Package 'LumiR'

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Type Package

Title Luminex multiplex array manipulation and analysis

Version 0.1.1

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Depends R(>= 2.15.0), Biobase

Imports flowCore, XML, gdata, tools, reshape2, ggplot2, drc, stats,multcomp

Suggests

Description
    Provides S4 structures and functions to deal with Luminex Bead Array Multiplex Assay data

biocViews

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R topics documented:

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blum-class   *blum class*

Description

The `blum` class is a container for the raw bead level information of a multiplex Luminex experiment. This is the base structure used in `LumiR`.

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Slots

phenodData An object of class `AnnotatedDataFrame`. Contains the information regarding the
samples (e.g: sample_type, sample_name, well, filename..).

featureData An object of class `AnnotatedDataFrame`. Contains the information regarding the
analytes: ID and name.

exprs A two level `list`. Contains the intensities measured for each bead. List(1) of lists(2), with
the first level being the samples, and the second being the analytes.

Author(s)

Renan Sauteraud

See Also

read.experiment

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read.experiment   *Read experiment folder*

Description

Parse the root folder of an experiment to store information in a `blum` object.

Usage

```
read.experiment(path="./")
```

Arguments

path   A `character`. The pathname of an experiment folder.

Value

An object of class blum that is the base structure for this package.

Note

The folder passed in path argument must be structured in a specific way and contain mapping files
describing the experiment. See the vignette LumiR user guide for more information.

Author(s)

Renan Sauteraud

See Also

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