Package 'mQTL'

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Type Package

Title Metabolomic Quantitative Trait Locus Mapping

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Author Lyamine Hedjazi and Jean-Baptiste Cazier

Maintainer Lyamine Hedjazi <l.hedjazi@fondation-ican.com>

Description mQTL provides a complete QTL analysis pipeline for metabolomic data. Distinctive features include normalisation using PQN approach, peak alignment using RSPA approach, dimensionality reduction using SRV approach and finally QTL mapping using R/qtl package.

License GPL

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R topics documented:

`mQTL-package` *Metabolomic Quantitative Trait Locus mapping*

Description

mQTL provides a complete QTL analysis pipeline for 1H NMR data. Distinctive features include normalisation using QPN approach, peak alignment using RSPA approach, dimensionality reduction using SRV approach and finally QTL mapping using R/qtl package.

Details

Package:	mQTL
Type:	Package
Version:	1.0
Date:	2013-09-18
License:	GPL (>= 3)

Main fucntions:

- `format_mQTL`: creates the proper format of data
- `align_mQTL`: peak alignment and normalisation
- `pre_mQTL`: dimension reduction by statistical recoupling of variables
- `process_mQTL`: computes LODs using extended Haley-Knott method
- `post_mQTL`: plots the results of a given run
- `summary_mQTL`: provides the results as a table

Author(s)

Lyamine Hedjazi and Jean-Baptiste Cazier

Maintainer: Lyamine Hedjazi <<l.hedjazi@fondation-ican.com>>

alignSp *Base function for Spectrum Alignment*

Description

Alignement of spectrum segement to a spectrum of interest

Usage

```
alignSp(refSp, refSegments, intSp, intSegments, recursion, MAX_DIST_FACTOR, MIN_RC)
```

Arguments

refSp	reference spectrum
refSegments	refrence segments
intSp	spectrum of intrest
intSegments	segments of intrest
recursion	parameters for recursive alignment
MAX_DIST_FACTOR	the distance matching parameter (0.5*peak width)
MIN_RC	minimum resamblance coefficient

Value

alignedSpectrum	aligned spectrum
extendedSegments	extended segments

Author(s)

Lyamine Hedjazi

Maintainer: Lyamine Hedjazi <<l.hedjazi@fondation-ican.com>>

See Also

align_mQTL

Examples

```
## Not run:
## Data

Sp=matrix(rnorm(10*13454,mean=0,sd=1), nrow=10,ncol=13454)
```

```
##Segmentation parameters

peakParam=list()
peakParam$ppmDist <- 0.03 #(ppm)  # distance to concatenate adjacent peaks #default 0.03#
peakParam$ampThr <- 0.3 # amplitude value to threshold small peaks
peakParam$minPeakWidth <- 0.005 # min peak width in ppm scale
peakParam$iFrameLen<-11 # Savitzky-Golay frame length in ppm scale
peakParam$iOrder<-3 # polynomial order of Savitzky - Golay filter
peakParam$peakEdgeMax<-0.2 # maximal peak edge

##Recusrsion alignment parameters

recursion=list()
recursion$resamblance<-0.95# Stop criterium of the recursion indicating
#the complete alignment of segment peaks
recursion$segShift<-0.02#(ppm)  max peak shift for large peaks
recursion$inbetweenShift<-0.02 #(ppm) max shift for small peaks
recursion$acceptance<-0.5 # if resemblance after the alignment between modified test
recursion$minSegWidth<-0.01 #(ppm) Stop criteria of the recursion - the size of the smallest peak
recursion$step<-0.02 # Recursion step (default 0.02)

## Normalisation

normD<-normalise(Sp,'prob')

## Reference spectrum selection

index<-selectRefSp(normD$Sp,recursion$step)
refSp<-normD$Sp[index,] # reference spectrum picked-up

##segmentate a reference spectrum

refSegments<- segmentateSp(refSp, peakParam) # segmentate reference spectrum

##segmentate a test spectrum

spectrum<-normD$Sp[10,]
testSegments<- segmentateSp(spectrum, peakParam) # segmentate test spectrum (10th sample)

#match test and reference segments

attachedSegs<-attachSegments(refSegments,testSegments)

refSegments<-attachedSegs$refSegmentsNew
testSegments<-attachedSegs$testSegmentsNew

##matching parameters

MAX_DIST_FACTOR<-0.5 # The distance matching parameter (0.5*peak_width)
MIN_RC<-0.25 # Minimum resamblance coefficient

Segs<-matchSegments(refSp,spectrum, testSegments,refSegments,MAX_DIST_FACTOR,MIN_RC)
```

```
#align a test spectrum

refSgs<-Segs$refSegs
tstSgs<-Segs$testSegs

SpAlg<- alignSp(refSp,refSgs,spectrum,tstSgs,recursion,MAX_DIST_FACTOR,MIN_RC)

## End(Not run)
```

