**IBD analysis (Isolation by descent analysis)**

For IBD analysis, you need to run beagle5\_v4.pl with -ibd argument first. The script can be found in “imputation/beagle5” folder.

Other arguments used for IBD analysis, please see the description in the script by -h tag.

After running script with -ibd tag, you might see some files with “ibd.gz” extension. Then, please execute “ibd2matrix.pl”.

Usage: perl ibd2matrix.pl -i ibd\_file(s) -vcf|-list vcf\_file|list\_file

-i: input files, can be directed to a file or a folder containing ibd.gz files

-vcf|-list: if you are using sample order from vcf file, please use -vcf VCF\_FILE; if you are using user defined sample order, please use -list LIST\_FILE. for the list file, one sample name per line.

After you got the matrix (output is in the sample folder of ibd files with extension “.matrix”), you can run “matrix\_plot.R” to visualize the data.

Usage: Rscript matrix\_plot.R MATRIX\_FILE POPULATION\_INFO\_FILE

Then, you will get a tiff file from the same folder of the matrix file.

\*\*for matrix\_plot.R, R modules “reshape2”, “ggplot2” are required.