Package ‘EstimateBreed’

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Type Package

Title Estimation of Environmental Variables and Genetic Parameters

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Description Performs analyzes and estimates of environmental covariates and genetic parameters related to selection strategies and development of superior genotypes. It has two main functionalities, the first being about prediction models of covariates and environmental processes, while the second deals with the estimation of genetic parameters and selection strategies. Designed for researchers and professionals in genetics and environmental sciences, the package combines statistical methods for modeling and data analysis. This includes the plastochron estimate proposed by Porta et al. (2024) <doi:10.1590/1807-1929/agriambi.v28n10e278299>, Stress indices for genotype selection referenced by Ghazvini et al. (2024) <doi:10.1007/s10343-024-00981-1>, the Environmental Stress Index described by Tazzo et al. (2024) <`https://revistas.ufg.br/vet/article/view/77035`>, industrial quality indices of wheat genotypes (Szareski et al., 2019), <doi:10.4238/gmr18223>, Ear Indexes estimation (Rigotti et al., 2024), <doi:10.13083/reveng.v32i1.17394>, Selection index for protein and grain yield (de Pelegrin et al., 2017), <doi:10.4236/ajps.2017.813224>, Estimation of the ISGR - Genetic Selection Index for Resilience for environmental resilience (Bandeira et al., 2024) <`https://www.cropj.com/Carvalho_18_12_2024_825_830.pdf`>, estimation of Leaf Area Index (Meira et al., 2015) <`https://www.fag.edu.br/upload/revista/cultivando_o_saber/55d1ef202e494.pdf`>, Restriction of control variability (Carvalho et al., 2023) <doi:10.4025/actasciagron.v45i1.56156>, Risk of Disease Occurrence in Soybeans described by Engers et al. (2024) <doi:10.1007/s40858-024-00649-1> and estimation of genetic parameters for selection based on balanced experiments (Yadav et al., 2024) <doi:10.1155/2024/9946332>.

License GPL (>= 3)

URL `https://github.com/willyanjnr/EstimateBreed`

Depends R (>= 4.1.0)

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Contents

`atsum` *Accumulated Thermal Sum*

Description

Calculates the daily and accumulated thermal sum, considering the subtraction of the average air temperature by the lower cardinal temperature for each crop.

Usage

```
atsum(AAT, crop = "maize", lbt = NULL, verbose = FALSE, plot = FALSE)
```

Arguments

`AAT`	The column with the average air temperature values.
`crop`	Parameter to define the culture. Use 'maize' for maize, 'soybean' for soybean, 'flax' for flaxseed, 'trit' for wheat or 'oat' for oat crop.
`lbt`	Parameter to define the value of the lower basal temperature to be used in the calculation. If not informed, the function will use the values of 10, 5, 2, 2 and 0 $^{\circ}C$ for maize, soybeans, flaxseed, wheat and oats, respectively.
`verbose`	Logical argument. Runs the code silently if FALSE.
`plot`	Logical argument. Plot a graph of thermal accumulation if TRUE.

Value

Returns the cumulative and total thermal sum considering the cultivation cycle of the selected crop. Also presents the following parameters:

* Total Cycle
The number of cycle days, for verification.

* TS
The value of the total thermal sum, in daily degree days (GDD).

* TBi
The value used for the lower base temperature.

* General Parameters
Considering the reported average air temperature values, it returns the maximum, minimum, and coefficient of variation.

Author(s)

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Examples

```
library(EstimateBreed)

data("clima")
clima <- get("clima")[1:150, ]

with(clima,atsum(TMED,crop="maize"))

#Adjusting lower basal temperature manually
with(clima,atsum(TMED,crop="maize",lbt=12))
```

`aveia` *Dataset: Oat data*

Description

Data set with oat genotypes and industry variables.

Usage

```
aveia
```

Format

A data.frame with 54 observations and 6 variables:

GEN 14 white oat genotypes.

BLOCO Experiment blocks.

NG2M Number of grains larger than 2 mm.

MG Grain mass

MC Caryopsis dough

RG Grain yield (in kg per ha)

Source

Real field data for use.

`clima` *Data: Climate Data Set for Predictions*

Description

Average air temperature and relative humidity data for the period of one year, with time, day and month.

Usage

```
clima
```

Format

A data.frame with 8760 observations and 5 variables:

MO Month of the year.

DY Day of the year.

HR Time of the day.

TMED Average Air Temperature - in degree C.

RH Relative Humidity - in %.

Source

Data obtained from the Nasa Power platform (https://power.larc.nasa.gov/).

`coefend` *Data: Data: Endogamy Coefficient Data Set*

Description

Data set of phenotypic and genotypic variance, heritability and differential selection for different variables.

Usage

```
coefend
```

Format

A data.frame with 7 observations and 5 variables:

Var	Variable name.
VF	Phenotypic Variance.
VG	Genotypic Variance.
h	Broad-sense heritability
DS	Selection Differential

Source

Real data for use.

`COI` *Inbreeding coefficient*

Description

Function for calculating the inbreeding coefficient

Usage

```
COI(var, VG, VF, generation = "all", verbose = FALSE)
```

Arguments

`var`	Column with the variable name
`VG`	Column with genotypic variance
`VF`	Column with phenotypic variance
`generation`	Parameter to select the generation. Use 'all' to get the parameters for all the generations or 'F3', 'F4', 'F5' and 'F6' for just one of the generations.
`verbose`	Logical argument. Runs the code silently if FALSE.

Value

Returns the total, additive and dominance variance values based on the variance components for a given variable.

Author(s)

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References

Falconer, D. S., & Mackay, T. F. C. (1996). Introduction to quantitative genetics (4th ed.). Longman.

