



# SANTIAGO GERARDO MEDINA | RESUME

bioinformatician

📍 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
---	---------

**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

## Scholarships

Colgate Academic Excellence - UNAM

2016

Stowers summer scholar - Stowers Insititute for Medical Research

2015

## Workshops

Bioinformatics Summer School - 2016

Institute of Mathematics  
UNAM, Querétaro

Statistical Data Analysis for Genome Scale Biology - 2017

Bressanone-Brixen

## 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. "Codon content predicts mRNA stability in vertebrates." *in production and to be available in bioRxiv on March 2020*

---

**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
- Dr. Cei
- Dr. Bazzini