Package 'toolStability'

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Type Package

Title Tool for Stability Indices Calculation

Version 0.1.3

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Description Tools to calculate stability indices with parametric,
non-parametric and probabilistic approaches. The basic data format requirement for 'toolStability' is a data frame with 3 columns including numeric trait values, genotype,and environmental labels. Output format of each function is the dataframe with chosen stability index for each genotype.
Function ``table_stability'' offers the summary table of all stability indices in this package.
This R package toolStability is part of the main publication:
Wang, Casadebaig and Chen (2023) <doi:10.1007/s00122-023-04264-7>.
Analysis pipeline for main publication can be found on github: <https://github.com/Illustratien/Wang_2023_TAAG>.
Sample dataset in this package is derived from another publication:
Casadebaig P, Zheng B, Chapman S et al. (2016) <doi:10.1371/journal.pone.0146385>.
For detailed documentation of dataset, please see on Zenodo <doi:10.5281/zenodo.4729636>.
Indices used in this package are from:
Döring TF, Reckling M (2018) <doi:10.1016/j.eja.2018.06.007>.
Eberhart SA, Russell WA (1966) <doi:10.2135/cropsci1966.0011183X000600010011x>.
Eskridge KM (1990) <doi:10.2135/cropsci1990.0011183X003000020025x>.
Finlay KW, Wilkinson GN (1963) <doi:10.1071/AR9630742>.
Hanson WD (1970) Genotypic stability. <doi:10.1007/BF00285245>.
Lin CS, Binns MR (1988).
Nassar R, Hühn M (1987).
Pinthus MJ (1973) <doi:10.1007/BF00021563>.
Römer T (1917).
Shukla GK (1972).
Wricke G (1962).

Depends R (>= 3.5.0)

VignetteBuilder knitr

RoxygenNote 7.2.3

Imports dplyr, data.table, Rdpack, nortest, stats

Suggests testthat (>= 3.0.0), ggplot2, knitr, rmarkdown, pkgdown,
     pander, XML, httr, RCurl, covr

RdMacros Rdpack

URL https://illustratien.github.io/toolStability/,

     https://link.springer.com/article/10.1007/s00122-023-04264-7,

     https://github.com/Illustratien/toolStability,

     https://github.com/Illustratien/Wang_2023_TAAG,

     https://doi.org/10.5281/zenodo.4729636

BugReports https://github.com/Illustratien/toolStability/issues

License GPL (>= 3)

Encoding UTF-8

LazyData true

LazyLoad true

Config/testthat/edition 3

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Contents

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adjusted_coefficient_of_variation

Adjusted coefficient of variaiton

Description

adjusted_coefficient_of_variation calculate variance of a genotype across environments.

Usage

```
adjusted_coefficient_of_variation(data, trait, genotype, environment)
```

Arguments

data	a dataframe containing trait, genotype and environment.
trait	colname of a column containing a numeric vector of interested trait to be analyzed.
genotype	colname of a column containing a character or factor vector labeling different genotypic varieties
environment	colname of a column containing a character or factor vector labeling different environments

Details

Adjusted coefficient of variaiton (Doering and Reckling, 2018) is calculatd based on regression function. Variety with low adjusted coefficient of variation is considered as stable. Equation of adjusted coefficient of variation can be found in vignette file.

Value

a data table with adjusted coefficient of variation

Author(s)

Tien-Cheng Wang

References

Döring TF, Reckling M (2018). "Detecting global trends of cereal yield stability by adjusting the coefficient of variation." *European Journal of Agronomy*, **99**, 30–36. ISSN 1161-0301, doi: 10.1016/j.eja.2018.06.007.

Examples

```
data(Data)
res <- adjusted_coefficient_of_variation(
 data = Data,
 trait = "Yield",
 genotype = "Genotype",
 environment = "Environment")
```

---

coefficient_of_determination

Coefficient of determination

Description

coefficient_of_determination calculate variance of a genotype across environments.