`align_mQTL` *Peak alignement and normalisation of metabolomic data*

Description

Recursive Segment-Wise Peak Alignment (RSPA) for accounting peak position variation across metabolomic data

Usage

```
align_mQTL(datafile, outdat)
```

Arguments

`datafile`	raw spectra
`outdat`	aligned spectra

Details

The algorithm is based on the following workflow:

1. Quotient probabilistic normalisation of metabolomic data.
2. Automatic selection of a reference spectrum.
3. Segmentate a reference spectrum.
4. Then for each test spectrum:
   - segmentate a test spectrum.
   - match test and reference segments.
   - align a test spectrum.

Value

It returns aligned data.

Author(s)

Lyamine Hedjazi

References

Veselkov,K. et al (2009) Recursive Segment-Wise Peak Alignment of Biological 1H NMR Spectra for Improved Metabolic Biomarker Recovery, Anal. Chem., 81(1), 56-66.

See Also

alignSp, attachSegments, matchSegments, segmentateSp,format_mQTL, format_mQTL

Examples

```
  ## Not run:
## Align metabolomic data profiles

  cleandat<-"CleanMetaboFile.dat" ## Metabolomic data file in csvs format
  aligdat<-"AlignData.dat" ## Aligned metabolomic profiles in csvs format

  align_mQTL(cleandat,aligdat)

## End(Not run)
```

---

attachSegments *Concatenation of test and reference segments*

Description

Concatenation of test and reference segments to ensure one-to-one correspondence.

Usage

```
attachSegments(refSegments,testSegments)
```

Arguments

refSegments	segments of the reference spectrum
testSegments	segments of the test spectrum

Details

The algorithm:

1. For each reference segment within segment boundaries, i.e. between initial and final positions, find all centre (middle) positions of test segments and merge those segments, if more than one centre position is found
2. Apply the same procedure for each test segment

Value

A list:

`segments$start` start of each concatenated test segment

`segments$PeakLeftBoundary`
peak left boundary of each concatenated test segment

`segments$PeakRightBoundary`
peak right boundary of each concatenated test segment

`segments$Peaks` peaks of each concatenated test segment

`segments$end` end of each concatenated test segment

`segments$end` center of each concatenated test segment

Author(s)

Lyamine Hedjazi

References

Veselkov,K. et al (2009) Recursive Segment-Wise Peak Alignment of Biological 1H NMR Spectra for Improved Metabolic Biomarker Recovery, Anal. Chem., 81(1), 56-66.

See Also

matchSegments

Examples

```
## Not run:

## Data

Sp=matrix(rnorm(10*13454,mean=0,sd=1), nrow=10,ncol=13454)

##Segmentation parameters

peakParam=list()
peakParam$ppmDist <- 0.03# (ppm)  # distance to concatenate adjacent peaks #default 0.03#
peakParam$ampThr <- 0.3 # amplitude value to threshold small peaks #
peakParam$minPeakWidth <- 0.005 #min peak width in ppm scale
peakParam$iFrameLen<-11 #Savitzky-Golay frame length in ppm scale
peakParam$iOrder<-3 #polynomial order of Savitzky - Golay filter
peakParam$peakEdgeMax<-0.2

##Reference spectrum selection

step<-0.02 # Recursion step (default 0.02)
index<-selectRefSp(Sp,step)
refSp<-Sp[index,]
```

```
#segmentate a reference spectrum

refSegments<- segmentateSp(refSp, peakParam) # segmentate reference spectrum

#segmentate a test spectrum

spectrum<-Sp[10,]
testSegments<- segmentateSp(spectrum, peakParam) # segmentate test spectrum (10th sample)

# match test and reference segments

attachedSegs<-attachSegments(refSegments,testSegments)


## End(Not run)
```

`format_mQTL` *Routine to reformat the data into the required format*

Description

This function enables to reformat data into the proper format. The user should provides in input metabolomic dataset, Genotype dataset and a dataset containing sex and pgm (parental grandmother).

