Package 'SIPI'

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Description Testing single nucleotide polymorphism (SNP) interactions is considered as a key for overcoming bottlenecks of genetic association studies. SNP Interaction Pattern Identifier (SIPI) evaluates SNP-SNP interactions associated with a binary or continuous outcome. The primary strengths of SIPI are (1) taking non-hierarchical models, reverse coding and inheritance modes (dominant, recessive and additive mode) into consideration and (2) using the Bayesian information criterion (BIC) to search for a best interaction pattern. For each SNP pair, the SIPI evaluates 45 interaction models. The best interaction pattern is the one with the lowest BIC value.

Reference (1) 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. (2) Lin HY, Huang PY, Chen DT, Tung HY, Sellers TA, Pow-Sang J, 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. doi: 10.1093/bioinformatics/bty461. PubMed PMID: 29878078.

LazyData true

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NeedsCompilation no

R topics documented:

`AA9int` *AA9int (Additive-Additive 9 interaction models): Detect SNP-SNP interactions through testing the 9 models*

Description

`AA9int` (Additive-Additive 9 interaction models), a mini version of `SIPI`, evaluates SNP-SNP interactions associated with a binary or continuous outcome through testing nine interaction models. `AA9int` treats both SNPs as an additive mode and takes reverse coding and non-hierarchical models into consideration. The best interaction pattern is the one with the lowest value of the Bayesian information criterion (BIC). The details of the nine models/patterns are listed in the reference.

Usage

```
AA9int(Outcome, SNPdata, PairInfo,
          X=NULL, categXNames=NULL,
          TestType="WaldTest", ModelType="binomial", OR=FALSE)
```

Arguments

`Outcome`	Binary (`1`: event of interest; `0`: reference) or continuous variable.
`SNPdata`	SNP data: All SNP variables should have a character variable attribute and contain two of four letters (C, T, A, and G). No other letters or numbers should be used. An invalid character or blank field are considered to be missing values.
`PairInfo`	3 types of PairInfo: (1) 2d-vector: names of the given SNP pair for one-pair analyses. ex: c(`'SNP1','SNP2'`) (2) 2d-matrix or 2d-dataframe: names for candidate SNP pair. (3) `"all"`: for pairwise analyses.
`X`	Covariate(s) to be adjusted in the model (for missing values, keep the field blank), NULL=without covariate. Default is NULL.
`categXNames`	The variable names of categorical variables, `NULL`=without categorical covariates. Default is `NULL`.
`TestType`	Specify the statistical test type: `"WaldTest"` = the Wald test; `"LRT"` = the likelihood ratio test. Default is `"WaldTest"`.
`ModelType`	Model type: `"binomial"`=logistic regression; `"gaussian"`=linear regression. Default is `"binomial"`.
`OR`	If `TRUE` print the odds ratios, 95% confidence intervals and corresponding p-values.

Value

Returns a list with the following attributes:

`selectedModel`	The results of the best model with the lowest BIC value among the 9 models.
`res9Models`	For one-pair analyses only: Detailed results with all 9 models sorted by BIC (lowest first). Output variables: Var1: SNP 1; Var2: SNP 2 (the pattern/model labels are based on this order); Model: interaction model/pattern; Wald_Chisq: the Wald chi-square value of the interaction term; Wald_p: the Wald p-value of the interaction term; LRT_Chisq: the chi-square value of likelihood ratio test (LRT) for the interaction term; LRT_p: the LRT p-value of the interaction term; BIC: the Bayesian information criterion. The model with the lowest BIC value is preferred.
`OR`	For the "all" pairs analyses, only results of the best model will show. The group coding, please see suppl. Figures 1-3 in the end of this manual.

Author(s)

Hui-Yi Lin and Po-Yu Huang

References

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 J, 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. doi: 10.1093/bioinformatics/bty461. PubMed PMID: 29878078.