Usage

```
coefficient_of_determination(data, trait, genotype, environment)
```

Arguments

data	a dataframe containing trait, genotype and environment.
trait	colname of a column containing a numeric vector of interested trait to be analysized.
genotype	colname of a column containing a character or factor vector labeling different genotypic varieties
environment	colname of a column containing a character or factor vector labeling different environments

Details

Coefficient of determination (Pinthus, 1976) is calculatd based on regression function. Variety with low coefficient of determination is considered as stable. Equation of coefficient of determination can be found in vignette file.

Value

a data table with coefficient of determination

Author(s)

Tien-Cheng Wang

References

Pinthus MJ (1973). "Estimate of genotypic value: A proposed method." *Euphytica*, **22**(1), 121–123. ISSN 1573-5060, doi: 10.1007/BF00021563.

Examples

```
data(Data)
coef.of.determination <- coefficient_of_determination(
 data = Data,
 trait = "Yield",
 genotype = "Genotype",
 environment = "Environment")
```

```
coefficient_of_regression
```
Coefficient of regression

Description

coefficient_of_regression calculate variance of a genotype across environments.

Usage

```
coefficient_of_regression(data, trait, genotype, environment)
```

Arguments

data	a dataframe containing trait, genotype and environment.
trait	colname of a column containing a numeric vector of interested trait to be analysized.
genotype	colname of a column containing a character or factor vector labeling different genotypic varieties
environment	colname of a column containing a character or factor vector labeling different environments

Details

Coefficient of regression (Finlay and Wilkinson, 1963) is calculatd based on regression function. Variety with low coefficient of regression is considered as stable. Under the linear model

$$Y = \mu + b_i e_j + g_i + d_{ij}$$

where Y is the predicted phenotypic values, g_i, e_j and μ denoting genotypic, environmental and overall population mean,respectively.

The effect of GE-interaction may be expressed as:

$$(ge)_{ij} = b_i e_j + d_{ij}$$

where b_i is the coefficient of regression and d_{ij} a deviation.

Coefficient of regression may be expressed as:

$$b_i = 1 + \frac{\sum_j (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..}) \cdot (\bar{X}_{.j} - \bar{X}_{..})}{\sum_j (\bar{X}_{.j} - \bar{X}_{..})^2}$$

where X_{ij} is the observed phenotypic mean value of genotype i(i=1,..., G) in environment j(j=1,...,E), with $\bar{X}_{i.}$ and $\bar{X}_{.j}$
denoting marginal means of genotype i and environment j,respectively.
$\bar{X}_{..}$ denote the overall mean of X.

Value

a data table with coefficient of regression

Author(s)

Tien Cheng Wang

References

Finlay KW, Wilkinson GN (1963). "The analysis of adaptation in a plant-breeding programme." *Australian Journal of Agricultural Research*, **14**(6), 742–754. doi: 10.1071/AR9630742.

Examples

```
data(Data)
coefficient.of.regression <- coefficient_of_regression(
 data = Data,
 trait = "Yield",
 genotype = "Genotype",
 environment = "Environment")
```

Data   *Wheat APSIM model simulated database*

Description

Multi-environment trail evaluating 5 genotypes in 4 locations for 4 years, with 2 nitrogen application rates, 2 sowing dates, and 2 CO2 levels of treatments (Casadebaig et al., 2016).

Usage

```
data(Data)
```

Format

A dataframe with 640 observations on the following 8 variables.

- Yield: kg*ha^-1.
- Genotype: genotypes, 5 varieties.
- Environment: 128 unique combination of environments for each genotype.
- Year: 4 years.
- Sites: 4 locations.

- Nitrogen: 2 nitrogen application levels.
- CO2: 2 CO2 concentration levels.
- Sowing: 2 sowing dates.

References

Casadebaig P, Zheng B, Chapman S, Huth N, Faivre R, Chenu K (2016). "Assessment of the Potential Impacts of Wheat Plant Traits across Environments by Combining Crop Modeling and Global Sensitivity Analysis." *PLOS ONE*, **11**(1), e0146385. doi: 10.1371/journal.pone.0146385.

