

Arun Durvasula

@arundurvasula

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Education

BS Biotechnology, Microbiology and Fermentation, University of California Davis 2015 (expected)

High School Diploma, Saint Francis High School, Mountain View, CA 2011

Experience

Student Assistant Level IV, Rowhani Lab. Foundation Plant Services. June 2014 - Present

Bioinformatics: supported research and discovery of novel viruses in diseased crop plants such as *Vitis vinifera*, *Pistacia vera*, and *Citrus sinensis*. Additionally, developed scripts and pipelines published on Github for the automated assembly, annotation, and aggregation of sequence information from high-throughput sequencing machines.

Writing: prepared reports summarizing methods and results for growers.

Research Intern, Ross-Ibarra Lab. University of California, Davis, Department of Plant Sciences. June 2013 - Present

angsd-wrapper: created a software package that simplifies population genetic analysis using ANGSD and streamlines graphical analysis using R and Shiny.

Re-estimation of the maize domestication bottleneck: used genetic simulations on a large computer cluster to re-estimate the strength of the maize domestication bottleneck using R and open source scientific software.

Lab documentation: wrote documentation and tutorials for computer cluster usage for use by lab.

Technical Reviewer, O'Reilly Media. December 2013 - Present

Bioinformatics Data Skills by Vince Buffalo: ensured accuracy of code and information in upcoming book.

Principal Programmer, Seqcoverage. July 2014

Seqcoverage: created an alignment web service that uses bedtools, BWA, and R to examine read coverage given a reference sequence and a set of reads (open source and available on Github).

Research Assistant, Tagkopulous Lab. University of California, Davis, Genome Center. January 2013 - June 2013

Escherichia coli simulator: created the methodology used to model the metabolism in a novel whole cell simulation of *E. coli* using Matlab.

Teaching

Teaching assistant: Ecological Genomics (Graduate), Winter 2015-present

Presentations

ANGSD-wrapper: scripts to streamline and visualize NGS population genetics analysis, Poster at Bay Area Population Genetics Conf, 2014.

Publications

Arun Durvasula, Tyler Kent, Siddharth Bhadra-Lobo, Jeffrey Ross-Ibarra. ANGSD-wrapper: scripts to streamline and visualize NGS population genetics analysis (2015). In preparation. <https://github.com/arundurvasula/angsd-wrapper-paper>.

Timothy Beissinger, Li Wang, Matthew Hufford, **Arun Durvasula**, Jeffrey Ross-Ibarra. Patterns of Demography and Selection Since Maize Domestication (2015). In preparation.

Skills

Programming: Python, Bash, Awk, Haxe, C, C++, Ruby, Java, Javascript, HTML, CSS

Frameworks/Libraries: Django, Rails, Scikit Learn, OpenFL, HaxeFlixel, Scipy, Numpy, Matplotlib,

Bioinformatics:

Assembly: Velvet, IDBA_UD, CLCBio

Alignment: BWA, bowtie

Other: samtools, bedtools, Bioconductor packages, SFS_CODE, SLiM, ANGSD

Tools: Git, R, Shiny, Matlab, SQL, Machine learning, IPython, LaTeX, Slurm, Sun Grid Engine

Molecular biology: PCR, Gel electrophoresis, RFLP, Bacterial transformation, Genomic DNA isolation

References

Jeffrey Ross-Ibarra

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