Package ‘affypdnn’

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Title Probe Dependent Nearest Neighbours (PDNN) for the affy package
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Depends R (>= 2.13.0), affy (>= 1.5)
Suggests affydata, hgu95av2probe
Description The package contains functions to perform the PDNN method described by Li Zhang et al.
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R topics documented:

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Description

A wrapper to perform the PDNN method.
Usage

```r
pdnn.scalevalue.exprSet(eset, scale.to=500)
expressopdnn(abatch,
  # background correction
  bg.correct = FALSE,
  bgcorrect.method = NULL,
  bgcorrect.param = list(),
  # normalize
  normalize = FALSE,
  normalize.method = NULL,
  normalize.param = list(),
  pmcorrect.method = c("pdnn", "pdnnpredict"),
  # pdnn
  findparams.param = list(),
  # expression values
  summary.subset = NULL,
  # PDNN expression values scaling
  eset.normalize = TRUE,
  scale.to = 500,
  # misc.
  verbose = TRUE)
```

Arguments

- **abatch**: object of `AffyBatch-class`
- **bg.correct**: a boolean to express whether background correction is wanted or not.
- **bgcorrect.method**: the name of the background adjustment method.
- **bgcorrect.param**: a list of parameters for bgcorrect.method (if needed/wanted).
- **eset**: an object of `ExpressionSet-class`.
- **normalize**: normalization step wished or not.
- **normalize.method**: the normalization method to use.
- **normalize.param**: a list of parameters to be passed to the normalization method (if wanted).
- **pmcorrect.method**: the name of the PM adjustment method (only two choices here, default to 'pdnn').
- **findparams.param**: a list of parameters to be passed to `find.params.pdnn`
- **eset.normalize**: is any normalization step on expression values to be performed.
- **scale.to**: a value to scale against.
- **summary.subset**: a list of 'affyids'. If NULL, then an expression summary value is computed for everything on the chip.
- **verbose**: logical value. If TRUE it writes out some messages.
find.params.pdnn

Details

expressopdnn is very similar to expresso. It is mainly a wrapper around the pre-processing steps ‘background correction’, ‘normalization’, ‘perfect match correction’ and the PDNN method to compute expression values (see the first reference for more details about the preprocessing steps and and the second reference for further details about the PDNN method).

The wrapper expresso has no way to handle easily the computation of chip-wide results that have to be used during the computeExprSet step. An easy way to overcome this was to write this simple wrapper.

pdnn.scalevalue is performed after the expression values have computed to somehow ‘normalize’ the values between different chips. When setting normalize to TRUE this step might be considered unnecessary (and the eset.normalize set to FALSE).

Value

An object of ExpressionSet-class, with an attribute pps.warnings as returned by the method computeExprSet.

See Also

expresso and generateExprVal.method.pdnn

Examples

```r
## load pre-computed parameters
data(hgu95av2.pdnn.params)

library(affydata)
data(Dilution)

## one CEL to go faster
afbatch <- Dilution[, 1]

## Take only few IDs (the 10 first)
ids <- ls(getCdfInfo(afbatch))[1:10]
eset <- expressopdnn(afbatch, bg.correct=FALSE, normalize=FALSE, findparams.param=list(params.chiptype=hgu95av2.pdnn.params, give.warnings=FALSE), summary.subset=ids)
```

find.params.pdnn

A function to find the experiment specific PDNN parameters

Description

A function to find the parameters specific to the chips in an AffyBatch object.

Usage

```r
find.params.pdnn(abatch, params.chiptype, optim.method = "BFGS", verbose = TRUE, give.warnings=TRUE)
```
Arguments

abatch an instance of AffyBatch-class.
params.chiptype chip-type specific parameters (see details)
optim.method method for the optimization function optim. When FALSE, a steepest-descent method of our own is used.
verbose verbosity (TRUE or FALSE)
give.warnings report probeset IDs in the abatch that could not be found in the params.chiptype

Details

This function fits PDNN parameters that are specific to experimental values. The parameters common to all the chips of a certain type are returned by the function pdnn.params.chiptype. If NULL, the parameter files included in the package will be used whenever possible...

