

## SIPI package

### Overview

'SIPI' (SNP Interaction Pattern Identifier) evaluates SNP-SNP interactions associated with a binary or continuous outcome. For each SNP pair, the SIPI evaluates 45 interaction models. The inheritance modes SIPI considered include dominant, recessive, and additive modes. 'AA9int' (Additive-Additive 9 interaction models) approach, a mini version of SIPI, evaluates SNP-SNP interactions associated with a binary or continuous outcome through testing 9 interaction models. AA9int treats both SNPs as an additive inheritance mode. The best interaction pattern for a given SNP pair is the model with the lowest value of the Bayesian information criterion (BIC).

### System requirements

#### Hardware requirements

The SIPI R package requires only a standard computer.

#### Software requirements

##### Operating system (OS) requirements

This SIPI R package can be installed on Windows, macOS, and Linux. Follow the instructions on CRAN website (<https://cran.r-project.org>).

This package has been tested on the following systems:

- Windows 10
- Linux: Enterprise\_Linux:7.7

### Installation Guide:

```
install.packages("https://raw.githubusercontent.com/LinHuiyi/SIPI/master/SIPI_0.64.tar.gz", repos = NULL, type = "source")
```

The SIPI package should take approximately 12 seconds to install with a standard computer.

### Demo

```
library(SIPI)
## example SNP data (1000 subjects, 10 SNPs and other 5 non-SNP variables)
data(simData)
```

```
## check variables in the simData
> names(simData)
```

```
[1] "id" "D" "SNP1" "SNP2" "SNP3" "SNP4" "SNP5" "SNP6" "SNP7" "SNP8"
"SNP9" "SNP10" "gender"
[14] "age" "group"
```

```
## define SNP variables
➤ snp=simData[,3:12]
```

```
## Run SIPI for all pairwise SNP-SNP interaction
```

- output=**SIPI**(simData\$D,snp,"all")
- output

\$selectedModel`					
Var1	Var2	Model	Wald_Chisq	Wald_p	
1	SNP1	SNP2	RR_M1_int_o1	0.864460377	3.524935e-01
2	SNP1	SNP3	RD_M1_int_r1	1.732129767	1.881391e-01
3	SNP1	SNP4	RD_M1_int_o1	4.366467158	3.665291e-02
4	SNP1	SNP5	RR_int_rr	52.366446228	4.605256e-13
5	SNP1	SNP6	RR_int_or	36.685383251	1.388164e-09
6	SNP1	SNP7	RR_int_rr	37.542213429	8.945582e-10
...					
44	SNP8	SNP10	RR_int_ro	2.750957919	9.719618e-02
45	SNP9	SNP10	DR_int_ro	2.750957919	9.719618e-02

```
## export a result file
```

```
>write.csv(output, file=("C:/file directory/SIPIoutput.csv"), row.names=F)
```

### Run Time:

It took ~16 seconds to run 45 SNP pairs (all pairwise SNP pairs for 10 SNPs) for a sample size of 1000 in a standard computer.

### Instructions for use

```
# input your own data
```

```
indata <- read.csv("C:/file directory/indata.csv")
```

```
# define SNP variable (from column 2-column 10)
```

```
SNPd=data[,2:10]
```

```
# follow the instructions showed in the SIPI manual
```

```
#### Reference:
```

Lin HY, Chen DT, Huang PY, Liu YH, Ochoa A, Zabaleta J, Mercante DE, Fang Z, Sellers TA, Pow-Sang JM, Cheng CH, Eeles R, Easton D, Kote-Jarai Z, Amin Al Olama A, Benlloch S, Muir K, Giles GG, Wiklund F, Gronberg H, Haiman CA, Schleutker J, Nordestgaard BG, Travis RC, Hamdy F, Pashayan N, Khaw KT, Stanford JL, Blot WJ, Thibodeau SN, Maier C, Kibel AS, Cybulski C, Cannon-Albright L, Brenner H, Kaneva R, Batra J, Teixeira MR, Pandha H, Lu YJ, Consortium P, Park JY. SNP interaction pattern identifier (SIPI): an intensive search for SNP-SNP interaction patterns. *Bioinformatics*. 2017;33(6):822-33. PubMed PMID:28039167.

Lin HY, Huang PY, Chen DT, Tung HY, Sellers TA, Pow-Sang JM, Eeles R, Easton D, Kote-Jarai Z, Amin Al Olama A, Benlloch S, Muir K, Giles GG, Wiklund F, Gronberg H, Haiman CA, Schleutker J, Nordestgaard BG, Travis RC, Hamdy F, Neal DE, Pashayan N, Khaw KT, Stanford JL, Blot WJ, Thibodeau SN, Maier C, Kibel AS, Cybulski C, Cannon-Albright L, Brenner H, Kaneva R, Batra J, Teixeira MR, Pandha H, Lu YJ, Consortium P, Park JY. AA9int: SNP interaction pattern search using non-hierarchical additive model set. *Bioinformatics*. 2018;34(24):4141-50. PubMed PMID: 29878078; PMCID: PMC6289141.