

Package ‘VPdtw’

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Type Package

Title Variable Penalty Dynamic Time Warping

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Description Variable Penalty Dynamic Time Warping for aligning GC-MS chromatograms to a master signal and more. With the appropriate penalty this method performs good alignment without altering the shape of peaks in GC-MS data.

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dilation

Compute a morphological dilation of a signal

Description

A dilation is a moving local maximum over a window of specific fixed width specified by span. This dilation is computed first in one direction and then in the other.

Usage

```
dilation(y, span)
```

Arguments

y	signal, a numeric vector
span	the width of the moving window, integer

Details

A dilation is a method often used in mathematical morphology and image analysis (Soille 1999). This function is for vectors not matrices or images though applying it to rows and columns of a matrix will give the corresponding results.

An erosion of a vector or image can also be computed easily from this by computing the dilation of -1 times the vector and transforming back.

We recommend using a dilation to form a penalty for use in VPdtw.

Value

res	Dilation of y with width span
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Author(s)

David Clifford

References

Soille, P. Morphological Image Analysis: Principles and Applications; Springer: New York, 1999.

Examples

```
## Example 1 - dilation of a signal
data(reference)
dref <- dilation(reference,150)
plot(reference,log="y",type="l")
lines(dref,col=2)

## Example 2 - dilation of an image
```

```
BIN <- (volcano>177)
dBIN <- t(apply(BIN,1,dilation,span=5))
dBIN <- apply(dBIN,2,dilation,span=5)
par(mfrow=c(2,2))
image(volcano)
image(BIN)
image(dBIN)
```

reference

GC-MS Chromatogram

Description

GC-MS chromatogram from a wine sample

Usage

```
data(reference)
```

Format

A numeric vector of length 10018

Details

This together with the query data are used in the VPdtw examples. The alignment of these two signals is usually carried out on the log scale. Plotting of this signal is best done also on the log scale (see example below).

Source

Amalia Berna, Stephen Trowell, CSIRO Food Futures Flagship

References

Amalia Z. Berna, Stephen Trowell, David Clifford, Wies Cynkar, Daniel Cozzolino, Geographical origin of Sauvignon Blanc wines predicted by mass spectrometry and metal oxide based electronic nose, *Analytica Chimica Acta*, Volume 648, Issue 2, 26 August 2009, Pages 146-152, ISSN 0003-2670, DOI: 10.1016/j.aca.2009.06.056. Keywords: Sauvignon Blanc; Electronic nose; Gas chromatography-mass spectrometry; Prediction

Examples

```
data(reference)
data(query)
plot(reference,log="y",type="l",main="Gas Chromatogram",ylab="log(intensity)",lwd=2,col=1)
lines(query,col=2)
```

VPdtw

*Variable Penalty Dynamic Time Warping function***Description**

Use variable penalty dynamic time warping to align one (or many) query signal(s) to a master signal. Penalties are incurred whenever a non-diagonal move is taken.

Usage

```
VPdtw(reference, query, penalty = 0, maxshift = 50, Reference.type=c("random", "median", "mean", "trimmed"))
```

Arguments

reference	Reference signal, NULL or a vector, see details.
query	Query signal, a vector or matrix, see details
penalty	Penalty term, a vector of same length as reference (not checked) or a matrix. See details. Default is 0 repeated to the length of reference
maxshift	Maximum allowable shift, an integer
Reference.type	Choices for reference if NULL is input

Details

Performs variable penalty dynamic time warping of query to reference. Sakoe Chiba dtw used with width maxshift.

The basic operation aligns a query vector to a reference vector.

If reference is not specified and query is a matrix then the reference is created based on the value of Reference.type. The four choices are random, median, mean and trimmed. These choose a column of query at random as a reference, or the piecewise median, mean or trimmed mean (with trim=0.1) with missing values removed.

If query is a matrix and penalty is a vector then the same penalty is used to align each column of query to the reference. Different alignment paths are chosen for each column of the query matrix.

If query is a vector and penalty is a matrix then the query is aligned to the reference several times, using each column of the penalty matrix in turn as the penalty for the alignment.

If query and penalty are matrices then nothing happens. If you wish to align many query vectors and test many penalty vectors at the same time then do the appropriate looping (over queries, or penalties) outside of VPdtw.

Value

xVals	For plotting everything to correct index
reference	reference vector used by VPdtw expanded by NAs for plotting
query	query passed to VPdtw

penalty	penalty passed to VPdtw
warpedQuery	result of alignment, same class as query
shift	shifts required to achieve alignment
summary	Summary information about the alignment. Used for print.VPdtw
information	Information about the alignment. Used for print.VPdtw

Author(s)

David Clifford, Glenn Stone

References

Alignment Using Variable Penalty Dynamic Time Warping by CLIFFORD, D; STONE, G; MON-TOLIU, I; et al. ANALYTICAL CHEMISTRY Volume: 81 Issue: 3 Pages: 1000-1007 Published: 2009

See Also

Also check out the [dtw](#) package by Toni Giorgino which covers many variations of dynamic time warping.

Examples

```
## Citation
citation("VPdtw")

## Basic Examples of zero-penalty DTW

## Example of exact fit in the middle
query <- c(1,5,4,3,9,8,5,2,6,5,4)
reference <- c(rnorm(5),query,rnorm(5))
lambda <- rep(0,length(reference))
maxshift <- 11
res <- VPdtw(reference,query,lambda,maxshift)
plot(res)
res

## Example of exact fit on one side
reference <- c(1,5,4,3,9,8,5,2,6,5,4)
query <- c(rnorm(5),reference)
reference <- c(reference,rnorm(5))
lambda <- rep(0,length(reference))
maxshift <- 6
res <- VPdtw(reference,query,lambda,maxshift)
plot(res)
res

## Example of exact fit on the other side
reference <- c(1,5,4,3,9,8,5,2,6,5,4)
query <- c(reference,rnorm(5))
```

```

reference <- c(rnorm(5),reference)
lambda <- rep(0,length(reference))
maxshift <- 6
res <- VPdtw(reference,query,lambda,maxshift)
plot(res)
res

## Example of exact fit except where one query gets dropped and its all on one side
reference <- c(1,5,4,3,9,8,5,2,6,5,4)
query <- c(reference[1:5],20,reference[6:11])
reference <- c(rnorm(5),reference)
query <- c(query,rnorm(5))
lambda <- rep(0,length(reference))
maxshift <- 6
res <- VPdtw(reference,query,lambda,maxshift)
plot(res)
res

## Examples that use penalty term. Examples with long signals

data(reference)
data(query)
## Do alignment on log scale
reference <- log(reference)
query <- log(query)

## VPdtw
result <- VPdtw(reference=reference[1:2500],query=query[1:2500],penalty=dilation(reference[1:2500],150)/4,maxsh
plot(result)
result

## Zero penalty DTW
result2 <- VPdtw(reference=reference[1:2500],query=query[1:2500],penalty=rep(0,length(reference)),maxshift=150)
plot(result2)

## Try both penalties at the same time
penalty <- dilation(reference,350)/5
penalty <- cbind(penalty,rep(0,length(penalty)))

result <- VPdtw(reference,query,penalty=penalty,maxshift=350)
plot(result,"After")
plot(result,"Shift")
result

## All three plots at once
plot(result)

```

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