Package ‘RFLPtools’

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Author Fabienne Flessa, Alexandra Kehl, Mohammed Aslam Imtiaz, Matthias Kohl
Maintainer Matthias Kohl <Matthias.Kohl@stamats.de>
Description RFLPtools provides functions to analyse DNA fragment samples
(i.e. derived from RFLP-analysis) and standalone BLAST report files
(i.e. DNA sequence analysis).
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RFLPtools-package  Tools to analyse RFLP-data

Description

RFLPtools provides functions to analyse DNA fragment samples (i.e. derived from RFLP-analysis) and standalone BLAST report files (i.e. DNA sequence analysis).

Details

Package: RFLPtools
Version: 1.6
Date: 2014-08-13
Depends: R(>= 3.0.0), stats, utils, graphics, grDevices, RColorBrewer
Suggests: lattice, MKmisc(>= 0.8)
License: LGPL-3

Author(s)

Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>,
Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>,
Mohammed Aslam Intiaz,
Matthias Kohl <Matthias.Kohl@stamats.de>

Maintainer: Matthias Kohl <Matthias.Kohl@stamats.de>

References


Matsumoto, Masaru; Furuya, Naruto; Takanami, Yoichi; Matsuyama, Nobuaki. RFLP analysis of the PCR-amplified 28S rDNA in Rhizoctonia solani. Mycoscience 1996 37:351-356.


Poussier, Stephane; Trigalet-Demery, Danielle; Vandewalle, Peggy; Goffinet, Bruno; Luisetti, Jacques; Trigalet, Andre. Genetic diversity of Ralstonia solanacearum as assessed by PCR-RFLP of the hrp gene region, AFLP and 16S rRNA sequence analysis, and identification of an African subdivision. Microbiology 2000 146:1679-1692.


Examples

data(RFLPdata)
res <- RFLPdist(RFLPdata)
plot(hclust(res[[1]]), main = "Euclidean distance")
par(mfrow = c(1,2))
plot(hclust(RFLPdist(RFLPdata, nrBands = 3)), cex = 0.7)
RFLPplot(RFLPdata, nrBands = 3, mar.bottom = 6, cex.axis = 0.8)
data(RFLPref)
RFLPrefplot(RFLPdata, RFLPref, nrBands = 6, cex.axis = 0.8)

library(mkmisc)
data(BLASTdata)
res <- simMatrix(BLASTdata, sequence.range = TRUE, Min = 500)
myCol <- colorRampPalette(brewer.pal(8, "RdYlGn"))(128)
simPlot(res, col = myCol, minVal = 0,
labels = colnames(res), title = "(Dis-)Similarity Plot")

Example data set for BLAST data

This is an example data set for BLAST data generated with standalone BLAST from NCBI.

Usage

data(RFLPdata)
Format

A data frame with 737 observations on the following four variables

query.id character: sequence identifier.
subject.id character: subject identifier.
identity numeric: identity between sequences (in percent).
alignment.length integer: number of nucleotides.
mismatches integer: number of mismatches.
gap.opens integer: number of gaps.
q.start integer: query sequence start.
q.end integer: query sequence end.
s.start integer: subject sequence start.
s.end integer: subject sequence end.
evalue numeric: evalue.
bit.score numeric: score value.

Details

The data was generated with standalone BLAST from NCBI. Pairwise similarities of DNA sequences are calculated among all sequences to analyse applying Standalone Blast with the parameters -m 8 -r 2 -G 5 -E 2.

Alternatively data can be generated with "local BLAST" implemented in BioEdit v7.0.9 using the additional parameters -m 8 -r 2 -G 5 -E 2 and by selecting "open output" and "tabular output".

Source

The data set was generated by F. Flessa.

References

BioEdit v7.0.9: Tom Hall, Ibis Biosciences; http://www.mbio.ncsu.edu/BioEdit/bioedit.html

Examples

data(BLASTdata)
str(BLASTdata)
Description

This function computes and returns the distance matrix computed by using the specified distance measure to compute the distances between the rows of a data matrix. Instead of the row values as in the case of `dist`, the successive differences of the row values are used.

Usage

diffDist(x, method = "euclidean", diag = FALSE, upper = FALSE, p = 2)

Arguments

x a numeric matrix, data frame or "dist" object.
method the distance measure to be used. This must be one of "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski". Any unambiguous substring can be given.
diag logical value indicating whether the diagonal of the distance matrix should be printed by print.dist.
upper logical value indicating whether the upper triangle of the distance matrix should be printed by print.dist.
p The power of the Minkowski distance.

Details

This function computes and returns the distance matrix computed by using the specified distance measure to compute the distances between the rows of a data matrix. Instead of the row values as in the case of `dist`, the successive differences of the row values are used.

It's a simple wrapper function around `dist`. For more details about the distances we refer to `dist`.

The function may be helpful, if there is a shift w.r.t. the measured bands; e.g. c(550, 500, 300, 250) vs. c(510, 460, 260, 210).

Value

diffDist returns an object of class "dist"; cf. `dist`.

Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

References

Examples

```r
## assume a shift in the measured bands
M <- rbind(c(550, 500, 300, 250), c(510, 460, 260, 210),
           c(550, 500, 300, 200))
dist(M)
diffDist(M)
```

FragMatch

*Compute matches for RFLP data via FragMatch.*

Description

Compute matches for RFLP data using FragMatch - a program for the analysis of DNA fragment data.

