

SOFÍA SALAZAR MAGAÑA

Senior undergraduate student of Genomic Sciences. Interested in AI applications in the analysis of genome data and its harmonization with bioinformatic techniques



EDUCATION

September
2020
|
Present

B.Sc., Genomic Sciences

National School of Superior Studies (ENES) Juriquilla, National Autonomous University of Mexico (UNAM)

📍 Querétaro, México

• Grade: 9.88/10

May
2017
|
May
2020

High School Diploma

Monterrey Institute of Technology and Higher Education (ITESM)

📍 Morelia, México

• Grade: 9.69/10



RESEARCH EXPERIENCE

September
2023
|
Present

Undergraduate Researcher

Im Lab, The University of Chicago

📍 Remotely

- Hae Kyung Im, PhD
- Conducted performance testing and workflow assembly for deep-learning software designed to predict genomic features.

January
2022
|
August
2023

Undergraduate Researcher

RegGenoLab, International Laboratory for Human Genome Research (LIIGH), National Autonomous University of Mexico (UNAM)

📍 Querétaro, México

- Alejandra Medina-Rivera, PhD
- Assembled a bioinformatic pipeline for analysis of RNA-seq data and conducted differential expression analysis across multiple datasets of Lupus patients and unaffected controls

CONTACT

✉ sogusama02@gmail.com

🐦 [ssalazar_02](https://twitter.com/ssalazar_02)

🐙 github.com/SophSM

🌐 sophsm.github.io

PROGRAMMING LANGUAGES

Expertise: R and Rstudio, Python, Git, Bash, C++, C#

Familiarity: MySQL, HTML, PHP, Perl

LANGUAGES

Spanish - Native

English - Proficient

French - Intermediate

Made with the R package
[pagedown](https://github.com/jgm/pagedown).

The source code is available [on
github.com/SophSM/CV](https://github.com/SophSM/CV).

Last updated on 2023-12-18.



TEACHING EXPERIENCE

2023



Guest lecturer at bioinformatics institutional course

Bioinformatic Fridays 2023 course, International Laboratory for Human Genome Research (LIIGH)

📍 Querétaro, México

- Lectured on introduction to R language usage for data analysis
- Undergraduate to graduate level class

2023



Guest Lecturer at RNA-seq analysis workshop

International Laboratory for Human Genome Research (LIIGH)

📍 Querétaro, México

- Lectured on RNA-seq analysis workflow using STAR and R
- Graduate level class



POSTERS

February
2023



Academic Days at LIIGH Symposium

Poster

📍 Querétaro, México

- Lupus peripheral blood meta-analysis with Recount3 & Recount3-like processed RNA-seq data

November
2022



ISCB-LA SolBio BioNetMX International Conference on Bioinformatics 2022

Poster

📍 Querétaro, México

- Lupus peripheral blood meta-analysis with Recount3 & Recount3-like processed RNA-seq data



COURSES

November
2022



Workshop: Analysis of biological and biomedical transcriptomic data using Artificial Intelligence (AI) and Machine Learning (ML) methods with R

ISCB-LA SolBio BioNetMX International Conference on Bioinformatics 2022

📍 Querétaro, México

- Multiple Instructors

January
2022



Introduction to the logical modeling of cellular networks, with applications to cancer and immunology.

International Laboratory for Human Genome Research (LIIGH)

📍 Querétaro, México

- Main instructor: Denis Thieffry, PhD, (ENS, Paris)

November
2021

Academic Writing in English course

National School of Superior Studies (ENES) Juriquilla, National
Autonomous University of Mexico (UNAM)

📍 Querétaro, México

• Main instructor: M.S. José Antonio Alonso-Pavón