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

Mark Dunning and Matt Ritchie

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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:

```r
> 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:


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:


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:

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()