

A bioinformatics workflow for detecting signatures of selection in genomic data

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1 Introduction

This selection analysis workflow utilizes genotype data derived from next-generation sequencing (NGS) or high-density microarray (e.g., “SNP chip”) experiments to identify the presence of signatures of selection. The tools used to detect selection are dependent on the selection signature being investigated (Sabeti *et al.*, 2006). The pipeline presented here generates various output files containing within- and between-population selection signatures. The starting point for the analysis is a variant call format (VCF) file of the genotype data and populations of interest (Danecek *et al.*, 2011). Both F_{ST} and Tajima’s D can be calculated from standard genotype data (Weir and Cockerham, 1984; Tajima, 1989). To compute iHS, Rsb and Fay and Wu’s H requires haplotype information, and thus the genotype data must be phased prior to calculation of these statistics (Voight *et al.*, 2006; Gautier and Vitalis, 2012; Fay and Wu, 2000). For phasing, shapeit2 is used, and for imputation impute2 is used (Howie *et al.*, 2009; Delaneau *et al.*, 2013). Furthermore these statistics also require ancestral allele information (Flicek *et al.*, 2012). The pipeline performs phasing if the VCF files do not contain phase information, and then performs ancestral allele annotation. ***** JAMES - IS THIS ONLY TRUE FOR HUMAN DATA? ***** Once complete, the rehh package for R provides a simple interface for implementing EHH-based analyses (Gautier and Vitalis, 2012). Here we have extended rehh to include penalties for gaps that match those used in the original iHS paper (Voight *et al.*, 2006). rehh is used to calculate iHH, iHS, iES and Rsb. To calculate Fay and Wu’s H, a C program, variscan, was utilised (Vilella *et al.*, 2005). The pipeline is implemented in Python, and takes a VCF file as input. The output is a collection of files relating to selection signatures detected by the various software tools.

2 Getting Started

2.1 Prerequisites

The selection pipeline was developed on a 64-bit Ubuntu 13.04 system and has been tested on 64-bit Centos and Ubuntu 13.10 installations. The pipeline should work on any 64-bit linux derivative assuming some basic libraries and tools are installed on the system. 8GB of RAM should be sufficient for all computation steps (imputation is the most RAM-intensive component of the pipeline).

- Python ≥ 2.6
- Bourne-again Shell (Bash)
- Perl5
- R $\geq 3.0.0$ (with the ability to install packages into a library within your home directory structure)
- GNU Autotools
- GCC

The software is installed with the same permissions as the user than runs the script: if the user is not root then a local (i.e., user-writeable) R library is required. The program also installs the scripts to the user’s `./local/bin` directory. This directory should be added to the system PATH to give direct access to the programs from the command-line.

2.2 Python dependencies

The following Python packages are required for the pipeline:

- python-setuptools
- python-numpy
- python-scipy

Most linux distributions provide these packages through the official package management repositories.

2.3 Downloading

The selection pipeline can be obtained at the url: <https://github.com/smilefreak/selectionTools>

For git users the following command will obtain the pipeline:

```
git clone https://github.com/smilefreak/selectionTools
```

Alternatively, wget can also be used:

```
wget https://github.com/smilefreak/selectionTools/archive/master.zip
```

2.4 Installation

To perform an automatic installation of the selection analysis pipeline, run the following command in the root of the directory in which the pipeline was installed (i.e., within the “selectionTools” directory).

```
./install.sh
```

The installation process creates a default configuration file located in the base directory of the pipeline. It also adds a program called selection_pipeline to the system path. To test that the program is installed correctly, run the following command at a terminal prompt.

```
selection_pipeline -h
```

If the above command does not work, make sure that `./local/bin/` is included in the PATH environment variable.

2.5 Genetic Maps and Impute Haplotypes

To use the phasing and imputation features of the pipeline requires both genetic map files and haplotype files. For humans, files that conform to the format required for shapeit and impute2 can be found [here](#). For impute2, one reference is available [here](#). Download and extract the archive to referencefiles/impute_ref and uncompress the contents. For shapeit2, a genetic map can be found [here](#). Download and extract the archive to referencefiles/shapeit_ref.

To use other reference files with the selection pipeline requires setting the following options in the config file. The question mark character “?” in the config is substituted by the chromosome number: this is used for

reference files that are split on chromosomes.

```
...
genetic_map_prefix=genetic_map_chr?_combined_b37.txt
...
impute_map_prefix=genetic_map_chr?_combined_b37.txt
impute_reference_prefix=ALL_1000G_phase1integrated_v3_chr?_impute
...
```

If you decide to store the reference files in another location, further options require alteration in the config file:

```
...
genetic_map_dir= \${HOME}/MerrimanSelectionPipeline/referencefiles/shapeit_ref
...
impute_map_dir= \${HOME}/MerrimanSelectionPipeline/referencefiles/impute_ref
impute_reference_dir= \${HOME}/MerrimanSelectionPipeline/referencefiles/impute_ref
...
```

2.6 Ancestral Fasta Files

The generation of results for iHS requires assigning the ancestral allele. The selection pipeline uses the ancestral alleles from the 6-way EPO (Enredo-Pecan-Ortheus) alignment pipeline. The files can be downloaded from [here](#). Be sure to extract the contents of the archive after download. The default directory to store the ancestral reference files is

```
referencefiles/ancestral_ref/
```

If you downloaded your reference to a different location you can alter the following setting in your config file.

```
...
ancestral_fasta_dir = # directory you downloaded alignment to #
...
```

3 Tutorial

3.1 Selection Signatures at the Lactase Locus

3.1.1 Getting the Data

In humans, lactase is encoded by the LCT gene, which is located on Chromosome 2 at the coordinates: 136,545,410-136,594,750. For this example we will use a 10 megabase region containing the LCT, and genotype data from the CEU and YRI populations from the 1000 Genomes Project. In order to demonstrate the functionality of the pipeline we will use the chromosome 2 region 130,000,000-140,000,000. The lactase gene is an example of strong selection in the last 5,000-10,000 years in human populations, specifically those of European ancestry (Bersaglieri *et al.*, 2004). To download the example dataset enter the following command:

```
wget https://github.com/smilefreak/SelectionPipelineTestData/blob/master/selection_pipeline_tutorial.tar.gz
```

Extract the example data into a new folder.

