

Steven R. Dea

srdea93.github.io
Mountain View, CA

Bioinformatics student and life scientist looking to establish and employ skills in computer science and engineering, data analytics, algorithm development, and next-generation sequencing analysis.

Education

Master of Science – Bioinformatics GPA: 3.86
Johns Hopkins University
Expected Graduation: September 2020

Bachelor of Science – Biology GPA: 3.53
University of California San Diego 2016

Skills

Technical

Python (Pandas DataFrame, Seaborn), Java, C++, R, MySQL, Relational Database Design, HTML, CSS, JavaScript, RESTful web services, Spring Boot/MVC, React/Node.js, Git

Bioinformatics Skills

Multi-omic data and Microarray data analysis and visualization, Phylogenetic analysis, GATK (using Docker instances)

Experience

Bioinformatics Intern – R&D

StemoniX 05/2020 – 06/2020

Developed and implemented an RNA-Seq data processing pipeline to take raw fastq files to expression matrices and differential gene expression data

- o Implemented pipeline with bash scripting and Python
- o Pipeline includes: fastqc, multiqc, HISAT2, samtools, stringtie, htseq-counts, gffcompare, DESeq2, and personally written bash scripts Python modules.

Developed analysis modules for differential gene expression using DESeq2 differential gene expression matrices

- o Analysis and visualization modules written in Python using Pandas data frames, matplotlib, seaborn
- o Generated differentially expressed gene analysis and visualizations for GO term enrichment, clustering, and extraction of expression information for genes of interest

Scientist I – Neurosciences

StemoniX 07/2016 – 05/2018

Developed a 3D screening platform for iPSC-derived neurons and astrocytes

- o Developed analysis tools and workflow for novel 3D model

Publications

Sirenko Oksana, Parham Frederick, Dea Steven et al. Functional and Mechanistic Neurotoxicity Profiling Using Human iPSC-Derived Neural 3D Cultures. Toxicological Sciences. 2018: kfy218.

<https://doi.org/10.1093/toxsci/kfy218>

Personal Achievements

Eagle Scout 2010

- o **Project Management:** Designed, planned, organized, and executed a project to develop and build six mobile uniform carts for the St. Francis high school marching band.

Projects

Portfolio: Bioinformatics Tools for Genome Analysis

- o **NGS Analysis:** NGS data preparation using FASTQ Groomer and Trimmer, alignment using Bowtie/BWA/HISAT. VCF file for variant calling produced using FreeBayes.
- o **Transcriptomic Analysis:** RNA-seq data prepared using FASTQ and aligned using HISAT2 and Stringtie used to merge comparison transcriptomes. GFFcompare used for annotations of transcripts and FeatureCount used to determine transcript expression levels. DeSeq2 used for graphical summary of datasets.
- o **Epigenomic Analysis:** ChIP-seq data analysis prepared using FASTQ and aligned using BWA to reference genome. MACS2 CallPeak used on output BAM file and loaded into IGV for visualization of epigenetic modifications on genome.

Animal Adoption Center Database

- o Used **MySQL** to design and implement a relational database
- o Implemented advanced database features such as stored procedures, triggers, and views
- o Database used to track animals, adopters, employees, donors, and other data fields to be used by an animal adoption company

Microarray Data Analysis Pipeline

- o Developed a data analysis pipeline for Affymetrix microarray data using R
- o Outlier filtering, feature selection, principal component analysis, classification and differential gene expression analysis.