

# Adaptive results visualization of sequences

## ARVoS

William Montgomery  
Gareth Halladay  
Anela Tosevska  
Frank Burkholder  
Adam Richards  
Andrew Gaines

May 2017

# What is ARVoS?

Adaptive results visualization of sequences (ARVoS)

## Motivation

A dockerized database and flask template for presentation of RNAseq results

<https://github.com/NCBI-Hackathons/arvos>

# Principal Objectives

## Motivation

- ① Create a dynamic and interactive results display environment (Flask)  
(Anela, Frank, William)
- ② Create an environment that encourages model comparison (Gareth, Adam)
- ③ Dockerize (Andrew)

# Pipeline

```
from arvos import Pipeline

results_dir = os.path.join(".", "results")
pline = Pipeline(results_dir)
countsPath = os.path.join(parentDir, "data", "est_counts.csv")
filteredCountsPath = pline.create_filtered(countsPath)
pline.run_deseq(filteredCountsPath, outFile)

deseq_file = os.path.join(results_dir, "deseq.csv")
deseq_matrix_file = os.path.join(results_dir, "deseq-samples.csv")
targets_file = os.path.join(".", "data", "targets.csv")

X, y = pline.generate_features_and_targets(deseq_file, deseq_matrix_file,
                                           targets_file)
```

# Demo

<http://54.213.27.230>

# Where do we go from here?

- More interactive plots for RNA-Seq
- Better Generalize for results versions
- Finish Pieris (Manuscript Supplement)
- Finish the Asthma (Manuscript Supplement)
- Docs in the style of PyMC3
- Blog post
- Publish as an application