

Package ‘EstimateBreed’

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Type Package

Title Estimation of Environmental Variables and Genetic Parameters

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Maintainer Willyan Junior Adorian Bandeira <bandeira.wjab@gmail.com>

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](https://doi.org/10.1590/1807-1929/agriambi.v28n10e278299)>, Stress indices for genotype selection referenced by Ghazvini et al. (2024) <[doi:10.1007/s10343-024-00981-1](https://doi.org/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](https://doi.org/10.4238/gmr18223)>, Ear Indexes estimation (Rigotti et al., 2024), <[doi:10.13083/reveng.v32i1.17394](https://doi.org/10.13083/reveng.v32i1.17394)>, Selection index for protein and grain yield (de Pelegrin et al., 2017), <[doi:10.4236/ajps.2017.813224](https://doi.org/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](https://doi.org/10.4025/actasciagron.v45i1.56156)>, Risk of Disease Occurrence in Soybeans described by Engers et al. (2024) <[doi:10.1007/s40858-024-00649-1](https://doi.org/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](https://doi.org/10.1155/2024/9946332)>.

License GPL (>= 3)

URL <https://github.com/willyanjnr/EstimateBreed>

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Author Willyan Junior Adorian Bandeira [aut, cre] (ORCID:
<<https://orcid.org/0000-0002-9430-3664>>),
Ivan Ricardo Carvalho [aut, ctb] (ORCID:
<<https://orcid.org/0000-0001-7947-4900>>),
Murilo Vieira Loro [aut, ctb] (ORCID:
<<https://orcid.org/0000-0003-0241-4226>>),
Leonardo Cesar Pradebon [aut, ctb] (ORCID:
<<https://orcid.org/0000-0001-7827-6312>>),
Jose Antonio Gonzalez da Silva [aut, ctb] (ORCID:
<<https://orcid.org/0000-0002-9335-2421>>)

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Contents

atsum	3
aveia	4
clima	5
coefend	6
COI	6
default_seg	7
desvamb	8
desv_clim	9
didint	10
genot	11
genot2	11
genpar	12
het	14
hw	15
indviab	16
isgr	17
is_ptnerg	19
is_qindustrial	20

itu	21
lai	22
leafarea	23
lin	24
linearest	24
maize	25
optemp	26
pheno	27
plast	27
ptermal	29
ptn	30
ptnrg	30
rend_ind	31
restr	32
risk	33
SG	34
stind	35
tamef	37
tdelta	38
termaldata	40
transg	40
trigo	41
vig	42

Index 43

atsum	<i>Accumulated Thermal Sum</i>
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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 °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)

Willyan Junior Adorian Bandeira

Ivan Ricardo Carvalho

Murilo Vieira Loro

Leonardo Cesar Pradebon

Jose Antonio Gonzalez da Silva

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)

Willyan Junior Adorian Bandeira
 Ivan Ricardo Carvalho
 Murilo Vieira Loro
 Leonardo Cesar Pradebon
 Jose Antonio Gonzalez da Silva

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	<i>Standard Segregation</i>
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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.

Author(s)

Willyan Junior Adorian Bandeira

Ivan Ricardo Carvalho

Murilo Vieira Loro

Leonardo Cesar Pradebon

Jose Antonio Gonzalez da Silva

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.

Author(s)

Willyan Junior Adorian Bandeira
Ivan Ricardo Carvalho
Murilo Vieira Loro
Leonardo Cesar Pradebon
Jose Antonio Gonzalez da Silva

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

<code>type</code>	Type of allelic interaction. Use 'ad' for additivity, 'dom' for complete dominance, 'domp' for partial dominance and 'sob' for overdominance.
<code>ge</code>	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)

Willyan Junior Adorian Bandeira
Ivan Ricardo Carvalho
Murilo Vieira Loro
Leonardo Cesar Pradebon
Jose Antonio Gonzalez da Silva

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	<i>Data: GxE Interaction</i>
-------	------------------------------

