Package ‘phenability’

February 24, 2015

Type Package
Title Nonparametric Stability Analysis
Version 2.0
Date 2015-02-24
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Description An alternative to carrying out phenotypic adaptability and stability analyses, taking into account nonparametric statistics. Can be used as a robust approach, less sensitive to departures from common genotypic, environmental, and GxE effects data assumptions (e.g., normal distribution of errors).
Depends calibrate, R (>= 2.12.0)
License GPL-3
NeedsCompilation no
Repository CRAN
Date/Publication 2015-02-24 20:22:46

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Description

An alternative to carrying out phenotypic adaptability and stability analysis, taking into account nonparametric statistics. Can be used as a robust approach, and less sensitive to departures from common genotypic, environmental, and GxE effects data assumptions (e.g., normal distribution of errors).

Arguments

- **function**: nahu, kang, fox, or thsu
- **data**: A numeric data.frame with fenotypic means values of MET, and genotypes and environments by rows and columns, respectively.
- **interaction**: do a interaction plot or not (FALSE = no interaction plot output, TRUE = draws a interaction plot between genotypes and environments).

Details

- **Package**: phenability
- **Type**: Package
- **Version**: 2.0
- **Date**: 2015-02-24
- **License**: GPU-3

The package can be applied to MET (multienvironment trials) data containing the phenotypic mean of genotype x environment (dataframe with genotypes by rows and environments into columns) and performs nonparametric analysis according to for criteria: Huehn (1979), and Nassar and Huehn (1987); Kang’s (1988); Fox et al. (1990) and; Thenarasu’s (1995).

Author(s)

Leonardo Castelo Branco

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References


Examples

```r
require(phenability)
data(bean.data)
bean.data
x <- bean.data

fox(x)
fox(x, interaction=TRUE)

kang(x)
kang(x, interaction=TRUE)

thsu(x)
thsu(x, interaction=TRUE)

nahu(x)
nahu(x, interaction=TRUE)
```

bean.data  
Bean Data

Description

A simulated bean yield data.frame

Usage

data(bean.data)
Format

A data frame with 20 genotypes on the following 10 environments.

amb1  a numeric vector
amb2  a numeric vector
amb3  a numeric vector
amb4  a numeric vector
amb5  a numeric vector
amb6  a numeric vector
amb7  a numeric vector
amb8  a numeric vector
amb9  a numeric vector
amb10 a numeric vector

Examples

data(bean.data)
## maybe str(bean.data) ; plot(bean.data) ...

---

fox  

Fox Function

Description

Performs a stability analysis based on the criteria of Fox et al. (1990), using the statistical "TOP third" only. In Fox function, a stratified ranking of the genotypes at each environment separately is done. The proportion of sites at which the genotype occurred in the top third are expressed in TOP output.

Usage

fox(data, interaction=FALSE)

Arguments

fox  fox function
data  A numeric data.frame with phenotypic means values of MET, and genotypes and environments by rows and columns, respectively.
interaction  do a interaction plot or not (FALSE = no interaction plot output, TRUE = draws a interaction plot between genotypes and environments).

Value

Is returned a list with numerical TOP ranking value by genotype, the ranking for the response variable in each environment, and the Spearman correlation matrix between environments.
kang

Author(s)

Leonardo Castelo Branco

References


Examples

```r
require("phenability")
data(bean.data)
bean.data
x <- bean.data

fox(x, interaction=TRUE)
```

---

**kang**

*Kang Function*

Description

Performs a stability analysis based on the Kang (1988) criteria. Kang nonparametric stability (ranksum) uses both "trait single value" and stability variance (Shukla, 1972), and the genotype with the lowest ranksum is commonly the most favorable one.

Usage

```r
kang(data, interaction=FALSE)
```

Arguments

- **kang**: kang function
- **data**: A numeric data.frame with phenotypic means values of MET, and genotypes and environments by rows and columns, respectively.
- **interaction**: do a interaction plot or not (FALSE = no interaction plot output, TRUE = draws a interaction plot between genotypes and environments).

Value

Is returned a list with "ranksum" value by genotype, the ranking for the response variable in each environment, and the Spearman correlation matrix between environments.

Author(s)

Leonardo Castelo Branco
References


Examples

```r
require("phenability")
data(bean.data)
bean.data
x <- bean.data
kang(x, interaction=TRUE)
```

---

**nahu**  
**Nassar and Huehn Function**

**Description**

Performs a stability analysis based on Nassar and Huehn (1987) and, Huehn (1979) statistics. The four nonparametric measures of phenotypic stability are: S1 (mean of the absolute rank differences of a genotype over the n environments), S2 (variance among the ranks over the k environments), S3 (sum of the absolute deviations), and S6 (relative sum of squares of rank for each genotype).

**Usage**

```r
nahu(data, interaction=FALSE)
```

**Arguments**

- `nahu`: nahu function
- `data`: A numeric data.frame with phenotypic means values of MET, and genotypes and environments by rows and columns, respectively.
- `interaction`: do a interaction plot or not (FALSE = no interaction plot output, TRUE = draws a interaction plot between genotypes and environments).

**Value**

Is returned a list with four numerical statistics values (S1, S2, S3, and S6) by genotype, the ranking for the response variable in each environment, and the Spearman correlation matrix between environments.

**Author(s)**

Leonardo Castelo Branco
References


Examples

```r
require("phenability")
data(bean.data)
bean.data
x <- bean.data

nahu(x, interaction = TRUE)
```

<table>
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<tr>
<th>thsu</th>
<th>Thennarasu Function</th>
</tr>
</thead>
</table>

Description

Performs a stability analysis according to Thennarasu (1995) methodology. Therefore the statistics N1, N2, N3, N4 are presented in output.

Usage

```
thsu(data, interaction=FALSE)
```

Arguments

```r
thsu function
data A numeric data.frame with fenotypic means values of MET, and genotypes and environments by rows and columns, respectively.
interaction do a interaction plot or not (FALSE = no interaction plot output, TRUE = draws a interaction plot between genotypes and environments).
```

Value

Is returned a list with four numerical statistics values (N1, N2, N3, and N4) by genotype, the ranking for the response variable in each environment, and the Spearman correlation matrix between environments.

Author(s)

Leonardo Castelo Branco
References

Examples

```r
require("phenability")
data(bean.data)
bean.data
x <- bean.data

thsu(x, interaction = TRUE)
```
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