See Also

`parAA9int`, `SIPI`, `parSIPI`

Examples

```
##load data
data(simData)

#### define SNP data
SNPdata = simData[,3:12]

########################
### run AA9int one-pair analyses <Wald test>
########################

##  For a SNP pair of SNP2 and SNP8
```

```
res_snp_2v8 = AA9int(simData$D,SNPdata,c('SNP2','SNP8'))

## print out the best model
res_snp_2v8$selectedModel

## list of 9 models for one SNP pair
res_snp_2v8$res9Models


########################
### run AA9int for a list of multiple SNP pairs <Wald test>
########################

##  For 5 SNP pairs(1 v.s. 6, 2 v.s. 7, 3 v.s. 8, 4 v.s. 9, and 5 v.s. 10)
pairMatrix = c("SNP1","SNP2", "SNP3", "SNP4","SNP5","SNP6","SNP7","SNP8","SNP9","SNP10")

pairMatrix = matrix(pairMatrix,5)

pairMatrix = as.data.frame(pairMatrix)

res_snp = AA9int(simData$D,SNPdata,pairMatrix)




########################
### run AA9int pairwise analyses <Wald test>
########################

res_all = AA9int(simData$D,SNPdata,"all")



########################
### run AA9int pairwise analyses <Wald test> adjusted for covariates
###  [age(numeric), gender (binary), and group (categorical)]
########################

X1 = simData[,c('age','gender','group')]

res_all_cov = AA9int(simData$D,SNPdata,"all",X1,c("gender","group"))

########################
## export ORs and p-values
########################

try = AA9int(simData$D,SNPdata,"all", OR=TRUE)
write_OR_csv(try$OR,'C:/OR.csv')
write_OR_csv(try$selectedModel,'C:/p.csv')
```

Description

Outcome proportions by the 3-by-3 genotype combinations of a give SNP pair.

Usage

```
Grid3by3(Outcome, SNPdata, PairInfo)
```

Arguments

Outcome	Binary outcome variable name: a binary variable with "1" as the event of interest and "0" as the reference.
SNPdata	SNP data. All SNP variables should have a character variable attribute and contain two of four letters (C, T, A, and G). No other letters or numbers should be used. An invalid character or blank field are considered to be missing values.
PairInfo	c('SNP1','SNP2'): names of the given SNP pairs for one-pair analyses

Value

maj_min	Major and minor allele
table3by3	Present outcome proportions by genotype combinations
table3by3Freq	Sample size by genotype combinations

Author(s)

Hui-Yi Lin and Po-Yu Huang

See Also

plot3by3

Examples

```
##load data
data(simData)

#### define SNP data
SNPdata = simData[,3:12]

########################
### run Grid3by3
########################
Grid3by3(simData$D,SNPdata,c('SNP1','SNP2'))
```

MAFinfo *SNP minor allele frequency (MAF)*

Description

Obtain minor allele frequency (MAF) and major and minor allele.

Usage

```
MAFinfo(SNPdata)
```

Arguments

SNPdata	SNP data

Value

maj/min	major and minor allele
MAF	minor allele frequency
Missing (%)	missing vales

Author(s)

Hui-Yi Lin and Po-Yu Huang

References

Gonzalez JR, Armengol L, Sole X, Guino E, Mercader JM, Estivill X, Moreno V. SNPassoc: an R package to perform whole genome association studies. Bioinformatics, 2007;23(5):654-5.

Examples

```
data(simData)
SNPdata = simData[,3:12]
MAFinfo(SNPdata)
```

parAA9int *Parallel computing for AA9int*

Description

parAA9int is a parallel computing version of AA9int. This function can decrease computing time, which is useful for large-scale data.

Usage

```
parAA9int(Outcome, SNPdata, PairInfo,
             X=NULL, categXNames=NULL,
           TestType="WaldTest", ModelType="binomial", core_ratio=0.9, OR=FALSE)
```

Arguments

`Outcome`	Binary (`1`: event of interest; `0`: reference) or continuous variable.
`SNPdata`	SNP data: All SNP variables should have a character variable attribute and contain two of four letters (C, T, A, and G). No other letters or numbers should be used. No other letters or numbers should be used. Invalid character or field blank is considered to be missing values.
`PairInfo`	3 types of PairInfo: (1) 2d-vector: names of the given SNP pair for one-pair analyses. ex: c(`'SNP1','SNP2'`) (2) 2d-matrix or 2d-dataframe: names for candidate SNP pair. (3) `"all"`: for pairwise analyses.
`X`	Covariate(s) to be adjusted in the model (for missing values, keep the field blank), `NULL`=without covariate. Default is `NULL`.
`categXNames`	The variable names of categorical variables, `NULL`=without categorical covariates. Default is `NULL`.
`TestType`	Specify the statistical test type: `"WaldTest"` = the Wald test; `"LRT"` = the likelihood ratio test. Default is `"WaldTest"`.
`ModelType`	Model type: `"binomial"`=logistic regression; `"gaussian"`=linear regression. Default is `"binomial"`.
`core_ratio`	The ratio of total cores for parallel computing. Default is `0.9`.
`OR`	If `TRUE` print the odds ratios, 95% confidence intervals and corresponding p-values.

