

SysBioSig Theme

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Installation

ITRC package can be installed using `devtools` package as following

```
install.packages("devtools") # if devtools package is not installed
require(devtools)
devtools::install_github("stork119/SysBioSigTheme", auth_token = [AUTHORISATION_TOKEN])
```

[AUTHORISATION_TOKEN] can be obtained on request after sending an email on address k.nienaltowski@sysbiosig.org (mailto:k.nienaltowski@sysbiosig.org).

To attach `SysBioSigTheme` functions use:

```
library(SysBioSigTheme)
```

Normalise data

To read data tables generated by Cell Profiler and IPIQA it is necessary to use normalisation function

```
data <- normalize_data(read.table([PATH_TO_FILE],
                                header=TRUE, sep=",")$data
```

Themes

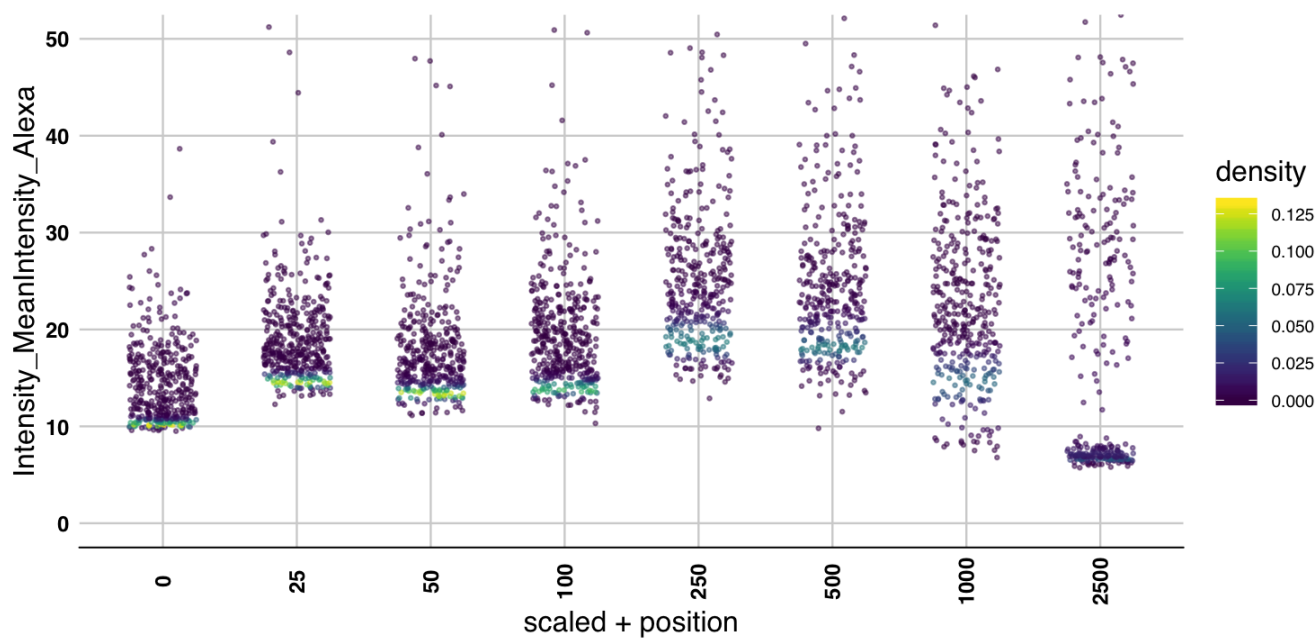
Instead of `theme_jetka()` you can use new theme function `theme_sysbiosig()`

Scatter plots

In order to plot novel scatter plots use functions `ScatterBoxplotGGplot` :

```
ScatterBoxplotGGplot(data = SysBioSigTheme::data.jarek,
                      x_ = "stimulation.1.1",
                      y_ = "Intensity_MeanIntensity_Alexa") +
  coord_cartesian(ylim = c(0,50))
```

```
## Joining, by = "stimulation.1.1"
```



Or `ScatterViolinGGplot` :

```
ScatterViolinGGplot(data = SysBioSigTheme::data.jarek,
  x_ = "stimulation.1.1",
  y_ = "Intensity_MeanIntensity_Alexa") +
  coord_cartesian(ylim = c(0,50))
```

```
## Joining, by = "stimulation.1.1"
```

