

Claudia R. Solís-Lemus

Curriculum Vitae

Employment

- 2019–present **Assistant Professor**, *Joint appointment in Wisconsin Institute for Discovery and Department of Plant Pathology*, University of Wisconsin-Madison.
UW Affiliations: Department of Statistics, Department of Mathematics, Department of Biostatistics and Medical Informatics, JF Crow Institute for the Study of Evolution, Quantitative Biology Initiative, Center for Genomic Innovation, Data Science Institute

Education

- 2010–2015 **Ph.D., Statistics**, *University of Wisconsin-Madison*, Madison.
2013 **M.A., Mathematics**, *University of Wisconsin-Madison*, Madison.
2003–2008 **B.S., Applied Mathematics**, *Instituto Tecnológico Autónomo de México (ITAM)*, Mexico City, Summa cum laude.
2003–2008 **B.S., Actuarial Sciences**, *Instituto Tecnológico Autónomo de México (ITAM)*, Mexico City, Summa cum laude.

Publications

Google Scholar link

Pre-prints (submitted to peer review)

- 2024 **HighDimMixedModels.jl: Robust High Dimensional Mixed Models across Omics Data**, Gorstein, E.*, Aghdam, R.* and C. Solís-Lemus, [bioRxiv:2024.05.09.593305](#).
- 2023 **Unsupervised Learning of Phylogenetic Trees via Split-Weight Embedding**, Kong, Y.*, Tiley, G. and C. Solís-Lemus, [arXiv:2312.16074](#).
- 2023 **Extracting diamonds: Identifiability of 4-node cycles in level-1 phylogenetic networks under a pseudolikelihood coalescent model**, Tiley, G. and C. Solís-Lemus, [biorXiv:2023/564087](#).
- 2023 **Human Limits in Machine Learning: Prediction of Plant Phenotypes Using Soil Microbiome Data**, Aghdam, R.*, Tang, X.*, Shan, S., Lankau, R., C. Solís-Lemus, [arXiv:2306.11157](#).
- 2022 **MiNAA: Microbiome Network Alignment Algorithm**, Nelson, R.*, Aghdam, R.*, C. Solís-Lemus, [arXiv:2212.05880](#).
- 2022 **Detectability of Varied Hybridization Scenarios using Genome-Scale Hybrid Detection Methods**, Bjorner, M.*, E. K. Molloy, C. N. Dewey, and C. Solís-Lemus, [arXiv:2211.00712](#).
- 2022 **BioKlustering: a web app for semi-supervised learning of maximally imbalanced genomic data**, Ozminkowski, S.*, Y. Wu*, L. Yang*, Z. Xu*, L. Selberg*, C. Huang* and C. Solís-Lemus, [arXiv:2209.11730](#).
- 2022 **Identifying microbial drivers in biological phenotypes with a Bayesian Network Regression model**, Ozminkowski, S.* and C. Solís-Lemus, [arXiv:2208.05600](#).
- 2022 **Sparse Gaussian chain graphs with the spike-and-slab LASSO: Algorithms and asymptotics**, Shen, Y.*, C. Solís-Lemus, S.K. Deshpande, [arXiv:2207.07020](#).
- 2021 **A Kernel Method for Dissecting Genetic Signals in Tests of High-Dimensional Phenotypes**, Solís-Lemus, C., A. M. Holleman, A. Todor, B. Bradley, K. J. Ressler, D. Ghosh, M. P. Epstein, [bioRxiv:2021.07.29.454336](#).

