

# Claudia R. Solís-Lemus

## Curriculum Vitae

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### 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

- 2018 **Fast reconstruction of phylogenetic networks via outlier detection**, *C. Solís-Lemus*.  
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*.

#### Journal papers

- 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

- 2018 **Enhanced genome-wide association studies leveraging family history**, with M. Epstein, Emory U.
- 2018 **Genome-wide association study of delta toxin production in *S. aureus***, with T. Read and M. Su, Emory U.
- 2018 **Bayesian importance sampling for phylogenetic inference**, with B. Larget, UW-Madison.
- 2018 **Modeling and inference of endogenous retrovirus dynamics**, with F. Nascimiento, U. of Oxford.
- 2018 **A new robust measure of relative dispersion**, with V. Guerrero, ITAM.

## Grants

### Pending

- 2018 **NIH K99/R00 Path to Independence**, *Enhanced Penalized Regression Methods for Detecting Trait Loci in GWAS*, Role: PI.  
Score: 36
- 2018 **NIH R01**, *Advanced Deep Learning Methods to Predict Disease Risk from a Variety of Health Data*, PI: Pimentel-Alarcón (GSU), Role: Significant Contributor.

## Fellowships and Awards

- 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–present **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

- 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

- 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*.

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#### Service

- since 2016 **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

- 2005-2008 **Sistema de preparatoria abierta para adultos**, *Math high-school teacher for adults*, ITAM, Mexico.

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#### 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

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