AgileROHFinder and AgileROHFilterer

Command line applications for the detection of autozygous regions from Exome or Affymetrix microarray SNP data.

Data format

AgileROHFinder identifies autozygous regions using genotype data formatted as either VCF files or older Affymetrix xls or birdseed text files. Similarly, AgileROHFilterer will process a VCF file (but not microarray genotype data), creating a second VCF that only contains variants within the autozygous regions. The format and required fields of the VCF and microarray input files is described here.

Note:

> These programs will only analyse one patient per file, if a file contains data on multiple individuals only one person will be analysed.

Creating the programs

The source code can be compiled on both Linux and Windows computers as described here.

Prebuild programs

Both programs have been prebuilt for Linux and Windows and placed in the Program folder. Select the appropriate OS version and download the programs (Linux or Windows). Due to the security policies of some organisations, downloading programs on a Windows computer may not be straight forward, however this guide may help.

Running the programs

These programs are console applications and so do not have a user interface. They run within a terminal environment. On Linux this will typically be in a bash terminal while on windows it will be a "Command Prompt" or "PowerShell" terminal. If the analysis is preformed on a remote server the application would typically be run from the inbuilt bash terminal on Linux or Mac or on windows via a third party terminal such as Putty. In both cases they connected to the remote server via an SSH connection.

The examples below use the Linux file structure were /data/in.vcf refers to a file in the "data" folder, the equivalent on Windows would be "C:\data\in.vcf".

Helpful scripts

The Program > scripts page contains a python and bash scripts that may be helpful.

Commands

Both programs require very similar commands, the structure of the commands to run `AgileROHFinder` and `AgileROHFilterer` are shown below and described in greater detail in the table.

`AgileROHFinder`

```
/path/AgileROHFinder.exe /data/in.vcf /data/out.txt -t
```

`AgileROHFilterer`

```
/path/AgileROHFilterer.exe /data/in.vcf /data/out.vcf /data/out.txt 500000 -t
```

Note

> If a folder or file name contains a space the file name and its location must be placed in speech marks i.e /my data/my file.vcf should be entered as "/my data/my file.vcf"

Table 1: Description of command parameters and options

Command fragment	Description	Note
/path/AgileROHFinder.exe or /path/AgileROHFilterer.exe	Name of the program with it's location	
/data/in.vcf	The name (with location) of the data file to process.	`AgileROHFilterer` will only process vcf files while `AgileROHFinder` will process vcf files and Affymetrix microarray genotype files
/data/out.vcf	Name of a file to save the filtered variant data too.	This option is only present in `AgileROHFilterer` While it will create this file, it will not create any directories, so the path to the location most exist before the program is run.
/data/out.txt	The name with location of the file to save the list of autozygous regions too	While it will create this file, it will not create any directories, so the path to the location most exist before the program is run.
Any whole positive number	The reported regions are be extended by this number of bases when `AgileROHFilterer` filters the variants by position, such that variants just outside a region are also retained	This option is only present in `AgileROHFilterer`
Export format options **-t**, **-b** or **-a**	Sets the format of the data results file	See Tables 2 to 4 for examples

Command fragment	Description	Note
Process all variants: **-Y**	By default only variants with an RS ID are processed, if **-Y** is set then all SNPs (with one alternative allele) will be used	Optional: only affects analysis of VCF data
Use genotypes in VCF file: **-V**	By default a variants genotype is calculated by the program, if **-V** is set the genotype in the VCF file is used (The file most have the 'GT' field)	Optional: only affects analysis of VCF data

Table 2

Autozygous regions output file format: Option -t (columns separated by tab character)

```
Chromosome  Start    End Length
2   25656880    29092679    3435799
2   179421694   180835792   1414098
2   182374534   189875421   7500887
11  48367050    55111584    6744534
17  21318629    26691321    5372692
```

Table 3

Autozygous regions output file format: Option -b (Each line can be entered in to the UCSC genome browser)

```
chr2:25656880-29092679
chr2:179421694-180835792
chr2:182374534-189875421
chr11:48367050-55111584
chr17:21318629-26691321
```

Table 4

Autozygous regions output file format: Option -a (Contains both formats)

```
Tabular data
Chromosome  Start    End Length
2   25656880    29092679    3435799
2   179421694   180835792   1414098
2   182374534   189875421   7500887
11  48367050    55111584    6744534
17  21318629    26691321    5372692

Genome browser
chr2:25656880-29092679
chr2:179421694-180835792
chr2:182374534-189875421
chr11:48367050-55111584
chr17:21318629-26691321
```

Feedback

As the programs run, the current status will be shown in the terminal window.