Examples

```
library(EstimateBreed)

var <- c("A","B","C","D","E")
VF <- c(2.5, 3.0, 2.8, 3.2, 2.7)
VG <- c(1.2, 1.5, 1.3, 1.6, 1.4)
data <- data.frame(var,VG,VF)

#Calculating for all generations
inbr1 <- with(data,COI(var,VG,VF,generation = "all"))

#Calculating for just one generation
inbr2 <- with(data,COI(var,VG,VF,generation = "F3"))
```

`default_seg` *Standard Segregation*

Description

Didactic table of standard segregation by generation

Usage

```
default_seg(verbose = TRUE)
```

Arguments

`verbose`	Logical argument. Runs the code silently if FALSE.

Value

Create a didactic table of standard segregation, considering allogamous and autogamous species and mutants. It shows the expected level of heterozygosity, probable number of genes, environmental effect and Wright's probabilistic coefficient.

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Examples

```
library(EstimateBreed)

default_seg(verbose=TRUE)
```

`desvamb` *Data: Data set for calculating the environmental deviation*

Description

Data set with average air temperature and precipitation values per environment

Usage

```
desvamb
```

Format

A data.frame with 449 observations and 3 variables:

ENV Selection environment.

TMED Average Air Temperature (in degree C).

PREC Precipitation (in mm)

Source

Real field data for use.

`desv_clim` *Auxiliary function for calculating ISGR*

Description

This function receives a dataframe with temperature and precipitation data and calculates the standard deviation of these parameters for each environment.

Usage

```
desv_clim(ENV, AAT, PREC)
```

Arguments

`ENV`	Identification of each selection environment (to differentiate if there is more than one cultivation cycle).
`AAT`	Average air temperature (in degree Celsius) during the cycle in each environment.
`PREC`	Rainfall (in mm) during the cultivation cycle in each environment

Value

A dataframe containing the identifier of the selection environment and the standard deviations for temperature and precipitation.

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Examples

```
library(EstimateBreed)
data("desvamb")
head(desvamb)

#Use DPclim for the ISGR function to identify deviations correctly
DPclim <- with(desvamb,desv_clim(ENV,TMED,PREC))
```

`didint` *Allelic and genotype-environment interactions*

Description

Didactic function - Examples of allelic and gene interactions

Usage

```
didint(type = NULL, ge = NULL)
```

Arguments

`type`	Type of allelic interaction. Use 'ad' for additivity, 'dom' for complete dominance, 'domp' for partial dominance and 'sob' for overdominance.
`ge`	Type of GxE interaction. Use 'aus' for no interaction, 'simple' for simple interaction and 'complex' for complex interaction.

Value

Plot graphs representing allelic and genotype x environment interactions.

Author(s)

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Examples

```
library(EstimateBreed)

didint (type="ad")
didint (type="dom")
didint (type="domp")
didint (type="sob")

didint (ge="aus")
didint (ge="simple")
didint (ge="complex")
```

`genot` *Data: GxE Interaction*

Description

Data set with strains and test subjects from a GxE experiment.

Usage

```
genot
```

Format

A data.frame with 55 observations and 5 variables:

GEN Selected lines in a GXE experiment.

ENV Selection environments.

NG Number of grains measured in the lines.

MG Grain mass measured in the lines (in g)

CICLO Length of crop cycle (in days)

Source

Real field data for use.

`genot2` *Data Set for obtaining genetic parameters.*

Description

Dataset with two breeding populations, 20 genotypes per population and three replicates per genotype.

Usage

```
genot2
```

Format

A data.frame with 60 observations and 4 variables:

Pop Column with population names.

Gen Column with genotype names.

Rep Column with replications.

VAR1 Column with numerical values of the random variable.

Source

Simulated data for use.

`genpar` *Genetic parameters for selection*

Description

Function for determining selection parameters, based on an experiment carried out on the rice crop. Intended for isolated evaluation of the performance of lines within a given population.

Usage

```
genpar(.data, GEN, REP, vars, K = 0.05, check = FALSE, verbose = FALSE)
```

Arguments

`.data`	The name of the object containing data.
`GEN`	The column with the selected genotypes within the population.
`REP`	The column with the repetitions (if any).
`vars`	The column with the variable of interest.
`K`	Selection pressure (Default 0.05).
`check`	Logical argument. Checks the model's assumptions statistical if the value is equal to TRUE.
`verbose`	Logical argument. Runs the code silently if FALSE.

Value

A list containing the following components:

`Environmental variance (sigmaE)`	The environmental variance (sigmaE) represents the variability in phenotypic traits attributable to environmental factors. This variance is important for understanding how environmental conditions influence the observed phenotype.
`Genotypic variance (sigmaG)`	The genotypic variance (sigmaG) reflects the variability in phenotypic traits attributable to genetic differences between individuals. It is crucial for assessing the genetic potential of a population for a specific trait.
`Phenotypic variance (sigmaP)`	The phenotypic variance (sigmaP) is the total observed variability in the phenotype, which is the sum of environmental and genotypic variances. This measure helps understand the overall range of variation observed in a given dataset.
`Environmental coefficient of variance (ECV)`	The environmental coefficient of variance (ECV) is the ratio of environmental variance to the mean of the phenotypic value, expressed as a percentage. It gives an idea of the magnitude of environmental variation relative to the mean value.

`Genotypic coefficient of variance (GCV)`
The genotypic coefficient of variance (GCV) is the ratio of genotypic variance to the mean of the phenotypic value, also expressed as a percentage. It is used to estimate how much genetic variability can be exploited for improving desirable traits.

