

# Daniela C. Soto, Ph.D.

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Gonda Neuroscience and Genetics Research Center  
695 Charles E Young Drive South  
Los Angeles, CA 90095

Phone: +1 530-979-4183  
E-mail: [dcsoto@ucla.edu](mailto:dcsoto@ucla.edu)  
Website: [dcsoto.github.io](http://dcsoto.github.io)

## Current position

Postdoctoral Scholar  
Department of Psychiatry  
University of California, Los Angeles

## Education

- 2022            Ph.D. Integrative Genetics and Genomics  
University of California Davis, Davis, CA, USA  
*Mentor: Megan Y. Dennis*
- 2015            M.S. Chemical Engineering  
Pontificia Universidad Católica de Chile, Santiago, Chile  
*Mentor: Loreto M. Valenzuela*
- 2012            B.S. Biological Engineering  
Pontificia Universidad Católica de Chile, Santiago, Chile  
*Summa cum laude*

## Employment

- 2023 - present    Postdoctoral Scholar - University of California Los Angeles, Los Angeles, CA, USA  
*Mentor: Jonathan Flint*
- 2023            Postdoctoral Scholar - University of California Davis, Davis, CA, USA  
*Mentor: Megan Y. Dennis*
- 2018 - 2022      Graduate Student Researcher - University of California Davis, Davis, CA, USA.  
*Mentor: Megan Y. Dennis*
- 2015 - 2017      Bioinformatics Analyst - Pontificia Universidad Católica de Chile, Santiago, Chile  
*Mentor: Rodrigo A. Gutiérrez*
- 2012 - 2014      Research Assistant - Pontificia Universidad Católica de Chile, Santiago, Chile  
*Mentor: Loreto M. Valenzuela*
- 2013            Part-Time R&D - Biofiltro SPA, Santiago, Chile

## Honors and awards

- 2023            ASHG Trainee Research Excellence Award (co-first author).
- 2021            UC Davis Summer Graduate Student Researcher Award.
- 2017 - 2021      Chilean Government scholarship "BecasChile" (Ph.D.)
- 2017 - 2021      Fulbright fellowship (Ph.D.)
- 2014 - 2015      Chilean Government scholarship (M.Sc.)

## Publications

\* These authors contributed equally to this work.

### Peer-reviewed

1. Libé-Philippot, B. *et al.* LRRC37B is a human modifier of voltage-gated sodium channels and axon excitability in cortical neurons. *Cell* 186, 5766–5783.e25 (2023)
2. Behera S, LeFaive J, Orchard P, Mahmoud M, Paulin LF, Farek J, **Soto DC**, et al. FixItFelix: improving genomic analysis by fixing reference errors. *Genome Biol.* 2023;24: 31.
3. **Soto DC**\*, Uribe-Salazar JM\*, Shew CJ\*, Sekar A, McGinty SP, Dennis MY. Genomic structural variation: A complex but important driver of human evolution. *Am J Biol Anthropol.* 2023. doi:10.1002/ajpa.24713
4. Nurk S, Koren S, Rhie A, Rautiainen M, Bzikadze AV, Mikheenko A, et al. The complete sequence of a human genome. *Science.* 2022;376: 44–53.
5. 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.
6. Mc Cartney AM, Shafin K, Alonge M, Bzikadze AV, Formenti G, Functammasan A, et al. Chasing perfection: validation and polishing strategies for telomere-to-telomere genome assemblies. *Nat Methods.* 2022.
7. 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.
8. 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.
9. 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.
10. 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.
11. 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.
12. **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.
13. 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.
14. 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.
15. 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.

### Pre-prints

1. Gutierrez Fugon, O. J. *et al.* Integration of CTCF Loops, Methylome, and Transcriptome in Differentiating LUHMES as a Model for Imprinting Dynamics of the 15q11-q13 Locus in Human Neurons. *bioRxiv* 2024.03.26.586689 (2024) doi:10.1101/2024.03.26.586689
2. Chen, P. B. *et al.* Complementation testing identifies causal genes at quantitative trait loci underlying fear related behavior. *bioRxiv* 2024.01.03.574060 (2024) doi:10.1101/2024.01.03.574060

### 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. Walker K, Kalra D, Lowdon R, Chen G, Molik D, **Soto DC**, et al. The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. *F1000Res*. 2022;11: 530.
2. 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.

