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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

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.*, bioarxiv 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 **Towards a robust out-of-the-box neural network model for genomic data**, *Zhang, Z.*, Cheng, S.* Solís-Lemus, C.*, arXiv:2012.05995.

2020 **WI Fast Stats: a collection of web apps for the visualization and analysis of WI Fast Plants data**, *Liu, Y.*, Solís-Lemus, C.*, arXiv:2012.03290.

2020 **On the identifiability of phylogenetic networks under a pseudolikelihood model**, *Solís-Lemus, C., Coen, Arrigo*, C. Ané*, arxiv: 2010.01758.

Journal papers

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. Solis-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

2020 **Wisconsin Potato and Vegetable Growers Association, Inc.**, *Development of bioinformatic tools to leverage certification data for enhanced seed potato production*, Role: PI.

2020 **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 **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

2020 Solis-Lemus et al (2016) paper listed in PLOS Genetics Top 10% Collection

2020 Hilldale Faculty/Undergraduate Research Fellowship *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*

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.

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

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

2021 **Seminario de Investigacion de la Escuela de Estadistica**, *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

2021 **Coloquio de la Sociedad Matemática Mexicana**, *Biologia 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 **Invited speaker selected by graduate students**, *Statistical challenges on phylogenetic networks*, Organisms and Evolution seminar at Duke University.

2021 **American Mathematical Society: Special Section on Phylogenetic Networks**, *Identifianility 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 **BISP12**, *Bayesian CAR-LASSO model to learn sparse networks with predictors*, (virtual in Italy).

2021 **INFORMS en español**, *Biologia 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 **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 **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 **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

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*.

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).

Volunteer work

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.

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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