beadarray: R classes and methods for Illumina bead-based data

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Introduction

beadarray is a Bioconductor package for the analysis of Illumina data. The main feature of the package is its ability to process raw data (text files and TIFFs) from BeadScan and store this information in convenient R classes. Access to this *bead-level data* offers users the choice between different image processing and background correction methods and allows for detailed quality assessments to be carried out for each array. The summarised intensities (*bead-summary data*) output by Illumina's BeadStudio software can also be imported using the *beadarray* package.

The documentation for this package is split into separate user guides: one for bead-level data and a second for bead-summary data. These documents may be accessed using the following commands:

```
library("beadarray")
beadarrayUsersGuide(topic="beadlevel")
beadarrayUsersGuide(topic="beadsummary")
```

Changes since Bioconductor 2.6 (beadarray 1.16)

There has been a major overhaul of *beadarray* since Bioconductor 2.6 with the intention of creating a more flexible package. Users now have more flexibility in the way quality assessment is performed at the bead-level and are allowed to modify the raw bead-level object. Summarisation is also more flexible and retrieval of annotation data can be performed from within the package. See the package vignettes for details and the package news for updates.

```
news(package="beadarray")
```

Companion packages to beadarray

In order to reduce the download size of *beadarray*, we have moved the example dataset to a Bioconductor data package (*beadarrayExampleData*) that can be downloaded in the usual way. An expanded dataset and more detailed commentary on the processing of BeadArray data is provided by the *BeadArrayUseCases* package. Finally, the *beadarray* package is also able to interact with various Illumina annotation packages in Bioconductor if they are installed.

```
source("http://www.bioconductor.org/biocLite.R")

biocLite(c("beadarrayExampleData", "beadarrayExampleData"))
```

Citing beadarray

If you use *beadarray* for the analysis or pre-processing of Illumina data please cite:

Dunning MJ, Smith ML, Ritchie ME, Tavaré S. *beadarray: R classes and methods for Illumina bead-based data*. Bioinformatics, 2007 Aug 15; 23(16):2183-4.

For recommendations on the low-level analysis of bead-level data, or if you make use of the spike-in data set available from

`http://www.compbio.group.cam.ac.uk/Resources/spike/`

please cite:

Dunning MJ, Barbosa-Morais NL, Lynch AG, Tavaré S, Ritchie ME. *Statistical issues in the analysis of Illumina data*. BMC Bioinformatics. 2008 Feb 6;9(1):85.

For a validation of the VST method (implemented in the *lumi* package) on the spike-in data set and a comparison of the results obtained from a full bead-level analysis, see

Dunning MJ, Ritchie ME, Barbosa-Morais NL, Tavaré S, Lynch AG. *Spike-in validation of an Illumina-specific variance-stabilizing transformation*. BMC Research Notes, 2008, 1:18.

If you use BASH to detect spatial artefacts, please cite

Cairns JM, Dunning MJ, Ritchie ME, Russell R, Lynch AG. *BASH: A tool for managing BeadArray spatial artefacts*. Bioinformatics, 2008, 15:24(24).

If you use the probe reannotation for Illumina expression arrays (used in the current Bioconductor annotation packages named *illuminaXXXXX.db*) please cite

Barbosa-Morais NL, Dunning MJ, Samarajiwa SA, Darot JF, Ritchie ME, Lynch AG, Tavaré S. *A re-annotation pipeline for Illumina BeadArrays: improving the interpretation of gene expression data.*. Nucleic Acids Research 2010 Jan;38(3)e17.Epub 2009 Nov 18.

Supplementary tables and supporting information for this annotation are available at

`http://www.compbio.group.cam.ac.uk/Resources/Annotation`.

1 Asking for help on beadarray

Wherever possible, please send all queries about *beadarray* to the Bioconductor mailing list at `bioconductor@stat.`. This will help maintain a searchable archive of questions and responses. When posting to the list, please include the commands you used along with the version of *beadarray* and `R` you are working with. Version information can be obtained by running the following command:

```
sessionInfo()
```

```
## R version 3.2.1 (2015-06-18)
## Platform: x86_64-apple-darwin10.8.0 (64-bit)
## Running under: OS X 10.6.8 (Snow Leopard)
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] knitr_1.10.5
##
## loaded via a namespace (and not attached):
## [1] BiocStyle_1.7.4 magrittr_1.5    formatR_1.2     tools_3.2.1     stringi_0.4-1
## [6] highr_0.5       stringr_1.0.0   evaluate_0.7
```