Package 'EvaluateCore'

February 17, 2020

Title Quality Evaluation of Core Collections

Version 0.0.0.9000

Description Implements various quality evaluation statistics to assess the
value of plant germplasm core collections using qualitative and quantitative
phenotypic trait data <doi:10.1007/s00122-012-1971-y>.

License GPL-2 | GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

RdMacros Rdpack

SystemRequirements Java JRE 8 or higher

Depends R (>= 3.5.0)

Imports agricolae,
car,
cluster,
corehunter,
dplyr,
entropy,
ggcorrplot,
ggplot2,
grDevices,
kSamples,
psych,
reshape2,
rJava (>= 0.9-8),
Rdpack,
stats,
vegan

Suggests ccChooser

R topics documented:

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bar.evaluate.core   *Bar Plots*

Description

Plot Bar plots to graphically compare the frequency distributions of qualitative traits between entire collection (EC) and core set (CS).

Usage

```
bar.evaluate.core(data, names, qualitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
qualitative	Name of columns with the qualitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Value

A list with the ggplot objects of relative frequency bar plots of CS and EC for each trait specified as qualitative.

See Also

barplot, geom_bar

Examples

```
#####################################
# Use data from R package ccChooser
#####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

#####################################
# EvaluateCore
#####################################

bar.evaluate.core(data = ec, names = "genotypes",
                  qualitative = qual, selected = core)
```

---

box.evaluate.core   *Box Plots*

Description

Plot Box-and-Whisker plots (Tukey 1970; McGill et al. 1978) to graphically compare the probability distributions of quantitative traits between entire collection (EC) and core set (CS).

Usage

```
box.evaluate.core(data, names, quantitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Value

A list with the ggplot objects of box plots of CS and EC for each trait specified as quantitative.

References

McGill R, Tukey JW, Larsen WA (1978). "Variations of Box Plots." *The American Statistician*, **32**(1), 12.

Tukey JW (1970). *Exploratory Data Analysis. Preliminary edition*. Addison-Wesley.

See Also

boxplot, geom_boxplot

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################

box.evaluate.core(data = ec, names = "genotypes",
                  quantitative = quant, selected = core)
```

---

chisquare.evaluate.core

Chi-squared Test for Homogeneity

Description

Compare the distribution frequencies of qualitative traits between entire collection (EC) and core set (CS) by Chi-squared test for homogeneity (Pearson 1900; Snedecor and Irwin 1933).

Usage

```
chisquare.evaluate.core(data, names, qualitative, selected)
```

Arguments

`data`	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
`names`	Name of column with the individual names as a character string
`qualitative`	Name of columns with the qualitative traits as a character vector.
`selected`	Character vector with the names of individuals selected in core collection and present in the `names` column.

Value

A a data frame with the following columns.

`Trait`	The qualitative trait.
`EC_No.Classes`	The number of classes in the trait for EC.
`EC_Classes`	The frequency of the classes in the trait for EC.
`CS_No.Classes`	The number of classes in the trait for CS.
`CS_Classes`	The frequency of the classes in the trait for CS.
`chisq_statistic`	
	The χ^2 test statistic.
`chisq_pvalue`	The p value for the test statistic.
`chisq_significance`	
	The significance of the test statistic (*: $p \leq 0.01$; **: $p \leq 0.05$; ns: $p > 0.05$).

References

Pearson K (1900). "X. On the criterion that a given system of deviations from the probable in the case of a correlated system of variables is such that it can be reasonably supposed to have arisen from random sampling." *The London, Edinburgh, and Dublin Philosophical Magazine and Journal of Science*, **50**(302), 157–175.

Snedecor G, Irwin M (1933). "On the chi-square test for homogeneity." *Iowa State College Journal of Science*, **8**, 75–81.

See Also

chisq.test

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################

chisquare.evaluate.core(data = ec, names = "genotypes",
                        qualitative = qual, selected = core)
```

---

corr.evaluate.core   *Phenotypic Correlations*

Description

Compute phenotypic correlations (Pearson 1895) between traits, plot correlation matrices as correl-ograms (Friendly 2002) and calculate mantel correlation (Legendre and Legendre 2012) between them to compare entire collection (EC) and core set (CS).

