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Education

- Australian National University, B Actuarial Studies (Honours), 12/2011
- Cornell University, M.S., Statistics, 01/2015
- Cornell University, Ph.D., Statistics, 05/2017

Professional Positions

- Senior Analyst, Macroeconomics, Canberra, Australia, 08/2009-06/2012
- Research, Data Management and Audit Officer, ACT NOWaste, Canberra, Australia, 11/2011-06/2012
- Statistical Consultant, Zadeh Laboratory, College of Human Ecology, Cornell University, 12/2014-05/2015
- Quantitative Analyst Intern, Google, Mountain View, CA, 05/2015-07/2015
- Associate Professor (with tenure), Department of Biostatistics, University of Washington, Seattle, WA, 07/2023-present
 - Assistant Professor (tenure-track), Department of Biostatistics, University of Washington, Seattle, WA, 06/2017-06/2023
 - Genentech Endowed Professorship in Biostatistics, 07/2018-06/2019
 - Adjunct Assistant Professor, Department of Statistics, 10/2017-present
 - Member, Center for Microbiome Sciences and Therapeutics (CMiST), UW Medicine, 2017-present
 - Program Faculty, Quantitative Ecology and Resource Management (QERM), UW College of the Environment, 2019-present
 - Affiliate Faculty, UW eScience Institute, 2019-present
 - Program Faculty, UW Computational Molecular Biology, 2019-present
- Scientific Advisory Board Member, Microbiome Biomarker Program, Takeda Pharmaceuticals, Boston, MA, 2020

Honors, Awards, Scholarships

- National Undergraduate Scholarship, Australian National University, 2008-2011
- Australian National University College of Business and Economics Summer Research Scholarship, 2009-2010.
- John XXIII College Academic Excellence Scholarship, 2008, 2009
- First Class Honours, Australian National University, 2011

- 3-Minute Thesis Finalist, Cornell University, 2015
- College Banner Bearer, Cornell University, 2017
- Outstanding Investigator Award, National Institutes of Health, 2019
- Outstanding Faculty Mentor Award, School of Public Health, University of Washington, 2021
- Outstanding Faculty Teaching Award, School of Public Health, University of Washington, 2022

Professional Activities

- Professional Memberships: American Statistical Association; International Biometric Society (Western North American Region); National Geographic Society
- Referee Service: Annals of Applied Statistics; Annals of Statistics; Bayesian Analysis; Bioinformatics; Biometrics; Biostatistics; Environmental and Ecological Statistics; Environmental Microbiology; Genome Biology; Journal of Applied Statistics; Journal of Agricultural, Biological, and Environmental Statistics; Journal of the American Statistical Association; Journal of Mathematical Biology; Journal of Nonparametric Statistics; mSystems; Microbiome; mSystems; Nature Ecology & Evolution; Nature Medicine; Nature Methods; PLoS Biology; PLoS Computational Biology; PLoS ONE; Scandinavian Journal of Statistics
- Guest Editor: PLoS Computational Biology (2017)
- Associate Editor: Microbiome (2018-2019)
- Associate Editor: Biostatistics (2018+)
- Associate Editor: Journal of the American Statistical Association, Applications & Case Studies (2019)
- Committee Member for Student Paper Competition, Conference on Statistical Learning, Data Science and Nonparametric Statistics (2020)
- External Doctoral Thesis Examiner: [university name redacted for confidentiality] (2020)

Bibliography

(a) Refereed research articles

(Student co-authors who I mentored are also highlighted in **bold**.)

- 1) John Bunge, **Amy Willis**, and Fiona Walsh. Estimating the Number of Species in Microbial Diversity Studies. *Annual Review of Statistics and Its Application*, 1(1):427–445, 2014.
- 2) Jacob P Christ, **Amy D Willis**, Eric D Brooks, Heidi Vanden Brink, Brittany Y Jarrett, Roger A Pierson, Donna R Chizen, and Marla E Lujan. Follicle number, not assessments of the ovarian stroma, represents the best ultrasonographic marker of polycystic ovary syndrome. *Fertility and sterility*, 101(1):280–287, 2014.
- 3) Arindam RoyChoudhury, **Amy Willis**, and John Bunge. Consistency of a phylogenetic tree maximum likelihood estimator. *Journal of Statistical Planning and Inference*, 161:73–80, 2015.
[Corresponding author]
- 4) **Amy D Willis** and John Bunge. Estimating diversity via frequency ratios. *Biometrics*, 71(4):1042–1049, 2015.

