

# Sergio Andreu Sánchez

Location: Delft

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## COMPUTATIONAL BIOLOGY SCIENTIST

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I am a computational biologist currently working in the Data Science team at dsm-firmenich. My work focuses on integrating multi-omics datasets and phenotypic readouts to support and develop products in the areas of healthy aging, cosmetics, and beauty.

Previously, I obtained a PhD at the University Medical Center Groningen, where I explored the drivers of interindividual variation in immunological and metabolic biomarkers in large, well-phenotyped population cohorts. I then completed a short postdoc at VIB in Leuven, Belgium, focusing on understanding temporal variation in subspecies diversity of the gut microbiome in both population-based and intervention settings.

## TECHNICAL SKILLS

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**Languages** : Python, R, bash  
**Data analysis** : Univariate statistics, longitudinal data analysis, multivariate statistics, machine learning  
**Other** : Snakemake, Django, Git, apptainer/docker

## EXPERIENCE

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**Associate Scientist** May 2025 –  
*dms-firmenichg, Data Science* Delft, the Netherlands

**Postdoctoral Fellow** July 2024 - May 2025  
*Raes Lab, Flemish institute for Biotechnology (VIB)* Leuven, Belgium

- Human microbiome genetic adaptation to human lifestyle. Longitudinal data analysis of intervention and observational cohorts.

**PhD candidate** January 2020 – June 2024  
*Groningen Microbiome Hub, University Medical Center Groningen* Groningen, The Netherlands

- May 2023 – September 2023 EMBO Visiting scholar at Nicola Segata group. Strain-resolved association study in over 30,000 metagenomes
- Large-scale epidemiological analyses using different omics techniques, particularly metagenomics, uncovering the aging of the immune system

**Research assistant** October 2019 – December 2019  
*Guojie Zhang lab, University of Copenhagen* Copenhagen, Denmark

- Continuation of MSc project after graduation. Working with NGS data from the Bird 10,000 Genome project

**Part-time bioinformatician** Oct 2018 – Sep 2019  
*Righospitalet* Copenhagen, Denmark

- Pipeline development for variant calling and different genetic diagnostic tasks
- Clinical microbiology. Tracking of microbial strains.

**Part-time bioinformatician** Dec 2017 – Nov 2018  
*EvaxionCopenhagen, Denmark*

- Student assistant. Database management. Ad-hoc bioinformatic tasks

## EDUCATION

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**University Medical Center Groningen** Groningen, The Netherlands  
*PhD in Computational Biology (Cum laude)* Jan 2020 – June 2024

**University of Copenhagen** Copenhagen, Denmark  
*MSc in Bioinformatics* Sep 2017 – Sep 2019

**Technical University of Valencia** Valencia, Spain  
*BSc in Biotechnology* Sep 2012 – Jan 2017

## UNDERGRADUATE PROJECTS

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**MSc Thesis** *Biodiversity Genomics Group. University of Copenhagen. Supervisor: Guojie Zhang*  
Mitochondrial genomics, quantification and data analysis

**MSc internship** *Genomic Medicine. Rigshospitalet. Supervisor: Rasmus Lykke Marvig*  
Strain analysis of post-surgical infections and air metagenomes

**MSc internship** *Center For Protein Research. University of Copenhagen. Supervisor: Søren Brunak*  
Genetic determinants of disease comorbidity

**BSc internship** *Bioengineering Institute. Miguel Hernandez University. Supervisor: Jose Luis Micol-Molina*  
Development of software for aiding mapping-by-sequencing

## CONGRESSES

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- 2023. The Human Microbiome (Heidelberg). Poster presentation.
- 2022. X Bioinformatics and Genomics Symposium (Valencia). Oral presentation.
- 2022. 9th Congress from the International Human Microbiome Consortium (Kobe). Poster presentation.
- 2022. 6th Translational Cardiovascular Research Meeting (Utrecht). Oral presentation.
- 2020. Word of Microbiome (online). Poster presentation.
- 2019. Congress European Society for Evolutionary Biology (Turku) . Poster presentation.