Usage

```
format_mQTL(datafile, genofile, physdat, outdat, outgeno)
```

Arguments

`datafile`	metabolomic data file
`genofile`	genotype data file
`physdat`	a file containing sex and pgm
`outdat`	phenotype data (metabolomic data + sex + pgm) in the format csvs
`outgeno`	genotype data

Value

It returns phynotype and genotype files in the proper format

Author(s)

Lyamine Hedjazi

See Also

`align_mQTL`,

Examples

```
  ## Not run:
## Clean the raw data to match the genotype and phenotype and create the proper format

  rawfile<-"MetaboFile.dat" ## Metabolomic data file
  genofile<-"GenoFile.dat" ## Genotype data file
  physiodat="physiodat.dat" ## data file containing sex and pgm
  cleandat<-"CleanMetaboFile.dat" ## Metabolomic data file in csvs format
  cleangen<-"CleanGenoFile.dat" ## Genotype data file in csvs format

  format_mQTL(rawfile,genofile,physiodat, cleandat,cleangen)

## End(Not run)
```

---

matchSegments *Matching of the segment of interest to the corresponding reference*

Description

The algorithm makes use of a fuzzy logic approach to match the segment of interest to the corresponding reference

Usage

```
matchSegments(refSp, intSp, intSegments, refSegments, MAX_DIST_FACTOR, MIN_RC)
```

Arguments

refSp	spectrum of reference
intSp	spetcrum of interest (test spectrum)
intSegments	segments of spectrum of interest
refSegments	segments of reference spectrum
MAX_DIST_FACTOR	the distance matching parameter (0.5*peak_width)
MIN_RC	minimum resamblance coefficient

Details

Algorithm:

1. take segment of interest
2. take reference segments
3. calculate relative distance between them
4. calculate relative resamblance between them
5. find min value of relative distance and resamblance
6. use it as representative of similiarity between target and reference segments
7. find the segment that has the highest value of both relative distance and resamblance

Value

A list:

testSegs	matched test segments
refSegs	matched reference segments

Author(s)

Lyamine Hedjazi

References

Veselkov,K. et al (2009) Recursive Segment-Wise Peak Alignment of Biological 1H NMR Spectra for Improved Metabolic Biomarker Recovery, Anal. Chem., 81(1), 56-66.

See Also

attachSegments

Examples

```
## Not run:

# Data

Sp=matrix(rnorm(10*13454,mean=0,sd=1), nrow=10,ncol=13454)

##Segmentation parameters

peakParam=list()
peakParam$ppmDist <- 0.03# (ppm)  # distance to concatenate adjacent peaks #default 0.03#
peakParam$ampThr <- 0.3 # amplitude value to threshold small peaks #
peakParam$minPeakWidth <- 0.005 #min peak width in ppm scale
peakParam$iFrameLen<-11 #Savitzky-Golay frame length in ppm scale
peakParam$iOrder<-3 #polynomial order of Savitzky - Golay filter
peakParam$peakEdgeMax<-0.2

##reference spectrum selection

step=0.02 # Recursion step (default 0.02)
index<-selectRefSp(Sp,step)
refSp<-Sp[index,]

#segmentate a reference spectrum

refSegments<- segmentateSp(refSp, peakParam) # segmentate reference spectrum

#segmentate a test spectrum

spectrum<-Sp[10,]
```

```
testSegments<- segmentateSp(spectrum, peakParam) # segmentate test spectrum (10th sample)

#attach test and reference segments
attachedSegs<-attachSegments(refSegments,testSegments)

##Matching parameters

MAX_DIST_FACTOR<-0.5 # The distance matching parameter (0.5*peak_width)
MIN_RC<-0.25 # Minimum resamblance coefficient

refSegments<-attachedSegs$refSegmentsNew
testSegments<-attachedSegs$testSegmentsNew
Segs<-matchSegments(refSp,spectrum, testSegments,refSegments,MAX_DIST_FACTOR, MIN_RC)

## End(Not run)
```

`normalise` *Normalisation of metabolomic data*

Description

Removing dilutions between biofluid samples (normalisation of spectra)

Usage

```
normalise(X, method)
```

Arguments

`X`	metabolomic data
`method`	total area (method<-"total") or quotient probabilistic method (method<-"prob")

Value

normalised spectrum

Author(s)

Lyamine Hedjazi

References

Dieterle,F., et al (2006) Probabilistic Quotient Normalization as Robust Method to Account for Dilution of Complex Biological Mixtures. Application in 1H NMR Metabonomics, Anal. Chem., 78(13), 42814290.

