John Paul Mendieta

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# Professional Experience

# Agricultural Genomic Initiative

### Computational Biologist | December 2015 - Present

* Designed in-house software utilizing a novel algorithm to assist with gene detection. Software currently being utilized by a team of 5+ other biologist tackling genome annotation for the Cannabaceae family
* Provided data quality metrics for various types of biological data (NGS reads). Created a reference database for the research group regarding current data quality (400+ Gb of data, 25+ individuals)
* Created custom bioinformatics software scripts in a range of languages (R, Python, Shell scripting) for common, simple procedures, allowing for ease of duplication of results, saving 100+ hours of work

## Nolan Kane’s Lab

### Computational Biologist, University of Colorado Boulder | January 2015 – January 2017

* Developed in-house software on demand for a wide range of projects, communicating with research groups studying different evolutionary phenomena. Created 20-30 different pieces of software and pipelines.
* Acted as an on call consultant for 6 different teams of graduate students and professors, recommended strategies and tools for computational analysis as well as provided trouble shooting solutions
* Introduced the Kane lab to concept of utilizing scripting languages with a specific emphasis on Python allowing lab members more flexibility when dealing with biological data sets
* Designed flexible pipelines to quantify and statistically analyze repetitive content of 96 different plant genomes. Results were visualized and presented at Evolution 2016
* Assisted in assembling, and error checking 20+ published chloroplast genomes, with a team of graduates and undergraduates (25 -30 students total), expanding global genomic resources (NCBI genomes) by 5%
* Performed rigorous computation analysis and statistics on multiple data sets to check for biologically relevant/significant results of alternative splicing in speciation genes in the *Helianthus* genus. Paper in preliminary draft.

# Education

## University of Colorado Boulder, 2011-2015

B.A. Ecology & Evolutionary Biology

B.A. Molecular Cellular & Developmental Biology

*Magna Cum Laude*

Dean’s List: Spring 2015, Fall 2015

Cumulative GPA: 3.5 Major GPA: 3.7

# Skills Summary

**GitHub:** https://github.com/Jome0169

**Programming Languages:** Python, R, Bash, HTML, CSS

**Software Engineering:** OOP, Test Driven Development

**Bioinformatics Tools:** Samtools suite, BWA, RepeatExplorer, Tuxedo Suite, Soapdenovo, Spades, Trinity, Trimmomatic, Blast Legacy

**Server Administration/IT:** Large Database Management, Bioinformatic technical issue trouble shooting, NCBI

**Operating Systems:** Mac OS, Linux OS, Unix Enviornments, Windows

**Functional:** Excellent communicator (verbal, written, and visual), able to work independently, self-motivated, fast-learner, highly organized, creative problem-solver, Excellent collaborator