

Package ‘dyebiasexamples’

July 11, 2024

Version 1.44.0

Date 2 March 2016

Title Example data for the dyebias package, which implements the GASSCO method.

Author Philip Lijnzaad and Thanasis Margaritis

Description Data for the dyebias package, consisting of 4 self-self hybridizations of self-spotted yeast slides, as well as data from Array Express accession E-MTAB-32

Maintainer Philip Lijnzaad <plijnzaad@gmail.com>

License GPL-3

Depends R (>= 1.4.1), marray, GEOquery

Suggests dyebias, convert, Biobase

URL http://www.holstegelab.nl/publications/margaritis_lijnzaad

biocViews ExperimentData, SAGEData, CGHData, MicroarrayData, TwoChannelData, ArrayExpress

git_url <https://git.bioconductor.org/packages/dyebiasexamples>

git_branch RELEASE_3_19

git_last_commit cf9bf87

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-07-11

Contents

data.raw	2
dyebias.geo2marray	3
dyebias.umcu.proper.estimators	4
Index	6

`data.raw`*Example data for the dyebias package*

Description

The dyebias-package, described in Margaritis et al. (2009) can be used to get rid of dye bias in two-colour microarrays. The `data.raw` and `data.norm` objects are used in its examples.

The objects represent four hybridizations of identical mRNA, with increasing Cy3 and Cy5 labeling percentages (identical per slide) and differently spiked-in external controls to judge the process of dyebias correction.

Usage

```
data(data.raw)
data(data.norm)
```

Format

The data uses the `marray`-package by Dudoit and Yang (2002). `data.raw` is a `marrayRaw` object, `data.norm` is a `marrayNorm` object derived from it by print-tip LOESS normalization. Neither is dyebias-corrected yet.

Details

The column `R.group` of `maInfo(maTargets(data.norm))` shows the details. Eg., `4%_2EC` indicates that the labeling (of both channels) was at 4%, and the external controls were spiked in at a concentration twice that of the green channel. See Margaritis et al. (2009) for details.

Note

The Tuteja data is also included in this package under the `(inst)/doc` directory, as this data is not proper `rda`, `tab` or `csv` data. For details, refer to the original publication and/or the `dyebias` vignette.

Author(s)

Philip Lijnzaad

Source

All accession numbers below refer to ArrayExpress (<http://www.ebi.ac.uk/microarray>).

This two-colour microarray data was obtained from identical mRNA extracts (protocol P-UMCU-37), spiked with external controls, dUTP-labeled with Cy3 and Cy5 (protocol P-UMCU-38). This was hybridized (protocol P-UMCU-39) onto self-spotted slides containing 70-mer oligonucleotides (2 replicates per oligo, Operon "Array-Ready", and including 2838 control features; protocol P-UMCU-34). Scanning was done with an Agilent G2565AA scanner (protocol P-UMCU-40) and images were quantified with BioDiscovery's ImaGene 7.x (protocol P-UMCU-42)

References

Margaritis, T., Lijnzaad, P., van-Leenen, D., Bouwmeester, D., Kemmeren, P., van-Hooff, S.R and Holstege, F.C.P. (2009). Adaptable gene-specific dye bias correction for two-channel DNA microarrays. *Molecular Systems Biology*, submitted

Dudoit, S. and Yang, Y.H. (2002) Bioconductor R packages for exploratory analysis and normalization of cDNA microarray data. In: Parmigiani, G., Garrett, E.S. , Irizarry, R.A., and Zeger, S.L. (eds.) *The Analysis of Gene Expression Data: Methods and Software*, New-York: Springer

Examples

```
data(data.raw)
data(data.norm)
```

dyebias.geo2marray *convenience function to convert GEO objects to marray objects*

Description

convenience function to convert GEO objects to marray objects

Arguments

gse	GSE data set
slide.ids	Return only the slides with these ids. If NULL, return all.
type	what to extract; must be either "norm" or "raw".
gene.selector	function(table) acting on Table(GPL) giving back an index with the rows considered to be genes.
reporterid.name	column containing the reporter.id, in Table(gpl).
cy3.name	The column name containing the factor value for the Cy3 (green) channel
cy5.name	The column name containing the factor value for the Cy5 (red) channel
R.name	column name for extracting the R data from Table(gsm)
G.name	column name for extracting the G data from Table(gsm)
M.name	column name for extracting the M data from Table(gsm)
A.name	column name for extracting the A data from Table(gsm)
Rf.name	column name for extracting the Rf data from Table(gsm)
Gf.name	column name for extracting the Gf data from Table(gsm)
Rb.name	column name for extracting the Rb data from Table(gsm)
Gb.name	column name for extracting the Gb data from Table(gsm)

Details

The XYZ.name mechanism is the same as that used in [read.marrayRaw](#); i.e. you specify the name of the column that contains the desired data.

Value

A full-fledged marrayRaw (if type was "raw") or marrayNorm (if type was "norm") is returned.

Note

At some point, this functionality should be merged into the convert package.

Author(s)

Philip Lijnzaad

References

Davis, S. and Meltzer, P.S (2007). GEOquery: a bridge between the Gene Expression Omnibus (GEO) and BioConductor. *Bioinformatics* 23, 1846–1847 (doi:10.1093/bioinformatics/btm254).

Dudoit, S. and Yang, Y.H. (2002) Bioconductor R packages for exploratory analysis and normalization of cDNA microarray data. In: Parmigiani, G., Garrett, E.S. , Irizarry, R.A., and Zeger, S.L. (eds.) *The Analysis of Gene Expression Data: Methods and Software*, New-York: Springer

Chen,S., de-Vries, M.A. and Bell, S.P. (2007) *Genes Dev.* 21, 2897–2907 "Orc6 is required for dynamic recruitment of Cdt1 during repeated Mcm2-7 loading" (doi:10.1101/gad.1596807)

Examples

```
## Not run:
## Running this example takes too much time; if you want that, see the
## second example in the vignette

## End(Not run)
```

```
dyebias.umcu.proper.estimators
```

Determine which spots should not be ruled out as slide bias estimators

Description

Some spots (reporters/probes) should not be used when estimating the slide bias. Typical examples are mitochondrial genes and spots known to cross-hybridize. This function finds the ones that are OK to use.

Arguments

reporter.info	A data.frame, one row per spot, with (at least) columns reporterId (e.g. gene id or oligo id) and any of the following characteristics: reporterGroup, chromosomeName, bioSeqType, crosshybRank and reporterSequence. They are used to get rid of reporters that are not suitable when estimating the slide bias.
verbose	Logical specifying whether to be verbose or not

Index

* **datasets**

data.raw, [2](#)

* **misc**

dyebias.geo2marray, [3](#)

dyebias.umcu.proper.estimators, [4](#)

data.norm (data.raw), [2](#)

data.raw, [2](#)

dyebias.apply.correction, [5](#)

dyebias.geo2marray, [3](#)

dyebias.umcu.proper.estimators, [4](#)

read.marrayRaw, [3](#)