- 5) Gennady Samorodnitsky, Sidney Resnick, Don Towsley, Richard Davis, **Amy Willis**, and Phyllis Wan. Nonstandard regular variation of in-degree and out-degree in the preferential attachment model. *Journal of Applied Probability*, 53(1):146–161, 2016.
- 6) Heidi Vanden Brink, **Amy D Willis**, Brittany Y Jarrett, Annie W Lin, Steven Soler, Siân Best, Erica L Bender, Andrew K Peppin, Kathleen M Hoeger, and Marla E Lujan. Sonographic markers of ovarian morphology, but not hirsutism indices, predict serum total testosterone in women with regular menstrual cycles. *Fertility and sterility*, 105(5):1322–1329, 2016.
- 7) **Amy D Willis**. Extrapolating abundance curves has no predictive power for estimating microbial biodiversity. *Proceedings of the National Academy of Sciences*, 113(35):E5096–E5096, 2016.
- 8) **Amy D Willis**, John Bunge, and Thea Whitman. Improved detection of changes in species richness in high-diversity microbial communities. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 66(5):963–977, 2016.
- 9) Nancy Chan, **Amy Willis**, Naomi Kornhauser, Maureen M Ward, Sharrell B Lee, Eleni Nackos, Bo Ri Seo, Ellen Chuang, Tessa Cigler, Anne Moore, Diana Donovan, Marta Vallee Cobham, Veronica Fitzpatrick, Sarah Schneider, Alysia Wiener, Jessica Guillaume-Abraham, Elnaz Aljom, Richard Zerkowitz, J David Warren, Maureen E Lane, Claudia Fischbach, Vivek Mittal, and Linda Vahdat. Influencing the Tumor Microenvironment: A Phase II Study of Copper Depletion Using Tetrathiomolybdate in Patients with Breast Cancer at High Risk for Recurrence and in Preclinical Models of Lung Metastases. *Clinical Cancer Research*, 23(3):666–676, 2017.
- 10) Clément P Bataille, **Amy Willis**, Xiao Yang, and Xiao-Ming Liu. Continental igneous rock composition: A major control of past global chemical weathering. *Science Advances*, 3(3):e1602183, 2017.
- 11) Sheena Sahota, Naomi Kornhauser, **Amy Willis**, Maureen M Ward, Tessa Cigler, Anne Moore, Eleni Andreopoulou, Veronica Fitzpatrick, Sarah E Schneider, Alysia Wiener, Anna Rubinchik, Sharrell Lee, Maureen E Lane, Vivek Mittal, and Linda T Vahdat. A phase II study of copper-depletion using tetrathiomolybdate (TM) in patients (pts) with breast cancer (BC) at high risk for recurrence: Updated results. *Journal of Clinical Oncology*, 35(15):2557–2557, 2017.
- 12) **Amy D Willis** and Rayna C Bell. Uncertainty in phylogenetic tree estimates. *Journal of Computational and Graphical Statistics*, 27(3):542–552, 2018.
- 13) **Amy Willis**. Confidence sets for phylogenetic trees. *Journal of the American Statistical Association*, 114(525):235–244, 2019.
- 14) Nicolas Tromas, Zofia E Taranu, **Bryan D Martin**, **Amy Willis**, Nathalie Fortin, Charles W Greer, and B Jesse Shapiro. Niche Separation Increases With Genetic Distance Among Bloom-Forming Cyanobacteria. *Frontiers in Microbiology*, 9:109, 2018.
- 15) **Amy D Willis**. Rigorous statistical methods for rigorous microbiome science. *mSystems*, 4(3), 2019.
- 16) Anna E Sarfaty, Caroline J Zeiss, **Amy D Willis**, Jorgen M Harris, and Peter C Smith. Concentration dependent toxicity following subcutaneous meloxicam administration in C57Bl/6N Mice. *Journal of the American Association of Laboratory Animal Science*, 58(6):802–809, 2019.
- 17) Evan Bolyen, Jai Ram Rideout, Matthew R Dillon, Nicholas A Bokulich, Christian C Abnet, Gabriel A Al-Ghalith, Harriet Alexander, Eric J Alm, Manimozhyan Arumugam, Francesco Asnicar, Yang Bai,

Jordan E Bisanz, Kyle Bittinger, Asker Brejnrod, Colin J Brislawn, C Titus Brown, Benjamin J Callahan, Andrés Mauricio Caraballo-Rodríguez, John Chase, Emily K Cope, Ricardo Da Silva, Christian Diener, Pieter C Dorrestein, Gavin M Douglas, Daniel M Durall, Claire Duvallet, Christian F Edwardson, Madeleine Ernst, Mehrbod Estaki, Jennifer Fouquier, Julia M Gauglitz, Sean M Gibbons, Deanna L Gibson, Antonio Gonzalez, Kestrel Gorlick, Jiarong Guo, Benjamin Hillmann, Susan Holmes, Hannes Holste, Curtis Huttenhower, Gavin A Huttley, Stefan Janssen, Alan K Jarmusch, Lingjing Jiang, Benjamin D Kaehler, Kyo Bin Kang, Christopher R Keefe, Paul Keim, Scott T Kelley, Dan Knights, Irina Koester, Tomasz Kosciolk, Jordan Kreps, Morgan G I Langille, Joslynn Lee, Ruth Ley, Yong-Xin Liu, Erikka Loftfield, Catherine Lozupone, Massoud Maher, Clarisse Marotz, **Bryan D Martin**, Daniel McDonald, Lauren J McIver, Alexey V Melnik, Jessica L Metcalf, Sydney C Morgan, Jamie T Morton, Ahmad Turan Naimy, Jose A Navas-Molina, Louis Felix Nothias, Stephanie B Orchanian, Talima Pearson, Samuel L Peoples, Daniel Petras, Mary Lai Preuss, Elmar Pruesse, Lasse Buur Rasmussen, Adam Rivers, Michael S Robeson, Patrick Rosenthal, Nicola Segata, Michael Shaffer, Arron Shiffer, Rashmi Sinha, Se Jin Song, John R Spear, Austin D Swafford, Luke R Thompson, Pedro J Torres, **Pauline Trinh**, Anupriya Tripathi, Peter J Turnbaugh, Sabah Ul-Hasan, Justin J J van der Hoof, Fernando Vargas, Yoshiki Vázquez-Baeza, Emily Vogtmann, Max von Hippel, William Walters, Yunhu Wan, Mingxun Wang, Jonathan Warren, Kyle C Weber, Charles H D Williamson, **Amy D Willis**, Zhenjiang Zech Xu, Jesse R Zaneveld, Yilong Zhang, Qiyun Zhu, Rob Knight, and J Gregory Caporaso. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, 37(8):852–857, 2019.