Value

Returns a data frame of the results of the best model with the lowest BIC value among the 9 models. For the "all" pairs analyses, only OR results of the best model will show. The group coding, please see suppl. Figures 1-3 in the end of this manual.)

Author(s)

Hui-Yi Lin and Po-Yu Huang

References

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 J, 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. doi: 10.1093/bioinformatics/bty461. PubMed PMID: 29878078.

See Also

AA9int, SIPI, and parSIPI

Examples

```
##load data
data(simData)

#### define SNP data
SNPdata = simData[,3:12]

########################
### run parAA9int pairwise analyses <Wald test>
########################

res_all = parAA9int(simData$D,SNPdata,"all")


########################
###run parAA9int pairwise analyses <Wald test> adjusted for covariates using SIPI with parallel computing
###[age(numeric), gender (binary), and group (categorical)]
########################

X1 = simData[,c('age','gender','group')]
res_all_X = parAA9int(simData$D,SNPdata,"all",X1,c("gender","group"))

########################
## export ORs and p-values
########################

try = parAA9int(simData$D,SNPdata,"all", OR=TRUE)
write_OR_csv(try$OR,'C:/OR.csv')
write_OR_csv(try$selectedModel,'C:/p.csv')
```

---

parSIPI *Parallel computing for SIPI*

Description

parSIPI is a parallel computing version of SIPI. This function can decrease computing time, which is useful for large-scale data.

Usage

```
parSIPI(Outcome, SNPdata, PairInfo,
        X=NULL, categXNames=NULL,
        TestType="WaldTest", ModelType="binomial", core_ratio=0.9, OR=FALSE)
```

Arguments

Outcome	Binary (1: event of interest; 0: reference) or continuous variable.

SNPdata	SNP data: All SNP variables should have a character variable attribute and contain two of four letters (C, T, A, and G). No other letters or numbers should be used. Invalid character or field blank is considered to be missing values.
PairInfo	3 types of PairInfo: (1) 2d-vector: names of the given SNP pair for one-pair analyses. ex: c('SNP1','SNP2') (2) 2d-matrix or 2d-dataframe: names for candidate SNP pair. (3) "all": for pairwise analyses.
X	Covariate(s) to be adjusted in the model (for missing values, keep the field blank), NULL=without covariate. Default is NULL.
categXNames	The variable names of categorical variables, NULL=without categorical covariates. Default is NULL.
TestType	Specify the statistical test type: "WaldTest" = the Wald test; "LRT" = the likelihood ratio test. Default is "WaldTest".
ModelType	Model type: "binomial"=logistic regression; "gaussian"=linear regression. Default is "binomial".
core_ratio	The ratio of total cores for parallel computing. Default is 0.9.
OR	If TRUE print the odds ratios, 95% confidence intervals and corresponding p-values.

Value

Returns a data frame of the results of the best model with the lowest BIC value among the 45 models for each SNP pair. For the "all" pairs analyses, only OR results of the best model will show. The group coding, please see suppl. Figures 1-3 in the end of this manual.)

Author(s)

Hui-Yi Lin and Po-Yu Huang

References

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.

See Also

SIPI

Examples

```
##load data
data(simData)

#### define SNP data
SNPdata = simData[,3:12]
```

```
########################
### run parSIPI pairwise analyses <Wald test>
########################

res_all = parSIPI(simData$D,SNPdata,"all")


########################
###run parSIPI pairwise analyses <Wald test> adjusted for covariates using SIPI with parallel computing
###[age(numeric), gender (binary), and group (categorical)]
########################

X1 = simData[,c('age','gender','group')]
res_all_X = parSIPI(simData$D,SNPdata,"all",X1,c("gender","group"))

########################
## export ORs and p-values
########################

try = parSIPI(simData$D,SNPdata,"all", OR=TRUE)
write_OR_csv(try$OR,'C:/OR.csv')
write_OR_csv(try$selectedModel,'C:/p.csv')
```

---

plot3by3 *Heatmap plot of outcome proportions by genotype combinations*

Description

Create a heatmap plot of outcome proportions by the 3-by-3 genotype combinations for a given SNP pair.