Usage

```r
FragMatch(newData, refData, maxvalue = 1000, errorBound = 25,
          weight = 1, na.rm = TRUE)
```

Arguments

- `newData` data.frame with new RFLP data; see `newDataGerm`.
- `refData` data.frame with reference RFLP data; see `refDataGerm`.
- `maxValue` numeric: maximum value for which the error bound is applied. Can be a vector of length larger than 1.
- `errorBound` numeric: error bound corresponding to `maxValue`. Can be a vector of length larger than 1.
- `weight` numeric: weight for weighting partial matches; see details section.
- `na.rm` logical: indicating whether NA values should be stripped before the computation proceeds.

Details

A rather simple algorithm which consists of counting the number of matches where it is considered a match if the value is inside a range of +/- `errorBound`.

If there is more than one enzyme, one can use weights to give the partial perfect matches for a certain enzyme a higher (or also smaller) weight.

Value

A character matrix with entries of the form "a_b" which means that there were a out of b possible matches.
germ

Author(s)

Mohammed Aslam Imtiaz, Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

newDataGerm, refDataGerm

Examples

data(refDataGerm)
data(newDataGerm)

res <- FragMatch(newDataGerm, refDataGerm)

germ

Compute matches for RFLP data via GERM.

Description

Compute matches for RFLP data using the Good-Enough RFLP Matcher (GERM) program.

Usage

germ(newData, refData, parameters = list("Max forward error" = 25,
                        "Max backward error" = 25,
                        "Max sum error" = 100,
                        "Lower measurement limit" = 100),
               method = "joint", na.rm = TRUE)

Arguments

newData data.frame with new RFLP data; see newDataGerm.
refData data.frame with reference RFLP data; see refDataGerm.
parameters list of the four program parameters of GERM; see details section.
method matching and ranking method used for computation; see details section.
na.rm logical: indicating whether NA values should be stripped before the computation proceeds.
Details

There are four matching and ranking methods which are "joint", "forward", "backward", and "sum". For more details see Dickie et al. (2003).

The parameters of the GERM software are: "Max forward error": Used if "matching and ranking method" is set to "forward" or "joint". "Max backward error": Used if "matching and ranking method" is set to "backward" or "joint". "Max sum error": Used for matching if "matching and ranking method" is set to "sum". "Lower measurement limit": The lower bound of measurements (often 100 or 50, depending on ladder used).

Value

A named list with the results.

Author(s)

Mohammed Aslam Imtiaz, Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

newdatagerm, refdatagerm

Examples

data(refdatagerm)
data(newdatagerm)

## Example 1
res1 <- germ(newdatagerm[1:7,], refdatagerm)

## Example 2
res2 <- germ(newdatagerm[8:15,], refdatagerm)

## Example 3
res3 <- germ(newdatagerm[16:20,], refdatagerm)

## all three examples in one step
res.all <- germ(newdatagerm, refdatagerm)
linCombDist  

**Linear Combination of Distances**

### Description

This function computes linear combinations of distances.

### Usage

```r
linCombDist(x, distfun1, w1, distfun2, w2, diag = FALSE, upper = FALSE)
```

### Arguments

- **x**: object which is passed to `distfun1` and `distfun2`.
- **distfun1**: function used to compute an object of class "dist".
- **w1**: weight for result of `distfun1`.
- **distfun2**: function used to compute an object of class "dist".
- **w2**: weight for result of `distfun2`.
- **diag**: see `dist`.
- **upper**: see `dist`.

### Details

This function computes and returns the distance matrix computed by a linear combination of two distance matrices.

### Value

`linCombDist` returns an object of class "dist"; cf. `dist`.

### Author(s)

Matthias Kohl <Matthias.Kohl@stamats.de>

### References

Examples

```r
## assume a shift in the measured bands
M <- rbind(c(550, 500, 300, 250),
           c(510, 460, 260, 210),
           c(700, 650, 450, 400),
           c(550, 490, 310, 250))
dist(M)
diffDist(M)

## convex combination of dist and diffDist
linCombDist(M, distfun1 = dist, w1 = 0.5, distfun2 = diffDist, w2 = 0.5)

## linear combination
linCombDist(M, distfun1 = dist, w1 = 2, distfun2 = diffDist, w2 = 5)

## maximum distance
linCombDist(M, distfun1 = function(x) dist(x, method = "maximum"), w1 = 0.5,
            distfun2 = function(x) diffDist(x, method = "maximum"), w2 = 0.5)
```

data(rflpdata)
distfun <- function(x) linCombDist(x, distfun1 = dist, w1 = 0.1, distfun2 = diffDist, w2 = 0.9)
par(mfrow = c(2, 2))
plot(hclust(RFLPdist(rflpdata, nbands = 3, distfun = distfun)), cex = 0.7, cex.lab = 0.7)
RFLPplot(RFLPdata, nbands = 3, distfun = distfun, mar.bottom = 6, cex.axis = 0.8)
plot(hclust(RFLPdist(rflpdata, nbands = 3)), cex = 0.7, cex.lab = 0.7)
RFLPplot(RFLPdata, nbands = 3, mar.bottom = 6, cex.axis = 0.8)
```

---

**newDataGerm**

*Example data set from GERM software*

---

### Description

This is the reference data taken from the GERM software.

### Usage

