

# Package ‘SNPmaxsel’

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**Title** Maximally selected statistics for SNP data

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**Depends** R (>= 2.2.1), mvtnorm, combinat

**Suggests** mvtnorm, combinat

**Description** This package implements asymptotic methods related to maximally selected statistics, with applications to SNP data.

**License** GPL (>= 2)

**URL** <http://cran.r-project.org/web/packages/SNPmaxsel/index.html>

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Fasymp	<i>Asymptotical distribution of the maximally selected chi-square statistic</i>
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### Description

This function computes the asymptotical distribution of the maximally selected chi-square statistic, where maximal selection is performed over the test statistics defined by type or user-defined through groups.

### Usage

```
Fasymp(t, a.vec, type=NULL, groups=NULL)
```

### Arguments

t	the value at which the distribution function has to be computed.
a.vec	A vector of length K giving the proportion of observations in each category. Its sum must be 1. If type="inter.ord" or "inter.cat", a.vec must have length 9.
type	must be one of "ordinal", "all.pairs", "all.partitions", "inter.ord", "inter.cat", "inter.ord.main". If type=NULL, the chi-square statistics are computed for the groups defined by groups
groups	If type=NULL, the chi-square statistics are computed for the groups defined by groups. groups must be a list with m elements, where m is the number of considered chi-square statistics. Each element is a list with two elements group1 and group2. groups\$group1 and groups\$group2 are numeric vectors giving the indices of the categories included in both groups. See example below.

### Details

This function uses the function pmvnorm from the package mvtnorm. If the considered test statistics are defined by groups, groups should not have more than 100 elements, since the pmvnorm function becomes unstable (or computationally prohibitive) for such a high dimension.

### Value

the value of the distribution function at t.

### Author(s)

Anne-Laure Boulesteix ([http://www.ibe.med.uni-muenchen.de/organisation/mitarbeiter/020\\_professuren/boulesteix/index.html](http://www.ibe.med.uni-muenchen.de/organisation/mitarbeiter/020_professuren/boulesteix/index.html))

### References

Boulesteix AL, Strobl C, Weidinger S, Wichmann HE, Wagenpfeil S, 2007. Multiple testing for SNP-SNP interactions. *Statistical Applications in Genetics and Molecular Biology* 6:37.

**See Also**

[maxsel.asymp.test](#), [maxsel](#).

**Examples**

```
# load SNPmaxsel library
# library(SNPmaxsel)

Fasymp(t=2,a.vec=c(0.2,0.1,0.05,0.05,0.6),type="ord")
Fasymp(t=2,a.vec=c(0.2,0.1,0.05,0.05,0.6),type="all.pairs")
Fasymp(t=2,a.vec=c(0.2,0.1,0.05,0.05,0.6),type="all.partitions")

Fasymp(t=2,a.vec=c(0.2,0.1,0.1,0.1,0.05,0.05,0.05,0.05,0.3),type="inter.ord")
Fasymp(t=2,a.vec=c(0.2,0.1,0.1,0.1,0.05,0.05,0.05,0.05,0.3),type="inter.cat")

# Creating a user-defined groups list
# (corresponding to type)="ord" with K=5)
my.groups<-list(list(group1=1,group2=2:5),list(group1=1:2,group2=3:5),
list(group1=1:3,group2=4:5),list(group1=1:4,group2=5))

Fasymp(t=2,a.vec=c(0.2,0.1,0.05,0.05,0.6),type=NULL,groups=my.groups)
```

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maxsel

*Computes maximally selected chi-square statistics*


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**Description**

The function `maxsel` computes the maximal chi-square statistic over some candidate binary splits specified by `type`.

**Usage**

```
maxsel(x1,x2=NULL,y,type="inter.ord")
```

**Arguments**

<code>x1</code>	a numeric vector of length <code>n</code> giving the values of the variable <code>x1</code> for the considered <code>n</code> observations. The classes must be coded as <code>1,...,K</code> .
<code>x2</code>	a numeric vector of length <code>n</code> giving the values of the variable <code>x2</code> for the considered <code>n</code> observations. <code>x2</code> should be <code>NULL</code> (default) for all types other than <code>"inter.ord"</code> , <code>"inter.cat"</code> and <code>"inter.ord.main"</code> . Since interactions are implemented for <code>K=3</code> only (SNPs), <code>x2</code> must be coded as <code>1,2,3</code> .
<code>y</code>	a numeric vector of length <code>n</code> giving the class (response variable <code>Y</code> ) of the considered <code>n</code> observations. The classes must be coded as <code>0</code> and <code>1</code> .
<code>type</code>	must be one of <code>"ordinal"</code> , <code>"all.pairs"</code> , <code>"all.partitions"</code> , <code>"inter.ord"</code> , <code>"inter.cat"</code> , <code>"inter.ord.main"</code> .

**Value**

the value of the maximally selected chi-square statistic.

**Author(s)**

Anne-Laure Boulesteix ([http://www.ibe.med.uni-muenchen.de/organisation/mitarbeiter/020\\_professuren/boulesteix/index.html](http://www.ibe.med.uni-muenchen.de/organisation/mitarbeiter/020_professuren/boulesteix/index.html))

**References**

Boulesteix AL, Strobl C, Weidinger S, Wichmann HE, Wagenpfeil S, 2007. Multiple testing for SNP-SNP interactions. *Statistical Applications in Genetics and Molecular Biology* 6:37.

**See Also**

[maxsel.asymp.test](#), [Fasymp](#).

