature](#) **617 (7960)**, 325-334 (2023)

TC Yu, ZT Thornton, WH Hannon, **WS DeWitt**, CE Radford, FA Matsen, JD Bloom. *A biophysical model of viral escape from polyclonal antibodies*. [Virus Evolution](#), Volume 8, Issue 2, (2022)

AF Magee^{*}, SK Hilton^{*}, **WS DeWitt**^{*}, *Robustness of phylogenetic inference to model misspecification caused by pairwise epistasis*. [Molecular Biology and Evolution](#), **38 (10)**, 4603-4615, (2021)

WS DeWitt, KD Harris, AP Ragsdale, K Harris. *Nonparametric coalescent inference of mutation spectrum history and demography*. [Proceedings of the National Academy of Sciences](#), 118(21) (2021).

Z Montague, H Lv, J Otwinowski, **WS DeWitt**, G Isacchini, GK Yip, WW Ng, OTY Tsang, M Yuan, H Liu, IA Wilson, M Peiris, NC Wu, A Nourmohammad, CKP Mok. *Dynamics of B cell repertoires and emergence of cross-reactive responses in patients with different severities of COVID-19*. [Cell Reports](#), **35 (8)** (2021)

J Feng, **WS DeWitt**, A McKenna, N Simon, A Willis, FA Matsen. *Estimation of cell lineage trees by maximum-likelihood phylogenetics*. [The Annals of Applied Statistics](#), **15 (1)** (2021)

J Carlson, **WS DeWitt**, K Harris. *Inferring evolutionary dynamics of mutation rates through the lens of mutation spectrum variation*. [Current Opinion in Genetics & Development](#) **62**, 50-57 (2020)

K Davidsen, BJ Olson, **WS DeWitt**, J Feng, E Harkins, P Bradley, FA Matsen. *Deep generative models for T cell receptor protein sequences*. [eLife](#) (2019)

WS DeWitt, A Smith, G Schoch, JA Hansen, FA Matsen, PH Bradley. *Human T cell receptor occurrence patterns encode immune history, genetic background, and receptor specificity*. [eLife](#). (2018)

DA Cusanovich, AJ Hill, D Aghamirzaie, RM Daza, HA Pliner, JB Berletch, GN Filippova, X Huang, L Christiansen, **WS DeWitt**, C Lee, SG Regalado, DF Read, FJ Steemers, CM Disteche, C Trapnell, J Shendure. *A single-cell atlas of in vivo mammalian chromatin accessibility*. [Cell](#) **174 (5)** (2018)

WS DeWitt, KK Quan, D Wilburn, A Sherwood, M Vignali, SC De Rosa, CL Day, TJ Scriba, HS Robins, W Swanson, RO Emerson, P Bradley, C Seshadri. *A diverse lipid antigen-specific TCR repertoire is clonally expanded during active tuberculosis*. [The Journal of Immunology](#) **201 (3)**, 888-896 (2018)

WS DeWitt, L Mesin, GD Victora, VN Minin, FA Matsen. *Using genotype abundance to improve phylogenetic inference*. [Molecular Biology and Evolution](#), Volume 35, Issue 5, 1 May 2018, Pages 1253-1265

RO Emerson*, **WS DeWitt***, M Vignali, J Gravley, JK Hu, EJ Osborne, C Desmarais, M Klinger, CS Carlson, JA Hansen, M Rieder, HS Robins. *Immunosequencing identifies signatures of cytomegalovirus exposure history and HLA-mediated effects on the T cell repertoire.* [Nature Genetics](#) 49, (2017)

WS DeWitt*, P Lindau*, TM Snyder*, AM Sherwood, M Vignali, CS Carlson, PD Greenberg, N Duerkopp, RO Emerson, HS Robins. *A Public Database of Memory and Naive B-Cell Receptor Sequences.* [PLoS ONE](#) 11(8) (2016)

WS DeWitt, RO Emerson, P Lindau, M Vignali, TM Snyder, C Desmarais, C Sanders, H Utsugi, EH Warren, J McElrath, KW Makar, A Wald, HS Robins. *Dynamics of the Cytotoxic T Cell Response to a Model of Acute Viral Infection.* [J Virol](#) 89:4517–4526 (2015)

WS DeWitt, P Lindau, TM Snyder, M Vignali, RO Emerson, HS Robins. *Replicate Immunosequencing as a Robust Probe of B Cell Repertoire Diversity.* [arXiv:1410.0350](#) [q-bio.QM] (2014)

WS DeWitt, K. Chu. *Imaging Protein Statistical Substate Occupancy in a Spectrum-Function Phase Space.* [Physical Review Letters](#) 105, 098101 (2010)