- 18) **Bryan Martin**, Daniela Witten* and **Amy Willis***. Modeling microbial abundances and dysbiosis with beta-binomial regression. *Annals of Applied Statistics*, 14(1):94–115, 2019. (* = joint senior author)
- 19) Samuel S Minot and **Amy D Willis**. Clustering co-abundant genes identifies components of the gut microbiome that are reproducibly associated with colorectal cancer and inflammatory bowel disease. *Microbiome*, 7(110), 2019.
- 20) Michael R McLaren, **Amy D Willis**, and Benjamin J Callahan. Consistent and correctable bias in metagenomic sequencing measurements. *eLife*, 8, 2019.
- 21) **Amy D Willis**. Rarefaction, alpha diversity, and statistics. *Frontiers in Microbiology*, 10:2407, 2019.
- 22) **Amy D Willis** and Samuel S Minot. Strategies to Facilitate Translational Advances from Microbiome Surveys. *Trends in Microbiology*, 2020.
- 23) **Amy D Willis** and **Bryan D Martin**. DivNet: Estimating diversity in networked communities. *Biostatistics*, 2020.
- 24) Alon Shaiber, **Amy D Willis**, Tom O Delmont, Simon Roux, Lin-Xing Chen, Abigail C Schmid, Mahmoud Yousef, Andrea R Watson, Karen Lolans, Özcan C Esen, Sonny T M Lee, Nora Downey, Hilary G Morrison, Floyd E Dewhirst, Jessica L Mark Welch, and A Murat Eren. Functional and genetic markers of niche partitioning among enigmatic members of the human oral microbiome. *Genome Biology*, 21(292), 2020.
- 25) **Alex Paynter** and **Amy D Willis**. Tuning parameter selection for a penalized estimator of species richness. *Journal of Applied Statistics*, 48(6):1053–1070, 2021.
- 26) Jean Feng, William S DeWitt III, Aaron McKenna, Noah Simon, **Amy D Willis**, and Frederick A Matsen IV. Estimation of cell lineage trees by maximum-likelihood phylogenetics. *The Annals of Applied Statistics*, 15(1):343 – 362, 2021.

- 27) A Murat Eren, Evan Kiefl, Alon Shaiber, Iva Veseli, Samuel E Miller, Matthew S Schechter, Isaac Fink, Jessica N Pan, Mahmoud Yousef, Emily C Fogarty, Florian Trigodet, Andrea R Watson, Özcan C Esen, Ryan M Moore, Quentin Clayssen, Michael D Lee, Veronika Kivenson, Elaina D Graham, Bryan D Merrill, Antti Karkman, Daniel Blankenberg, John M Eppley, Andreas Sjödin, Jarrod J Scott, Xabier Vázquez-Campos, Luke J McKay, Elizabeth A McDaniel, Sarah L R Stevens, Rika E Anderson, Jessika Fuessel, Antonio Fernandez-Guerra, Lois Maignien, Tom O Delmont, and **Amy D Willis**. Community-led, integrated, reproducible multi-omics with anvi'o. *Nature Microbiology*, 6(1):3–6, 2021.
 - 28) Samuel S Minot, Kevin C Barry, Caroline Kasman, Jonathan L Golob, and **Amy D Willis**. geneshot: gene-level metagenomics identifies genome islands associated with immunotherapy response. *Genome Biology*, 22(1):1–10, 2021.
 - 29) **Brian D Williamson**, James P Hughes, and **Amy D Willis**. A multiview model for relative and absolute microbial abundances. *Biometrics*, 2021.
 - 30) Matthew J Wooller, Clement Bataille, Patrick Druckenmiller, Gregory M Erickson, Pamela Groves, Norma Haubenstock, Timothy Howe, Johanna Irrgeher, Daniel Mann, Katherine Moon, Ben A Potter, Thomas Prohaska, Jeffrey Rasic, Joshua Reuther, Beth Shapiro, Karen J Spaleta, and **Amy D Willis**. Lifetime mobility of an arctic woolly mammoth. *Science*, 373(6556):806–808, 2021.
 - 31) Melissa Kordahi, Mariion Avril, Ian Stanaway, Denise Chac, B Ross, C Diener, Sumita Jain, P McCleary, Anika Parker, Vince Friedman, J Huang, Wynn Burke, Sean Gibbons, **Amy D Willis**, Richard Darveau, WM Grady, Cynthia Ko, and R William DePaolo. Genomic and functional characterization of a mucosal symbiont involved in early-stage colorectal cancer. *Cell Host and Microbe*, 2021.
 - 32) Emily Kuehn, **David S Clausen**, Ryan W Null, Bria M Metzger, **Amy D Willis** and B Duygu Özpolat. Segment number threshold determines juvenile onset of germline cluster proliferation in *Platynereis dumerilii*. *Journal of Experimental Zoology Part B: Molecular and Developmental Evolution*, 338(4):225–240, 2022.
 - 33) **David S Clausen** and **Amy D Willis**. Evaluating Replicability in Microbiome Data. *Biostatistics*, In Press, 2022.
 - 34) Yiqun T Chen, Brian D Williamson, Taylor Okonek, Charles J Wolock, Andrew J Spieker, Travis Y Hee Wai, James P Hughes, Scott S Emerson, and **Amy D Willis**. rigr: Regression, Inference, and General Data Analysis Tools in R. *The Journal of Open Source Software*, In Press, 2022.
- (b) Other refereed scholarly publications
- 1) **Amy Donaldson Willis**. Confidence procedures for phylogenetic trees. May 2017. (PhD Thesis, Cornell University)
- (c) Other non-refereed published scholarly publications
- 1) **David S Clausen** and **Amy D Willis**. Modeling complex measurement error in microbiome experiments.
 - [arxiv: arxiv.org/abs/2204.12733](https://arxiv.org/abs/2204.12733)
 - 2) **Pauline Trinh**, **David S Clausen** and **Amy D Willis**. happi: a Hierarchical Approach to Pangenomics Inference.
 - [bioRxiv: biorxiv.org/content/10.1101/2022.04.26.489591v1](https://bioRxiv.org/content/10.1101/2022.04.26.489591v1)

