Package: agrostab (via r-universe)

June 4, 2026

Type Package

Title Stability Analysis for Agricultural Research

Version 0.1.0

Date 2019-10-01

Author Anna Cheshkova [aut, cre]

Maintainer Anna Cheshkova <`cheshanf@gmail.com`>

Description Statistical procedures to perform stability analysis in plant breeding and to identify stable genotypes under diverse environments. It is possible to calculate coefficient of homeostaticity by Khangildin et al. (1979), variance of specific adaptive ability by Kilchevsky&Khotyleva (1989), weighted homeostaticity index by Martynov (1990), steadiness of stability index by Udachin (1990), superiority measure by Lin&Binn (1988) <doi:10.4141/cjps88-018>, regression on environmental index by Erberhart&Rassel (1966) <doi:10.2135/cropsci1966.0011183X000600010011x>, Tai's (1971) stability parameters <doi:10.2135/cropsci1971.0011183X001100020006x>, stability variance by Shukla (1972) <doi:10.1038/hdy.1972.87>, ecovalence by Wricke (1962), nonparametric stability parameters by Nassar&Huehn (1987) <doi:10.2307/2531947>, Francis&Kannenberg's parameters of stability (1978) <doi:10.4141/cjps78-157>.

Depends R (>= 3.1)

Imports ggplot2, dplyr, graphics, stats, rlang

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

NeedsCompilation no

Repository https://cheshanf.r-universe.dev

Date/Publication 2019-10-16 10:50:06 UTC

RemoteUrl https://github.com/cran/agrostab

RemoteRef HEAD

RemoteSha f4eab432941757473f94ce2642f105dab190dba2

Contents

`agrostab` *Stability Analysis for Agricultural Research*

Description

The `agrostab` package provides functionalities to perform stability analysis in plant breeding. The package includes statistical procedures to identify stable genotypes under diverse environments.

Author(s)

Anna Cheshkova <cheshanf@gmail.com>

`exp_data` *Experimental data for stability analysis*

Description

Data obtained from the agrotechnical experiments carried out in 2009-2011 to evaluate grain yield of seven Siberian common winter wheat cultivars.

Usage

```
data(exp_data)
```

Format

A `data.frame` 126 obs. of 4 variables.

Details

- env Environment
- gen Genotype
- rep Replicate
- yield Yield Response

References

Siberian Research Institute of Plant Growing and Breeding - Branch of the Institute of Cytology and Genetics, Krasnoobsk, Novosibirsk region, Russia

Examples

```
data(exp_data)
```

`stability.cv` *Coefficient of variation*

Description

This function calculates the Francis&Kannenberg's parameters of stability

Usage

```
stability.cv(dataf, res_var, gen_var, env_var, rep_var, plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

Returns a data frame:

CV the genotype's coefficient of variation

Mean the genotype's mean

References

Francis, T.R. and L.W. Kannenberg. 1978. Yield stability studies in short-season maize. I. A descriptive method for grouping genotypes. Can J Plant Sci 58: 1029?1034. doi: 10.4141/cjps78-157

Examples

```
data(exp_data)
stability.cv(exp_data,"yield","gen","env","rep")
```

`stability.env_var` *Environmental variance*

Description

This function calculates the Roemer's environmental variance.

Usage

```
stability.env_var(dataf, res_var, gen_var, env_var, rep_var,
  plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

A numeric vector with environmental variances of genotypes.

References

Becker, H.C. and J. Leon. 1988. Stability analysis in plant breeding. Plant Breeding 101: 1-23.

Examples

```
data(exp_data)
stability.env_var(exp_data,"yield","gen","env","rep")
```

`stability.er` *Regression on Environmental Index*

Description

This function calculates the Erberhart&Rassel's stability parameters and the Dragavtsev's coefficient of multiplicativity.