A successful analysis:

Figure 1: `AgileROHFiinder`

```
msjimc@login1.arc4:~/myPrograms/AgileROH
Reading data file CHRNG-6.vcf
Including SNPs without RS ids
Calculating genotypes
Saved 34261 SNPs and rejected 617 SNPs
Processing data
Created homozygous run data
SNP counts per chromosome
3429    on 1
2236    on 2
1811    on 3
1287    on 4
1536    on 5
2315    on 6
1606    on 7
1192    on 8
1413    on 9
1454    on 10
2480    on 11
1805    on 12
547     on 13
1160    on 14
1076    on 15
1566    on 16
2158    on 17
561     on 18
2329    on 19
980     on 20
414     on 21
860     on 22
Completed task
(base) [msjimc@loginl.arc4 AgileROH]$
```

Figure 2: `AgileROHFilterer`

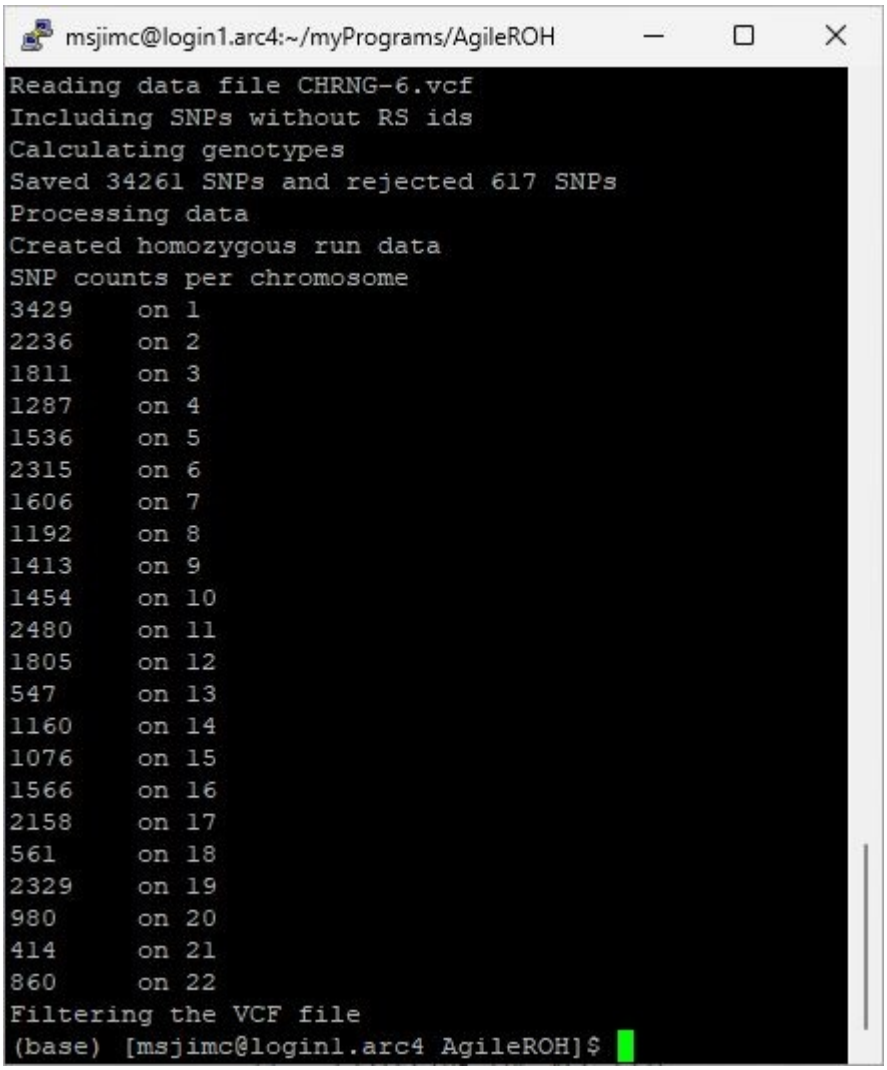


Figure 1

Figures 1 and 2 show a typical status report of the analysis of a exome vcf file by `AgileROHFinder` and `AgileROHFilterer` respectively where only variants with an RS id were used and their genotypes were calculated by the programs.

Output description:

- Initially, the program states which file is being process.
- Next it states whether it will process variants without an RS ID. "*Including SNP without RS ids*" indicates it will process all variants, while "*Ignoring SNP without RS IDs*" indicates unnamed variants will be excluded.
- The program that declares whether it is calculating the genotypes from the allele read depths (Calculating genotypes)or using those in the VCF file (Using genotypes in VCF file (No validated in paper)): Using genotypes in the VCF file was not validated in the linked paper.