3.2 Setting up the Pipeline Run

3.3 Population Files

Population files are required for any cross population comparisons. The commands below will initiate the data generation step. Population files are line separated files, where the first line contains the population name, and every successive line contains an individual ID from that population.

```
<POPULATION_IDENTIFIER>
<INDIVIDUAL ID 1>
<INDIVIDUAL ID 2>
.....
<INDIVIDUAL ID N>
```

3.4 Run The Tutorial

The default configuration file is located in the base directory of the selection pipeline. To run the pipeline, execute the command below in the folder in which the example data were extracted, and change the `--config-file` parameter to match the location where the pipeline is installed.

```
multipop_selection_pipeline -p CEU_ids.txt -p YRI_ids.txt \
-i CEU_YRI_lactase.vcf --config-file defaults.cfg \
--fst-window-size 1000 --fst-window-step 1000
```

***** JAMES - I added backslashes to the code above in case people try to paste directly in the command line - good or stupid? *****

The generated folders and current folder have all the data required to perform further selection analysis. Within each population folder four output files are generated. These contain Tajima's D, iHH, an updated VCF, and Fay and Wu's H statistic. The files are located in the results folder inside each population subfolder. F_{ST} is calculated between each population and results are located in the fst folder. F_{ST} results are calculated using the Weir and Cockerham estimator.

3.5 Data Visualisation

The purpose of the analysis pipeline is to generate standard signatures of selection from a VCF formatted input file. In order to assist with exploring/interpreting the results, visualization of the pipeline output can be extremely useful. The next section describes some basic approaches to plotting these data using the R programming language. All of the following commands are run in an R session with the working directory set as the base directory from which the tutorial is being run. In each of the plots that follow, the vertical blue lines indicate the position of the lactase gene (LCT).

3.5.1 Visualizing F_{ST} values

Read in the F_{ST} data:

```
CEUYRIfst=read.table("fst/2CEUYRI.fst", header=TRUE)
```

Plot the F_{ST} results across a region 1 megabase on each side of the lactase gene. Weighted F_{ST} is being plotted in each case.

```
plot(CEUYRIfst[,5]~CEUYRIfst[,2], pch=16, cex=.4, type="p",xlab='',ylab='FST')
rect(136545410,0,136594750,1,border="Blue")
```

Figure 1 shows clustering of high F_{ST} values close to the lactase gene plotting one megabase downstream and upstream either side of the gene.

[*** JAMES - HOW INTERESTING IS THIS? THERE ARE A LOT OF APPARENT SPIKES. :) Also, the axis labels for the graphs could be improved by using the “expression” function in R. Within the plot command, “ylab=expression(F[ST])”, will produce a subscript for “ST”. Also, a label is needed for the x axis (I’d suggest “Chromosome 2, position (bp)”). ***]

3.5.2 Fay and Wu’s H

Plot the Fay and Wu’s H values for the CEU population:

```
CEUFay=read.table('CEU/results/CEU2.faw',comment.char="#")
#Plot Fay and Wu's H
plot(CEUFay[,15] ~ CEUFay[,1],xlim=c(136545410-1e6,136594750+1e6),pch='.',cex=2,
xlab='',ylab="H Statistic")
rect(136545410,-1000,136594750,100,border="Blue")
```

Figure 2 shows the Fay and Wu’s H statistic one megabase downstream and upstream of the lactase gene. Plot the Fay and Wu’s H values for the YRI population:

```
YRIFay=read.table('YRI/results/YRI2.faw',comment.char="#")
#Plot Fay and Wu's H
plot(YRIFay[,15] ~ YRIFay[,1],xlim=c(136545410-1e6,136594750+1e6),pch='.',cex=2,
xlab='',ylab="H Statistic")
rect(136545410,-1900,136594750,100,border="Blue")
```

Figure 3 shows Fay and Wu’s H statistic one megabase downstream and upstream of the lactase gene.

3.5.3 iHS

Plot the iHS values around the lactase gene for the CEU population:

```
CEUihs = read.table('CEU/results/CEUchr2.ihs')
#plot iHS pvalues
plot(CEUihs[,3] ~ CEUihs[,2],xlim=c(136545410-1e6,136594750+1e6),pch='.',cex=2)
rect(136545410,-10,136594750,10,border="Blue")
```

Figure 4 shows iHS pvalues around the lactase gene one megabase upstream and downstream. Plot the iHS

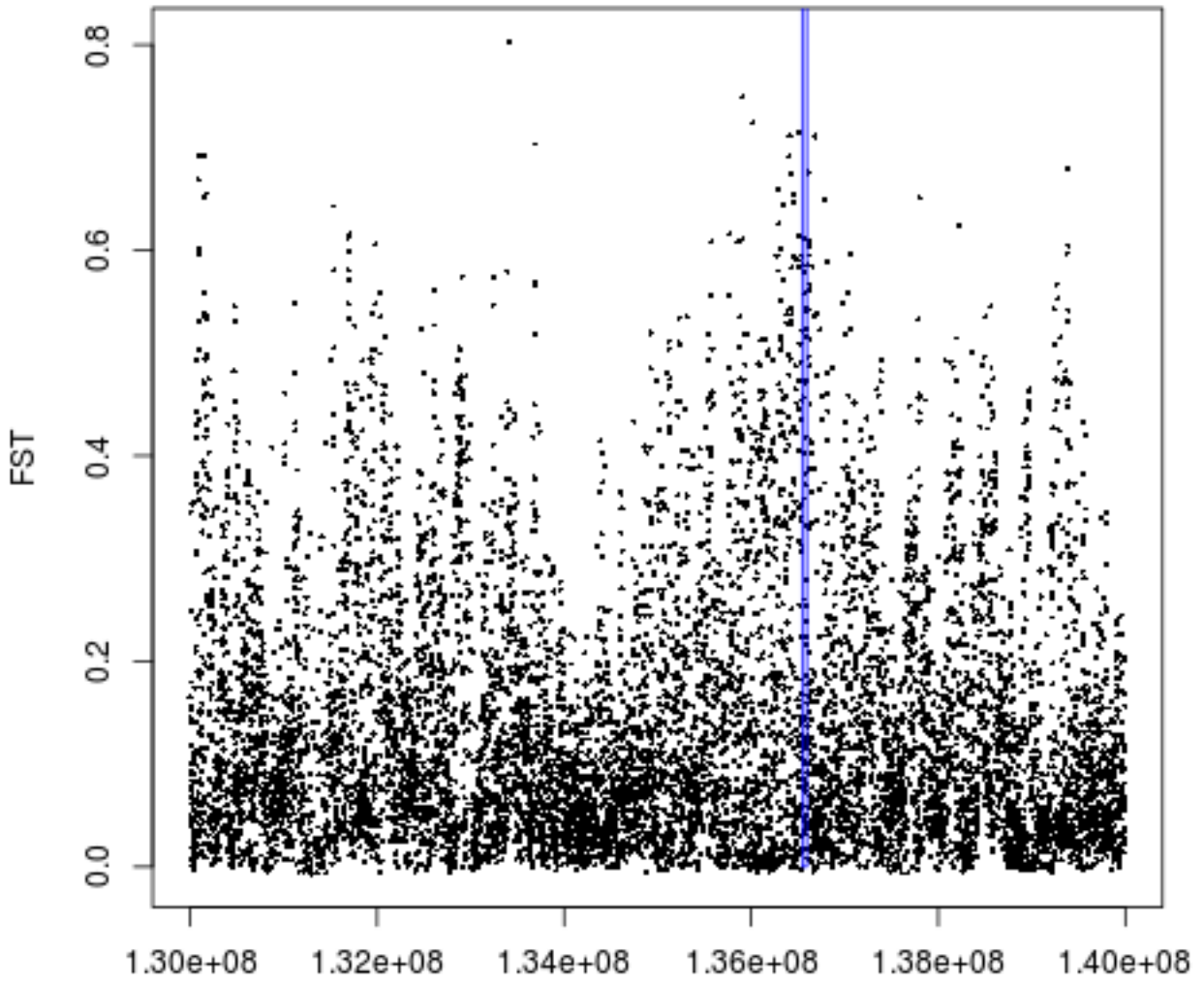


Figure 1: Values of F_{ST} generated for comparing the YRI and CEU populations across a ten megabase region around the LCT gene.