Usage

```
corr.evaluate.core(data, names, quantitative, qualitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.

qualitative	Name of columns with the qualitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Value

A list with the following components.

Correlation Matrix

The matrix with phenotypic correlations between traits in EC (below diagonal) and CS (above diagonal).

Correologram   A correlogram of phenotypic correlations between traits in EC (below diagonal) and CS (above diagonal) as a ggplot object.

Mantel Correlation

A data frame with Mantel correlation coefficient (r) between EC and CS phenotypic correlation matrices, it's p value and significance (*: $p \leq 0.01$; **: $p \leq 0.05$; ns: $p > 0.05$).

References

Friendly M (2002). "Corrgrams." *The American Statistician*, **56**(4), 316–324.

Legendre P, Legendre L (2012). "Interpretation of ecological structures." In *Developments in Environmental Modelling*, volume 24, 521–624. Elsevier.

Pearson K (1895). "Note on regression and inheritance in the case of two parents." *Proceedings of the Royal Society of London*, **58**, 240–242.

See Also

cor, cor_pmat ggcorrplot, mantel

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")
```

```
####################################
# EvaluateCore
####################################

corr.evaluate.core(data = ec, names = "genotypes", quantitative = quant,
                    qualitative = qual, selected = core)
```

---

coverage.evaluate.core

Class Coverage

Description

Compute the Class Coverage (Kim et al. 2007) to compare the distribution frequencies of qualitative traits between entire collection (EC) and core set (CS).

Usage

```
coverage.evaluate.core(data, names, qualitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
qualitative	Name of columns with the qualitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Details

Class Coverage (Kim et al. 2007) is computed as follows.

$$Class\,Coverage = \left(\frac{1}{n} \sum_{i=1}^{n} \frac{A_{CS_i}}{A_{EC_i}} \right) \times 100$$

Where, A_{CS_i} is the sets of categories in the CS for the ith trait, A_{EC_i} is the sets of categories in the EC for the ith trait and n is the total number of traits.

Value

The Class Coverage value.

References

Kim K, Chung H, Cho G, Ma K, Chandrabalan D, Gwag J, Kim T, Cho E, Park Y (2007). "PowerCore: A program applying the advanced M strategy with a heuristic search for establishing core sets." *Bioinformatics*, **23**(16), 2155–2162.

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################

coverage.evaluate.core(data = ec, names = "genotypes",
                       qualitative = qual, selected = core)
```

---

cr.evaluate.core   *Coincidence Rate of Range*

Description

Compute the Coincidence Rate of Range (CR) (Diwan et al. 1995; Hu et al. 2000) to compare quantitative traits of the entire collection (EC) and core set (CS).

Usage

```
cr.evaluate.core(data, names, quantitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Details

The Coincidence Rate of Range (CR) is computed as follows.

$$CR = \left(\frac{1}{n} \sum_{i=1}^{n} \frac{R_{CS_i}}{R_{EC_i}} \right) \times 100$$

Where, R_{CS_i} is the range of the ith trait in the CS, R_{EC_i} is the range of the ith trait in the EC and n is the total number of traits.

Value

The CR value.

References

Diwan N, McIntosh MS, Bauchan GR (1995). "Methods of developing a core collection of annual Medicago species." *Theoretical and Applied Genetics*, **90**(6), 755–761.

Hu J, Zhu J, Xu HM (2000). "Methods of constructing core collections by stepwise clustering with three sampling strategies based on the genotypic values of crops." *Theoretical and Applied Genetics*, **101**(1), 264–268.

See Also

wilcox.test

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################
```

```
cr.evaluate.core(data = ec, names = "genotypes",
                 quantitative = quant, selected = core)
```

---

dist.evaluate.core   *Distance Measures*

Description

Compute average Entry-to-nearest-entry distance (E-EN), Accession-to-nearest-entry distance (A-EN) and Entry-to-entry distance (E-E) (Odong et al. 2013) to evaluate a core set (CS) selected from an entire collection (EC).