See Also

SRV

Examples

```
## Data
Sp=matrix(rnorm(10*13454,mean=0,sd=1), nrow=10,ncol=13454)

## Quotient probabilistic normalisation
NormDat<-normalise(abs(Sp),'prob')
```

---

peakPeaks *Peak picking algorithm*

Description

Identification of peaks in metabolomic data based on the calculation of smoothed derivates using Savitzky-Golay filter. The peak is identified if derivative crosses zero, i.e. sign(X'(i))>sing(X'(i+1)).

Usage

```
peakPeaks(SpSmooth, dpDerivs, Sp)
```

Arguments

SpSmooth	smoothed spectrum
dpDerivs	smoothed derivative of the spectrum
Sp	Spectrum of intrest

Value

identified peaks

Author(s)

Lyamine Hedjazi

References

Veselkov,K. et al (2009) Recursive Segment-Wise Peak Alignment of Biological 1H NMR Spectra for Improved Metabolic Biomarker Recovery, Anal. Chem., 81(1), 56-66.

See Also

sgolayDeriv

Examples

```
## Data
Sp=matrix(rnorm(10*13454,mean=0,sd=1), nrow=10,ncol=13454)

## Peak picking
Spectrum<-Sp[1,]
iOrder <- 3
iFrameLen<- 11

SpDerivs=sgolayDeriv(Spectrum,iOrder,iFrameLen,2)
SpSmooth = sgolayDeriv(Spectrum,iOrder,iFrameLen,1)
peaks=peakPeaks(SpSmooth,SpDerivs,Spectrum)
```

`post_mQTL` *Plot top LOD results*

Description

Function to plot the results of a given run

Usage

```
post_mQTL(results, probs = c(0.95, 0.99, 0.999, 0.9999))
```

Arguments

`results`	results of mQTL analysis.
`probs`	numeric vector of probabilities with values in [0,1]. (Values up to 2e-14 outside that range are accepted and moved to the nearby endpoint.).

Details

This function plots differents results corresponding to top LOD marker

Value

It returns graphs and summaries

Author(s)

Jean-Baptiste Cazier

See Also

`pre_mQTL`

Examples

```
  ## Not run:
## Pre-process data

    infile<-"ReducedData.dat" ## Reduced data by SRV
    cleangen<-"CleanGenoFile.dat" ## Genotype data file in csvs format
    nperm <- 0 ## Number of permutations
    MQTL_results<-process_mQTL(infile, cleangen, nperm))

    post_mQTL(results)## Plot mQTL results


## End(Not run)
```

`ppersp` *Plot a 3-D profile of LODs*

Description

Plot 3-D profile of LODs as function of genomic position and chemical shift

Usage

```
ppersp(z, ppm, titre, theta=-15, phi=15, r=50)
```

Arguments

`z`	table of results
`ppm`	chemical shift
`titre`	title
`theta`	angle defining the viewing direction (azimuthal direction)
`phi`	angle defining the viewing direction (colatitude direction)
`r`	the distance of the eyepoint from the centre of the plotting box.

Value

plot 2D-profile

Author(s)

Jean-Baptiste Cazier

See Also

`pplot`

Examples

```
## Plot 3D profile

## Not run:
x11(width=5,height=5,pointsize=5)
titel<-"Example plot"
ppersp(results, ppm, title)

## End(Not run)
```

`pplot` *Plot a color scale layer*

Description

Plot the results with a color scale y layer over 3 in 2D

Usage

```
pplot(z, titre, ppm, res, LT = c(5,10,15,20))
```

Arguments

`z`	mQTL's whole results
`titre`	figure title
`ppm`	chemical shift
`res`	results to be plotted
`LT`	quantil(res,probs), res: results and probs: vector of probabilities

Value

2-D profile

Author(s)

Jean-Baptiste Cazier

See Also

`ppersp`

Examples

```
## Not run:

## Plot 3D profile

x11(width=5,height=5,pointsize=5)
titel<-"Example plot"

probs=c(0.95,0.99,0.999,0.9999) ## probabilities

pplot(res,"Full 2D Profile", ppm, best, quantile(res,probs=probs))

## End(Not run)
```

---

pre_mQTL *Statistical Recoupling of variables for mQTL analysis*

Description

Makes use of SRV to preprocess metabolomic data for dimensionality reduction by statistical recoupling of variables

Usage

```
pre_mQTL(infile, outfile, met, corrT = 0.9)
```

Arguments

infile	metabolomic datafile
outfile	reduced metabolomic datafile
met	used statistical summary
corrT	correlation threshold

Details

The SRV algorithm forms clusters of variables using a measure of a local spectral dependency. Then tests whether consecutive clusters are correlated to aggregate them into a single supercluster.

