Package ‘genstab’

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Type Package
Title Resampling Based Yield Stability Analyses
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Description Several yield stability analyses are mentioned in this package: variation and regression based yield stability analyses. Resampling techniques are integrated with these stability analyses. The function stab.mean() provides the genotypic means and ranks including their corresponding confidence intervals. The function stab.var() provides the genotypic variances over environments including their corresponding confidence intervals. The function stab.fw() is an extended method from the Finlay-Wilkinson method (1963). This method can include several other factors that might impact yield stability. Resampling technique is integrated into this method. A few missing data points or unbalanced data are allowed too. The function stab.fw.check() is an extended method from the Finlay-Wilkinson method (1963). The yield stability is evaluated via common check line(s). Resampling technique is integrated.
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maize

Maize yield trial data

Description
Maize yield trial data

Usage
maize

Format
An object of class data.frame with 260 rows and 4 columns.

References

Examples
str(maize)

stab.fw

F-W Regression Based Yield Stability Analysis

Description
F-W Regression Based Yield Stability Analysis

Usage
stab.fw(y, Gen, Env, times, Rep, X = NULL, alpha = NULL)

Arguments
y A vector of yield data
Gen A vector of Genotypes
Env A vector of Environments
times Replication number for resampling
Rep Replication included or not included
X Independent variables matrix or vector
alpha Preset alpha value
Value

A list of yield stability results

References


Examples

```r
require(genstab)
data(maize)
#names(maize)
Geno=as.vector(maize$Cultivar)
Env=paste(maize$Location,maize$Year,sep=":")
y=maize$Yld
res=stab.fw(y,Gen=Geno,Env=Env,times=10,Rep=TRUE)
res
```

---

**stab.fw.check**

*Check-based yield stability analysis*

Description

Check-based yield stability analysis

Usage

```r
stab.fw.check(y, Gen, Env, times, check, Rep, X = NULL, alpha = NULL)
```

Arguments

- **y**
  A response variable vector used for stability analysis
- **Gen**
  A vector of genotypes.
- **Env**
  A vector of environments.
- **times**
  Times of resampling used for stability analysis.
- **check**
  One or more checks used for stability analysis.
- **Rep**
  An argument with replication: Rep=TRUE or with replication: Rep=FALSE
- **X**
  A vector or matrix of other predictable variables. Default is NULL.
- **alpha**
  A nominal probability values used for statistical tests. Default is NULL, 0.05
stab.mean

Value

A list of yield stability results

References


Examples

data(maize)
#names(maize)
Geno=as.vector(maize$Cultivar)
Env=paste(maize$Location,maize$Year,sep=":")
y=maize$Yld
res=stab.fw.check(y,Geno=Geno,Env=Env,times=10,check=c("Hai He"),Rep=FALSE)
res

stab.mean

Group means and ranks with resampling

Description

Group mean and rank calculation with two resampling techniques: permutation and bootstrapping

Usage

stab.mean(Y, class, cls2 = NULL, resample, times = NULL, alpha = NULL)

Arguments

Y
A matrix including One or more traits

class
A vector of the first factor for calculating variance. For example, a vector of genotypes.

cls2
A vector of the second factor used within-group bootstrapping for variance. It can be default

resample
Resampling technique option. resample="Boot" is for bootstrapping. resample="Perm" is for permutation.

times
Number of resampling used. The default number is 1000.

alpha
A nominal probability used for statistical test. The default value is 0.05.
Value

A list of variances and confidence intervals for genotypes or environments

Author(s)

Jixiang Wu <jixiang.wu@sdstate.edu>

References


Examples

data(maize)
#names(maize)

Geno=as.vector(maize$Cultivar)
Env=paste(maize$Location,maize$Year,sep=":")
y=maize$Yld

res=stab.mean(y,class=Geno,cls2=Env,resample="Boot",times=100)
res

res=stab.mean(y,class=Geno,resample="Perm",times=100)
res

stab.var

Group variances with resampling

Description

Group variance calculation with two resampling techniques: permutation and bootstrapping

Usage

stab.var(Y, class, cls2 = NULL, resample, times = NULL, alpha = NULL)

Arguments

Y A matrix including one or more traits
class A vector of the first factor for calculating variance. For example, a vector of genotypes.
cls2 A vector of the second factor used within-group bootstrapping for variance. It can be default
resample Resampling technique option. resample="Boot" is for bootstrapping. resample="Perm" is for permutation.
times Number of resampling used. The default number is 1000.
alpha A nominal probability used for statistical test. The default value is 0.05.

Value
A list of variances and confidence intervals for genotypes or environments

Author(s)
Jixiang Wu <jixiang.wu@sdstate.edu>

References

Examples
data(maize)
#names(maize)
Geno=as.vector(maize$Cultivar)
Env=paste(maize$Location,maize$Year,sep=":")
y=maize$Yld
res=stab.var(y,class=Geno,cls2=Env,resample="Boot",times=100)
res
res=stab.var(y,class=Geno,resample="Perm",times=100)
res
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