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	<i>Data Set for obtaining genetic parameters.</i>
--------	---

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	<i>Genetic parameters for selection</i>
--------	---

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 (h²_b)

Heritability (h²_b) 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)

Willyan Junior Adorian Bandeira

Ivan Ricardo Carvalho

Murilo Vieira Loro

Leonardo Cesar Pradebon

Jose Antonio Gonzalez da Silva

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")

#Getting 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)

Willyan Junior Adorian Bandeira

Ivan Ricardo Carvalho

Murilo Vieira Loro

Leonardo Cesar Pradebon

Jose Antonio Gonzalez da Silva

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	<i>Hectolitre weight of cereals</i>
----	-------------------------------------

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 It 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)

Willyan Junior Adorian Bandeira
 Ivan Ricardo Carvalho
 Murilo Vieira Loro
 Leonardo Cesar Pradebon
 Jose Antonio Gonzalez da Silva

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)

Willyan Junior Adorian Bandeira
Ivan Ricardo Carvalho
Murilo Vieira Loro
Leonardo Cesar Pradebon
Jose Antonio Gonzalez da Silva

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	<i>ISGR - Genetic Selection Index for Resilience</i>
------	--

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)

Willyan Junior Adorian Bandeira
 Ivan Ricardo Carvalho
 Murilo Vieira Loro
 Leonardo Cesar Pradebon
 Jose Antonio Gonzalez da Silva

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)

Willyan Junior Adorian Bandeira
 Ivan Ricardo Carvalho
 Murilo Vieira Loro
 Leonardo Cesar Pradebon
 Jose Antonio Gonzalez da Silva

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	<i>Industrial quality of wheat</i>
----------------	------------------------------------

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)

Willyan Junior Adorian Bandeira
 Ivan Ricardo Carvalho
 Murilo Vieira Loro
 Leonardo Cesar Pradebon
 Jose Antonio Gonzalez da Silva

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 $\geq$ 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).

Author(s)

Willyan Junior Adorian Bandeira
Ivan Ricardo Carvalho
Murilo Vieira Loro
Leonardo Cesar Pradebon
Jose Antonio Gonzalez da Silva

References

Tazzo, I. F., Tarouco, A. K., Allem Junior P. H. C., Bremm, C., Cardoso, L. S., & Junges, A. H. (2024). Índice de Temperatura e Umidade (ITU) ao longo do verão de 2021/2022 e estimativas dos impactos na bovinocultura de leite no Rio Grande do Sul, Brasil. *Ciencia Animal Brasileira*, 25, e-77035P.

lai	<i>Leaf Area Index (LAI)</i>
-----	------------------------------

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)

- Willyan Junior Adorian Bandeira
- Ivan Ricardo Carvalho
- Murilo Vieira Loro
- Leonardo Cesar Pradebon
- Jose Antonio Gonzalez da Silva

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 morfológicos 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	<i>Data Set for Leaf Area Index</i>
----------	-------------------------------------

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	<i>Data: Wheat Data Set with Protein and Grain Yield</i>
-----	--

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	<i>Estimates using polynomial equations.</i>
-----------	--

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)

Willyan Junior Adorian Bandeira

Ivan Ricardo Carvalho

Murilo Vieira Loro

Leonardo Cesar Pradebon

Jose Antonio Gonzalez da Silva

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	<i>Plotting the optimum and cardinal temperatures for crops</i>
--------	---

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 Attribute",
  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)

Willyan Junior Adorian Bandeira
 Ivan Ricardo Carvalho
 Murilo Vieira Loro
 Leonardo Cesar Pradebon
 Jose Antonio Gonzalez da Silva

