

SANDRO VALENZUELA

Bioinformatician

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 Mensinkweg 68, 7442 TE, Nijverdal, Netherlands

 Born on December 8, 1989, Curicó, Chile

I am a bioinformatician with deep expertise in the human gut microbiome, and I love turning complex sequencing data into clear biological insight. On top of a solid foundation in computer science and next-generation sequencing, I work fluently with SQL, several programming languages, and a broad range of bioinformatics tools. Analytical, proactive, and a genuine team player, I stay effective under pressure and enjoy building things that people actually rely on.

COMPETENCES

Programming Languages	R, Python, awk, bash, tcl, C++, JavaScript.
Data bases	MySQL, PostgreSQL, MongoDB.
Frameworks	Rshiny (advance), Django(medium), .NET(basic).
Genomic bioinformatic	NGS analyses (read quality, abundance calculation, expression analysis, taxa assignment), De novo assembly, sequence tools manipulation (samtools, seqtk, gatk, bedtools and more), prokariotic and eukariotic annotation and visualization .

PROFESSIONAL EXPERIENCE

To date
March 2023

PhD student, UNIVERSITY OF HELSINKI, Finland

- Assessing the effect of a viral enrichment protocol on the characterisation of the infant gut virome.
- Modelling ecological time series to elucidate the role of bacteriophages in regulating bacterial population dynamics.
- Benchmarking taxonomic profiling software for microbiome analysis across a cohort of 1,300 samples.
- Developed www.questomics.app, a web platform for analysing the human gut microbiome.

    

December 2022
November 2020

Bioinformatician, MERISTEM SPA, Chile

- Designed and implemented the Viroscope platform and its associated pipeline for viral diagnosis.
- Developed and maintained the company's software infrastructure in preparation for base-editing data.
- Delivered curated datasets to the laboratory, serving as the interface between wet-lab and dry-lab operations.

      

August 2020
March 2020

Bioinformatician | Research assistant at BeatsonLab, UNIVERSITY OF QUEENSLAND, Brisbane, Australia

- Investigated the influence of read aligners and variant callers on phylogenetic inference for closely and distantly related prokaryotic genomes.
- Conducted read quality control and taxonomic classification across 131 sequencing projects generated on heterogeneous platforms.

        

March 2020
August 2019

Bioinformatic Contractor, CENTRO DE INVESTIGACIONES BIOLÓGICAS (CIBA), Puerto Montt, Chile

- Advised CIBA on the phylogenetic classification of Piscine orthoreovirus (PRV), drawing on all available NCBI data to establish an optimal classification framework.
- Advised CIBA on SNP calling and phylogenetic analysis of Renibacterium salmoninarum, incorporating local Chilean isolates.

     

May 2019 October 2017	Bioinformatician Production Analytics, uBIOME, Chile > Generated monthly, quarterly, and semiannual reports tracking processed sequences over time. > Developed applications to automate data acquisition and improve operational efficiency. > Supported laboratory operations through read quality control and the provision of data from diverse database sources. Rstudio shiny shinydashboard MongoDB PostgreSQL MySQL Bash
September 2017 October 2015	Bioinformatician Research assistant, LABORATORIO DE GENÉTICA MICROBIANA, CENTRO DE BIOINFORMÁTICA Y BIOLOGÍA INTEGRATIVA, Universidad Andres Bello, Santiago > Provided cross-disciplinary support and conducted microbiome research spanning diverse sample sources. > Developed pipelines to automate the analysis of heterogeneous microbial samples. > Supported other faculty groups by delivering bioinformatics solutions and analyses. Rstudio shiny Microsoft Excel Slurm Illustrator Bash

LANGUAGES

Spanish
English

FORMATION

2023 PhD - Ongoing | Integrative Life Science, University of Helsinki
2016 Bachelor | Bachelor with honours in Bioinformatics, Universidad de Talca

PUBLICATIONS

- > **Valenzuela-Diaz, S.**, Dikareva, E., Hickman, B., Kiljunen, S., Kolho, K., de Vos, W., Salonen, A., Korpela, K. (2026). Impact of phage enrichment on the observed infant gut phageome. Microbiology Spectrum, 14. <https://doi.org/10.1128/spectrum.02153-25>
- > Gätjens-Boniche, O., Jiménez-Madrigal, J. P., Whetten, R. W., **Valenzuela-Diaz, S.**, Alemán-Gutiérrez, A., Hanson, P. E., & Pinto-Tomás, A. A. (2023). Microbiome and plant cell transformation trigger insect gall induction in cassava. Frontiers in Plant Science, 14. <https://doi.org/10.3389/fpls.2023.1237966>
- > **Valenzuela, S. L.**, Norambuena, T., Morgante, V., García, F., Jiménez, J. C., Núñez, C., Fuentes, I., & Pollak, B. (2022). Viro-scope: Plant viral diagnosis from high-throughput sequencing data using biologically-informed genome assembly coverage. Frontiers in Microbiology, 13. <https://doi.org/10.3389/fmicb.2022.967021>
- > Godoy M, Medina DA, Suarez R, **Valenzuela S**, Romero J, Kibenge M, Wang Y, Kibenge F. Extensive Phylogenetic Analysis of Piscine Orthoreovirus Genomic Sequences Shows the Robustness of Subgenotype Classification. Pathogens. 2021 Jan 7;10(1):41. PMID: 33430212; PMCID: PMC7825714. <https://doi.org/10.3390/pathogens10010041>
- > Miossec MJ, **Valenzuela SL**, Pérez-Losada M, Johnson WE, Crandall KA, Castro-Nallar E. Evaluation of computational methods for human microbiome analysis using simulated data. PeerJ. 2020 Aug 11;8:e9688. PMID: 32864214; PMCID: PMC7427543. <https://doi.org/10.7717/peerj.9688>
- > Gutierrez-Urrutia I, Miossec MJ, **Valenzuela SL**, Meneses C, Dos Santos VAPM, Castro-Nallar E, Poblete-Castro I. Genome sequence of two members of the chloroaromatic-degrading MT community: Pseudomonas reinekei MT1 and Achromobacter xylosoxidans MT3. J Biotechnol. 2018 Jun 10;275:13-16. Epub 2018 Mar 29. PMID: 29605637. <https://doi.org/10.1016/j.jbiotec.2018.03.019>
- > Miossec MJ, **Valenzuela SL**, Mendez KN, Castro-Nallar E. Computational Methods for Human Microbiome Analysis. Current Protocols in Microbiology. 2017 Nov 9;47(1). <https://doi.org/10.1002/cpmc.41>

This list shows a selection of my recent publications. For the complete and up-to-date record, please visit my Google Scholar profile: <https://scholar.google.com/citations?user=ZzNZg8MAAAA>