Value

The algorithm:

1. variables are associated into a series of clusters.
2. integration of clusters into superclusters.

Author(s)

Jean-Baptiste Cazier and Lyamine Hedjazi

References

Blaise,B. et al (2009) Statistical recoupling prior to significance testing in nuclear magnetic resonance based metabonomics, Anal. Chem., 81(15), 6242-6251.

See Also

SRV,post_mQTL

Examples

```
  ## Not run:
## Pre-process data

    infile<-"AlignData.dat" ## Aligned metabolomic profiles in csvs format
    outfile<-"ReducedData.dat" ## Reduced data by SRV
    met<- "rectangle" ## Summary measure (mean, max,...)
    corrT<- 0.9 ## Correlation threshold (default 0.9)
    (pre_mQTL(infile, outfile, met, corrT)

## End(Not run)
```

`process_mQTL` *mQTL mapping*

Description

Function to process the tissue extract of the individuals for QTL analysis

Usage

```
process_mQTL(datfile, genfile, nperm = 0)
```

Arguments

`datfile`	phenotype data
`genfile`	genotype data
`nperm`	nperm

Details

This function makes use of metabolomic and genotype data to perform QTL analysis based on the R/QTL package, for mapping quantitative trait loci. In particular, it makes use of the extended Haley-Knott method to optimize the LOD score evaluation and avoid problems with missing genotypes.

Value

2D LOD score table

Author(s)

Jean-Baptiste Cazier and Hedjazi Lyamine

References

Broman,K., et al (2006) R/qtl: QTL mapping in experimental crosses, Bioinformatics, 19(7), 889-890.

See Also

post_mQTL

Examples

```
  ## Not run:
## Pre-process data
    infile<-"ReducedData.dat" ## Reduced data by SRV
    cleangen<-"CleanGenoFile.dat" ## Genotype data file in csvs format
    nperm <- 0 ## Number of permutations
    MQTL_results<-process_mQTL(infile, cleangen, nperm))

## End(Not run)
```

---

segmentateSp *Segmentation of a spectrum of interest*

Description

Determination of highly intensive peaks in the spectrum of interest and subsequent concatenation of closely located peaks into larger segments

Usage

```
segmentateSp(Sp, peakParam)
```

Arguments

Sp	spectrum
peakParam	a list:

- ampThr: amplitude threshold [default 2*median(peaksMaxValues)]
- iFrameLen: Savitzky-Golay frame length
- iOrder: polynomial order of Savitzky - Golay filter
- iFrameLen: Savitzky-Golay frame length
- minPeakWidth: min peak size
- ppmDist: distance to concatenate adjacent peaks

Value

A list:

`testSegmentsNew` new test segments

`refSegmentsNew` new reference segments

Author(s)

Lyamine Hedjazi

References

Veselkov,K. et al (2009) Recursive Segment-Wise Peak Alignment of Biological 1H NMR Spectra for Improved Metabolic Biomarker Recovery, Anal. Chem., 81(1), 56-66.

See Also

attachSegments, matchSegments

Examples

```
# Data

Sp=matrix(rnorm(10*13454,mean=0,sd=1), nrow=10,ncol=13454)

##Segmentation parameters

peakParam=list()
peakParam$ppmDist <- 0.03# (ppm)  # distance to concatenate adjacent peaks #default 0.03#
peakParam$ampThr <- 0.3 # amplitude value to threshold small peaks #
peakParam$minPeakWidth <- 0.005 #min peak width in ppm scale
peakParam$iFrameLen<-11 #Savitzky-Golay frame length in ppm scale
peakParam$iOrder<-3 #polynomial order of Savitzky - Golay filter
peakParam$peakEdgeMax<-0.2

#segmentate a test spectrum (10th sample)

Spectr<-Sp[10,]
testSegments<- segmentateSp(Spectr, peakParam)
```

---

selectRefSp *Automated selection of a reference spectrum*

Description

The selection of reference spectrum among all spectrums is based on the highest similarity to all other spectra

Usage

```
selectRefSp(X, step)
```

Arguments

X	spectra
step	used to scale spectral regions down to specific bin size

Value

returns the index of selected spectrum

Author(s)

Lyamine Hedjazi

See Also

alignSp

Examples

```
# Data

Sp=matrix(rnorm(10*13454,mean=0,sd=1), nrow=10,ncol=13454)

# Reference spectrum selection

step=0.02 # Recursion step (default 0.02)
index<-selectRefSp(Sp,step)
```

---

sgolay *Find the matrix of differentiation filters*

Description

designs a Savitzky-Golay (polynomial) FIR smoothing filter. The polynomial order must be less than the frame size which must be odd.