Value

A list of

lambda The lambda’s
Bs The B’s
Ns The N’s
Fs The F’s

References

Li Zhang, Michael F. Miles and Kenneth D. Aldape - A model of molecular interactions on short oligonucleotide arrays, 2003, Nature Biotech., vol. 21, n.7

See Also

pdnn.params.chiptype, generateExprVal.method.pdnn

Examples

## load a chip-specific parameter file
## (as returned by the function pdnn.params.chiptype)
data(hgu95av2.pdnn.params)

## load experimental data
library(affydata)
data(Dilution)

## one CEL to go faster
afbatch <- Dilution[, 1]
params <- find.params.pdnn(afbatch, hgu95av2.pdnn.params, optim.method = FALSE, give.warnings=FALSE)
**generateExprVal.method.pdnn**

*Compute PM correction and summary expression value*

---

**Description**

Computes PM correction and summary expression value with PDNN method.

**Usage**

```r
pmcorrect.pdnn(object, params, gene=NULL, gene.i=NULL, params.chiptype=NULL, outlierlim=3, callingFromExpresso=FALSE)
pmcorrect.pdnnpredict(object, params, gene=NULL, gene.i=NULL, params.chiptype=NULL, outlierlim=3, callingFromExpresso=FALSE)
generateExprVal.method.pdnn(probes, params)
```

**Arguments**

- `object` object of `ProbeSet`
- `probes` matrix of PM-corrected signals (should be coming out of `pmcorrect.pdnn`).
- `params` experiments specific parameters.
- `gene` gene (probe set) ID (from which the `gene.i` would be derived).
- `gene.i` gene index (see details).
- `params.chiptype` chip-specific parameters.
- `outlierlim` threshold for tagging a probe as an outlier.
- `callingFromExpresso` is the function called through expresso. DO NOT play with that.

**Details**

Only one of `gene`, `gene.i` should be specified. For most the users, this is `gene`. `pmcorrect.pdnn` and `pmcorrect.pdnnpredict` return what is called GSB and GSB + NSB + B in the paper by Zhang Li and collaborators.

**Value**

`pmcorrect.pdnn` and `pmcorrect.pdnnpredict` return a matrix (one row per probe, one column per chip) with attributes attached. `generateExprVal` returns a list:

- `exprs` expression values
- `se.exprs` se expr. val.

**See Also**

`pdnn.params.chiptype`
Examples

data(hgu95av2.pdnn.params)
library(affydata)
data(Dilution)

## only one CEL to go faster
abatch <- Dilution[, 1]

## get the chip specific parameters
params <- find.params.pdnn(abatch, hgu95av2.pdnn.params)

## The thrill part: do we get like in the Figure 1-a of the reference?
par(mfrow=c(2,2))
#ppset.name <- sample(featureNames(abatch), 2)
ppset.name <- c("41206_r_at", "31620_at")
ppset <- probeset(abatch, ppset.name)
for (i in 1:2) {
  #ppset[[i]] <- transform(ppset[[i]], fun=log) # take the log as they do
  probes.pdnn <- pmcorrect.pdnnpredict(ppset[[i]], params,
                                       params.chiptype=hgu95av2.pdnn.params)
  #probes.pdnn <- log(probes.pdnn)
  plot(ppset[[i]], main=paste(ppset.name[i], "(raw intensities)")
       matplotProbesPDNN(probes.pdnn, main=paste(ppset.name[i], "(predicted intensities)"))
}

## pick the 50 first probeset IDs
## (to go faster)
ids <- featureNames(abatch)[1:100]

## compute the expression set (object of class 'ExpressionSet')
eset <- computeExprSet(abatch, pmcorrect.method="pdnn",
                        summary.method="pdnn", ids=ids,
                        summary.param = list(params, params.chiptype=hgu95av2.pdnn.params))


hgu133a.pdnn.params  

Chip-type specific data

Description

Chip-type specific data structure.

Usage

data(hgu95av2.pdnn.params)

Format

The format is a list:

**Eg** environment (one entry per dinucleotide)

**Wg** numerical vector.
**En** environment (one entry per dinucleotide)

**Wn** numerical vector.

**gene.Sn** list (one entry per affyID)

**gene.Sg** list (one entry per affyID)

**gene.xy** list (one entry per affyID)

**params.gene** environment

**Details**

These chip-specific data structures are generated from the data files made available by the author of the PDNN paper (see the section source). They are stored as data to save some computation time. The data structures were made using the function `pdnn.params.chiptype`. The data files are included in the the directory ‘data’ of the package.

**Note**

To lower the size of the package, the only chip-specific data structures included in the package is the one for HG-U95Av2.