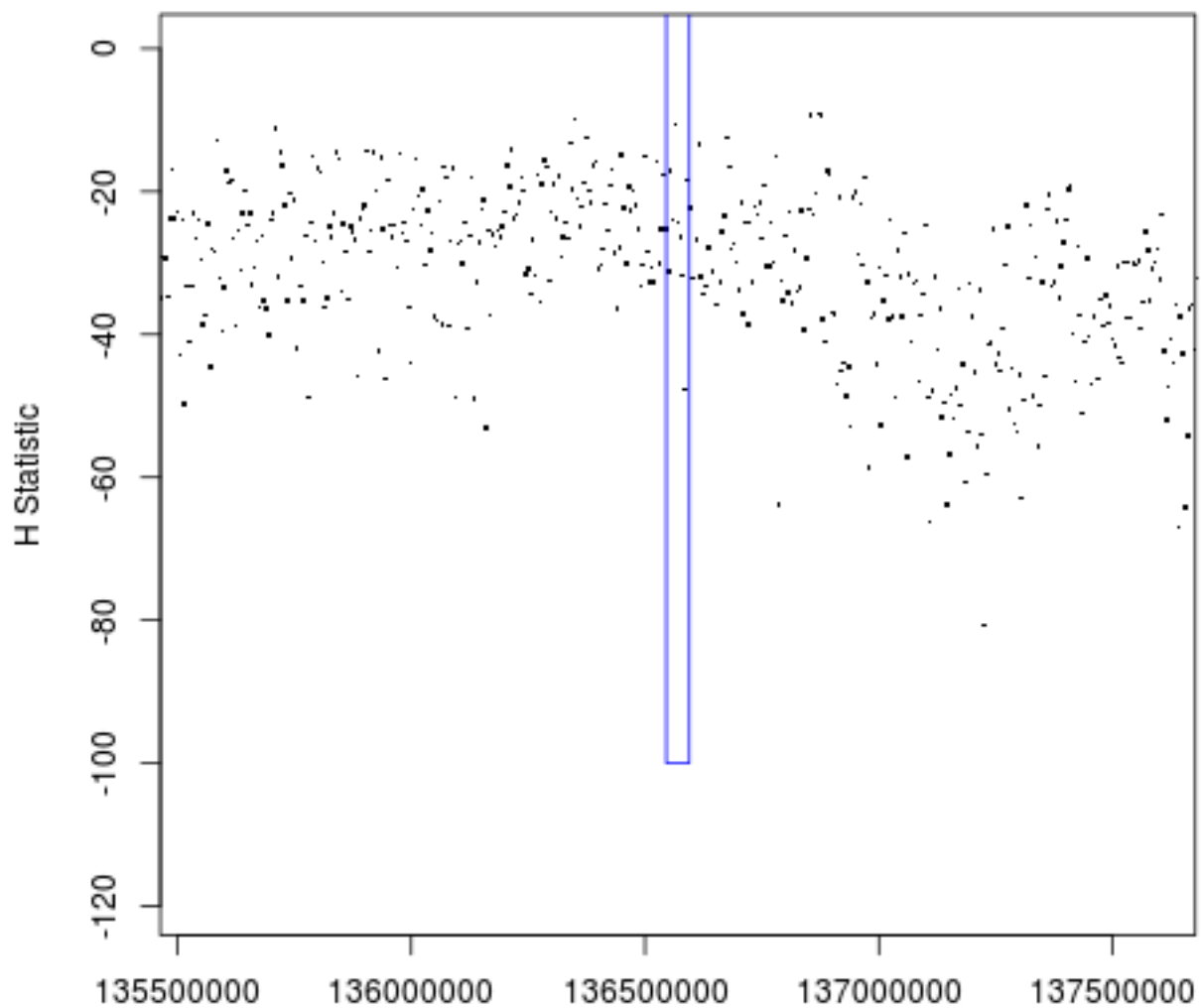


Figure 2: Fay and Wu's H statistic in the CEU population, across a two megabase region around the LCT gene. ***** NEED X-AXIS LABEL. Also, code for plot has blue rectangle extending down to -1000, but figure only has it to -100: need to update figure. *****

