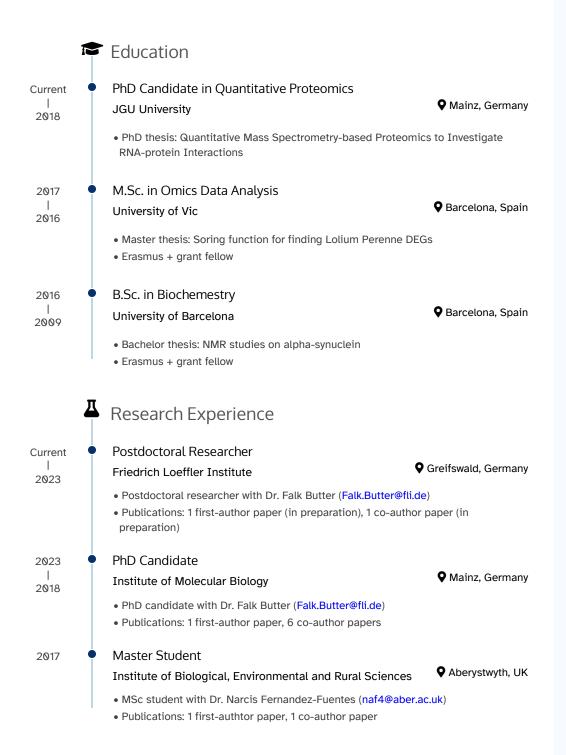
Albert Fradera Sola

Bioinformatician | Data Scientist | Proteomics & Genomics Scientist

I consider myself both collaborative and adaptable. I am always eager to take on new and diverse projects. I am very enthusiastic about sharing and continuously developing my data visualization skills as a means to enhance scientific communication. I am an open-minded person and enjoy fostering strong relationships with my colleagues.





Contact

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Language Skills

Catalan	
Spanish	
English	
German	

My CV as a network



Bullet points (for $rac{a}$, \underline{A} , $\underline{=}$, and \underline{s}) are interconnected by year. Interactive version here

oxplus Dry Lab Projects and Related Skills

Network-based Assignment of RNA-Binding Proteins' Functionality

- Functionality was inferred from associations with annotations at the domain, molecular function, and pathway levels.
- Function-based networks were created from quantitative proteomics data and made accessible through an interactive, user-friendly web interface.
- Keywords: Network | Functional analysis | Pfam | GO | KEGG | R Shiny

Infectome Profiling of Three Leishmania Species

- *M. musculus* proteome changes were investigated after infection with *Leishmania*.
- Protein orthologs between the *Leishmania* species were established.
- Keywords: Proteome | Differential expression | Protein orthology

Embryonic Development Proteome Profiling of Xenopus Species

- Clustering (Self Organizing Maps) and dimensionality reduction techniques (Principal Component Analysis) were applied.
- Keywords: Proteome | Differential expression | SOM | PCA | Clustering

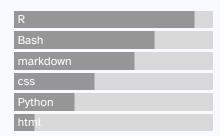
Scoring Function for RNA-Seq Differential Expression Assessment

- A scoring function was developed around three RNA-Seq differential expression assessment R packages (DESeq2, edgeR, limma+voom)
- Keywords: NGS | RNA-Seq | Quality control | Differential expression
- ChIP-Seq Characterization of a Novel ATPase in T. brucei
- H2A.Z deposition was investigated and visualized with genome tracks
- Keywords: NGS | ChIP-Seq | Genome tracks

Wet Lab Projects and Related Skills

- Immunoprecipitation of RNA-binding Proteins in S. cerevisiae
 - I was responsible for designing the experimental setup and generating the data for the RNA-binding protein interactome investigation.
 - Keywords: Yeast | Protein Immunoprecipitation | Experimental design
- Mass Spectrometry Quantitative Proteomics
- I used chemical labeling (DML) and label-free mass spectrometry sample preparation protocols on several projects
- Keyword: Mass spectrometry | DML | LFQ | In-gel digestion

Coding Skills



Some R packages I have experience with:



Proteomics Software Skills

MaxQuant	
Proteinortho	
InterPro	

Genomics Software Skills

STAR
Bowtie
FastQC
MultiQC
fastqscreen
deepTools
HTSeq
MACS2
rMATS

Publications

Articles with Genomics Analysis

- 2022 | PLoS Pathogens | https://doi.org/10.1371/journal.ppat.1010514
- 2021 | Nature Comunications | https://doi.org/10.1038/s41467-021-22861-2
- 2021 | PLoS One | https://doi.org/10.1371/journal.pone.0249636
- 2019 | PLoS One | https://doi.org/10.1371/journal.pone.0220518

Articles with Proteomics Analysis

- 2023 | Nucleic Acid Research | https://doi.org/10.1093/nar/gkad245
- 2023 | iScience | https://doi.org/10.1016/j.isci.2023.106778
- 2023 | PLoS Pathogens | https://doi.org/10.1371/journal.ppat.1011486
- 2021 | Journal of Cell Science | https://doi.org/10.1242/jcs.254300
- 2020 | RNA | https://doi.org/10.1261/rna.076281.120

Conferences and Courses

Conferences

- 2022 | Statistical data analysis for genome-scale biology | Flash talk
- 2021 | Network biology | Plenary talk
- 2019 | FEBS advanced course | Poster presentation

Courses

- 2022 | Data visualization for scientists
- 2021 | Scientific writing
- 2020 | Convincing scientific presentations
- 2020 | Regression Models | Coursera certificate
- 2020 | Statistical Inference | Coursera certificate

Abstract word cloud



Abstracts from the publications are summarized into a word cloud.

Document created with the R packages pagedown and datadrivency.

The source code is available on github.

Last updated on 2023-11-20.