- Once the file has been read, the program displays the number of SNPs saved and the number rejected. Only single base SNPs on the autosomal chromosomes are counted with the main reasons for a variant being rejected are low total read count or skewed allele read ratios.
  (Issues with the file format may also cause the SNPs to be rejected, in this case an excessive number or all the SNPs may be rejected.)
- Next the program states that it is analysing the SNP data to find autozygous regions ("*Processing data and finding autozygous regions*") followed by "*Created homozygous run data*" when the analysis is

completed.

- The next 23 lines form a table of the number of SNPs analysed on each autosomal chromosome. Typically, the number of variants depends on the length of the chromosome and for exome data the number of genes on the chromosome.
- Finally, `AgileROHFilterer` will state "*Filtering the VCF file*" indicating it is creating the results files. Since `AgileROHFinder` does not filter the variants, it just states "*Completed task*".

Failed analysis

Wrong input file name

Figure 3: Wrong input file

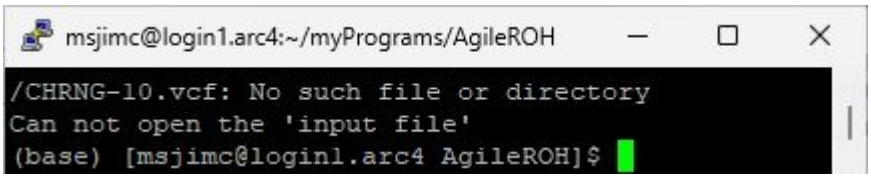


Figure 3: Feedback if the input file is incorrectly entered. A similar message will be displayed if the program can not open the file because it is open for editing in another program or you don't have permission to write to the file.

Trying to export data to a folder that doesn't exist

Figure 4: Folder does not exist

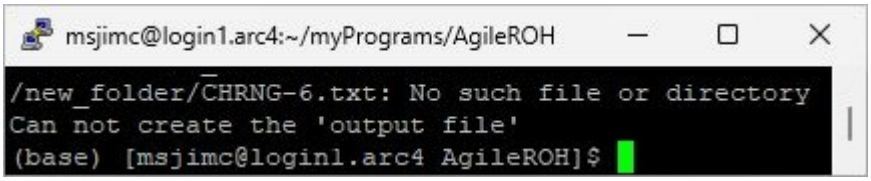


Figure 4: Feedback if the folder the export file is to be saved in does not exist. The programs can create results files, but will not create folders/directories.