Usage

```
plot3by3(x, SNP_info = T, outcome = T, freq=T, legend = T, monochrome = F,
            scale = "fixed", axis_fs = 1, outcome_fs = 1, freq_fs = 1, lgd_fs = 1)
```

Arguments

x	List object output from function Grid3by3.
SNP_info	Put SNP information(SNP name and major/minor allele) on plot. Default is TRUE.
outcome	Include outcome proportions in each cell of plot. Default is TRUE. When no observations is in the given cell, 'NaN' will be shown. If there is no observation and outcome=FALSE, a warning will be shown.
freq	Include frequency in each cell. Default is TRUE.
legend	Include legend. Default is TRUE.
monochrome	Output monochrome plot. Default is FALSE
scale	A character string specifying the colour gradient scale type. "fixed" will lend color to heatmap with fixed color gradient scale from 0 to 1, "sliding" will lend color to heatmap with sliding gradient scale between minimum and maximum outcome proportion. Default is "fixed".

axis_fs	Axis font size. Adjusted both axis title font size and axis label font size. Number greater than 1 will enlarge the font size, less than 1 will reduce the font size. Default is 1.
outcome_fs	Outcome font size. Number greater than 1 will enlarge the font size, less than 1 will reduce the font size. Default is 1.
freq_fs	Frequency font sizr. Number greater than 1 will enlarge the font size, less than 1 will reduce the font size. Default is 1.
lgd_fs	Legend font size. Number greater than 1 will enlarge the font size, less than 1 will reduce the font size. Default is 1.

Details

This function creates a heatmap plot based on the output of Grid3by3, which generates outcome proportions by genotype combinations of a given SNP pair.

Value

A heatmap plot of outcome proportions, which is a ggplot object.

Author(s)

Hui-Yi Lin and Heng-Yuan Tung

References

H. Wickham. ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York, 2009.

See Also

Grid3by3

Examples

```
##load data
data(simData)

#### define SNP data
SNPdata = simData[,3:12]

########################
### run plot3by3
########################
x = Grid3by3(simData$D, SNPdata, c('SNP1', 'SNP2'))
plot3by3(x, SNP_info = F, outcome = F, legend = T, scale = "fixed", monochrome = T, lgd_fs = 1.2)

x = Grid3by3(simData$D, SNPdata, c('SNP4', 'SNP6'))
plot3by3(x, scale = "sliding", axis_fs = 1.2, outcome_fs = 0.9, freq_fs = 0.8)
plot3by3(x, scale = "sliding", freq = F, axis_fs = 1.2, outcome_fs = 0.9)
```

simData *An example data set*

Description

simData is an example dataset with one binary outcome variable (D), the 10 SNPs, and three covariates [age (numeric), gender (binary), and group (categorical)].

Usage

```
data(simData)
```

Format

A data frame with 1000 observations on the following 12 variables.

id A numeric vector for identification.

D A numeric vector for a binary outcome with "1" as the event of interest and "0" as the reference.

SNP1 to SNP10 A factor has three genotypes, which are composed of two of the four letters (C, T, A, and G), such as CC, TC and TT.

age numeric age.

gender 0: female, 1: male.

group 1: Group 1; 2: Group 2; and 3: Group 3.

Examples

```
data(simData)
```

SIPI *SNP Interaction Pattern Identifier (SIPI): Detect SNP-SNP interactions through testing the 45 models*

Description

SNP Interaction Pattern Identfier (SIPI) evaluates SNP-SNP interactions associated with a binary or continuous outcome. The primary strengths of SIPI are (1) taking non-hierarchical models, reverse coding and inheritance modes (dominant, recessive and additive mode) into consideration and (2) using BIC to search for a best interaction pattern. For each SNP pair, the SIPI evaluates 45 interaction models. The best interaction pattern is the one with the lowest value of the Bayesian information criterion (BIC). The details of the 45 models/patterns are listed in the SIPI published paper.

