

# Package ‘charmData’

October 8, 2016

**Type** Package

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

**Version** 1.8.0

**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
<b>Index</b>	<b>3</b>

---

charmData-package	<i>An example dataset for the charm package</i>
-------------------	---

---

### 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](#)