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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 <i>Thesis: Characterization of primate structural variation using diverse sequencing technologies. Mentor: Megan Y. Dennis</i>
2015	M.S. Chemical Engineering Pontificia Universidad Católica de Chile, Santiago, Chile <i>Mentor: Loreto M. Valenzuela</i>
2012	B.S. Biological Engineering Pontificia Universidad Católica de Chile, Santiago, Chile <i>Summa cum laude</i>

Employment

2025 - present	Postdoctoral Fellow - University of California Santa Barbara, Santa Barbara, CA, USA <i>Mentor: Soojin Yi; co-mentor: Kirk Lohmueller (UCLA)</i>
2023 - 2024	Postdoctoral Scholar - University of California Los Angeles, Los Angeles, CA, USA <i>Mentor: Jonathan Flint</i>
2023	Postdoctoral Scholar - University of California Davis, Davis, CA, USA <i>Mentor: Megan Y. Dennis</i>
2018 - 2022	Graduate Student Researcher - University of California Davis, Davis, CA, USA. <i>Mentor: Megan Y. Dennis</i>
2015 - 2017	Bioinformatics Analyst - Pontificia Universidad Católica de Chile, Santiago, Chile <i>Mentor: Rodrigo A. Gutiérrez</i>
2012 - 2014	Research Assistant - Pontificia Universidad Católica de Chile, Santiago, Chile <i>Mentor: Loreto M. Valenzuela</i>
2013	Part-Time R&D - Biofiltro SPA, Santiago, Chile

Selected honors and awards

2025 - present	HHMI Hanna H. Gray Postdoctoral Fellow
2023	ASHG Trainee Research Excellence Award (co-first author)
2021	UC Davis Summer Graduate Student Researcher Award
2017 - 2021	Fulbright Chile – Ph.D. fellowship
2017 - 2021	Chilean National Agency for Research and Development – Ph.D. scholarship
2014 - 2015	Chilean National Agency for Research and Development – M.Sc. scholarship

Publications

* co-first authors; [†] mentored student

Google Scholar: <https://scholar.google.com/citations?user=c7K5YbUAAAAJ&hl=en>

Total citations (as of September 2025): 5019; h-index: 15

Peer-reviewed

1. **Soto DC***, Uribe-Salazar JM*, Kaya G, Valdarrago R, Sekar A, Haghani NK, et al. Human-specific gene expansions contribute to brain evolution. *Cell*. 2025. doi:10.1016/j.cell.2025.06.037
2. Greenfield S, Stevens NC, Bishop L, Rabow Z, **Soto DC**, Abdullah AO, et al. Drug-Based Lifespan Extension in Mice Strongly Affects Lipids Across Six Organs. *Aging Cell*. 2025. doi:10.1111/acel.14465
3. Ostridge HJ, Fontseré C, Lizano E, **Soto DC**, Schmidt JM, Saxena V, et al. Local genetic adaptation to habitat in wild chimpanzees. *Science*. 2025. doi:10.1126/science.adn7954
4. 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.
5. 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.
6. 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.
7. 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.
8. **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
9. Nurk S, Koren S, Rhee A, Rautiainen M, Bzikadze AV, Mikheenko A, et al. The complete sequence of a human genome. *Science*. 2022.
10. 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.
11. 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.
12. 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.
13. 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. *PNAS*. 2021.
14. 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.
15. 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.
16. Miga KH, Koren S, Rhee A, Vollger MR, Gershman A, Bzikadze A, et al. Telomere-to-telomere assembly of a complete human X chromosome. *Nature*. 2020.
17. **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.
18. Díaz FP, Latorre C, Carrasco-Puga G, Wood JR, Wilmhurst JM, **Soto DC**, et al. Multiscale climate change impacts on plant diversity in the Atacama Desert. *Glob Chang Biol*. 2019.

19. 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.
20. 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.

Pre-prints

1. 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. 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.

Community sprints

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, Agustinho 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.

Non-technical publications

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

Selected presentations

Invited talks

1. Ecology, Evolution and Marine Biology Seminar, UCSB, Santa Barbara, CA. November 2025. “Gene duplications and regulatory changes contributing to human brain evolution.”
2. Department of Anthropology Colloquium Series, UCSB, Santa Barbara, CA. May 2025. “Genetic and epigenetic changes contributing to human brain evolution.”
3. Instituto Nacional de Medicina Genómica, INMIGEN, México. August 2022. “Genetic variant detection in complex genomic regions using long-read sequencing.”
4. Nanopore Community Meeting. December 2020. “Identification of Structural Variation in Chimpanzees Using Optical Mapping and Nanopore Sequencing.” (Virtual)
5. 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. Southern California Evolutionary Genetics and Genomics Meeting, Los Angeles, CA. November 2025. "Human-specific splice isoforms contributing to brain evolution."
2. American Society of Human Genetics Meeting, Washington, D.C. November 2023. "Long-read Khoe-San genomes reveal structurally divergent loci overlapping genic regions."
3. 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."
4. 7th Annual UC Davis Health Human Genomics Symposium. Virtual event. November 2020. "Genomic variant detection within human segmental duplications."
5. American Society of Human Genetics Virtual Meeting. Virtual event. October 2020. "Genomic variant detection within human segmental duplications."
6. Integrative Genetics and Genomics Colloquium, Davis, CA. September 2019. "Genomic variant detection within human-specific segmental duplications." (Best poster award)
7. 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."