## PRIZES & HONORS

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- 2025. EMBO postdoctoral fellowship awarded (636-2025), funding Postdoctoral work 'Game of Strains: Decoding Gut Microbial Adaptation to Perturbations' at the Raes lab
- 2024. PhD awarded with *Cum laude* distinction (top 5%)
- 2023. EMBO Scientific Exchange Grant (10263) funding academic stay at Nicola Segata's group
- 2022. Simonsfonds funding for attendance of IHMC Kobe 2022
- 2021. JXTX Foundation scholarship for attendance of 2021 Cold Spring Harbor's Genome Informatics meeting
- 2016. Technical University of Valencia PROMOE scholarship for international stay in Tsinghua University
- 2012. High school completion with *Cum laude* distinction

## SUPERVISION

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- Supervision of two MSc students

## OUTREACH

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- Interview for *Nutraingredients* link
- Participation on Podcast *El Disfraz de Polifemo* (Spanish) link
- Interview in *Ciencias.com* (Spanish) link

## REFERENCES

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- Jingyuan Fu - PhD Supervisor [j.fu@umcg.nl](mailto:j.fu@umcg.nl)
- Alexandra Zhernakova - PhD Supervisor [a.zhernakova@umcg.nl](mailto:a.zhernakova@umcg.nl)
- Rasmus Lykke Marvig - Supervisor during employment at Rigshospitalet [rasmus.lykke.marvig@regionh.dk](mailto:rasmus.lykke.marvig@regionh.dk)
- Josefin Stiller - Daily supervisor during MSc thesis [josefin.stiller@bio.ku.dk](mailto:josefin.stiller@bio.ku.dk)

- Manosalva, Ailine G Lopez, Tess Yntema, Nurul Wirusanti, Daoming Wang, Sergio Andreu-Sánchez, Melany Rios-Morales, Vincent W Bloks, Martijn Koehorst, Jingyuan Fu, Folkert Kuipers, et al. (n.d.). "Dietary fat and cholesterol contents modulate oral and gut microbiota in diet-induced obesity in mice". In: ().
- Andreu-Sánchez, Sergio, Aitor Blanco-Miguez, Daoming Wang, Davide Golzato, Paolo Manghi, Vitor Heidrich, Gloria Fackelmann, Daria V Zhernakova, Alexander Kurilshikov, Mireia Valles-Colomer, et al. (2025). "Global genetic diversity of human gut microbiome species is related to geographic location and host health". In: *Cell*.
- Bourgonje, Arno R, Sergio Andreu-Sánchez, Ranko Gacesa, Gabriel Innocenti, Iris N Kalka, Shelley Klompus, Sigal Leviatan, Yishay Schlesinger, David Krongauz, Adina Weinberger, et al. (2025). "Crohn's disease and ulcerative colitis exhibit prediagnostic antibody signatures with shared and divergent changes towards disease onset". In: *Gut*.
- Ennis, Dena, Sergio Andreu-Sanchez, Yarden Levin, Omer Goldberger, Cyrus A Mallon, Yuvashankar Kavanal Jayaprakash, Yan Shao, Shijie Zhao, Trishla Sinha, Jingyuan Fu, et al. (2025). "Bifidobacterium longum subsp. nexus nov., a novel subspecies isolated from infant stool". In: *bioRxiv*, pp. 2025–06.
- Fu, Jingyuan, Haoran Peng, Sergio Andreu-Sánchez, Angel Ruiz-Moreno, Asier Fernández-Pato, Jiafei Wu, Ranko Gacesa, Alexandra Zhernakova, and Daoming Wang (2025). "Longitudinal Gut Microbiota Tracking Reveals the Persistent Spread of Mobile Genes and HGT-Driven Community Stabilization". In: .
- Fu, Jingyuan, Yue Zhang, Daria Zhernakova, Ranko Gacesa, Sergio Andreu-Sánchez, Jiafei Wu, Alexander Kurilshikov, Jiqui Wu, Godfrey Temba, Vesla Kullaya, et al. (2025). "Microbial Adaptation in Healthy Ageing: Insights from Age-associated Structural Variation in the Human Gut Microbiome". In: .
