

Package ‘GCSscore’

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Type Package

Title GCSscore: an R package for microarray analysis for
Affymetrix/Thermo Fisher arrays

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Description

For differential expression analysis of 3'IVT and WT-style microarrays from Affymetrix/Thermo-Fisher. Based on S-score algorithm originally described by Zhang et al 2002.

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calcSF	<i>calculates Scaling Factor (SF) values</i>
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Description

This internally called function calculates the scaling factor (SF) values for Affymetrix microarrays, for use in computing GCS-score values

Usage

```
calcSF(diff, probetab, trim)
```

Arguments

diff	The GC-content background corrected probe groupings for every probesetID or transcriptionclusterID on the given array type. This is generated internally by the computeSscore function
probetab	The internal datafile that contains the probe groupings and annotations for each array type and method type
trim	The internal setting for the trimmed mean of every probe grouping on the array, as used in the calculation of SF. For 3' IVT arrays, the trim is set to 0.02 by default. For all newer WT-type arrays, the trim is set to 0.04 by default

Value

calcSF returns a numeric SF value for a given CEL file

Examples

```
if (length(list.files(path = ".", pattern = "*.CEL")) != 0){
  #Example of input, as the function would be called internally:
  calcSF(diff, probetab, trim)
}
```

computeScore	<i>Computes GCS-score values</i>
--------------	----------------------------------

Description

This internally called function computes the GCS-score values between two Affymetrix-style microarrays. The computeScore function contains the majority of the GCS-score algorithm.

Usage

```
computeScore(ce1, ce2, probeFile, bgp, method, infoKey, SF1 = NULL, SF2 = NULL,
             verbose = FALSE, trim = NULL)
```

Arguments

ce1	The 1st Affymetrix CEL file, as read in by the affxparser package
ce2	The 2nd Affymetrix CEL file, as read in by the affxparser package
probeFile	The internal datafile that contains the probe groupings and annotations for each array type and method type
bgp	The index of the probe location, GC-content, and annotations of the background probes of a given chip type. For WT-type arrays, the bgp consists of 16,943 antigenomic background probes. For 3' IVT arrays, the MisMatch (MM) probes are used to calculate the bgp list in both methods
method	Determines the method used to group and tally the probes when calculating GCS-score values
infoKey	The key of how to group the probes together for the GCS-score calculations. Determines the method used to group and tally the probes when calculating GCS-score values. For example, exon-level analysis groups probes by probe-set_ids while gene-level groups probes by transcript_cluster_ids
SF1	If the user has predetermined scaling factors, input user Scaling Factor (SF) for the 1st CEL file. Otherwise, the computeScore function will calculate SF1 directly from the 1st CEL file
SF2	If the user has predetermined scaling factors, input user Scaling Factor (SF) for the 2nd CEL file. Otherwise, the computeScore function will calculate SF2 directly from the 2nd CEL file
verbose	If set to TRUE, additional information will be printed to the console while the algorithm is running.
trim	Internal parameter determined by chip type .trim=0.04 for WT-type arrays and 0.02 for 3' IVT type arrays

Details

This internally called function computes the raw difference scores between the probes on each microarray, then groups the probes into probesets or transcript cluset ids, and normalizes the results to produce GCS-score values. The function returns the values to the main GCscore2, where BioConductor-based annotations are added to either the exon-level or gene-level probe groupings

Value

A data.table object with GCS-Score values for the probe groupings (determined by the method argument)

Examples

```
if (length(list.files(path = ".", pattern = "*.CEL")) != 0){

#Example of input, as the function would be called internally:
computeSscore(ce1, ce2, probeFile, bgp, infoKey, method, SF1 = NULL, SF2 = NULL,
              verbose = FALSE, trim = NULL)

}
```

GCSscore

*Main GCS-score Function***Description**

The main function used to call and run the GCS-score algorithm.

