

# Sergio Andreu Sánchez

Location: Delft

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## POSTDOCTORAL RESEARCH COMPUTATIONAL BIOLOGY

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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.
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