

Dylan Gallinson
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Education

St. Petersburg College
Bachelor of Science in Biology
2012 – 2017

East Lake High School
Standard High School Diploma
2007 – 2011

Honors and Awards

Federal Pell Grant

2014 – 2015

2015 – 2016

Excellence in Biology

2014 – 2015

Outstanding Student Tutor

2015 – 2016

STEM Scholar Recipient

Spring 2017

Excellence in Scientific Writing

2017

Excellence in Undergraduate Research

2017

Professional Experience

St. Petersburg College Instructional Support Specialist (2014 – Present)

- Helped students with: Biology I and II, General Chemistry I and II, and Organic Chemistry I and II, Bachelor Biology courses, and math through Calculus I

University of South Florida Research Assistant (August 2021 – Present)

Research Experience

RNA-Seq Data Mining Workflow (2016 – Present)

An RNA-Seq study of human pancreatic exocrine cells involving transcriptome assembly, differential expression analysis, data curation using command-line tools, and the creation of custom parsing scripts written in Python.

USF Codeathon (2021)

A three-day intensive online coding competition. My team focused on characterizing the airborne microbiome using an abundance time-series dataset of bacterial operational taxonomic units. I developed a Python script to detect outliers through seasonal trend decomposition using LOESS.

USF Genomics Microbiome Data-Analysis Training (2021)

A three-day intensive online training session detailing microbiome data analysis pipelines. The training utilized the R programming language to generate Amplicon Sequence Variants (ASVs) from raw FASTQ reads. The training session then described downstream analyses involving microbiota abundances, feature extraction, and data visualization.

USF Tasmanian Devil and DFTD Coevolution (2021 – Present)

A study conducted for my thesis using a GWA approach to look at the coevolution between Tasmanian devils and a transmissible tumor, Devil Facial Tumor Disease (DFTD). The project is computationally driven and utilizes a cluster for data processing, generating SNPs from FASTQ reads. Downstream statistical models are then used to look at possible coevolutionary interactions between SNPs, and to generate estimated breeding values (EBVs).

Software Knowledge

Linux

- Distributions include Ubuntu, Raspbian, and RedHat
- Ability to setup a distribution from scratch
- Usage of the BASH terminal

SLURM

- Setting up a basic batch script
- Running parallel jobs

BLAST

- Blastn, blastp, and blastx

- Ability to modify parameters in a meaningful way (filter results with entrez queries, exclude/include specific organisms, employ species-specific repeat-masking)
- Interpretation of BLAST alignments

Primer3

- Generate primers around a region of interest
- Meaningfully select primers with desirable physical characteristics (e.g. GC content, specificity of primer to target)

RNA-seq Pipeline Tools

- Preprocessing and quality control of raw sequence reads
 - FastQC
 - Cutadapt
 - Trimmomatic
 - MultiQC
- HISAT2
- STAR
- Samtools
- StringTie
- FeatureCounts
- DESeq2
- IGV

Programming knowledge

- Python
 - Numpy
 - Pandas
 - PyTorch (basic working knowledge)
- R Programming Language
- Java
- C++ (basic working knowledge)
- HTML
- CSS
- Javascript
- PHP
- MySQL
- Dart
 - Flutter SDK