Examples

```
data(Data)

ggplot2::ggplot(Data,ggplot2::aes(x=Sites,y=Yield,col=Genotype))+
  ggplot2::geom_boxplot()+
  ggplot2::facet_grid(Sowing~Nitrogen,labeller =ggplot2::label_both)+
  ggplot2::ylab(bquote('Wheat yield (ton' %.%'ha'^'-1'*')'))
```

---

deviation_mean_squares

Deviation mean squares

Description

deviation_mean_squares calculate variance of a genotype across environments.

Usage

```
deviation_mean_squares(
  data,
  trait,
  genotype,
  environment,
  unit.correct = FALSE
)
```

Arguments

data	a dataframe containing trait, genotype and environment.
trait	colname of a column containing a numeric vector of interested trait to be analysized.
genotype	colname of a column containing a character or factor vector labeling different genotypic varieties
environment	colname of a column containing a character or factor vector labeling different environments

unit.correct	logical, default is FALSE, returning the stability index with unit equals to squared unit of trait; when TRUE, returning stability index with the unit as same as unit of trait.

Details

Deviation mean squares (Eberhart and Russell, 1966) is calculatd based on regression function. Variety with low stability variance is considered as stable. Equation of deviation mean squares can be found in vignette file.

Value

a data table with deviation mean squares

Author(s)

Tien Cheng Wang

References

Eberhart SA, Russell WA (1966). "Stability parameters for comparing varieties." *Crop Science*, **6**(1), 36–40. ISSN 0011-183X, doi: 10.2135/cropsci1966.0011183X000600010011x.

Examples

```
data(Data)
deviation.mean.squares <- deviation_mean_squares(
 data = Data,
 trait = "Yield",
 genotype = "Genotype",
 environment = "Environment",
 unit.correct = FALSE)
```

---

ecovalence	*Ecovalence*

Description

ecovalence calculate genetic and environmental interaction.

Usage

```
ecovalence(
  data,
  trait,
  genotype,
  environment,
  unit.correct = FALSE,
  modify = FALSE
)
```

Arguments

`data`	a dataframe containing trait, genotype and environment.
`trait`	colname of a column containing a numeric vector of interested trait to be analysized.
`genotype`	colname of a column containing a character or factor vector labeling different genotypic varieties
`environment`	colname of a column containing a character or factor vector labeling different environments
`unit.correct`	logical, default is `FALSE`, returning the stability index with unit equals to squared unit of trait; when `TRUE`, returning stability index with the unit as same as unit of trait.
`modify`	logical, default is `FALSE`, returning the original ecovalence; when `TRUE`, returning modified ecovalence in consideration of number of environment.

Details

Ecovalence (Wricke, 1962) is calcualted based on square and sum up the genotype–environment interaction all over the environment. Variety with low ecovalence is considered as stable. Equation of ecovalence can be found in vignette file.

Value

a data table with ecovalence

Author(s)

Tien-Cheng Wang

References

Wricke G (1962). "Ãœber eine Methode zur Erfassung der Ã–kologischen Streubreite in Feldversuchen." *Zeitschrift fÃ¼r PflanzenzÃ¼chtung*, **47**, 92–96.

Examples

```
data(Data)
eco.valence <- ecovalence(
 data = Data,
 trait = "Yield",
 genotype = "Genotype",
 environment = "Environment",
 unit.correct = FALSE,
 modify=FALSE)
```

---

environmental_variance

Environmental variance

Description

environmental_variance is used to calculate variance of a genotype across environments.

Usage

```
environmental_variance(data, trait, genotype, unit.correct = FALSE)
```

Arguments

data	a dataframe containing trait, genotype and environment.
trait	colname of a column containing a numeric vector of interested trait to be analysized.
genotype	colname of a column containing a character or factor vector labeling different genotypic varieties
unit.correct	logical, default is FALSE, returning the stability index with unit equals to squared unit of trait; when TRUE, returning stability index with the unit as same as unit of trait.'