PATENTS

Multiplexed digital quantitation of rearranged lymphoid receptors in a complex mixture
[US 2016/0138011 A1](#) (2016)

Characterization of adaptive immune response to vaccination or infection using immune repertoire sequencing
[US 11,066,705 B2](#) (2021)

Methods for diagnosing infectious disease and determining HLA status using immune repertoire sequencing
[US 11,047,008 B2](#) (2021)

FUNDING

Santa Fe Institute Micro Working Groups. Role: co-organizer of four one-week collaborative workshops:

<i>Slow-fast dynamics in biological systems I</i>	March 23–28, 2023
<i>Slow-fast dynamics in biological systems II</i>	Oct 7–11, 2023
<i>Evolutionary dynamics of cheating in viral infections I</i>	April 10–15, 2024
<i>Evolutionary dynamics of cheating in viral infections II</i>	Nov 2–7, 2024

Postdoctoral Fellowship in Understanding Dynamic and Multi-scale Systems, James S. McDonnell Foundation. Role: PI, full salary support and travel/equipment budget. May 2022 – July 2024

Kirschstein Predoctoral Individual National Research Service Award (F31AI150163). NIAID, NIH. Role: PI. Impact Score: 13 Jan 2020 – Dec 2022

Genome Training Grant (T32HG000035-23). NHGRI, NIH. Role: trainee Sept 2017 – Sept 2019

PROFESSIONAL EMPLOYMENT

Fred Hutchinson Cancer Center	Programmer/Analyst II	Aug 2016 – Sep 2017
Adaptive Biotechnologies	Sr. Computational Biologist	Apr 2015 – Aug 2016
	Sr. Bioinformatics Scientist	Oct 2012 – Mar 2015
Columbia Genome Center	Senior Scientific Programmer	Nov 2011 – Sep 2012
Bloomberg L.P.	R&D Developer	Aug 2011 – Oct 2011
Ascension Technology Corp.	Computational Physicist	Jun 2010 – Aug 2011
	Numerical Analyst Intern	Jun 2007 – Jun 2010

TEACHING EXPERIENCE

University of Washington Genome Sciences	Instructor of record for GENOME 541: Population Genetic Inference	Spring 2020
	Teaching Assistant for GENOME 361: Introduction to Genetics	Winter 2020
UVM Physics Dept.	Teaching Assistant / Tutor	Feb 2007 – May 2007
VT HITEC Inc.	Teaching Consultant	Jul 2006 – Sep 2006

INVITED TALKS

<i>Effective theories and response functions for germinal center evolutionary dynamics.</i> Kavli Institute for Theoretical Physics, Santa Barbara. Hosted by Thierry Mora.	October 2, 2024
<i>Dynamics, prediction, and computation for evolutionary mechanisms in immune responses.</i> Stanford University, Biomedical Data Science Seminar. Hosted by Chiara Sabatti.	March 7, 2024
<i>Dynamics, prediction, and computation for evolutionary mechanisms in immune responses.</i> University of Washington, Genome Sciences Seminar. Hosted by Douglas Fowler.	February 14, 2024
<i>Experiments, theory, and inference for parallel replay of B-cell evolution.</i> Aspen Center for Physics, Aspen, Colorado. Program on statistical physics & adaptive immunity. Hosted by Armita Nourmohammad	August 18, 2023
<i>Evolution of antibody affinity maturation in replica germinal centers.</i> Ohio State University, Biomedical Informatics seminar. Hosted by Dr. Brian Searle.	October 7, 2022
<i>Inferring evolutionary processes across scales: from germline mutagenesis to adaptive immunity.</i> Columbia University, Program for Mathematical Genomics. Hosted by Dr. Mohammed AlQuraishi.	March 10, 2022
<i>Inferring evolutionary processes across scales: from germline mutagenesis to adaptive immunity.</i> Arizona State University, Dept. of Physics and Center for Mechanisms of Evolution. Hosted by Dr. Banu Ozkan and Dr. Michael Lynch.	February 16, 2022
<i>Evolutionary inference for mutagenesis, demography, and adaptive immunity.</i> Cornell University Dept. of Computational Biology. Hosted by Dr. Philipp Messer [virtual].	November 16, 2020
<i>Adaptive immune repertoires: a structured space of chemical sensors.</i> Princeton Institute for Theoretical Sciences: Sensing chemical spaces.	December 12, 2019
<i>Inferring ancient dynamics of mutational processes that shape modern genetic variation.</i> University of Oregon The Institute of Ecology and Evolution. Hosted by Dr. Peter Ralph.	November 22, 2019
<i>Antibody affinity maturation as a model system for sequence evolution.</i> ETH Zürich Dept. of Environmental Systems Science. Hosted by Prof. Dr. Joshua Payne.	July 29, 2019
<i>Computational approaches to adaptive immune repertoires.</i> Roche Sequencing, Pleasanton, CA. Hosted by Dr. Jan Berka.	June 27, 2018
<i>Quantitative methods for analysis of immunosequencing data.</i> Google Life Sciences (formerly Google[x], currently Verily)	October 9, 2015
<i>Imaging Protein Statistical Substate Occupancy in a Spectrum-Function Phase Space.</i> Bio-computing Department, DFG Research Center MATHEON, Freie Universität Berlin. Hosted by Prof. Dr. Frank Noé	December 14, 2010