## Select presentations

### Talks

1. Inaugural Symposium Celebrating Hispanic Heritage Month, Davis, CA. October 2023. "Assessment of duplicated genes in a complete human telomere-to-telomere genome implicates novel paralogs in brain evolution."
2. Stanford Genetics Conference on Structural Variants and DNA Repeats SVAR23, Stanford, CA. September, 2023. "Long-read Khoe-San genomes reveal structurally divergent loci overlapping genic regions."
3. *Invited panelist*. Instituto Nacional de Medicina Genómica, INMIGEN, México. August, 2022. "Genetic variant detection in complex genomic regions using long-read sequencing."
4. *Invited panelist*. Nanopore Community Meeting [Online]. December, 2020. "Identification of Structural Variation in Chimpanzees Using Optical Mapping and Nanopore Sequencing."
5. *Invited speaker*. Technology Networks - Oxford Nanopore Technologies [Online]. July, 2020. "Identification of Structural Variation in Chimpanzees Using Optical Mapping and Nanopore Sequencing."
6. 6th Annual UC Davis Health Human Genomics Symposium, Davis, California. November, 2019. "Long-read sequencing to assay complex regions of the human genome."
7. *Best Talk Award*. XI Chilean Plant Biology Meeting, Chillán, Chile. November, 2016. "Metatranscriptomic approach reveals conserved adaptive processes in Atacama Desert plants."

### Posters

1. American Society of Human Genetics Meeting, Washington, D.C. November 2023. "Long-read Khoe-San genomes reveal structurally divergent loci overlapping genic regions."
2. American Society of Human Genetics Meeting, Los Angeles, CA. October 2022. "Population diversity and selection of recent gene duplications detected using a complete human genome sequence."
3. 7th Annual UC Davis Health Human Genomics Symposium. Virtual event. November 2020. "Genomic variant detection within human segmental duplications."
4. American Society of Human Genetics Virtual Meeting. Virtual event. October 2020. "Genomic variant detection within human segmental duplications."
5. *Best poster award*. Integrative Genetics and Genomics Colloquium, Davis, CA. September 2019. "Genomic variant detection within human-specific segmental duplications."
6. 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 and mentoring

### Courses

#### University of California Davis

2024 Winter      *Guest lecturer*. Genomics (1 lecture, 1 bioinformatics lab)

2023 Winter      *Guest lecturer*. Genomics (2 lectures, 1 bioinformatics lab).

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 programming lab).  
2013 Spring      *Teaching Assistant.* Biopolymers.  
2012 Fall      *Teaching Assistant.* Microbial Biotechnology.  
2012 Spring      *Teaching Assistant.* Biopolymers.

#### **Undergraduate mentoring**

2021 - present      Jeffrey Zang. B.S. Computer Science. University of California, Davis.  
2019 - 2020      Mira Mastoras. B.S. Cellular and Molecular Biology. University of California, Davis.

#### **Service and community**

##### Dennis Lab, UC Davis

May 2023      *Volunteer.* Molecular Biology Laboratory, Sacramento Charter High School.  
Summer 2022      *Mentor.* UC Davis Biochemistry & Molecular Medicine-Sacramento Charter High School Summer Research Program.  
Apr 2022      *Volunteer.* Molecular Biology Laboratory, Sacramento Charter High School.

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

March 2023      *Volunteer.* UC Davis Postdoctoral Association, 8th Annual Postdoctoral Research Symposium organizing committee.  
2020 - 2021      *Member.* Diversity, equity, inclusion committee.  
2019 - 2020      *Vice-chair,* Student Executive Committee.  
2018 - 2021      *Volunteer.* UC Davis Picnic Day K-12 science activities.  
2018 - 2019      *Mentoring and Advising Coordinator,* Student Executive Committee.

