

# Package ‘agrostab’

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**Type** Package

**Title** Stability Analysis for Agricultural Research

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**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&Kannenbergs parameters of stability (1978) <doi:10.4141/cjps78-157>.

**Depends** R (>= 3.1)

**Imports** ggplot2, dplyr, graphics, stats, rlang

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**LazyData** true

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agrostab	<i>Stability Analysis for Agricultural Research</i>
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### 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>

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exp_data	<i>Experimental data for stability analysis</i>
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### 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	<i>Coefficient of variation</i>
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**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")
```

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stability.env_var	<i>Environmental variance</i>
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## 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&Russel'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

<code>dataf</code>	the name of the data frame containing the data to analyze.
<code>res_var</code>	the response variable.
<code>gen_var</code>	the genotypes variable.
<code>env_var</code>	the environments variable.
<code>rep_var</code>	the replications variable.
<code>plotIt</code>	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 (chosen alpha level)/(number of genotypes) and one degree of freedom
- chi.sum chi-squared for chosen 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	<i>Variance of specific adaptive ability</i>
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### 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	<i>Superiority measure</i>
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## 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  $P_i$  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	<i>Weighted homeostaticity index</i>
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### 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")
```

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stability.shu	<i>Stability variance</i>
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### 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  $b_i=0$
- **p\_value** p-values for gypothesis that  $b_i=0$
- **sigma** Shukla's stability variance value
- **pf\_value** p-values for gypothesis that  $\sigma_i=0$

### 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	<i>Tai's stability analysis</i>
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---

### 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	<i>Steadiness of stability index</i>
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**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**

<code>dataf</code>	the name of the data frame containing the data to analyze.
<code>res_var</code>	the response variable.
<code>gen_var</code>	the genotypes variable.
<code>env_var</code>	the environments variable.
<code>rep_var</code>	the replications variable.
<code>plotIt</code>	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")
```

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