

# Package ‘BeadArrayUseCases’

April 11, 2019

**Version** 1.20.0

**Date** 2012-03-17

**Title** Analysing Illumina BeadArray expression data using Bioconductor

**Author** Mark Dunning, Wei Shi, Andy Lynch, Mike Smith, Matt Ritchie

**Description** Example data files and use cases for processing Illumina BeadArray expression data using Bioconductor

**Imports** beadarray (>= 2.3.18), limma, GEOquery

**Suggests** Biostrings, GenomicRanges, illuminaHumanv1.db, illuminaHumanv2.db, illuminaHumanv3.db

**Maintainer** Mike Smith <mike.smith@embl.de>

**License** GPL-2

**biocViews** MicroarrayData

**git\_url** <https://git.bioconductor.org/packages/BeadArrayUseCases>

**git\_branch** RELEASE\_3\_8

**git\_last\_commit** b369e83

**git\_last\_commit\_date** 2018-10-30

**Date/Publication** 2019-04-11

**R topics documented:**