- 2021 **CARlasso: An R package for the estimation of sparse microbial networks with predictors**, Shen, Y.*, Solís-Lemus, C., arXiv:2107.13763.
- 2021 **The Effect of the Prior and the Experimental Design on the Inference of the Precision Matrix in Gaussian Chain Graph Models**, Shen, Y.*, Solís-Lemus, C., arXiv:2107.01306.
- 2021 **Phasing Alleles Improves Network Inference with Allopolyploids**, Tiley, G., Crawl, A., Manos, P., Sessa, E., Solís-Lemus, C., Yoder, A., Burleigh, G., bioRxiv doi: <https://doi.org/10.1101/2021.05.04.442457>.
- 2020 **Bayesian Conditional Auto-Regressive LASSO Models to Learn Sparse Networks with Predictors**, Shen, Y.*, Solís-Lemus, C., arXiv:2012.08397.
- 2020 **On the identifiability of phylogenetic networks under a pseudolikelihood model**, Solís-Lemus, C., Coen, Arrigo*, C. Ané, arXiv: 2010.01758.
- Journal papers
- 2024 **Ultrafast learning of 4-node hybridization cycles in phylogenetic networks using algebraic invariants**, Wu, Z.*, C. Solís-Lemus, Bioinformatics Advances.
DOI: 10.1093/bioadv/vbae014
- 2024 **Novel Symmetry-preserving Neural Network Model for Phylogenetic Inference**, Tang, X.*, Zepeda-Nunez, L., S. Yang*, Z. Zhao*, C. Solís-Lemus, Bioinformatics Advances.
DOI: 10.1093/bioadv/vbae022
- 2023 **Machine learning identification of Pseudomonas aeruginosa strains from colony image data**, Ratray, JB, Walden, R., Marquez-Zacarias, P., Molotkova, E., Perron, G., Solís-Lemus, C., Pimentel-Alarcon, D., Brown, S, PLoS Comp Bio.
DOI: 10.1371/journal.pcbi.1011699
- 2023 **SiPhyNetwork: An R package for simulating phylogenetic networks**, J. Justison, Solís-Lemus, C., T. Heath, bioRxiv:10.1101/2022.10.26.513953, Methods of Ecology and Evolution.
DOI: 10.1111/2041-210X.14116
- 2022 **Classification of animal sounds in a hyperdiverse rainforest using Convolutional Neural Networks**, Y. Sun*, T. M. Maeda, Solís-Lemus, C., D. Pimentel-Alarcon, Z. Burivalova, arXiv:2111.14971, Ecological Indicators.
DOI: 10.1016/j.ecolind.2022.109621
- 2022 **WI Fast Stats: a collection of web apps for the visualization and analysis of WI Fast Plants data**, Liu, Y.*, Solís-Lemus, C., JOSE, DOI:10.21105/jose.00159.
arXiv:2012.03290
- 2022 **Towards a robust out-of-the-box neural network model for genomic data**, Zhang, Z.*, Cheng, S.* Solís-Lemus, C., BMC Bioinformatics, DOI:10.1186/s12859-022-04660-8.
arXiv (2020):2012.05995
- 2022 **Efficient Estimation of Indirect Effects in Case-Control Studies Using a Unified Likelihood Framework**, G. A. Satten, S. W. Curtis, C. Solís-Lemus, E. J. Leslie, M. P. Epstein, Statistics in Medicine: DOI 10.1002/sim.9390, bioRxiv:10.1101/2021.07.16.452552.
- 2021 **Effect of genetic background on the evolution of Vancomycin-Intermediate Staphylococcus aureus (VISA)**, Su, M., Hargita Davis, M.N., Peterson, J., Solís-Lemus, C., Satola, S.W. and T. Read, PeerJ, DOI: 10.7717/peerj.11764.
- 2021 **Genes influencing phage host range in Staphylococcus aureus on a species-wide scale**, Moller, A., Winston, K., Ji, S., Wang, J.*, Hargita Davis, M.N., Solís-Lemus, C. and T. Read, mSphere, DOI: 10.1128/mSphere.01263-20.
- 2020 **A generalized measure of relative dispersion**, Guerrero, V. and C. Solís-Lemus, Stat. and Prob. Letters.
- 2020 **Genomic analysis of variability in delta-toxin levels between Staphylococcus aureus strains**, M. Su, J. Lyles, R. A. Petit III, J. M. Peterson, M. Hargita, H. Tang, C. Solís-Lemus, C. Quave, T. D. Read, PeerJ, doi:10.7717/peerj.8717.

- 2020 **Leveraging family history in case-control analyses of rare variation**, *C. Solís-Lemus, S.T. Fischer, A. Todor, C. Liu, E.J. Leslie, D. Cutler, D. Ghosh, M.P. Epstein*, Genetics, doi: 10.1534/genetics.119.302846.
(Genetics editors Highlights of February 2020)
- 2020 **Prediction of functional markers of mass cytometry data via deep learning**, *C. Solís-Lemus, X. Ma, M. Hostetter II, S. Kundu, P. Qiu, D. Pimentel-Alarcón*, Statistical Modeling in Biomedical Research, Springer.
- 2018 **Greatly reduced phylogenetic structure in the cultivated potato clade (*Solanum* section *Petota pro parte*)**, *Spooner, D.M., H. Ruess, C. Arbizu, F. Rodríguez, and C. Solís-Lemus*, American Journal of Botany, doi:10.1002/ajb2.1008.
- 2018 **Phylogenetic comparative methods on phylogenetic networks with reticulations**, *Bastide, P., C. Solís-Lemus, R. Kriebel, K.W. Sparks, and C. Ané*, Systematic Biology, doi: 10.1093/sysbio/syy033.
- 2017 **PhyloNetworks: a package for phylogenetic networks**, *Solís-Lemus, C., P. Bastide and C. Ané*, Molecular Biology and Evolution, doi: 10.1093/molbev/msx235.
- 2016 **Inferring phylogenetic networks with maximum pseudolikelihood under incomplete lineage sorting**, *Solís-Lemus, C. and C. Ané*, PLoS Genetics 12(3):e1005896, doi:10.1371/journal.pgen.1005896. (PLOS Genetics Top 10%)
- 2016 **Inconsistency of species-tree methods under gene flow**, *Solís-Lemus, C., M. Yang and C. Ané*, Systematic Biology, doi: 10.1093/sysbio/syw030.
- 2016 **Statistical evidence for common ancestry: application to primates**, *Baum, D., C. Ané, B. Larget, C. Solís-Lemus, L.S.T. Ho, P. Boone, C. Drummond, M. Bontrager, S. Hunter, B. Saucier*, Evolution, doi: 10.1111/evo.12934.
- 2015 **Bayesian species delimitation combining multiple genes and traits in a unified framework**, *Solís-Lemus, C., L.L. Knowles and C. Ané*, Evolution, 2:69,492–507.