Details

Environmental variance (Roemer, 1917) is calculated by squared and suming up all deviation from genotypic mean for each genotype. The larger the environmental variance of one genotype is, the lower the stability. Equation of environmental variance can be found in vignette file.

Value

a data table with environmental variance

Author(s)

Tien-Cheng Wang

References

Römer T (1917). "Sind die ertragdreichen Sorten ertagissicherer?" *Mitteilungen der Deutschen Landwirtschaftlichen Gesellschaft*, **32**(1), 87–89.

Examples

```
data(Data)
environmental.variance <- environmental_variance(
 data = Data,
 trait = "Yield",
 genotype = "Genotype",
 unit.correct = FALSE)
```

---

genotypic_stability   *Genotypic stability*

Description

genotypic_stability calculate variance of a genotype across environments.

Usage

```
genotypic_stability(data, trait, genotype, environment, unit.correct = FALSE)
```

Arguments

data	a dataframe containing trait, genotype and environment.
trait	colname of a column containing a numeric vector of interested trait to be analysized.
genotype	colname of a column containing a character or factor vector labeling different genotypic varieties
environment	colname of a column containing a character or factor vector labeling different environments
unit.correct	logical, default is FALSE, returning the stability index with unit equals to squared unit of trait; when TRUE, returning stability index with the unit as same as unit of trait.'

Details

Genotypic stability (Hanson, 1970) is calculatd based on regression function. Variety with low stability variance is considered as stable. Equation of genotypic stability can be found in vignette file.

Value

a data table with genotypic stability

Author(s)

Tien-Cheng Wang

References

Hanson WD (1970). "Genotypic stability." *Theoretical and Applied Genetics*, **40**(5), 226–231. ISSN 1432-2242, doi: 10.1007/BF00285245.

Examples

```
data(Data)
genotypic.stability <- genotypic_stability(
 data = Data,
 trait = "Yield",
 genotype = "Genotype",
 environment = "Environment",
 unit.correct = FALSE)
```

---

genotypic_superiority_measure

Genotypic superiority measure

Description

genotypic_superiority_measure calculate variance of a genotype across environments.

Usage

```
genotypic_superiority_measure(
  data,
  trait,
  genotype,
  environment,
  unit.correct = FALSE
)
```

Arguments

data	a dataframe containing trait, genotype and environment.
trait	colname of a column containing a numeric vector of interested trait to be analysized.
genotype	colname of a column containing a character or factor vector labeling different genotypic varieties
environment	colname of a column containing a character or factor vector labeling different environments
unit.correct	logical, default is FALSE, returning the stability index with unit equals to squared unit of trait; when TRUE, returning stability index with the unit as same as unit of trait.'

Details

Genotypic superiority measure (Lin and Binns, 1988) is calculatd based on means square distance between maximum value of environment j and genotype i. Variety with low genotypic superiority measure is considered as stable. Equation of genotypic superiority measure can be found in vignette file.

Value

a data table with genotypic superiority measure

Author(s)

Tien-Cheng Wang

References

Lin CS, Binns MR (1988). "A superiority measure of cultivar performance for cultivar $\times$ location data." *Canadian Journal of Plant Science*, **68**(1), 193–198. ISSN 0008-4220.

Examples

```
data(Data)
res <- genotypic_superiority_measure(
 data = Data,
 trait = "Yield",
 genotype = "Genotype",
 environment = "Environment",
 unit.correct = FALSE)
```

---

safety_first_index   *Safety-first Index*

Description

safety_first_index calculate variance of a genotype across environments.