- 3) Evan Kiefl, Ozcan C Esen, Samuel E Miller, Kourtney Kroll, **Amy D Willis**, Michael S Rappé, Tao Pan and A Murat Eren. Structure-informed microbial population genetics elucidate selective pressures that shape protein evolution.
 - bioRxiv: doi.org/10.1101/2022.03.02.482602
- 4) **Pauline Trinh**, **Amy D Willis**, Milagros Zavaleta, Kathleen Connery, Georgios Kotsakis, Joseph Zunt, Leann Andrews, Jorge A Alarcon, Krisopher A Kerns, Ella I Lamont, Jeffrey S McLean and Peter Rabinowitz. Shifts in Microbial Gut Composition Following a Landscape Intervention in Iquitos, Peru.
- 5) **Xiaochuan Cecilia Shi** and **Amy D Willis**. Removing sample-to-sample cross-contamination in high-throughput sequencing data.
- 6) Taylor E Reiter, Luiz C Irber Jr, Alicia A Gingrich, Dylan Haynes, N Tessa Pierce-Ward, Phillip T Brooks, Yosuke Mizutani, Dominik Moritz, Felix Reidl, **Amy D Willis**, Blair D Sullivan and C Titus Brown. Meta-analysis of metagenomes via machine learning and assembly graphs reveals strain switches in Crohn's disease.
 - bioRxiv: [biorxiv.org/content/10.1101/2022.06.30.498290v1](https://www.biorxiv.org/content/10.1101/2022.06.30.498290v1)
- 7) Michael R McLaren, Jacob T Nearing, **Amy D Willis**, Karen G Lloyd and Benjamin J Callahan. Differential abundance analysis of taxonomically-biased microbiome measurements.
 - bioRxiv: <https://www.biorxiv.org/content/10.1101/2022.08.19.504330v2>
- 8) **Amy Willis**. Species richness estimation with high diversity but spurious singletons.
 - arXiv: [arXiv:1604.02598](https://arxiv.org/abs/1604.02598)

Patents and Other Intellectual Property

- Publicly available software
 1. anvio, "an analysis and visualization platform for 'omics data"
 - Specific contributions: Developed hypothesis test for functional enrichment in pangenomic data
 - anvio is developed and maintained by the Meren Lab at the Helmholtz Institute for Functional Marine Biodiversity (HIFMB) at Oldenburg.
 2. breakaway, an R package for estimating and modelling species richness and microbial diversity
 - Stable release: cran.r-project.org/web/packages/breakaway/index.html
 - Development version: github.com/adw96/breakaway
 - QIIME2 plug-in: github.com/statdivlab/q2-breakaway
 3. corncob, an R package for modeling microbial abundances
 - Stable release: github.com/bryandmartin/corncob (mentored student author: Bryan Martin)
 - QIIME2 plug-in: github.com/statdivlab/q2-corn-cob (mentored student author: Pauline Trinh)
 - Docker container: quay.io/repository/fhcr-microbiome/corncob
 4. DivNet, an R package for estimating diversity in networked communities
 - Stable release: github.com/adw96/DivNet
 5. find-cags, Python code and a Docker image for finding co-abundant genes in microbial shotgun metagenomic data
 - Development version: github.com/FredHutch/find-cags (in collaboration with Sam Minot)

6. geneshot, a Nextflow workflow for identifying and modelling the abundance of microbial genes from shotgun metagenomic sequencing data
 - Installation and documentation: github.com/Golob-Minot/geneshot/wiki/Getting-Started (in collaboration with Sam Minot and Jonathan Golob)
 7. happi, an R package for modeling gene presence and functional enrichment in microbial genomes
 - Development version: github.com/statdivlab/happi (mentored student authors: Pauline Trinh and David S Clausen)
 8. KikWalk, an R package implementing a isotopically-guided Markov Chain for reconstructing lifetime mobility histories based on one or more isotopes
 - Stable version: github.com/statdivlab/KikWalk (in collaboration with Clément Bataille)
 9. metacal, an R package for calibrating high-throughput sequencing data
 - Development version: mikec.github.io/metacal (in collaboration with Michael McLaren and Benjamin Callahan)
 10. paramedic, an R package for jointly modeling relative and absolute microbial abundances
 - Development version: github.com/statdivlab/paramedic (mentored student author: Brian Williamson)
 11. radEmu, an R package to estimate fold-changes in absolute means from relative data
 - Development version: github.com/statdivlab/radEmu (mentored student author: David S Clausen)
 12. rigr, an R package to streamline data analysis in R
 - Stable release: cran.r-project.org/web/packages/rigr/index.html
 - Development version: github.com/statdivlab/rigr
 - Coauthors and contributors: Scott S Emerson, Brian D Williamson, Charles Wolock, Taylor Okonek, Jim Hughes, Andrew J Spieker and Travis Y Hee Wai.
 13. rre, an R package for estimating diversity with replicate frequency count tables
 - Development version: github.com/statdivlab/rre (mentored student author: Alex Paynter)
 14. tinyvamp, an R package for modeling complex measurement error in microbiome experiments
 - Development version: github.com/statdivlab/tinyvamp (mentored student author: David S Clausen)
- Patents
 - Patents Pending
 1. Systems and methods for identifying associations between microbial strains and phenotypic features (US20210319848A1). Inventors: Samuel S. Minot, Amy D. Willis, and Jonathan L. Golob.

Funding History

1. Funded projects

- (a) National Institutes of Health, NIGMS, R35. 1R35GM133420-01.
 - Role: Principal Investigator
 - Budget: \$1,566,054 in total costs; \$323,394/year in total costs; \$230,147/year in direct costs
 - 40% FTE 09/01/2019 – 06/30/2024
 - Project Period: 09/01/2019 – 06/30/2024
 - Title: Statistical Methods to Enhance Reproducible Microbiome Discovery.
 - Collaborators: Sam Minot (co-I, Fred Hutchinson Cancer Research Center)

