

Package ‘saturation’

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Type Package

Title Combining multiple laser scans of microarrays by means of a two-way ANOVA model

Version 1.0

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Description The main function of the saturation package is the `cms2a` function. This function can be used to correct the microarray saturated spots obtained at high PMT voltage by using the corresponding spots acquired at lower PMT voltage. The `cms2a` algorithm is based on a two-way ANOVA model and on a maximum likelihood estimation of the scanner optical bias.

License GPL-2

LazyLoad yes

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saturation-package	<i>Combining multiple laser scans of spotted microarrays by means of a two-way ANOVA model.</i>
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Description

The main function of the saturation package is `cms2a`, an algorithm which combines microarray data acquired at multiple PMT voltage to correct saturated spots obtained at high PMT Voltage. When microarray data are acquired at low PMT Voltage, spots foreground tend to be lower than the local background. On the other hand, data acquired at higher PMT voltage suffer from saturation. A solution is to scan the microarray at different PMT Voltage and to use `cms2a` to correct saturated spot acquired high PMT voltage.

Details

```

Package:    saturation
Type:      Package
Version:    1.0
Date:      2011-05-26
License:    GPL-2?
LazyLoad:  yes

```

The package contains the msc2a function and the MAQCEPPS3A1 data set.

Author(s)

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See Also

multiscan

Examples

```

data(MAQCEPPS3A1)
corrected <- cms2a(MAQCEPPS3A1$foreground,MAQCEPPS3A1$background)

```

cms2a

Combining multiple scan by means of a two-way ANOVA model

Description

cms2a is an algorithm which combines microarray data acquired at multiple PMT voltage to correct saturated spots obtained at high PMT Voltage. When microarray data are acquired at low PMT Voltage, spots foreground tend to be lower than the local background. On the other hand, data acquired at higher PMT voltage suffer from saturation. A solution is to scan the microarray at different PMT Voltage and to use cms2a to correct saturated spot acquired high PMT voltage.

Usage

```
cms2a(foreground, background)
```

Arguments

foreground	a data frame which contain spots foreground intensities acquired at different PMT voltage.Each line corresponds to a spot and each column corresponds to a PMT voltage. The first column corresponds to the lower PMT voltage while successive columns correspond to increasing PMT voltage
background	a data frame which contain spots foreground intensities acquired at different PMT voltage.Each line corresponds to a spot and each column corresponds to a PMT voltage. The first column corresponds to the lower PMT voltage while successive columns correspond to increasing PMT voltage

Value

a list which contain the spot foreground intensities acquired at high PMT voltage corrected for saturation problem and the spot local background intensities acquired at high PMT voltage

Author(s)

Jerome Amrboise

References

Combining multiple laser scans of spotted microarrays by means of a two-way ANOVA model

Examples

```
data(MAQCEPPS3A1)
corrected <- cms2a(MAQCEPPS3A1$foreground,MAQCEPPS3A1$background)
```

MAQCEPPS3A1	<i>Microarray intensities acquired at multiple PMT voltage generated from the MAQC project</i>
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Description

Data set generated on Eppendorf Microarray platform in Site 3 (sample A1) in the MAQC I project

Usage

```
data(MAQCEPPS3A1)
```

Format

List of 2 components:

1. foreground: A data.frame with foreground intensities. 1 row for each spot and 1 column for each PMT Voltage.
2. background: A data.frame with local background intensities. 1 row for each spot and 1 column for each PMT Voltage.

Details

Data set generated on Eppendorf Microarray platform in Site 3 (sample A1) in the MAQC I project

Source

GEO

References

The MicroArray Quality Control (MAQC) project shows inter- and intraplatform reproducibility of gene expression measurements

Examples

```
data(MAQCEPPS3A1)
```

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