The LumiR User Guide

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March 18, 2013

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1 Introduction

1.1 Technology

Luminex xMAP technology is a multiplex assay using flow cytometry to concurrently measure up to 500 analytes in a single reaction volume.

1.2 LumiR

`LumiR` is an R package that provides data structure and functions to read, store and analyze Luminex xMAP experiment.

As with any R package, it should first be loaded in the session

```
> library(LumiR)
```

2 blum

The first step is to read the data into R using the function `read.experiment`. Assuming the folder to read meets all the requirements, the function will automatically detect what software has been used for the acquisition. `read.experiment` returns an object of class `blum`. This object contains the bead level data and all the information extracted from the mapping files.

```
> XP.path <- system.file("extdata", package = "LumiR")
> bl <- read.experiment(XP.path)
```

---

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phenotype mapping file missing.
Some information may be missing.

0%

0%

0%

89%

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0%

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0%

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68%

94%

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98%

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```
0%

> bl

An object of class blum with 27 analytes:
        CHEX.1 CHEX.2 CHEX.3 ... IL.7 IL.8 IP10
885047 measures of expression in 176 wells, on 2 plates.
And slots: phenoData featureData exprs
```

LumiR makes use of the `ggplot2` package to quickly visualize the design of an experiment. The `plot_layout` method can plot phenotype data for the selected plate.

```
> plot_layout(bl, plate = "plate1", fill = "sample_type")
```

Here, we use colors to plot the sample_type for each well of plate1.
This method uses `ggplot2`'s `geom_polygon` function, therefore, the same arguments can be used here.

3   bsum

The second step is to summarize the data using `slummarize`. It returns an object of class `slum`. It is used for 'classic' standardization methods as it only contains the median fluorescence intensity (MFI) for each well and not the raw bead events. For this step, the package needs a user provided 'layout.csv' file with at least the location and expected concentration of the standards. The file provided in the extdata folder of this package is an example of such file.

```
> sl <- slummarize(bl)
```

Since `slum` objects retain the phenotype information from the mapping file, they may be used as first argument in `plot_layout`.

`slummarize` does the standard curve fitting using a 5-Parameters Logigistic curve by default. `LumiR` defines a new method to be used in `ggplot2` for standard curve visualisation.

In the following example, we melt the object into a big data.frame in order to display the standards FI on the same plot using `ggplot2::geom_point`.

```
> library(ggplot2)
> msl <- melt(sl)
> msl.ss <- subset(msl, tolower(sample_type) == "standard")
> ggplot(msl.ss, aes(color = plate), alpha = 0.5) + scale_x_log10() +
+     scale_y_log10() + facet_wrap(~analyte) + geom_sc(sl) + geom_point(aes(x = concentration,
+     y = mfi))
```

Here again, any argument will be passed to the underlying `ggplot2`'s method `geom_line`.