- (b) National Institutes of Health, NIAID, R21. R21 AI168679-01.
 - Role: Principal Investigator
 - Budget: \$233,250 in total costs; \$75,000/year in direct costs
 - 8% FTE 05/25/2022 – 04/30/2024
 - Project Period: 05/25/2022 – 04/30/2024
 - Title: Statistical pangenomics to study the effects of zoonotic exposure on the gut microbiome.
 - Collaborators: Peter Rabinowitz (co-I, UW Department of Environmental and Occupational Health Sciences).
- (c) UW Cystic Fibrosis Foundation, Research Development Program. SINGH15Ro (PI Singh)
 - Role: subaward Principal Investigator
 - Budget: \$98,234 in total costs to subaward PI Willis
 - 20% FTE 07/01/2021 – 06/30/2023
 - Project Period: 07/01/2021 – 06/30/2023
 - Title: Estimating the composition of the cystic fibrosis pulmonary microbiome.
 - Collaborators: Pradeep Singh (collaborator, University of Washington)
- (d) University of Wisconsin-Madison Data Science Initiative.
 - Role: co-Principal Investigator
 - Title: Addressing misclassification in the microbiome: A data-scientific approach to propagating uncertainty in microbial community composition.
 - Collaborators: Thea Whitman (co-PI, University of Wisconsin-Madison, Department of Soil Science) and Karl Broman (co-I, University of Wisconsin-Madison, Department of Biostatistics and Medical Informatics).
- (e) Amazon Web Services Cloud Credits for Research.
 - Role: Principal Investigator
 - Title: Scaling statistical methods for the analysis of shotgun metagenomics data using distributed computing.
 - Budget: \$12,000 for computing on Amazon Web Services
 - Project Period: 03/11/2019 – present
- (f) National Institutes of Health, NIEHS, R01. 1R01ES030197-01.
 - Role: co-Investigator
 - 10% FTE 01/01/19 – 12/31/21
 - \$51,298 in total direct costs to co-I Willis
 - Title: Developmental PBDE exposure, gut microbiome, and diabetes.
 - Collaborators: Julia Yue Cui (PI, University of Washington, Department of Environmental and Occupational Health Sciences)
- (g) New Frontiers in Research Fund – Exploration, Canada Research Coordinating Committee.
 - Role: co-Investigator
 - 0% FTE
 - \$0 in total direct costs to co-I Willis
 - Title: Phenotype-genotype associations for migratory behaviour in insects: combining isotope geolocation and next-generation sequencing tools.
 - Collaborators: Clement Bataille (PI, University of Ottawa, Department of Earth and Environmental Sciences).

Conferences and Symposia

Keynote & Plenary presentations

1. January 2019: 2019 Workshop on Genomics, Český Krumlov; **Keynote speaker** on *Microbiome Data & Analysis*.
2. December 2019: 4th Thünen Symposium on Soil Metagenomics; Braunschweig, Germany; **Keynote speaker**; organizer: Christoph Tebbe.
3. July 2020: Intelligent Systems for Molecular Biology & European Conference on Computational Biology 2020; Montreal, Canada and online; **Keynote speaker**; organizer: Alice C. McHardy, Microbiome Community of Special Interest of International Society for Computational Biology.
4. May 2022: Purdue Applied Microbiome Sciences Symposium; West Lafayette, Indiana; **Keynote lecturer**; organizer: Stephen R. Lindemann.
5. June 2022: Having IMPACTT: Advancing Microbiome Research; Canmore, Alberta, Canada; **Plenary lecturer** (Bioinformatics & Multi-Omics); organizer: Kathy McCoy, Canadian Microbiome Research Core.
6. July 2022: Bioc2022; Seattle, WA; **Keynote speaker**.
7. (December 2022: Microbiome Virtual International Forums (MVIF); **Keynote speaker**.)

Invited and contributed presentations

* = invited

1. March 2014: Ordered Data Analysis, Models, and Health Research Methods: HNN60; A ratio-based method for estimating an unknown number of classes
2. August 2014: Joint Statistical Meetings; id.
3. October 2014: Université de Montréal, Microbial Evolutionary Genomics Group*; Statistical inference for estimating and modeling diversity
4. June 2015: Google, Decision Support Research Group*; Species Richness Estimation
5. August 2015: Joint Statistical Meetings, Microbiome in Epidemiology Section*; Righting some wrongs in the statistical analysis of microbial community data
6. December 2015: Queensland University of Technology, ARC Centre of Excellence for Mathematical & Statistical Frontiers*; Taxonomic richness: estimation and comparison
7. September 2016: Pontificia Universidad Javeriana, Departamento de Matemáticas*; Teoremas del límite central y conjuntos de confianza para árboles
8. September 2016: Universidad de los Andes, Departamento de Matemáticas*; id.
9. October 2016: University of Glasgow, School of Mathematics and Statistics*; Biodiversity Statistics
10. October 2016: Newcastle University, School of Mathematics and Statistics*; Confidence Sets for Phylogenetic Trees
11. December 2016: Université de Montreal, Département de mathématiques et de statistique*; id.
12. January 2017: Pennsylvania State University, Department of Statistics*; id.
13. January 2017: University of Texas at Austin, Department of Statistics and Data Sciences*; id.

14. January 2017: University of Michigan, Department of Statistics*; id.
15. January 2017: Carnegie Mellon University, Department of Statistics*; id.
16. February 2017: University of Wisconsin-Madison, Department of Biostatistics and Medical Informatics*; id.
17. February 2017: University of Pennsylvania, The Wharton School, Statistics Department*; id.
18. February 2017: Columbia University, Department of Statistics*; id.
19. February 2017: University of Washington, Department of Biostatistics*; id.
20. February 2017: Broad Institute of MIT, Second Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis*; Visualizing uncertainty in phylogenetic trees.
21. March 2017: Cornell University, Department of Statistics; Confidence Procedures for Phylogenetic Trees.
22. October 2017: University of Washington, Department of Statistics*; id.
23. October 2017: University of Washington, Centre for Microbiome Sciences and Therapeutics; Statistical Analysis of Alpha Diversity.
24. November 2017: Rice University, Department of Statistics*; Confidence Sets for Phylogenetic Trees.
25. November 2017: University of Connecticut, Department of Statistics*; id.
26. November 2017: University of Washington, Centre for Microbiome Sciences and Therapeutics*; Adjusting for Multiple Testing in Microbiome Data Analysis.
27. December 2017: University of Washington, Microbiome Symposium*; Statistical Considerations for Microbiome Research.
28. January 2018: University of Washington, Mini-Symposium: Emerging Opportunities in Microbiomes and Environmental Health*; Statistical summaries and uncertainties in microbiome data analysis.
29. March 2018: Fred Hutchinson Cancer Research Centre, Public Health Sciences Division: Microbiome Data to Knowledge*; Microbial community structure & data analysis.
30. June 2018: 4th Conference of the International Society for Nonparametric Statistics; Invited Session *Graphs and Trees in Object Oriented Data Analysis**. Estimation and testing of functions of phylogeny and abundance.
31. February 2019: University of Washington, Department of Genome Sciences and the Computational Molecular Biology Program, COMBI seminar*. Estimating diversity and relative abundance in microbial communities.
32. February 2019: Indiana University, Department of Statistics*; id.
33. February 2019: Fred Hutchinson Cancer Research Center, Biostatistics division*; id.
34. March 2019: Institute for Systems Biology, Seattle, Washington*; id.
35. March 2019: University of Georgia, Department of Marine Sciences*; id.
36. March 2019: University of Georgia, Department of Statistics; id.
37. April 2019: Third Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis*; Measurement Error and Inference in Human 16S Studies (collaborative work presented by trainee David Clausen).

