# Guidance to reproduce SUMMIT's results

## Simulation

#### Figure 2(a) and 2(b)

```
Rscript /gpfs/research/chongwu/zichenzhang/SUMMIT-test/code/Simulation.R \
--h2_e A \
--h2_p 0.2 \
--p_causal B \
--n 31684 \
--sumstats TRUE \
--gene_ENSG ENSG00000258289 \
--UKB TRUE \
--folder_output SIM \
--t1e FALSE \
--seed SEED \
```

Α	В	SEED
0.005	0.01	1
0.005	0.05	2
0.005	0.10	3
0.005	0.20	4
0.01	0.01	5
0.01	0.05	6
0.01	0.10	7
0.01	0.20	8
0.1	0.01	9
0.1	0.05	10
0.1	0.10	11
0.1	0.20	12

## Figure 2(c)

```
Rscript /gpfs/research/chongwu/zichenzhang/SUMMIT-test/code/Simulation.R \
--h2_e A \
--h2_p 0.2 \
--p_causal 0.05 \
--n B \
--sumstats TRUE \
--gene_ENSG ENSG000000258289 \
--UKB TRUE \
--folder_output SIM \
--t1e FALSE \
--seed SEED \
```

Α	В	SEED
0.005	300	13
0.005	600	14
0.005	3000	15
0.005	10000	16
0.005	31684	17
0.01	300	18
0.01	600	19
0.01	3000	20
0.01	10000	21
0.01	31684	22
0.1	300	23
0.1	600	24
0.1	3000	25
0.1	10000	26
0.1	31684	27

```
Rscript /gpfs/research/chongwu/zichenzhang/SUMMIT-test/code/Simulation.R \
--h2_e A \
--h2_p 0.1 \
--p_causal B \
--n 31684 \
--sumstats TRUE \
--gene_ENSG ENSG00000258289 \
--UKB TRUE \
--folder_output SIM \
--t1e FALSE \
--seed SEED \
```

To reproduce this figure, use exact same options for Figure 2(a) and 2(b) but change the flag p\_causal to 0.1, 0.5, and 0.8.

```
Rscript /gpfs/research/chongwu/zichenzhang/SUMMIT-test/code/Simulation.R \
--h2_e 0.05 \
--h2_p 0.2 \
--p_causal 0.2 \
--n A \
--sumstats B \
--gene_ENSG ENSG00000258289 \
--UKB TRUE \
--folder_output SIM \
--t1e FALSE \
--seed SEED \
```

Α	В	SEED
300	FALSE	28
600	FALSE	29
3000	FALSE	30
10000	FALSE	31
31684	FALSE	32
31684	TRUE	33

```
Rscript /gpfs/research/chongwu/zichenzhang/SUMMIT-test/code/Simulation.R \
--h2_e A \
--h2_p 0.2 \
--p_causal B \
--n 31684 \
--sumstats TRUE \
--gene_ENSG ENSG000000003147 \
--UKB TRUE \
--folder_output SIM \
--t1e FALSE \
--seed SEED \
```

Α	В	SEED
0.005	0.01	34
0.005	0.05	35
0.005	0.10	36
0.005	0.20	37
0.01	0.01	38
0.01	0.05	39
0.01	0.10	40
0.01	0.20	41
0.1	0.01	42
0.1	0.05	43
0.1	0.10	44
0.1	0.20	45

```
Rscript /gpfs/research/chongwu/zichenzhang/SUMMIT-test/code/Simulation.R \
--h2_e A \
--h2_p 0.2 \
--p_causal B \
--n 31684 \
--sumstats TRUE \
--gene_ENSG ENSG00000001631 \
--UKB TRUE \
--folder_output SIM \
--t1e FALSE \
--seed SEED \
```