Usage

```
SIPI(Outcome, SNPdata, PairInfo,
     X=NULL, categXNames=NULL,
     TestType="WaldTest", ModelType="binomial", OR=FALSE)
```

Arguments

`Outcome`	Binary (`1`: event of interest; `0`: reference) or continuous variable.
`SNPdata`	SNP data: All SNP variables should have a character variable attribute and contain two of four letters (C, T, A, and G). No other letters or numbers should be used. Invalid character or field blank is considered to be missing values.
`PairInfo`	3 types of PairInfo: (1) 2d-vector: names of the given SNP pair for one-pair analyses. ex: `c('SNP1','SNP2')` (2) 2d-matrix or 2d-dataframe: names for candidate SNP pair. (3) `"all"`: for pairwise analyses.
`X`	Covariate(s) to be adjusted in the model (for missing values, keep the field blank), `NULL`=without covariate. Default is `NULL`.
`categXNames`	The variable names of categorical variables, `NULL`=without categorical covariates. Default is `NULL`.
`TestType`	Specify the statistical test type: `"WaldTest"` = the Wald test; `"LRT"` = the likelihood ratio test. Default is `"WaldTest"`.
`ModelType`	Model type: `"binomial"`=logistic regression; `"gaussian"`=linear regression. Default is `"binomial"`.
`OR`	If `TRUE` print the odds ratios, 95% confidence intervals and corresponding p-values.

Value

Returns a list with the following attributes:

`selectedModel`	The results of the best model with the lowest BIC value among the 45 models.
`res45Models`	For one-pair analyses only: Detailed results with all 45 models sorted by BIC (lowest first). Output variables: Var1: SNP 1; Var2: SNP 2 (the pattern/model labels are based on this order); Model: interaction model/pattern; Wald_Chisq: the Wald chi-square value of the interaction term; Wald_p: the Wald p-value of the interaction term; LRT_Chisq: the chi-square value of likelihood ratio test (LRT) for the interaction term; LRT_p: the LRT p-value of the interaction term; BIC: the Bayesian information criterion. The model with the lowest BIC value is preferred.
`OR`	For the "all" pairs analyses, only results of the best model will show. The group coding, please see suppl. Figures 1-3 in the end of this manual.

Author(s)

Hui-Yi Lin and Po-Yu Huang

References

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.

See Also

parSIPI, AA9int, and parAAint

Examples

```
##load data
data(simData)

#### define SNP data
SNPdata = simData[,3:12]

########################
### run SIPI one-pair analyses <Wald test>
########################

##  For a SNP pair of SNP2 and SNP8
res_snp_2v8 = SIPI(simData$D,SNPdata,c('SNP2','SNP8'))

## print out the best model
res_snp_2v8$selectedModel

## list of 45 models for one SNP pair
res_snp_2v8$res45Models


########################
### run SIPI for a list of multiple SNP pairs <Wald test>
########################

##  For 5 SNP pairs(1 v.s. 6, 2 v.s. 7, 3 v.s. 8, 4 v.s. 9, and 5 v.s. 10)
pairMatrix = c("SNP1","SNP2", "SNP3", "SNP4","SNP5","SNP6","SNP7","SNP8","SNP9","SNP10")

pairMatrix = matrix(pairMatrix,5)

pairMatrix = as.data.frame(pairMatrix)

res_snp = SIPI(simData$D,SNPdata,pairMatrix)


########################
### run SIPI pairwise analyses <Wald test>
########################

res_all = SIPI(simData$D,SNPdata,"all")


########################
### run SIPI pairwise analyses <Wald test> adjusted for covariates
###  [age(numeric), gender (binary), and group (categorical)]
########################

X1 = simData[,c('age','gender','group')]

res_all_cov = SIPI(simData$D,SNPdata,"all",X1,c("gender","group"))

########################
```

```
## export ORs and p-values
########################

try = SIPI(simData$D,SNPdata,"all", OR=TRUE)
write_OR_csv(try$OR,'C:/OR.csv')
write_OR_csv(try$selectedModel,'C:/p.csv')
```