38. May 2019: Symposium on Data Science and Statistics; Invited session *Computational Statistics for Large-Scale Biological Data*; organizer: Jacob Bien* (collaborative work presented by trainee Bryan Martin). Inference for Diversity under Networked Models.
39. May 2019: Symposium on Data Science and Statistics; Invited session *Deciphering Biological Systems via Innovative Statistical Learning Methods*; organizer: Tian Zhang* (collaborative work presented by trainee David Clausen). Assessing Replicability in Human Microbiome Studies.
40. June 2019: 2019 WNAR/IMS/JR Annual Meeting; Invited session *Microbiome Data Analysis*; organizer: Debashis Mondal*. The implications for inference of taxon-specific biases in microbial metagenomics.
41. October 2019: Women in Statistics and Data Science Conference; Session organizer and panelist: *Working and thriving with disability in the statistical sciences*. Co-panelists: Regina Nuzzo, Anna Plantinga and Andrea Lane.
42. October 2019: Oregon State University, Department of Statistics*; Measurement error in microbiome data.
43. March 2020: Colorado State University, Department of Statistics*; Measurement error in compositional data and its effect on the replicability of microbiome studies.
44. July 2020: Northwest Data Science Summit*; Paradoxes arising from model misspecification: a case study in microbiome data analysis.
45. September 2020: Brigham and Women's Hospital Precision Medicine, Division of Computational Pathology, Junior Investigator Advanced Biomedical Computation Series; The analysis of microbiome data from biased high-throughput sequencing.*
46. November 2020: University of Massachusetts Amherst, Department of Mathematics and Statistics; Measurement error in compositional data and the replicability of microbiome studies.*
47. November 2020: University of Florida, Department of Biostatistics*; id.
48. January 2021: Washington State Department of Health; Office of Communicable Disease Epidemiology*.
49. March 2021: ENAR 2021 Spring Meeting; Invited session *Statistical Innovation in Microbiome Data Science*; organizer: Hongzhe Li*.
50. April 2021: Department of Defense (DoD) Tri-Service Microbiome Consortium Bioinformatics meeting; organizer: Matthew Perisin*.
51. April 2021: Developing Data-Driven Cancer Researchers Training Grant Seminar, Fred Hutchinson Cancer Research.*
52. May 2021: Cornell University, Department of Microbiology.*
53. May 2021: Harvard Chan Microbiome in Public Health Center (HCMPH) Symposium; organizers: Curtis Huttenhower and Wendy Garrett.*
54. June 2021: University College London, Department of Statistical Science.*
55. September 2021: 2021 International Chinese Statistical Association Applied Statistics Symposium; session organizer: Anru Zhang*
56. September 2021: UK Conference of Bioinformatics and Computational Biology (UKCBCB) 2021; session organizer: Melanie Schirmer.*
57. November 2021: Carnegie Mellon University, Department of Statistics and Data Science.*
58. November 2021: Indiana University, Department of Biostatistics.*
59. March 2022: Vanderbilt University, Department of Biostatistics.*

60. March 2022: Channing Division of Network Medicine, Brigham and Women's Hospital and Harvard Medical School, Microbiome Working Group, Channing Microbiome Seminar Series.*
61. April 2022: University of Wisconsin-Madison, Department of Biostatistics & Medical Informatics.*
62. May 2022: Johns Hopkins University, Department of Biostatistics*.
63. May 2022: Brigham and Women's Hospital Precision Medicine, Division of Computational Pathology, Junior Investigator Advanced Biomedical Computation Series.*
64. August 2022: 2022 NIST-Hosted Workshop on Standards for Microbiome and Multi-Omics Measurements.
65. October 2022: University of Pennsylvania, The Wharton School, Statistics Department.*
66. October 2022: Northwestern University, Environmental Engineering and Science Seminar Series.*
67. November 2022: Rice University, Department of Computer Science.*
68. November 2022: University of Washington, Department of Genome Sciences and the Computational Molecular Biology Program, COMBI seminar*.

