INPower Package

February 21, 2026

Introduction

An R package to estimate the number of susceptibility loci and the distribution of their effect sizes for a trait on the basis of discoveries from existing genome-wide association studies (GWASs).

```
> library(INPower)
```

Height example

Get the path to the data which contains a known set of susceptibility SNPs for height.

```
> datafile <- system.file("sampleData", "data.rda", package="INPower")
```

Load and print the data frame.

```
> load(datafile)
> data
```

```
          SNP  MAF        Beta       Power
1    rs314277 0.13  0.03538462 0.01005508
2   rs4713858 0.14 -0.03900000 0.02774654
3  rs12198986 0.50  0.03300000 0.12273508
4   rs1492820 0.48 -0.03353846 0.13659137
5  rs10946808 0.28 -0.04830769 0.57978559
6   rs2274432 0.37  0.04500000 0.58359100
7    rs678962 0.22  0.05400000 0.65003547
8   rs8007661 0.30 -0.05015385 0.70992649
9  rs12735613 0.24 -0.05500000 0.75566530
10   rs724016 0.48  0.04723077 0.76483843
11  rs1812175 0.14 -0.06900000 0.79323028
12  rs4800148 0.21 -0.05900000 0.80022419
13  rs4896582 0.27 -0.05615385 0.86294616
14 rs11205277 0.44  0.05400000 0.94813202
15  rs4549631 0.50  0.05500000 0.96621958
16  rs7153027 0.48 -0.05700000 0.98270897
17  rs3760318 0.37 -0.06000000 0.98802127
18  rs2844479 0.33 -0.06300000 0.99289585
```

1

```
19  rs6060369 0.36   0.06307692 0.99593942
20  rs3791675 0.23   0.07500000 0.99879522
21  rs6830062 0.11  -0.10500000 0.99969644
22  rs2282978 0.31   0.07150000 0.99976245
23  rs2814993 0.15   0.09500000 0.99991429
24  rs1042725 0.50   0.06792308 0.99991841
25   rs798544 0.28  -0.07700000 0.99996252
26       rs8756 0.48  -0.07200000 0.99999452
27  rs6060373 0.38  -0.07500000 0.99999710
28  rs3748069 0.26  -0.08300000 0.99999711
29  rs6440003 0.44   0.09500000 1.00000000
30  rs6763931 0.45   0.13500000 1.00000000
```

For each known susceptibility SNP, we will need the MAF, effect size and power of detection.

```
> MAFs  <- data[, "MAF"]
> betas <- data[, "Beta"]
> pow   <- data[, "Power"]
```

Suppose that a one-stage design with a genome-wide significant level of 1e-7 is considered for a future study. It is known that the heritability of height is 0.8. It is of interest to predict the expected number of discoveries with sample sizes from 25,000 to 125,000 with an increment of 25,000. In addition, for the given sample sizes, it is also of interest to find power to detect at least k loci, with k ranging from 25 to 125 with an increment of 25.

```
> INPower(MAFs, betas, pow, span=0.5, binary.outcome=FALSE,
+          sample.size=seq(25000,125000,by=25000),
+          signif.lvl=10^(-7), tgv=0.8, k=seq(25,125,by=25))

[1] FALSE
$esdist.summary
$esdist.summary$t.n.loci
[1] 200.8


$esdist.summary$gve
[1] "16.39% of the total genetic variance"


$esdist.summary$es.dist
   MAFs      betas        pow  effect.size est.num.loci
1  0.13  0.03538462 0.01005508 0.0002832185         54.0
2  0.14 -0.03900000 0.02774654 0.0003662568         47.3
3  0.50  0.03300000 0.12273508 0.0005445000         33.4
4  0.48 -0.03353846 0.13659137 0.0005615143         32.2
5  0.28 -0.04830769 0.57978559 0.0009409209          3.1
6  0.37  0.04500000 0.58359100 0.0009440550          3.0
7  0.22  0.05400000 0.65003547 0.0010007712          2.3
8  0.30 -0.05015385 0.70992649 0.0010564715          1.7
9  0.24 -0.05500000 0.75566530 0.0011035200          1.4
10 0.48  0.04723077 0.76483843 0.0011135882          1.4
```

```
11 0.14 -0.06900000 0.79323028 0.0011464488          1.3
12 0.21 -0.05900000 0.80022419 0.0011549958          1.3
13 0.27 -0.05615385 0.86294616 0.0012430129          1.2
14 0.44  0.05400000 0.94813202 0.0014370048          1.1
15 0.50  0.05500000 0.96621958 0.0015125000          1.1
16 0.48 -0.05700000 0.98270897 0.0016219008          1.0
17 0.37 -0.06000000 0.98802127 0.0016783200          1.0
18 0.33 -0.06300000 0.99289585 0.0017550918          1.0
19 0.36  0.06307692 0.99593942 0.0018333841          1.0
20 0.23  0.07500000 0.99879522 0.0019923750          1.0
21 0.11 -0.10500000 0.99969644 0.0021586950          1.0
22 0.31  0.07150000 0.99976245 0.0021870205          1.0
23 0.15  0.09500000 0.99991429 0.0023013750          1.0
24 0.50  0.06792308 0.99991841 0.0023067722          1.0
25 0.28 -0.07700000 0.99996252 0.0023905728          1.0
26 0.48 -0.07200000 0.99999452 0.0025878528          1.0
27 0.38 -0.07500000 0.99999710 0.0026505000          1.0
28 0.26 -0.08300000 0.99999711 0.0026508872          1.0
29 0.44  0.09500000 1.00000000 0.0044475200          1.0
30 0.45  0.13500000 1.00000000 0.0090213750          1.0
```