`Phenotypic coefficient of variance (PCV)`
The phenotypic coefficient of variance (PCV) is the ratio of phenotypic variance to the mean of the phenotypic value, expressed as a percentage. It provides insight into the overall impact of both genetic and environmental factors on the observed variation.

`Heritability (h2b)`
Heritability (h2b) is the proportion of phenotypic variance attributable to genotypic variance. It indicates the potential for selecting specific traits within a population.

`Genetic advance (GA)`
Genetic advance (GA) represents the amount of genetic progress that can be achieved in one generation by selecting the best individuals for specific traits.

`Genetic advance as percentage of the mean (GAM)`
Genetic advance as a percentage of the mean (GAM) is a measure of how much genetic progress represents relative to the population's mean. This value helps assess the effectiveness of selection strategies.

Author(s)

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References

Yadav, S. P. S., Bhandari, S., Ghimire, N. P., Mehata, D. K., Majhi, S. K., Bhattarai, S., Shrestha, S., Yadav, B., Chaudhary, P., & Bhujel, S. (2024). Genetic variability, character association, path coefficient, and diversity analysis of rice (Oryza sativa L.) genotypes based on agro-morphological traits. International Journal of Agronomy, 2024, Article ID 9946332. doi:10.1155/2024/9946332

Examples

```
library(EstimateBreed)
data("genot2")

#Geting parameters without cheking model assumptions
parameters <- genpar(genot2,Gen,Rep,var =c("VAR1", "VAR2"))
parameters$anova
parameters$gp

#Checking model assumptions
```

```
parameters <- genpar(genot2,Gen,Rep,var =c("VAR1", "VAR2"),check=TRUE)
parameters$anova
parameters$gp
```

---

het *Heterosis and Heterobeltiosis*

Description

Calculation of heterosis and heterobeltiosis parameters of hybrids

Usage

```
het(GEN, GM, GP, PR, REP, param = "all", verbose = FALSE)
```

Arguments

`GEN`	The column with the genotype name
`GM`	The column with the average of the maternal parent
`GP`	The column with the average of the paternal parent
`PR`	The column with the average of the progeny
`REP`	The column with the repetitions (if exists)
`param`	Value to determine the parameter to be calculated. Default is 'all'. To calculate heterosis only, use 'het'. To calculate only heterobeltiosis, use 'hetb'.
`verbose`	Logical argument. Runs the code silently if FALSE.

Value

Returns heterosis values based on the performance of the tested parents and progenies. The standard error (SE) is also reported for each parameter.

Author(s)

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Examples

```
library(EstimateBreed)

data("maize")
#Extract heterosis and heterobeltiosis
general <- with(maize,het(GEN,GM,GP,PR,REP,param="all"))

#Only extract heterosis
het <- with(maize,het(GEN,GM,GP,PR,REP,param = "het"))

#Extract only heterobeltiosis
hetb <- with(maize,het(GEN,GM,GP,PR,REP,param = "hetb"))
```

`hw` *Hectolitre weight of cereals*

Description

Useful function for characterizing the hectolitre weight (HW) of experiments with cereals.

Usage

```
hw(GEN, HL, crop = "trit", stat = "all")
```

Arguments

`GEN`	The column with the genotype name
`HL`	Weight obtained on a 1qt lt scale, as determined by the Rules for Seed Analysis (RAS), Ministry of Agriculture, Livestock and Supply (2009).
`crop`	Argument for selecting culture. Use 'trit' for wheat, 'oat' for white oats, 'rye' for rye and 'barley' for barley
`stat`	Argument to select the function output type. Use 'all' to estimate the HW for all replicates, or 'mean' to extract the mean for each genotype.

Value

Returns the estimated value for the hectoliter weight considering the selected cereal.

Author(s)

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References

Brasil. Ministerio da Agricultura, Pecuaria e Abastecimento. Secretaria de Defesa Agropecuaria. Regras para Analise de Sementes. Brasilia: MAPA/ACS, 2009. 399 p. ISBN 978-85-99851-70-8.

Examples

```
library(EstimateBreed)

GEN <- rep(paste("G", 1:5, sep=""), each = 3)
REP <- rep(1:3, times = 5)
MG <- c(78.5, 80.2, 79.1, 81.3, 82.0, 80.8, 76.9, 78.1, 77.5, 83.2,
84.1, 82.9, 77.4, 78.9, 79.3)

data <- data.frame(GEN, REP, MG)

trit <- with(data,hw(GEN,MG,crop="trit"))

#Extract the average PH per genotype
trit <- with(data,hw(GEN,MG,crop="trit",stat="mean"))
```

`indviab` *Ear Indexes*

Description

Estimating the viability index from the combination of two field variables.

Usage

```
indviab(
  GEN,
  var1,
  var2,
  ylab = "Index",
  xlab = "Genotype",
  stat = "all",
  verbose = FALSE,
  plot = FALSE
)
```

Arguments

`GEN`	The column with the name of the genotypes
`var1`	The column containing the first variable
`var2`	The column containing the second variable
`ylab`	The name of the chart's Y axis
`xlab`	The name of the chart's X axis

`stat`	Logical argument. Use 'all' to return the values obtained for all observations or 'mean' to return the mean per genotype.
`verbose`	Logical argument. Runs the code silently if FALSE.
`plot`	Logical argument. Plot a graphic if 'TRUE'.

Value

Returns the index obtained between the reported variables. The higher the index, the better the genotype.