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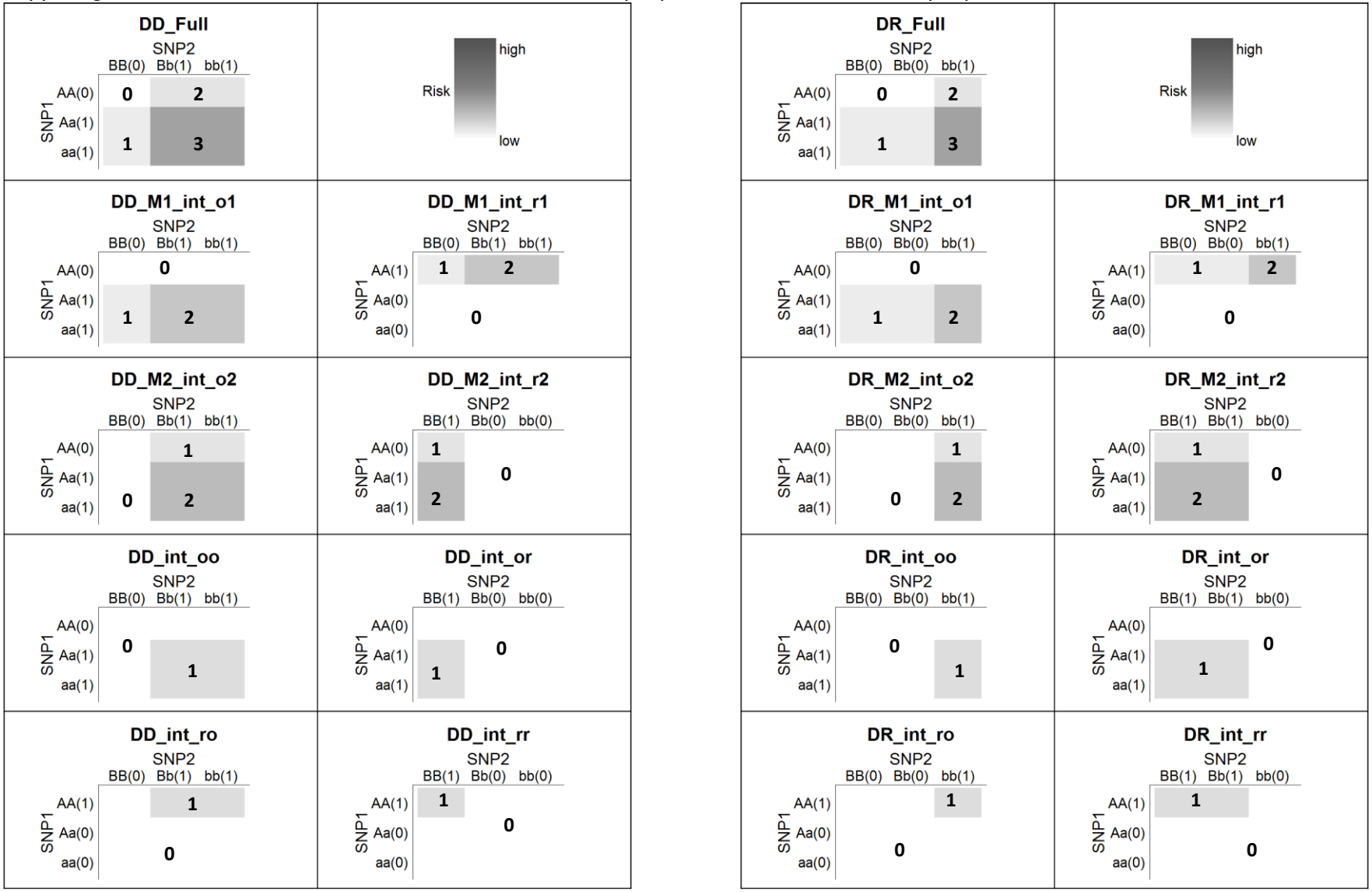
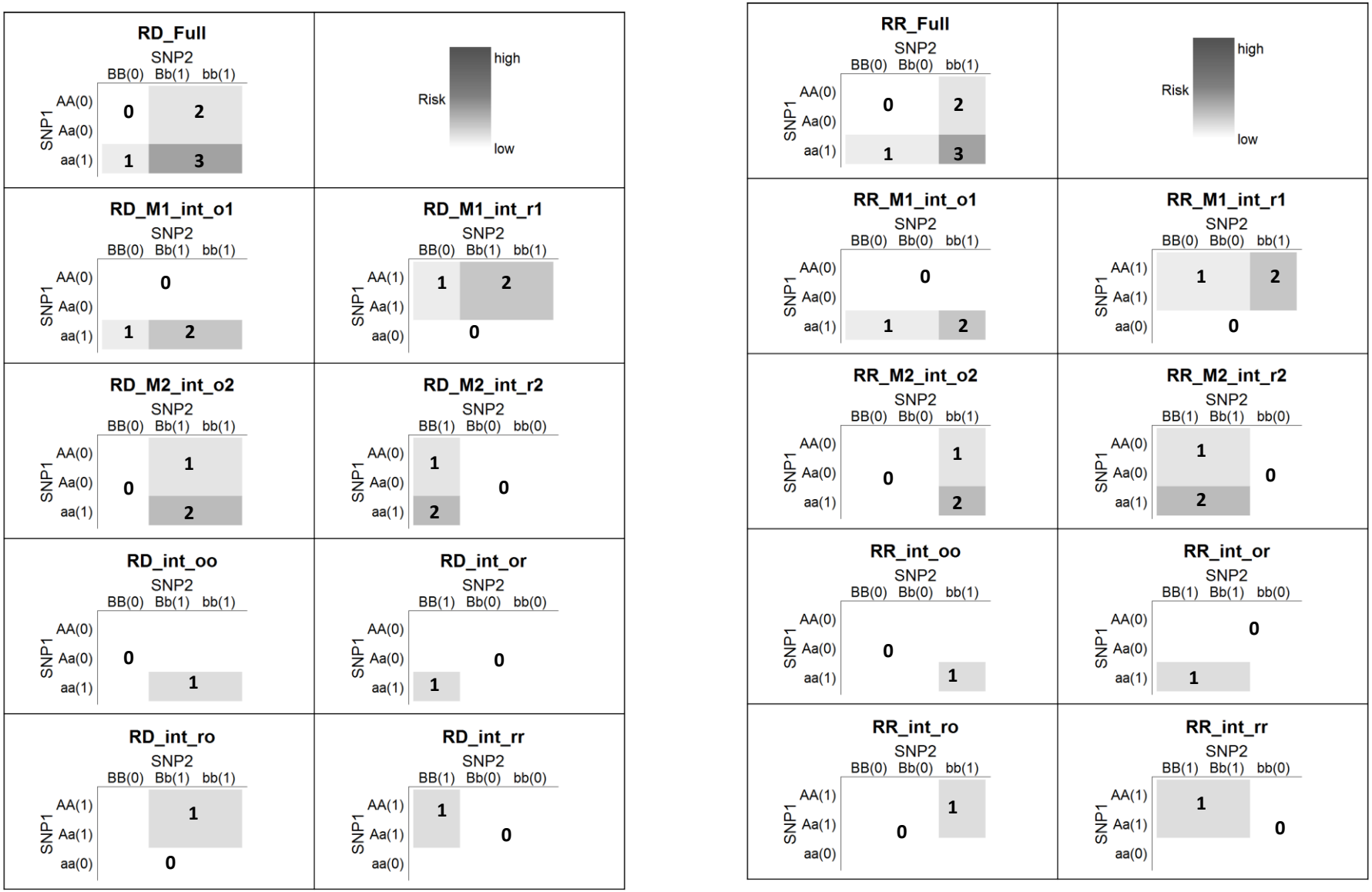
Suppl. Figure 1. SIPI interaction models: dominant-dominant (DD) and dominant-recessive (DR) modes[1,2]