$future.study.summary
$future.study.summary$e.discov
```
  sample.size e.discov
1       25000     27.3
2       50000     74.4
3       75000    125.6
4      100000    161.5
5      125000    182.8
```

$future.study.summary$e.gve
```
  sample.size                               e.gve
1       25000  6.58% of the total genetic variance
2       50000 10.28% of the total genetic variance
3       75000 13.17% of the total genetic variance
4      100000 14.85% of the total genetic variance
5      125000 15.71% of the total genetic variance
```

$future.study.summary$prob.k
```
   k Pr(X>=k).n=25000   k Pr(X>=k).n=50000   k Pr(X>=k).n=75000    k
1 24             0.90  25             1.00  25             1.00   25
2 25             0.82  50             1.00  50             1.00   50
3 25             0.82  68             0.91  75             1.00   75
4 26             0.72  70             0.83 100             1.00  100
5 27             0.59  72             0.71 119             0.90  125
6 28             0.46  74             0.57 121             0.82  155
7 28             0.46  75             0.49 123             0.71  158
8 29             0.34  75             0.49 125             0.57  159
9 30             0.23  76             0.42 125             0.57  161
```

```
10  32           0.09  78           0.28 126           0.50 162
11  50           0.00  79           0.22 127           0.43 163
12  75           0.00  82           0.09 129           0.30 165
13 100           0.00 100           0.00 131           0.19 166
14 125           0.00 125           0.00 133           0.11 168
   Pr(X>=k).n=1e+05   k Pr(X>=k).n=125000
1             1.00  25           1.00
2             1.00  50           1.00
3             1.00  75           1.00
4             1.00 100           1.00
5             1.00 125           1.00
6             0.92 178           0.90
7             0.78 180           0.79
8             0.72 181           0.72
9             0.58 182           0.63
10            0.50 183           0.53
11            0.42 184           0.43
12            0.27 185           0.34
13            0.21 187           0.18
14            0.11 188           0.12
```

