



# SANTIAGO GERARDO MEDINA | RESUME

bioinformatician (Stowers Institute for Medical Research)

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

☎ +1 816 267 2239

✉ [smedina@stowers.org](mailto:smedina@stowers.org)

## Personal Details

Date of Birth -	June 17, 1995
Place of Birth -	Guanajuato, Mexico (Mexican nationality)
Marital Status -	Single

## Education

<b>Bachelor in Genomic Sciences</b> - Universidad Nacional Autónoma de México- León, Mexico	2013-17
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**2018 - (current):** *I work as a bioinformatician in Ariel Bazzini's lab at the Stowers Institute for Medical Research.*  
I collaborate with experimentalists by providing help in analyzing omics-data to study how genes are regulated and how that regulation can impact development or affect human diseases. Also, I have the opportunity to carry my own research projects developing statistical models to understand post-transcriptional gene regulation.

## Research Experience

<b>2014</b> - 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
<b>2015</b> - 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
<b>2016</b> - 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
<b>2017</b> - undergraduate thesis, Stowers Institute, supervised by Dr. Ariel Bazzini  - I employed Bayesian hierarchical GLMs 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

## Skills

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

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

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

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## Scholarships

**Colgate Academic Excellence** - UNAM

2016

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

2015

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## Workshops

**Bioinformatics Summer School** - 2016

Institute of Mathematics  
UNAM, Querétaro

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**Statistical Data Analysis for Genome Scale Biology** - 2017

Bressanone-Brixen

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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.

## Meetings

**XVI National Congress of Plant Biochemistry and Molecular Biology & IX Symposium Mexico /USA**, - Querétaro-2016

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

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**Biological Data Science** - CSHL-2018

Deciphering mRNA  
decay programs during  
embryogenesis (poster)

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## Publications

- Wu, Qiushuang, **Santiago Gerardo Medina**, Gopal Kushawah, Michelle Lynn DeVore, Luciana A. Castellano, Jacquelyn 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. "Codon content predicts mRNA stability in vertebrates." *in production and to be available in bioRxiv on March 2020*

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**Languages:** Fully bilingual (Spanish / English)

**outside the lab**, I enjoy reading, mainly non-fiction, and outdoor activities including mountain biking, hiking, and horseback riding.

## References

- Dr. Julio Vega Arreguin [jvega.arreguin@gmail.com](mailto:jvega.arreguin@gmail.com)
- Dr. Cei Abreu-Goodger [cei.abreu@cinvestav.mx](mailto:cei.abreu@cinvestav.mx)
- Dr. Ariel Bazzini [arb@stowers.org](mailto:arb@stowers.org)