```r
data(newDataGerm)
```

### Format

A data frame with 20 observations on the following six variables:

- **Sample** character: sample identifier.
- **Enzyme** character: enzyme used.
- **Band** integer: band number.
- **MW** integer: molecular weight.
- **Genus** character: genus of sample.
- **Species** character: species of sample.
nrBands

Details
See GERM software.

Source
The data set was taken from the GERM software (table ‘Example Unknowns’).

References

Examples
data(newdatagerm)
str(newdatagerm)

nrBands
Function to compute number of bands.

Description
Computes groups based on the number of bands per sample in a RFLP data set. Each group comprises RFLP-samples with equal number of bands.

Usage
nrBands(x)

Arguments
x data.frame with RFLP data; see RFLPdata.

Details
The function computes groups based on the number of bands per sample in a RFLP data set. Each group comprises RFLP-samples with equal number of bands.

Value
Number of bands per RFLP-samples.

Author(s)
Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>,
Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>,
Matthias Kohl <Matthias.Kohl@stamats.de>
read.blast

References


See Also

RFLPdata, RFLPdist2, dist

Examples

data(RFLPdata)
nrBands(RFLPdata)

Description

Function to read BLAST data generated with standalone BLAST from NCBI.

Usage

read.blast(file, sep = "\t")

Arguments

file character: BLAST file to read in.
sep the field separator character. Values on each line of the file are separated by this character. Default "\t".

Details

The function reads data which was generated with standalone BLAST from NCBI; see ftp://ftp.ncbi.nih.gov/blast/executables/release/.

Possible steps:
1) Install NCBI BLAST
2) Generate and import database(s)
3) Apply BLAST with options outfmt and out; e.g.
   blastn -query Testquery -db Testdatabase -outfmt 6 -out out.txt
   or
   blastn -query Testquery -db Testdatabase -outfmt 10 -out out.csv
   One can also call BLAST from inside R by using function system
   system("blastn -query Testquery -db Testdatabase -outfmt 6 -out out.txt")
4) Read in the results
   test.res <- read.blast(file = "out.txt")
   or
   test.res <- read.blast(file = "out.csv", sep = ",")
Value

A data.frame with variables

query.id character: sequence identifier.
subject.id character: subject identifier.
identity numeric: identity between sequences (in percent).
alignment.length integer: number of nucleotides.
mismatches integer: number of mismatches.
gap.opens integer: number of gaps.
q.start integer: query sequence start.
q.end integer: query sequence end.
s.start integer: subject sequence start.
s.end integer: subject sequence end.
evalue numeric: evalue.
b.bit.score numeric: score value.

Author(s)

Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>,
Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>,
Matthias Kohl <Matthias.Kohl@stamats.de>

References

Flessa, F., Kehl, A., Kohl, M. Analysing diversity and community structures using PCR-RFLP: a

See Also

BLASTdata, simMatrix

Examples

Dir <- system.file("extdata", package = "RFLPtools")  # input directory
filename <- file.path(Dir, "BLASTexample.txt")
BLAST1 <- read.blast(file = filename)
str(BLAST1)
Description
Function to read RFLP data (e.g. generated with software package Gene Profiler 4.05 (Scanalytics Inc.)) for DNA fragment analysis and genotyping, and exported to a text file.

Usage
read.rflp(file)

Arguments
file character: RFLP file to read in.

Details
The function reads data from a text file which was generated e.g. with the software package Gene Profiler 4.05 (Scanalytics Inc.) for DNA fragment analysis and genotyping. The data file contains sample identifier (Sample), band number (Band), molecular weight (MW) and gel identifier (Gel) (see RFLPdata).

If gel identifier Gel is missing it is extracted from the sample identifier Sample.

Value
A data.frame with variables
Sample character: sample identifier.
Band integer: band number.
MW integer: molecular weight.
Gel character: gel identifier.

Author(s)
Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>,
Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>,
Matthias Kohl <Matthias.Kohl@stamats.de>

References

See Also
RFLPdata,RFLPdist
refDataGerm

Examples

```r
Dir <- system.file("extdata", package = "RFLPtools") # input directory
filename <- file.path(Dir, "RFLPexample.txt")
RFLP1 <- read.rflp(file = filename)
str(RFLP1)

filename <- file.path(Dir, "AZ091016_report.txt")
RFLP2 <- read.rflp(file = filename)
str(RFLP2)
```

---

**Description**

This is the reference data taken from the GERM software.

**Usage**

```r
data(refDataGerm)
```

**Format**

A data frame with 250 observations on the following six variables

- **Sample** character: sample identifier.
- **Enzyme** character: enzyme used.
- **Band** integer: band number.
- **MW** integer: molecular weight.
- **Genus** character: genus of sample.
- **Species** character: species of sample.

**Details**

See GERM software.

**Source**

The data set was taken from the GERM software (table 'Example Data').

**References**


**Examples**

