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Education

2022 (expected)	Ph.D. Integrative Genetics and Genomics University of California Davis
2015	M.Sc.Eng. Chemical and Bioprocess Engineering Pontificia Universidad Católica de Chile
2015	Biological Engineering Pontificia Universidad Católica de Chile Completed coursework in 2012. <i>Summa cum laude</i> .

Professional experience

2018 - present	Dennis Lab, University of California Davis, California, USA As a graduate student researcher to Dr. Megan Dennis, I currently study complex variation in great apes using short- and long-read sequencing technologies.
2015 - 2017	Plant Systems Biology Lab, Pontificia Universidad Católica de Chile, Chile As a bioinformatics support, I worked on <i>de novo</i> transcriptome assembly, RNA-seq differential expression analysis, and DNA metabarcoding analysis of endemic Atacama Desert plants.
2012 - 2014	Fondecyt Project, Pontificia Universidad Católica de Chile, Chile As a research assistant to Dr. Loreto Valenzuela, I studied the degradation profile of polymers intended for biomedical applications.
2013	Research and Development, Biofiltro SPA, Chile As a part-time researcher, I was tasked with improving the performance of an earthworm-based wastewater filter, for which we designed and set up a pilot plant, and interpreted the data using mathematical models.

Honors and awards

2017 - 2021	Chilean Government scholarship “BecasChile” for Ph.D. studies.
2017 - 2021	Fulbright fellowship for Ph.D. studies.
2014 - 2015	Chilean Government scholarship for M.Sc. studies.

Publications

Pre-prints	1. Shew CJ, Carmona-Mora P, Soto DC , Mastoras M, Roberts E, Rosas J, et al. Diverse molecular mechanisms contribute to differential expression of human duplicated genes. Cold Spring Harbor Laboratory. 2020. p. 2020.11.27.401752. doi:10.1101/2020.11.27.401752
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Peer reviewed

1. Carrasco-Puga G, Díaz FP, **Soto DC**, Hernández-Castro C, Contreras-López O, Maldonado A, et al. Revealing hidden plant diversity in arid environments. *Ecography*. 2020;75: 55.
2. Miga KH, Koren S, Rhie A, Vollger MR, Gershman A, Bzikadze A, et al. Telomere-to-telomere assembly of a complete human X chromosome. *Nature*. 2020. doi:10.1038/s41586-020-2547-7
3. **Soto DC***, Shew C*, Mastoras M, Schmidt JM, Sahasrabudhe R, Kaya G, et al. Identification of Structural Variation in Chimpanzees Using Optical Mapping and Nanopore Sequencing. *Genes*. 2020;11: 276.
4. Díaz FP, Latorre C, Carrasco-Puga G, Wood JR, Wilmshurst JM, **Soto DC**, et al. Multiscale climate change impacts on plant diversity in the Atacama Desert. *Glob Chang Biol*. 2019;25: 1733–1745.
5. Vidal EA, Moyano TC, Bustos BI, Pérez-Palma E, Moraga C, Riveras E, et al. Whole Genome Sequence, Variant Discovery and Annotation in Mapuche-Huilliche Native South Americans. *Sci Rep*. 2019;9: 2132.
6. Sánchez BJ, **Soto DC**, Jorquera H, Gelmi CA, Pérez-Correa JR. HIPPO: An Iterative Reparametrization Method for Identification and Calibration of Dynamic Bioreactor Models of Complex Processes. *Ind Eng Chem Res*. 2014;53: 18514–18525.

Book chapters

1. Contreras-López O, Moyano TC, **Soto DC**, Gutiérrez RA. Step-by-Step Construction of Gene Co-expression Networks from High-Throughput Arabidopsis RNA Sequencing Data. *Root Development*. Humana Press, New York, NY; 2018. pp. 275–301.

Selected presentations

Talks

1. *Invited panelist*. Nanopore Community Meeting Online. December 2020. “Identification of Structural Variation in Chimpanzees Using Optical Mapping and Nanopore Sequencing.”
2. *Invited webinar speaker*. Technology Networks - Oxford Nanopore Technologies. July 2020. “Identification of Structural Variation in Chimpanzees Using Optical Mapping and Nanopore Sequencing.”
3. 6th Annual UC Davis Health Human Genomics Symposium, Davis, California. November 2019. “Long-read sequencing to assay complex regions of the human genome.”
4. *Best talk award*. XI Chilean Plant Biology Meeting, Chillán, Chile. November 2016. “Metatranscriptomic approach reveals conserved adaptive processes in Atacama Desert plants.”

Posters

1. 7th Annual UC Davis Health Human Genomics Symposium Online. November 2020. “Genomic variant detection within human segmental duplications.”
2. American Society of Human Genomics Virtual Meeting. October 2020. “Genomic variant detection within human segmental duplications.”
3. *Best poster award*. Integrative Genetics and Genomics Colloquium, Davis, CA. September 2019. “Genomic variant detection within human-specific segmental duplications.”

4. Nanopore Community Meeting, San Francisco, CA. November 2018.
“Whole-genome sequencing of CHM1 and CHM13 haploid human cell lines for variant discovery in complex genomic regions.”

Teaching experience

University of California Davis

2019 Winter	<i>Teaching assistant.</i> Genomics.
2018 Summer	<i>Helper.</i> Data Intensive Biology Summer Institute: Analyzing High Throughput Sequencing Data Workshop.

Pontificia Universidad Católica de Chile

2013 Fall	<i>Teaching assistant.</i> Mathematics Applied to Process Engineering (MATLAB lab).
2013 Spring	<i>Teaching assistant.</i> Biopolymers.
2012 Fall	<i>Teaching assistant.</i> Microbial Biotechnology.
2012 Spring	<i>Teaching assistant.</i> Biopolymers.

Service

Integrative Genetics and Genomics Graduate Group

2020 - present	<i>Member.</i> Diversity, equity, inclusion committee.
2018 - present	<i>Volunteer.</i> K-12 science activities.
2019 - 2020	Vice-chair, Student Executive Committee
2018 - 2019	Mentoring and Advising Coordinator, Student Executive Committee.

Other service

October 2019	<i>Organizing committee.</i> Northern California Computational Biology Symposium 2019, Davis, California.
November 2016	<i>Organizing committee.</i> International Plant Biology Course, Santiago, Chile.

Skills and Qualifications

- Operating systems: Linux/Unix.
- Programming languages: Python, R, AWK, MATLAB.
- Bioinformatics toolbox: Git/GitHub, Conda/Bioconda, Snakemake, Markdown, R Shiny.
- Graphic design and illustration: Adobe Illustrator, Adobe Photoshop, Procreate.
- Languages: Spanish (native), English (full professional proficiency).