- Innocenti, Gabriel, Sergio Andreu-Sánchez, Nicolai V Hörstke, Hesham Elabd, Iros Barozzi, Andre Franke, Máté Manczinger, and Thomas Vogl (2025). "Associations between HLA-II variation and antibody specificity are predicted by antigen properties". In: *Genome Medicine* 17.1, p. 65.
- Andreu-Sánchez, Sergio, Shahzad Ahmad, Alexander Kurilshikov, Marian Beekman, Mohsen Ghanbari, Martijn van Faassen, Inge CL van den Munckhof, Marinka Steur, Amy Harms, Thomas Hankemeier, et al. (2024). "Unraveling interindividual variation of trimethylamine N-oxide and its precursors at the population level". In: *iMeta*, e183.
- Andreu-Sánchez, Sergio, Aida Ripoll-Cladellas, Anna Culinscaia, Ozlem Bulut, Arno R Bourgonje, Mihai G Netea, Peter Lansdorp, Geraldine Aubert, Marc Jan Bonder, Lude Franke, et al. (2024). "Antibody signatures against viruses and microbiome reflect past and chronic exposures and associate with aging and inflammation". In: *IScience* 27.6.
- Fernández-Pato, Asier, Trishla Sinha, Ranko Gacesa, Sergio Andreu-Sánchez, Milla F Brandao Gois, Jody Gelderloos-Arends, Dianne BH Jansen, Marloes Kruk, Martin Jaeger, Leo AB Joosten, et al. (2024). "Choice of DNA extraction method affects stool microbiome recovery and subsequent phenotypic association analyses". In: *Scientific Reports* 14.1, p. 3911.
- Fu, Jingyuan, Daoming Wang, Sergio Andreu-Sánchez, Haoran Peng, Angel Ruiz-Moreno, Daria Zhernakova, Alexander Kurilshikov, Ranko Gacesa, Godfrey Temba, Vesla Kullaya, et al. (2024). "Microbiome-wide PheWAS links gut microbial SNVs to human health and exposures". In: .
- Garmaeva, Sanzhima, Trishla Sinha, Anastasia Gulyaeva, Nataliia Kuzub, Johanne E Spreckels, Sergio Andreu-Sánchez, Ranko Gacesa, Arnau Vich Vila, Siobhan Brushett, Marloes Kruk, et al. (2024). "Transmission and dynamics of mother-infant gut viruses during pregnancy and early life". In: *Nature Communications* 15.1, p. 1945.
- Hidding, Iwan J, Arnau Vich Vila, Shixian Hu, Arno R Bourgonje, Marielle Van Gijn, Willem Theodorus Kars Maassen, Gerben Van der Vries, Renate AAA Ruigrok, Sergio Andreu-Sanchez, Bernadien H Jansen, et al. (2024). "Intestinal somatic mutations in inflammatory bowel disease patients are enriched in very early onset IBD and primary immunodeficiency genes". In: *medRxiv*, pp. 2024–12.
- Ioannou, Magdalini, Jenny Borkent, Sergio Andreu-Sánchez, Jiafei Wu, Jingyuan Fu, Iris EC Sommer, and Bartholomeus CM Haarman (2024). "Reproducible gut microbial signatures in bipolar and schizophrenia spectrum disorders: A metagenome-wide study". In: *Brain, Behavior, and Immunity* 121, pp. 165–175.
- Piperni, Elisa, Long H Nguyen, Paolo Manghi, Hanseul Kim, Edoardo Pasolli, Sergio Andreu-Sánchez, Alberto Arrè, Kate M Bermingham, Aitor Blanco-Miguez, Serena Manara, et al. (2024). "Intestinal Blastocystis is linked to healthier diets and more favorable cardiometabolic outcomes in 56,989 individuals from 32 countries". In: *Cell* 187.17, pp. 4554–4570.
- Prins, Femke M, Valerie Collij, Hilde E Groot, Johannes R Björk, J Casper Swarte, Sergio Andreu-Sánchez, Bernadien H Jansen, Jingyuan Fu, Hermie JM Harmsen, Alexandra Zhernakova, et al. (2024). "The gut