Conference papers

- 2018 **Breaking the Limits of Subspace Inference**, *Solís-Lemus, C., D. Pimentel-Alarcón*, 56th Annual Allerton Conference on Communication, Control, and Computing.
- 2017 **Processus d'évolution réticulée: tests de signal phylogénétique**, *Ané, C., P. Bastide, M. Mariadassou, S., and C. Solís-Lemus*, Journées de Statistique.
- 2017 **Adversarial Principal Component Analysis**, *Pimentel-Alarcón, D., A. Biswas and C. Solís-Lemus*, IEEE International Symposium on Information Theory (ISIT).
- 2016 **Crime detection via crowdsourcing**, *Pimentel-Alarcón, D. and C. Solís-Lemus*, 8th Mexican Conference on Pattern Recognition, Springer International.

* Member of Solis-Lemus lab

Grants

Awarded

- 2024–2028 **USDA-Individual hatch**, *Enhanced interaction and network statistical models for microbiome data*, Role: PI.
- 2023–2027 **NSF IntBIO Collaborative Research**, *Assessing drivers of the nitrogen-fixing symbiosis at continental scales*, Role: co-PI, (co-PI: Ryan Folk, Mississippi State U).
- 2022–2027 **USDA NIFA**, *Unraveling The Microbial Mechanisms That Mediate Disease Resurgence In Plants Following Fungicide Application*, Role: co-PI, (co-PI: Paul Koch, UW-Madison).
- 2022–2027 **NSF CAREER**, *Towards robust and scalable inference of phylogenetic networks*, Role: PI.
- 2020 **Wisconsin Potato and Vegetable Growers Association, Inc.**, *Development of bioinformatic tools to leverage certification data for enhanced seed potato production*, Role: PI.
- 2020–2022 **DOE – Computational Tool Development for Integrative Systems Biology**, *Harnessing the power of big omics data: Novel statistical tools to study the role of microbial communities in fundamental biological processes*, Role: PI, (NCE to 2023).

- 2020–2021 **USDA-hatch**, *Novel interaction and network statistical models for microbiome data*, Role: PI.
- 2019 **NIH K99/R00 Path to Independence**, *Enhanced Penalized Regression Methods for Detecting Trait Loci in GWAS*, Role: PI.
Score: 20 (withdrawn due to faculty job)

Fellowships and Awards

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| 2024 | Holstrom Environmental Undergraduate Research Fellowship (Tianyi Xu) | <i>UW-Madison</i> |
| 2022 | Hilldale Faculty/Undergraduate Research Fellowship (Bella Wu) | <i>UW-Madison</i> |
| 2021 | Holstrom Environmental Undergraduate Research Fellowship (Yuren Sun) | <i>UW-Madison</i> |
| 2020 | Solis-Lemus et al (2016) paper listed in PLOS Genetics Top 10% Collection | |
| 2020 | Hilldale Faculty/Undergraduate Research Fellowship (Zhaoyi Zhang) | <i>UW-Madison</i> |
| 2020 | Madison Teaching and Learning Excellence Fellow | <i>UW-Madison</i> |
| 2019 | Reviewers' choice award | <i>American Society of Human Genetics</i> |
| 2015 | Student travel support | <i>Society for Systematic Biologists</i> |
| 2015 | Vilas conference presentation funds | <i>UW-Madison</i> |
| 2014 | Advanced Computing Infrastructure Fellowship | <i>UW-Madison</i> |
| 2012 | College of Letters and Science Teaching Fellowship | <i>UW-Madison</i> |
| 2009 | Ex-ITAM Research Award in Actuarial Sciences | <i>ITAM</i> |
| 2008 | Social Responsibility Award | <i>ITAM</i> |
| 2003 | Academic Excellence Scholarship | <i>ITAM</i> |

Software development

- 2024 **HighDimMixedModels.jl**, <https://github.com/solislemuslab/HighDimMixedModels.jl>, A Julia package for fitting regularized linear mixed-effect models on high-dimensional omics data..
- 2023 **PhyloClustering.jl**, <https://github.com/solislemuslab/PhyloClustering.jl>, A Julia package to perform unsupervised learning on phylogenetic trees.
- 2023 **PhyloDiamond.jl**, <https://github.com/solislemuslab/PhyloDiamond.jl/>, A Julia package to estimate phylogenetic networks from algebraic invariants.
- 2022 **MiNAA**, <https://github.com/solislemuslab/minaa>, C++ software to align two biological networks based on topology and biology.
- 2022 **BioKlustering**, <https://bioklustering.wid.wisc.edu/>, Web app to cluster unaligned genomics sequences for partially labelled samples.
- 2022 **BayesianNetworkRegression.jl**, <https://github.com/solislemuslab/BayesianNetworkRegression.jl/>, A Julia package for fitting Bayesian Network Regression models to infer the relationships between microbiome networks and biological phenotypes.
- 2021 **CARlasso**, <https://yunyishen.ml/CAR-LASSO/dev/>, An R package for the reconstruction of microbial networks with predictors.
- 2020 **WI Fast Stats**, <https://wi-fast-stats.wid.wisc.edu/>, A collection of web apps for the data analysis and data visualization for WI Fast Plants.
- 2015 **PhyloNetworks**, <https://github.com/crsl4/PhyloNetworks>, Julia package for phylogenetic networks including estimation method SNaQ.
- 2014 **iBPP**, <https://github.com/cecileane/iBPP>, Bayesian species delimitation integrating genes and traits.

