Package ‘flowPloidyData’

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Title Example Flow Cytometry Data

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Description A collection of raw flow cytometry data for use in vignettes for the flowPloidy package.

License GPL-3

Encoding UTF-8

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VignetteBuilder knitr

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Contents

`flowPloidyData` *Example flow cytometry datasets from analysis of ploidy in plants.*

Description

A list of LMD files from analyses of the plant leaf tissue samples, co-chopped with standards with known GC (e.g., tomato, soybean etc.).

Usage

```
flowPloidyFiles()

fpBad()

fpVac()
```

Format

The function `flowPloidyFiles` returns a vector of filenames corresponding to the LMD files provided by this package. Individual elements of this vector (e.g., `flowPloidyFiles()[1]` can be passed to functions that load a single FCS file, such as `flowCore::read.FCS`. The entire vector can be passed to functions that load multiple files, such as `flowPloidy::histBatch`.

Each element is named with the filename (without the path), so that you can select an individual filename either by numeric index (i.e., `flowPloidyFiles()[7]`) or by name (`flowPloidyFiles()["248+S.LMD"]`). The names aren't meaningful to you, of course! I added them to provide a more robust way to select an individual file, as the order of files may change in package updates.

The individual files named in `flowPloidyFiles` are LMD files generated by a Beckman-Coulter Gallios flow cytometer. They represent a variety of samples, and some of them are low quality. They are not ideal data sets, but rather represent a range of data quality for assessing the performance of `flowPloidy`.

`fpBad()` and `fpVac()` each return the path to a single LMD file. These are particularly poor quality files that are used in some of the unit tests for `flowPloidy`. They're probably not useful to regular users.

Value

A named character vector of file names, including their full path in the local file system.

Examples

```
flowPloidyFiles()   ## a character vector of file names

## Read in the first file:
library(flowCore)
fcs <- read.FCS(flowPloidyFiles()[1], dataset = 1,
                          alter.names = TRUE)
```

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