Usage

```
stability.er(dataf, res_var, gen_var, env_var, rep_var, plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

Returns a list of three objects:

ANOVA the analysis of variance table

scores the data frame object of stability analysis results:

- `bi` regression of genotype means on environmental index
- `t_value` t-values for gypothesis that bi=1
- `p_value` p-values for gypothesis that bi=1
- `s2di` individual squared deviation from regression
- `pf_value` p-values for gypothesis that s2di=0
- `ai` Dragavtsev's coefficient of multiplicativity

Ij enviromental indexes

References

Eberhart, S.A. and W.A. Russell. 1966. Stability parameters for comparing varieties. Crop Sci 6: 36-40. doi:10.2135/cropsci1966.0011183X000600010011x

Examples

```
data(exp_data)
stability.er(exp_data,"yield","gen","env","rep")
```

`stability.hom` *Coefficient of homeostaticity*

Description

This function calculates the Khangildin's coefficient of homeostaticity

Usage

```
stability.hom(dataf, res_var, gen_var, env_var, rep_var, plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

Returns a data frame:

mean_all the genotype's mean

mean_opt the genotype's max yield value

mean_lim the genotype's min yield value

sd the genotype's standard deviation

hom the genotype's coefficient of homeostaticity

References

Khangildin V.V., Shayakhmetov I.F., Mardamshin A.G. 1979. Homeostasis of crop components and prerequisites for creating a model of a spring wheat variety. In Genetic analysis of quantitative traits of plants, 5-39. Ufa. (In Russian)

Examples

```
data(exp_data)
stability.hom(exp_data,"yield","gen","env","rep")
```

`stability.hue` *Nonparametric stability analysis*

Description

This function calculates the Nassar&Huehn's stability parameters.

Usage

```
stability.hue(dataf, res_var, gen_var, env_var, rep_var, alpha = 0.05,
  plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`alpha`	the significance level; default is 0.5
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

Returns a list of two objects:

statistic the data frame object of stability analysis results:

- `S1`-value of genotype
- `Z1`-value of genotype
- `S2`-value of genotype
- `Z2`-value of genotype

scores the data frame object of summary results:

- `Z1.sum` sum of Z1
- `Z2.sum` sum of Z2
- `chi.ind` chi-squared for (choosen alpha level)/(number of genotypes) and one degree of freedom
- `chi.sum` chi-squared for choosen alpha level and number of genotypes degree of freedom

References

Nassar, R. and M. Huehn. 1987. Studies on estimation of phenotypic stability: Tests of significance for nonparametric measures of phenotypic stability. Biometrics 43: 45-53. doi: 10.2307/2531947

Examples

```
data(exp_data)
stability.hue(exp_data,"yield","gen","env","rep")
```

`stability.kilch` *Variance of specific adaptive ability*

Description

This function calculates several stability parameters suggested by Kilchevsky & Khotyleva.

Usage

```
stability.kilch(dataf, res_var, gen_var, env_var, rep_var, plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

Returns a list of two objects:

ANOVA the analysis of variance table

scores the data frame object of stability analysis results:

- `mean` mean value
- `OAC` common adaptive ability
- `sigma_ge` variance of GE interaction
- `sigma_CAC` variance of specific adaptive ability
- `S_g` relative stability

References

Kilchevsky A.V., Khotyleva L.V. 1989. Genotype and environment in plant breeding. - Minsk: Science and technology. (In Russian).

Examples

```
data(exp_data)
stability.kilch(exp_data,"yield","gen","env","rep")
```

`stability.linbin` *Superiority measure*

Description

This function calculates the Lin&Binn's superiority measure.

Usage

```
stability.linbin(dataf, res_var, gen_var, env_var, rep_var,
  plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

A numeric vector with superiority measure Pi of genotypes.

References

Lin, C.S. and M.R. Binns. 1988. A superiority measure of cultivar performance for cultivar x location data. Can J Plant Sci 68: 193?198. doi: 10.4141/cjps88-018

Examples

```
data(exp_data)
stability.linbin(exp_data,"yield","gen","env","rep")
```

`stability.mart` *Weighted homeostaticity index*

Description

This function calculates the Martynov's weighted homeostaticity index.

Usage

```
stability.mart(dataf, res_var, gen_var, env_var, rep_var, alpha = 0.05,
  plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`alpha`	alpha level of LSD; default is 0.05.
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

A numeric vector with weighted homeostaticity index of genotypes.

