Julio Gamboa

Preferred name: **Julen**

I bring extensive experience in R, Python, Bash, and SQL (>5 years) applied across a range of scientific domains. I'm a keen user of machine learning and deep learning libraries applied to large datasets and problems to generate actionable insights. As an experienced university level instructor (>5 years) I am in my element when trusted with communicating complex problems. I'm currently looking for opportunities to use my skills as a data scientist across multiple sectors.

Essential contact details

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Github/Portfolio:

J. Gamboa · GitHub

Personal website:

jgamboa.github.io

Key skills | Core skills

- **Programming languages**: R/Tidyverse, Python, GNU Bash scripting, Julia, Perl.
- **Relational databases**: SQL/MySQL.
- **Version control**: Git, GitHub, GitLab.
- **Reporting and dashboards**: R Shiny, Flexdashboard, Quarto, RMarkdown, Tableau.
- **Statistical and Machine learning approaches**: R (mlr, xgboost, stan), Python (scikit-learn, xgboost, keras, tensorflow, huggingface).
- **Other:** MS Excel/Office.
- **Project management.**
- **Emotional intelligence.**
- **Public speaking.**
- **Creativity and problem solving.**
- **Languages at native proficiency: English and Spanish**

Work Experience

Texas A&M University, USA — Ph.D researcher | 2018 to Present

- I have analysed how the informational content (annotated protein domains and motifs) of animal proteomes (the library of proteins of an organism) evolves using a combination of bioinformatic and machine learning methods, this has led to previously unreported patterns of protein domain architecture.
- Using >10 TB of human genome variation (mutation) data I have developed a pipeline to classify and cluster this information to describe existing patterns of functional divergence of proteins involved in circadian biology across human populations.
- I was involved in the development and deployment of an amphibian karyotype database which is now the main point of reference in the field of amphibian genome evolution. The database was published in 2019 (https://doi.org/10.1007/s10577-019-09613-1) and it is maintained and accessible via the following R Shiny app: https://evobir.shinyapps.io/AmphibianDB/
- I used mathematical modelling to answer how different population genetic forces interact to affect the fate of traits that are beneficial to one sex but detrimental to the other when the ratio of mating individuals is unequal.

Texas A&M University, USA — Selected teaching experience | August 2018 - 2023

- **Computational Genomics (BIOL350)/(BIOL650)**
- **Digital Biology (BIOL647)**.
- **Critical Writing in Biology (BIOL401)**
- **Communicating Biological Research to the Public (BIOL402)**

EDUCATION

Texas A&M University, College Station, Texas, USA | **2018 - Present**

Ph.D in Biology (in progress)
 Focus: Comparative genomics analysis of clinal evolution of circadian proteins.

University College London, London, UK | **2013-2017**

MSci Cell and Developmental Biology - 2:1
Thesis: Altered circadian control of cell cycle progression in the context of wound healing *in vitro*.

References are available upon request