Author(s)

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References

Rigotti, E. J., Carvalho, I. R., Loro, M. V., Pradebon, L. C., Dalla Roza, J. P., & Sangiovo, J. P. (2024). Seed and grain yield and quality of wheat subjected to advanced harvest using a physiological ripening process. Revista Engenharia na Agricultura - REVENG, 32, 54-64. doi:10.13083/reveng.v32i1.17394

Examples

```
library(EstimateBreed)

data("trigo")
#Ear viability index
index1 <- with(trigo,indviab(TEST,NGE,NEE))

#Ear harvest index
index2 <- with(trigo,indviab(TEST,MGE,ME))

#Spikelet deposition index in the ear
index3 <- with(trigo,indviab(TEST,NEE,CE))
```

`isgr` *ISGR - Genetic Selection Index for Resilience*

Description

Estimation of the selection index for environmental resilience (Bandeira et al., 2024).

Usage

```
isgr(GEN, ENV, NG, MG, CICLO, req = 3.5, stage = NULL)
```

Arguments

`GEN`	Column referring to genotypes. Lines must have the prefix 'L' before the number. Ex: L139.
`ENV`	The column for the selection environment.
`NG`	Number of grains of all genotypes evaluated
`MG`	Grain mass of all genotypes evaluated
`CICLO`	Number of days in the cycle to define rainfall ideal (value of 3.5 mm per day). Can be changed manually in the 'req' argument.
`req`	Average daily water demand for the soybean crop (standard 3.5 mm). May change depending on the phenological stage.
`stage`	Parameter to define the phenological stage the crop is in Use 'veg' for vegetative and 'rep' for reproductive, if the evaluations have only been carried out in a given period.

Value

The ISGR - Genetic Selection Index for Resilience defines the ability of genotypes to express their productivity components under the conditions of air temperature and rainfall offered by the environment. The lower the index, the more resilient the genotype.

Author(s)

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References

Bandeira, W. J. A., Carvalho, I. R., Loro, M. V., da Silva, J. A. G., Dalla Roza, J. P., Scarton, V. D. B., Bruinsma, G. M. W., & Pradebon, L. C. (2024). Identifying soybean progenies with high grain productivity and stress resilience to abiotic stresses. Aust J Crop Sci, 18(12), 825-830.

Examples

```
library(EstimateBreed)

#Obtain environmental deviations
data("desvamb")
head(desvamb)
```

```
#Use DPclim for the ISGR function to identify deviations correctly
DPclim <- with(desvamb,desv_clim(ENV,TMED,PREC))

#Calculate the ISGR
data("genot")
head(genot)
isgr_index <- with(genot, isgr(GEN,ENV,NG,MG,CICLO))

#Define the water requirement per stage
isgr_index <- with(genot, isgr(GEN,ENV,NG,MG,CICLO,req=5,stage="rep"))
```

`is_ptnerg` *Selection index for protein and grain yield*

Description

Selection index for protein and grain yield (Pelegrin et al., 2017).

Usage

```
is_ptnerg(GEN, PTN, RG, verbose = TRUE)
```

Arguments

`GEN`	The column with the name of the genotype
`PTN`	The column with the crude protein values
`RG`	The column with the grain yield values (in kg per ha)
`verbose`	Logical argument. Runs the code silently if FALSE.

Value

Returns an industrial wheat quality index based solely on protein and grain yield.

Author(s)

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References

de Pelegrin, A. J., Carvalho, I. R., Nunes, A. C. P., Demari, G. H., Szareski, V. J., Barbosa, M. H., ... & da Maia, L. C. (2017). Adaptability, stability and multivariate selection by mixed models. American Journal of Plant Sciences, 8(13), 3324.

Examples

```
library(EstimateBreed)

Gen <- c("G1", "G2", "G3", "G4", "G5")
PTN <- c(12.5, 14.2, 13.0, 11.8, 15.1)
RG <- c(3500, 4000, 3700, 3300, 4100)

data <- data.frame(Gen,PTN,RG)

iqptn <- with(data,is_ptnerg(Gen,PTN,RG))
```

`is_qindustrial` *Industrial quality of wheat*

Description

Function for determining industrial quality indices of wheat genotypes, described by Szareski et al. (2019).

Usage

```
is_qindustrial(GEN, NQ, W, PTN, verbose = TRUE)
```

Arguments

`GEN`	The column with the genotype name
`NQ`	The column with the falling number
`W`	The column with the gluten force (W)
`PTN`	The column with the protein values
`verbose`	Logical argument. Runs the code silently if FALSE.

Value

Determines the industrial quality index for wheat crops, when considering variables used to classify wheat cultivars.

Author(s)

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References

Szareski, V. J., Carvalho, I. R., Kehl, K., Levien, A. M., Lautenchleger, F., Barbosa, M. H., ... & Aumonde, T. Z. (2019). Genetic and phenotypic multi-character approach applied to multivariate models for wheat industrial quality analysis. Genetics and Molecular Research, 18(3), 1-14.

Examples

```
library(EstimateBreed)

data("ptn")
with(ptn,is_qindustrial(Cult,NQ,W,PTN))
```

`itu` *Environmental Stress Index*

Description

Determining the UTI (temperature and humidity index) from the air temperature and relative humidity values over a given period of time

Usage

```
itu(AAT, RH)
```

Arguments

`AAT`	The column with the average air temperature values
`RH`	The column with the relative humidity values

Value

Returns the stress condition based on the reported air temperature and relative humidity values, being: Non-stressful condition (ITU>=70), Heat stress condition (ITU between 71 and 78), Severe heat stress (ITU between 79 and 83), and Critical heat stress condition (ITU above 84).

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References

Tazzo, I. F., Tarouco, A. K., Allem Junior P. H. C., Bremm, C., Cardoso, L. S., & Junges, A. H. (2024). Indice de Temperatura e Umidade (ITU) ao longo do verao de 2021/2022 e estimativas dos impactos na bovinocultura de leite no Rio Grande do Sul, Brasil. Ciencia Animal Brasileira, 2,5, e-77035P.

