

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 **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 **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. 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

- 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

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 , <i>NIH-supported project</i> , Epilepsy consortium and 22q11.1 deletion syndrome consortium, PI: Michael Epstein. Emory University
2016–2017	Postdoctoral research , <i>NSF-supported project</i> , Improved Bayesian phylogenetic inference based on approximate conditional independence, PI: Bret Larget. University of Wisconsin-Madison
2014–2015	Research assistant , <i>NSF-supported project</i> , 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 , <i>NSF-supported project</i> , 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	Invited Faculty , <i>Virtual Species Delimitation workshop</i> , National Museum of Natural History, (virtual).
Spring 2021	Botany 563 , <i>Phylogenetic analysis of molecular data</i> , 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 , <i>Readings in phylogenomics</i> , This course will be a journal club where students will read and discuss the current literature related to phylogenomic analyses, UW-Madison.
2020	Invited Faculty , <i>Molecular Evolution Workshop: Phylogenetic networks</i> , Marine Biology Lab (MBL), Woods Hole, MA. (cancelled due to COVID19)
2019	Invited Faculty , <i>Molecular Evolution Workshop: Phylogenetic networks</i> , Marine Biology Lab (MBL), Woods Hole, MA.
2016	Guest lecturer , <i>Botany 563: Phylogenetic networks</i> , UW-Madison.
2014	Statistics tutorial , <i>PhD qualifying examination summer camp</i> , 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 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

- 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**, *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 **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 **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)	<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>

Media

2021	"The Tree of Life is rooted in Math" article	<i>GROW Magazine</i>
2021	WID Women's history month	<i>YouTube video</i>
2020	Code conversations with Casey Dunn	<i>YouTube interview</i>
2020	"The flip of a coin" article	<i>Badger Vibes stories</i>

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