The function call below shows the same results as the above, but without the tgv (total genetic variance) argument. As a result, the genetic variance explained is expressed as a percentage of the total variance of the outcome, not of the total genetic variance.

```
> INPower(MAFs, betas, pow, span=0.5, binary.outcome=FALSE,
+         sample.size=seq(25000,125000,by=25000),
+         signif.lvl=10^(-7), k=seq(25,125,by=25))

[1] FALSE
$esdist.summary
$esdist.summary$t.n.loci
[1] 200.8


$esdist.summary$gve
[1] "13.11% of the total variance of the outcome"


$esdist.summary$es.dist
   MAFs       betas        pow  effect.size est.num.loci
1  0.13  0.03538462 0.01005508 0.0002832185         54.0
2  0.14 -0.03900000 0.02774654 0.0003662568         47.3
3  0.50  0.03300000 0.12273508 0.0005445000         33.4
4  0.48 -0.03353846 0.13659137 0.0005615143         32.2
5  0.28 -0.04830769 0.57978559 0.0009409209          3.1
6  0.37  0.04500000 0.58359100 0.0009440550          3.0
7  0.22  0.05400000 0.65003547 0.0010007712          2.3
8  0.30 -0.05015385 0.70992649 0.0010564715          1.7
9  0.24 -0.05500000 0.75566530 0.0011035200          1.4
10 0.48  0.04723077 0.76483843 0.0011135882          1.4
11 0.14 -0.06900000 0.79323028 0.0011464488          1.3
```

```
12 0.21 -0.05900000 0.80022419 0.0011549958          1.3
13 0.27 -0.05615385 0.86294616 0.0012430129          1.2
14 0.44  0.05400000 0.94813202 0.0014370048          1.1
15 0.50  0.05500000 0.96621958 0.0015125000          1.1
16 0.48 -0.05700000 0.98270897 0.0016219008          1.0
17 0.37 -0.06000000 0.98802127 0.0016783200          1.0
18 0.33 -0.06300000 0.99289585 0.0017550918          1.0
19 0.36  0.06307692 0.99593942 0.0018333841          1.0
20 0.23  0.07500000 0.99879522 0.0019923750          1.0
21 0.11 -0.10500000 0.99969644 0.0021586950          1.0
22 0.31  0.07150000 0.99976245 0.0021870205          1.0
23 0.15  0.09500000 0.99991429 0.0023013750          1.0
24 0.50  0.06792308 0.99991841 0.0023067722          1.0
25 0.28 -0.07700000 0.99996252 0.0023905728          1.0
26 0.48 -0.07200000 0.99999452 0.0025878528          1.0
27 0.38 -0.07500000 0.99999710 0.0026505000          1.0
28 0.26 -0.08300000 0.99999711 0.0026508872          1.0
29 0.44  0.09500000 1.00000000 0.0044475200          1.0
30 0.45  0.13500000 1.00000000 0.0090213750          1.0


$future.study.summary
$future.study.summary$e.discov
  sample.size e.discov
1       25000     27.3
2       50000     74.4
3       75000    125.6
4      100000    161.5
5      125000    182.8


$future.study.summary$e.gve
  sample.size                                     e.gve
1       25000  5.26% of the total variance of the outcome
2       50000  8.23% of the total variance of the outcome
3       75000 10.54% of the total variance of the outcome
4      100000 11.88% of the total variance of the outcome
5      125000 12.57% of the total variance of the outcome


$future.study.summary$prob.k
     k Pr(X>=k).n=25000   k Pr(X>=k).n=50000   k Pr(X>=k).n=75000   k
1   24             0.90  25             1.00  25             1.00  25
2   25             0.82  50             1.00  50             1.00  50
3   25             0.82  68             0.91  75             1.00  75
4   26             0.72  70             0.83 100             1.00 100
5   27             0.59  72             0.71 119             0.90 125
6   28             0.46  74             0.57 121             0.82 155
7   28             0.46  75             0.49 123             0.71 158
8   29             0.34  75             0.49 125             0.57 159
9   30             0.23  76             0.42 125             0.57 161
10  32             0.09  78             0.28 126             0.50 162
```

11	50	0.00	79	0.22	127	0.43	163
12	75	0.00	82	0.09	129	0.30	165
13	100	0.00	100	0.00	131	0.19	166
14	125	0.00	125	0.00	133	0.11	168

	Pr(X>=k).n=1e+05	k	Pr(X>=k).n=125000
1	1.00	25	1.00
2	1.00	50	1.00
3	1.00	75	1.00
4	1.00	100	1.00
5	1.00	125	1.00
6	0.92	178	0.90
7	0.78	180	0.79
8	0.72	181	0.72
9	0.58	182	0.63
10	0.50	183	0.53
11	0.42	184	0.43
12	0.27	185	0.34
13	0.21	187	0.18
14	0.11	188	0.12

Now a two-stage study is considered with all the other conditions remaining the same (including the estimate of total heritability). In addition, the selection criterion for SNPs taken toward the second stage is 5e-5 and 30assigned to the first stage (and hence 70

```
> INPower(MAFs, betas, pow, span=0.5, binary.outcome=FALSE,
+         sample.size=seq(25000,125000,by=25000),
+         signif.lvl=10^(-7), multi.stage.option=list(al=5*10^(-5), pi=0.3),
+         tgv=0.8 , k=seq(25,125,by=25))

$esdist.summary
$esdist.summary$t.n.loci
[1] 200.8

$esdist.summary$gve
[1] "16.39% of the total genetic variance"

$esdist.summary$es.dist
```