Grants and fellowships

Active

2025 - present	Howard Hughes Medical Institute Hanna Gray Fellowship Postdoctoral Phase <u>The role of human-specific mRNA isoforms in brain function and disease</u> 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 for 4 yr, 15K supplemental research fund Total: \$415,000 Role: Postdoctoral fellow
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Past

2017-2021	Chilean National Agency for Research and Development Ph.D. scholarship covering 4 years of Ph.D. tuition Total: \$147,983 Role: Ph.D. student
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Teaching and mentoring

Courses

University of California, Davis

2025 Winter	<i>Guest lecturer.</i> GGG201B Genomics (1 lab).
2024 Winter	<i>Guest lecturer.</i> GGG201B Genomics (1 lecture, 1 lab).
2023 Winter	<i>Guest lecturer.</i> GGG201B Genomics (2 lectures, 1 lab).
2019 Winter	<i>Teaching assistant.</i> Genomics.
2018 Summer	<i>Volunteer.</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 programming laboratory).
2013 Spring	<i>Teaching assistant.</i> Biopolymers.
2012 Fall	<i>Teaching assistant.</i> 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

Peer-review activities

2025 *Ad hoc reviewer.* NAR Genomics and Bioinformatics, Nature Communications.

2024 *Ad hoc abstract reviewer.* American Society of Human Genetics Annual Meeting.

2023-2024 *Ad hoc reviewer.* Science, NAR Genomics and Bioinformatics, Scientific Reports.

University service

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

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 and 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.

Professional development

2025	Leadership and Management in Action Program (LMAP), Molly Grisham Company.
2023 - 2025	Genetics Society of America – Early Career Leadership Program, Communication and Outreach Subcommittee.
2022 - 2023	Genetics Society of America – Peer Review Training Program, Genome & Systems Biology Group.

Media coverage

- Fell, Andy (July 21, 2025). *Finding Human Brain Genes in Duplicated DNA* [University press release]. UC Davis News. <https://biology.ucdavis.edu/news/finding-human-brain-genes-duplicated-dna>
- Tasoff, Harrison (February 6, 2025). *UCSB postdoc receives competitive award to investigate the genetic changes that shaped the human mind* [University press release]. UCSB News – The Current. <https://news.ucsb.edu/2025/021743/ucsb-postdoc-receives-competitive-award-investigate-genetic-change-s-shaped-human-mind>
- Lane, C. (January 10, 2025). *Chimpanzees are genetically adapted to local habitats and infections such as malaria* [University press release]. UCL News. <https://www.ucl.ac.uk/news/2025/jan/chimpanzees-are-genetically-adapted-local-habitats-and-infections-such-malaria>
- Duran, E., & Venegas, L. (May 9, 2022). *Descubriendo los secretos del genoma* [Discovering the secrets of the genome] [Podcast episode] En un Mar de Ciencia. <https://open.spotify.com/episode/16ket90cLPlfcfyOOEBC74?si=xMjj3r32Q92U1VyBHs4ikq>
- Aravena, F. (April 25, 2022). *La importancia de la secuenciación completa del genoma humano* [The importance of the complete sequencing of the human genome] [Podcast episode]. El Café Diario, La Tercera. <https://www.latercera.com/podcast/noticia/el-cafe-diario-la-importancia-de-la-secuenciacion-completa-del-genoma-humano/WFRPQUY4C5F4FNP5T4BV5G227M/>
- Reyes, M. (April 5, 2022). *Las principales conclusiones del último informe del IPCC* [The main conclusions of the latest IPCC report] [Radio program segment]. 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>
- Romero, M. (April 5, 2022). *El ADN al descubierto: hablamos con una de las bioinformáticas que ayudó a secuenciar el genoma humano* [DNA uncovered: We talk with one of the bioinformaticians who helped sequence the human genome] [Television news segment]. France 24. <https://www.france24.com/es/programas/salud/20220405-adn-secuencia-genoma-humano-daniela-soto>
- Ansede, M. (March 31, 2022). *El primer genoma completo de un ser humano abre una nueva era en la ciencia* [Newspaper article]. 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>
- Fell, A. (March 31, 2022). *New Human Reference Genome Opens Unexplored Regions* [University press release]. UC Davis News. <https://www.ucdavis.edu/health/news/new-human-reference-genome-opens-unexplored-regions>
- Yehya, N. A. (February 15, 2022). *Placenta may hold clues for early autism diagnosis and intervention* [University Press Release]. 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.
- Sequencing data types: genomic short- and long-read (PacBio HiFi, Nanopore) sequencing, ChIP-seq, ATAC-seq, Hi-C, RNA-seq, PacBio Iso-Seq, scRNA-seq, scATAC-seq.
- Web applications: R Shiny, Python Dash/Plotly.
- Graphic design and illustration: Adobe Illustrator, iPad Procreate.
- Languages: Spanish (native), English (full professional proficiency).