

# Package ‘charmData’

February 14, 2019

**Type** Package

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

**Version** 1.19.0

**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

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

**git\_branch** master

**git\_last\_commit** ffa8cd

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

**Date/Publication** 2019-02-14

## 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](#)