

# VALERIA VELASQUEZ-ZAPATA

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## SUMMARY

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My research currently focuses on developing mathematical models and methods for understanding disease emergence. I study pathogenic mechanisms and host immune responses through the combination of statistical modeling and wet lab approaches, such as the production and analysis of high-throughput data (like Y2H-Seq and RNA-Seq), the use of systems biology to build biological networks, and the integration multi-omics data. Multidisciplinary collaborations have led me to interact with molecular biologists, geneticists, statisticians, and computer scientists in the development of solutions in the field. I hope to find opportunities where I can find fulfillment in my work by continuing to expand my understanding of biological systems and apply my data analysis expertise.

## EDUCATION

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<b>PhD, Bioinformatics and Computational Biology (minor in Statistics)</b> Iowa State University, USA	GPA: 4/4 July 2021
<b>MS, Biomedical Research</b> University of Valladolid, Spain	GPA: 9.2/10 July 2015
<b>BS, Biology</b> University of Antioquia, Colombia	GPA: 4.4/5 October 2013
<b>BS, Biological Engineering</b> National University of Colombia	GPA: 4.1/5 July 2010

## EXPERIENCE AND PROJECTS

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### Y2H-SCORES

[Y2H-SCORES](#) is a software developed to rank protein-protein interactions from yeast two-hybrid next generation interaction screening (Y2H-NGIS) data. Besides the software, I developed a [Y2H-NGIS simulator](#) to generate Y2H-NGIS data, and a [Benchmarking](#) section that proves the performance of the software across published datasets.

### Interact-omics

I developed [Interact-omics](#), a series of workflows to integrate interactome data with other omics like eQTL, RNASeq and Y2H-NGIS. Different network analyses are presented and applied to characterize the signaling of the *Mla* receptor.

### TranscriptoNET

I am developing different data analysis workflows for transcriptome data. [TranscriptoNET](#) include generation and integration of Gene Regulatory Networks (GRNs), prioritization of transcription factors for their role in regulating expression, data visualization and epistatic analysis of gene effects on gene expression.

## SELECTED PUBLICATIONS

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**Velásquez-Zapata V**, Elmore J, Banerjee S, Dorman K, Wise R. *Next-generation yeast-two-hybrid analysis with Y2H-SCORES identifies novel interactors of the MLA immune receptor*. PLoS Computational Biology (2021).  
**Banerjee S, Velásquez-Zapata V**, Fuerst G, Elmore J, Wise R. *NGPINT: A Next-generation protein-protein interaction software*. Briefings in Bioinformatics (2020)  
**Reyes-Herrera P, Muñoz-Baena L, Velásquez-Zapata V**, Patiño L, Delgado O, Díaz-Diez C, Navas-Arboleda A, Cortés A. *Inheritance of Rootstock Effects in Avocado (Persea americana Mill.) cv. Hass*. Frontiers in Plant Science (2020).  
**Gemmell N, et al.** *The tuatara genome reveals ancient features of amniote evolution*. Nature (2020).  
**Fraile E, Díez-Gómez B, Velásquez-Zapata V**, Acedo A, Sanz D, Velasco E. *Functional classification of DNA variants by hybrid minigenes: Identification of 30 spliceogeanic variants of BRCA2 exons 17 and 18*. PLoS Genetics (2017).

## SKILLS

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**Proficient:** R, Python, MATLAB, L<sup>A</sup>T<sub>E</sub>X, Git, BASH, Slurm, Excel, Benchling, Biorender

**Familiar:** SQL, SAS, Adobe illustrator

**Languages:** Spanish, English, Portuguese