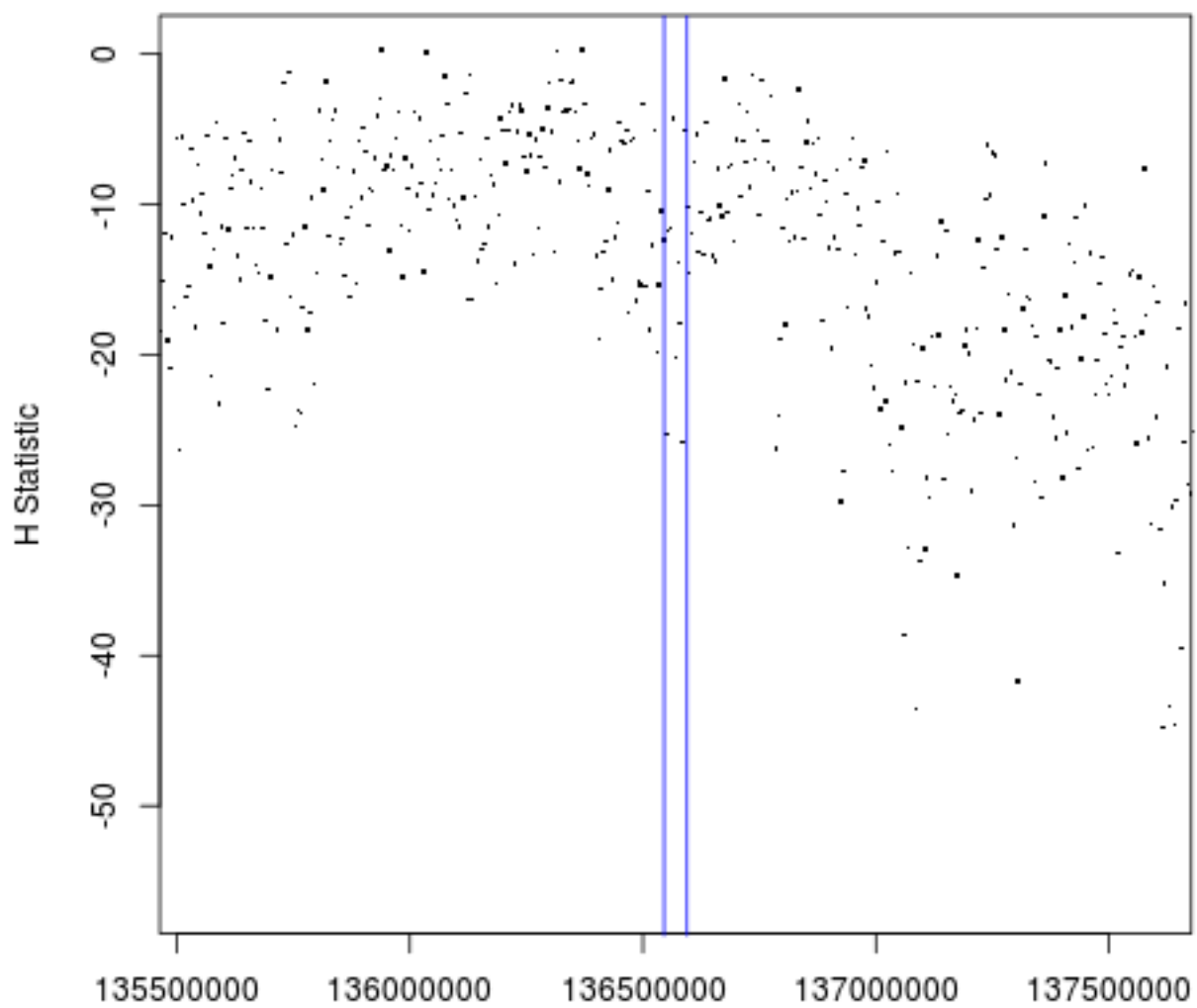


Figure 3: Fay and Wu's H statistic in the YRI population, across a two megabase region around the LCT gene.
 [*** NEED X-AXIS LABEL. ***]

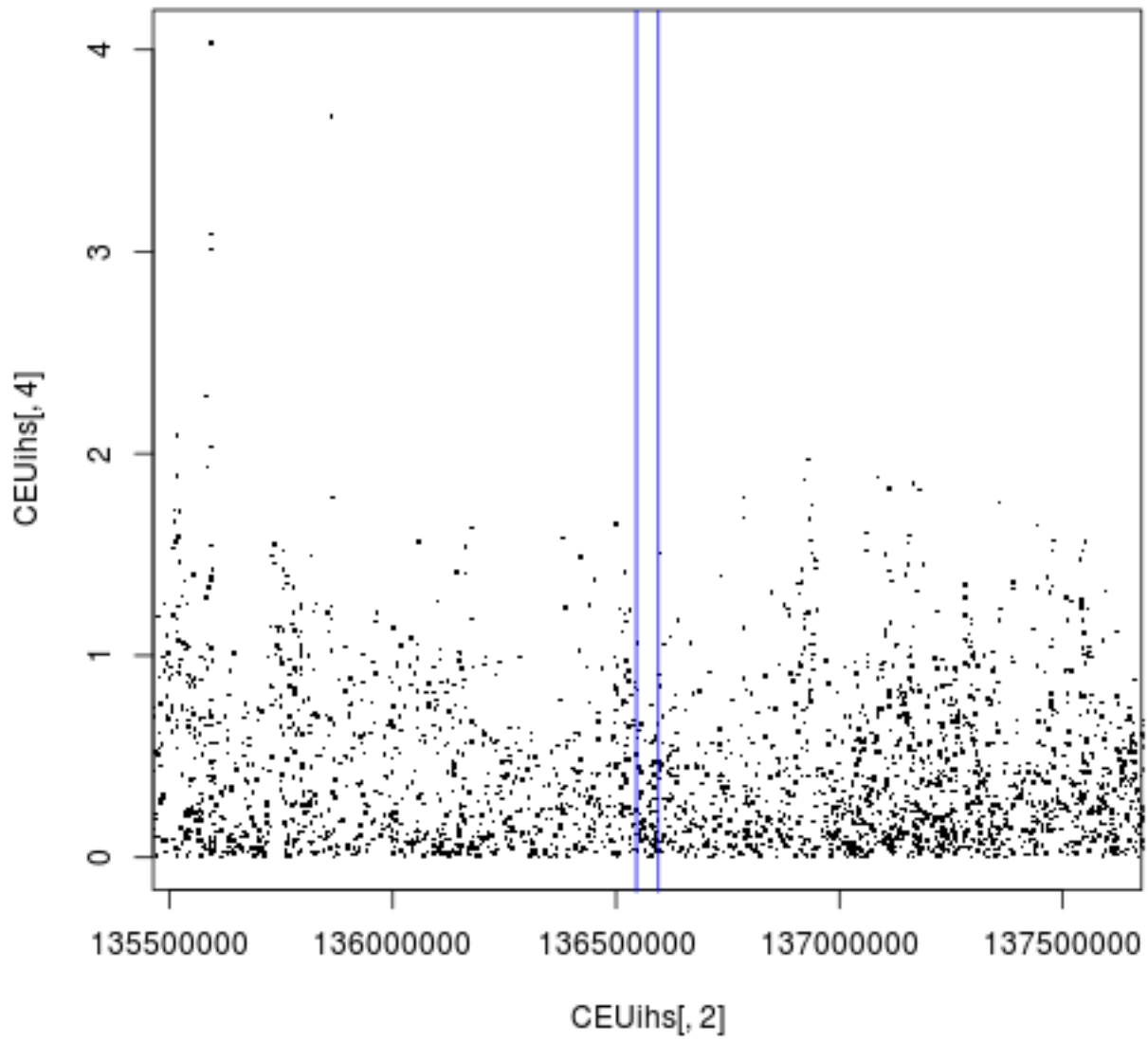


Figure 4: iHS statistic in the CEU population, across a two megabase region around the LCT gene. ***** NEED BETTER AXIS LABELS *****

values around the lactase gene for the YRI population:

```
YRIihs = read.table('YRI/results/YRIchr2.ihs')
#plot IHS pvalues
plot(YRIihs[,3] ~ YRIihs[,2],xlim=c(136545410-1e6,136594750+1e6),pch='.',cex=2)
rect(136545410,-10,136594750,10,border="Blue")
```

Figure 5 shows iHS pvalues around the lactase gene one megabase upstream and downstream.

To visualize individual SNPs, a haplotype bifurcation diagram can be used (Gautier and Vitalis, 2012). The SNP displayed a strong signal of selection using iHS. We construct a bifurcation diagram for both alleles at this SNP.