`lai` *Leaf Area Index (LAI)*

Description

Utility function for estimating crop LAI

Usage

```
lai(GEN, W, L, TNL, TDL, crop = "soy", sp = 0.45, sden = 14, verbose = TRUE)
```

Arguments

`GEN`	The column with the genotype name
`W`	The column with the width of the leaf (in meters).
`L`	The column with the length of the leaf (in meters).
`TNL`	The column with the total number of leaves.
`TDL`	The column with the total number of dry leaves.
`crop`	Crop sampled. Use 'soy' for soybean and 'maize' for maize, 'trit' for wheat, 'rice' for rice, 'bean' for bean, 'sunflower' for sunflower, 'cotton' for cotton, 'sugarcane' for sugarcane, 'potato' for potato and 'tomato' for tomato.
`sp`	Row spacing (Standard sp=0.45).
`sden`	Sowing density, in plants per linear meter (standard sden=14).
`verbose`	Logical argument. Runs the code silently if FALSE.

Value

Returns the accumulated leaf area, the potential leaf area index (considering the total number of leaves) and the actual leaf area index (making the adjustment considering the number of dry leaves) for each genotype

Author(s)

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References

Meira, D., Queiroz de Souza, V., Carvalho, I. R., Nardino, M., Follmann, D. N., Meier, C., Brezolin, P., Ferrari, M., & Pelegrin, A. J. (2015). Plastocrono e caracteres morfologicos da soja com habito de crescimento indeterminado. Revista Cultivando o Saber, 8(2), 184-200.

Examples

```
library(EstimateBreed)

data("leafarea")
#Crop selection
soy_lai<-with(leafarea,lai(GEN,C,L,TNL,TDL,crop="soy"))

#Changing row spacing and sowing density
maize_lai<-with(leafarea,lai(GEN,C,L,TNL,TDL,crop="maize",sp=0.45,sden=4))
```

`leafarea` *Data Set for Leaf Area Index*

Description

Data set with 10 genotypes and values for leaf length, leaf width, number of total leaves and number of dry leaves

Usage

```
leafarea
```

Format

A data.frame with 10 observations and 5 variables:

GEN Column with the genotypes.

C Leaf lenght

L Leaf width

TNL Total number of leaves.

TDL Total dry leavesh.

Source

Simulated data.

`lin` *Data: Wheat Data Set with Protein and Grain Yield*

Description

Data set with wheat genotypes, protein percentage and grain yield.

Usage

```
lin
```

Format

A data.frame with 24 observations and 7 variables:

POP Base population.

MGP_MF Phenotypic average of grain mass per plant.

MGP_GP Genotypic average of grain mass per plant.

VF Phenotypic variance

VG Genetic variance

H2 Heritability in the broad sense

Test Witness parameters

Source

Real field data for use.

`linearest` *Estimates using polynomial equations.*

Description

Determination of maximum technical efficiency (MTE) and plateau regression.

Usage

```
linearest(indep, dep, type = NULL, alpha = 0.05, verbose = FALSE)
```

Arguments

`indep`	Name of the column with the independent variable.
`dep`	Name of the dependent variable column
`type`	Type of analysis to be carried out. Use 'MTE' to extract the maximum technical efficiency or 'plateau' for plateau regression.
`alpha`	Significance of the test.
`verbose`	Logical argument. Runs the code silently if FALSE.

Value

Calculates the maximum technical efficiency (MTE) based on a quadratic polynomial model, if it is significant. The MTE is given by:

$$MTE = -\frac{\beta_1}{2\beta_2}$$

It also calculates plateau regression parameters, returning: - The plateau value:

$$Y_{plateau} = \beta_0 + \beta_1 X_{plateau} + \beta_2 X_{plateau}^2$$

- The growth rate:

$$\beta_1$$

- The inflection point:

$$X_{inflection} = -\frac{\beta_1}{2\beta_2}$$

Author(s)

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Examples

```
library(EstimateBreed)
data("mtcars")

met<-with(mtcars,linearest(wt,mpg,type = "MTE",verbose=TRUE))
```

`maize` *Data: Maize Dataset*

Description

Data set with progenies and maternal and paternal maize genitors.

Usage

```
maize
```

Format

A data.frame with 4 observations and 3 variables:

P Progenies.

GM Maternal Parent

GP Patern Parent

Source

Simulated Data.

`optemp` *Plotting the optimum and cardinal temperatures for crops*

Description

Utility function for plotting graphs of thermal preferences for crops. It is necessary to inform the temperature values (minimum, average or maximum).

Usage

```
optemp(
  VAR,
  crop = NULL,
  verbose = FALSE,
  plot = TRUE,
  ylab = "Meteorological Atribute",
  xlab = "Days After Sowing"
)
```

Arguments

`VAR`	The column with air temperature values (minimum, average or maximum).
`crop`	Parameter to define the culture. Use 'soybean' for soybean crop, 'maize' for maize crop and 'trit' for wheat crop.
`verbose`	Logical argument. Runs the code silently if FALSE.
`plot`	Logical argument. Plot a graph of optimal temperatures if TRUE.
`ylab`	The name of the Y axis.
`xlab`	The name of the X axis.

Value

Returns the parameters of lower basal and optimum temperature, upper basal and optimum temperature, maximum temperature and average temperature.

Author(s)

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Examples

```
library(EstimateBreed)

data("clima")
clima <- get("clima")[1:150, ]

with(clima,optemp(TMED,crop="soybean"))
```

`pheno` *Soybean Plastochron Estimation Data Set*

Description

Fictitious data set for estimating soybean plastochron based on on the number of nodes

Usage

```
pheno
```

Format

A data.frame with 135 observations and 5 variables:

CICLO Days in the soybean cycle.

