beadarray: R classess 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 the ability to read in an process the raw data from BeadScan (text files and tiffs) and store it in convenient R classes. Users may choose between different image processing and background correction methods. Alternatively, data which has been processed by Illumina's BeadStudio software may be read in (currently only single channel summary data can be imported).

The documentation for this package is split into two separate user guides for raw (bead level) data and summarised (bead summary) data. These documents may be found in the inst/doc directory of the downloaded beadarray folder, or can be downloaded from the bioconductor website.

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, 23(16):2183-4. Epub 2007 Jun 22.

2 Getting help with beadarray

Wherever possible, please send all queries about beadarray to the Bioconductor mailing list at `bioconductor@stat.math.ethz.ch`. This will help to maintain a searchable archive of questions and responses visible to all users of the package.