FRANCISCO ZORRILLA

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SUMMARY

Computational Biologist and NCCR Microbiomes Flagship Project Lead with a Ph.D. from Cambridge and 7+ years of expertise in metagenomics, metabolic modeling, and structural bioinformatics. Proven track record of developing high-throughput computational products (e.g., metaGEM) and directing multi-lab consortia to establish predictive rules for synthetic community (SynCom) assembly. Expert in applying data-driven systems biology to solve complex challenges in environmental resilience, soil health, and agricultural biotechnology.

TECHNICAL SKILLS

Bioinformatics & Genomics

- *Metagenomics:* Quality control (fastp), assembly (MEGAHIT, metaSPAdes), read mapping (BWA-MEM), binning (CONCOCT, MetaBAT2), MAG consolidation (MetaWRAP), relative abundance estimation, and taxonomic assignment (GTDB-Tk) from complex environmental and host samples.
- *Functional Annotation & Pangenomics:* Database mapping (KEGG, UniProt, eggNOG, CAZy, mOTUs-db), predicting core conserved traits, and trait-based niche profiling.

Systems Biology & Metabolic Modeling

- *Modeling Frameworks:* Constraint-based modeling, genome-scale metabolic (GEM) reconstruction, experimental data integration, Flux Balance Analysis (FBA), and Flux Variability Analysis (FVA).
- *Community Design:* Rational design of synthetic communities (SynComs), predicting trophic interactions and cross-feeding, and bioaugmentation strategies.
- *Domain Tools:* metaGEM (lead developer), CarveMe, SMETANA, MEMOTE, RAVEN, and COBRA Toolbox.

AI, Data Science & Structural Biology

- *Structural Bioinformatics:* Protein structure-mediated annotation (Foldseek, AlphaFold2) and protein language models (ProstT5).
- *Machine Learning & AI:* Deep learning frameworks (PyTorch, TensorFlow) and predictive trait modeling.
- *Statistics & Visualization:* Multi-omics data wrangling, terabyte-scale heterogeneous dataset processing, and advanced biostatistics.

Programming & Infrastructure

- *Languages:* Python (Pandas, NumPy), R (Tidyverse), MATLAB, and Unix/Bash.
- *High-Performance Computing:* HPC cluster management (Slurm), GPU optimization, and parallel processing.
- *Workflow Automation:* Building end-to-end scalable pipelines (Snakemake) and version control (Git/GitHub).

PROFESSIONAL EXPERIENCE

ETH Zurich **Zurich, Switzerland**

Postdoctoral Researcher & National Centres of Competence in Research (NCCR) Flagship Project Lead October 2024 – Present

- **Scientific Leadership (NCCR Flagship Project**): Co-leading a multi-center NCCR Microbiomes Flagship Project across **5+ labs**; designed the **4-year computational roadmap** to establish predictive rules for community assembly and the rational design of resilient Synthetic Communities (SynComs).
- **AI & Structural Bioinformatics Pipeline:** Co-designing a scalable functional annotation pipeline, pivoting from AlphaFold to a protein language model approach (ProstT5) for rapid structure-alignment (FoldSeek). Leveraged GPU-optimized Slurm cluster for rapid sequence-to-3Di translation (ProstT5), increasing throughput **100x** and shrinking a 2-month custom database generation bottleneck down to 1 week.
- **Data-Driven SynCom Design:** Applying constraint-based metabolic modeling, pangenomics, and machine learning approaches to heterogeneous datasets; identifying trophic interactions and niche-filling strains to drive rational bioaugmentation strategies in plant-associated and environmental microbiomes.
- **Cross-Functional Management:** Managing the technical lifecycle from conceptualization to execution; currently directing a team of computational PhDs and Postdocs to integrate pangenomics, co-occurrence networks, and metabolic models, defining computational milestones and monitoring progress.
- **Technical Mentorship:** Designed and delivered advanced bioinformatics and modeling curricula for 50+ international researchers at the ETH Block Course, NCCR Winter School, and the EMBO Practical Course (Metabolite and species dynamics in microbial communities, Bangalore); supervised external Master's theses (Oxford University).