The input data file's extension is not recognised

Figure 5: Unrecongised file extension

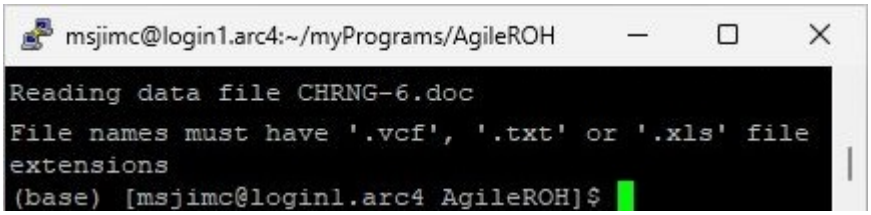


Figure 5: Feedback if the input file does not recognise the file extension. While Linux itself does not use file extensions, these programs do use them to decide what type of data file is being used. If the file extension is not '.vcf', '.txt' or '.xls' the program will not process them.

The input data file's extension does not match the data type

Figure 6: Wrong file extension

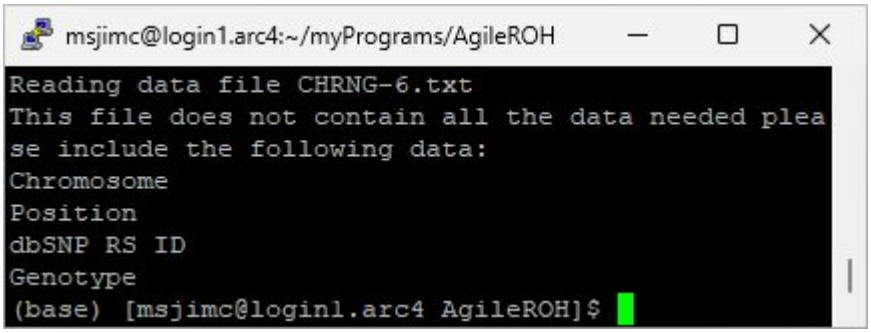


Figure 6: Feedback if the input file's extension does not match it's format. In this case the file is a vcf file, but its extension has been changed to txt. Consequently, the program tries to processed it as a microarray file and found that it does not contain the expected data fields/columns.

The input data file does not contain all the required data fields/columns

Figure 7: Missing data fields

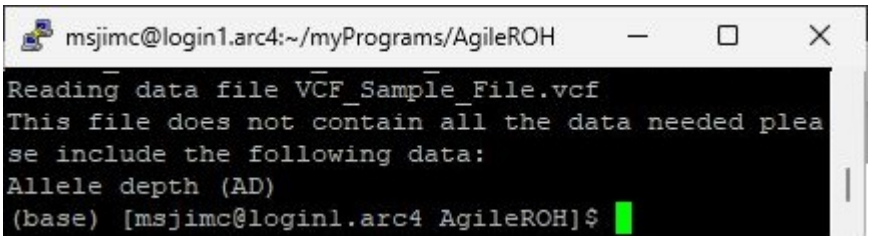


Figure 7 shows the program feedback if input file does not contain the expected data fields/columns. In this case the vcf file contains the total read depth value for each variant, but not the read depths for each allele.

The input data file's format is completely wrong

Figure 8: Wrong totally file format

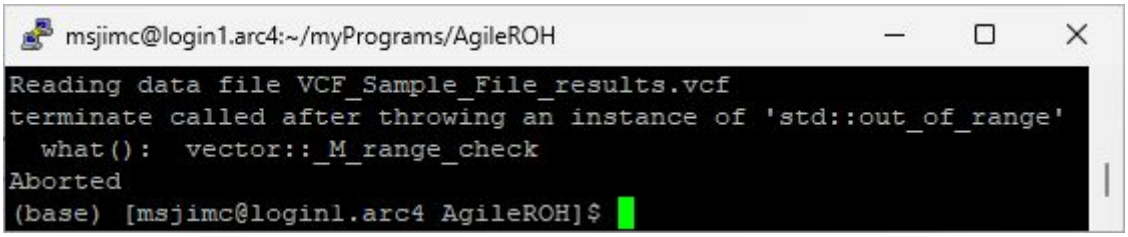


Figure 8: Feedback if the input file format is totally wrong and the program crashes reading it. In this case a results text file was given a vcf file extension and then entered as a vcf data file. The program as attempted to read data that does not exist and crashed. This will create a cryptic error message, if the problem persists after checking the files format, you may need to contact me.

