Adaptive results visualization of sequences ARVoS

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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)

Node and edge attributes

```python
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