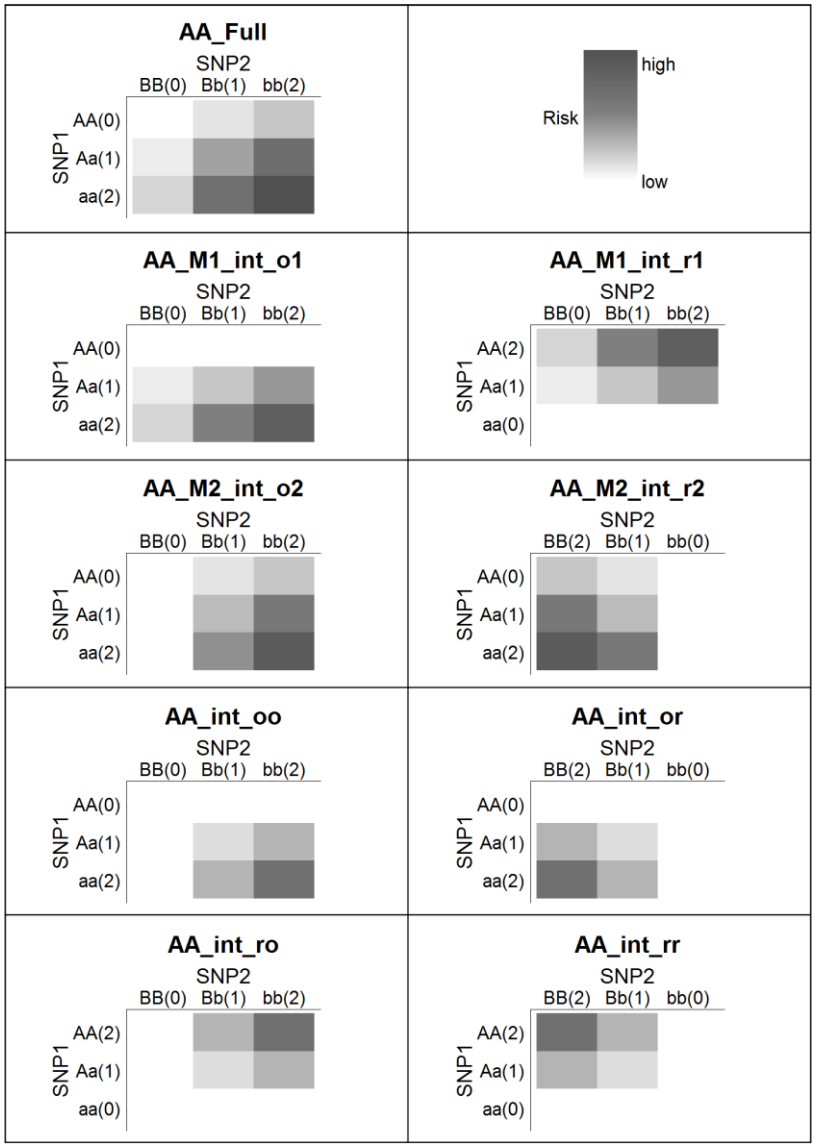
[1] **Model label**: 'D' (dominant), 'R' (recessive); 'Full' (full interaction), 'M1_int' (SNP1 main effect plus interaction); coding direction: 'o1' (original for SNP1), 'o2' (original for SNP2), r1' (reverse for SNP1), 'r2' (reverse for SNP2), 'oo' (original-original for SNP1-SNP2), 'or' (reverse-original), 'ro' (reverse-original), and 'rr' (reverse-reverse). The labels of two axes are '**genotype (coding)**'. A lowercase and capital letter denotes the minor and major allele, respectively. Color levels represent present outcome proportions. The darker the color, the higher the outcome proportion. For the 'Full' model, the figure is an example pattern based on both minor alleles as risk alleles. These plots are the SIPI pattern examples based on positive model coefficients in SIPI models. If coding direction ('o'/'r') is not specified, the original coding is applied. [2] **The bold numbers inside table are the group labels for modeling (0: reference).**