- microbiome across the cardiovascular risk spectrum". In: *European Journal of Preventive Cardiology* 31.8, pp. 935–944.
- Sinha, Trishla, Siobhan Brushett, Asier Fernández-Pato, Sanzhima Garmaeva, Sergio Andreu-Sánchez, Johanne Spreckels, Cyrus Mallon, Nataliia Kuzub, Milla Brandao Gois, Marloes Kruk, et al. (2024). "Pregnancy and Early Life Gut Microbiome: Influencing Factors and Health Implications". In: Vochteloo, Martijn, Patrick Deelen, Britt Vink, BIOS Consortium, Ellen A Tsai, Heiko Runz, Sergio Andreu-Sánchez, Jingyuan Fu, Alexandra Zhernakova, Harm-Jan Westra, et al. (2024). "PICALO: principal interaction component analysis for the identification of discrete technical, cell-type, and environmental factors that mediate eQTLs". In: *Genome Biology* 25.1, p. 29.
- Wu, Jiafei, Victoria Palasantzas, Sergio Andreu-Sánchez, Torsten Plösch, Sam Leonard, Shuang Li, Marc Jan Bonder, Harm-Jan Westra, Joyce van Meurs, Mohsen Ghanbari, et al. (2024). "Epigenome-wide association study on the plasma metabolome suggests self-regulation of the glycine and serine pathway through DNA methylation". In: *Clinical Epigenetics* 16.1, p. 104.
- Zhernakova, Daria V, Daoming Wang, Lei Liu, Sergio Andreu-Sánchez, Yue Zhang, Angel J Ruiz-Moreno, Haoran Peng, Niels Plomp, Ángela Del Castillo-Izquierdo, Ranko Gacesa, et al. (2024). "Host genetic regulation of human gut microbial structural variation". In: *Nature* 625.7996, pp. 813–821.
- Andreu-Sánchez, Sergio, Arno R Bourgonje, Thomas Vogl, Alexander Kurilshikov, Sigal Leviatan, Angel J Ruiz-Moreno, Shixian Hu, Trishla Sinha, Arnau Vich Vila, Shelley Klompus, et al. (2023). "Phage display sequencing reveals that genetic, environmental, and intrinsic factors influence variation of human antibody epitope repertoire". In: *Immunity*.
- Andreu-Sánchez, Sergio, Jiafei Wu, and Jingyuan Fu (2023). "Beyond personal space: unveiling the transmission pattern of the human gut and oral microbiome". In: *iMeta* 2.2.
- Bourgonje, Arno R, Sergio Andreu-Sánchez, Thomas Vogl, Shixian Hu, Arnau Vich Vila, Ranko Gacesa, Sigal Leviatan, Alexander Kurilshikov, Shelley Klompus, Iris N Kalka, et al. (2023). "Phage-display immunoprecipitation sequencing of the antibody epitope repertoire in inflammatory bowel disease reveals distinct antibody signatures". In: *Immunity*.
- Brushett, S, R Gacesa, A Vich Vila, MF Brandao Gois, S Andreu-Sánchez, JC Swarte, MAY Klaassen, V Collij, T Sinha, LA Bolte, et al. (2023). "Gut feelings: the relations between depression, anxiety, psychotropic drugs and the gut microbiome". In: *Gut Microbes* 15.2, p. 2281360.
- Sinotte, Veronica M, Justinn Renelies-Hamilton, Sergio Andreu-Sánchez, Mireille Vasseur-Cognet, and Michael Poulsen (2023). "Selective enrichment of founding reproductive microbiomes allows extensive vertical transmission in a fungus-farming termite". In: *Proceedings of the Royal Society B* 290.2009, p. 20231559.
- Vila, Arnau Vich, Shixian Hu, Sergio Andreu-Sánchez, Valerie Collij, Bernadien H Jansen, Hannah E Augustijn, Laura A Bolte, Renate AAA Ruigrok, Galeb Abu-Ali, Cosmas Giallourakis, et al. (2023). "Faecal metabolome and its determinants in inflammatory bowel disease". In: *Gut* 72.8, pp. 1472–1485.
- Zhang, Yue, Sergio Andreu-Sánchez, Nadira Vadaq, Daoming Wang, Vasiliki Matzaraki, Wouter A van der Heijden, Ranko Gacesa, Rinse K Weersma, Alexandra Zhernakova, Linos Vandekerckhove, et al. (2023). "Gut dysbiosis associates with cytokine production capacity in viral-suppressed people living with HIV". In: *Frontiers in Cellular and Infection Microbiology* 13.
- Andreu-Sánchez, Sergio, Geraldine Aubert, Aida Ripoll-Cladellas, Sandra Henkelman, Daria V Zhernakova, Trishla Sinha, Alexander Kurilshikov, Maria Carmen Cenit, Marc Jan Bonder, Lude Franke, et al. (2022). "Genetic, parental and lifestyle factors influence telomere length". In: *Communications biology* 5.1, p. 565.
- Chen, Lianmin, Daria V Zhernakova, Alexander Kurilshikov, Sergio Andreu-Sánchez, Daoming Wang, Hannah E Augustijn, Arnau Vich Vila, Lifelines Cohort Study, Rinse K Weersma, Marnix H Medema, et al. (2022). "Influence of the microbiome, diet and genetics on inter-individual variation in the human plasma metabolome". In: *Nature Medicine* 28.11, pp. 2333–2343.
- Gacesa, R, A Kurilshikov, A Vich Vila, T Sinha, MAY Klaassen, LA Bolte, S Andreu-Sánchez, L Chen, V Collij, S Hu, et al. (2022). "Environmental factors shaping the gut microbiome in a Dutch population". In: *Nature*, pp. 1–8.
- Lopera-Maya, Esteban A, Alexander Kurilshikov, Adriaan van der Graaf, Shixian Hu, Sergio Andreu-Sánchez, Lianmin Chen, Arnau Vich Vila, Ranko Gacesa, Trishla Sinha, Valerie Collij, et al. (2022). "Effect of host genetics on the gut microbiome in 7,738 participants of the Dutch Microbiome Project". In: *Nature genetics* 54.2, pp. 143–151.
- Peters, Vera, Laura Bolte, Eva Schuttert, Sergio Andreu-Sánchez, Gerard Dijkstra, Rinse Weersma, and Marjo Campmans-Kuijpers (2022). "Western and carnivorous dietary patterns are associated with greater likelihood of IBD development in a large prospective population-based cohort". In: *Journal of Crohn's and Colitis* 16.6, pp. 931–939.
- Zhernakova, Daria V, Trishla Sinha, Sergio Andreu-Sánchez, Jelmer R Prins, Alexander Kurilshikov, Jan-Willem Balder, Serena Sanna, Lifelines Cohort Study, Lude Franke, Jan A Kuivenhoven, et al. (2022).