Usage

```
GCSscore(ce1File1 = NULL, ce1File2 = NULL, ce1Table = NULL, ce1Tab.names = FALSE,
          typeFilter = 1, method = 1, rm.outmask = FALSE, SF1 = NULL, SF2 = NULL, fileout = FALSE,
          gzip = FALSE, verbose = FALSE)
```

Arguments

ce1File1	If a one comparison run is desired, enter the filename and path to the 1st Affymetrix CEL file
ce1File2	If a one comparison run is desired, enter the filename and path to the 2nd Affymetrix CEL file
ce1Table	If a batch run is desired, enter the filename and path to the CSV file containing the batch information
ce1Tab.names	If set to TRUE, then the GCS-score batch output is assigned the user-designated name (specified in the first column of the ce1Table CSV file (see examples))
typeFilter	If set to 0, all available probe types are included in the calculation and normalization of the GCS-score values. If set to 1, only probes well-annotated probe_ids (from BioConductor .db packages) are included in the calculation and normalization of the GCS-score output
method	This determines the method used to group and tally the probes_ids when calculating GCS-scores. For Whole Transcriptome (WT) arrays, for gene-level (transcript_cluster_id-based) analysis, set method = 1, and for exon-level (probeset_id-based) analysis, set method = 2. For the older generation arrays (3' IVT-style), if a PM-MM based background correction is desired, set method = 1 (PM-MM gives identical results to the original sscore package). If a GC-content based background correction is desired on the 3' IVT arrays, set method = 2
rm.outmask	If set to TRUE, then probes that are flagged as MASKED or OUTLIER in either CEL file 1 or CEL file 2 will be removed from the analysis. If set to FALSE, these probes are not filtered out and will be used in the GCS-score calculation

SF1	Input a pre-determined Scaling Factor (SF) for the 1st CEL file
SF2	Input a pre-determined Scaling Factor (SF) for the 2nd CEL file
fileout	Determines if the resulting GCS-score output is written to disk in a CSV format following the completion of the function. By default, this is set to FALSE so unnecessary GCS-score outputs are not saved to disk after each run
gzip	If set to TRUE, the GCSscore output that is written to disk is compressed. This could prove useful if a large number runs are input using the batch submission
verbose	If set to TRUE, more information will be printed to the console during while the algorithm is running

Details

The input accepts individual CEL files or reads in a CSV file for batch runs. The user also inputs parameters to determine the method used by the GCS-score algorithm to group and tally the individual probes on a given array.

Value

An ExpressionSet object with GCS-score values for the probe groupings (determined by the method argument) and the relevant annotation information

Examples

```
if (length(list.files(path = ".", pattern = "*.CEL")) != 0){

##Single run example:
# get the path to example CEL files in the package directory:
celpath1 <- system.file("extdata/ex_dat",
                        "MN_2_3.CEL", package = "GCSscore")
celpath2 <- system.file("extdata/ex_dat",
                        "MN_4_1.CEL", package = "GCSscore")
# run GCSscore() function directly on two .CEL files:
Ss2_clarS <- GCSscore(celFile1 = celpath1, celFile2 = celpath2)

# display selected columns of GCSscore output:
Ss2_clarS[1:6,c(1,3,6,7,8,11)]

## Batch run example:
# get the path to example CSV file in the package directory:
celtab_path <- system.file("extdata/ex_dat",
                           "Ss2_BATCH_example.csv", package = "GCSscore")
# read in the .CSV file with fread():
celtab <- fread(celtab_path)
# view structure of 'celTable' input:
celtab

# For the following example, the .CEL files are not in the working
# directory. The path to the .CEL files must be added to allow
# the GCSscore() function to find them.

# add path to celFile names in batch input:
path <- system.file("extdata/ex_dat",
                    "", package = "GCSscore")
celtab$CelFile1 <- celtab[,paste(path,CelFile1,sep="")]
celtab$CelFile2 <- celtab[,paste(path,CelFile2,sep="")]
}
```

```
# run GCSscore() function with batch input:
Ss_clarS_batch <- GCSscore(celTable = celTab, celTab.names = TRUE)
# display selected columns of GCSscore batch output:
Ss_clarS_batch[1:6,c(1,3,11,12,13,14,15,16)]
}
```

```
get3primeIVTprobeFileData
```