Usage

```
sgolay(k,F,W)
```

Arguments

k	polynomial order
F	frame size
W	weighting matrix

Value

matrix of differentiators

Author(s)

Lyamine Hedjazi

References

Sophocles J. Orfanidis, INTRODUCTION TO SIGNAL PROCESSING, Prentice-Hall, 1995, Chapter 8

See Also

sgolayDeriv

Examples

```
k <- 3
F <- 11

Sg=sgolay(k,F)
```

---

sgolayDeriv *Calculate smoothed derivates*

Description

Calculate smoothed derivates using Savitzky-Golay filter

Usage

```
sgolayDeriv(dpSpectr, iOrder, iFrameLen, j)
```

Arguments

dpSpectr	input spectrum
iOrder	polynomial order of Savitzky - Golay filter
iFrameLen	Savitzky-Golay frame length in ppm scale
j	order of derivative

Value

jth dervitative of the spectrum

Author(s)

Lyamine Hedjazi

See Also

sgolay

Examples

```
## Data

Sp=matrix(rnorm(10*13454,mean=0,sd=1), nrow=10,ncol=13454)

## Peak picking
Spectrum<-Sp[10,]
iOrder <- 3
iFrameLen<- 11
j<-2

SpDerivs=sgolayDeriv(Spectrum,iOrder,iFrameLen,j)
```

SRV *Statistical Recoupling of Variables*

Description

Base function for dimensionality reduction by statistical recoupling of variables

Usage

```
SRV(X, minsize, correl, clustf = median)
```

Arguments

X	data matrix
minsize	singlet size
correl	bucketting resolution
clustf	correlation threshold

Value

A list:

indicesdebf	starting border of superclusters
indicesfinf	ending border of superclusters

Author(s)

Jean-Baptiste Cazier

References

Blaise,B. et al (2009) Statistical recoupling prior to significance testing in nuclear magnetic resonance based metabonomics, Anal. Chem., 81(15), 6242-6251.

See Also

pre_mQTL

Examples

```
## Not run:

## Statistical recoupling of variables

    corrT=0.9 # correlation threshold
    minsize=10 # singlet size
    met="rectangle" # summary measure

#Perform the SRV analysis to reduce the number of dimension of Spectra data (Sp)

    SRV<-SRV(Sp, minsize, corrT,clustf=met)


## End(Not run)
```

SRV_Corr *Statistical recoupling of variables in a supervised context*

Description

Correlation generation for Statistical Recoupling of Variables.

Usage

```
SRV_Corr(X, Y, minsize, correl)
```

Arguments

X	data matrix
Y	class matrix
minsize	bucketting resolution
correl	correlation threshold

Value

A list:

Pfinal	pvalue vector
indicesdebf	starting border of cluster
indicesfinfl	ending border of cluster
Correlation	Correlation of superclusters/clusters

Author(s)

Jean-Baptiste Cazier

References

Blaise,B. et al (2009) Statistical recoupling prior to significance testing in nuclear magnetic resonance based metabonomics, Anal. Chem., 81(15), 6242-6251.

See Also

SRV, pre_mQTL

---

summary_mQTL *Function to summarize the results of a all the runs and their differences*

Description

This function generates a table containing the genetic markers and thier associated metabolomic variables and estimated LOD score.

Usage

```
summary_mQTL(results, Th = 5)
```

Arguments

results	mQTL mapping results
Th	Threshold of the top accepted LOD

Details

Generates a text file containing a table of results

Value

returns Summaries

Author(s)

Jean-Baptiste Cazier and Lyamine Hedjazi

See Also

pre_mQTL

Examples

```
  ## Not run:

## Pre-process data

    infile<-"ReducedData.dat" ## Reduced data by SRV
    cleangen<-"CleanGenoFile.dat" ## Genotype data file in csvs format
    nperm <- 0 ## Number of permutations
    MQTL_results<-process_mQTL(infile, cleangen, nperm))

    T=10 ## LOD threshold
    summary_mQTL(results,T=8)## summarizes mQTL results in a table


## End(Not run)
```

Index