grape.pipeline.runner Documentation

Release 1.0

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Grape (Grape RNA-Seq Analysis Pipeline Environment) is a pipeline for processing and analyzing RNA-Seq data developed at the Bioinformatics and Genomics unit of the Centre for Genomic Regulation (CRG) in Barcelona.

The grape.buildout packages installs the command line tools of the grape.pipeline.runner package for automatically running your configured pipelines.

To learn more about Grape, and to download and install it, go to the Bioinformatics and Genomics website at:

Grape Homepage

Note: The grape.pipeline.runner package is a Buildout recipe used by grape.buildout, and is not a standalone Python package. It is only going to be useful as installed by the grape.buildout package.

MOTIVATION

Here at the CRG, we configure all our RNASeq pipeline runs in a central place before running the Grape pipelines. Once all the accessions and pipeline profiles have been defined and the buildout parts have been created, we start and execute them.

When we receive Fastq or bam files for a project, we typically have to:

1. Define the accessions and profiles in:

    ```
    grape.buildout/accessions/MyProject/db.cfg
    grape.buildout/profiles/MyProject/db.cfg
    ```

2. Create a pipeline project folder in:

    ```
    grape.buildout/pipelines/MyProject
    ```

3. Configure the buildout in:

    ```
    grape.buildout/pipelines/MyProject/buildout.cfg
    ```

4. Run the buildout in:

    ```
    grape.buildout/pipelines/MyProject
    ```

5. Run the pipeline with the console script:

    ```
    cd grape.buildout/pipelines/MyProject
    ./bin/grape-runner
    ```

The grape.pipeline.runner package installs the grape-runner console script that is used in step number 5. The buildout uses the recipe to produce the individual pipelines and preconfigure the start and execute scripts with all the necessary command line options, used by the grape-runner console script.

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