```r
data(refDataGerm)
str(refDataGerm)
```
RFLPcombine  Combine RFLP data sets

Description
Function to combine an arbitrary number of RFLP data sets.

Usage
RFLPcombine(...) 

Arguments
... two or more data.frames with RFLP data.

Details
The data sets are combined using \texttt{rbind}.
If data sets with identical sample identifiers are given, the identifiers are made unique using \texttt{make.unique}.

Value
A \texttt{data.frame} with variables 
Sample character: sample identifier.
Band integer: band number.
MW integer: molecular weight.
Gel character: gel identifier.

Author(s)
Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>,
Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>,
Matthias Kohl <Matthias.Kohl@stamats.de>

References

See Also
RFLPdata

Examples
data(RFLPdata)
res <- RFLPcombine(RFLPdata, RFLPdata, RFLPdata)
RFLPplot(res, nrBands = 4)
Example data set for RFLP data

Description

This is an example data set for RFLP data.

Usage

data(RFLPdata)

Format

A data frame with 737 observations on the following four variables

- Sample character: sample identifier.
- Band integer: band number.
- MW integer: molecular weight.
- Gel character: gel identifier.

Details

The molecular weight was determined using the software package Gene Profiler 4.05 (Scanalytics Inc.) for DNA fragment analysis and genotyping, and exported to a text file.

Source

The data set was generated by F. Flessa.

References


Examples

data(RFLPdata)
str(RFLPdata)
RFLPdist

Compute distances for RFLP data.

Description

Within each group containing RFLP-samples exhibiting an equal number of bands, the distance between the molecular weights is computed.

Usage

RFLPdist(x, distfun = dist, nrBands, LOD = 0)

Arguments

- **x**: data.frame with RFLP data; see `RFLPdata`
- **distfun**: function computing the distance with default `dist`; cf. `dist`
- **nrBands**: if not missing, then only samples with the specified number of bands are considered.
- **LOD**: threshold for low-bp bands.

Details

For each number of bands the given distance between the molecular weights is computed. The result is a named list of distances where the names correspond to the number of bands which occur in each group.

- If `nrBands` is specified only samples with this number of bands are considered.
- If `LOD > 0` is specified, all values below `LOD` are removed before the distances are calculated.

Value

A named list with the distances; see `dist`.

In case `nrBands` is not missing, an object of S3 class `dist`.

Author(s)

Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>,
Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>,
Matthias Kohl <Matthias.Kohl@stamats.de>

References

Poussier, Stephane; Trigalet-Demery, Danielle; Vandewalle, Peggy; Goffinet, Bruno; Luisetti, Jacques; Trigalet, Andre. Genetic diversity of Ralstonia solanacearum as assessed by PCR-RFLP of the hrp

Matsumoto, Masaru; Furuya, Naruto; Takanami, Yoichi; Matsuyama, Nobuaki. RFLP analysis of the PCR-amplified 28S rDNA in Rhizoctonia solani. Mycoscience 1996 37:351 - 356

See Also

RFLPdata, dist

Examples

```r
## Euclidean distance
data(RFLPdata)
res <- RFLPdist(RFLPdata)
names(res) ## number of bands
res$"6"

RFLPdist(RFLPdata, nbands = 6)

## Other distances
res1 <- RFLPdist(RFLPdata, distfun = function(x) dist(x, method = "manhattan"))
res2 <- RFLPdist(RFLPdata, distfun = function(x) dist(x, method = "maximum"))
res[[1]]
res1[[1]]
res2[[1]]

## cut dendrogram at height 50
clust4bd <- hclust(res[[2]])
cgroups50 <- cutree(clust4bd, h=50)
cgroups50

## or
library(mkmisc)
res3 <- RFLPdist(RFLPdata, distfun = corDist)
res3$"9"

## hierarchical clustering
par(mfrow = c(2,2))
plot(hclust(res[[1]]), main = "Euclidean distance")
plot(hclust(res1[[1]]), main = "Manhattan distance")
plot(hclust(res2[[1]]), main = "Maximum distance")
plot(hclust(res3[[1]]), main = "Pearson correlation distance")

## Similarity matrix
library(mkmisc)
myCol <- colorRampPalette(brewer.pal(8, "RdYlGn")(128))
ord <- order.dendrogram(as.dendrogram(hclust(res[[1]])))
temp <- as.matrix(res[[1]])
simPlot(temp[ord,ord], col = rev(myCol), minVal = 0,
       labels = colnames(temp), title = "(Dis-)Similarity Plot")
```
RFLPdist2

Compute distances for RFLP data.

Description

If gel image quality is low, faint bands may be disregarded and may lead to wrong conclusions. This function computes the distance between the molecular weights of RFLP samples, including samples containing one or more additional bands. Thus, failures during band detection could be identified. Visualisation of band patterns using this method can be done by RFLPplot using the argument nrMissing.

Usage

RFLPdist2(x, distfun = dist, nrBands, nrMissing, LOD = 0, diag = FALSE, upper = FALSE)

Arguments

x data.frame with RFLP data; see RFLPdata.
distfun function computing the distance with default dist; cf. dist.
nrBands samples with number of bands equal to nrBands are to be considered.
nrMissing number of bands that might be missing.
LOD threshold for low-bp bands.
diag see dist
upper see dist
Details

For a given number of bands the given distance between the molecular weights is computed. It is assumed that a number of bands might be missing. Hence all samples with number of bands in \( nrBands, nrBands+1, \ldots, nrBands+nrMissing \) are compared.

If \( LOD > 0 \) is specified, it is assumed that missing bands can only occur for molecular weights smaller than \( LOD \). As a consequence only samples which have \( nrBands \) bands with molecular weight larger or equal to \( LOD \) are selected.

For computing the distance between the molecular weight of a sample \( S1 \) with \( x \) bands and a Sample \( S2 \) with \( x+y \) bands the distances between the molecular weight of sample \( S1 \) and the molecular weight of all possible subsets of \( S2 \) with \( x \) bands are computed. The distance between \( S1 \) and \( S2 \) is then defined as the minimum of all these distances.

If \( LOD > 0 \) is specified, only all combinations of values below \( LOD \) are considered.

This option may be useful, if gel image quality is low, and the detection of bands is doubtful.

Value

An object of class "dist" returned; cf. \texttt{dist}.

Author(s)

Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>, Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>, Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

\texttt{RFLPdata, nrBands, RFLPdist, dist}

Examples

