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 made on 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 two 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")
```

1 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. Epub 2007 Jun 22.

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.

Probe reannotation for Illumina expression arrays are available from:

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

If you make use of these, please cite:

Barbosa-Morais NL, Dunning MJ, Ritchie ME, Lynch AG, Tavaré S. *Reannotation of Illumina BeadArray probes improves the interpretation of gene expression data*. (in preparation).

2 Asking for help on beadarray

Wherever possible, please send all queries about beadarray to the Bioconductor mailing list at `bioconductor@stat.math.ethz.ch`. 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()
```