*** JAMES - STILL NEED CODE FOR THIS (AND A PLOT). :) ***

```
# Plot bifurcation diagram.
```

3.5.4 Tajima's D

```
tajimaD=read.table(file="CEU/results/CEU2.taj_d", header=TRUE)
plot(tajimaD[,4] ~ tajimaD[,2],xlim=c(136545410-1e6,136594750+1e6),pch='.',cex=2)
rect(136545410,-10,136594750,10,border="Blue")
```

Figure 6 show the Tajima's D statistic one megabase downstream and upstream of the lactase gene in the CEU population

```
tajimaD=read.table(file="YRI/results/YRI2.taj_d", header=TRUE)
plot(tajimaD[,4] ~ tajimaD[,2],xlim=c(136545410-1e6,136594750+1e6),pch='.',cex=2)
rect(136545410,-10,136594750,10,border="Blue")
```

Figure 7 show the Tajima's D statistic one megabase downstream and upstream of the lactase gene in the YRI population

3.5.5 Rsb

*** JAMES - WHAT IS HAPPENING HERE? ***



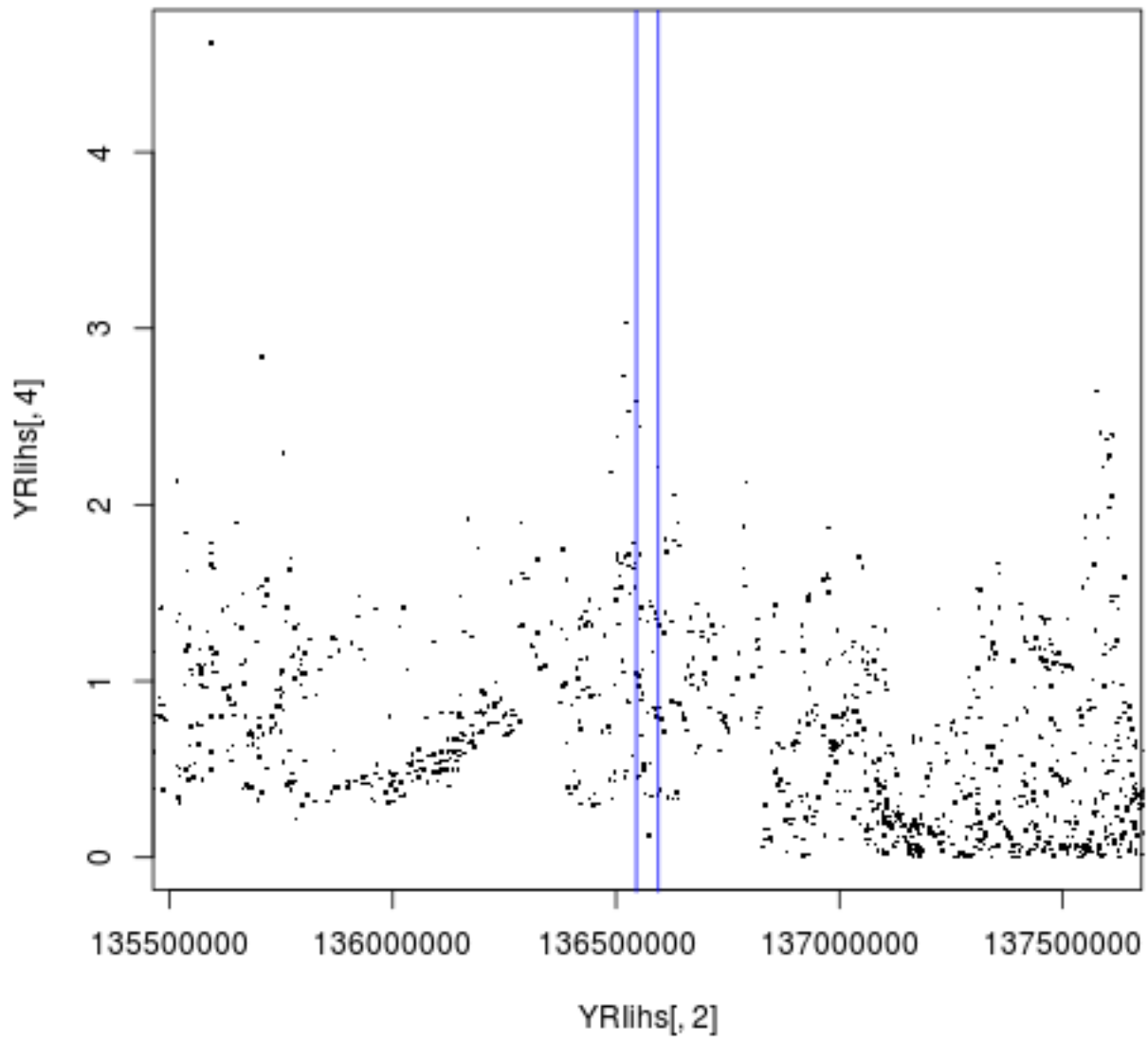


Figure 5: iHS statistic in the YRI population, across a two megabase region around the LCT gene. ***** NEED BETTER AXIS LABELS *****