Read a data file describing the probe sequences on an Affymetrix genechip

Description

Read a data file describing the probe sequences on an Affymetrix genechip

Usage

```
get3primeIVTprobeFileData(arraytype, datafile, pkgname = NULL, comparewithcdf = FALSE)
```

Arguments

arraytype	Character. Array type (e.g. 'HG-U133A')
datafile	Character with the filename of the input data file, or a connection (see example). If omitted a default name is constructed from arraytype (for details you will need to consult this function's source code).
pkgname	Character. Package name. If NULL the name is derived from arraytype.
comparewithcdf	Logical. If TRUE, run a consistency check against a CDF package of the same name (what used to be Laurent's "extraparanoia".)

Details

This function serves as an interface between the (1) representation of array probe information data in the packages that are generated by [makeProbePackage](#) and (2) the vendor- and possibly version-specific way the data are represented in datafile.

datafile is a tabulator-separated file with one row per probe, and column names 'Probe X', 'Probe Y', 'Probe Sequence', and 'Probe.Set.Name'. See the vignette for an example.

Value

A list with three components

dataEnv	an environment which contains the data frame with the probe sequences and the other probe data.
symVal	a named list of symbol value substitutions which can be used to customize the man pages. See createPackage .
pkgname	a character with the package name; will be the same as the function parameter pkgname if it was specified; otherwise, the name is constructed from the parameter arraytype.

See Also

makeProbePackage

Examples

```
if (length(list.files(path = ".", pattern = "*.CEL")) != 0){
  ## Example using the "Mouse430 2.0" chip-type

  ## Input the clean name for the given chip:
  chip <- "mouse4302"

  ## Input the .probe_tab file, as generated using the internal function:
  ## IVT3primePBuilder()

  probedata <- "GCSs.mouse4302.probeFile.probe_tab"

  ## Run function:
  get3primeIVTprobeFileData(arraytype = chip, datafile = probedata)
}
```

getClariomSprobeFileData

Read a data file describing the probe sequences on an Affymetrix genechip

Description

Read a data file describing the probe sequences on an Affymetrix genechip

Usage

```
getClariomSprobeFileData(arraytype, datafile, pkgname = NULL, comparewithcdf = FALSE)
```

Arguments

arraytype	Character. Array type (e.g. 'HG-U133A')
datafile	Character with the filename of the input data file, or a connection (see example). If omitted a default name is constructed from arraytype (for details you will need to consult this function's source code).
pkgname	Character. Package name. If NULL the name is derived from arraytype.
comparewithcdf	Logical. If TRUE, run a consistency check against a CDF package of the same name (what used to be Laurent's "extraparanoia".)

Details

This function serves as an interface between the (1) representation of array probe information data in the packages that are generated by [makeProbePackage](#) and (2) the vendor- and possibly version-specific way the data are represented in datafile.

datafile is a tabulator-separated file with one row per probe, and column names 'Probe X', 'Probe Y', 'Probe Sequence', and 'Probe.Set.Name'. See the vignette for an example.

Value

A list with three components

dataEnv	an environment which contains the data frame with the probe sequences and the other probe data.
symVal	a named list of symbol value substitutions which can be used to customize the man pages. See createPackage .
pkgname	a character with the package name; will be the same as the function parameter pkgname if it was specified; otherwise, the name is constructed from the parameter arraytype.

