

affyILM

April 20, 2011

ILM-class

Class to contain the results of an ilm calculation

Description

S4 object to contain background intensities, results from parameter fit and concentrations

Slots

intens: A "matrix" of size (number of probes) x (2x number of CEL-files). A set of two columns corresponds to one CEL-file where the first column contains the raw PM and the second one the background intensities per feature.

concs: A "matrix" of size (number of probe sets) x (number of CEL-files) holding the concentration per probe set (picoMolar) calculated according to the Langmuir model.

parameter: A "matrix" holding the 50 optimized parameter values/fitted parameters for each CEL-file (number of columns)

satLim: Is the "numeric" saturation limit of the intensities of the Langmuir Isotherm, i.e. where the concentration is high or the probe-target binding free energies are large. The default value of `satLim` is 10000.

Methods

[Subset

getIntens Get background intensity (of a particular probe set)

getConcs Get concentration in pM

getParams Optimized parameters

plotIntens Plot PM and calculated background intensities per probe set

Author(s)

Myriam Kroll, Fabrice Berger and Enrico Carlon

Examples

```
showClass("ILM")
```

Description

These methods allow to access the results of the function `ilm` stored in an object of type `ILM`.

Usage

```
getIntens(object, y)
getConcs(object, y)
getParams(object)
```

Arguments

<code>object</code>	An object of type <code>ILM</code>
<code>y</code>	A character string or vector of probe set name(s). If <code>y</code> is missing, values are retrieved for all probesets.

Details

A linear function is used to approximate the shape of the background intensities. By means of the linear least square method the 50 parameters characterizing this function are determined. The optimized set of parameters can be accessed using `getParams()`.

`getIntens()` is used to access the calculated background intensities.

The concentrations are calculated on behalf of the Langmuir model. For each probe (of a probeset) the concentration is estimated in picoMolar. Its median value is then considered as the concentration/probeset. The results can be accessed via `getConcs()`.

If `y` is missing, the results for all probe sets are shown.

Value

A matrix of dimension (number of probes) x (2x(number of CEL-files)) for `getIntens()` A matrix of dimension 50 x (number of CEL-files) and for `getParams()` A matrix of dimension (number of probesets) x (number of CEL-files) for `getConcs()`

An object of the class `ILM` when subsetting [

Author(s)

Myriam Kroll, Fabrice Berger and Enrico Carlon

See Also

`ILM`

Examples

```
## Locate and read in CEL-file
file1 <- system.file("rawData","FusionSDK_HG-Focus","HG-Focus","2.Calvin","HG-Focus-1-121")
## Calculation of background estimates and expression values (concentrations)
result <- ilm(file1)
## Background intensities of all probes
getIntens(result)
## Background intensities for one or more probesets
getIntens(result,"203561_at")
getIntens(result,c("203561_at","40359_at"))

## Get concentrations of all probesets
getConcs(result)
## Get concentrations (in picoMolar)
getConcs(result,"203561_at")
getConcs(result,c("203561_at","40359_at"))

## Parameter
getParams(result)

## Subsetting
result["203561_at"]
```

 ilm

affyILM

Description

This function is the working horse of the package and is used as an overall function to calculate the background intensities as well as the concentrations.

Usage

```
result <- ilm(celfiles, threshold = 350, satLim = 10000)
```

Arguments

<code>celfiles</code>	filenames of CEL-files
<code>threshold</code>	Criterion to filter probes used for background calculation. By default set to 350,~i.e.~use only probes with intensity values below threshold value.
<code>satLim</code>	Saturation Limit of the Langmuir isotherm (determined by scanner). Default value 10000.

Details

A linear function with 50 parameters is used to describe the background intensity. On behalf of the linear-least square method these 50 parameters are determined of which 18 reflect the influence of the neighboring spots on the background intensity of a particular feature. The next 16 parameters incorporate the nearest-neighbor free energies (sequence dependence) with and the last 16 parameters modify the strength of the sequence dependence based upon the position of a nucleotide along the sequence. The parameters are determined through the linear least square method making use of a standard algorithm implementing singular value decomposition. (SVD).

Value

An object of class [ILM](#)

Note

The AffymetrixDataTestFiles-package must be installed to run examples.

Author(s)

Myriam Kroll, Fabrice Berger, Gerard Barkema and Enrico Carlon

References

KM Kroll, E Carlon and GT Barkema (2009), Linear method for fast background subtraction in oligonucleotide microarrays, *Algorithms for Molecular Biology* 2009, 4:15

G Mulders, GT Barkema and E Carlon, Inverse Langmuir method for oligonucleotide microarray analysis, *BMC Bioinformatics* (2009) 10, 64

E. Carlon and T. Heim, Thermodynamics of RNA/DNA hybridization in high-density oligonucleotide microarrays, *Physica A* (2006), 362, 433

See Also

[getIntens](#), [getConcs](#)

Examples

```
## Locate and read in CEL-file
file1 <- system.file("rawData", "FusionSDK_HG-Focus", "HG-Focus", "2.Calvin", "HG-Focus-1-121")
## Calculation of background estimates and expression values (concentrations)
result <- ilm(file1)
## show all
show(result)

## per probeset (example probeset randomly chosen)
result["AFFX-r2-P1-cre-5_at"]

## Analysis of two files
file2 <- system.file("rawData", "FusionSDK_HG-Focus", "HG-Focus", "2.Calvin", "HG-Focus-2-121")
result2 <- ilm(c(file1, file2))
```

plotIntens

plotIntens

Description

Plot the PM intensity and the calculated background of one probe set.

Usage

```
plotIntens(object, y, z, ...)
```

Arguments

<code>object</code>	An object of type ILM
<code>y</code>	A probe set
<code>z</code>	The name of a sample
<code>...</code>	Graphical parameters can be given as arguments to par

Details

`plotIntens` plots one graph for each CEL-file. Note that it is only possible to plot one probe set at a time (if `y` (or `z`) is a vector, only the first value is used). If `y` is missing, no plot is output. If `z` is missing, the probeset `y` of first CEL-file is used by default.

Author(s)

Myriam Kroll and Fabrice Berger

See Also

[ILM](#)

Examples

```
file1 <- system.file("rawData","FusionSDK_HG-Focus","HG-Focus","2.Calvin","HG-Focus-1-121502.CEL")
file2 <- system.file("rawData","FusionSDK_HG-Focus","HG-Focus","2.Calvin","HG-Focus-2-121502.CEL")
result2 <- ilm(c(file1,file2))
## plot output
plotIntens(result2,"203561_at","HG-Focus-1-121502.CEL")
```

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