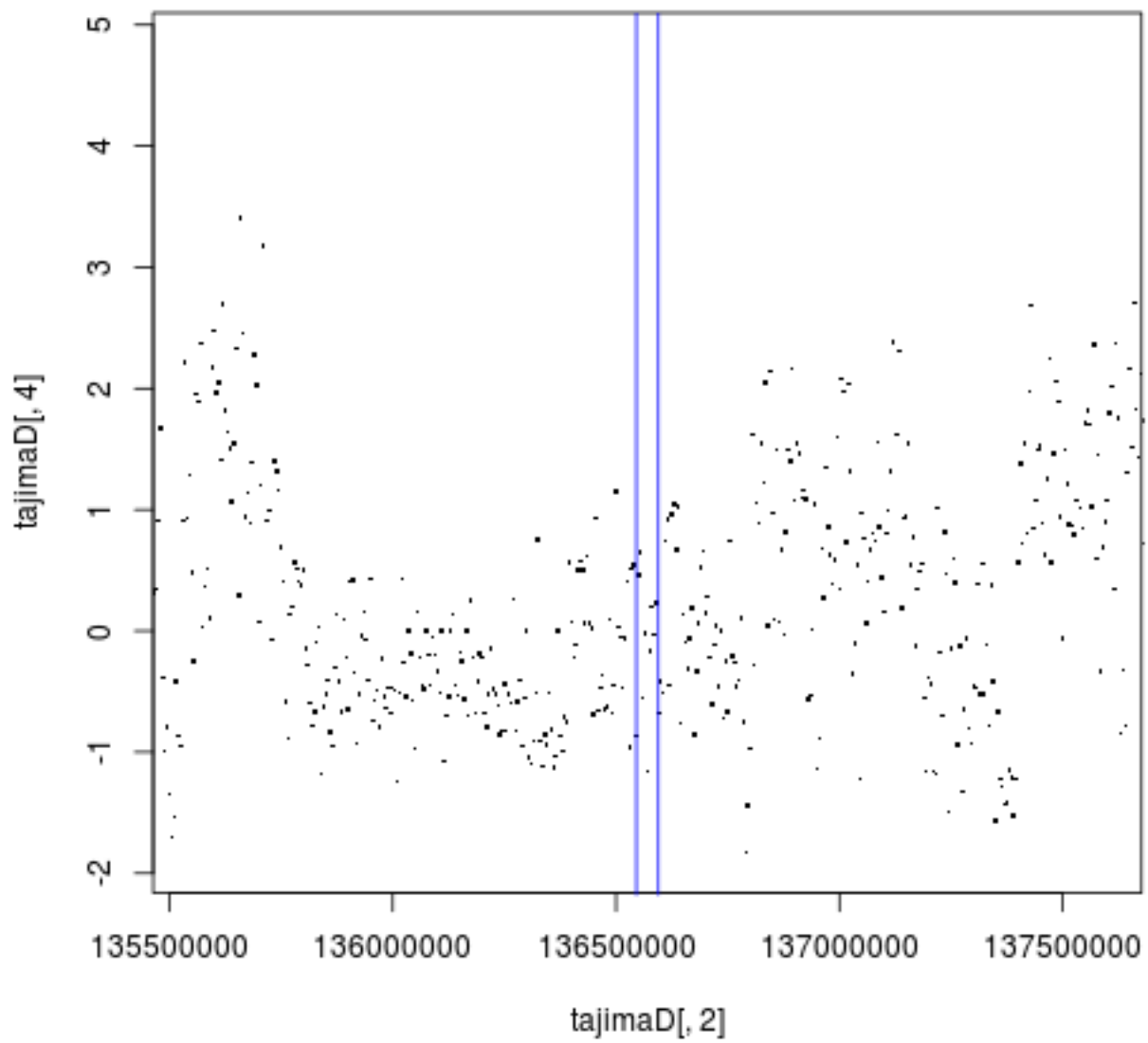


Figure 6: Tajima's D statistic in the CEU population, across a two megabase region around the LCT gene. ***** NEED BETTER AXIS LABELS *****

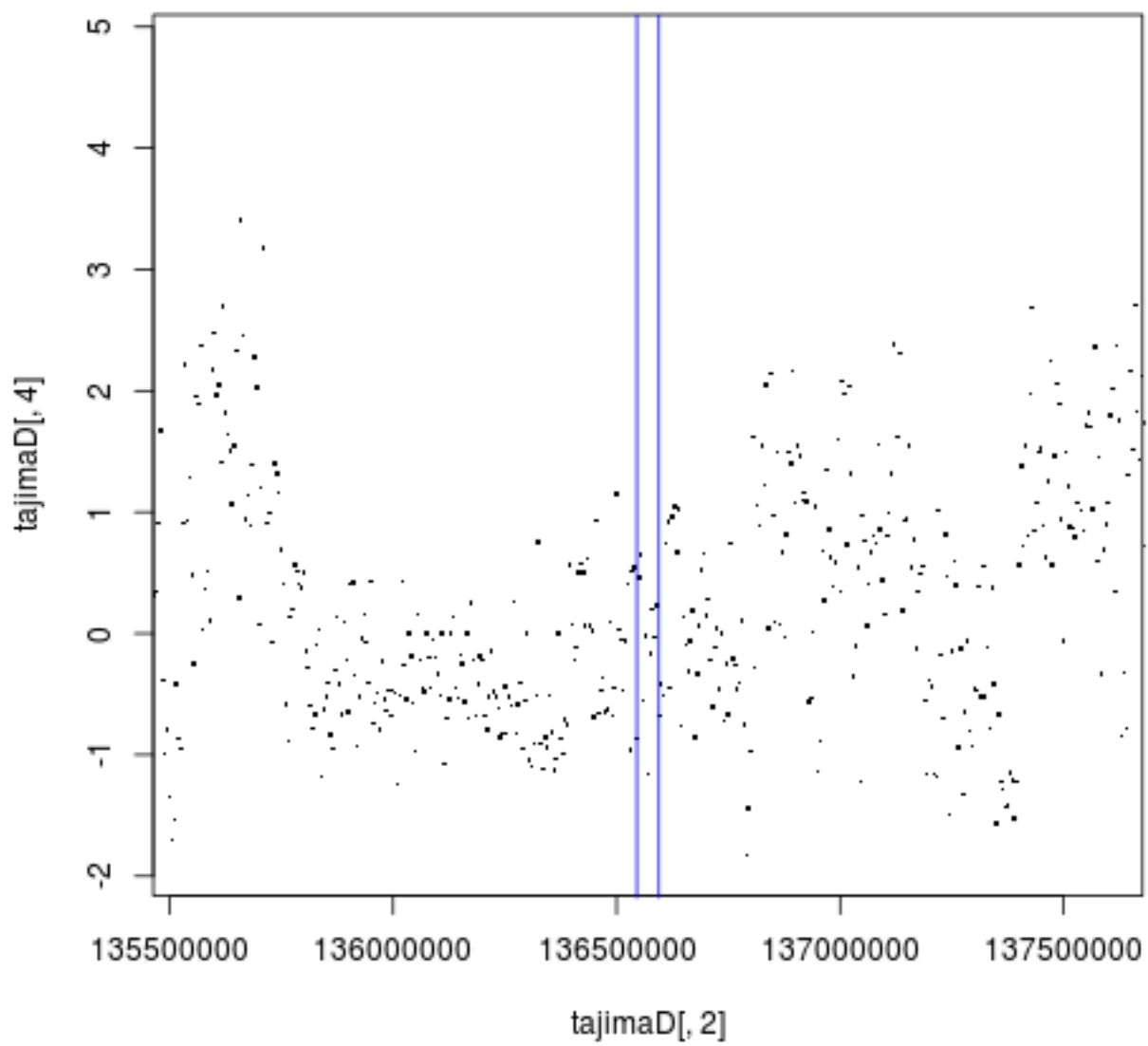


Figure 7: Tajima's D statistic in the YRI population, across a two megabase region around the LCT gene. ***** NEED BETTER AXISLABELS *****

4 Output Files

The output files are preserved in the same state as the original output from the program used to generate the data.

4.1 multi_population

4.1.1 Fst

Located in the fst folder. Tab-delimited data file containing 1 header line followed data on each subsequent line

CHROM	BIN_START	BIN_END	N_VARIANTS	WEIGHTED_FST	MEAN_FST
2	130000001	130010000	94	0.133102	0.0680276

4.2 selection_pipeline

All the outputs for each population are contained in the results folder. If you ran the tool using *multi_population* the outputs are located in <pop name>/results.

4.2.1 Fay and Wu's H

Space-delimited data file containing header line that start with a hash character (#). Contains lots of columns. If you are only interested in Fay and Wu's H, column 1 provides the position and column 15 provides the H statistic.

