

# 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.

### 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

- 2022 **Accurate Phylogenetic Inference with a Symmetry-preserving Neural Network Model**, [C. Solís-Lemus](#), [S. Yang\\*](#), [L. Zepeda-Nunez](#), [arXiv:2201.04663](#).
- 2021 **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](#).
- 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.](#), [Crowl, 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

- 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. Mariadasou, 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.

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## Grants

### Awarded

- 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.
- 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)

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## Fellowships and Awards

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

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## Software development

- 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.

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## 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

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## Teaching Experience

- 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*.
- 2021 **Invited Faculty**, *Virtual Species Delimitation workshop*, National Museum of Natural History, (virtual).
- 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).
- 2020 **Invited Faculty**, *Molecular Evolution Workshop: Phylogenetic networks*, Marine Biology Lab (MBL), Woods Hole, MA.  
(cancelled due to COVID19)
- 2019 **Invited Faculty**, *Molecular Evolution Workshop: Phylogenetic networks*, Marine Biology Lab (MBL), Woods Hole, MA.
- 2016 **Guest lecturer**, *Botany 563: Phylogenetic networks*, UW-Madison.
- 2014 **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.
- 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.

## Tutorials

- 2022 **Julia for Data Science**, *ISMB 2022*, Co-taught with Doug Bates.
- 2022 **Scalable inference of phylogenetic networks**, *RADsequencing for phylogenOMICs*, Taxon-OMICS partners from Göttingen, München and Braunschweig.
- 2021 **Seminario de Investigación 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 **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 **Molecular Evolution Workshop – Woods Hole, MA**, *PhyloNetworks: julia package for 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*.
- 2016 **Botany 563 – UW Madison**, *Small tutorial on PhyloNetworks and SNaQ*.
- 2015 **The hacker within series – UW Madison**, *Short introduction to Julia*.
- 2015 **Statistics student seminar – UW Madison**, *Short introduction to HTCondor*.

## Presentations

### Invited talks

- 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 traves de los ojos de Ciencias de Datos*.
- 2021 **ISCB EvolCompGen: Evolution and Comparative Genomics**, *Scalable inference of phylogenetic networks*.
- 2021 **I Congreso Latinoamericano de Evolucion**, *Metodos estadisticos para reconstruir redes filogeneticas*.
- 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 Latinoamerica**, *Metodos Estadisticos 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 traves 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 **Taming the BEAST – Squamish, BC**, *Bayesian phylogenetic inference for big data*.
- 2019 **Taming the BEAST – Squamish, BC**, *Statistical models on phylogenetic networks*.
- 2019 **Molecular Evolution Workshop – Woods Hole, MA**, *Statistical models on phylogenetic networks*.
- 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 **JSM – Advanced statistical inference for stochastic models of evolutionary biology**, *Comparative methods in phylogenetic networks*.
- 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
- 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 **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

- 2022 **Guest lecture: Statistics in Forensics 101**, *National Forensic College.*
- 2022 **Guest lecture: Basics of statistics for defense attorneys**, *Forensic University, (WI public defenders).*
- 2021 **WI Science Festival: Stumble into Science**, *UW-Madison.*
- 2021 **WI Science Festival: Stumble into Science**, *UW-Madison, Science talk at Delta Beer Lab.*
- 2021 **Biological Interactions Program**, *UW-Madison, Hosting undergraduate student Kaitilyn Abshire (CUNY) in the lab during Summer 2021.*
- 2021 **NSF**, *Grants review panel.*
- 2021 **Evolution conference**, *Bilingual Mentoring Program.*
- 2021–present **Frontiers in Ecology and Evolution - Phylogenetics, Phylogenomics, and Systematics**, *Review Editor.*
- 2021–2024 **Society of Systematic Biology**, *Elected Council Member.*
- 2019–present **Systematic Biology**, *Associate Editor.*
- 2016–present **Systematic Biology**, *Editorial Board Member.*
- 2019 **Atlanta Science Festival**, *Complete the circuit: meet a woman scientist, Atlanta, GA.*
- 2018 **Career Day**, *Bridge the diversity gap in science, Campbell Middle School, Atlanta, GA.*
- 2005–2008 **Sistema de preparatoria abierta para adultos**, *Math high-school teacher for adults, ITAM, Mexico.*
- UW-Madison
- 2020–present **Justice, Equity, Diversity and Inclusion (JEDI) committee**, *Chair.*
- 2020–present **PSGSC Plant Sciences Graduate Student Council**, *Invited to mentor students of color.*
- 2019–2020 **Graduate Admissions committee.**
- 2021 **Summer reading group**, *Machine learning in phylogenetics.*

## Symposium organization

- 2020–present **El Zoominario**, *Short scientific talks from Latinx in STEM*, (Organizer of this virtual seminar series to increase visibility of Latinx STEM speakers and inspire the next generation of Latinx scientists).
- 2020 **Systematic Biology Meeting**, *Coalescent-based methods in the age of big data*.
- 2018 **SACNAS symposium**, *Data Science: The Rise of the Machines*, Co-organizer: D.Pimentel-Alarcón.
- 2016 **Evolution meeting SSB symposium**, *Advances in the analysis of reticulate population networks*, Co-organizer: David Baum (UW-Madison).

## 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)

## Computer skills

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

## Certifications

- Exam C Society of Actuaries (SOA) *Construction of Actuarial Models Certificate*
- Exam FM Society of Actuaries (SOA) *Financial Mathematics Certificate*
- Exam P Society of Actuaries (SOA) *Probability Certificate*

## Media

- 2021 En Nuestro Patio Radio Interview on my work 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*
- 2020 “The flip of a coin” article *Badger Vibes stories*

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