Usage

```
safety_first_index(data, trait, genotype, environment, lambda)
```

Arguments

data	a dataframe containing trait, genotype and environment.
trait	colname of a column containing a numeric vector of interested trait to be analyzed.
genotype	colname of a column containing a character or factor vector labeling different genotypic varieties.

environment   colname of a column containing a character or factor vector labeling different
                   environments.

lambda   the minimal acceptable value of trait that the user expected from crop across
                   environments. Lambda should between the ranges of trait vlaue.

Details

Safety-first index (Eskridge, 1990) is calculated based on the assumption of that the trait from
each genotype follows normal distribution over enviornments. Among different environments, trait
below a given cirtical level λ is defined as failure of trait. The probability of trait failure can
be obtained by entering mean and variance of trait and λ into the cumulated density function of
normal distribution. Variety with low safety first index is considered as stable. Equation of adjusted
coefficient of variation can be found in vignette file.

Value

a data table with coefficient of determination

Author(s)

Tien-Cheng Wang

References

Eskridge KM (1990). "Selection of Stable Cultivars Using a Safety-First Rule." *Crop Science*,
30(2), 369. ISSN 0011-183X, doi: 10.2135/cropsci1990.0011183X003000020025x.

Examples

```
data(Data)
safety.first.index <- safety_first_index(
 data = Data,
 trait = "Yield",
 genotype = "Genotype",
 environment = "Environment",
 lambda = median(Data$Yield))
```

---

stability_variance   *Stability variance*

Description

stability_variance calculate variance of a genotype across environments.

Usage

```
stability_variance(data, trait, genotype, environment, unit.correct = FALSE)
```

Arguments

`data`	a dataframe containing trait, genotype and environment.
`trait`	colname of a column containing a numeric vector of interested trait to be analyzed.
`genotype`	colname of a column containing a character or factor vector labeling different genotypic varieties.
`environment`	colname of a column containing a character or factor vector labeling different environments.
`unit.correct`	logical, default is `FALSE`, returning the stability index with unit equals to squared unit of trait; when `TRUE`, returning stability index with the unit as same as unit of trait.#'

Details

Stability variance (Shukla, 1972) is calculatd based on lindear combination of ecovalence and mean square of genotype-environment interaction. Variety with low stability variance is considered as stable. Negative values of stability variance is replaced with 0. Equation of stability variance can be found in vignette file.

Value

a data table with stability variance

Author(s)

Tien-Cheng Wang

References

Shukla GK (1972). "Some statistical aspects of partitioning genotype environmental components of variability." *Heredity*, **29**(2), 237–245.

Examples

```
data(Data)
stability.variance <- stability_variance(
 data = Data,
 trait = "Yield",
 genotype = "Genotype",
 environment = "Environment")
```

---

table_stability   *Table of stability indices*

Description

table_stability export all the stability indices in the package.

Usage

```
table_stability(
  data,
  trait,
  genotype,
  environment,
  lambda,
  normalize = FALSE,
  unit.correct = FALSE
)
```

Arguments

data	a data frame containing trait, genotype and environment.
trait	colname of a column containing a numeric vector of interested trait to be analyzed.
genotype	colname of a column containing a character or factor vector labeling different genotypic varieties.
environment	colname(s) of a column containing a character or factor vector labeling different environments, if input is a vector containing multiple column names, then it will be merged into single environment column in the function.
lambda	the minimal acceptable value of trait that the user expected from crop across environments. Lambda should between the ranges of trait vlaue.
normalize	logical, default is FALSE, indicating whether stability indices should be normalized to the range from 0 to 1, where 1 refer to stable and 0 is unstable.
unit.correct	logical, default is FALSE, returning the stability index with unit equals to squared unit of trait; when TRUE, returning stability index with the unit as same as unit of trait.

Details

Combine all stability indices in this package and export as a table, including mean trait, normality of the trait across environment.

