

Claudia R. Solís-Lemus

Curriculum Vitae

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👤 crsl4

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

Submitted

2020 **A Kernel Method for Dissecting Genetic Signals in Tests of High-Dimensional Phenotypes**, C. Solís-Lemus, A.M. Holleman, A. Todor, L.M. Almli, B. Bradley, K.J. Ressler, D. Ghosh, M.P. Epstein.

2019 **Data Augmentation and Transfer Learning for Image-Based Prediction in Microbial Data**, R. Walden, J. Rattray, S. Brown, C. Solis-Lemus, D. Pimentel-Alarcon.

Journal papers

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.

2019 **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, *Biostatistics and Bioinformatics*, 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.

Grants

Pending

- 2019 **NIH R01**, *Microbiome structure and response to antibiotics in chronic polymicrobial infections*, Role: co-I, (PI: Samuel Brown, GaTech).
Score: 35, Percentile:30
- 2020 **NIH R01**, *Novel integrative machine-learning tools for the prediction of complex phenotypes from high-dimensional biological data*, Role: co-PI, (co-PI: Daniel Pimentel-Alarcon).
- 2020 **NIH R01**, *Enhanced Penalized Regression Methods for Detecting Trait Loci in Genome-scale Studies*, Role: PI.
- 2020 **NSF**, *Microbiome beyond abundances: novel statistical theory on microbial phylogenetic networks*, Role: PI, (co-PI: Renee Rioux, Rick Lankau, Paul Koch).
- 2020 **DOE**, *Harnessing the power of big omics data: Novel statistical tools to study the role of microbial communities in fundamental biological processes*, Role: PI.

Awarded

- 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)

Unsuccessful

- 2019 **UW2020**, *Novel data integration and machine-learning tools for mycovirus data in the biological control of plant fungi pathogens*, Role: co-PI, (co-PI: Aurelie Rakotondrafara).
- 2019 **UW2020**, *Stethoscope for the rainforests: a near-real time biodiversity monitoring tool to curb extinctions*, Role: co-I, (PI: Zuzana Burilova).

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

- 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.

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

- 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

- 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*.

Tutorials

- 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*.

Service

- 2019–present **Systematic Biology**, *Associate Editor*.
- 2016–present **Systematic Biology**, *Editorial Board Member*.

Symposium organization

- 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)	<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>

Statistical consulting

2016	Analysis of education programs for adults in indigenous populations	<i>INEA, Mexico</i>
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References

- **Cécile Ané**, Professor of Statistics and Botany, UW-Madison cecile.ane@wisc.edu
- **Bret Larget**, Professor of Statistics and Botany, UW-Madison bret.larget@wisc.edu
- **Douglas Bates**, Emeritus Professor of Statistics, UW-Madison bates@wisc.edu
- **David Baum**, Chair of Botany, UW-Madison dbaum@wisc.edu
- **Kevin Packard**, Statistical consultant, Cornell U. (to address teaching), kcp48@cornell.edu
- **Ron Gangnon**, Professor of Biostatistics and Population Health (to address teaching) ronald@biostat.wisc.edu
- **Mike Epstein**, Professor of Human Genetics, Emory University mpepste@emory.edu