Usage

```
dist.evaluate.core(data, names, quantitative, qualitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.
qualitative	Name of columns with the qualitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Details

This function is a wrapper around the [evaluateCore](#) function of the [corehunter](#) package.

Value

A data frame with the average values of E-EN, A-EN and E-E.

References

Odong TL, Jansen J, van Eeuwijk FA, van Hintum TJL (2013). "Quality of core collections for effective utilisation of genetic resources review, discussion and interpretation." *Theoretical and Applied Genetics*, **126**(2), 289–305.

See Also

[evaluateCore](#)

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################

dist.evaluate.core(data = ec, names = "genotypes", quantitative = quant,
                   qualitative = qual, selected = core)
```

---

iqr.evaluate.core   *Interquartile Range*

Description

Compute the Interquartile Range (IQR) (Upton and Cook 1996) to compare quantitative traits of the entire collection (EC) and core set (CS).

Usage

```
iqr.evaluate.core(data, names, quantitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Value

A data frame with the IQR values of the EC and CS for the traits specified as `quantitative`.

References

Upton G, Cook I (1996). "General summary statistics." In *Understanding statistics*. Oxford University Press.

See Also

IQR

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################

iqr.evaluate.core(data = ec, names = "genotypes",
                  quantitative = quant, selected = core)
```

`levene.evaluate.core`   *Levene's Test*

Description

Test for of variances of the entire collection (EC) and core set (CS) for quantitative traits by Levene's test (Levene 1960).

Usage

```
levene.evaluate.core(data, names, quantitative, selected)
```

Arguments

`data`	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
`names`	Name of column with the individual names as a character string
`quantitative`	Name of columns with the quantitative traits as a character vector.
`selected`	Character vector with the names of individuals selected in core collection and present in the `names` column.

Value

A data frame with the following columns

`Trait`	The quantitative trait.
`EC_V`	The variance of the EC.
`CS_V`	The variance of the CS.
`EC_CV`	The coefficient of variance of the EC.
`CS_CV`	The coefficient of variance of the CS.
`Levene_Fvalue`	The test statistic.
`Levene_pvalue`	The p value for the test statistic.
`Levene_significance`	
	The significance of the test statistic (*: $p \leq 0.01$; **: $p \leq 0.05$; ns: $p > 0.05$).

References

Levene H (1960). "Robust tests for equality of variances." In Olkin I, Ghurye SG, Hoeffding W, Madow WG, Mann HB (eds.), *Contribution to Probability and Statistics: Essays in Honor of Harold Hotelling*, 278–292. Stanford University Press, Palo Alto, CA.

See Also

leveneTest

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
```

```
                                         function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))

head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")


####################################
# EvaluateCore
####################################

levene.evaluate.core(data = ec, names = "genotypes",
                     quantitative = quant, selected = core)
```

---

pca.evaluate.core   *Principal Component Analysis*

Description

Compute Principal Component Analysis Statistics (Mardia et al. 1979) to compare the probability distributions of quantitative traits between entire collection (EC) and core set (CS).

Usage

```
pca.evaluate.core(
  data,
  names,
  quantitative,
  selected,
  center = TRUE,
  scale = TRUE,
  npc.plot = 6
)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.
center	either a logical value or numeric-alike vector of length equal to the number of columns of x, where 'numeric-alike' means that as.numeric(.) will be applied successfully if is.numeric(.) is not true.

scale   either a logical value or a numeric-alike vector of length equal to the number of
                       columns of x.

npc.plot   The number of principal components for which eigen values are to be plotted.
                       The default value is 6.

Value

A list with the following components.

EC PC Importance
                       A data frame of importance of principal components for EC

EC PC Loadings   A data frame with eigen vectors of principal components for EC

CS PC Importance
                       A data frame of importance of principal components for CS

CS PC Loadings   A data frame with eigen vectors of principal components for CS

Scree Plot   The scree plot of principal components for EC and CS as a ggplot object.

