

# Daniela C. Soto

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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  
Courses completed in 2012. *Summa cum laude*.

## Professional experience

- 2018 - present     **Dennis Lab, University of California Davis, California, USA**  
As a graduate student researcher to Dr. Megan Dennis, I study complex genomic variation—including structural variants and segmental duplications—in great apes using short- and long-read sequencing technologies.
- 2015 - 2017     **Plant Systems Biology Lab, Pontificia Universidad Católica de Chile, Chile**  
As bioinformatics support, I worked on *de novo* transcriptome assembly, RNA-seq differential expression analysis, and DNA metabarcoding analysis of endemic plants from the Chilean Atacama Desert.
- 2012 - 2014     **Fondecyt Project, Pontificia Universidad Católica de Chile, Chile**  
As a research assistant to Dr. Loreto Valenzuela, I studied the degradation profile of tyrosine-derived polymers intended for biomedical applications.
- 2013     **Researcher, 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

- 2021     UC Davis Summer Graduate Student Researcher Award.
- 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

\* These authors contributed equally to this work.

- Peer-reviewed**
1. Nurk S, Koren S, Rhie A, Rautiainen M, Bizikadze AV, Mikheenko A, et al. The complete sequence of a human genome. *Science*. 2022;376: 44–53.
  2. Aganezov S\*, Yan SM\*, **Soto DC\***, Kirsche M\*, Zarate S\*, Avdeyev P, et al. A complete reference genome improves analysis of human genetic variation. *Science*. 2022;376: eabl3533.

3. Mc Cartney AM, Shafin K, Alonge M, Bzikadze AV, Formenti G, Fungtammasan A, et al. Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. *Nat Methods*. 2022. doi:10.1038/s41592-022-01440-3
4. Zhu Y, Gomez JA, Laufer BI, Mordaunt CE, Mouat JS, **Soto DC**, et al. Placental methylome reveals a 22q13.33 brain regulatory gene locus associated with autism. *Genome Biol*. 2022;23: 1–32.
5. Eshel G\*, Araus V\*, Undurraga S, **Soto DC**, Moraga C, Montecinos A, et al. Plant ecological genomics at the limits of life in the Atacama Desert. *Proc Natl Acad Sci U S A*. 2021;118. doi:10.1073/pnas.2101177118
6. 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. *Mol Biol Evol*. 2021. doi:10.1093/molbev/msab131
7. 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.
8. 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
9. **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.
10. 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.
11. 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.
12. 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.

#### Other

1. Mc Cartney AM, Mahmoud M, Jochum M, Agostinho DP, Zorman B, Al Khleifat A, et al. An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. *F1000Res*. 2021;10: 246.

### 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 Genetics 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."

## Additional Training

### Genetics Society of America

2022-2023                      Genetics Peer Review Training Program. Genome & Systems Biology.

## Teaching experience

### University of California Davis

2019 Winter                      *Teaching assistant.* Genomics.

2018 Summer                      *Helper.* Data-Intensive Biology Summer Institute: Analyzing High Throughput Sequencing Data Workshop.

### Pontificia Universidad Católica de Chile

2013 Fall                              *Teaching assistant.* Mathematics Applied to Process Engineering (MATLAB lab).

2013 Spring                        *Teaching assistant.* Biopolymers.

2012 Fall                              *Teaching assistant.* Microbial Biotechnology.

2012 Spring                        *Teaching assistant.* Biopolymers.

## Mentoring

### Undergraduate Students

2021                                  Jeffrey Zang                      B.S. Computer Science. University of California, Davis.

2019                                  Mira Mastoras                      B.S. Cellular and Molecular Biology. University of California, Davis.

## Service and Community

### Dennis Lab, UC Davis

Apr 2022                              **Volunteer. Molecular Biology Laboratory, Sacramento Charter School.** We organized and executed a molecular biology workshop for junior and senior classes.

### Integrative Genetics and Genomics Graduate Group, UC Davis

2020 - 2021                              **Member. Diversity, equity, inclusion committee.** As part of the survey subcommittee, we designed, distributed, and analyzed a survey to study the diversity of identities within our graduate group.

2019 - 2020                              **Vice-chair, Student Executive Committee.** During a year-long period, I served as vice-chair of my graduate group.

2018 - 2021	<b>Volunteer. UC Davis Pic Nic Day K-12 science activities.</b> I volunteered in several science outreach activities, including extraction of DNA from strawberries and making “DNA bracelets”.
2018 - 2019	<b>Mentoring and Advising Coordinator, Student Executive Committee.</b> I oversaw the IGG’s peer-mentoring program where senior students are matched with incoming students.
<b>Other activities</b>	
2022	<b>Mentee. Graduate Students of Color Mentoring Program.</b>
Dec 2021	<b>Invited instructor. Central Asia Genomics Workshop: Command-Line Fundamentals.</b> I was invited to teach an introductory lecture on the Linux command line for bioinformatics to a group of students from Uzbekistan.
Oct 2021	<b>Participant. Baylor College of Medicine Virtual Structural Variation Hackathon. Team: k-var.</b> For three days, I worked along with other 70+ scientists developing software and pipelines to aid with structural variation research.
Sep-Nov 2021	<b>Organizing Committee. Chilean Society of Bioinformatics Annual Meeting.</b> I designed graphic materials for the annual meeting, including the logotype of the event and website banners.
Feb 2021	<b>Invited panelist. Graduate Student Panel, California Undergraduate Bioinformatics Virtual Conference.</b> I was invited to share my experience as a computational biologist and bioinformatician with undergraduate students from all UCs.
Jan 2021	<b>Invited panelist. Graduate Student Panel, UC Davis CompBio Virtual Symposium.</b> I was invited to share my experience as a computational biologist and bioinformatician with undergraduate students from UC Davis.
Nov 2020	<b>Participant. Baylor College of Medicine Virtual Structural Variation Hackathon. Team: CoronaSV.</b> For three days, I work along with other 70+ scientists developing software and pipelines to aid with structural variation research.
Oct 2019	<b>Organizing committee. Northern California Computational Biology Symposium 2019, Davis, California.</b> I designed the graphic materials for the symposium, including a logotype for the organization and for the event, flyers, and T-shirts.
Oct 2018	<b>Invited panelist. SACNAS Student Chapter Panel Discussion.</b> I was invited to share my experience as a Latino graduate student along with other scientists coming from underrepresented backgrounds at Sacramento State University.
Nov 2016	<b>Organizing committee. International Plant Biology Course, Santiago, Chile.</b> I designed the graphic materials for the promotion of the course.
July 2016	<b>Logotype design. Chilean Society of Plant Biologists.</b> I designed the official logo of the Chilean Society of Plant Biologists available at <a href="http://www.biologiavegetal.cl">www.biologiavegetal.cl</a> .
2016-2017	<b>Volunteer. Girls in Tech Chile.</b> Member of the Chilean chapter of Girls in Tech, where I attended group meetings and volunteered in activities to inspire girls to pursue STEM careers.

## Skills and Qualifications

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