

Daniela C. Soto, Ph.D.

1125 Biological Sciences II
University of California, Santa Barbara
Santa Barbara, CA 93106

Phone: +1 530-979-4183
Email: dcsoto@ucsb.edu
Website: dcsoto.github.io

Current position

Postdoctoral Scholar
Neuroscience Research Institute
University of California, Santa Barbara

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

2025 - present Postdoctoral Scholar - University of California Santa Barbara, Santa Barbara, CA, USA
 Mentor: Soojin Yi; co-mentor: Kirk Lohmueller (UCLA)

2023 - 2024 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

2025 - present HHMI Hanna H. Gray Fellow

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. Ostridge HJ, Fonsere C, Lizano E, **Soto DC**, Schmidt JM, Saxena V, et al. Local genetic adaptation to habitat in wild chimpanzees. *Science*. 2025;387. doi:10.1126/science.adn7954
2. Gutierrez Fugón OJ, Sharifi O, Heath N, **Soto DC**, Gomez JA, Yasui DH, 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. *Hum Mol Genet*. 2024; ddae111.
3. Chen PB, Chen R, LaPierre N, Chen Z, Mefford J, Marcus E, et al. Complementation testing identifies genes mediating effects at quantitative trait loci underlying fear-related behavior. *Cell Genom*. 2024; 100545.
4. Libé-Philippot B, Lejeune A, Wierda K, Louros N, Erkol E, Vlaeminck I, et al. LRRC37B is a human modifier of voltage-gated sodium channels and axon excitability in cortical neurons. *Cell*. 2023;186: 5766-5783.e25.
5. 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.
6. **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
7. 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.
8. 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.
9. McCartney 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.
10. 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.
11. 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.
12. 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.
13. 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.
14. 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.
15. **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.
16. 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.
17. 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.
18. 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. **Soto DC***, Uribe-Salazar JM*, Kaya G, Valdarrago R, Sekar A, Haghani NK, et al. Gene expansions contributing to human brain evolution. bioRxiv. 2024. p. 2024.09.26.615256. doi:10.1101/2024.09.26.615256.
2. Uribe-Salazar JM, Kaya G, Weyenberg KB, Radke B, Hino KK, **Soto DC**, et al. Zebrafish models of human-duplicated gene SRGAP2 reveal novel functions in microglia and visual system development. bioRxiv. 2024. p. 2024.09.11.612570. doi:10.1101/2024.09.11.612570.

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

Invited talks

1. Instituto Nacional de Medicina Genómica, INMIGEN, México. August 2022. “Genetic variant detection in complex genomic regions using long-read sequencing.”
2. Nanopore Community Meeting. December 2020. “Identification of Structural Variation in Chimpanzees Using Optical Mapping and Nanopore Sequencing.” (Virtual.)
3. Technology Networks - Oxford Nanopore Technologies. July 2020. “Identification of Structural Variation in Chimpanzees Using Optical Mapping and Nanopore Sequencing.” (Virtual.)

Contributed 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. 6th Annual UC Davis Health Human Genomics Symposium, Davis, California. November 2019. “Long-read sequencing to assay complex regions of the human genome.”
4. XI Chilean Plant Biology Meeting, Chillán, Chile. November 2016. “Metatranscriptomic approach reveals conserved adaptive processes in Atacama Desert plants.” (Best Talk Award.)

Contributed 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. Integrative Genetics and Genomics Colloquium, Davis, CA. September 2019. “Genomic variant detection within human-specific segmental duplications.” (Best poster award.)
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.”

Non-technical presentations and publications

1. **Soto DC**, Kirsche M, Yan SM, Zarate S. The human reference genome is finally complete. TheScienceBreaker. 2023;9.

Research funding

Active

2025 - present **Howard Hughes Medical Institute** Hanna Gray Fellowship Postdoctoral Phase
The role of human-specific mRNA isoforms in brain function and disease
The goal of this project is to systematically characterize human-specific forms of messenger RNA exhibiting signatures of natural selection and evaluate their roles in brain development and function using single-cell and long-read RNA isoform sequencing.
Salary \$80K/yr for 4 yr, flexible fund \$20K/yr
Role: Postdoctoral fellow

Teaching and mentoring

Courses

University of California, Davis

2025 Winter *Guest lecturer.* GGG201B Genomics (1 lab).
2024 Winter *Guest lecturer.* GGG201B Genomics (1 lecture, 1 lab).
2023 Winter *Guest lecturer.* GGG201B Genomics (2 lectures, 1 lab).
2019 Winter *Teaching assistant.* Genomics.
2018 Summer *Volunteer.* 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 laboratory).
2013 Spring *Teaching assistant.* Biopolymers.
2012 Fall *Teaching assistant.* Microbial Biotechnology.
2012 Spring *Teaching assistant.* Biopolymers.

