

Example data for use with the flowFit package

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1 Data Introduction

This package provides two lightweight datasets for those wishing to try out the examples within the *flowFit* package.

The package contains two datasets:

1. PKH26data
2. QuahAndParish

2 Loading the data

The example datasets can be loaded using the `data` function.

```
> library(flowFitExampleData)
> data(PKH26data)
> PKH26data
```

A flowSet with 2 experiments.

```
An object of class 'AnnotatedDataFrame'  
  rowNames: NONPROL.FCS PROL.FCS  
  varLabels: PatientID GroupID ... name (6 total)  
  varMetadata: labelDescription  
  
column names(4): FSC-Height SSC-Height FL1-Height LOG  
  FL2-Height LOG
```

```
> data(QuahAndParish)  
> QuahAndParish
```

A flowSet with 4 experiments.

```
An object of class 'AnnotatedDataFrame'  
  rowNames: Fig 2a All CD4 T Nonstim.fcs Fig 2a CFSE CD4 T  
  Stim.fcs Fig 2a CPD CD4 T Stim.fcs Fig 2a CTV CD4 T  
  Stim.fcs  
  varLabels: Filename SampleType Stain CellType  
  varMetadata: labelDescription  
  
column names(13): FSC-A FSC-H ... <APC-A> <APC-Cy7-A>
```

```
>
```

3 Data creation

The following commands were used to create the QuahAndParish data included with this package.

```
> require(flowCore)  
> flowData <- read.flowSet(path = ".", phenoData = "annotationfig2.txt", transformationId="truncate")  
> wf <- workflow(flowData, name = "FACSCANTO LOG workflow")  
> trunTrans <- truncateTransform(transformationId="truncate", a=1)  
> tr <- transformList(c("<FITC-A>", "<PE-A>", "<PE-Cy5-A>", "<Alexa Fluor 405-A>", "<APC-A>"))  
> add(wf, tr)  
> logTrans <- logTransform(transformationId="log10-transformation", logbase=10, r=1,  
> tf <- transformList(c("<FITC-A>", "<PE-A>", "<PE-Cy5-A>", "<Alexa Fluor 405-A>", "<APC-A>"))
```

```
> add(wf, tf, parent="truncate")
> mDataLog <- Data(wf[["log"]])
>
```