GEN The column with the name of the genotype.

TMED The column with the average temperature values.

EST The column with the phenological stage.

NN The column with the number of nodes.

Source

Simulated data for use.

`plast` *Soybean plastochron estimation*

Description

Estimation of soybean plastochron using average air temperature and number of nodes

Usage

```
plast(GEN, AAT, STAD, NN, habit = "ind", verbose = FALSE, plot = FALSE)
```

Arguments

`GEN`	The column with the genotype name.
`AAT`	The column with the average air temperature values.
`STAD`	The column with the phenological stages of soybean, as described by Fehr & Caviness (1977).
`NN`	The column with the number of nodes measured in field.
`habit`	Growth habit of the genotype (default = "ind"). Use "ind" for indeterminate and "det" for determinate.
`verbose`	Logical argument. Runs the code silently if FALSE.
`plot`	Logical argument. Returns a graph with the linear models if TRUE.

Value

If the growth habit is determined, the function returns a linear model for the V1 to R1 stages (Early Pheno) and a linear model for the R1 to R5 stages (Late Pheno). If the growth habit is indeterminate, returns three linear models: Early Pheno (V1 to R1), Intermediate Pheno (R1 to R3) and Late Pheno (R3 to R5).

Author(s)

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References

Porta, F. S. D., Streck, N. A., Alberto, C. M., da Silva, M. R., & Tura, E. F. (2024). Improving understanding of the plastochron of determinate and indeterminate soybean cultivars. Revista Brasileira de Engenharia Agricola e Ambiental, 28(10), e278299. doi:10.1590/18071929/agriambi.v28n10e278299

Fehr, W. R., & Caviness, C. E. (1977). Stages of soybean development. Iowa State University of Science and Technology Special Report, 80, 1-11.

Examples

```
library(EstimateBreed)
data("pheno")

mod1 <- with(pheno, plast(GEN,TMED,EST,NN,habit="ind",plot=TRUE))
mod1
```

`ptermal` *Photothermal Index*

Description

Calculation of the photothermal index based on average temperature and radiation

Usage

```
ptermal(DAY, AAT, RAD, PER, verbose = FALSE)
```

Arguments

`DAY`	The column with the cycle days
`AAT`	The column with the average air temperature values
`RAD`	The column with the incident radiation values
`PER`	The column with the period (use VEG for vegetative and REP for reproductive)
`verbose`	Logical argument. Runs the code silently if FALSE.

Value

Retorna o ind fototermal

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References

Zanon, A. J., & Tagliapietra, E. L. (2022). Ecofisiologia da soja: Visando altas produtividades (2a ed.). Field Crops.

Examples

```
library(EstimateBreed)
data("termaldata")

termal <- with(termaldata,ptermal(Day,Temperature,Radiation,Period))
termal
```

`ptn` *Data: Wheat Dataset 1*

Description

Data set with wheat cultivars and grain rheological characters.

Usage

```
ptn
```

Format

A data.frame with 360 observations and 5 variables:

Cult Wheat cultivars.
Am Sample identification number.
NQ Falling Number.
W Gluten Strength (W).
PTN Grain Protein.

Source

Real laboratory data.

`ptnrg` *Data: Wheat Dataset 2*

Description

Wheat genotype, protein and grain yield data set

Usage

```
ptnrg
```

Format

A data.frame with 360 observations and 5 variables:

CULTIVAR Wheat cultivars.
REP Repetition number.
PTN Grain protein.
RG Grain yield (kg ha)

Source

Real field data.

`rend_ind` *Peeling Index and Industrial Yield*

Description

Calculating the Hulling Index and Industrial Yield of White Oats

Usage

```
rend_ind(GEN, NG2M, MG, MC, RG, stat = "all", verbose = FALSE, ...)
```

Arguments

`GEN`	The column with the name of the genotypes.
`NG2M`	The column with values for the number of grains larger than 2mm.
`MG`	The column with grain mass values.
`MC`	The column with karyopsis mass values.
`RG`	The column with the grain yield values (kg per ha).
`stat`	Logical argument. Use 'all' to keep all the observations or 'mean' to extract the overall average.
`verbose`	Logical argument. Runs the code silently if FALSE.
`...`	General parameters of ggplot2 for utilization

Value

Returns the peeling index and industrial yield considering the standards desired by the industry.

Author(s)

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Examples

```
library(EstimateBreed)

data("aveia")
# Calculate the industrial yield without extracting the average
with(aveia, rend_ind(GEN,NG2M,MG,MC,RG))

# Calculate the industrial yield by extracting the average per genotype
with(aveia, rend_ind(GEN,NG2M,MG,MC,RG,stat="mean"))
```

`restr` *Restriction of control variability*

Description

Method for restricting the variability of control proposed by Carvalho et al. (2023). It uses the restriction of the mean plus or minus one standard deviation. standard deviation, which restricts variation by removing asymmetric values.

Usage

```
restr(TEST, REP, Xi, scenario = NULL, zstat = NULL, verbose = FALSE)
```

Arguments

`TEST`	The column with the name of the witness
`REP`	The column with the replications
`Xi`	The column with the observed value for a given genotype.
`scenario`	Scenario to be used for the calculation. Use 'original' to do not restrict the witnesses by the mean plus or minus the standard deviations, or 'restr' to apply the restriction.
`zstat`	Logical argument. Applies Z-notation normalization if 'TRUE'.
`verbose`	Logical argument. Runs the code silently if FALSE.

Value

Describes controls that were removed from the dataset to restrict variability.