	MAFs	betas	pow	effect.size	est.num.loci
1	0.13	0.03538462	0.01005508	0.0002832185	54.0
2	0.14	-0.03900000	0.02774654	0.0003662568	47.3
3	0.50	0.03300000	0.12273508	0.0005445000	33.4
4	0.48	-0.03353846	0.13659137	0.0005615143	32.2
5	0.28	-0.04830769	0.57978559	0.0009409209	3.1
6	0.37	0.04500000	0.58359100	0.0009440550	3.0
7	0.22	0.05400000	0.65003547	0.0010007712	2.3
8	0.30	-0.05015385	0.70992649	0.0010564715	1.7
9	0.24	-0.05500000	0.75566530	0.0011035200	1.4
10	0.48	0.04723077	0.76483843	0.0011135882	1.4
11	0.14	-0.06900000	0.79323028	0.0011464488	1.3
12	0.21	-0.05900000	0.80022419	0.0011549958	1.3

```
13 0.27 -0.05615385 0.86294616 0.0012430129          1.2
14 0.44  0.05400000 0.94813202 0.0014370048          1.1
15 0.50  0.05500000 0.96621958 0.0015125000          1.1
16 0.48 -0.05700000 0.98270897 0.0016219008          1.0
17 0.37 -0.06000000 0.98802127 0.0016783200          1.0
18 0.33 -0.06300000 0.99289585 0.0017550918          1.0
19 0.36  0.06307692 0.99593942 0.0018333841          1.0
20 0.23  0.07500000 0.99879522 0.0019923750          1.0
21 0.11 -0.10500000 0.99969644 0.0021586950          1.0
22 0.31  0.07150000 0.99976245 0.0021870205          1.0
23 0.15  0.09500000 0.99991429 0.0023013750          1.0
24 0.50  0.06792308 0.99991841 0.0023067722          1.0
25 0.28 -0.07700000 0.99996252 0.0023905728          1.0
26 0.48 -0.07200000 0.99999452 0.0025878528          1.0
27 0.38 -0.07500000 0.99999710 0.0026505000          1.0
28 0.26 -0.08300000 0.99999711 0.0026508872          1.0
29 0.44  0.09500000 1.00000000 0.0044475200          1.0
30 0.45  0.13500000 1.00000000 0.0090213750          1.0


$future.study.summary
$future.study.summary$e.discov
  sample.size e.discov
1       25000    10.8
2       50000    31.5
3       75000    56.0
4      100000    82.1
5      125000   106.7

$future.study.summary$e.gve
  sample.size                             e.gve
1       25000   3.75% of the total genetic variance
2       50000   6.81% of the total genetic variance
3       75000   8.89% of the total genetic variance
4      100000 10.61% of the total genetic variance
5      125000 12.04% of the total genetic variance

$future.study.summary$prob.k
    k Pr(X>=k).n=25000   k Pr(X>=k).n=50000   k Pr(X>=k).n=75000   k
1   8             0.93  25             0.98  25             1.00  25
2   9             0.84  27             0.92  50             0.91  50
3  10             0.70  29             0.79  50             0.91  75
4  11             0.53  30             0.70  52             0.82  75
5  11             0.53  31             0.60  54             0.69  78
6  12             0.36  32             0.49  55             0.62  80
7  12             0.36  33             0.38  56             0.54  81
8  13             0.22  34             0.29  58             0.38  83
9  14             0.12  35             0.20  59             0.30  84
10 25             0.00  37             0.09  61             0.18  86
11 50             0.00  50             0.00  63             0.10  87
```

```
12  75              0.00  75              0.00  75              0.00  90
13 100              0.00 100              0.00 100              0.00 100
14 125              0.00 125              0.00 125              0.00 125
   Pr(X>=k).n=1e+05    k  Pr(X>=k).n=125000
1                1.00   25                1.00
2                1.00   50                1.00
3                0.91   75                1.00
4                0.91  100                0.89
5                0.79  100                0.89
6                0.67  102                0.81
7                0.60  104                0.70
8                0.47  106                0.58
9                0.40  107                0.51
10               0.27  109                0.38
11               0.22  110                0.32
12               0.10  112                0.21
13               0.00  115                0.10
14               0.00  125                0.00
```

Session Information

```
> sessionInfo()

R version 4.5.2 (2025-10-31)
Platform: x86_64-pc-linux-gnu
Running under: Ubuntu 24.04.3 LTS

Matrix products: default
BLAS:   /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblasp-r0.3.26.so;  LAPACK versio

locale:
 [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8        LC_COLLATE=C
 [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
 [9] LC_ADDRESS=C               LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

time zone: Etc/UTC
tzcode source: system (glibc)

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] INPower_1.47.0 mvtnorm_1.3-3

loaded via a namespace (and not attached):
```

```
[1] compiler_4.5.2   cli_3.6.5       tools_4.5.2     maketools_1.3.2
[5] buildtools_1.0.0 knitr_1.51      xfun_0.56       rlang_1.1.7
[9] sys_3.4.3        evaluate_1.0.5
```