PC Loadings Plot
                       A plot of the eigen vector values of principal components for EC and CS as
                       specified by npc.plot as a ggplot2 object.

References

Mardia KV, Kent JT, Bibby JM (1979). *Multivariate analysis*. Academic Press, London; New York.
ISBN 0-12-471250-9 978-0-12-471250-8 0-12-471252-5 978-0-12-471252-2.

See Also

[prcomp](#)

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
```

```
# EvaluateCore
####################################

pca.evaluate.core(data = ec, names = "genotypes",
                  quantitative = quant, selected = core,
                  center = TRUE, scale = TRUE, npc.plot = 4)
```

---

pdfdist.evaluate.core   *Distance Between Probability Distributions*

Description

Compute Kullback-Leibler (Kullback and Leibler 1951), Kolmogorov-Smirnov (Kolmogorov 1933; Smirnov 1948) and Anderson-Darling distances (Anderson and Darling 1952) between the probability distributions of collection (EC) and core set (CS) for quantitative traits.

Usage

```
pdfdist.evaluate.core(data, names, quantitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Value

A data frame with the following columns.

Trait	The quantitative trait.
KL_Distance	The Kullback-Leibler distance (Kullback and Leibler 1951) between EC and CS.
KS_Distance	The Kolmogorov-Smirnov distance (Kolmogorov 1933; Smirnov 1948) between EC and CS.
KS_pvalue	The p value of the Kolmogorov-Smirnov distance.
AD_Distance	Anderson-Darling distance (Anderson and Darling 1952) between EC and CS.
AD_pvalue	The p value of the Anderson-Darling distance.
KS_significance	
	The significance of the Kolmogorov-Smirnov distance (*: $p \leq 0.01$; **: $p \leq 0.05$; ns: $p > 0.05$).
AD_pvalue	The significance of the Anderson-Darling distance (*: $p \leq 0.01$; **: $p \leq 0.05$; ns: $p > 0.05$).

See Also

KL.plugin, ks.test, ad.test

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################

pdfdist.evaluate.core(data = ec, names = "genotypes",
                      quantitative = quant, selected = core)
```

---

percentdiff.evaluate.core

Percentage Difference of Means and Variances

Description

Compute the following differences between the entire collection (EC) and core set (CS).

- Percentage of significant differences of mean ($MD\%_{Hu}$) (Hu et al. 2000)

- Percentage of significant differences of variance ($VD\%_{Hu}$) (Hu et al. 2000)

- Average of absolute differences between means ($MD\%_{Kim}$) (Kim et al. 2007)

- Average of absolute differences between variances ($VD\%_{Kim}$) (Kim et al. 2007)

- Percentage difference between the mean squared Euclidean distance among accessions ($\bar{d}D\%$) (Studnicki et al. 2013)

Usage

