

Rafael Soler Ortuno

Computational Biologist | Immuno-Oncology | Biomarker Discovery & Patient Stratification

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Professional summary

Computational biologist with a PhD in bioinformatics and 2+ years of postdoctoral experience (6+ years total) in immuno-oncology and tumor biology, using single-cell and spatial transcriptomics, multi-omics integration, and ML/AI to drive **biomarker discovery, validation, and patient stratification**. Industry experience spanning antibody-based immunotherapies (TNFR2, FcγRIIB), drug mode-of-action studies, and translational research across oncology and autoimmune disease. Builds reproducible R/Python pipelines on HPC and AWS, and communicates findings directly to clinical, translational, and non-technical stakeholders and teammates.

Professional experience

Bioinformatics Research Scientist | BioInvent International AB | Lund, Sweden *Aug 2025 – Aug 2026*

- Led multi-omics analysis integrating scRNA-seq, CITE-seq, spatial transcriptomics, bulk RNA-seq, proteomics, and clinical metadata across the BI-1206 (anti-FcγRIIB) and BI-1808 (anti-TNFR2) antibody programs, connecting evidence across patient, mouse, and in vitro samples to advance drug mode-of-action and resistance-mechanism understanding.
- Uncovered a non-canonical myeloid cell activation pathway underlying antibody response, as measured by resolving distinct immune activation states across a 30-patient clinical PBMC cohort spanning the BI-1808 and BI-1910 programs, by extending the mode-of-action pipeline to integrate clinical single-cell RNA-seq data with targeted pathway-level analysis.
- Characterised drug mechanism of action using scRNA-seq, spatial transcriptomics, and targeted gene module scoring, resolving antibody-responsive immune cell states, macrophage polarisation profiles, and tissue niches in blood and tumour microenvironments to support early-stage patient selection.
- Validated cell-type-specific genetic regulation of a candidate autoimmune target using a public single-cell eQTL atlas, auditing raw alignment quality and dataset chemistry protocols to protect expression quantification against multi-mapping-driven read loss within a polymorphic gene family, directly informing a target validation go/no-go decision.
- Established a novel biomarker and therapeutic target for autoimmune disease, as measured by demonstrating marker specificity restricted to M1 macrophages, inflammatory monocytes, and neutrophils, by curating and integrating public single-cell RNA-seq atlases across multiple autoimmune indications, beginning with three published inflammatory bowel disease cohorts spanning ulcerative colitis, Crohn's disease, and healthy controls.
- Strengthened the biological rationale for a novel bispecific target by integrating clinical single-cell and spatial transcriptomics data into the biomarker strategy, identifying a significant expression correlation with a canonical regulatory T cell (Treg) marker gene ahead of experimental validation.
- Built and trained a variational autoencoder (VAE) to separate strain-level technical variability from tumor biomarker signal across genetically diverse mouse strains, designed to extrapolate candidate biomarkers to human population heterogeneity.
- Delivered a reusable single-cell and spatial immune atlas alongside an AWS-based, Docker-containerised HPC environment built from scratch, enabling reproducible computing across the team; communicated results through well-documented R/Python pipelines with automated QC and reporting for both technical and non-technical stakeholders.

Visiting Scientist, Computational Biology | Bristol Myers Squibb | Sevilla, Spain *Sep 2024 – Jan 2025*

- Designed gene signatures from patient tumor samples across lung, pancreatic, and breast cancers, applying SNV and mutation analysis to inform precision medicine and drug resistance strategies.
- Mapped preclinical models (cell lines, xenografts, organoids) to clinical tumor subtypes using TCGA and DepMap (Celligner), improving the translational validity of preclinical findings.
- Performed spatial transcriptomics analysis with NanoString CosMx and 10x Visium HD to resolve tissue-level gene expression programs across tumor sample cohorts.

Bioinformatics Research Scientist (PhD) | Institute of Neurosciences CSIC-UMH | Alicante, Spain *Sep 2020 – Sep 2024*

- Built automated Python, R, Bash, and AWK pipelines to integrate RNA-seq and ATAC-seq data across phylogenetically distant species, resolving conserved and species-specific genes and enhancers governing cortical development.
- Integrated scRNA-seq with RNA-seq and ATAC-seq datasets to define conserved cortical stem cell types and their gene regulatory programs across species.
- Identified tumor gene signatures in pediatric brain tumors through meta-analysis of public GEO/EGA datasets, benchmarking findings against mouse scRNA-seq, ATAC-seq, and bulk RNA-seq models.
- Applied deep learning to protein sequence data to predict candidate transcription factor sequences from structural features, scaling automated workflows across large public datasets.
- Built and published an interactive R Shiny single-cell atlas application for non-programmer researchers, broadening public access to cortical single-cell data; mentored two MSc students (<http://cortevo-scRNA-ferret.in.umh-csic.es/>) for public data navigation.

