

Package ‘lxb’

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Title Fast LXB File Reader

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Description Functions to quickly read LXB parameter data.

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lxb-package	<i>Fast LXB file reader</i>
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Description

This package provides functions to quickly read LXB parameter data. LXB is the format used by Luminex bead arrays and is based on the FCS v3.0 standard.

Details

Note that the functions in this package were written to run as fast as possible and with very specific LXB files in mind. It will not work with general files based on the FCS v3.0 standard and it must run on a little endian machine (e.g. Intel is ok, PowerPC is not). Adding support for more features of FCS v3.0 and other machines should be simple.

Here are some assumptions made:

- The LXB file must be smaller than 100 Mb (\$BEGINDATA and \$ENDDATA are ignored)
- The data must be integral, in list mode, and in little endian byte order (\$DATATYPE = I, \$MODE = L, \$BYTEORD = 1,2,3,4)
- At most 99 parameters are supported
- Unicode in the text segment is not supported
- Keys or values containing the separator character are not supported

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Examples

```
## Not run:
## Typically your LXB files should be organized with one folder per
## plate, with each plate consisting of multiple wells and each well
## corresponding to one LXB file. Assuming the folder 'plate1' contains
## all LXB files for the first plate, here is how to read all parameter
## data for plate 1 into a list of matrices (each list item is one well,
## each column in a matrix corresponds to one parameter):
y <- readLxb('plate1/*.lxb')

## It is now possible inspect individual wells, e.g. the dimensions of
## the first well are given by:
dim(y[[1]])

## .. and the names of the parameters for well 1 are given by:
colnames(y[[1]])

## If the LXB files have names like "XXXX_B1.lxb" (where 'B1' indicates
## that the LXB file corresponds to the first well on the second row),
## then it is also possible to index 'y' by the well name, e.g.:
dim(y$B1)

## .. which is the same as:
dim(y[[2]])

## You can see all well names (and the order of the wells in 'y') by
## typing:
names(y)

## End(Not run)
```

readLxb	<i>Read LXB files</i>
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Description

Read one or more LXB files.

Usage

```
readLxb(paths, filter=TRUE, text=FALSE)
```

Arguments

paths	character vector of patterns for relative or absolute filepaths. Missing values will be ignored.
filter	set filter=TRUE to drop reads with an invalid bead ID or which did not pass the doublet discriminator test. If filter=FALSE then all data is included in the output.
text	include text segment in output if TRUE.

Value

Returns a list of LXB files read. Each item in the list may consist of a text component and a data component. The former is a vector of the values in the text segment of the LXB file, the latter is a matrix of all parameters in the LXB file where each column corresponds to one parameter.

If text=FALSE then each item only consists of the data matrix. Set text=TRUE to return the text segment of the LXB file as well. This can be useful for debugging purposes.

If only one LXB file was read then the first item of the list is returned instead of a list with only one item.

The names attribute of the returned list is set to the well names, if all LXB files have names of the form XXX_B1.lxb (i.e. if they end in a letter and a number). Otherwise the file names are used.

Examples

```
## Not run:
## Read file 'name.lxb' from current directory and include all
## information about the LXB file
x <- readLxb('name.lxb', filter=FALSE, text=TRUE)
dim(x$data)
names(x$text)

## Read all LXB files from current directory
xs <- readLxb('*.*.lxb')
length(xs)
dim(xs[[1]])

## If the LXB files end in a letter and digit, then this can be used to
```

```
## index 'xs', e.g. to inspect the first few rows of well "C10", type:  
head(xs$C10)  
  
## End(Not run)
```

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