```
percentdiff.evaluate.core(data, names, quantitative, selected, alpha = 0.05)
```

Arguments

`data`	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
`names`	Name of column with the individual names as a character string
`quantitative`	Name of columns with the quantitative traits as a character vector.
`selected`	Character vector with the names of individuals selected in core collection and present in the `names` column.
`alpha`	Type I error probability (Significance level) of difference.

Details

The differences are computed as follows.

$$MD\%_{Hu} = \left(\frac{S_t}{n}\right) \times 100$$

Where, S_t is the number of traits with a significant difference between the means of the EC and the CS and n is the total number of traits.

$$VD\%_{Hu} = \left(\frac{S_t}{n}\right) \times 100$$

Where, S_t is the number of traits with a significant difference between the variances of the EC and the CS and n is the total number of traits.

$$MD\%_{Kim} = \frac{1}{n}\sum_{i=1}^{n}\frac{|M_{EC_i} - M_{CS_i}|}{M_{CS_i}}$$

Where, M_{EC_i} is the mean of the EC for the ith trait, M_{CS_i} is the mean of the CS for the ith trait and n is the total number of traits.

$$VD\%_{Kim} = \frac{1}{n}\sum_{i=1}^{n}\frac{|V_{EC_i} - V_{CS_i}|}{V_{CS_i}}$$

Where, V_{EC_i} is the variance of the EC for the ith trait, V_{CS_i} is the variance of the CS for the ith trait and n is the total number of traits.

$$\overline{d}D\% = \frac{\overline{d}_{CS} - \overline{d}_{EC}}{\overline{d}_{EC}} \times 100$$

Where, $\overline{d}_{CS}$ is the mean squared Euclidean distance among accessions in the CS and $\overline{d}_{EC}$ is the mean squared Euclidean distance among accessions in the EC.

Value

A data frame with the values of $MD\%_{Hu}$, $VD\%_{Hu}$, $MD\%_{Kim}$, $VD\%_{Kim}$ and $\overline{d}D\%$.

References

Hu J, Zhu J, Xu HM (2000). "Methods of constructing core collections by stepwise clustering with three sampling strategies based on the genotypic values of crops." *Theoretical and Applied Genetics*, **101**(1), 264–268.

Kim K, Chung H, Cho G, Ma K, Chandrabalan D, Gwag J, Kim T, Cho E, Park Y (2007). "PowerCore: A program applying the advanced M strategy with a heuristic search for establishing core sets." *Bioinformatics*, **23**(16), 2155–2162.

Studnicki M, Madry W, Schmidt J (2013). "Comparing the Efficiency of Sampling Strategies to Establish a Representative in the Phenotypic-based Genetic Diversity Core Collection of Orchardgrass (*Dactylis glomerata* L.)." *Czech Journal of Genetics and Plant Breeding*, **49**(1), 36–47.

See Also

snk.evaluate.core, snk.evaluate.core

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################

percentdiff.evaluate.core(data = ec, names = "genotypes",
                          quantitative = quant, selected = core)
```

---

qq.evaluate.core   *Quantile-Quantile Plots*

Description

Plot Quantile-Quantile (QQ) plots (Wilk and Gnanadesikan 1968) to graphically compare the probability distributions of quantitative traits between entire collection (EC) and core set (CS).

Usage

```
qq.evaluate.core(data, names, quantitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Value

A list with the ggplot objects of QQ plots of CS vs EC for each trait specified as quantitative.

References

Wilk MB, Gnanadesikan R (1968). "Probability plotting methods for the analysis for the analysis of data." *Biometrika*, **55**(1), 1–17.

See Also

[qqplot](#)

Examples

```
#####################################
# Use data from R package ccChooser
#####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")
```

```
####################################
# EvaluateCore
####################################

qq.evaluate.core(data = ec, names = "genotypes",
                 quantitative = quant, selected = core)
```

shannon.evaluate.core   *Shannon-Weaver Diversity Index*

Description

Compute the Shannon-Weaver Diversity Index (H'), Maximum diversity (H'_{max}) and Shannon Equitability Index (E_H) (Shannon and Weaver 1949) to compare the phenotypic diversity for qualitative traits between entire collection (EC) and core set (CS).

Usage

```
shannon.evaluate.core(data, names, qualitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
qualitative	Name of columns with the qualitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Details

Shannon-Weaver Diversity Index (H') is computed as follows.

$$H' = -\sum_{i=1}^{k} p_i log(p_i)$$

Where p_i denotes the proportion in the group k.

The maximum value of the index (H'_{max}) is $\ln(k)$. This value occurs when each group has the same frequency.

The Shannon equitability index (E_H) is the Shannon diversity index divided by the maximum diversity.

$$E_H = \frac{H}{\ln(k)}$$

Value

A data frame with the following columns.

Trait	The qualitative trait.
EC_H	The Shannon-Weaver Diversity Index (H') for EC.
EC_H	The Shannon-Weaver Diversity Index (H') for CS.
EC_Hmax	The Maximum diversity value (H'_{max}) for EC.
CS_Hmax	The Maximum diversity value (H'_{max}) for CS.
EC_EH	The Shannon Equitability Index (E_H) for EC.
CS_EH	The Shannon Equitability Index (E_H) for CS.

References

Shannon C, Weaver W (1949). *The Mathematical Theory of Communication*, number v. 2 in The Mathematical Theory of Communication. University of Illinois Press.