**Source**

Li Zhang, Michael F. Miles and Kenneth D. Aldape - A model of molecular interactions on short oligonucleotide arrays, 2003, Nature Biotech., vol. 21, n.7

**Examples**

```r
## give the path the original energy parameter files included in the package
dataset <- list.files(system.file("exampleData", package="affypdnn"),
  "^pdnn-energy-parameter_", full.names=TRUE)
```

**matplotProbesPDNN**  
Plot the PDNN computed probe intensities

**Description**

Plot the probe intensities as computed by `pmcorrect.pdnn` or `pmcorrect.pdnnpredict`

**Usage**

```r
matplotProbesPDNN(x, type="l", ...)
```

**Arguments**

- **x**: a matrix (and attributes) as returned by `pmcorrect.pdnn` or `pmcorrect.pdnnpredict`.
- **type**: type of plot (same as in `matplot`)
- **...**: optional arguments to be passed to `matplot`

**Details**

The crosses are the probe intensities which are considered ‘ok’ by the outlier detection part of the algorithm, while the circles are the ones considered ‘outliers’
pdnn.params.chiptype

Value

Only used for its side-effect.

See Also

pmcorrect.pdnn and pmcorrect.pdnnpredict

Examples

# see 'pmcorrect.pdnn'

params.dilution  Parameters for the Dilution dataset

Description

PDNN parameters for the Dilution dataset

Usage

data(params.dilution)

Format

The format is: List of 6 $ lambda :List of 12625 (probesets) ... $ Bs : num [1:4] 111.9 57.3 120.5 50.1 $ Ns : num [1:4] 2967 2998 2992 2999 $ Fs : num [1:4] 0.607 0.662 0.600 0.656 $ names.abatch: chr [1:12625] "1000\_at" "1001\_at" "1002\_f\_at" ... $ names.i : int [1:12625] 1 2 3 4 5 6 7 8 9 10 ...

Details

These data are provided to reduce the time needed to run the vignette.

Examples

data(params.dilution)

pdnn.params.chiptype  A function to fit PDNN parameters

Description

A function to fit PDNN parameters that are chip-type specific

Usage

pdnn.params.chiptype(energy.param.file, probes.file = NULL, probes.pack = NULL, probes.data.frame = NULL, seq.name, x.name, y.name, affyid.name, verbose = TRUE)
Arguments

energy.param.file
  Path to the energy data file (see details)

probes.file
  Path to the probe files (see details)

probes.pack
  Name of the probe pack (see details)

probes.data.frame
  A data.frame

seq.name, x.name, y.name, affyid.name
  The names of the columns in the data.frame from probes.pack or probes.file for the probe sequences, the X positions, the Y positions and the probe set ID respectively

verbose
  verbosity (TRUE or FALSE)

Details

The parameters probes.file, probes.pack and probes.data.frame are mutually exclusive. The function fits PDNN parameters that are specific to chip-types (hence specific to the probe sequences). It requires data files like the one found on Li Zhang’s web page: (http://odin.mdacc.tmc.edu/~zhangli/PerfectMatch/) This should be computed once for all for a given chip type. Computed values for the chips are included in the package. This allows ‘automagic’ use of them when these chip types are used (as done in the function expressopdnn).

Value

A list of:

Eg
  environment. One entry per dinucleotide.

Wg
  numerical vector

En
  environment. One entry per dinucleotide.

Wn
  numerical vector

params.gene
  environment. One entry per gene, each entry is a list of elements Sg, Sn, xy and gene.i

warning

The X and Y positions in the data.frame are expected to be original ones in the Affymetrix files (starting at zero). They are offset by one within this function.

See Also

find.params.pdnn

Examples

if (interactive()) {
  energy.file <- system.file("exampleData", "pdnn-energy-parameter_hg-u95av2.txt", package="affypdnn")

  params.chiptype <- pdnn.params.chiptype(energy.file, probes.pack="hgu95av2probe")
}
transform.ProbeSet  

A function to transform a `ProbeSet`

Description

A function to transform the PMs and MM in a `ProbeSet`.

Usage

```r
## S3 method for class 'ProbeSet'
transform(~data~, fun = I, ...)
```

Arguments

- `~data~` object of `ProbeSet`-class.
- `fun` a function. The identity function by default.
- `...` optional arguments for `fun`.

Details

The function `fun` is applied to the slots `pm` and `mm`. The function `vsnh` in the package `vsn` is a recommended argument for `fun`.

Value

An object of class `ProbeSet`.

Note

This function should make to the package `affy` for the version 1.4.x.

Author(s)

Laurent

Examples

```r
library(affydata)
data(Dilution)

ppset.name <- sample(featureNames(Dilution), 1)
ppset <- probeset(Dilution, ppset.name)[[1]]
ppset.log <- transform(ppset, fun=log)

par(mfrow=c(1,2))
plot(ppset)
plot(ppset.log)
```
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