See Also

[makeProbePackage](#)

Examples

```
if (length(list.files(path = ".", pattern = "*.CEL")) != 0){
  ## Example using the "Clariom S mouse" chip-type

  ## Input the clean name for the given chip:
  chip <- "clarionmouse"

  ## Input the .probe_tab file, as generated using the internal function:
  ## ClarionSpFBuilder()

  probedata <- "GCSs.clarionmouse.probeFile.probe_tab"

  ## Run function:
  getClariomSprobeFileData(arraytype = chip, datafile = probedata)
}
```

getWTgeneexonprobeFileData

Read a data file describing the probe sequences on an Affymetrix genechip

Description

Read a data file describing the probe sequences on an Affymetrix genechip

Usage

```
getWTgeneexonprobeFileData(arraytype, datafile, pkgname = NULL, comparewithcdf = FALSE)
```

Arguments

arraytype	Character. Array type (e.g. 'HG-U133A')
datafile	Character with the filename of the input data file, or a connection (see example). If omitted a default name is constructed from arraytype (for details you will need to consult this function's source code).

pkgname Character. Package name. If NULL the name is derived from arraytype.

comparewithcdf Logical. If TRUE, run a consistency check against a CDF package of the same name (what used to be Laurent's "extraparanoia".)

Details

This function serves as an interface between the (1) representation of array probe information data in the packages that are generated by [makeProbePackage](#) and (2) the vendor- and possibly version-specific way the data are represented in datafile.

datafile is a tabulator-separated file with one row per probe, and column names 'Probe X', 'Probe Y', 'Probe Sequence', and 'Probe.Set.Name'. See the vignette for an example.

Value

A list with three components

dataEnv an environment which contains the data frame with the probe sequences and the other probe data.

symVal a named list of symbol value substitutions which can be used to customize the man pages. See [createPackage](#).

pkgname a character with the package name; will be the same as the function parameter pkgname if it was specified; otherwise, the name is constructed from the parameter arraytype.

See Also

[makeProbePackage](#)

Examples

```
if (length(list.files(path = ".", pattern = "*.CEL")) != 0){
## Example using the "Mouse Gene 1.0-ST v1" chip-type

## Input the clean name for the given chip:
chip <- "mogene10stv1"

## Input the .probe_tab file, as generated using the internal function:
## WTgeneexonPFBuilder()

probedata <- "GCSs.mogene10stv1.probeFile.probe_tab"

## Run function:
getWTgeneexonprobefileData(arraytype = chip, datafile = probedata)
}
```

getXTAprobeFileData *Read a data file describing the probe sequences on an Affymetrix genechip*

Description

Read a data file describing the probe sequences on an Affymetrix genechip

Usage

```
getXTAprobeFileData(arraytype, datafile, pkgname = NULL, comparewithcdf = FALSE)
```

Arguments

arraytype	Character. Array type (e.g. 'HG-U133A')
datafile	Character with the filename of the input data file, or a connection (see example). If omitted a default name is constructed from arraytype (for details you will need to consult this function's source code).
pkgname	Character. Package name. If NULL the name is derived from arraytype.
comparewithcdf	Logical. If TRUE, run a consistency check against a CDF package of the same name (what used to be Laurent's "extraparanoia".)

Details

This function serves as an interface between the (1) representation of array probe information data in the packages that are generated by [makeProbePackage](#) and (2) the vendor- and possibly version-specific way the data are represented in datafile.

datafile is a tabulator-separated file with one row per probe, and column names 'Probe X', 'Probe Y', 'Probe Sequence', and 'Probe.Set.Name'. See the vignette for an example.

Value

A list with three components

dataEnv	an environment which contains the data frame with the probe sequences and the other probe data.
symVal	a named list of symbol value substitutions which can be used to customize the man pages. See createPackage .
pkgname	a character with the package name; will be the same as the function parameter pkgname if it was specified; otherwise, the name is constructed from the parameter arraytype.