- “Age-dependent sex differences in cardiometabolic risk factors”. In: *Nature Cardiovascular Research* 1.9, pp. 844–854.
- Andreu-Sánchez, Sergio, Lianmin Chen, Daoming Wang, Hannah E Augustijn, Alexandra Zhernakova, and Jingyuan Fu (2021). “A Benchmark of Genetic Variant Calling Pipelines Using Metagenomic Short-Read Sequencing”. In: *Frontiers in Genetics* 12, p. 537.
- Andreu-Sánchez, Sergio, Wanjun Chen, Josefin Stiller, and Guojie Zhang (2021). “Multiple origins of a frameshift insertion in a mitochondrial gene in birds and turtles”. In: *GigaScience* 10.1, gaa161.
- Gabrielaite, Migle, Mathias Husted Torp, Malthe Sebro Rasmussen, Sergio Andreu-Sánchez, Filipe Garrett Vieira, Christina Bligaard Pedersen, Savvas Kinalis, Majbritt Busk Madsen, Miyako Kodama, Gül Sude Demircan, et al. (2021). “A comparison of tools for copy-number variation detection in germline whole exome and whole genome sequencing data”. In: *Cancers* 13.24, p. 6283.
- Li, Rumei, Sergio Andreu-Sánchez, Folkert Kuipers, and Jingyuan Fu (2021). “Gut microbiome and bile acids in obesity-related diseases”. In: *Best Practice & Research Clinical Endocrinology & Metabolism* 35.3, p. 101493.
- Lup, Samuel Daniel, David Wilson-Sánchez, Sergio Andreu-Sánchez, and José Luis Micol (2021). “Easymap: a user-friendly software package for rapid mapping-by-sequencing of point mutations and large insertions”. In: *Frontiers in plant science* 12, p. 655286.
- Plachokova, Adelina S, Sergio Andreu-Sánchez, Marlies P Noz, Jingyuan Fu, and Niels P Riksen (2021). “Oral Microbiome in Relation to Periodontitis Severity and Systemic Inflammation”. In: *International Journal of Molecular Sciences* 22.11, p. 5876.
- Wang, Daoming, Marwah Doestzada, Lianmin Chen, Sergio Andreu-Sánchez, Inge CL van den Munckhof, Hannah E Augustijn, Martijn Koehorst, Angel J Ruiz-Moreno, Vincent W Bloks, Niels P Riksen, et al. (2021). “Characterization of gut microbial structural variations as determinants of human bile acid metabolism”. In: *Cell Host & Microbe* 29.12, pp. 1802–1814.
- Feng, Shaohong, Josefin Stiller, Yuan Deng, Joel Armstrong, Qi Fang, Andrew Hart Reeve, Duo Xie, Guangji Chen, Chunxue Guo, Brant C Faircloth, et al. (2020). “Dense sampling of bird diversity increases power of comparative genomics”. In: *Nature* 587.7833, pp. 252–257.
- Stauning, Marius Ahm, Antoinette Bediako-Bowan, Stephanie Bjerrum, Leif Percival Andersen, Sergio Andreu-Sánchez, Appiah-Korang Labi, JAL Kurtzhals, Rasmus L Marvig, and Japheth A Opintan (2020). “Genetic relationship between bacteria isolated from intraoperative air samples and surgical site infections at a major teaching hospital in Ghana”. In: *Journal of Hospital Infection* 104.3, pp. 309–320.