Author(s)

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Jose Antonio Gonzalez da Silva

References

Carvalho, I. R., Silva, J. A. G. da, Moura, N. B., Ferreira, L. L., Lautenchleger, F., & Souza, V. Q. de. (2023). Methods for estimation of genetic parameters in soybeans: An alternative to adjust residual variability. Acta Scientiarum. Agronomy, 45, e56156. doi:10.4025/actasciagron.v45i1.56156

Examples

```
library(EstimateBreed)

TEST <- rep(paste("T", 1:5, sep=""), each=3)
REP <- rep(1:3, times=5)
Xi <- rnorm(15, mean=10, sd=2)

data <- data.frame(TEST,REP,Xi)

#Apply the control variability constraint
Control <- with(data, restr(TEST,REP,Xi,scenario = "restr",zstat = FALSE))

#Apply control variability restriction with normalization (Z statistic)
Control <- with(data, restr(TEST,REP,Xi,scenario = "restr",zstat = TRUE))
```

`risk` *Risk of Disease Occurrence in Soybeans*

Description

Calculation of the Risk of Disease Occurrence in Soybeans as a Function of Variables meteorological variables (Engers et al., 2024).

Usage

```
risk(DAY, MONTH, AAT, RH, disease = "rust", verbose = FALSE, plot = FALSE)
```

Arguments

`DAY`	The column for the day of the month.
`MONTH`	The column for the month of the year (numeric value).
`AAT`	The average air temperature column (in degree Celsius).
`RH`	The relative humidity column (in %).
`disease`	Define the soybean disease (Standard = 'rust').
`verbose`	Logical argument. Runs the code silently if FALSE.
`plot`	Plot a graph of the accumulation (Default is F (FALSE)).

Value

Returns the parameters of the incidence probability of the selected disease in the soybean crop, being:

* RHrisk
Risk caused by relative humidity.

* TEMPrisk

Risk caused by air temperature.

* TOTALrisk
Product of the multiplication between RHrisk and TEMPrisk.

* RELrisk
Relative risk obtained from the highest value of TOTALrisk.

Author(s)

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References

de Oliveira Engers, L.B., Radons, S.Z., Henck, A.U. et al. Evaluation of a forecasting system to facilitate decision-making for the chemical control of Asina soybean rust. Trop. plant pathol. 49, 539-546 (2024). doi:10.1007/s40858024006491

Examples

```
library(EstimateBreed)

# Rust Risk Prediction
data("clima")
with(clima, risk(DY, MO, TMED, RH, disease = "rust"))
```

`SG` *General Selection Gain Function*

Description

Computes selection gain using different selection methods

Usage

```
SG(
  Var,
  h,
  VF = NULL,
  P = "1",
  DS = NULL,
  Year = NULL,
  method = "pressure",
  verbose = FALSE
)
```

Arguments

`Var`	The column with the name of the variables of interest
`h`	The column with the restricted heritability values
`VF`	The column with the phenotypic variance values (optional)
`P`	The column with the progeny values or selection pressure (optional)
`DS`	The column with the selection differential values (optional)
`Year`	The column with the year of selection (optional)
`method`	The selection method: 'pressure', 'differential', 'genitor_control", or 'year_weighted'
`verbose`	Logical argument. Runs the code silently if FALSE.

Value

A data frame with selection gain results

Author(s)

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Examples

```
library(EstimateBreed)

SG(Var = c("A", "B", "C"), h = 0.5, VF = 1.2, P = "10", method = "pressure")
SG(Var = c("A", "B", "C"), h = 0.5, DS = 1.5, method = "differential")
SG(Var = c("A", "B", "C"), h = 0.5, VF = 1.2, P = "10", method = "genitor_control")
SG(Var = c("A", "B", "C"), h = 0.5, VF = 1.2, P = "10", Year = 5, method = "year_weighted")
```

`stind` *Stress indices for genotype selection*

Description

Selection indices for genotypes conducted under stress conditions cited by Ghazvini et al. (2024).

Usage

```
stind(
  GEN,
  YS,
  YC,
  index = "ALL",
  bygen = TRUE,
  verbose = FALSE,
  plot = FALSE,
  xlab = "Genotype",
  ylab = "Values",
  ...
)
```

Arguments

`GEN`	The column with the genotypes to be selected.
`YS`	Productivity of the genotype without stress conditions.
`YC`	Genotype productivity under stressful conditions.
`index`	Index to be calculated (Standard 'ALL'). The indices to be used are: 'STI' - Stress Tolerance Index, 'YI' - Yield Index, 'GMP' - Geometric Mean Productivity, 'MP' - Mean Productivity, 'MH' - Harmonic Mean, 'SSI' - Stress Stability Index, 'YSI' - Yield Stability Index, 'RSI' - Relative Stress Index.
`bygen`	Returns the average of each genotype if 'TRUE'. Only in this way it will be possible to plot graphs.
`verbose`	Logical argument. Runs the code silently if FALSE.
`plot`	Plot graph if equal to 'TRUE' (Standard 'FALSE').
`xlab`	Adjust the title of the x-axis in the graph.
`ylab`	Adjust the title of the y-axis in the graph.
`...`	General ggplot2 parameters for graph customization.

Value

Returns a table with the genotypes and the selected indices. The higher the index value, the more resilient the genotype.

Author(s)

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References

Ghazvini, H., Pour-Aboughadareh, A., Jasemi, S.S. et al. A Framework for Selection of High-Yielding and Drought-tolerant Genotypes of Barley: Applying Yield-Based Indices and Multi-index Selecion Models. Journal of Crop Health 76, 601-616 (2024). doi:10.1007/s10343024009811

Examples

```
library(EstimateBreed)

data("aveia")

#General
index <- with(aveia,stind(GEN,MC,MG,index = "ALL",bygen=TRUE))

#Only the desired index
STI <- with(aveia,stind(GEN,MC,MG,index = "STI",bygen=TRUE))
```

`tamef` *Effective Population Size*

Description

Estimates the effective population size (N_e) adapted from Morais (1997). The function provides two different calculation methods: 'classic' and 'alternative'.

