

Package ‘phenability’

February 24, 2015

Type Package

Title Nonparametric Stability Analysis

Version 2.0

Date 2015-02-24

Author Leonardo Castelo Branco

Maintainer Leonardo C. Branco <leonardocb@usp.br>

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

R topics documented:

phenability-package	2
bean.data	3
fox	4
kang	5
nahu	6
thsu	7

Index	9
--------------	----------

 phenability-package *Nonparametric Stability Analysis*

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 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).

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; Thennarasu's (1995).

Author(s)

Leonardo Castelo Branco

Maintainer: Leonardo C. Branco <leonardocb@usp.br>

References

Fox, P.N., B. Skovmand, B.K. Thompson, H.J. Braun, and R. Cormier. 1990. Yield and adaptation of hexaploid spring triticale. *Euphytica* 47:57.

Huehn, V.M. 1979. Beitrage zur erfassung der phanotypischen stabilitat. *EDV Med. Biol.* 10:112.

Kang, M.S. 1988. A ranksum method for selecting high yielding, stable corn genotypes. Cereal Res. Comm. 16:113.

Lin, C.S., and M.R. Binns. 1994. Concepts and methods for analyzing regional trial data for cultivar and location selection. Plant Breed. Rev. 12:271.

Lin, C.S., M.R. Binns, and L.P. Lefkovitch. 1986. Stability analysis: Where do we stand? Crop Sci. 26:894.

Nassar, R., and M. Huehn. 1987. Studies on estimation of phenotypic stability: Tests of significance for nonparametric measures of phenotypic stability. Biometrics 43:45.

Shukla, G.K. 1972. Some aspects of partitioning genotype environmental components of variability. Heredity 28:237.

Thennarasu, K. 1995. On certain nonparametric procedures for studying genotype x environment interactions and yield stability. Ph.D. thesis. P.J. School, IARI, New Delhi, India.

Examples

```
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.

Author(s)

Leonardo Castelo Branco

References

Fox, P.N., B. Skovmand, B.K. Thompson, H.J. Braun, and R. Cormier. 1990. Yield and adaptation of hexaploid spring triticale. *Euphytica* 47:57.

Examples

```
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

```
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

Kang, M.S. 1988. A ranksum method for selecting high yielding, stable corn genotypes. *Cereal Res. Comm.* 16:113.

Shukla, G.K. 1972. Some aspects of partitioning genotype environmental components of variability. *Heredity* 28:237.

Examples

```
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

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

Arguments

nahu	nahu 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 (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

Nassar, R., and M. Huehn. 1987. Studies on estimation of phenotypic stability: Tests of significance for nonparametric measures of phenotypic stability. *Biometrics* 43:45.

Huehn, V.M. 1979. Beitrage zur erfassung der phanotypischen stabilitat. *EDV Med. Biol.* 10:112.

Examples

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

nahu(x, interaction = TRUE)
```

thsu

Thennarasu Function

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

thsu	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

Thennarasu, K. 1995. On certain nonparametric procedures for studying genotype x environment interactions and yield stability. Ph.D. thesis. P.J. School, IARI, New Delhi, India.

Examples

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

thsu(x, interaction = TRUE)
```


Index

- *Topic **Fox**
 - fox, [4](#)
 - *Topic **\textasciitildeThemmarasu**
 - thsu, [7](#)
 - *Topic **\textasciitildephenability**
 - thsu, [7](#)
 - *Topic **datasets**
 - bean.data, [3](#)
 - *Topic **huehn**
 - nahu, [6](#)
 - *Topic **kang**
 - kang, [5](#)
 - *Topic **phenability**
 - fox, [4](#)
 - kang, [5](#)
 - nahu, [6](#)
 - phenability-package, [2](#)
- bean.data, [3](#)
- fox, [4](#)
- kang, [5](#)
- nahu, [6](#)
- phenability (phenability-package), [2](#)
- phenability-package, [2](#)
- thsu, [7](#)