Imaging Protein Statistical Substate Occupancy in a Spectrum-Function Phase Space. Max Planck Institute for Biophysical Chemistry, Göttingen. Hosted by Prof. Dr. Helmut Grubmüller October 1, 2010

CONTRIBUTED TALKS

Tractable phylodynamic processes with lineage interactions. Evo-WIBO 2025, Blaine WA. April 5, 2025

Evolutionary dynamics of antibody affinity maturation in replica germinal centers. SMBE 2023, Ferrara, Italy. July 24, 2023

Evolutionary dynamics of antibody affinity maturation in replica germinal centers. Probabilistic Modeling in Genomics 2023, CSHL March 12, 2023

Evolution of antibody affinity maturation in replica germinal centers. Bay Area Population Genetics, UC Berkeley. October 15, 2022

Reconstructing human mutation spectrum evolution over thousands of generations. Probabilistic Modeling in Genomics 2021 [virtual] April 14, 2021

~~*Joint non-parametric inference of demography and time-calibrated mutation spectrum histories.*~~ SMBE-2020 [meeting canceled due to COVID-19] July 1, 2020

Coalescent inference of mutation spectrum histories from sample frequency spectra. TAGC 2020, lightning talk [converted to virtual poster Q&A due to COVID-19] May 1, 2020

Antibody affinity maturation as a model system for sequence evolution. Nordic Institute for Theoretical Physics: Predictability and control of evolution. July 25, 2019

HONORS, AWARDS

SMBE 2023 Young Investigator Award

Probabilistic Modeling in Genomics 2018 registration award

University of Washington Graduate School international conference travel award, 2018

Cover art submission selected for May 2018 issue of *Molecular Biology and Evolution*.

SMBE 2018 Yokohama, Registration Award

WORKSHOPS AND TRAININGS

Interactions and Co-evolution between Viruses and Immune Systems
Kavli Institute for Theoretical Physics, Santa Barbara 3-week program
Sep 24–Oct 11, 2024

Inclusive Research Mentor-Manager Training
UCSF-CCSF 4 hours per week, 5 weeks
Oct 11–Nov 17, 2023

Program on Statistical Physics & Adaptive Immunity
Aspen Center for Physics 2-week workshop
Aug 14–25, 2023

Sensing Chemical Spaces
Princeton Center for Theoretical Sciences 1-week workshop
December 11-13, 2019

10th annual summer institute in statistics and modeling in infectious diseases: Evolutionary dynamics and molecular epidemiology of viruses
University of Washington Intensive course
Jul 18–20, 2018

SERVICE

Peer Review: Molecular Biology & Evolution, Genetics, PLoS Comp Bio, eLife, Bioinformatics, Nature Scientific Reports, Science, Royal Society Interface

Co-founder and organizer of Evo-Hub, UW evolution community meetings, Fall 2024 – present

Faculty organizer for UW Genome Sciences departmental retreat – Fall 2025

Co-organizer for Berkeley Center for Theoretical Evolutionary Genetics, Spring 2023 – Spring 2024

Organizer for departmental seminars in UW Genome Sciences, Spring 2020 – Fall 2020

Graduate student representative in UW Genome Sciences monthly faculty meetings, 2018 – 2019

UW / Fred Hutch Molecular Evolution Supergroup, organizer of ~monthly meetings, 2019 – 2020

UW Genome Sciences 1st year mentor. 2019 – 2022

UW Popgen Lunch seminar series organizer, weekly Spring 2021

OUTREACH

Imagine Science Films

- Unit still photography, B-roll camera, and scientific production assistant on the set of The Fly Room, a short film about the geneticist Calvin Bridges, which we shot in the reconstructed "fly room" of Thomas Hunt Morgan in its original location at Columbia University.
- Video editor for ISF's mixed media exhibit at the [dOCUMENTA \(13\)](#) art exbo in Kassel Germany
- Ambassador for the [Scenes](#) project