Value

a data table with multiple stability indices

Author(s)

Tien-Cheng Wang

References

DÃ¶ring TF, Reckling M (2018). "Detecting global trends of cereal yield stability by adjusting the coefficient of variation." *European Journal of Agronomy*, **99**, 30–36. ISSN 1161-0301, doi: 10.1016/j.eja.2018.06.007. Pinthus MJ (1973). "Estimate of genotypic value: A proposed method." *Euphytica*, **22**(1), 121–123. ISSN 1573-5060, doi: 10.1007/BF00021563. Finlay KW, Wilkinson GN (1963). "The analysis of adaptation in a plant-breeding programme." *Australian Journal of Agricultural Research*, **14**(6), 742–754. doi: 10.1071/AR9630742. Eberhart SA, Russell WA (1966). "Stability parameters for comparing varieties." *Crop Science*, **6**(1), 36–40. ISSN 0011-183X, doi: 10.2135/cropsci1966.0011183X000600010011x. Wricke G (1962). "Ãœber eine Methode zur Erfassung der Ã¶kologischen Streubreite in Feldversuchen." *Zeitschrift fÃ¼r PflanzenzÃ¼chtung*, **47**, 92–96. RÃ¶mer T (1917). "Sind die ertragdreichen Sorten ertagissicherer?" *Mitteilungen der Deutschen Landwirtschaftlichen Gesellschaft*, **32**(1), 87–89. Hanson WD (1970). "Genotypic stability." *Theoretical and Applied Genetics*, **40**(5), 226–231. ISSN 1432-2242, doi: 10.1007/BF00285245. Lin CS, Binns MR (1988). "A superiority measure of cultivar performance for cultivar × location data." *Canadian Journal of Plant Science*, **68**(1), 193–198. ISSN 0008-4220. Shukla GK (1972). "Some statistical aspects of partitioning genotype environmental components of variability." *Heredity*, **29**(2), 237–245. Nassar R, HÃ¼hn M (1987). "Studies on estimation of phenotypic stability: Tests of significance for nonparametric measures of phenotypic stability." *Biometrics*, **43**(1), 45–53. ISSN 0006-341X. Eskridge KM (1990). "Selection of Stable Cultivars Using a Safety-First Rule." *Crop Science*, **30**(2), 369. ISSN 0011-183X, doi: 10.2135/cropsci1990.0011183X003000020025x.

See Also

adjusted_coefficient_of_variation

coefficient_of_determination

coefficient_of_regression

deviation_mean_squares

ecovalence

environmental_variance

genotypic_stability

genotypic_superiority_measure

stability_variance

variance_of_rank

safety_first_index

Examples

```
data(Data)
tb <- table_stability(
 data = Data,
 trait = "Yield",
```

```
genotype = "Genotype",
environment = "Environment",
lambda = median(Data$Yield),
normalize = TRUE,
unit.correct=TRUE)
```

---

variance_of_rank   *variance of rank*

Description

variance_of_rank calculate variance of a genotype across environments.

Usage

```
variance_of_rank(data, trait, genotype, environment, unit.correct = FALSE)
```

Arguments

data	a dataframe containing trait, genotype and environment.
trait	colname of a column containing a numeric vector of interested trait to be analy-sized.
genotype	colname of a column containing a character or factor vector labeling different genotypic varieties
environment	colname of a column containing a character or factor vector labeling different environments
unit.correct	logical, default is FALSE, returning the stability index with unit equals to squared unit of trait; when TRUE, returning stability index with the unit as same as unit of trait.#'

Details

Variance of rank (Nassar and Huehn, 1987) is calculatd based on regression function. Variety with low variance of rank is considered as stable. Equation of variance of rank can be found in vignette file.

Value

a data table with variance of rank

Author(s)

Tien-Cheng Wang

References

Nassar R, Hühn M (1987). "Studies on estimation of phenotypic stability: Tests of significance for nonparametric measures of phenotypic stability." *Biometrics*, **43**(1), 45–53. ISSN 0006-341X.

Examples

```
data(Data)
variance.of.rank <- variance_of_rank(
 data = Data,
 trait = "Yield",
 genotype = "Genotype",
 environment = "Environment",
 unit.correct = FALSE)
```

Index