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

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.

2017 **Greatly reduced phylogenetic structure in the cultivated potato clade of Solanum section Petota**, *D. M. Spooner, H. Ruess, C. Arbizu, F. Rodríguez, and C. Solís-Lemus.*

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/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 **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

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`