

VALERIA VELASQUEZ-ZAPATA

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SUMMARY

My research currently focuses on developing mathematical models and methods for understanding biological systems. I combine 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. 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

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

EXPERIENCE AND PROJECTS

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 omics like eQTL, RNASeq and Y2H-NGIS. Different network analyses are presented and applied to characterize the *Mla* receptor signaling.

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.

Genetic resources: I have collaborated in different projects exploring the genomics and population structure of different groups of organisms. These had different applications going from [genome evolution](#) to the assessment of genetic diversity linked with [agronomic](#) or [clinical](#) traits.

SELECTED PUBLICATIONS

- **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 spliceogenic variants of BRCA2 exons 17 and 18*. PLOS Genetics (2017).

SKILLS

Proficient: R, Python, MATLAB, L^AT_EX, Git, BASH, Slurm, Excel, Benchling, Biorender

Familiar: SQL, SAS, Adobe illustrator

Languages: Spanish, English, Portuguese