

Instructions for running iRIGS

1. Download the zipped file iRIGS_code.tar.gz and unzip it.
2. Enter the iRIGS_code folder. Type Rscript Gibbs.R -h on linux platform for help information.
3. Usage: Rscript Gibbs.R SNP_file flank res_path res_pref
4. Explanation of arguments:
 - 4.1 SNP_file File name of GWAS SNPs. The file must include three columns: SNP, Chr, and Pos_hg19.
 - 4.2 flank An integer indicating the flanking region (bp) for choosing candidate genes. 1000000 is recommended.
 - 4.3 res_path Path of result files. Optional; "./iRIGS_result/" used by default if not designated.
 - 4.4 res_pref Prefix of the result file. Optional; SNP_file name used by default if not designated.
5. Type the following code to run our example and iRIGS will be implemented on the 108 SCZ loci used in our manuscript:

```
Rscript Gibbs.R ./SNP_file/SCZ_108_loci 1000000 ./iRIGS_result_108_loci/ SCZ &
```