University of Cambridge & EMBL **Cambridge, UK / Heidelberg, Germany**

Doctoral Researcher (2020 - 2024) & Computational Biologist (2019 - 2020) August 2019 – August 2024

- **Software Product & Pipeline Engineering:** Executed the development and release of metaGEM, an open-source software product for high-throughput metabolic modeling. Managed the full product lifecycle including user-centric design, comprehensive documentation, and version control (Git/GitHub). Scaled workflows across HPC environments, resolving critical data bottlenecks for the microbiome community by automating the terabyte-scale reconstruction of 14,000+ Genome-Scale Metabolic Models (GEMs).
- **Mechanistic Modeling & Applied Systems Biology:** Applied constraint-based modeling approaches to decipher microbial interactions across diverse commercial and clinical contexts. This included predicting metabolic drivers of flavor formation in cheese fermentation (partnered with **Chr. Hansen**), modeling obligate cross-feeding in soil communities, and investigating metabolic niches in *C. difficile* infection models.
- **Multi-Omics Integration & Data-Driven Discovery:** Synthesized heterogeneous datasets (genomic, transcriptomic, metabolomic) to develop predictive frameworks for microbial behavior. Established data-driven approaches to identify plastic degrading enzymes (mBio), metabolic auxotrophies (bioRxiv), and ecological dynamics (Nature Microbiology).

EDUCATION & DISTINCTIONS

University of Cambridge **Cambridge, UK**

Ph.D. in Biology - Medical Research Council Toxicology Unit (MRCTU) & Darwin College October 2020 – August 2024

- Ph.D. placement via the Vice-Chancellor's provisions (Cambridge Trust) and MRCTU.

Chalmers University of Technology **Gothenburg, Sweden**

M.Sc. in Biotechnology, Systems & Synthetic Biology Division August 2017 – June 2019

- Elected Treasurer for the Society for Biological Engineering students at Chalmers; managed events and budgets.
- Awarded gold medal and best modelling nominee at iGEM 2018 (International Synthetic Biology Competition).

University of California, Davis **Davis, USA**

B.Sc. in Biological Systems Engineering September 2013 - June 2017

KEY PROJECTS & IMPACT

Yousif, G.*, **Zorrilla, F.***, Dash, S., Oña, L., Shekhar, A., Giri, S., ... & Kost, C. (2025). Obligate cross-feeding of metabolites is common in soil microbial communities. *bioRxiv*, 2025-01. *co-first authors

- Applied a computational framework to identify metabolic dependencies in soil, providing a roadmap for the **rational design of resilient synthetic communities** for agricultural and environmental restoration.

Zorrilla, F., Buric, F., Patil, K. R., & Zelezniak, A. (2021). metaGEM: reconstruction of genome scale metabolic models directly from metagenomes. **Nucleic Acids Research**, 49(21), e126-e126.

- Architected and launched an open-source software solution. Successfully **scaled the product** to enable the broader scientific community to conduct large-scale functional analysis of microbiomes without requiring deep metabolic modeling expertise.

Yin, Q., da Silva, A. C., **Zorrilla, F.**, Almeida, A. S., Patil, K. R., & Almeida, A. (2025). Ecological dynamics of Enterobacteriaceae in the human gut microbiome across global populations. **Nature Microbiology**, 10(2), 541-553.

- Served as **subject matter expert in metabolic modeling**, guiding a multi-disciplinary team to integrate mechanistic insights into a global metagenomic study.

Zrimec, J., Kokina, M., Jonasson, S., **Zorrilla, F.**, & Zelezniak, A. (2021). Plastic-degrading potential across the global microbiome correlates with recent pollution trends. **mBio**, 12(5), 10-1128.

- Enabled a global metagenomic screen of enzymatic potential, establishing a **predictive data-driven approach** for identifying novel biocatalysts with industrial bioremediation and sustainability applications.

Melkonian, C., **Zorrilla, F.**, Kjærbølling, I., Blasche, S., Machado, D., Junge, M., ... & Zeidan, A. A. (2023). Microbial interactions shape cheese flavour formation. **Nature Communications**, 14(1), 8348.

- Applied mechanistic metabolic modeling to decipher how inter-species interactions dictate chemical outputs, showcasing the use of **systems biology to optimize commercial fermentation and product quality.**

LANGUAGES & INTERESTS

- **Languages:** English (C2), Spanish (C2), Italian (B1), French (A1), German (A1).
- **Interests:** Lived in **11 countries** (Americas, Europe, and Asia); Amateur multi-instrumentalist; Long-distance runner.