See Also

[shannon](#)

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################

shannon.evaluate.core(data = ec, names = "genotypes",
                      qualitative = qual, selected = core)
```

---

signtest.evaluate.core

Sign Test

Description

Test difference between means and variances of entire collection (EC) and core set (CS) for quantitative traits by Sign test (+ versus −) (Basigalup et al. 1995; Tai and Miller 2001).

Usage

```
signtest.evaluate.core(data, names, quantitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Details

The test statistic for Sign test (χ^2) is computed as follows.

$$\chi^2 = \frac{(N_1 - N_2)^2}{N_1 + N_2}$$

Where, where N_1 is the number of variables for which the mean or variance of the CS is greater than the mean or variance of the EC (number of + signs); N_2 is the number of variables for which the mean or variance of the CS is less than the mean or variance of the EC (number of − signs). The value of χ^2 is compared with a Chi-square distribution with 1 degree of freedom.

Value

A data frame with the following components.

Comparison	The comparison measure.
ChiSq	The test statistic (χ^2).
p.value	The p value for the test statistic.
significance	The significance of the test statistic (*: $p \leq 0.01$; **: $p \leq 0.05$; ns: $p > 0.05$).

References

Basigalup DH, Barnes DK, Stucker RE (1995). "Development of a Core Collection for Perennial Medicago Plant Introductions." *Crop Science*, **35**(4), 1163–1168.

Tai PYP, Miller JD (2001). "A Core Collection for *Saccharum spontaneum* L. from the World Collection of Sugarcane." *Crop Science*, **41**(3), 879–885.

Examples

```
#####################################
# Use data from R package ccChooser
#####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

#####################################
# EvaluateCore
#####################################

signtest.evaluate.core(data = ec, names = "genotypes",
                       quantitative = quant, selected = core)
```

---

snk.evaluate.core	*Student-Newman-Keuls Test*

Description

Test difference between means of entire collection (EC) and core set (CS) for quantitative traits by Newman-Keuls or Student-Newman-Keuls test (Newman 1939; Keuls 1952).

Usage

```
snk.evaluate.core(data, names, quantitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Value

A data frame with the following components.

`Trait`	The quantitative trait.
`EC_Min`	The minimum value of the trait in EC.
`EC_Max`	The maximum value of the trait in EC.
`EC_Mean`	The mean value of the trait in EC.
`EC_SE`	The standard error of the trait in EC.
`CS_Min`	The minimum value of the trait in CS.
`CS_Max`	The maximum value of the trait in CS.
`CS_Mean`	The mean value of the trait in CS.
`CS_SE`	The standard error of the trait in CS.
`SNK_pvalue`	The p value of the Student-Newman-Keuls test for equality of means of EC and CS.
`SNK_significance`	
	The significance of the Student-Newman-Keuls test for equality of means of EC and CS.

References

Keuls M (1952). "The use of the „studentized range" in connection with an analysis of variance." *Euphytica*, **1**(2), 112–122.

Newman D (1939). "The distribution of range in samples from a normal population, expressed in terms of an independent estimate of standard deviation." *Biometrika*, **31**(1-2), 20–30.

See Also

SNK.test

Examples

```
#####################################
# Use data from R package ccChooser
#####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
```

```
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################

snk.evaluate.core(data = ec, names = "genotypes",
                  quantitative = quant, selected = core)
```

---

ttest.evaluate.core   *Student's t Test*

Description

Test difference between means of entire collection (EC) and core set (CS) for quantitative traits by Student's t test (Student 1908).

Usage

```
ttest.evaluate.core(data, names, quantitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Value

Trait	The quantitative trait.
EC_Min	The minimum value of the trait in EC.
EC_Max	The maximum value of the trait in EC.
EC_Mean	The mean value of the trait in EC.
EC_SE	The standard error of the trait in EC.
CS_Min	The minimum value of the trait in CS.
CS_Max	The maximum value of the trait in CS.
CS_Mean	The mean value of the trait in CS.
CS_SE	The standard error of the trait in CS.
ttest_pvalue	The p value of the Student's t test for equality of means of EC and CS.
ttest_significance	
	The significance of the Student's t test for equality of means of EC and CS.