Research Experience

- 2017–2019 **Postdoctoral fellow**, *NIH-supported project*, Epilepsy consortium and 22q11.1 deletion syndrome consortium, PI: Michael Epstein.
Emory University

- 2016–2017 **Postdoctoral research**, *NSF-supported project*, Improved Bayesian phylogenetic inference based on approximate conditional independence, PI: Bret Larget.
University of Wisconsin-Madison
- 2014–2015 **Research assistant**, *NSF-supported project*, ATOL: Assembling a taxonomically balanced genome-scale reconstruction of the evolutionary history of the Enterobacteriaceae, PI: Nicole Perna, Bret Larget, Cécile Ané, Colin Dewey.
University of Wisconsin-Madison
- 2013–2014 **Research assistant**, *NSF-supported project*, Reconciling gene trees: Deciphering the source and extent of genealogical discordance, PI: David Spooner, David Baum, Bret Larget, Cécile Ané, Gregory Thain.
University of Wisconsin-Madison

Teaching Experience

At UW-Madison

- Spring 2024 **Botany/Plant Path 563**, *Phylogenetic analysis of molecular data*, A course in the theory and practice of phylogenetic inference from DNA sequence data. Students will learn all the necessary components of state-of-the-art phylogenomic analyses and apply the knowledge to the data analyses of their own organisms, UW-Madison.
- Spring 2023 **Botany 563**, *Phylogenetic analysis of molecular data*, A course in the theory and practice of phylogenetic inference from DNA sequence data. Students will learn all the necessary components of state-of-the-art phylogenomic analyses and apply the knowledge to the data analyses of their own organisms, UW-Madison.
- 2023 **Guest lecture**, *LAW 915: Statistics for Forensic Science*, (Spring and Fall).
- 2023 **Guest lecture**, *BMI 826: Inferring Biological Networks*.
- 2022 **Guest lecture**, *ENVIR ST 400: Deep learning in Biology*.
- 2022 **Guest lecture**, *STAT 609/849: Statistical models for biological applications*.
- 2022 **Guest lecture**, *LAW 915: Statistics for Forensic Science*.
- Spring 2022 **Botany 563**, *Phylogenetic analysis of molecular data*, A course in the theory and practice of phylogenetic inference from DNA sequence data. Students will learn all the necessary components of state-of-the-art phylogenomic analyses and apply the knowledge to the data analyses of their own organisms, UW-Madison.
- Spring 2022 **Plant Path 875**, *Readings in phylogenomics*, This course will be a journal club where students will read and discuss the current literature related to phylogenomic analyses, UW-Madison.
- 2021 **Guest lecture**, *BME 780: An overview of phylogenetic inference*.
- 2021 **Guest lecture**, *STAT 609/849: Statistical models for biological applications*.
- Spring 2021 **Botany 563**, *Phylogenetic analysis of molecular data*, A course in the theory and practice of phylogenetic inference from DNA sequence data. Students will learn all the necessary components of state-of-the-art phylogenomic analyses and apply the knowledge to the data analyses of their own organisms, UW-Madison.
- Spring 2021 **Plant Path 875**, *Readings in phylogenomics*, This course will be a journal club where students will read and discuss the current literature related to phylogenomic analyses, UW-Madison.
- 2020 **Guest lecture**, *STAT 609/849: Statistical models for biological applications*, (virtual).
- 2016 **Guest lecture**, *Botany 563: Phylogenetic networks*, UW-Madison.
- 2015 **The hacker within series – UW Madison**, *Short introduction to Julia*.
- 2015 **Statistics student seminar – UW Madison**, *Short introduction to HTCondor*.
- 2014 **Teaching assistant**, *Statistics tutorial: PhD qualifying examination summer camp*, UW-Madison.
- 2012–2013 **Teaching assistant**, *Regression methods for population health*, UW-Madison, Professor Ron Gangnon.
- 2011–2012 **Teaching assistant**, *Introduction to Biostatistics for population health*, UW-Madison, Professor Ron Gangnon.
- 2011 **Teaching assistant**, *Introduction to Statistical methods*, UW-Madison, Professor Kevin Packard (Spring), Kam Wah Tsui (Summer).