Examples

```
library(EstimateBreed)

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

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

pheno	<i>Soybean Plastochron Estimation Data Set</i>
-------	--

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	<i>Soybean plastochron estimation</i>
-------	---------------------------------------

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)

Willyan Junior Adorian Bandeira
 Ivan Ricardo Carvalho
 Murilo Vieira Loro
 Leonardo Cesar Pradebon
 Jose Antonio Gonzalez da Silva

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 Agrícola 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	<i>Photothermal Index</i>
---------	---------------------------

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 fotothermal

Author(s)

Willyan Junior Adorian Bandeira
Ivan Ricardo Carvalho
Murilo Vieira Loro
Leonardo Cesar Pradebon
Jose Antonio Gonzalez da Silva

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	<i>Peeling Index and Industrial Yield</i>
----------	---

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)

Willyan Junior Adorian Bandeira
 Ivan Ricardo Carvalho
 Murilo Vieira Loro
 Leonardo Cesar Pradebon
 Jose Antonio Gonzalez da Silva

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	<i>Restriction of control variability</i>
-------	---

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)

Willyan Junior Adorian Bandeira
Ivan Ricardo Carvalho
Murilo Vieira Loro
Leonardo Cesar Pradebon
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	<i>Risk of Disease Occurrence in Soybeans</i>
------	---

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)

Willyan Junior Adorian Bandeira

Ivan Ricardo Carvalho

Murilo Vieira Loro

Leonardo Cesar Pradebon

Jose Antonio Gonzalez da Silva

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](https://doi.org/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)

Willyan Junior Adorian Bandeira
Ivan Ricardo Carvalho
Murilo Vieira Loro
Leonardo Cesar Pradebon
Jose Antonio Gonzalez da Silva

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	<i>Stress indices for genotype selection</i>
-------	--

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)

Willyan Junior Adorian Bandeira
 Ivan Ricardo Carvalho
 Murilo Vieira Loro
 Leonardo Cesar Pradebon
 Jose Antonio Gonzalez da Silva

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	<i>Effective Population Size</i>
-------	----------------------------------

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:

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

The alternative method is calculated as:

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

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)

Willyan Junior Adorian Bandeira
 Ivan Ricardo Carvalho
 Murilo Vieira Loro
 Leonardo Cesar Pradebon
 Jose Antonio Gonzalez da Silva

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)

Willyan Junior Adorian Bandeira
Ivan Ricardo Carvalho
Murilo Vieira Loro
Leonardo Cesar Pradebon
Jose Antonio Gonzalez da Silva

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 threshold. Also plot a representative graph of the selected genotypes based on the mean and standard deviations.

Author(s)

Willyan Junior Adorian Bandeira
 Ivan Ricardo Carvalho
 Murilo Vieira Loro
 Leonardo Cesar Pradebon
 Jose Antonio Gonzalez da Silva

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

* datasets

- aveia, [4](#)
- clima, [5](#)
- coefend, [6](#)
- desvamb, [8](#)
- genot, [11](#)
- genot2, [11](#)
- leafarea, [23](#)
- lin, [24](#)
- maize, [25](#)
- pheno, [27](#)
- ptn, [30](#)
- ptnrg, [30](#)
- termaldata, [40](#)
- trigo, [41](#)
- vig, [42](#)

atsum, [3](#)

aveia, [4](#)

clima, [5](#)

coefend, [6](#)

COI, [6](#)

default_seg, [7](#)

desv_clim, [9](#)

desvamb, [8](#)

didint, [10](#)

genot, [11](#)

genot2, [11](#)

genpar, [12](#)

het, [14](#)

hw, [15](#)

indviab, [16](#)

is_ptnrg, [19](#)

is_qindustrial, [20](#)

isgr, [17](#)

itu, [21](#)

lai, [22](#)

leafarea, [23](#)

lin, [24](#)

linearest, [24](#)

maize, [25](#)

optemp, [26](#)

pheno, [27](#)

plast, [27](#)

ptermal, [29](#)

ptn, [30](#)

ptnrg, [30](#)

rend_ind, [31](#)

restr, [32](#)

risk, [33](#)

SG, [34](#)

stind, [35](#)

tamef, [37](#)

tdelta, [38](#)

termaldata, [40](#)

transg, [40](#)

trigo, [41](#)

vig, [42](#)