snpFC Documentation

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CHAPTER 1

Introduction

snpFC - a python tool for filtering and comparing SNPs from two or multiple VCF files.

CHAPTER 2

How can I get it

At the moment, latest snpFC tool can be obtained from github repo link . Just clone the repository or download as a compressed file.

I have a target to upload snpFC to python repository enabling to install using pip command.

CHAPTER 3

Pre-requisites

Assuming you have python3 already, install pyVCF

```
pip install pyvcf
```

CHAPTER 4

Quick Start

If you don't have patience, here is how to run snpFC

```
python scripts/filter_and_comparesnps.py --vcf testfiles/test1.vcf testfiles/test2.
↪vcf --filter --compare --show --frequency 70 --pvalue 0.05 --genotype heterozygous -
↪-quality 10 --rawreaddepth 5 --qualityreaddepth 5 --depthreference 5 --depthvariant␣
↪5 --outdir ./testfiles
```

The above command will output as following

```
Common and Unique SNPS in vcf File :  testfiles/test1.vcf
tig00000003 775 A G common
tig00000003 776 T C common
tig00000003 836 G C unique
tig00000004 1166 G A common
tig00000004 1190 G A unique
Common and Unique SNPS in vcf File :  testfiles/test2.vcf
tig00000003 775 A G common
tig00000003 776 T C common
tig00000003 836 G T unique
tig00000004 1166 G A common
tig00000004 1190 G A,C unique
The outputs are saved in these files : /home/shrestha/Sites/test1_snpanalysis.txt /
↪home/shrestha/Sites/test2_snpanalysis.txt
```

CHAPTER 5

Options

Available options:

```
--vcf                   space separated two or more vcf files
--filter                filter snps
--compare               compare snps between vcf files
--frequency             frequency threshold value to filter (default: 70)
--pvalue                pvalue threshold value to filter ( default: 0.05)
--genotype              genotype to filter (default: heterozygous)
--quality               genotype quality threshold to filter (default: 10)
--rawreaddepth          raw read depth threshold to filter (default: 5)
--qualityreaddepth      quality read depth threshold to filter (default:5)
--depthreference        depth in reference threshold to filter (default:5)
--depthvariant          depth in variant threshold to filter (default:5)
--show                  show the compared snps on screen
--outdir                output directory
```

To check the options:

```
python scripts/filter_and_comparesnps.py --help
```

5.1 Modules

5.1.1 filter_and_comparesnps

5.1.2 vcfFilter

5.2 Contributions

The project is contributed by Dr Dan Maclean and Dr Ram Krishna Shrestha

The project is supported by Gatesby Foundation.

5.3 Contact

For help, please contact ram_krishna.shrestha@tsl.ac.uk

CHAPTER 6

Indices and tables

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