University Service

- Faculty Fellows Program 2017, Participant
- Department of Biostatistics Diversity Committee, Member (07/2017-08/2018)
- Department of Biostatistics Seminar Organizer (01/2018-03/2018)
- Panelist at University of Washington Career and Internship Center's 2018 workshop *Academic Salary Negotiations*
- Search committee member, Center for Microbiome Sciences and Therapeutics, UW Medicine (07/2018-present)
- Department of Biostatistics & Statistics First-Year Theory Qualifying Exam Committee, Member (2018-2019)
- Department of Biostatistics Emergency Preparedness committee, Chair (09/2019-06/2021)
- School of Public Health COVID-19 Workplace Preparedness committee, Member (02/2020-06/2021)
- Department of Biostatistics PhD Admissions Committee, Member, 2020-2021
- Quantitative Ecology and Resource Management (QERM) PhD Admissions Committee, Member, 2020-2021
- School of Public Health, Dean's Office Fellowship Selection Committee, Member 2021, 2022
- Department of Biostatistics PhD Applied Exam Committee, Member, 2021
- UW Medicine, Center for Microbiome Sciences and Therapeutics (CMiST), Steering Committee Member (2020-present)
- UW School of Public Health, Environmental Health and Microbiome Research Center (EHMBRACE), Steering Committee Member (2022-present)
- Statisticians and Biostatisticians of Underrepresented Genders (SBUG) Faculty Liaison (08/2018-present). *Prior to August 2021, this group was known as WiBS: Womxn in Biostatistics and Statistics.*

- School of Public Health, Dean's Office Undergraduate Scholarship Selection Committee, Member 2022
- UW Medicine, Center for Microbiome Sciences and Therapeutics (CMiST), Director Search Committee Member, 2022-2023
- Department of Biostatistics Faculty Search Committee, Member, 2022-2023
- (Department of Biostatistics & Statistics First-Year Theory Qualifying Exam Committee, Member, 2022-2023)

Other Information

- Popular media
 - Twitter: @AmyDWillis
 - Blog: <http://statisticaldiversitylab.com/blog>. The Statistical Diversity Lab Blog discusses microbiome data analysis tools and recommendations for practitioners.

Teaching History

1. Formal courses

- Summer Institute in Statistical Genetics, and Summer Institute in Statistics and Modelling in Infectious Diseases (crosslisted courses)
 - Module 1: Probability and Statistical Inference, July 2017
 - Module 1: Probability and Statistical Inference, July 2018
- Department of Biostatistics, University of Washington
 - BIOST 561: Computational Skills for Biostatistics I, Autumn 2017
 - Advanced R programming for graduate students (1 credit)
 - BIOST 582: Student Seminar, Winter 2018
 - BIOST 561: Computational Skills for Biostatistics I, Spring 2019
 - Advanced R programming for graduate students (2 credits)
 - BIOST 533: Theory of Linear Models, Spring 2019
 - Semiparametric, parametric and non-parametric theory of the linear model. Emphasis on distribution-free asymptotics using probability theory and linear algebraic tools (3 credits)
 - BIOST 509: Introduction to R for Data Analysis in the Health Sciences, Autumn 2019
 - Skills and strategies for data analysis in R using the tidyverse, including readr, dplyr and ggplot (2 credits)
 - BIOST 533: Theory of Linear Models, Spring 2020
 - BIOST 509: Introduction to R for Data Analysis in the Health Sciences, Autumn 2020
 - BIOST 515/518: Applied Biostatistics II, Winter 2021
 - Covers fitting and interpretation of regression analyses that are commonly-used in biomedical research (4 credits)
 - BIOST 515/518: Applied Biostatistics II, Winter 2022
 - (BIOST 515/518: Applied Biostatistics II, Winter 2023)
 - (BIOST 561: Computational Skills for Biostatistics, Spring 2023)

2. Other teaching

- Teaching Assistantships at Cornell University
 - STSCI2100: Introductory Statistics; Fall 2012

- (b) STSCI4100: Multivariate Analysis; Spring 2013
 - (c) BTRY6010: Statistical Methods 1; Fall 2013
 - (d) STSCI4140: Applied Design; Spring 2015, Spring 2017
 - (e) STSCI3100: Statistical Sampling; Fall 2014, Fall 2015
 - Teaching Assistantships at Australian National University
 - (a) STAT1008: Quantitative Research Methods; Semester 2 2009, Semester 1 2010, Semester 2 2010, Semester 2 2011
 - (b) STAT1003: Statistical Techniques; Semester 1 2011
 - Lecturing at Marine Biological Laboratory
 - (a) Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS)
 - i. August 2013: *breakaway: Diversity estimation software*
 - ii. August 2014: *The peanut butter sandwich of beta diversity*
 - iii. August 2015: *Biodiversity: A practical guide*
 - iv. August 2016: *Honest statistics for microbial ecologists; Species richness for microbial ecologists; Rarefaction and why you shouldn't*
 - v. August 2017: *Introduction to R; R lab; alpha and beta diversity analysis; Diversity lab*
 - vi. August 2018: *Statistics & statistical thinking; Statistical estimation: diversity, abundance, shotgun data; Diversity lab*
 - vii. July 2019: *Statistics Bootcamp; Estimating abundance and diversity (lecture + lab); Microbiome data is wrong, and what to do about it*
 - viii. July 2022: *Statistics Bootcamp; Modeling Microbiome Data; Modeling Shotgun Sequencing Data*
- ### 3. Independent Study Supervision
- University of Washington, Department of Biostatistics
 - (a) Edward Zhao, University of Washington, Department of Biostatistics, PhD Candidate, Winter Quarter 2018.
 - (b) Kaleigh Ervin, University of Washington, Department of Biostatistics, PhD Candidate, Winter Quarter 2018.
 - (c) Alex Paynter, University of Washington, Department of Biostatistics, MS Candidate, Spring Quarter 2018, Summer Quarter 2018, Autumn Quarter 2018, Winter Quarter 2019, Spring Quarter 2019.
 - (d) Jean Feng, University of Washington, Department of Biostatistics, PhD Candidate, Spring Quarter 2018.
 - (e) Kendrick Qijun Li, University of Washington, Department of Biostatistics, PhD Candidate, Spring Quarter 2018, Summer Quarter 2018, Autumn Quarter 2018, Winter Quarter 2019.
 - (f) Charles Wolock, University of Washington, Department of Biostatistics, PhD Candidate, Autumn Quarter 2018, Winter Quarter 2019 and Spring Quarter 2019.
 - (g) Eva Tourangeau, University of Washington, Department of Statistics, PhD Candidate, Winter Quarter 2021 and Spring Quarter 2021.
 - (h) Bryan Martin, University of Washington, Department of Statistics, PhD Candidate, every quarter beginning Summer Quarter 2018 to Spring 2021.
 - (i) Pauline Trinh, University of Washington, Department of Environmental and Occupational Health Sciences, PhD Candidate, every quarter beginning Spring Quarter 2018 to present.
 - (j) David Clausen, University of Washington, Department of Biostatistics, PhD Candidate, every quarter beginning Summer Quarter 2018 to present.
 - (k) Sarah Teichman, University of Washington, Department of Statistics, PhD Candidate, every quarter beginning Summer Quarter 2020 to present.
 - (l) María Valdez, University of Washington, Department of Biostatistics, PhD Candidate, every quarter beginning Fall Quarter 2020 to present.

