William S. DeWitt

Department of Genome Sciences, University of Washington
Foege Building S130C, 3720 15th Ave NE, Seattle WA 98195-5065
wsdewitt@uw.edu | dewitt-lab.github.io

Education

PhD, 2022	Genome Sciences, University of Washington, Seattle Advisors: Kelley Harris, Erick Matsen Dissertation: *Some problems in probabilistic modeling of germline and somatic evolutionary processes*
MS, BA, 2011	Physics, University of Vermont Advisor: Kelvin Chu Thesis: *Imaging protein statistical substate occupancy in a spectrum-function phase space*

Academic Appointments

Sep 2024 – present	Assistant Professor	University of Washington, Seattle Department of Genome Sciences
May 2022 – Jun 2024	McDonnell Foundation Fellow	University of California, Berkeley Department of Electrical Engineering & Computer Sciences Host: Yun S. Song

Academic Affiliations

Molecular Engineering & Sciences Institute University of Washington, Seattle	Faculty Member Apr 2025 – present
Computational Biology Program Fred Hutchinson Cancer Center, Seattle	Affiliate Investigator Dec 2024 – present
Computational Molecular Biology Program University of Washington, Seattle	Training Faculty Oct 2024 – present
NIH/NHGRI Genome Training Grant University of Washington, Seattle	Training Faculty Sep 2024 – present
Santa Fe Institute Santa Fe, NM	JSMF-SFI Postdocs in Complexity Apr 2022 – Apr 2024

Professional Employment

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

Publications And Preprints

** = co-first authorship, ° = co-senior authorship*

M Celentano, **WS DeWitt**, S Prillo, YS Song. *Exact and efficient phylodynamic simulation from arbitrarily large populations.* PNAS 122 (20) e2412978122 (2025)

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 Vandi, 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. (2024)

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)

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:

- Mar 23–28, 2023, *Slow-fast dynamics in biological systems I*
- Oct 7–11, 2023, *Slow-fast dynamics in biological systems II*
- Apr 10–15, 2024, *Evolutionary dynamics of cheating in viral infections I*
- Nov 2–7, 2024, *Evolutionary dynamics of cheating in viral infections II*

May 2022 – Jul 2024	*Postdoctoral Fellowship in Understanding Dynamic and Multi-scale Systems.* James S. McDonnell Foundation. Role: PI.
Jan 2020 – Dec 2022	*Kirschstein Predoctoral Individual National Research Service Award* (F31AI150163). NIAID, NIH. Role: PI. Impact Score: 13
Sep 2017 – Sep 2019	*Genome Training Grant* (T32HG000035-23). NHGRI, NIH. Role: trainee.

Trainees

Postdoctoral Researchers

Magdelena Russell	*Postdoctoral Researcher / T32 Fellow*	Apr 2025 – present

Graduate Students

Carlo Melendez	*Genome Sciences rotation*	Spring 2025
Arnav Nagle	*MolES rotation*	Spring 2025

Teaching

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

Invited Talks

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

Dec 14, 2010	*Imaging Protein Statistical Substate Occupancy in a Spectrum-Function Phase Space.* Biocomputing Department, DFG Research Center MATHEON, Freie Universität Berlin. Hosted by Prof. Dr. Frank Noé
Oct 1, 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

CONTRIBUTED TALKS

Apr 5, 2025	*Tractable phylodynamic processes with lineage interactions.* Evo-WIBO 2025, Blaine WA.
Jul 24, 2023	*Evolutionary dynamics of antibody affinity maturation in replica germinal centers.* SMBE 2023, Ferrara, Italy.
Mar 12, 2023	*Evolutionary dynamics of antibody affinity maturation in replica germinal centers.* Probabilistic Modeling in Genomics 2023, CSHL.
Oct 15, 2022	*Evolution of antibody affinity maturation in replica germinal centers.* Bay Area Population Genetics, UC Berkeley.
Apr 14, 2021	*Reconstructing human mutation spectrum evolution over thousands of generations.* Probabilistic Modeling in Genomics 2021 [virtual].
Jul 1, 2020	*Joint non-parametric inference of demography and time-calibrated mutation spectrum histories.* SMBE 2020 [meeting canceled due to COVID-19].
May 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].
Jul 25, 2019	*Antibody affinity maturation as a model system for sequence evolution.* Nordic Institute for Theoretical Physics: Predictability and control of evolution.

HONORS AND AWARDS

2023	Young Investigator Award, SMBE (Ferrara, Italy)
2018	Registration Award, Probabilistic Modeling in Genomics (CSHL)
2018	International Conference Travel Award, University of Washington Graduate School
2018	Cover art selected for May issue of Molecular Biology and Evolution.
2018	Registration Award, SMBE (Yokohama, Japan)

WORKSHOPS AND TRAININGS

Sep 24 – Oct 11, 2024	*Interactions and Co-evolution between Viruses and Immune Systems.* Kavli Institute for Theoretical Physics, Santa Barbara. 3-week program.
Oct 11 – Nov 17, 2023	*Inclusive Research Mentor-Manager Training.* UCSF-CCSF. 4 hours per week, 5 weeks.
Aug 14–25, 2023	*Program on Statistical Physics & Adaptive Immunity.* Aspen Center for Physics. 2-week workshop.
Dec 11–13, 2019	*Sensing Chemical Spaces.* Princeton Center for Theoretical Sciences. 1-week workshop.
Jul 18–20, 2018	*10th annual summer institute in statistics and modeling in infectious diseases: Evolutionary dynamics and molecular epidemiology of viruses.* University of Washington. Intensive course.

SERVICE

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

Dissertation committee member (GSR), Jack Castelli (UW M3D program), Spring 2025

Dissertation committee member, Lucas Kampman (UW MCB program), Spring 2025 – present

Dissertation opponent, Andrei Slabodkin, Immunology, University of Oslo, Norway, Spring 2025 – present

Genome Sciences Seminar Committee member, Winter 2025 – present

Co-founder and organizer of Evo-Hub, UW evolution community meetings, Winter 2025 – 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 expo in Kassel, Germany
- Ambassador for the Scenes project