

# Auxiliary scripts

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**AgileROHFinder** and **AgileROHFilterer** are designed to be used as part of a pipeline. The first two scripts are designed to show how they can be automated in a Bash script

## AgileROHFinder\_bash\_script.sh

This script highlights how to **AgileROHFinder** can be automated. Rather than manually enter a series of commands to process each file in a folder of VCF data files, this script iterates through the files, and instructs **AgileROHFinder** to save the regions data to a file with the same name as the input file, but with a 'txt' file extension.

The scripts command line structure is:

```
bash /script/AgileROHFinder_bash_script.sh /program/AgileROHFinder.exe /data/Files/ format
```

### Where

- /script/AgileROHFinder\_bash\_script.sh: the name with location of this bash script
- /program/AgileROHFinder.exe: the name and location of the program to use
- /data/Files/: the name and location of the folder of the VCF files (the script expects the file extension to be lower case 'vcf')
- format: The format of the regions file (**-a**, **-t** or **-b**). If you wish to process SNPs without an RS id, the **-Y** option could be combined by adding the **-Y** option to the format option and putting them all in speech marks i.e. "**-t -Y**". Note space between the **-t** and the **-Y**.

## AgileROHFilterer\_bash\_script.sh

Like the previous script this script shows how to **AgileROHFilterer** can be automated. This script iterates through the files, and instructs **AgileROHFinder** to save the regions data to a file with the same name as the input file, but with a 'txt' file extension and save the filtered variants to a file with the same name as the input VCF file, but with 'filtered' inserted before the file extension. As before the format option can be modified to include the **-Y** option to process SNPs without an RS id.

The scripts command line structure is:

```
bash /script/AgileROHFilterer_bash_script.sh /program/AgileROHFinder.exe /data/Files/ format
```

### Where

- /script/AgileROHFilterer\_bash\_script.sh: the name with location of this bash script
- /program/AgileROHFilterer.exe: the name and location of the program to use
- /data/Files/: the name and location of the folder of the VCF files (the script expects the file extension to be lower case 'vcf')
- 500000: any positive integer by which the autozygous regions are extended to include variants close to the regions
- format: The format of the regions file (**-a**, **-t** or **-b**). If you wish to process SNPs without an RS id, the **-Y** option could be combined by adding the **-Y** option to the format option and putting them all in

speech marks i.e. "-t -Y". Note space between the -t and the -Y.

## p\_FindCommonRegions.py script

Neither program attempt to combine the results of two are more analysis to identify common autozygous regions. This python script will attempt to read all the text files (\*.txt) created by **AgileROHfinder** or **AgileROHFilterer** with the -t format option in a folder and identify the location of the autozygous regions and then create a minimum list of regions present in all the files. Since the analysis files could originate from different data types and different families with a similar phenotype, the script makes no attempt to match the haplotype of common regions. Similarly, it does not exclude regions present in unaffected relatives as they may be autozygous for a different haplotype.

### Note

The folder should only contain results files: If other text files are present the script will attempt to read then and probably crash as they will not contain the expected data/format.

The scripts command line structure is:

```
python /script/p_FindCommonRegions.py /data/ResultFiles/
```

### Where

- /script/p\_FindCommonRegions.py : the name with location of this python script
- /data/ResultFiles/: the name and location of the folder of the txt files (the script expects the file extension to be lower case 'txt')