```r
## Euclidean distance
data(RFLPdata)
nrBands(RFLPdata)
res0 <- RFLPdist(RFLPdata, nrBands = 4)
res1 <- RFLPdist2(RFLPdata, nrBands = 4, nrMissing = 1)
res2 <- RFLPdist2(RFLPdata, nrBands = 4, nrMissing = 2)
res3 <- RFLPdist2(RFLPdata, nrBands = 4, nrMissing = 3)

## assume missing bands only below LOD
res1.lod <- RFLPdist2(RFLPdata, nrBands = 4, nrMissing = 1, LOD = 60)
```
## RFLPdist2ref

This function computes the distance between RFLP data and RFLP reference data. It is part of the `RFLP` package and is used for hierarchical clustering and similarity matrix calculations.

### Hierarchical Clustering

```r
## hierarchical clustering
par(mfrow = c(2,2))
plot(hclust(res0), main = "0 bands missing")
plot(hclust(res1), main = "1 band missing")
plot(hclust(res2), main = "2 bands missing")
plot(hclust(res3), main = "3 bands missing")
```

### Missing Bands Only Below LOD

```r
## missing bands only below LOD
par(mfrow = c(1,2))
plot(hclust(res0), main = "0 bands missing")
plot(hclust(res1lod), main = "1 band missing below LOD")

## Similarity matrix
library(Misc)
myCol <- colorRampPalette(brewer_pal(8, "RdYlGn"))(128)
ord <- order.dendrogram(as.dendrogram(hclust(res1))
temp <- as.matrix(res1)
simPlot(temp[ord,ord], col = rev(myCol), minVal = 0,
       labels = colnames(temp), title = "(Dis-)Similarity Plot")

## missing bands only below LOD
ord <- order.dendrogram(as.dendrogram(hclust(res1lod)))
temp <- as.matrix(res1lod)
simPlot(temp[ord,ord], col = rev(myCol), minVal = 0,
       labels = colnames(temp), title = "(Dis-)Similarity Plot\1 band missing below LOD")

## or
library(lattice)
levelPlot(temp[ord,ord], col.regions = rev(myCol),
          at = do.breaks(c(0, max(temp)), 128),
          xlab = "", ylab = "",
          ## Rotate label of x axis
          scales = list(x = list(rot = 90)),
          main = "(Dis-)Similarity Plot")
```

### Other Distances

```r
## Other distances
res11 <- RFLPdist2(RFLPdata, distfun = function(x) dist(x, method = "manhattan"),
                   nrBands = 4, nrMissing = 1)
res12 <- RFLPdist2(RFLPdata, distfun = corDist, nrBands = 4, nrMissing = 1)
res13 <- RFLPdist2(RFLPdata, distfun = corDist, nrBands = 4, nrMissing = 1, LOD = 60)
par(mfrow = c(2,2))
plot(hclust(res1), main = "Euclidean distance\1 band missing")
plot(hclust(res11), main = "Manhattan distance\1 band missing")
plot(hclust(res12), main = "Pearson correlation distance\1 band missing")
plot(hclust(res13), main = "Pearson correlation distance\1 band missing below LOD")
```

---

**RFLPdist2ref**

*Compute distance between RFLP data and RFLP reference data.*
Description

Function to compute distance between RFLP data and RFLP reference data.

Usage

RFLPdist2ref(x, ref, distfun = dist, nrBands, LOD = 0)

Arguments

x data.frame with RFLP data; e.g. RFLPdata.
ref data.frame with RFLP reference data; e.g. RFLPref.
distfun function computing the distance with default dist; cf. dist.
nrBands only samples and reference samples with this number of bands are considered.
LOD threshold for low-bp bands.

Details

For each sample with nrBands bands the distance to each reference sample with nrBands bands is computed. The result is a matrix with the corresponding distances where rows represent the samples and columns the reference samples.

If LOD > 0 is specified, all values below LOD are removed before the distances are calculated. This applies to x and ref.

Value

A matrix with distances.

Author(s)

Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>,
Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>,
Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

RFLPdata, dist
RFLPlod

Remove bands below LOD

Description

Function to exclude bands below a given LOD.

Usage

RFLPlod(x, LOD)

Arguments

x  
data.frame with RFLP data.

LOD  
threshold for low-bp bands.

Details

Low-bp bands may be regarded as unreliable. Function RFLPlod can be used to exclude such bands, which are likely to be absent in some other samples, before further analyses.

Value

A data.frame with variables

Sample  character: sample identifier.

Band  integer: band number.

MW  integer: molecular weight.

Gel  character: gel identifier.
**Author(s)**

Fabienne Flessa <fabienne.flessa@uni-bayreuth.de>,
Alexandra Kehl <alexandra.kehla@botgarten.uni-tuebingen.de>,
Matthias Kohl <matthias.kohl@stamats.de>

**References**


**See Also**

RFLPdata

**Examples**

