Package ‘agrostab’

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agrostab .................................................. 2
exp_data .................................................. 2
The `agrostab` package provides functionalities to perform stability analysis in plant breeding. The package includes statistical procedures to identify stable genotypes under diverse environments.

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**exp_data**

**Description**

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

**Usage**

```r
data(exp_data)
```

**Format**

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

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

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

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

```r
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 hypothesis that `bi=1`
  - `p_value`: p-values for hypothesis that `bi=1`
  - `s2di`: individual squared deviation from regression
  - `pf_value`: p-values for hypothesis that `s2di=0`
  - `ai`: Dragavtsev’s coefficient of multiplicativity
- **Ij**: environmental indexes

References


Examples

```r
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**

```r
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**


**Examples**

```r
data(exp_data)
stability.hom(exp_data,"yield","gen","env","rep")
```
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 choosen alpha level and number of genotypes degree of freedom

References


Examples

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

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

### Usage

```r
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


### Examples

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

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


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**

```r
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**


**Examples**

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

**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 hypothesis that bi=0
  - `p_value`: p-values for hypothesis that bi=0
  - `sigma`: Shukla’s stability variance value
  - `pf_value`: p-values for hypothesis that sigma=0

**References**


**Examples**

```r
data(exp_data)
stability.shu(exp_data,"yield","gen","env","rep")```
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 hypothesis that alpha=0
  • p_value p-values for hypothesis that alpha=0
  • lambda deviation from linear responses
  • pf_value p-values for hypothesis that lambda=0

References

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")
Description

This function calculates the Wricke’s ecovalence.

Usage

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dataf</td>
<td>the name of the data frame containing the data to analyze.</td>
</tr>
<tr>
<td>res_var</td>
<td>the response variable.</td>
</tr>
<tr>
<td>gen_var</td>
<td>the genotypes variable.</td>
</tr>
<tr>
<td>env_var</td>
<td>the environments variable.</td>
</tr>
<tr>
<td>rep_var</td>
<td>the replications variable.</td>
</tr>
<tr>
<td>plotIt</td>
<td>a logical value specifying if plot should be drawn; default is TRUE</td>
</tr>
</tbody>
</table>

Value

A numeric vector with genotype’s ecovalence.

References


Examples

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

* datasets
  exp_data, 2

agrostab, 2
agrostab-package (agrostab), 2

exp_data, 2

stability.cv, 3
stability.env_var, 4
stability.er, 5
stability.hom, 6
stability.hue, 7
stability.kilch, 8
stability.linbin, 9
stability.mart, 10
stability.shu, 11
stability.tai, 12
stability.udach, 13
stability.wricke, 14