Visiting Scientist, Bioinformatics | Helmholtz Munich | Munich, Germany *Mar 2023 – Jun 2023*

- Combined Hi-C analysis with the ENCODE ATAC-seq pipeline (Docker, Snakemake) to resolve open chromatin regions, enhancers, and transcription factor motifs across the genome.
- Trained a deep learning model (ChromBPNet) to predict open chromatin regions, transcription factor binding sites, and sequence motifs directly from DNA sequence, and built a custom Python/R/Bash visualization pipeline for genomic rearrangements.

Junior Scientist | SUEZ | London, UK

Aug 2018 – Jun 2019

Junior Scientist | IMDEA | Madrid, Spain

Sep 2017 – Jul 2018

Projects

TargetIntel-IO | Explainable target discovery and prioritisation

- Python tool that brings together scientific, clinical and experimental evidence to identify and rank promising cancer drug targets, with clear explanations for every score [GitHub](#).

DrugMatch-Confidence | Interpretable cancer drug-response prediction

- XGBoost-based machine-learning tool that predicts which cancer cell models are likely to respond to specific drugs and explains the main biological factors behind each prediction [GitHub](#).

Activation Liability | Inflammation-aware surface-target risk audit

- Python tool that checks whether a cancer target may also appear in healthy cells during inflammation or immune activation, helping identify potential safety risks early [GitHub](#).

Dev Autopilot | Auditable AI-agent workflow for scientific software

- Python/SQLite workflow coordinating AI implementation and independent review through deterministic safety gates, resumable execution and human approval [GitHub](#).

Segmentation Fragility | Spatial segmentation robustness audit

- Python tool that tests whether spatial-transcriptomics results change when different cell-segmentation methods are used.

V2G Fragility | Variant-to-gene evidence robustness audit

- Python tool that tests whether variant-to-gene links remain stable across evidence sources and analysis settings.

Reach Gap | Spatial drug-reach and target-coverage audit

- Python tool that identifies target-positive tissue regions a therapy may fail to reach.

FM Value Audit | Single-cell foundation-model value audit

- Python tool that tests whether single-cell foundation models outperform simpler methods for target discovery.

Education

PhD, Bioinformatics — Helmholtz Munich / CSIC / UMH 2020 – 2025

MSc, Bioinformatics & Biostatistics — University of Barcelona 2018 – 2020

MSc, Molecular Biology — Autonomous University of Madrid (UAM) 2017 – 2018

BSc, Biology — University of Alicante 2013 – 2017

Technical skills

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- **Domains:** Computational Biology · Immuno-Oncology · Inflammation · Tumor Biology · Biomarker Discovery · Patient Stratification · Drug Mode-of-Action · Translational Research · Neuroscience
 - **Single-cell:** scRNA-seq · CITE-seq · scATAC-seq · RNA velocity · Perturbation modelling
 - **Spatial:** 10x Visium HD · NanoString CosMx
 - **Bulk omics:** RNA-seq · ATAC-seq · ChIP-seq · CUT&Tag/CUT&RUN · Hi-C · Ribo-seq · miRNA · Proteomics · SNV/mutation analysis
 - **Functional genomics:** DepMap · CCLE · PRISM · CRISPR/RNAi dependency screens · drug sensitivity analysis · target discovery · biomarker validation
 - **ML, statistical modelling & AI:** Random Forest · XGBoost · Survival analysis (Cox regression, Kaplan–Meier) · Risk modelling · Variational autoencoders (VAE) · Single-cell foundation models (Geneformer, scGPT, Cell2Sentence) · ChromBPNet
 - **Multi-omics integration:** Seurat WNN · totalVI · MultiVI
 - **Programming:** R Seurat/Shiny/DESeq2/edgeR · Python scanpy/scvi-tools/PyTorch/pandas · Bash · AWK
 - **Pipelines & infrastructure:** Nextflow · Snakemake · Docker · HPC/Slurm · AWS
 - **Version control:** Git
 - **Databases & resources:** GEO · EGA · TCGA · UCSC Genome Browser · Ensembl · NCBI · UniProt

Publications

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- Singh, A. et al. Gene regulatory landscape of cerebral cortex folding. Science Advances 10 (2024).
 - Del-Valle-Anton, L. et al. Multiple parallel cell lineages in the developing mammalian cerebral cortex. Science Advances 10 (2024).
 - Chinnappa, K. et al. Secondary loss of miR-3607 reduced cortical progenitor amplification during rodent evolution. Science Advances 8 (2022).
 - Fernández, V. et al. Repression of Irs2 by let-7 miRNAs is essential for homeostasis of the telencephalic neuroepithelium. EMBO Journal 39 (2020).
 - Espinós, A.; Soler, R. et al. Cross-Species Multi-Omic Analysis of Apical Radial Glia Cells in Cortical Development Evolution. In preparation.
 - Soler, R. Prediction of novel mammalian membrane transcription factors with deep learning. In preparation.

Certifications & training

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- Generative AI & Prompt Engineering (IBM) · Single-cell RNA-seq (EMBL-EBI) · HPC/Slurm (University of Cambridge) · Cloud Computing (Google) · Drug Discovery & Biomarker Validation (GSK)

Languages

Spanish (native) · **English** (CEFR C1) · **Catalan** (CEFR C1) · **Swedish** (CEFR A2) · **Japanese** (CEFR A2)