- 2010 **Teaching assistant**, *Introduction to theory and methods of mathematical statistics I*, UW-Madison, Professor Zhengjun Zhang.
- Outside of UW-Madison
- 2023 **Workshop on Methodological Advances in Reticulate Evolution**, *Invited faculty*, Edinburgh Botanical Gardens, Edinburgh, Scotland.
- 2023 **Workshop on Methodological Advances in Reticulate Evolution**, *Invited faculty*, Kew Botanical Gardens, Richmond, UK.
- 2023 **Botany conference 2023**, *Workshop: Estimating phylogenetic networks with SNaQ*.
- 2023 **Molecular Evolution Workshop: Phylogenetic networks**, *Invited Faculty*, Marine Biology Lab (MBL), Woods Hole, MA.
- 2023 **SSB 2023 Satellite**, *Workshop: Introduction to PhyloNetworks*, Mexico City.
- 2022 **AI Summer School**, *Deep learning in Biology*, August 10, 2022, UChicago.
- 2022 **Molecular Evolution Workshop: Phylogenetic networks**, *Invited Faculty*, Marine Biology Lab (MBL), Woods Hole, MA.
- 2022 **International Society of Molecular Biology Meeting**, *Workshop: Julia for Data Science*, Co-taught with Doug Bates.
- 2022 **Scalable inference of phylogenetic networks**, *RADsequencing for phylogenOMICS*, Taxon-OMICS partners from Göttingen, München and Braunschweig.
- 2021 **Virtual Species Delimitation workshop**, *Invited Faculty*, National Museum of Natural History, (virtual).
- 2021 **Seminario de Investigacion de la Escuela de Estadística**, *Julia workshop for Data Science*, Universidad de Los Andes, Mérida, Venezuela, (taught in Spanish).
- 2021 **WID Data Science Research Bazaar**, *Julia workshop for Data Science*, (co-taught with Douglas Bates).
- 2020 **Molecular Evolution Workshop: Phylogenetic networks**, *Invited Faculty*, Marine Biology Lab (MBL), Woods Hole, MA.
(cancelled due to COVID19)
- 2020 **Mexicanas en Ciencias de Datos**, *Julia workshop for Data Science*, Virtual event organized by CIMAT.
- 2020 **WI Fast Plants webinar**, *Data analysis tools for WI Fast plants data*, (webinar for high-school teachers in Biology).
- 2019 **R developer workshop – Nantucket, MA**, *From mindful programming to reproducible research*.
- 2019 **Taming the BEAST – Squamish, BC**, *Invited Faculty*, Bayesian phylogenetic inference for big data.
- 2019 **Taming the BEAST – Squamish, BC**, *Invited Faculty*, Statistical models on phylogenetic networks.
- 2019 **Molecular Evolution Workshop – Woods Hole, MA**, *Invited Faculty*, Statistical models on phylogenetic networks.
- 2017 **Human Genetics Meeting – Emory University**, *Julia: why do we need another language?*.
- 2016 **Instituto de Biología – UNAM**, *PhyloNetworks: julia package for phylogenetic networks*.
- 2016 **Phylogenomics symposium and software school – Evolution meeting**, *PhyloNetworks: julia package for phylogenetic networks*.
- 2010 **Instructor in Mathematics**, *Advanced Algebra II*, ITAM.
- 2010 **Instructor in Mathematics**, *Calculus II*, ITAM.
- 2009 **Instructor in Mathematics**, *Calculus III*, ITAM.
- 2009–2010 **Instructor in Actuarial Sciences**, *Actuarial Mathematics I*, ITAM.
- 2009–2010 **Instructor in Actuarial Sciences**, *Actuarial Mathematics III*, ITAM.

Presentations

Invited talks

- 2024 **Data Science Symposium**, *Inferring Biological Networks*, Loyola University.

- 2024 **WID Seminar**, *Statistical and Computational Challenges in Phylogenetic Inference*, Co-presenter: Kris Sankaran, Lab presenters: Nathan Kolbow, Hailey Louw, Yibo Kong.
- 2023 **American Statistical Association**, *Reproducibility and mindful programming*.
- 2023 **Algebraic Statistics for Ecological and Biological Systems**, *Ultrafast learning of 4-node hybridization cycles using phylogenetic invariants*, Institute for Mathematical and Statistical Innovation (IMSI), University of Chicago.
- 2023 **BMI Seminar**, *Inferring networks*, (UW-Madison).
- 2023 **Evolution conference**, *Identifiability of 4-node hybridization cycles in phylogenetic networks*.
- 2023 **Botany conference**, *Inferring phylogenetic networks*.
- 2023 **Toronto Workshop on Reproducibility**, *Accessible reproducibility for biological researchers*.
- 2023 **Biological Interactions Program**, *Biological Data Science*, (UW-Madison).
- 2023 **WID seminar**, *Biological Networks from Adaptable Mathematics*, (UW-Madison).
- 2023 **SSB Standalone Meeting**, *Statistical models on phylogenetic networks*, (Mexico City, remote).
- 2022 **PBEE seminar at Emory University**, *From phylogenetic networks to microbial networks: novel tools for networked data*.
- 2022 **Statistics seminar – UW-Madison**, *Inferring networks*, (Lightning talk).
- 2022 **Evolution conference**, *Invited panelist for the iEvoBio panel "Build it right from the start"*.
- 2022 **Evolution conference**, *Statistical challenges to infer phylogenetic networks*, Symposium: Towards the Network of Life.
- 2022 **EEOB seminar at Iowa State University**, *Statistical challenges to infer phylogenetic networks*.
- 2021 **Coloquio de la Sociedad Matemática Mexicana**, *Biología Evolutiva a través de los ojos de Ciencias de Datos*.
- 2021 **ISCB EvolCompGen: Evolution and Comparative Genomics**, *Scalable inference of phylogenetic networks*.
- 2021 **I Congreso Latinoamericano de Evolución**, *Metodos estadísticos para reconstruir redes filogenéticas*.
- 2021 **Organisms and Evolution seminar at Duke University**, *Statistical challenges on phylogenetic networks*, Invited speaker selected by graduate students.
- 2021 **American Mathematical Society: Special Section on Phylogenetic Networks**, *Identifiability of phylogenetic networks under the multispecies coalescent model*.
- 2021 **Delta Beer Lab: The adventures of the statistician's rule of thumb**, *WI Science Festival*.
- 2021 **Biology seminar series – University of Florida**, *From phylogenetic networks to microbial networks: statistical tools for networked data*.
- 2021 **Kenneth B. Raper Symposium – UW-Madison**, *Novel methods to reconstruct microbial networks with environmental or experimental predictors*.
- 2021 **ClubEcoEvo Latinamerica**, *Metodos Estadísticos para estudiar comunidades microbianas*.
- 2021 **Think STEM**, *Career Exploration Center at UW-Madison*, (audience: high school students).
- 2021 **Universidad de La Paz**, *Through the looking glass of Data Science*.
- 2021 **BISP12**, *Bayesian CAR-LASSO model to learn sparse networks with predictors*, (virtual in Italy).
- 2021 **INFORMS en español**, *Biología evolutiva a través de los ojos de Ciencias de Datos*, (Rice University).
- 2021 **NZ seminar in Algorithms and Complexity in Phylogenetics**, *Scalable inference of phylogenetic networks*.
- 2021 **University of Georgia – Athens**, *Scalable inference of phylogenetic networks*.
- 2021 **Department of Statistics – Ohio State University**, *Scalable inference of phylogenetic networks*.
- 2021 **Department of Ecology and Evolutionary Biology – Ohio State University**, *Scalable inference of phylogenetic networks*.
- 2021 **Bioinformatics Institute – University of North Carolina**, *Scalable inference of phylogenetic networks*.
- 2021 **CIBM – UW-Madison**, *New challenges in phylogenetic inference*.

