

# Package ‘dyebiasexamples’

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

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**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

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**License** GPL-3

**Depends** R (>= 1.4.1), marray, GEOquery

**Suggests** dyebias, convert, Biobase

**URL** [http://www.holstegelab.nl/publications/margaritis\\_lijnzaad](http://www.holstegelab.nl/publications/margaritis_lijnzaad)

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

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

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## 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 | <i>convenience function to convert GEO objects to marray objects</i> |
|--------------------|----------------------------------------------------------------------|

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## Description

convenience function to convert GEO objects to marray objects

## Arguments

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

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dyebias.umcu.proper.estimators

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

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**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                                                                                                                                                                                                                                                                   |

## Details

This function is particular to the slides and database set-up at the Holstege lab, but might serve as inspiration.

## Value

Returns and index vector that can be used as the estimator `.subset`-argument to `dyebias.application.subset`.

**Author(s)**

Philip Lijnzaad &lt;p.lijnzaad@umcutrecht.nl&gt;

## 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

## See Also

dyebias.apply.correction

## Examples

[illegible]

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