

Julen Gamboa

I am a computational biologist by training with expertise in a wide range of tools and languages such as R, Python, and GNU Bash, as well as statistical and machine learning methods such as XGBoost and HDBSCAN. What truly motivates me is thinking deeply about the underlying processes that generate any dataset I work with. I believe in the power of interdisciplinary knowledge, as it allows me to approach challenges from different perspectives and find innovative solutions.

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boa.github.io/

*Willing to relocate

EXPERIENCE

Texas A&M University, USA — Ph.D student Aramayo Lab

January 2020 - Present

- Currently I am assessing the evolution of informational content in eukaryotic proteome using a cross-disciplinary approach involving machine learning methods (CD-HIT + BIRCH/HDBSCAN)
- I have also analysed human variation data from the gnomAD v3.1.2 database (>2TB of compressed data) to classify mutations using a combination of characterisation and clustering algorithms (CD-HIT/BIRCH/HDBSCAN/AlphaFold/Rosetta). The question I want to answer is whether differences in latitude (clinal variation) over our evolutionary history has led to significant and adaptive changes in protein function and architecture.

Tools: R/Tidyverse, GNU Bash, AWK, SED, regex, Perl, org-mode, emacs, Python, Git, GitHub, SQL.

Texas A&M University, USA — Ph.D student Blackmon Lab

August 2018 - 2019

- I was the second author on an amphibian karyotype database developed and deployed for the Blackmon Lab. <https://evobir.shinyapps.io/AmphibianDB/>
- Using forward-time population genetic modelling I explored the effect that different population genetic forces have on populations with skewed sex ratios of mating individuals. The results are displayed on this shiny app: <https://evoclock.shinyapps.io/osrbias/>.

Tools: R/Tidyverse, Shiny.

Texas A&M University, USA — Selected teaching and mentoring experience

August 2018 - 2023

- **Computational Genomics (BIOL350)/Genomics(BIOL650)** - 3 semesters - Introductory course for applied genome assembly and comparative genomics.
- **Digital Biology (BIOL647)** - 2 semesters - Fast-paced graduate level course that takes the principles learned in BIOL650 applied to bioinformatic analyses using the command line.

- **Critical Writing in Biology (BIOL401)** - 1 semester - This course aims to teach the student how to prepare and write a manuscript for publication in scientific journals.
 - **Communicating Biological Research to the Public (BIOL402)** - 1 semester - This course guides students to take high level scientific writing and transform it into content for general audiences.
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Volunteering

Texas A&M University, College Station, Texas, USA

Open Source for Open Science Workshop 2020 - Volunteer - I generated materials for Carl Hjelman's presentation.

(<https://eeb.tamu.edu/open-source-open-science/open-source-open-science-workshop-2020/>)

Open Source for Open Science Workshop 2019 - Volunteer

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EDUCATION

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

Ph.D in Biology (in progress)

Main focus: Comparative genomics analysis of clinal evolution of photoperiodic/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*.

Skills

- R/Tidyverse, Shiny, Python, GNU Bash, SSH, AWK, SED, Perl, Julia, SQL, LaTeX, Quarto, RMarkdown, Git/GitHub, SLURM, Tableau.
 - Descriptive and inferential statistics/Bayesian statistics and mathematical modelling.
 - Machine learning models in R and Python (scikit-learn, mlr, and xgboost)
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Publications and posters

[R.D. Perkins, J.R. Gamboa, M.M. Jonika, J. Lo, A. Shum, R.H. Adams, H. Blackmon. The Amphibian Karyotype Database. Chromosome Research. https://doi.org/10.1007/s10577-019-09613-1](https://doi.org/10.1007/s10577-019-09613-1)

Poster presentation at Evolution Conference 2019 in Providence, RI, USA.

Poster presentation at STEGG 2019 in College Station, Texas, USA.