

Claudia R. Solís-Lemus

Curriculum Vitae

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📄 <http://crsl4.github.io/>

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

- 2016 **PhyloNetworks: Julia package for inference and manipulation of phylogenetic networks**, *Solís-Lemus, Claudia and Ané, Cécile*, Submitted.
- 2016 **Inferring phylogenetic networks with maximum pseudolikelihood under incomplete lineage sorting**, *Solís-Lemus, Claudia and Ané, Cécile*, *PLoS Genetics* 12(3): e1005896, doi:10.1371/journal.pgen.1005896, arXiv:1509.06075.
- 2016 **Inconsistency of species-tree methods under gene flow**, *Solís-Lemus, Claudia and Yang, Mengyao and Ane, Cecile*, *Systematic Biology*, doi: 10.1093/sysbio/syw030.
- 2016 **Statistical evidence for common ancestry: application to primates**, *Baum, D., Ané, C., Larget, B., Solís-Lemus, C., Ho, L.S.T, Boone, P., Drummond, C., Bontrager, M., Hunter, S., Saucier, B.*, *Evolution*, doi: 10.1111/evo.12934.
- 2015 **Bayesian species delimitation combining multiple genes and traits in a unified framework**, *Solís-Lemus, Claudia, Knowles, L. Lacey and Ané, Cécile*, *Evolution*, 2. 69, 492–507

Conference papers

- 2016 **Crime detection via crowdsourcing**, *Pimentel-Alarcon, D. and C. Solís-Lemus*, 8th Mexican Conference on Pattern Recognition, Springer International.

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

- 2016 **Postdoctoral research**, *NSF-supported project*, Improved Bayesian phylogenetic inference based on approximate conditional independence, PI: Bret Larget.
- 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.
- 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.

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

- 2015 **Statistics Senior Honors Thesis**, *Inconsistency of species-tree methods under gene flow*, Mengyao Yang – University of Wisconsin-Madison.
- 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

- 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

- 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

Symposium organization

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

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*

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

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*