

# Example data for use with the flowFit package

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## Contents

<b>1</b>	<b>Data Introduction</b>	<b>1</b>
<b>2</b>	<b>Loading the data</b>	<b>1</b>
<b>3</b>	<b>Data creation</b>	<b>2</b>

## 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:
 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:
 FSC-A FSC-H FSC-W SSC-A SSC-H SSC-W <FITC-A> <PE-A> <PE-Cy5-A> <Alexa Fluor 405-A> <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>", "<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>", "<A  
> add(wf, tf, parent="truncate")  
> mDataLog <- Data(wf[["log"]])  
>
```