Α	В	SEED
0.005	0.01	46
0.005	0.05	47
0.005	0.10	48
0.005	0.20	49
0.01	0.01	50
0.01	0.05	51
0.01	0.10	52
0.01	0.20	53
0.1	0.01	54
0.1	0.05	55
0.1	0.10	56
0.1	0.20	57

```
Rscript /gpfs/research/chongwu/zichenzhang/SUMMIT-test/code/Simulation.R \
--h2_e 0.05 \
--h2_p 0.2 \
--p_causal 0.2 \
--n A \
--sumstats B \
--gene_ENSG ENSG00000003147 \
--UKB TRUE \
--folder_output SIM \
--t1e FALSE \
--seed SEED \
```

Α	В	SEED
300	FALSE	58
600	FALSE	59
3000	FALSE	60
10000	FALSE	61
31684	FALSE	62
31684	TRUE	63

```
Rscript /gpfs/research/chongwu/zichenzhang/SUMMIT-test/code/Simulation.R \
--h2_e 0.05 \
--h2_p 0.2 \
--p_causal 0.2 \
--n A \
--sumstats B \
--gene_ENSG ENSG00000001631 \
--UKB TRUE \
--folder_output SIM \
--t1e FALSE \
--seed SEED \
```

Α	В	SEED
300	FALSE	64
600	FALSE	65
3000	FALSE	66
10000	FALSE	67
31684	FALSE	68
31684	TRUE	69

```
Rscript /gpfs/research/chongwu/zichenzhang/SUMMIT-test/code/Simulation.R \
--h2_e A \
--h2_p 0.2 \
--p_causal 0.01 \
--n B \
--sumstats FALSE \
--gene_ENSG ENSG000000258289 \
--UKB TRUE \
--folder_output SIM \
--t1e FALSE \
--seed SEED \
```

Α	В	SEED
0.005	300	70
0.005	600	71
0.005	3000	72
0.005	10000	73
0.005	31684	74
0.01	300	75
0.01	600	76
0.01	3000	77
0.01	10000	78
0.01	31684	79
0.05	300	80
0.05	600	81
0.05	3000	82
0.05	10000	83
0.05	31684	84
0.1	300	85
0.1	600	86
0.1	3000	87

Α	В	SEED
0.1	10000	88
0.1	31684	89

```
Rscript /gpfs/research/chongwu/zichenzhang/SUMMIT-test/code/Simulation.R \
--h2_e 0.05 \
--h2_p 0.2 \
--p_causal 0.01 \
--n 31684 \
--sumstats TRUE \
--gene_ENSG ENSG000000258289 \
--UKB TRUE \
--folder_output SIM \
--t1e TRUE \
--seed 90 \
```

#### Real-data results

To reproduce SUMMIT's real-data results, please follow our steps:

- 1. Download GWAS summary data through the links provided in Supplementary Table 1
- 2. Preprocess the downloaded GWAS summary data using APSS.R
- 3. Get the real-data result using TestAssociation.R
- 4. Use our plotting code to draw the plots

#### **Tips**

Since we were working on a SLURM-managed environment, in line 55 of Simulation.R, we used

```
Sys.getenv("SLURM_ARRAY_TASK_ID")
```

to get the sub-job's index from the global environment. Depending on your computing environment, you may need to manually modify this line.

In line 663 of Simulation. R, you can change runs to a smaller number to save time and still get results that are very similar to ours.

#### **Notes**

We made every effort to help users replicate our results exactly. All results were tested on CentOS Linux 8. For each figure and table, you may need to change the parameters (denoted by A, B, and SEED) as we suggested. The codes can also serve as a launching point for your own studies.

All the above codes are for replication purposes and the users may need to change the directory and install the necessary packages to run it smoothly. If you have any questions, feel free to contact us (Zichen Zhang, zz17@fsu.edu)

#### Disclaimer

The codes are provided "as is" and the author disclaims all warranties with regard to these codes including all implied warranties of merchantability and fitness. In no event shall the author be liable for any special, direct, indirect, or consequential damages or any damages whatsoever resulting from loss of use, data or profits, whether in an action of contract, negligence or other tortious action, arising out of or in connection with the use or performance of these codes.

#### **Author**

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