
snpFC Documentation

Release 0.0.1

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Feb 25, 2019

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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
tig000000003 775 A G common
tig000000003 776 T C common
tig000000003 836 G C unique
tig000000004 1166 G A common
tig000000004 1190 G A unique
Common and Unique SNPS in vcf File : testfiles/test2.vcf
tig000000003 775 A G common
tig000000003 776 T C common
tig000000003 836 G T unique
tig000000004 1166 G A common
tig000000004 1190 G A,C unique
The outputs are saved in these files : /home/shrestha/Sites/test1_snpanalysis.txt /
↪home/shrestha/Sites/test2_snpanalysis.txt
```


Options

Available options:

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

To check the options:

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

5.1 Modules

5.1.1 filter_and_comparesnps module

5.1.2 vcfFilter module

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

- `genindex`
- `modindex`
- `search`