# RefStart	Refend	...	FayWu_H
130000040	130005039	...	-22.2438460

4.2.2 iHS

Space-delimited data file containing one header line followed by data on each subsequent line.

"CHR"	"POSITION"	"iHS"	"Pvalue"
"rs4662641"	2	130000272	0.0644902912148128 0.0229261107107533

4.2.3 iHH

Space-delimited data file containing one header line followed by data on each subsequent line.

"CHR"	"POSITION"	"FREQ_a"	"IHHa"	"IHHd"	"IES"
"rs1251176"	2	130000040	0.9823	11558.89	83915.49 11571.13

4.2.4 Tajima's D

Space-delimited data file containing one header line followed by data on each subsequent line.

CHROM	BIN_START	N_SNPS	TajimaD
2	130000000	22	0.775224

5 Command line Arguments

The selection pipeline contains three programs: *selection_pipeline*, *aa_annotate* and *multi_population*. The selection pipeline does all the intra-population statistics calculations. The multi_population program calculates all the inter-population statistics and calls the selection pipeline. The aa_annotate program annotates a haplotype file or a phased vcf file with the ancestral allele from the 6-way EPO alignment, for other species or alternative ancestral annotation, the feature will be added in the future.

5.1 Multipopulation

5.1.1 Input Files

- `-i <vcf input file>` VCF file containing all the populations you want to analyse from one chromosome or a part of a chromosome only.

5.1.2 Output Files

- FST
Fst results are stored in the fst folder with the chromosome number followed by the two populations. e.g 2CEUYRI.fst
- Selection Pipeline Results
All single population pipeline results are stored in the subdirectory of the population in a folder named results. These contain the iHH, Tajima's D and a population VCF file.

5.1.3 Other parameters (Compulsory)

- `-l <log_file>`
Name for the log file. Moved into the logs folder at the end of program run.
- `-c <Chromosome>`
Integer for the chromosome being used.
- `-a <Arguments to the selection pipeline>`
Quoted string containing any extra arguments to the selection_pipeline program. e.g `"-imputation"`
- `-config-file <path to config file>`
Path to the selection pipeline config file an example config file is located in the base directory of the extracted package.

5.1.4 Other parameters (Optional)

- `-no-clean-up`
Do not clean up intermediate data files.
- `-fst-window-size <FST window size>`
Fst calculation sliding window size in kilobases (default = 1kb).

- `-fst-window-step <FST window step>`

Fst calculation window jump in kilobases, if window size is equal to the jump size non-overlapping windows are used (default = 1kb).

- `-cores`

Number of cores available for the pipeline overrides setting in the config file.

5.2 Selection Pipeline

5.2.1 Input Files

- `-i <VCF input file>`

Single population single chromosome VCF input file. VCF should be unzipped

5.2.2 Output Files

The Results directory contains all the output files.

- `.ihh` file

The outputted iHH data for each SNP

- `.taj_d` file

Tajima's D output

- `.vcf` file

Single population VCF updated by the pipeline, can contain.

5.2.3 Other parameters(Compulsory)

- `-config-file <Config File path>`

Path to the selection pipeline config file an example config file is located in the base directory of the extracted package.

5.2.4 Other parameters(Optional)

- `-l <log_file>`

Name for the log file. Moved into the logs folder at the end of program run.

- `-maf <minimum MAF>`

Minor allele frequency filter threshold any SNPs below this threshold will be discarded from the analysis (default = 0.01).

- `-hwe <hardy-weinberg minimum p-value>`

A hardy weinberg test is performed on every snp any snps failing the test will be discarded (default = 0.001).

- `-remove-missing <Inclusion threshold for missing genotypes>`

Inclusion criteria for SNPs with missing data. SNPs with less than this value will be removed from analysis (default = 0.99).

- `-fay-Window-Width <window width>`

Sliding window width for Fay and Wu's H calculation in kb (default = 5kb).

- `-fay-Window-Jump <Window Jump>`

Window jump for Fay and Wu's H calculation, if equal to `fay-Window-Width` non-overlapping windows will be used (default = 5kb).

- `-TajimaD <tajimas D bin size>`

Tajima's D statistic bin size in kb (default = 5kb).

- `-no-clean-up`

Do not clean up intermediate data files

- `-ehh-window-size`

Window size for multicore rehh calculations in Megabases (Mb) (default = 5Mb).

- `-ehh-overlap`

Window overlap for multicore rehh calculations in Megabases (Mb) (default = 2Mb).

- `-daf <Minimum derived allele frequency>`

Derived allele frequencies below this minimum will be discarded (default = 0.0).

- `-big-gap`

Gap size in kb for not calculating iHH if the gap is too large. If set to zero the big-gap rule is not applied (default = 0kb).

- `-small-gap`

Gap size in kb for applying a penalty to the area calculated by iHH. If set to zero the small-gap rule is not applied (default = 0kb).

- `-small-gap-penalty`

Penalty multiplier for intergration step in iHH calculation. $multiplier/gap_size * area$ is the formula we use. Setting the multiplier to the same value as the small gap threshold is recommended (default = 0kb).

- `-cores`

Number of cores available for the pipeline overrides setting in the config file.

5.3 Ancestral Annotation

The program *ancestral_annotation* is installed in the program path. The program annotates .haps and .vcf files with ancestral allele annotation from the 6-way IPO alignment or the human reference genome.

5.3.1 Input Files

- `-i` or `-haps` <HAPS File>

Haplotype File (.haps)

- `-v` <Phased VCF file>

Phased VCF file (.vcf), phased VCF genotypes denoted by a bar (|) for each sample.

- `-a` or `-aa` <Ancestral allele fasta>

Ancestral allele annotation file. Currently only works on a the full 1000 Genomes Project GRCh3764 reference file or the single chromosome fasta files from the 6-way EPO alignment.

5.3.2 Output Files

- `-o` or `-output` <Output file name>

Output file name optional argument by default output is sent to the stdout stream.

- `-s` or `-sample-file` <Sample file output>

Sample file output name (currently only works with phased vcf option)

5.3.3 Other parameters

- `-header-regex`

Compulsory argument: it is a regex (regular expression) with a question mark denoting substitution for the chromosome number. The regex should match the header in the fasta file and when the question mark is replaced selectively return only the chromosome of interest. Optional for single chromosome fasta files.

- `-single-chromosome`

Single chromosome pipeline run option.

- `-c` <chromosome number>

The number or symbol of the chromosome being used.

- `-f` or `-format` <format>

The 6-way EPO alignment denotes ancestral alleles with both high and low confidence. To use only ancestral alleles with high confidence use `-format upper`. To use both high and low confident alleles use `-format lower`. By default the program will use only highly confident alleles. The highly confident alleles are in uppercase.

By default it uses all the valid bases in the file that are one of either A,T,C,G,a,t,c or g.