References

Martynov S.P. 1990. A Method for the Estimation of Crop Varieties Stability. Biom. J. 7: 887-893.

Examples

```
data(exp_data)
stability.mart(exp_data,"yield","gen","env","rep")
```

`stability.shu` *Stability variance*

Description

This function calculates the Shukla's stability variance.

Usage

```
stability.shu(dataf, res_var, gen_var, env_var, rep_var, plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

Returns a list of two objects:

ANOVA the analysis of variance table

scores the data frame object of stability analysis results:

- `bi` regression of genotype means on environmental means
- `t_value` t-values for gypothesis that bi=0
- `p_value` p-values for gypothesis that bi=0
- `sigma` Shukla's stability variance value
- `pf_value` p-values for gypothesis that sigmai=0

References

Shukla, G.K. 1972. Some statistical aspects of partitioning genotype-environmental components of variability. Heredity 29: 237-245. doi: 10.1038/hdy.1972.87

Examples

```
data(exp_data)
stability.shu(exp_data,"yield","gen","env","rep")
```

`stability.tai` *Tai's stability analysis*

Description

This function calculates the Tai's stability parameters.

Usage

```
stability.tai(dataf, res_var, gen_var, env_var, rep_var, plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

Returns a list of two objects:

ANOVA the analysis of variance table

scores the data frame object of stability analysis results:

- `alpha` regression of genotype means on environmental means
- `t_value` t-values for gypothesis that alpha=0
- `p_value` p-values for gypothesis that alpha=0
- `lambda` deviation from linear responses
- `pf_value` p-values for gypothesis that lambda=0

References

Tai, G.C.C. 1971. Genotypic stability analysis and application to potato regional trials. Crop Sci. 11: 184-190. doi:10.2135/cropsci1971.0011183X001100020006x

Examples

```
data(exp_data)
stability.tai(exp_data,"yield","gen","env","rep")
```

`stability.udach` *Steadiness of stability index*

Description

This function calculates the Udachin's parameters of stability

Usage

```
stability.udach(dataf, res_var, gen_var, env_var, rep_var, plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

Returns a data frame:

Ust the genotype's Steadiness of stability index

intensity the genotype's intensity value

max_val the genotype's yield max value

min_val the genotype's yield min value

S_opt the genotype's standard deviation at optimal environment

S_lim the genotype's standard deviation at limited environment

I_opt the genotype's stability index at optimal environment

I_lim the genotype's stability index at limited environment

References

Udachin R.A. 1990. Methods of assessing the ecological plasticity of wheat varieties. Selection and seed production. 5: 2-6. (In Russian)

Examples

```
data(exp_data)
stability.udach(exp_data,"yield","gen","env","rep")
```

`stability.wricke` *Ecovalence*

Description

This function calculates the Wricke's ecovalence.

Usage

```
stability.wricke(dataf, res_var, gen_var, env_var, rep_var,
  plotIt = TRUE)
```

Arguments

`dataf`	the name of the data frame containing the data to analyze.
`res_var`	the response variable.
`gen_var`	the genotypes variable.
`env_var`	the environments variable.
`rep_var`	the replications variable.
`plotIt`	a logical value specifying if plot should be drawn; default is TRUE

Value

A numeric vector with genotype's ecovalence.

References

Wricke, G., 1962. Tjber eine Methode zur Erfassung der okologischen Streubreite in Feldversuchen. Z. Pflanzenzuchtg. 47: 92-96.

Examples

```
data(exp_data)
stability.wricke(exp_data,"yield","gen","env","rep")
```

Index