



JESÚS VÉLEZ SANTIAGO

Genomic Scientist | Data Scientist




I love analyzing and visualizing data to improve our understanding of what is around us. Besides, I am fascinated by software development, and I hope to contribute valuable packages to the scientific community one day. I am known for being a passionate, curious person and be always open to new challenges. Do you have any challenges? Good! Let's do it. Let's be problem solvers.








EDUCATION AND TRAINING

- 2021 • **Datacamp Inc.**
Data Scientist Professional  Certificate
- The following knowledge was assessed:
- Data Management
 - Model Development
 - Exploratory Analysis
 - Coding for Production Environments
 - Statistical Experimentation
 - Communication and Reporting
- 2017 | 2021 • **National Autonomous University of Mexico (UNAM)**
B.S. in Genomic Sciences  Cuernavaca, Morelos, Mexico
- Thesis: Bacterial filamentation: a bet for survival in stressful environments

RESEARCH EXPERIENCE

- 2018 | 2021 • **Undergrad Thesis Student**
Center for Genomic Sciences  Cuernavaca, Morelos, Mexico
- I combined mathematical models with experimental microbiology to understand how exposure to antimicrobial substances triggers bacterial cells' stress responses. I have mainly focused on postulating a mathematical model showing that cell elongation can promote transient resistance to individual bacterial cells by diluting the antibiotic's intracellular concentration.
- 2020 | 2021 • **Developer of R Software**
Universität Heidelberg  Remote work, Germany
- Over the years, many different regulatory networks and statistical algorithms have been developed, mostly in a fixed combination of one network and one algorithm. To systematically evaluate both networks and algorithms, we developed `decoupleR`, an R package that allows users to apply efficiently any combination provided.
- 2019 | 2020 • **Assitant of National Researcher Level III or Emeritus**
Center for Genomic Sciences  Cuernavaca, Morelos, Mexico
- Perform analysis of collections of massive expression experiments (e.g., RNA-seq) from *E. coli* using uniform bioinformatic pipelines that allowed comparison with the transcriptional regulation network's classical experimental knowledge.

CONTACT INFO

 jvelezmagic.com
 [@jvelezmagic](https://github.com/jvelezmagic)
 [@jvelezmagic](https://twitter.com/jvelezmagic)
 [@jvelezmagic](https://in.jvelezmagic)
 jvelezmagic@gmail.com

SKILLS

Experienced in machine learning, statistical and mathematical modeling, data analysis, and data visualization.

Highly skilled in R, Python, Git, and Conda.

Last updated on 2021-08-22.

- 2019 ● **Bioinformatician and Genomist**
 Centré de Regulació Genòmica 📍 Barcelona, Spain
- Differential expression analysis between the different conditions (e.g., deletions, overexpression, wild type) of transcriptional factors.
 - Comparison of the expression profiles of genes regulated by transcriptional factors with the information available in *E. coli* gene regulation databases (e.g., RegulonDB).
- 2018 ● **Visiting Scientist**
 Center for Genomic Sciences 📍 Cuernavaca, Morelos, Mexico
- Design of R programs for the study of the topological properties of the *E. coli* transcriptional regulatory network.

PROFESSIONAL EXPERIENCE

- 2021 ● **Data Science Professor**
 Platzi Inc. 📍 Remote work
- Complete design and planning of two data science courses.
 - Courses promotional writing.
 - Creation of exams and support materials.
 - Courses promotional live class.


TEACHING EXPERIENCE

- 2021 ● **Advanced Customization of Environment for Data Science**
 Platzi Inc. 📍 Link to my course
- Learn how to customize a data science workbench based on Python, Conda, and Jupyter Notebooks. With these tools, you will achieve harmony in your work environment and increase your productivity as a data scientist.
- 2021 ● **Jupyter Notebooks for Data Science**
 Platzi Inc. 📍 Link to my course
- Learn about the different types of Jupyter notebook, the fundamental work tool for any data scientist.
- 2021 ● **Teaching Assistant of “Analysis of transcriptomic data of single cell (scRNA-seq) with R and Bioconductor.” Course**
 Bioinformatics Meeting in Mexico 2021 📍 Course material
- Provide support to students.
 - Guide discussions and exercises in breakout rooms.
 - Solve configurations of work environments.
- 2020 ● **Teaching Assistant of Linear Algebra Course**
 Center for Genomic Sciences 📍 Cuernavaca, Morelos, Mexico
- Monitoring of student performance accompanied by personalized and group tutorials.
 - Review of assignments and exams.



HONORS AND AWARDS


2020

- **Winner of first “Olimpiadas Platzi: Data Triathlon” – Platzi**
Platzi Inc.  [Award link](#)


2020

|

2021

- **Support Program for Research and Technological Innovation Projects (PAPIIT)**
National Autonomous University of Mexico (UNAM)  Mexico


2019

- **Program for Special Inter-institutional Cooperation Activities (PAECI)**
National Autonomous University of Mexico (UNAM)  Mexico



SELECTED PUBLICATIONS AND POSTERS

2019

- **Filamentation: a bet for survival.**
Poster for 2019 Fall School of Mathematical Biology (EOBM).
 Merida, Yucatan, Mexico
Velez-Santiago J, Peña-miller R.