

# Auxiliary scripts

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## example\_bash\_script.sh

**AgileROHFinder** and **AgileROHFilterer** are designed to be used as part of a pipeline, consequently, this script highlights how **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 script's command line structure is:

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

### Where

- /script/example\_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**.

## p\_FindCommonRegions.py script

Neither program attempts to combine the results of two more analyses 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 them and probably crash as they will not contain the expected data/format.

The script's 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')