Note

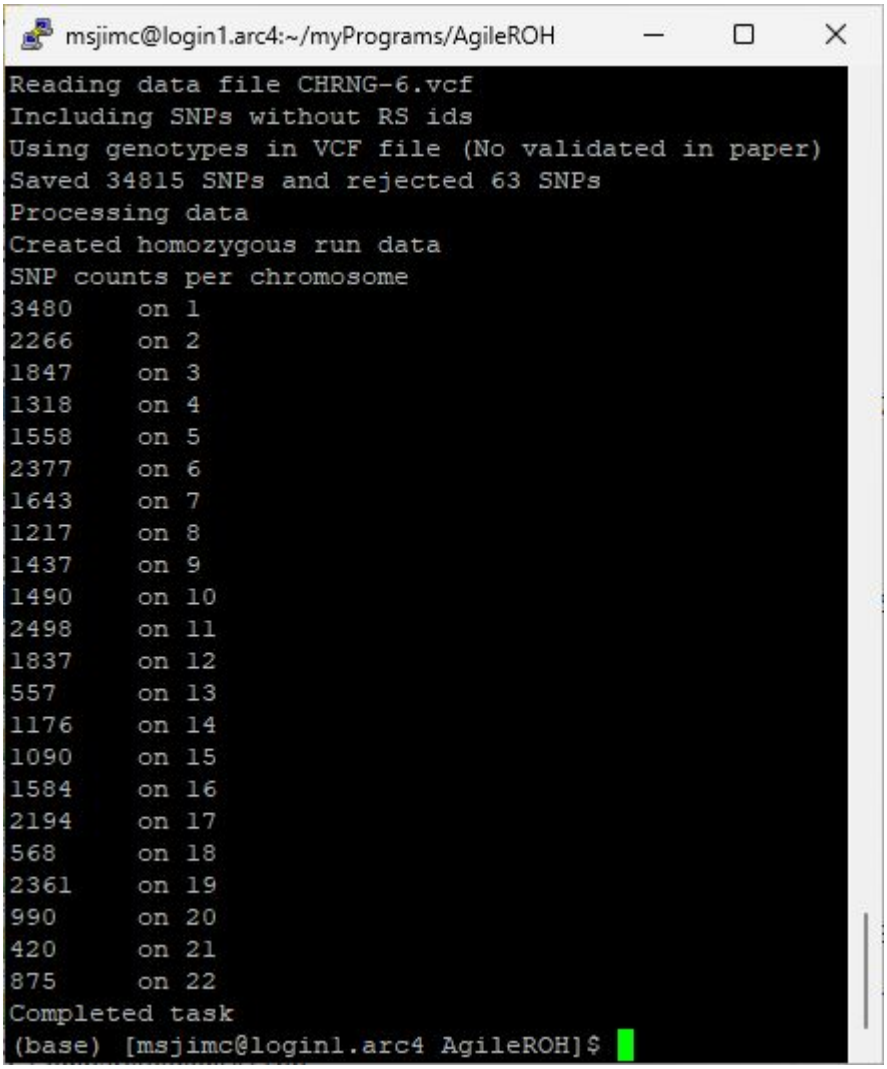
There are many ways in which the input data or command line arguments lead the analysis to fail. While the commonest reasons have been listed above its possible that some combinations of input data format and

command options will result in unexpected behaviour. In these cases always check that the file format matches the expected format as listed on the data format page.

Identifying regions in VCF files without read depth data

While many VCF files include read depth data for each variant, some VCF files do not. To allow the processing of this data, it is possible to instruct the programs to ignore read depth data and use the genotypes in the VCF file. In these cases the VCF file must contain the '**GT**' field and have have the genotypes declared as 0/0, 0/1, 1/0 or 1/1. Figure 9 shows the feedback of the analysis by `AgileROHFinder` with the optional **-V** used to set this behaviour.

Figure 9: Use of genotypes in VCF file



The results from this type of analysis was not investigated in the paper and so it is not supported. The quality of the results is highly likely to be dependant on the variant calling software and parameters used in its operation.