**Examples**

```
# load SNPmaxsel library
# library(SNPmaxsel)

x1<-sample(5,1000,replace=TRUE)
y<-sample(c(0,1),1000,replace=TRUE)

maxsel(x1=x1,y=y,type="ord")
maxsel(x1=x1,y=y,type="all.pairs")
maxsel(x1=x1,y=y,type="all.partitions")

x1<-sample(3,1000,replace=TRUE)
x2<-sample(3,1000,replace=TRUE)

maxsel(x1=x1,x2=x2,y=y,type="inter.ord")
maxsel(x1=x1,x2=x2,y=y,type="inter.cat")
maxsel(x1=x1,x2=x2,y=y,type="inter.ord.main")
```

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maxsel.asymp.test

*Test of independence based on maximally selected statistics*

---

**Description**

The function `maxsel.test` computes the probability that the maximally selected chi-square statistic is  $\leq$  than the value observed from the data, under the null-hypothesis of no association between  $X$  and  $Y$ , given the proportions of observations with  $X=1, \dots, X=K$ . The candidate binary splits over which the chi-square statistic is maximized is specified by `type`. If  $x$  denotes the output of the function `maxsel.asymp.test`,  $1-x$  may be seen as the p-value of an independence test.

**Usage**

```
maxsel.asymp.test(x1,x2=NULL,y,type)
```

**Arguments**

x1	a numeric vector of length n giving the values of the variable x1 for the considered n observations. The classes must be coded as 1,...,K.
x2	a numeric vector of length n giving the values of the variable x2 for the considered n observations. x2 should be NULL (default) for all types other than "inter.ord", "inter.cat" and "inter.ord.main". Since interactions are implemented for K=3 only (SNPs), x2 must be coded as 1,2,3.
y	a numeric vector of length n giving the class (response variable Y) of the considered n observations. The classes must be coded as 0 and 1.
type	must be one of "ordinal", "all.pairs", "all.partitions", "inter.ord", "inter.cat", "inter.ord.main".

**Details**

See Boulesteix et al (2007).

**Value**

maxselstat	the observed maximally selected statistic.
value	the value of the distribution function of the maximally selected statistic at maxselstat.

**Author(s)**

Anne-Laure Boulesteix ([http://www.ibe.med.uni-muenchen.de/organisation/mitarbeiter/020\\_professuren/boulesteix/index.html](http://www.ibe.med.uni-muenchen.de/organisation/mitarbeiter/020_professuren/boulesteix/index.html))

**References**

Boulesteix AL, Strobl C, Weidinger S, Wichmann HE, Wagenpfeil S, 2007. Multiple testing for SNP-SNP interactions. *Statistical Applications in Genetics and Molecular Biology* 6:37.

**See Also**

[maxsel](#), [Fasymp](#).

**Examples**

```
# load SNPmaxsel library
# library(SNPmaxsel)

x1<-sample(5,1000,replace=TRUE)
y<-sample(c(0,1),1000,replace=TRUE)

maxsel.asymp.test(x1=x1,y=y,type="ord")
maxsel.asymp.test(x1=x1,y=y,type="all.pairs")
```

```
maxsel.asymp.test(x1=x1,y=y,type="all.partitions")

x1<-sample(3,1000,replace=TRUE)
x2<-sample(3,1000,replace=TRUE)

maxsel.asymp.test(x1=x1,x2=x2,y=y,type="inter.ord")
maxsel.asymp.test(x1=x1,x2=x2,y=y,type="inter.cat")
maxsel.asymp.test(x1=x1,x2=x2,y=y,type="inter.ord.main")
```

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transf.inter

*Transforms a pair of SNPs into a single variable with nine categories*

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### Description

The function `transf.inter` creates a new variable with 9 categories out of a pair of variables with 3 categories (e.g. SNPs). The new variable is generated as described in Boulesteix et al (2007): =1 if  $x_1=1$  and  $x_2=1$ , =2 if  $x_1=2$  and  $x_2=1$ , =3 if  $x_1=3$  and  $x_2=1$ , =4 if  $x_1=1$  and  $x_2=2$ , =5 if  $x_1=2$  and  $x_2=2$ , =6 if  $x_1=3$  and  $x_2=2$ , =7 if  $x_1=1$  and  $x_2=3$ , =8 if  $x_1=2$  and  $x_2=3$ , =9 if  $x_1=3$  and  $x_2=3$ .

### Usage

```
transf.inter(x1,x2)
```

### Arguments

`x1` a numeric vector of length `n` giving the first SNP, coded as 1,2,3.  
`x2` a numeric vector of length `n` giving the second SNP, coded as 1,2,3.

### Value

a numeric vector of length `n` containing the new variable with 9 categories.

### Author(s)

Anne-Laure Boulesteix ([http://www.ibe.med.uni-muenchen.de/organisation/mitarbeiter/020\\_professuren/boulesteix/index.html](http://www.ibe.med.uni-muenchen.de/organisation/mitarbeiter/020_professuren/boulesteix/index.html))

### References

Boulesteix AL, Strobl C, Weidinger S, Wichmann HE, Wagenpfeil S, 2007. Multiple testing for SNP-SNP interactions. *Statistical Applications in Genetics and Molecular Biology* 6:37.

### See Also

[maxsel](#), [maxsel.asymp.test](#).

**Examples**

```
# load SNPmaxsel library
# library(SNPmaxsel)

x1<-sample(3,100,replace=TRUE)
x2<-sample(3,100,replace=TRUE)

transf.inter(x1,x2)
```

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