- 2021 **Wednesday at the Lab – University of Wisconsin-Madison**, *Through the looking glass of Data Science*, (audience: general public).
- 2021 **El Zoominario**, *Learning the Tree of Life*, (audience: general public).
- 2020 **Biology seminar – University of Central Florida**, *Comparative methods on phylogenetic networks*.
- 2020 **Department of Statistics – University of British Columbia**, *Scalable inference of phylogenetic networks*.
- 2020 **The Biology Department – George Washington University**, *Scalable inference of phylogenetic networks*, (invited by graduate students).
- 2020 **Department of Biological Sciences – Auburn University**, *Scalable inference of phylogenetic networks*.
- 2020 **BadgerTalks – Cedarburg Public Library**, *Through the looking glass of Data Science*, (talk for general audience interested in women in STEM).
- 2020 **WID symposium – Lightning talk**, *Statistical methods for biological applications*.
- 2020 **SBE Meeting – Methods in phylogenomics**, *What are phylogenetic networks and why should we care?*.
- 2020 **Microbiome Hub Seminar – WID**, *Scalable Inference of Phylogenetic Networks*.
- 2020 **Illuminating connections – WID**, *Identifying Genetic Factors Driving Microbial Phenotypes Through the Power of Data Science*.
- 2020 **Statistics seminar – UW-Madison**, *New challenges in phylogenetic inference*.
- 2019 **R developer workshop – Nantucket, MA**, *From mindful programming to reproducible research*.
- 2019 **Bio-mathematics seminar – Georgia Tech, Atlanta, GA**, *Phylogenetic inference for big data*.
- 2019 **HAMLET seminar – UW-Madison**, *Using neural networks to predict antibiotic-resistance from genomic data*.
- 2019 **Women in STEM conference – Georgia State University**, *Through the looking glass of Data Science*.
- 2018 **Statistics seminar – Creighton University**, *Statistical methods to identify genes associated with disease*.
- 2018 **BUGS seminar – Georgia Institute of Technology**, *Statistical methods to reconstruct phylogenetic networks*.
- 2017 **Microbiome group – Emory University**, *Statistical methods to reconstruct phylogenetic networks*.
- 2017 **CIBS Seminar – Emory University**, *Statistical methods and Julia computings tools for the reconstruction of the tree of life*.
- 2017 **Human Genetics Seminar – Emory University**, *Phylogenetic inference for big data*.
- 2017 **Mathematical Approaches to Evolutionary Trees and Networks – BIRS**, *Likelihood challenges for big trees and networks*.
- 2016 **Statistics Seminar – UW-Madison**, *Phylogenetic inference for Big Data*.
- 2016 **Instituto de Biología UNAM – Mexico City, Mexico**, *Quartet-based inference of phylogenetic networks*.
- 2016 **Simposio de Inferencia y modelación estadística – Guanajuato, Mexico**, *Bayesian phylogenetic inference for big data*.
- 2016 **SSB symposium: Advances in the analysis of reticulate population networks – Evolution meeting**, *Quartet-based inference of phylogenetic networks*.
- 2016 **Phylogenomics symposium and software school – Evolution meeting**, *Quartet-based estimation of reticulate evolution*.
- 2015 **System Information Learning Optimization Seminar – UW Madison**, *Statistical inference of phylogenetic networks*.
- 2015 **Evolution Seminar Series – UW Madison**, *Fast reconstruction of hybridization networks from multilocus data*.

- 2015 **Networks seminar – UW Madison**, *Statistical inference on phylogenetic networks*.
- 2015 **Statistics student seminar – UW Madison**, *Statistical inference on phylogenetic networks*.
- 2014 **Seminario Aleatorio – ITAM**, *The role of Statistics in the inference of the Tree of Life*.