Other universities

July 2024 *Guest lecturer.* Research seminar (1 lecture). Master of Science in Biomolecular Medicine, School of Medicine, Universidad Autónoma de Sinaloa, Sinaloa, México.
December 2021 *Guest lecturer.* Central Asia Genomics Workshop: Command-Line Fundamentals.

Undergraduate mentoring

2021 - 2023 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

Academic and university service

Reviewer

2024 *Ad hoc abstract reviewer.* American Society of Human Genetics Annual Meeting.
2023-2024 *Ad hoc reviewer.* Science, NAR Genomics and Bioinformatics, Scientific Reports.

Administrative responsibilities

2020 - 2021	UC Davis Integrative Genetics and Genomics Graduate Program, Diversity, Equity, and Inclusion Committee Member.
2019 - 2020	UC Davis Integrative Genetics and Genomics Graduate Program, Student Executive Committee, Vice-chair.
2018 - 2019	UC Davis Integrative Genetics and Genomics Graduate Program, Student Executive Committee, Mentoring and Advising Coordinator.
March 2023	UC Davis Postdoctoral Association, 8th Annual Postdoctoral Research Symposium Organizing Committee.
Oct 2019	UC Davis Northern California Computational Biology Symposium 2019, Organizing Committee.

Other professional activities

2023 - present	Genetics Society of America Early Career Scientists Program, Communication and Outreach Subcommittee.
2022 - 2023	Data Science Affiliate, UC Davis DataLab.
2022 - 2023	Genetics Society of America Peer Review Training Program, Genome & Systems Biology Group.
Nov 2022	Chilean Society of Bioinformatics Annual Meeting, Organizing Committee.
Oct 2021	Baylor College of Medicine Virtual Structural Variation Hackathon.
Feb 2021	California Undergraduate Bioinformatics Virtual Conference Graduate Student Panel, Invited Panelist.
Jan 2021	UC Davis CompBio Virtual Symposium Graduate Student Panel, Invited Panelist.
Nov 2020	Baylor College of Medicine Virtual Structural Variation Hackathon.
Nov 2016	International Plant Biology Course, Santiago, Chile, Organizing Committee.
July 2016	Chilean Society of Plant Biologists, Logotype Design.

Outreach and public engagement

May 2023	Molecular Biology Laboratory, Sacramento Charter High School, Co-Instructor.
Summer 2022	UC Davis Biochemistry & Molecular Medicine-Sacramento Charter High School Summer Research Program, Co-Mentor.
Apr 2022	Molecular Biology Laboratory, Sacramento Charter High School, Co-Instructor.
Jan - Jun 2022	UC Davis Graduate Students of Color Mentoring Program, Member.
2018 - 2021	UC Davis Picnic Day, K-12 science outreach, Co-Facilitator.
Oct 2018	SACNAS Student Chapter Panel Discussion, Sacramento State University, Invited Panelist.
2016 - 2017	Chilean Chapter of Girls in Tech, Member.

Media coverage

- [University Press] Tasoff, Harrison (February 6, 2025). "*UCSB postdoc receives competitive award to investigate the genetic changes that shaped the human mind.*" UCSB News: The Current.
<https://news.ucsb.edu/2025/021743/ucsb-postdoc-receives-competitive-award-investigate-genetic-change-s-shaped-human-mind>
- [University Press] Lane, C. (January 10, 2025). "*Chimpanzees are genetically adapted to local habitats and infections such as malaria.*" UCL News.

<https://www.ucl.ac.uk/news/2025/jan/chimpanzees-are-genetically-adapted-local-habitats-and-infections-such-malaria>

- [Podcast] Duran, E., & Venegas, L. (May 9, 2022). "Descubriendo los secretos del genoma." En un Mar de Ciencia. <https://open.spotify.com/episode/16ket90cLPlfcyOOEBC74?si=xMjj3r32Q92U1VyBHs4ikg>
- [Podcast] 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/>
- [Radio Show] 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>
- [TV News] 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>
- [Newspaper] Ansedé, 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>
- [University Press] 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>
- [University Press] Yehya, N. 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, Python Dash.
- Graphic design and illustration: Adobe Illustrator, iPad Procreate.
- Languages: Spanish (native), English (full professional proficiency).