```r
data(rflpdata)
# remove bands with MW smaller than 60
RFLPdata.lod <- RFLPlod(RFLPdata, LOD = 60)
par(mfrow = c(1, 2))
RFLPplot(RFLPdata, nrBands = 4, ylim = c(40, 670))
RFLPplot(RFLPdata.lod, nrBands = 4, ylim = c(40, 670))
title(sub = "After applying RFLPlod")
```

---

**Function to plot RFLP data.**

**Description**

Given RFLP data is plotted where the samples are sorted according to the corresponding dendrogram.

**Usage**

```r
RFLPplot(x, nrBands, nrMissing, distfun = dist,
         hclust.method = "complete", mar.bottom = 5,
         cex.axis = 0.5, colBands, xlab = ",",
         ylab = "molecular weight", ylim, ...)
```

**Arguments**

- `x` data.frame with RFLP data; see RFLPdata.
- `nrBands` if not missing, then only samples with the specified number of bands are considered.
- `nrMissing` if not missing, then it is assumed that some bands may be missing. That is, all samples with number of bands in `nrBands`, `nrBands+1`, ..., `nrBands+nrMissing` are considered.
RFLPplot

distfun function computing the distance with default dist; see dist.
hclust.method method used for hierarchical clustering; see hclust.
mar.bottom bottom margin of the plot; see par.
cex.axis size of the x-axis annotation.
colBands color for the bands. Has to be of length 1 or number of samples. If missing, "Set1" of RColorBrewer is used; see ColorBrewer.
xlab passed to function plot.
ylab passed to function plot.
ylim passed to function plot. If missing an appropriate range of y-values is computed.
... additional arguments passed to function plot except xlim which is defined inside of RFLPplot.

Details

RFLP data is plotted. The samples are sorted according to the corresponding dendrogram which is computed via function hclust.

The option to specify nrMissing may be useful, if gel image quality is low, and the detection of bands is doubtful.

Value

invisibility

Author(s)

Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>, Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>, Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

RFLPdata, dist

Examples

data(RFLPdata)
par(mfrow = c(1,2))
plot(hclust(RFLPdist(RFLPdata, nrbands = 3)), cex = 0.7)
RFLPplot(RFLPdata, nrbands = 3, mar.bottom = 6, cex.axis = 0.8)

par(mfrow = c(1,2))
plot(hclust(RFLPdist2(RFLPdata, nrbands = 9, nrMissing = 1)), cex = 0.7)
### RFLPqc

Quality control for RFLP data

**Description**

Function to perform quality control for RFLP data based on a comparison between the total length of the digested PCR amplification product and the sum of the fragment lengths. If the sum is smaller or larger than the PCR amplification product (within a certain range to define), the samples can be excluded from further analyses. This function is helpful for data sets containing faint or uncertain bands. It is necessary to include the total length of the PCR amplification product for each sample as largest fragment in the data set, see `RFLPdata`.

**Usage**

