

# Package ‘charmData’

October 18, 2017

**Type** Package

**Title** An example dataset for use with the charm package

**Version** 1.12.0

**Date** 2010-10-13

**Author** Martin Aryee

**Maintainer** Martin Aryee <aryee@jhu.edu>

**Description** An example dataset for use with the charm package

**License** LGPL (>= 2)

**Depends** R(>= 2.11.0), charm, pd.charm.hg18.example

**biocViews** ExperimentData, MicroarrayData

**ZipData** no

**LazyLoad** yes

**NeedsCompilation** no

## R topics documented:

charmData-package . . . . . 1

**Index** 3

---

charmData-package      *An example dataset for the charm package*

---

## Description

This is a small example DNA methylation microarray dataset for use with the charm package. It contains Nimblegen xys (raw data) files for 8 samples and the corresponding sample description file.

## Author(s)

Martin Aryee <aryee@jhu.edu>

**Examples**

```
dataDir <- system.file("data", package="charmData")  
setwd(dataDir)  
dir()
```

# Index

charmData (charmData-package), [1](#)  
charmData-package, [1](#)