See Also

[makeProbePackage](#)

Examples

```

if (length(list.files(path = ".", pattern = "*.CEL")) != 0){
## Example using the "MTA_1-0" chip-type:

## Input the clean name for the given chip:
chip <- "mta10"

## Input the .probe_tab file, as generated using the internal function:
## ClariomDXTApFBuilder()

probedata <- "GCSs.mta10.probeFile.probe_tab"

## Run function:
getXTAprobeFileData(arraytype = chip, datafile = probedata)
}

```

mismatch

Calculates mismatch values for probes

Description

This internally called function calculates the background correction for each probe based on the median intensity of all background probes with the same GC-content of as the target probe in question

Usage

```
mismatch(probes, bgp, intensity)
```

Arguments

probes	probe indices for target probes. Each probe index contains the gc-content of the probe
bgp	contains probe location (indices), GC-content, and annotations of the background probes of a given chip type. For WT-type arrays, the bgp consists of 16,943 antigenomic background probes. For 3' IVT arrays, the mismatch (MM) probes are used to calculate the bgp list in both methods
intensity	The intensities value of the bgp probes as read in from the .CEL file

Details

This internally called function calculates the probe background correction based on the median intensity of all background probes with the same gc-content of as the target probe in question

Value

`mismatch` returns a numeric vector containing the gc-content based background correction for every probe included in the analysis

Examples

```

if (length(list.files(path = ".", pattern = "*.CEL")) != 0){

#Example of input, as the function would be called internally:
mismatch(probes, bgp, intensity)
}

```

normalize

Normalization of GCS-score values

Description

Normalizes the GCS-score values using all scores within 3*SD of the mean. This normalization step occurs after the probes have been tallied and grouped into probe_ids, according to the method (probeset_id for exon-level or transcription_cluster_id for gene-level)

Usage

```
normalize(Score)
```

Arguments

Score	The unnormalized GCS-score values (grouped and tallied according to the method selection) that are generated in the computeScore function
-------	---

Value

normalize Returns a numeric vector containing normalized GCS-score values for every probe_id grouping included in the analysis

Examples

```

if (length(list.files(path = ".", pattern = "*.CEL")) != 0){

#Example of input, as the function would be called internally:
normalize(Score)
}

```

rawScore

Calculates the rawScore values

Description

Calculates rawScore values based on differences between the two background corrected arrays in a given GCS-score analysis (e.g. CEL_1 vs. CEL_2), using the internally generated Statistical Difference Threshold (SDT) values.

Usage

```
rawScore(diff1, diff2, SDT1, SDT2)
```

Arguments

diff1	The gc-background-corrected values for the probe intensities on the 1st array
diff2	The gc-background-corrected values for the probe intensities on the 2nd array
SDT1	The internally calculated Statistical Difference Threshold ($SDT=4*rawQ*SF$) for the 1st array
SDT2	The internally calculated Statistical Difference Threshold ($SDT=4*rawQ*SF$) for the 2nd array

Value

rawScore returns a numeric vector containing the raw, ungrouped scores for every probe grouping included in the analysis (as determined by method)

Examples

```
if (length(list.files(path = ".", pattern = "*.CEL")) != 0){
  #Example of input, as the function would be called internally:
  rawScore(diff1, diff2, SDT1, SDT2)
}
```

zoneRQ

Calculates the zone-based RawQ values

Description

This internally called function calculates the zone-based RawQ values. RawQ is a measure of the noise within a given zone on a microarray chip. This noise value is used in the error model contained in the GCS-score algorithm

Usage

```
zoneRQ(DT, affyCel, trim)
```

Arguments

DT	Internally generated data.table containing the .CEL data, generated from the list that is created by the affxparser package
affyCel	The .CEL file data, in list structure, as read in using the readCel function included in the affxparser package
trim	The internal setting for the trimmed mean of every probe grouping on the array. For 3' IVT arrays, the trim is set to 0.02 by default. For all newer WT-type arrays, the trim is set to 0.04 by default

Value

zoneRQ returns a numeric vector containing zone-based rawQ values for a given array

Examples

```
if (length(list.files(path = ".", pattern = "*.CEL")) != 0){  
  
#Example of input, as the function would be called internally:  
zoneRQ(DT, affyCel, trim)  
}
```

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