Contributed talks

- 2023 **Botany conference**, *Phylogenetic networks to study reticulate evolution*, (co-organized symposium with George Tiley).
- 2021 **JuliaCon (virtual)**, *PhyloNetworks: a julia package for phylogenetic networks*.
- 2021 **Evolution conference (virtual)**, *Behind the scenes of phylogenetic reconstructions with SNaQ*.
- 2020 **JSM – Statistical Methods in Phylogenetics**, *Fast reconstruction of Phylogenetic Networks*.
- 2018 **JSM – Advanced statistical inference for stochastic models of evolutionary biology**, *Comparative methods in phylogenetic networks*.
- 2018 **SACNAS – Data Science: The Rise of the Machines**, *Identifying genes associated with disease*.
- 2018 **SACNAS – Postdoc talks**, *Machine-learning the Tree of Life*.
- 2018 **20th IMS New Researchers Conference**, *Statistical inference of the Tree of Life*.
- 2016 **8th Mexican Conference on Pattern Recognition – Guanajuato, Mexico**, *Crime detection via crowdsourcing*.
- 2015 **Evolutionary System Biology and Modeling Workshop – UW Madison**, *Statistical inference of phylogenetic networks*.
- 2015 **JSM – Bayesian Models and Inference**, *Bayesian species delimitation combining multiple genes and traits in a unified framework*.
- 2015 **Mathematical and Computational Evolutionary Biology Conference**, *Inferring phylogenetic networks from quartets with maximum pseudolikelihood estimation*.
- 2009 **XXIV Foro Nacional de Estadística**, *A parametric measure of dispersion derived from the generalized mean*.

Service

University

- 2024 **Reviewer of Sophomore Undergraduate Research Fellowships**.
- 2023–2024 **Graduate admissions committee**, *Department of Plant Pathology*.
- 2024 **Data in Action Research Bazaar**, *Co-organizer of the Collaboration Matching Exercise: Want to find your match?*, Co-organizer: Michael Ferris.
- 2023 **MANRRS Women in STEM panel**, *Invited faculty*.
- 2023 **Research Forward committee**.
- 2023 **Biological Interactions Mentoring Program**, *Invited speaker*, Biological Data Science.
- 2023 **WID Research Bazaar**, *Co-organizer of the Collaboration Matching Exercise: Want to find your match?*, Co-organizer: Michael Ferris.
- 2022 **MOSAIC mentor**, *Lauren English*.
- 2022 **Pre-awards recruitment committee**, *WID*.
- 2022 **Creator of Latinx UW-Madison Faculty group**.
- 2022 **Reviewer for Research Forward 2**.
- 2021 **Pre-award recruitment committee**, *WID*.
- 2021 **A-JEDI committee**, *WID*.
- 2021 **Biological Interactions Mentoring Program**, *Summer mentor of Kaitilyn Abshire (CUNY)*.
- 2020 **Whiteness in STEM Discussions**, *WID*.
- 2020 **Anti-racist working group**, *WID*.
- 2020–2021 **Phylogenomics bookclub**, *Organizer*.

- 2020 **Meet and Greet**, *with students of color, first generation students, students with varying abilities, or students from low-income backgrounds*, Division of Diversity, Equity and Educational Achievement.
- 2020 **Women in Science and Engineering (WISE) Learning Community**, *Faculty Guest*.
- 2020 **SciMed GRS Poster Session**, *Judge*, (cancelled due to COVID).
- 2020–present **Justice, Equity, Diversity and Inclusion (JEDI) committee**, *Chair*.
- 2020–present **PSGSC Plant Sciences Graduate Student Council**, *Invited to mentor students of color*.
- 2019 **International Year of Plant Health committee**, *Department of Plant Pathology*, (activities canceled due to COVID).
- 2019–2020 **Graduate admissions committee**, *Department of Plant Pathology*.
- Editorial
- 2024 **75th anniversary of Systematic Biology**, *Invited “Evolving views” article on phylogenetic networks*.
- 2024 **PNAS special issue Speciation-Introgression-Conservation**, *Invited review article on phylogenetic networks*, (co-author: George Tiley).
- 2023–2024 **Co-editor Special Edition**, *Seeing the web for the tree: advances in reticulate evolution*, *Bulletin of Society of Systematic Biology*, (co-editor: George Tiley).
- 2023–present **Journal of Agricultural, Biological and Environmental Statistics**, *Associate Editor*.
- 2023–present **Journal of Open Source Software**, *Associate Editor*.
- 2021–present **Frontiers in Ecology and Evolution - Phylogenetics, Phylogenomics, and Systematics**, *Review Editor*.
- 2019–present **Systematic Biology**, *Associate Editor*.
- 2016–present **Systematic Biology**, *Editorial Board Member*.
- Reviewer:**, *Syst Bio, MBE, Bioinformatics, Genetics, eLIFE, Evolution, PLoS Comp Bio, Bulletin of Math Bio, Nature Methods, JOMB, BSSB, ISMB, Nature Microbiology, Science*.
- Conferences, Symposia, Workshops
- 2024 **Methods for Biological Data Workshop Series**, *Department of Plant Pathology, UW-Madison*, Co-organizer with Emile Gluck-Thaler.
- 2023 **Botany Meeting Symposium**, *Seeing the network for the trees: novel methods in phylogenetic networks*, Co-organizer: George Tiley.
- 2021 **Evolution Meeting**, *Bilingual Mentoring Program*.
- 2020 **Systematic Biology Meeting**, *Coalescent-based methods in the age of big data*.
- 2020 **Future of Systematics Invited Session**, *SSB-Standalone Meeting*.
- 2020–present **El Zoominario**, *Short scientific talks to increase visibility of Latinx in STEM*, Co-organizer: Daniel Pimentel-Alarcon.
- 2018 **SACNAS Symposium**, *Data Science: The Rise of the Machines*, Co-organizer: Daniel Pimentel-Alarcón.
- 2016 **Evolution Meeting Symposium**, *Advances in the analysis of reticulate population networks*, Co-organizer: David Baum.
- Grant panels
- 2022 **Dutch Research Council**, *Grant review*.
- 2022 **NSF**, *Grants review panel (Summer)*.
- 2022 **NSF**, *Grants review panel (April)*.
- 2022 **DOE**, *Grants review panel (Summer)*.
- 2022 **DOE**, *Grants review panel (April)*.
- 2021 **NSF**, *Grants review panel*.
- 2020 **NIH NHGRI Genomics**, *Strategic Planning Finale Meeting*.
- 2020 **DOE**, *Grants review panel*.

