

# Santiago Gerardo Medina Resume

bioinformatician (Stowers Institute for Medical Research)

♥ 1000 E. 50th Street, Kansas City, MO 64110, USA

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Date of Birth - June 17, 1995 (gender: male)

Place of Birth - Guanajuato, Mexico (Mexican nationality)

Marital Status - Single

#### **Education**

**Bachelor in Agro-genomic Sciences** - Escuela Nacional de Estudios Superiores Unidad León, UNAM

2013-17

## **Research Experience**

**2018** - Bioinformatician (current position), Stowers Institute, supervised by Dr. Ariel Bazzini. I have worked on multiple projects in the lab in collaboration with other lab members. Also, I have the opportunity to carry my own research projects developing statistical models to understand post-transcriptional gene regulation.

**Codon Optimality** 

**2017** - undergraduate thesis, Stowers Institute, supervised by Dr. Ariel Bazzini. I employed Bayesian hierarchical models to estimate the effect of each codon on gene expression across human tissues. For this, I analyzed hundreds of RNA-seq profiles from ENCODE. My analysis showed that the effect of each codon on the mRNA level varies across tissues. This is still ongoing work and now, with a successful collaboration of a graduate student in the lab, we are experimentally validation these results in zebrafish.

Tissue-specific codon effect on gene expression

**2016** - undergraduate research, UNAM-Leon, supervised by Dr. Julio Vega Arreguin. I identified NBS domains of immune resistance genes in the genomes of 30 plant species with BLAST searches. Then I looked at the evolution of these domains with phylogenetic approaches.

Evolution of NBS domains in plant resistance genes

**2015** - Stowers summer scholar, Stowers Institute, MO USA, supervised by Dr. Julia Zeitlinger. I benchmarked different tools for ChiP-seq data analysis with the purpose of developing a pipeline to analyze ChiP-nexus data.

A pipeline for peak calling and motif discovery in ChIP-nexus data

**2014** - undergraduate summer research, National Laboratory of Genomics for Biodiversity, Mexico, supervised by Dr. Cei Abreu. Using microarrays and RNA-seq data I evaluated if the microRNA's target sites of homologous genes were conserved and also the conservation of expression pattern due to microRNA effect.

Conservation of microRNAs targets in homologous genes

#### **Publications**

- Wu, Qiushuang, **Santiago Gerardo Medina**, Gopal Kushawah, Michelle Lynn DeVore, Luciana A. Castellano, Jacqelyn M. Hand, Matthew Wright, and Ariel Alejandro Bazzini. "Translation affects mRNA stability in a codon-dependent manner in human cells." Elife 8 (2019): e45396.
- Santiago Gerardo Medina, Gopal Kushawah, Maria Jose Blanco, and Ariel Alejandro Bazzini. "Interplay between codon optimality and 3' UTR cis-elements controls mRNA stability." *in review*

## **Meetings**

- **Deciphering mRNA decay programs during embryogenesis.** Santiago Gerardo Medina and Ariel A. Bazzini. (poster) *Biological Data Science. CSHL-2018*
- A pipeline for peak calling and motif discovery in ChIP-nexus data. Santiago Gerardo Medina and Julia Zeitlinger. (poster) XVI National Congress of Plant Biochemistry and Molecular Biology & IX Symposium Mexico /USA. Querétaro-2016

## Workshops

Statistical Data Analysis for Genome Scale Biology - 2017

Bressanone-Brixen

**Bioinformatics Summer School** - 2016

Institute of Mathematics UNAM, Querétaro

In 2018 I did an intensive one-week workshop with students at my university where I introduced them to scientific Python, data analysis, and data visualization.

## **Scholarships**

Colgate Academic Excellence - UNAM

2016

**Stowers summer scholar** - Stowers Insititute for Medical Research

2015

#### **Skills**

**Communication** - technical presentation, data analysis report, scientific publications, data visualization

**Programing** - R/Bioconductor (advanced), R package development, shiny. Python (Scikit Learn, Pandas, NumPy, SciPy, Keras). Bash scripting, Pipeline development: Snakemake. Software development, git, and github

**Statistics** - machine learning, data analysis, generalized linear regression, cluster analysis, principal components analysis, cross validation, generalized linear models, Monte Carlo simulation, Bayesian statistics

• Languages: Fully bilingual (Spanish / English)

outside the lab, I enjoy reading and outdoor activities including mountain biking, hiking, and horseback riding.

#### References

- Dr. Julio Vega Arrequin jvega.arreguin@gmail.com
- Dr. Cei Abreu-Goodger cei.abreu@cinvestav.mx
- Dr. Ariel Bazzini arb@stowers.org