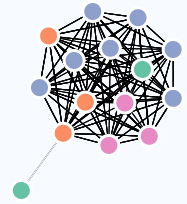


ALBERT FRADERA SOLA

I consider myself both collaborative and adaptable. I am always eager to tackle new and different projects. I am very enthusiastic to always share and develop my data visualization skills as a means towards better science communication. I am an open-minded person and enjoy having great relationships with my colleagues.



EDUCATION

- Current | 2018
- **PhD Candidate, Quantitative Proteomics**
JGU University 📍 Mainz, Germany
 - PhD thesis: Computational approaches to mass spectrometry based quantitative proteomics
- 2017 | 2016
- **M.Sc. in Omics Data Analysis**
University of Vic 📍 Barcelona, Spain
 - Master thesis: Development of a scoring function for finding differential expression - application to Lolium Perenne
 - Erasmus + grant fellow

View this CV online with links at <https://github.com/AFraderaSola/CV/blob/master/cv.html>

RESEARCH EXPERIENCE

- Current | 2018
- **PhD candidate**
Butter laboratory - Institute Molecular Biology 📍 Mainz, Germany
 - PhD candidate with Dr. Falk Butter (F.Butter@imb-mainz.de)
 - Publications: 1 first-author paper (in submission), 5 co-author papers
- 2017
- **Master student**
Narcis Fernandez-Fuentes - IBERS 📍 Aberystwyth, UK
 - MSc student with Dr. Narcs Fernandez-Fuentes (naf4@aber.ac.uk)
 - Publications: 1 first-author paper, 1 co-author paper

CONTACT

✉ A.FraderaSola@imb.de

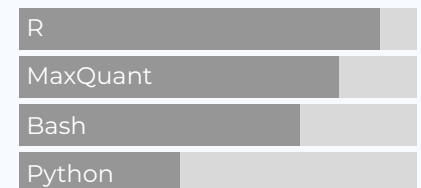
📞 +49 179 3469988



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 that allowed 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

SOFTWARE SKILLS



LANGUAGE SKILLS





DRY LAB PROJECTS AND RELATED SKILLS

- **Network-based assignment of RNA binding proteins functionality**

- Function-based networks were created from quantitative proteomics data and made accessible through a shiny app.
- Keywords: Network | Functional analysis | KEGG | GO | R Shiny

- Temporal proteome profiling of *Xenopus* and *Leishmania* species

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

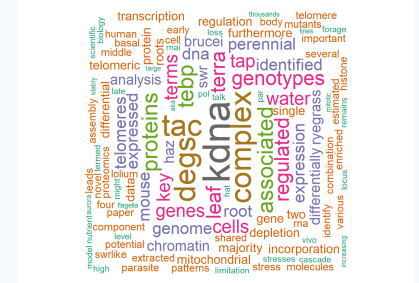
- **Scoring function for RNAseq differential expression assessment**

- A scoring function was developed around three RNAseq differential expression assessment R packages (DESeq2, edgeR, limma+voom)
- Keywords: NGS | RNA-Seq | Quality control | Differential expression

ChIPseq characterization of a novel ATPase in *T. brucei*

- H2A.Z deposition was investigated and visualized with genome tracks
- Keywords: NGS | ChIP-Seq | Genome tracks

"I enjoy using multiomics tools to integrate different research disciplines"



Publication abstract's wordcloud



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

"I nurture data visualization skills as a path towards better science communication"



SELECTED PUBLICATIONS

- Genomics

- 2022 | PLoS Pathogens | <https://doi.org/10.1371/journal.ppat.1010514>
- 2021 | Nature Communications | <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>

Proteomics

- 2021 | Journal of Cell Science | <https://doi.org/10.1242/jcs.254300>
- 2020 | RNA | <https://doi.org/10.1261/rna.076281.120>

Document created with the R
packages **pagedown** and
datadrivency.

The source code is available on github.com/AFraderaSola/CV.

Last updated on 2022-07-20.