```r
RFLPqc(x, rm.band1 = TRUE, QC.lo = 0.8, QC.up = 1.07, QC.rm = FALSE)
```

**Arguments**

- `x` : data.frame with RFLP data.
- `rm.band1` : logical: remove first band.
- `QC.lo` : numeric: a real number in (0,1).
- `QC.up` : numeric: a real number larger than 1.
- `QC.rm` : logical: remove samples with insufficient quality.

**Details**

In case the first band corresponds to the total length of the fragment one can perform a quality control comparing the length of the first band with the sum of the lengths of the remaining bands for each sample. If the sum is smaller than `QC.lo` times the length of the first band or larger than `QC.up` times the length of the first band, respectively, a text message is printed.

If `rm.band1 = TRUE` band 1 of all samples is removed and the remaining band numbers are reduced by 1.

If `QC.rm = TRUE` samples of insufficient quality are entirely removed from the given data and the resulting `data.frame` is returned.
Value

A data.frame with variables

Sample character: sample identifier.
Band integer: band number.
MW integer: molecular weight.
Gel character: gel identifier.

Author(s)

Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>,
Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>,
Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

RFLPdata, RFLPdist

Examples

Dir <- system.file("extdata", package = "RFLPtools") # input directory
filename <- file.path(Dir, "AZ091016_report.txt")
RFLP1 <- read.rflp(file = filename)
str(RFLP1)

RFLP2 <- RFLPqc(RFLP1, rm.band1 = FALSE) # identical to RFLP1
identical(RFLP1, RFLP2)

RFLP3 <- RFLPqc(RFLP1)
str(RFLP3)

RFLP4 <- RFLPqc(RFLP1, rm.band1 = TRUE, QC.rm = TRUE)
str(RFLP4)

---

RFLPref

Example data set for RFLP reference

Description

This is an example data set for RFLP reference.
Usage
    data(RFLPref)

Format
    A data frame with 35 observations on the following five variables
    Sample character: sample identifier.
    Band integer: band number.
    MW integer: molecular weight.
    Taxonname character: taxon name.
    Accession character: accession number.

Details
    This example data set for RFLP reference consists of seven RFLP reference samples. Taxon names
    are assigned by sequence comparison with GenBank database (http://www.ncbi.nlm.nih.gov/BLAST/),
    and supplemented with imaginary accession numbers.

Source
    The data set was generated by F. Flessa.

References
    Flessa, F., Kehl, A., Kohl, M. Analysing diversity and community structures using PCR-RFLP: a

Examples
    data(RFLPref)
    str(RFLPref)

RFLPrefplot  Function for a visual comparison of RFLP samples with reference samples.

Description
    Given RFLP samples are plotted together with reference samples and sorted by their distance to the
    reference sample.

Usage
    RFLPrefplot(x, ref, distfun = dist, nrBands, mar.bottom = 5,
                cex.main = 1.2, cex.axis = 0.5, devNew = FALSE,
                colBands, xlab = "", ylab = "molecular weight",
                ylim, ...)
Arguments

- **x**: data.frame with RFLP data; e.g. `RFLPdata`.
- **ref**: data.frame with RFLP reference data; e.g. `RFLPref`.
- **distfun**: function computing the distance with default `dist`; see `dist`.
- **nrBands**: if not missing, then only samples with the specified number of bands are considered.
- **mar.bottom**: bottom margin of the plot; see `par`.
- **cex.main**: size of the plot title.
- **cex.axis**: size of the x-axis annotation.
- **devNew**: logical. Open new graphics device for each plot.
- **colBands**: color for the bands. Has to be of length 1 or number of samples. If missing, “Set1” of `RColorBrewer` is used; see `ColorBrewer`.
- **xlab**: passed to function `plot`.
- **ylab**: passed to function `plot`.
- **ylim**: passed to function `plot`. If missing an appropriate range of y-values is computed.
- **...**: additional arguments passed to function `plot` except `xlim` which is defined inside of `RFLPplot`.

Details

Given RFLP samples are plotted together with reference samples and sorted by their distance to the reference sample.

Value

invisible

Author(s)

Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>, Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>, Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

`RFLPplot`
Examples

data(RFLPdata)
data(RFLPref)
deVnew(width = 12)
RFLPrefplot(RFLPdata, RFLPref, nrBands = 4, cex.axis = 0.5)
deVnew()
RFLPrefplot(RFLPdata, RFLPref, nrBands = 6, cex.axis = 0.8)
RFLPrefplot(RFLPdata, RFLPref, nrBands = 9, cex.axis = 0.8)
RFLPrefplot(RFLPdata, RFLPref[ RFLPref$Sample == "Ni_29_A3" , ], nrBands = 4, cex.axis = 0.7)

Dir <- system.file("extdata", package = "RFLPtools") # input directory
filename <- file.path(Dir, "AZ091016_report.txt")
RFLP1 <- read.rflp(file = filename)
RFLP2 <- RFLPqc(RFLP1)

deVnew(width = 12)
RFLPrefplot(RFLP1, RFLPref, nrBands = 4, cex.axis = 0.8)
deVnew()
RFLPrefplot(RFLP1, RFLPref, nrBands = 5, cex.axis = 0.8)

---

**sim2dist**

*Convert similarity matrix to dist object.*

**Description**

Function to convert similarity matrix to object of S3 class "dist".

**Usage**

```r
sim2dist(x, maxSim = 1)
```

**Arguments**

- `x` symmetric matrix: similarity matrix.
- `maxSim` maximum similarity possible.

**Details**

Similarity is converted to distance by `maxSim - x`. The resulting matrix is converted to an object of S3 class "dist" by as.dist

**Value**

Object of S3 class "dist" is returned; see `dist`.
Author(s)

Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>,
Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>,
Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

BLASTdata, simMatrix

Examples

data(BLASTdata)

## without sequence range
## Not run:
res <- simMatrix(BLASTdata)

## End(Not run)

## with sequence range
range(BLASTdata$alignment.length)
res1 <- simMatrix(BLASTdata, sequence.range = TRUE, Min = 100, Max = 450)
res2 <- simMatrix(BLASTdata, sequence.range = TRUE, Min = 500)

## visualize similarity matrix
library(MKmisc)
simPlot(res2, minVal = 0,
labels = colnames(res2), title = "(Dis-)Similarity Plot")

## or
library(lattice)
myCol <- colorRampPalette(brewer.pal(8, "RdYlGn"))(128)
levelplot(res2, col.regions = myCol,
at = do.breaks(c(0, max(res2)), 128),
lab = "", ylab = "",
## Rotate label of x axis
scales = list(x = list(rot = 90)),
main = "(Dis-)Similarity Plot")

## convert to distance
res.d <- sim2dist(res2)

## hierarchical clustering
plot(hclust(res.d))
simMatrix

**SimMatrix**

**Similarity matrix for BLAST data.**

**Description**

Function to compute similarity matrix for all-vs-all BLAST results of rDNA sequences generated with standalone BLAST from NCBI or local BLAST implemented in BioEdit.

**Usage**