References

Student (1908). "The probable error of a mean." *Biometrika*, **6**(1), 1–25.

See Also

t.test

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################

ttest.evaluate.core(data = ec, names = "genotypes",
                    quantitative = quant, selected = core)
```

---

vr.evaluate.core   *Variable Rate of Coefficient of Variation*

Description

Compute the Variable Rate of Coefficient of Variation (VR) (Hu et al. 2000) to compare quantitative traits of the entire collection (EC) and core set (CS).

Usage

```
vr.evaluate.core(data, names, quantitative, selected)
```

Arguments

`data`	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
`names`	Name of column with the individual names as a character string
`quantitative`	Name of columns with the quantitative traits as a character vector.
`selected`	Character vector with the names of individuals selected in core collection and present in the `names` column.

Details

The Variable Rate of Coefficient of Variation (VR) is computed as follows.

$$VR = \left(\frac{1}{n} \sum_{i=1}^{n} \frac{CV_{CS_i}}{CV_{EC_i}} \right) \times 100$$

Where, CV_{CS_i} is the coefficients of variation for the ith trait in the CS, CV_{EC_i} is the coefficients of variation for the ith trait in the EC and n is the total number of traits

Value

The VR value.

References

Hu J, Zhu J, Xu HM (2000). "Methods of constructing core collections by stepwise clustering with three sampling strategies based on the genotypic values of crops." *Theoretical and Applied Genetics*, **101**(1), 264–268.

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")
```

```
####################################
# EvaluateCore
####################################

vr.evaluate.core(data = ec, names = "genotypes",
                 quantitative = quant, selected = core)
```

---

wilcox.evaluate.core   *Wilcoxon Rank Sum Test*

Description

Compare the medians of quantitative traits between entire collection (EC) and core set (CS) by
Wilcoxon rank sum test or Mann-Whitney-Wilcoxon test or Mann-Whitney U test (Wilcoxon 1945;
Mann and Whitney 1947).

Usage

```
wilcox.evaluate.core(data, names, quantitative, selected)
```

Arguments

data	The data as a data frame object. The data frame should possess one row per individual and columns with the individual names and multiple trait/character data.
names	Name of column with the individual names as a character string
quantitative	Name of columns with the quantitative traits as a character vector.
selected	Character vector with the names of individuals selected in core collection and present in the names column.

Value

Trait	The quantitative trait.
EC_Med	The median value of the trait in EC.
CS_Med	The median value of the trait in CS.
Wilcox_pvalue	The p value of the Wilcoxon test for equality of medians of EC and CS.
Wilcox_significance	
	The significance of the Wilcoxon test for equality of medians of EC and CS.

References

Mann HB, Whitney DR (1947). "On a Test of Whether one of Two Random Variables is Stochastically Larger than the Other." *The Annals of Mathematical Statistics*, **18**(1), 50–60.

Wilcoxon F (1945). "Individual Comparisons by Ranking Methods." *Biometrics Bulletin*, **1**(6),
80.

See Also

wilcox.test

Examples

```
####################################
# Use data from R package ccChooser
####################################

library(ccChooser)
data("dactylis_CC")
data("dactylis_EC")

ec <- cbind(genotypes = rownames(dactylis_EC), dactylis_EC[, -1])
ec$genotypes <- as.character(ec$genotypes)
rownames(ec) <- NULL
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) cut(x, breaks = 4))
ec[, c("X1", "X6", "X7")] <- lapply(ec[, c("X1", "X6", "X7")],
                                    function(x) factor(as.numeric(x)))
head(ec)

core <- rownames(dactylis_CC)

quant <- c("X2", "X3", "X4", "X5", "X8")
qual <- c("X1", "X6", "X7")

####################################
# EvaluateCore
####################################

wilcox.evaluate.core(data = ec, names = "genotypes",
                     quantitative = quant, selected = core)
```

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