Claudia R. Solís-Lemus

Curriculum Vitae

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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

2019 **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.*

2019 **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.*

2019 **Mediation analysis 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.*

Journal papers

2018 **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.

In preparation

2019   **Bayesian importance sampling for phylogenetic inference**, *with B. Larget*, UW-Madison.

2019   **Modeling and inference of endogenous retrovirus dynamics**, *with F. Nascimiento*, U. of Oxford.

2019   **A new robust measure of relative dispersion**, *with V. Guerrero*, ITAM.

Grants

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)

Fellowships and Awards

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/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

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

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

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

| 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*
Exam P	Society of Actuaries (SOA)	*Probability Certificate*

Statistical consulting

| 2016 | Analysis of education programs for adults in indigenous populations | *INEA, Mexico* |

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

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