

Claudia R. Solís-Lemus

Curriculum Vitae

Discovery Building Suite 3164
330 Orchard St
Madison, WI, 53715
☎ +1 (608) 609 4032
✉ solislemus@wisc.edu
📄 solislemuslab.github.io
🌐 [crl4](#)
🐦 [solislemuslab](#)

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

- 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 **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.
- 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 **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 **UW-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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| 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

- 2015 **PhyloNetworks**, <https://github.com/crs14/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

- 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

- 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*.

Mentoring Experience

- 2020 **Undergraduate research**, *Machine-learning to understand plant microbiome*, Songyang Cheng, Haoming Chen, Katherine Fu – UW-Madison.
- 2020 **Undergraduate research**, *Neural network models to predict biocontrol potential in mycovirus*, Liule Yang, Luke Selberg, Yifan Wu, Zhiwen Xu, Chunrong Huang – UW-Madison.
- 2020 **Undergraduate research**, *Neural network models to predict antibiotic-resistance*, Aryan Adhlakha, Zhaoyi Zhang, Lareina Liu – UW-Madison.
- 2018 **Software Development Project**, *Fast reconstruction and visualization of phylogenetic networks*, Harnoor Singh and Naman Kanwar – Georgia State University.
- 2018 **Software Development Project**, *Julia package for GAMuT*, Anna Voss – Emory University.
- 2018 **Statistics Senior Honors Thesis**, *GWAS for epilepsy*, Mengtong Hu – Emory University.
- 2016 **Software Development Project**, *Parallelization of SNaQ in PhyloNetworks*, Josh McGrath – University of Wisconsin-Madison.
- 2016 **Undergraduate Research Scholar**, *Computing tools for bayesian phylogenetic inference*, Jordan Vonderwell – University of Wisconsin-Madison.
- 2016 **Statistics Senior Honors Thesis**, *Computing tools and performance of PhyloNetworks*, Nan Ji – University of Wisconsin-Madison.
- 2015 **Statistics Senior Honors Thesis**, *Inconsistency of species-tree methods under gene flow*, Mengyao Yang – University of Wisconsin-Madison, published work.
- 2015 **Integrated Biological Sciences Summer Research Program**, *Visualizing inferred phylogenetic networks in Julia*, John Spaw – University of Wisconsin-Madison.
- 2014 **Integrated Biological Sciences Summer Research Program**, *Using quartets to estimate phylogenetic networks*, John Malloy – University of Wisconsin-Madison.

Presentations

Invited talks

- 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

- 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

- 2021–2024 **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: Daniel Pimentel-Alarcón (GSU).
- 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*

Statistical consulting

2016 Analysis of education programs for adults in indigenous populations

INEA, Mexico

Last updated: February 15, 2021