

Claudia R. Solís-Lemus

Curriculum Vitae

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Education

- 2010–2015 **Ph.D., Statistics**, *University of Wisconsin-Madison*, Madison.
2014 **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

- 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.
2017 **Phylogenetic comparative methods on phylogenetic networks with reticulations**, Bastide, P., C. Solís-Lemus, R. Kriebel, K.W. Sparks, and C. Ané, bioRxiv:194050.
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

- 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.

Submitted

2017 **Phylogenetic comparative methods on phylogenetic networks with reticulations**, *P. Bastide, C. Solís-Lemus, R. Kriebel, K. W. Sparks, C. Ané*.

In preparation

2017 **Bayesian importance sampling for phylogenetic inference**, *with Bret Larget*, UW-Madison.

2017 **Modeling and inference of endogenous retrovirus dynamics**, *with Fabricia Nascimiento*, U. of Oxford.

2017 **A new robust measure of relative dispersion**, *with Victor Guerrero*, ITAM.

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 **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

- 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

- 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 **SSB spotlight: Next generation phylogenetic inference – Evolution meeting**, *Bayesian Phylogenetics with Importance Sampling*, (speaker Bret Larget).
- 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

- 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 **Bayesian Models and Inference – Contributed speed talk JSM**, *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.*
- 2012 **Data, skewness and testing – Contributed papers JSM**, *A parametric measure of dispersion derived from the generalized mean.*
(presenter: Victor Guerrero)
- 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.*

Service

- 2016 – 2017 **Systematic Biology**, *Editorial Board Member.*
Symposium organization
- 2016 **Evolution meeting SSB symposium**, *Advances in the analysis of reticulate population networks*, Co-organizer: David Baum.
Volunteer work
- 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

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| 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 *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