Package ‘agrostab’
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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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**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` with 126 observations 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
stability.env_var

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")
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 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

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")
```
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

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


Examples

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

Description
This function calculates the Lin&Binn’s superiority measure.

Usage

```r
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


Examples

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

**Description**

This function calculates the Shukla’s stability variance.

**Usage**

```r
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")
```
stability.tai  
**Tai’s stability analysis**

**Description**
This function calculates the Tai’s stability parameters.

**Usage**
```r
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**
```r
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

```r
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

Examples

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