Michael Alonge

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Education

University of California, Santa Cruz
- B.S. Biomolecular Engineering (2014)
- Undergraduate Thesis: *De novo* genome assembly of *Rubus arcticus* (Arctic Raspberry) and k-mer frequency based non-nuclear read filtration

Relevant Coursework

- **Research Programming in the Life Sciences**
Introduction to the fundamentals of python applied to common research topics in the biological sciences.

- **Computational Biology Tools**
An overview of computational biology tools, such as genome assemblers, gene finders, and sequence aligners.

- **Accelerated Introduction to Programming**
Introduction to computer science fundamentals via the Java programming language.

Work History

Research Associate I (November 2014 - present)
Driscoll Strawberry Associates, Watsonville CA

Use of computational biology tools as well as novel programming to support marker assisted breeding of berry species. Exploration of different sequencing technologies and genome assembly/improvement algorithms to establish high-quality reference genomes.

Responsibilities:
- Work with modern sequencing technologies and associated computational tools to establish high-quality reference genomes for use in marker assisted breeding.
- Use the python programming language to develop computational tools to assist the molecular biology team with processing and analyzing data.
- Contribute to the development, maintenance, and testing of a database for the molecular biology team.
- Maintain in-house instances of genome browsers and associated data.
- Archive and curate all primary data acquired by the molecular biology team.

Molecular Biology and Strawberry Breeding Intern (June 2013 - November 2014)
Driscoll Strawberry Associates, Watsonville CA

Coordinated a research project to identify a volatile organic compound marker in strawberry. Assisted in general wet lab and computational projects to support molecular biology projects that focused on strawberry breeding.

Responsibilities:
- Processed datasets using python for downstream analysis.
- Performed RNA extractions for plant virus screening.

Research Experience

***de novo* assembly of the red raspberry genome**
Currently working on establishing a PacBio draft assembly with the FALCON assembler. I am also analyzing how well the FALCON Unzip software phases haplotypes of this draft assembly. Finally, I am using chromatin interaction data to order and orient this draft assembly into a chromosome scale assembly. This assembly is being compared to a preexisting reference which used a separate genome assembly pipeline. A Jupyter Notebook describing some of this work is available on my GitHub.

Filtration of chloroplast sequencing reads via kmer-spectra analysis (undergraduate thesis project)
Tested a novel way of extracting chloroplast specific sequencing reads without the need for a closely related reference genome. Reads were filtered by peaks in kmer-spectra plots characteristic of non-nuclear kmers.

***de novo* assembly of the Arctic Raspberry genome (undergraduate thesis project)**
Established a draft genome assembly using Illumina fragment and mate pair data. Analyzed accuracy and contiguity of various draft assemblies to find the optimal genomic coverage.

Computational Tools Developed

Genome assembly lift-over tool
Wrote a python program that "lifts over" genomic features from a scaffold level assembly to its ordered and oriented assembly.

Raspberry postharvest color change image analysis
Used the scikit-image API to develop a tool that measures the postharvest change in color in raspberries.

Strawberry leaf necrosis image analysis
Used the scikit-image API to develop a tool that measures the amount of necrotic leaf tissue in strawberries.

Sequencing Sample Database and Web App
Created a PostgreSQL database of in-house sequencing sample metadata. Used python and Django to create a web app with query tools for users to obtain information regarding samples.

Relevant Skills

- **Programming Languages**
  - Intermediate python programmer
    - Experience with numpy, scipy, pandas, matplotlib, scikit-image, and virtualenv
  - Beginner Java, BASH, and R programmer

- **Data Analysis**
  - Pandas Data Frames, matplotlib, R Data Frames

- **Software Development and Databases**
  - Relational database design, PostgreSQL, SQLite, and MySQL.
  - Object Oriented Design
  - Git and GitHub
  - Django, HTML, CSS, and JavaScript

- **Computational Biology Tools**
  - FALCON, FALCON-Unzip, DALIGNER, DAZZ_DB, DAVIEWER, DAMASKER, ALLPATHS, ABySS, BLASR, BLAST, PBJelly, Bowtie2, BWA, SAMtools, bcftools, bedtools.
  - UCSC Genome Browser, JBrowse

- **Sequencing Datasets**
  - Illumina, Oxford Nanopore, PacBio

- **Operating Systems**
  - RedHat, CentOS, OS X, Windows

- **Laboratory**
  - DNA/RNA extractions, PCR, Gel Electrophoresis

Conferences Attended

- Plant Animal Genome 2015 and 2016, San Diego CA
- Sequencing, Finishing, Analysis, and the Future 2015 and 2016, Santa Fe NM
- PyCon 2016, Portland OR

Awards and Grants

- **Alumni College Service Award (2013)**
  For involvement in the Stevenson College community

- **College Board AP Scholar With Distinction Award (2009)**
  For receiving a score of "4" on a total of five AP tests

Volunteer Work

- **Founder of Stevenson College Secular Humanism Club (2010)**
  A UCSC Stevenson College student group that facilitated philanthropic activities for on-campus residents.

- **American Cancer Society Relay For Life**
  Participated as a Team Captain for the 2011 UCSC Stevenson College Relay For Life team.

References

Judson Ward, Ph.D.
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