1. Program

Program : Executing the ANNOVAR package

Program Version : 0.1a

Author : Ryan

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Development Language : python 2.7 (it should be compatible to all 2.Xs)

Filename : runAnnovar.py

2. Introduction

ANNOVAR is an efficient software tool to utilize update-to-date information to functionally annotate genetic variants detected from diverse genomes

http://www.openbioinformatics.org/annovar/

3. How to run

Usage: python runAnnovar.py [options]

Options:

-h, --help show this help message and exit

-i FILE VCF input files

-t ANNOTATIONTYPE annotationType : gene, region, filter (default Gene-

based)

-d DBDIR Directory that the database are written to

-b DBTYPE Datebase type

-r REFERENCE Reference i.e., hg19, hg18, (default hg19)

-g GFFDB dff3db file, it is required when dbType is gff3

4. Testing