- (m) Sarah Kim, University of Washington, Department of Environmental and Occupational Health Sciences, PhD Candidate, Winter Quarter 2022.
- (n) Jess Kunke, University of Washington, Department of Statistics, PhD Candidate, Winter to Summer Quarters, 2022.

4. Teaching and Other Professional Development

- Evidence-based Teaching Program, Center for Teaching and Learning, University of Washington: Participant, Spring 2020.
 - *“The Evidence-Based Teaching Program offers collaborative peer support, as well as support from teaching and technology consultants, in cross-disciplinary groups facilitated by UW faculty.”*
- Intergroup Dialogue Faculty Training (IGD), University of Washington: Participant, Summer 2020.
 - *“IGD is a communication technique that facilitates dialogue across group differences. The goal for this training is to increase faculty members’ cultural proficiency using the IGD framework by increasing their ability to hold difficult conversations (about race, class, or gender, for example) between and among different groups.”*
- University of Washington School of Public Health Equity, Diversity and Inclusion Level 1A Universal Anti-Racism Training, Participant, Autumn 2020.
- University of Washington School of Public Health Equity, Level 1B Universal Anti-Racism Training, Participant, Autumn 2021.

Advising and Formal Mentoring

1. PhD Dissertations, chair

- (a) David Clausen (PhD 2022), University of Washington, Department of Biostatistics
- (b) Pauline Trinh (PhD 2022), University of Washington, Department of Environmental & Occupational Health Sciences (co-chair with Peter Rabinowitz)
- (c) Sarah Teichman, University of Washington, Department of Statistics, PhD Candidate
- (d) María Valdez, University of Washington, Department of Biostatistics, PhD Candidate
- (e) Bryan Martin, University of Washington, Department of Statistics, PhD Candidate (co-chair with Daniela Witten)

2. Masters Theses, chair

- (a) Alex Paynter (MS 2019), University of Washington, Department of Biostatistics, MS Candidate
 - Alex was the Winner of the Outstanding MS Student Award in Biostatistics, 2019
 - Current position: Biostatistician at Cystic Fibrosis Foundation, Seattle WA

3. Mentored Scientists and Postdoctoral Fellows

- Postdoctoral Supervision
 - (a) Jacob Price, University of Wisconsin, Department of Soil Science (co-supervised with Thea Whitman), December 2018 – December 2020
 - (b) Pauline Trinh, University of Washington, Department of Biostatistics, September 2022+

4. MS and PhD committees in non-chair role

- Doctoral Committee Member
 - (a) Kelsey Grinde (PhD 2019), University of Washington, Department of Biostatistics
 - (b) Yiqun Chen (PhD 2022), University of Washington, Department of Biostatistics, PhD Candidate

- (c) Nicklas Bohmann, University of Washington, Department of Molecular Engineering and Sciences, PhD Candidate
 - (d) Matthew Schechter, University of Chicago, Committee on Microbiology, PhD Candidate
 - (e) Kristof Glauninger, University of Washington, Department of Statistics, PhD Candidate
 - (f) Hassan Nasif, University of Washington, Department of Statistics, PhD Candidate
 - (g) Seth Temple, University of Washington, Department of Statistics, PhD Candidate
 - Graduate Student Representative
 - (a) Leandra Brettner (PhD 2020), University of Washington, Department of Bioengineering, PhD Candidate
 - (b) Andrew Gustin (PhD 2021), University of Washington, Pathobiology - Department of Global Health, PhD Candidate
 - (c) Andria Ellis (PhD 2022), University of Washington, Department of Genome Sciences, PhD Candidate
 - (d) Alex Carr, University of Washington, Department of Molecular Engineering and Sciences, PhD Candidate
 - (e) Anne Massey, University of Washington, Department of Epidemiology, PhD Candidate
 - (f) Nok Chhun, University of Washington, Department of Global Health, PhD Candidate
5. Other Mentoring
- Project Supervision (outside of independent study supervision)
 - (a) Jean Feng, University of Washington, Department of Biostatistics, PhD (2020) (project co-supervised with Erick Matsen and Noah Simon)
 - (b) Brian Williamson, University of Washington, Department of Biostatistics, PhD (2021) (project co-supervised with Jim Hughes)
 - (c) Xiaochuan (Cecilia) Shi, University of Washington, Department of Statistics, MS (2021)
6. Academic Advising
- Department-assigned Academic Advisor
 - (a) Alexander Paynter, University of Washington, Department of Biostatistics, MS (2019)
 - (b) Jiawen Liu, University of Washington, Department of Biostatistics, MS (2022)
 - (c) Taylor Keating, University of Washington, Department of Biostatistics, MS (2022)
 - (d) Niki Petrakos, University of Washington, Department of Biostatistics, MS (2022)
 - (e) Ning Yang, University of Washington, Department of Biostatistics, MS (2022)
 - (f) Ivy Zhang, University of Washington, Department of Biostatistics, MS (2022)
 - (g) Xuehan (Jennifer) Ci, University of Washington, Department of Biostatistics, MS Candidate
 - (h) Han Liu, University of Washington, Department of Biostatistics, MS Candidate
 - (i) Lan Shui, University of Washington, Department of Biostatistics, MS Candidate
 - (j) Hanyi Wang, University of Washington, Department of Biostatistics, MS Candidate
 - (k) Awan Afiaz, University of Washington, Department of Biostatistics, PhD Candidate