**RegAnnotator v1.0**

**Introduction**

This program is part of a pipeline that is used to analyze metagenomic samples. This script merges different files showing the depth of coverage, breadth of coverage and the regions covered for different organisms identified in a sample into a summary file showing all three along with the genes that correspond to the regions from different organisms as shown in their GFF files downloaded from NCBI.

**Requirements**

This bash script uses **python v2.7.15** with the following python libraries installed:

* argparse==1.1
* bcbio-gff==0.6.4
* bio==0.1.0
* collections
* csv==1.0
* ftputil==3.4
* glob
* itertools
* os
* re
* shutil
* subprocess
* urllib==1.25.6

Some of the packages mentioned above are inbuilt in python27.

**Sample Usage**

Download Annotator-master.zip from <https://github.com/GayathriRajan/Annotator>

Unzip the file and run

cd regAnnotator-master/

bash reg\_Annotator\_v1.0/regAnnotator.sh

bash reg\_Annotator\_v1.0/regAnnotator.sh -s test -d reg\_Annotator\_v1.0/

Check for result files test/test.sum, test/test\_region.sum

**Input**

test.cov: breadth of coverage file for all organisms identified

test.b.sum: depth of coverage file for all organisms identified

test.gt4c: individual regions for all organisms identified

**Output**

test.sum:

summary file showing depth of coverage, breadth of coverage, regions and their corresponding genes for all organisms identified

test\_region.sum

summary file showing individual regions with depth and gene information for all organisms identified

**Output**