The bladderbatch data User’s Guide

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The `bladderbatch` package contains gene expression data on 57 samples from a bladder cancer study [1] which have been normalized with RMA and pre-processed according to a previously defined protocol [2]. The data are in an expression set object with pData including the variables “sample”, “outcome”, “batch”, and “cancer”. The first variable is the sample number, the second variable is the outcome as defined in the original study, the third variable is a batch variable defined based on the date the microarrays were processed and the cancer variable is a simplified outcome grouping all the cancers together. The data can be accessed as follows:

```r
> library(bladderbatch)
> data(bladderdata)
> # Get the expression data
> edata = exprs(bladderEset)
> # Get the pheno data
> pdata = pData(bladderEset)
```

The data in this package are used as an example data set in the `sva` package.
References
