

Adaptive results visualization of sequences

ARVoS

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

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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)

Node and edge attributes

```
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