##### Other activities

2023-2024      *Member.* Genetics Society of America Early Career Scientists Program. Communication and outreach subcommittee.  
2022-2023      *Member.* Data Science Affiliate, UC Davis DataLab.  
2022-2023      *Member.* Genetics Peer Review Training Program. Genome & Systems Biology.  
Jan-Jun 2022      *Mentee.* UC Davis Graduate Students of Color Mentoring Program.  
Dec 2021      *Invited instructor.* Central Asia Genomics Workshop: Command-Line Fundamentals.  
Oct 2021      *Participant.* Baylor College of Medicine Virtual Structural Variation Hackathon. Team: k-var.  
Nov 2021      *Organizing committee and graphic design.* Chilean Society of Bioinformatics Annual Meeting.  
Feb 2021      *Invited panelist.* California Undergraduate Bioinformatics Virtual Conference Graduate Student Panel.  
Jan 2021      *Invited panelist.* UC Davis CompBio Virtual Symposium Graduate Student Panel.

Nov 2020	<i>Participant.</i> Baylor College of Medicine Virtual Structural Variation Hackathon. Team: CoronaSV.
Oct 2019	<i>Organizing committee and graphic design.</i> Northern California Computational Biology Symposium 2019.
Oct 2018	<i>Invited panelist.</i> SACNAS Student Chapter Panel Discussion, Sacramento State University.
Nov 2016	<i>Organizing committee and graphic design.</i> International Plant Biology Course, Santiago, Chile.
July 2016	<i>Logotype design.</i> Chilean Society of Plant Biologists.
2016-2017	<i>Volunteer.</i> Girls in Tech Chilean Chapter.

## Media coverage

1. Duran, E. & Venegas, L. May 9, 2022. "Descubriendo los secretos del genoma." *En un Mar de Ciencia*. <https://open.spotify.com/episode/16ket90cLPficyOOEBC74?si=xMjj3r32Q92U1VyBHs4ikg>
2. Aravena, F. April 25, 2022. "La importancia de la secuenciación completa del genoma humano." *El Café Diario, La Tercera*. <https://www.latercera.com/podcast/noticia/el-cafe-diario-la-importancia-de-la-secuenciacion-completa-del-genoma-humano/WFRPQUY4C5F4FNP5T4BV5G227M/>
3. Reyes, M. April 5, 2022. "Las principales conclusiones del último informe del IPCC." *Congreso Futuro, Radio Cooperativa*. <https://www.cooperativa.cl/noticias/sociedad/ciencia/congreso-futuro/congreso-futuro-las-principales-conclusiones-del-ultimo-informe-del-ipcc/2022-04-10/125605.html>
4. Romero, M. April 5, 2022. "El ADN al descubierto: hablamos con una de las bioinformáticas que ayudó a secuenciar el genoma humano." *France 24*. <https://www.france24.com/es/programas/salud/20220405-adn-secuencia-genoma-humano-daniela-soto>
5. Ansele, M. March 31, 2022. "El primer genoma completo de un ser humano abre una nueva era en la ciencia." *El País*. <https://elpais.com/ciencia/2022-03-31/el-primer-genoma-completo-de-un-ser-humano-abre-una-nueva-era-en-la-ciencia.html>
6. Fell, A. March 31, 2022. "New Human Reference Genome Opens Unexplored Regions." *UC Davis News*. <https://www.ucdavis.edu/health/news/new-human-reference-genome-opens-unexplored-regions>
7. Yehya, Nadine A. February 15, 2022. "Placenta may hold clues for early autism diagnosis and intervention." *UC Davis Health News*. <https://health.ucdavis.edu/news/headlines/placenta-may-hold-clues-for-early-autism-diagnosis-and-intervention/2022/02>

## Skills and qualifications

- Operating systems: Linux/Unix.
- Job schedulers: Slurm, Sun Grid Engine.
- Programming languages: Python, R, shell scripting.
- Bioinformatics toolbox: Git/GitHub, Conda/Bioconda, Snakemake, Markdown.
- Web applications: R Shiny.
- Graphic design and illustration: Adobe Illustrator, iPad Procreate.
- Languages: Spanish (native), English (full professional proficiency).