

Steven R. Dea

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: May 2020

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

Skills

Technical

Java, Python, C++, R, SQL, Relational Databases

Bioinformatics Tools

Multi-omic data analysis and visualization (Genome, Proteome, Transcriptome, Epigenome), Microarray data analysis and visualization, Phylogenetic analysis, Gene prediction

Cell Culture

iPSC/NPC culturing, Immunofluorescence microscopy, Flow cytometry, qPCR, HTS, FLIPR, MEA, ImageXpress

Experience

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
- o Performed large compound screenings and data analysis to characterize and validate novel 3D model
- o Directed training of new hires and interns

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

Proteomic Investigation of a novel variant

- o Comparisons between normal and variant R195K of CACNA1A gene using various proteomic analysis techniques.
- o Basic physical properties, hydropathicity, coil prediction, secondary and tertiary structure prediction and their effects on normal vs. variant protein function.

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

Python HTS data analysis and visualization

- o **Python:** script to import data from csv files
- o **NumPy:** transform data sets and provide aggregates of replicates
- o **Pandas DataFrames:** Generate summary statistics on aggregates
- o **Matplotlib:** generate graphs for visualization

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.