Suppl. Figure 2. SIPI interaction models: recessive-dominant (RD) and recessive-recessive (RR) modes[1,2]



[1] **Model label**: 'D' (dominant), 'R' (recessive); 'Full' (full interaction), 'M1_int' (SNP1 main effect plus interaction); coding direction: 'o1' (original for SNP1), 'o2' (original for SNP2), r1' (reverse for SNP1), 'r2' (reverse for SNP2), 'oo' (original-original for SNP1-SNP2), 'or' (reverse-original), 'ro' (reverse-original), and 'rr' (reverse-reverse). The labels of two axes are '**genotype (coding)**'. A lowercase and capital letter denotes the minor and major allele, respectively. Color levels represent present outcome proportions. The darker the color, the higher the outcome proportion. For the 'Full' model, the figure is an example pattern based on both minor alleles as risk alleles. These plots are the SIPI pattern examples based on positive model coefficients in SIPI models. If coding direction ('o'/'r') is not specified, the original coding is applied. [2] **The bold numbers inside table are the group labels for modeling (0: reference).**

Suppl. Figure 3. SIPI interaction models: additive-additive (AA) mode[1,2]



[1] **Model label**: 'A' (additive); 'Full' (full interaction), 'M1_int' (SNP1 main effect plus interaction); coding direction: 'o1' (original for SNP1), 'o2' (original for SNP2), r1' (reverse for SNP1), 'r2' (reverse for SNP2), 'oo' (original-original for SNP1-SNP2), 'or' (reverse-original), 'ro' (reverse-original), and 'rr' (reverse-reverse). The labels of two axes are '**genotype (coding)**'. A lowercase and capital letter denotes the minor and major allele, respectively. Color levels represent present outcome proportions. The darker the color, the higher the outcome proportion. For the 'Full' model, the figure is an example pattern based on both minor alleles as risk alleles. These plots are the SIPI pattern examples based on positive model coefficients in SIPI models. If coding direction ('o'/'r') is not specified, the original coding is applied.