Outreach and Public Engagement

- 2024 **Guest lecture: Statistics in Forensics 101**, *Forensic Justice Institute*.
- 2023 **Celebrating Latinx voices in STEM Symposium**, *UW-Madison*, organizer of the event with the support of WID and CALS.
- 2023 **Crossroads of ideas: Comparing the Creative Process in Science and Art**, *WI Science Fest and WI Book Fest*.
- 2023 **Uncontrolled Variables**, *Invited speaker at the comedy show about scientific presentations*.
- 2023 **Technical to Beautiful: Data as Art Exhibition**, *UW-Madison*, Co-organizer: Kris Sankaran.
- 2023 **Guest lecture: Statistics in Forensics 101**, *DNA Bootcamp 2023 by California State University Los Angeles, Los Angeles Innocence Project, Federal Defender Central District of California, and Los Angeles County Public Defender*.
- 2023 **Women in STEM – UNAM**, *De las mates a las plantas: mi camino en ciencia*.
- 2023 **Latino Youth Summit**, *From math to plants: my winding path in science*.
- 2023 **Girls Who Code**, *What is a statistician doing in Plant Pathology?*.
- 2022 **Dreamers of Wisconsin Mentoring Program Kickoff Event**, *UW-Madison School of Education*, Invited speaker.
- 2022 **Guest lecture: Statistics in Forensics 101**, *National Forensic College*.
- 2022 **Guest lecture: Basics of statistics for defense attorneys**, *Forensic University*, (WI public defenders).
- 2022 **Virtual Science Event**, *Data Decoders*, Mauston High School.
- 2022 **Día Internacional de la Mujer y la Niña en la Ciencia**, *Universidad Anahuac*, Invited speaker.
- 2021 **WI Science Festival: Stumble into Science**, *UW-Madison*.
- 2021 **WI Science Festival: Stumble into Science**, *UW-Madison*, Science talk at Delta Beer Lab.
- 2020 **SACNAS Women in Science Forum**, *UW-Madison*, (cancelled due to COVID).
- 2020 **Cientifico Latino mentoring program**.
- 2020 **Latina in Science presentation**, *Universidad Nacional de Colombia*.
- 2019 **Atlanta Science Festival**, *Complete the circuit: meet a woman scientist*.
- 2018 **Career Day**, *Bridge the diversity gap in science*, Campbell Middle School.
- 2005-2008 **Sistema de preparatoria abierta para adultos**, *ITAM*, Math high-school teacher for adults, Mexico.

Societies

- 2021–2024 **Society of Systematic Biologists**, *Elected Council Member*.
- 2022 **American Statistical Association**, *Creator of LatinxInStat database*.
- Member**, *Society of Systematic Biologists, American Statistical Association, SACNAS*.

Media

- 2024 Faculty Spotlight *Madison Chapter of Graduate Women in Science (GWIS-Beta Chapter)*
- 2023 There are no bugs in winter *Zero budget sci-fi movie screening*
- 2023 Faces of Data Science: Claudia Solis-Lemus *Data Science at UW*
- 2023 El Zoominario: giving a voice to Latinx scientists and inspiring the next generation *CGSI Newsletter*
- 2022 "Behind the scientist" *Interview for WID Kohler fellowship*
- 2022 Wisconsin Latinx History Collective (WLHP) *Interview with Tess Arenas*
- 2021 En Nuestro Patio Radio Interview on diversity in STEM *WORT FM*
- 2021 Meet the Lab: Data Decoders *PBS*
- 2021 Invited publication about me *Mujeres Haciendo Ciencia @mujeres.haciendo.ciencia*
- 2021 Rotating Curator of Twitter @WomenInStat in Sept 13-17 *American Statistical Association (ASA)*
- 2021 "The Tree of Life is rooted in Math" article *GROW Magazine*
- 2021 WID Women's history month *YouTube video*
- 2020 Code conversations with Casey Dunn *YouTube interview*

Computer skills

Programming C++, Java, Julia, Perl, Python
Statistics R, SAS, SPSS
Mathematics Matlab, Mathematica, Macaulay2
HTC HTCCondor, OSG, SLURM

Certifications

Exam C	Society of Actuaries (SOA)	<i>Construction of Actuarial Models Certificate</i>
Exam FM	Society of Actuaries (SOA)	<i>Financial Mathematics Certificate</i>
Exam P	Society of Actuaries (SOA)	<i>Probability Certificate</i>

Languages

Spanish Native language
English Proficient level: TOEFL iBT (2009), IELTS (2009)
French Advanced level: DALF C1 (2007)
Portuguese Advanced level: CELPE-BRAS (2008)
German Beginner level: A1 Start Deutsch 1 (2008)

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