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 hybrizations of self-spotted yeast slides, as well as data from Array Express accession E-MTAB-32

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Depends R (>= 1.4.1), marray, GEOquery

Suggests dyebias, convert, Biobase

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

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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 microarrray 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 speficying 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)

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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

```
### choose the estimators and which spots to correct:
estimator.subset <- dyebias.umcu.proper.estimators(maInfo(maGnames(data.norm)))

summary(estimator.subset)

### do the correction
## Not run:
   correction <- dyebias.apply.correction(data.norm=data.norm,
                                          iGSDBs = iGSDBs.estimated,
                                          estimator.subset=estimator.subset,
                                          application.subset = TRUE,
                                          verbose=TRUE)

## End(Not run)
```

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