Resume

David Angeles Albores

Contact Information

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Professional Summary

Motivated computational and molecular biologist who specializes in the design, generation and analysis of deep sequencing experiments, with multiple peer-reviewed articles on this subject. Ensures maximal transparency and reproducibility by performing analyses using Python or R with version control (Git) following PEP8 standards. Deep knowledge of advanced statistical methods that can be applied to any biological problem. **Experienced scientist who can translate biological intuition into computational solutions.** Values collaborations and seeks them out actively.

Education

Caltech, PhD, Biochemistry and Molecular Biophysics, 2018 (Expected)
Cornell University, BA, *cum laude*, Molecular and Computational Biology, 2013

Skills

RNA-seq; NGS; Python; R; Matlab; Java; Unix; Linux; Statistical methods; Programming; Molecular Biology; Genetics; Genomics; Mathematical Modeling; Chromatin; Chromatin Modification; Enhancer Biology; Quantitative Genetics; Bayesian Probability; Developmental Biology; Leadership; Teamwork; Collaboration; Dataviz; Data Visualization; Data Science; Big Data;

Experience and Professional Accomplishments

I am first author in all publications listed below.

- **Genetic reconstruction of an animal genetic pathway using RNA-seq.** Led a project that sequenced the expression profiles of 4 single and 2 double mutants of the hypoxia pathway in the nematode *C. elegans*. Developed statistical tools that reconstructed the hypoxia pathway blindly and provided proof-of-principle that genetic networks can be reconstructed from whole-animal expression profiles and culminated in a publication in the prestigious *Proceedings of the National Academy of Sciences*.
- **Identification of a novel life cycle state in the roundworm *C. elegans*.** Transcriptomic profiling coupled with General Linear Models (GLM) inferred a state in the life cycle of this organism that could not be observed otherwise. This project used a modeling technique known as a linear model with interactions to measure genetic epistasis. This technique was later adopted in single-cell sequencing to map genetic pathways. This project was published in the peer-reviewed journal *G3*.

- **Study of an allelic series using transcriptomic phenotypes.** Leveraging tools developed in the above projects, analyzed different alleles of a Mediator subunit that have distinct developmental and transcriptomic phenotypes. This analysis, the first ever of its kind, identified novel functions encoded within Mediator. This project culminated in a manuscript currently undergoing peer-review in *Genetics*.
- **Development of the WormBase Enrichment Suite.** Developed the WormBase Enrichment Suite, a Python library that allows genomics researchers to identify any anatomical regions; phenotypes; and cellular or molecular structures that are enriched in their genomic data. This tool was published in *BMC Bioinformatics*.

Awards

- Florence C. Rose and S. Meryl Rose Endowed Scholarship, 2015
- Amgen Fellowship, 2014
- Frank and Sara McKnight Award in Molecular Sciences, Finalist, 2012
- James A. Perkins Award for Interracial Understanding and Harmony, 2012
- HHMI EXROP Capstone Award, 2012

Scientific Societies

- Genetics Society of America (since 2014)
- Society for Developmental Biology (since 2015)