

Silvia Diz de Almeida

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Personal site: <https://silviaadiz.github.io/>

BIOSTATISTICIAN

Biostatistician with 4+ years in genomics research and 5+ years of expertise in R programming. Experienced in statistical analysis, genetic risk prediction, and biomarker identification for large-scale biomedical studies. Proven ability to mentor junior researchers and contribute to high-impact publications. Seeking to apply statistical expertise to drug development and clinical trials in the pharmaceutical industry.

PROFESSIONAL EXPERIENCE

Center for Research in Molecular Medicine and Chronic Diseases - Genomic Medicine Group

Biostatistician | Research technician

Jun 2020-Jul 2024

- **Led** statistical analyses to identify **genetic biomarkers** with potential for clinical and drug development applications. **Discovered five novel genes** linked to COVID-19 severity, small-cell lung cancer, and aggressive periodontal disease, contributing to three first-author publications in high-impact journals
- Executed and designed analyses for the COVID-19 host genetics SCOURGE consortium, involving **multi-country clinical and genetic data from +10,000 patients**, to identify genetic determinants of disease severity.
- Developed **risk prediction models** on a large patient cohort. Assessed the **incremental value of genetic biomarkers in clinical risk stratification**, supporting their potential integration into precision medicine applications.
- **Applied multiple statistical methods** such as hypothesis testing, classification and clustering, fixed-effects meta-analysis, PCA, logistic mixed models and regularized regression, ANOVA, univariate analysis and descriptive statistics.
- Collaborated with **interdisciplinary teams**, including clinicians, geneticists, odontologists and psychology researchers, across national and international projects. Contributed with both design and execution of studies, resulting in successful project completions and co-authorship on +10 publications.
- **Mentored junior researchers** in R programming, statistical methods, and bioinformatics, including the co-supervision of a MSc thesis awarded a grade of 10/10.
- Built and **automated R pipelines** to handle statistical analyses more efficiently, creating **reusable scripts** to eliminate redundancy and allowing the team to run analyses across multiple projects simultaneously.
- **Harmonized** and cleaned a **multi-center dataset involving 30+ research units** for large-scale analysis.

Intern

Feb 2020-Jun 2020

- Assisted in database wrangling and data preparation using R, supporting data analysis workflows.
- Acquired and applied research methodologies in bioinformatics and genomics.

EDUCATION

PhD in Molecular Medicine - University of Santiago de Compostela - 2024

- Statistical Genetics; Bioinformatics (*Summa Cum Laude*)

MSc in Statistical Techniques - University of Santiago de Compostela - 2021

- Relevant courses: multivariate analysis, spatial analysis, probability models, mixed models, parametric and non parametric regression, survival analysis, time series

BSc in Biology - University of Santiago de Compostela

SKILLS

Statistics and programming: Advanced R, R-markdown, exploratory data analysis, frequentist statistics, regression modelling (GLMs, mixed models), classification, parametric and non parametric statistics, data visualization, analysis of variance, survival analysis, multivariate statistics, statistical learning, bash, beginner python.

Soft skills: Time management, adaptability, self-learning, resourcefulness.

COURSES AND CERTIFICATIONS

- Hands on clinical reporting using R (Genentech - Coursera) - November 2024
 - ADAM datasets, statistical programming, admiral, TLFs, NEST, teal
 - A crash course in causality (University of Pennsylvania - Coursera) - December 2024
 - Causality, propensity score matching, IPTW, IVs
 - Python Programming (Udemy) - In progress
 - Certificate of Proficiency in English - Cambridge C2 (2021)
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PROJECTS

Genetic determinants of COVID-19 (SCOURGE consortium):

Role: Co-lead biostatistician.

- Worked with genetic and clinical data from +10,000 patients recruited in Spain and 6 countries from Latin-America to identify genetic variants associated with the disease and integrated expression data to prioritize potential therapeutic targets such as the gene *AQP3*.
- Tested an alternative approach for training PRS models in genetically diverse cohorts based on genetic similarity between individuals.
- Explored the behaviour of the genetic score in relation to key clinical variables and related subgroups, such as age, sex, and relevant comorbidities, and its association with other COVID-19 complications.
- Actively participated in subprojects derived from the study.

Genetics of aggressive periodontitis (PERIOGEN study):

- Role: Assistant biostatistician.
 - Performed quality control of genetic and clinical data.
 - Contributed with R workflows for polygenic risk score development and analysis.
 - Assisted in drafting the grant proposal that secured funding for the Phase II study, contributing to the design and analysis plan for the continuation of the project.
 - Role: Co-lead biostatistician.
 - Coordinated a remote collaboration, managing task distribution and timelines for analysis, report generation, and manuscript preparation.
 - Meta-analyzed cohort data from large genetic association studies to identify novel biomarkers for the disease.
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SELECTED PUBLICATIONS

ORCID: 0000-0003-2813-8928

- **Diz-de Almeida, S.**, Cruz, R., ..., Carracedo, A. (2024) Novel risk loci for COVID-19 hospitalization among admixed American populations. *eLife* 13:RP93666.
- **Diz-de Almeida, S.**, Richter, G., ... ,Cruz, R., Schaefer, A. S. (2023). A genome-wide association study meta-analysis in a European sample of stage III/IV grade C periodontitis patients 35 years of age identifies new risk loci. *Journal of clinical periodontology*. <https://doi.org/10.1111/jcpe.13922>
- **Diz-de Almeida, S.**, Cruz, R., ... , Flores, C., Carracedo, A. (2022). Novel genes and sex differences in COVID-19 severity. *Human molecular genetics*, 31(22), 3789–3806. <https://doi.org/10.1093/hmg/ddac132>
- Alemany-Navarro, M., **Diz-de Almeida, S.**, ... ,Carracedo, A. (2023). Psychiatric polygenic risk as a predictor of COVID-19 risk and severity: insight into the genetic overlap between schizophrenia and COVID-19. *Translational psychiatry*, 13(1), 189. <https://doi.org/10.1038/s41398-023-02482-7>