```r
simMatrix(x, sequence.range = FALSE, Min, Max)
```

**Arguments**

- `x`  
  data.frame with BLAST data; see `BLASTdata`.
- `sequence.range`  
  logical: use sequence range.
- `Min`  
  minimum sequence length.
- `Max`  
  maximum sequence length.

**Details**

The given BLAST data is used to compute a similarity matrix using the following algorithm: First, the length of each sequence (LS) comprised in the input data file is extracted. If there is more than one comparison for one sequence including different parts of the respective sequence, that one with maximum base length is chosen. Subsequently, the number of matching bases (mB) is calculated by multiplying two variables comprised in the BLAST output: the identity between sequences (%) and the number of nucleotides divided by 100. The, resulting value is rounded to integer. Furthermore, the similarity is calculated by dividing mB by LS. Finally, the similarity matrix including all sequences is built. If the similarity of a combination is not shown in the BLAST report file (because the similarity was lower than 70%), this comparison is included in the similarity matrix with the result zero.

**Value**

Similarity matrix.

**Author(s)**

Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>,  
Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>,  
Matthias Kohl <Matthias.Kohl@stamats.de>
References

BioEdit v7.0.9: Tom Hall, Ibis Biosciences; http://www.mbio.ncsu.edu/BioEdit/bioedit.html

See Also

BLASTdata, sim2dist

Examples

data(BLASTdata)

## without sequence range
## code takes some time
## Not run:
res <- simMatrix(BLASTdata)

## End(Not run)

## with sequence range
range(BLASTdata$alignment.length)
res1 <- simMatrix(BLASTdata, sequence.range = TRUE, Min = 100, Max = 450)
res2 <- simMatrix(BLASTdata, sequence.range = TRUE, Min = 500)

simulateRFLPdata

Simulate RFLP data.

Description

Simulates RFLP data for comparisons of algorithms.

Usage

simulateRFLPdata(N = 10, nrBands = 3:12, bandCenters = seq(100, 800, by = 100),
delta = 50, refData = FALSE)
simulateRFLPdata

Arguments

- **n**: integer: number samples which shall be simulated per number of bands.
- **nrbands**: integer: vector of number of bands.
- **bandcenters**: numeric: vector of band centers.
- **delta**: numeric: uniform distribution with \( \text{min} = \text{bandCenter} - \delta \) and \( \text{max} = \text{bandCenter} + \delta \) is used.
- **refdata**: logical: if TRUE, additional columns Taxonname and Accession are generated.

Details

The function can be used to simulate RFLP data. For every number of band specified in nrbands a total number of N samples are generated.

First the band centers are randomly selected (with replacement) from bandCenter which form the centers of intervals of length 2*delta. From these intervals uniform random numbers are drawn leading to randomly generated RFLP data.

Value

A data frame with N*length(nrbands) observations on the following four variables:

- **Sample**: character: sample identifier.
- **Band**: integer: band number.
- **MW**: integer: molecular weight.
- **Enzyme**: character: enzyme name.

is generated. If refData = TRUE then the following two additional variables are added.

- **Taxonname**: character: taxon name.
- **Accession**: character: accession number.

Author(s)

Mohammed Aslam Imtiaz, Matthias Kohl <Matthias.Kohl@stamats.de>

See Also

RFLPdata, RFLPref

Examples

```r
simData <- simulateRFLPdata()
```
write.hclust

Cut a hierarchical cluster tree and write cluster identifiers to a text file.

Description

The tree obtained by a hierarchical cluster analysis is cut into groups by using cutree and the results are exported to a text file.

Usage

write.hclust(x, file, prefix, h = NULL, k = NULL, append = FALSE, dec = ",",)

Arguments

x object of class hclust: result of hierarchical cluster analysis computed via function hclust.
file either a character string naming a file or a connection open for writing. "" indicates output to the console.
prefix character. Information about the cluster analysis.
h numeric scalar or vector with heights where the tree should be cut.
k an integer scalar or vector with the desired number of groups.
append logical. Only relevant if file is a character string. If TRUE, the output is appended to the file. If FALSE, any existing file of the name is destroyed.
dec the string to use for decimal points in numeric or complex columns: must be a single character.

Details

The results are written to file by a call to write.table where the columns in the resulting file are seperated by tabulators (i.e. sep="\t") and no row names are exported (i.e. row.names = FALSE).

Author(s)

Fabienne Flessa <Fabienne.Flessa@uni-bayreuth.de>,
Alexandra Kehl <Alexandra.Kehl@botgarten.uni-tuebingen.de>,
Matthias Kohl <Matthias.Kohl@stamats.de>

References


See Also

write.table, cutree
Examples

data(RFLPdata)
res <- RFLPdist(RFLPdata, nbands = 4)
c1 <- hclust(res)
write.hclust(c1, file = "Test.txt", prefix = "Bd4", h = 50)

res <- RFLPdist2(RFLPdata, nbands = 4, nrMissing = 1)
c1 <- hclust(res)
write.hclust(c1, file = "Test.txt", append = TRUE, prefix = "Bd4_Mis1", h = 60)
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