5.4 Configuration File

The selection pipeline requires a configuration file. By default the program looks in the current working directory for a file named defaults.cfg but you can point the program to any file using command line argument `-config-file` <config_file_location>. There are two main programs in the selection pipeline namely *selection_pipeline* and

multi_population. These programs share a config file but certain configuration parameters can be omitted when using the *selection_pipeline* program exclusively. A clean install of the pipeline generates an example configuration file containing default arguments for all the compulsory parameters. The default config file contains an example of the format.

5.4.1 system

- `cores_avaliable`

Certain programs in the pipeline can take advantage of multicore computers. This option instructs the pipeline about the maximum number of concurrent processes it is allowed to use.

5.4.2 environment

- `LD_LIBRARY_PATH`

Set the library path when running the pipeline, this enables the pipeline to use the shared libraries that are used for some programs in the pipeline (alter this option with caution!)

- `PERL5LIB`

Sets the PERL5LIB environment variable, this enables the pipeline to use the perl libraries required by VCFTOOLS (alter this option with caution!)

5.4.3 selection_pipeline

- `selection_pipeline_executable`

Points to the location of the `selection_pipeline_executable`.

5.4.4 vcf_tools

- `vcf_tools_executable`

Points to the `vcftools` executable, by default it points to the `vcftools` executable installed with the pipeline.

- `vcf_subset_executable`

Points to the `vcf-subset` executable, by default pointing to the `vcf-subset` installed with the pipeline.

- `vcf_merge_executable`

Points to the `vcf-merge` executable, by default pointing to the `vcf-subset` installed with the pipeline.

- `extra_args`

A quoted string containing extra arguments to send to the `vcf_tools` executable.

5.4.5 shapeit

- `shapeit_executable`

Location of the `shapeit` executable.

- `genetic_map_dir`

Directory containing the genetic map for shapeit.

- `genetic_map_prefix`

The full file for the genetic map files with a "?" character representing the changing chromosome number.

- `extra_args` extra arguments to send to shapeit (Warning: Certain options could potentially break the pipeline - use with caution).

5.4.6 **impute2**

- `impute_executable`

Location of the impute2 executable

- `impute_map_dir`

Directory containing the genetic map for impute2

- `impute_reference_dir`

Directory containing the reference panel (`.legend` and `.hap`) files for impute2.

- `chromosome_split_size`

Window size for imputation calculation.

- `impute_map_prefix`

The full file name for the genetic map files with a "?" character representing the changing chromosome number

- `impute_reference_prefix`

The full file name for the reference panels minus the extension with a "?" character representing the changing chromosome number.

- `extra_args`

extra arguments to send to impute2 (Warning: Certain options could potentially break to pipeline use with caution).

5.4.7 **plink**

- `plink_executable`

Location of the plink executable

5.4.8 **Rscript**

- `rscript_executable`

Location of the rscript executable (Program usually in path so just Rscript is the default).

- `indel_filter`

Location of the rscript `indel_filter` (`hap_indel_and_maf_filter.R`)i

5.4.9 python

- python_executable

location of the python executable (2 or 3)

5.4.10 ancestral_allele

- split_by_chromosome

Option determines whether the ancestral fasta file is split by chromosome or not. If the ancestral fasta is split by chromosome the ancestral_fasta_dir and ancestral_prefix arguments are required. If the ancestral fasta is just one flat file the ancestral_fasta_file options is required which is just merely the location of the ancestral fasta option.

- ancestral_fasta_header_regex

This options specifies a regular expression that will extract each chromosome from the fasta file. The '?' denotes the chromosome number and will be replaced in the regular expression for the chromosome number of interest. Even when using one fasta per chromosome this is required as the python library used to extract the sequence uses the fasta header for extraction. Only required if your fasta file is not split by chromosome.

- ancestral_fasta_file

Ancestral fasta file used if the split_by_chromosome is set to false.

- ancestral_allele_script

Location of the ancestral_annotation script (aa_annotate.py)

- ancestral_fasta_dir

Directory containing the ancestral reference files

- ancestral_prefix

Full file name for ancestral fasta files containing a "?" character

5.4.11 qctool

- qctool_executable

Location of the qctool executable.

5.4.12 multicore_ihh

- multicore_ihh

Location of the multicore_iHH.R script

The rehh package source included with the pipeline has been altered to match the output filters used in Voight's paper. If the $EHH > 0.05$ reaches the end of a chromosome or the start of a gap $> \text{big_gap_threshold}$, then no value is returned for the core snp. The small_gap_threshold specifies the gap distance to reduce the distance spanned by the gap by a multiplicative factor specified by small_gap_multiplier. The formula

for the penalty is $\frac{\text{small_gap_multiplier}}{\text{gap_size}}$. To match the parameters used by Voight, a value of 200,000 should be used for `big_gap_threshold`, 20,000 for `small_gap_threshold` and 20,000 for `small_gap_multiplier` (Voight *et al.*, 2006).

6 Log Files

6.1 multi_population

The location of the log file for *multi_population* defaults is located in the log directory. It contains all the logging information for the between population selection signature calculations.

6.2 selection_pipeline

The location of the log file for *selection_pipeline* is located in the log directory. The log file contains all the logging information for the within population selection signature calculations.

7 Extra Features

7.1 Galaxy Intergration

The galaxy folder contains the scripts required to add the selection pipeline to a local galaxy installation. The pipeline is also available on the galaxy toolshed at `galaxy_url`. To do intergrate the pipeline into galaxy.

[JAMES - is this stuff available for Galaxy? **]**

8 F.A.Q

1. How do I run *multi_population* with a phased VCF?

In the `-a` argument for *multi_population* merely add `-phased-vcf` between the quotes. This will ensure phasing and imputation will be skipped when *selection_pipeline* is called.

2. My populations are in seperate VCF-Files: how do I run *multi_population*?

To run the pipeline you will need to merge the VCF-files into one large multipopulation VCF file and generate the appropriate population files.

To merge your vcfs you can use the `vcf-merge` program. For this to work correctly outside the selection pipeline you will need to add the following to your `.bashrc` file or equivalent dot-file for another shell.

```
export PERL5LIB=\${PERL5LIB}:<path to selection pipeline>/lib/perl5
```

The command to run `vcf-merge` is as follows.

```
vcf-merge <vcf1.vcf> <vcf2.vcf> ..... > big_vcf.vcf
```

3. My VCF file is not split by chromosome how do I get my VCF into a single chromosome?

The vcftools program can be used to extract each chromosome from your full vcf file. If you do not have the vcftools program installed the bin/ directory contains exactly what you need. For example, for human 1000 genomes data to extract chromosome 2 from your VCF file use the following command.

```
vcf-tools --vcf big_vcf.vcf --chr 2 --out chr2 --recode
```

The command will generate a vcf file named chr2.recode.vcf containing only data from chromosome 2.

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