The classic method follows the equation:

$$N_e = \frac{(\sum SI)^2}{\sum\left(\frac{SI^2}{NE}\right)}$$

The alternative method is calculated as:

$$N_e = \frac{4\sum SI}{2 + \sum\left(\frac{SI}{NE}\right)}$$

Usage

```
tamef(GEN, SI, NE, remove_na = TRUE, method = "classic", verbose = TRUE)
```

Arguments

`GEN`	The column with the name of the genotype (progeny).
`SI`	The column with the number of individuals selected.
`NE`	Number of individuals conducted during the selection period.
`remove_na`	Logical argument. If 'TRUE', missing values will be removed.
`method`	Character string specifying the calculation method. Options are classic' (default) or 'alternative'. 'classic' uses the variance-based method, while 'alternative' uses an adjusted method that accounts for reproductive variation.
`verbose`	Logical argument. Runs the code silently if FALSE.

Value

The result is the effective population size for any variable, based on the number of individuals conducted and selected.

Author(s)

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References

Morais, R. P. (1997). Effective population size and genetic diversity in improved populations of self-pollinated plants (Doctoral dissertation, University of Campinas).

Examples

```
library(EstimateBreed)

GEN <- c("Genotype1", "Genotype2", "Genotype3", "Genotype4", "Genotype5")
SI <- c(10, 15, 12, 18, 14)
NE <- c(100, 150, 120, 180, 140)
data <- data.frame(GEN,SI,NE)

with(data, tamef(GEN, SI, NE, method = "classic"))
```

`tdelta` *Optimum conditions for pesticide application*

Description

Determining the ideal time for pesticide application using TDELTA

Usage

```
tdelta(
  LON,
  LAT,
  type = 2,
  days = 7,
  control = NULL,
  details = FALSE,
  verbose = TRUE,
  dates = NULL,
  plot = FALSE
)
```

Arguments

`LON`	Longitude (in decimal)
`LAT`	Latitude (in decimal)
`type`	Type of analysis. Use 1 for forecast and 2 for temporal data.
`days`	Number of days (only use this argument if type=1).
`control`	Type of product to be applied. Use 'fung' for fungicide, 'herb' for herbicide, 'ins' for insecticides, 'bio' for biological products.
`details`	Returns the result in detail if TRUE.
`verbose`	Logical argument. Runs the code silently if FALSE.
`dates`	Only use this argument if type=2. Start and end date for obtaining weather data for a crop cycle.
`plot`	Logical argument. Plots a graphic if 'TRUE'.

Value

Returns the ideal application times, considering each scenario. Taking as a parameter a TDELTA between 2 and 8, wind speed between 3 and 8, and no precipitation.

Author(s)

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Examples

```
library(EstimateBreed)

# Forecasting application conditions
forecast <- tdelta(-53.6969,-28.0638,type=1,days=10,verbose=TRUE)

# Retrospective analysis of application conditions
retrosp <- tdelta(-53.6969,-28.0638,type=2,days=10,
                 dates=c("2023-01-01","2023-05-01"),
                 verbose=TRUE)
```

`termaldata` *Data Set with air temperature and incident radiation.*

Description

Data Set with air temperature and incident radiation.

Usage

```
termaldata
```

Format

A data.frame with 100 observations and 4 variables:

Day Column with cycle lenght.

Period Column with two periods (vegetative and reproductive).

Temperature Average air temperature values.

Radiation Incident radiation values.

Source

Simulated data for use.

`transg` *Selection Differential (Mean and Deviations)*

Description

Selection of Transgressive Genotypes - Selection Differential (SD)

Usage

```
transg(
  Gen,
  Var,
  Control,
  verbose = FALSE,
  plot = FALSE,
  ylab = "Selection",
  xlab = "Genotypes"
)
```

Arguments

`Gen`	The column with the genotype name
`Var`	The column with the values for the variable of interest
`Control`	The column with the value of the variable 'X' for the controls
`verbose`	Logical argument. Runs the code silently if FALSE.
`plot`	Logical argument. Plots a graphic if 'TRUE'.
`ylab`	The name of the Y axis.
`xlab`	The name of the X axis.

Value

Returns the general parameters and the genotypes selected for each treshold. Also plot a representative graph of the selected genotypes based on the mean and standard deviations.

Author(s)

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Examples

```
library(EstimateBreed)

Gen <- paste0("G", 1:20)
Var <- round(rnorm(20, mean = 3.5, sd = 0.8), 2)
Control <- rep(3.8, 20)

data <- data.frame(Gen,Var,Control)

transg_sel <- with(data,transg(Gen,Var,Control,verbose=FALSE,plot=TRUE))
```

`trigo` *Data: Wheat Dataset 3*

Description

Data set from a wheat experiment with different herbicide management.

Usage

```
trigo
```

Format

A data.frame with 19 observations and 6 variables:

TEST Treatment identification.

CE Ear length.

ME Ear mass

NGE Number of grains on the cob.

MGE Grain mass of ear.

NEE Number of spikelets per spike

Source

Real field data for use.

`vig` *Data Set for Seed Vigor Extraction*

Description

Data set from experiment with wheat genotypes subjected to different sowing density.

Usage

```
vig
```

Format

A data.frame with 54 observations and 6 variables:

Trat Column with treatments.

PC First Count

G Germination percentage.

CPA Length of aerial part.

RAD Root length.

MS Seedling dry mass.

EC See what EC is.

Source

Real field data for use.

Index