

Making your packages accessible to non-programmer collaborators using the VisRseq framework

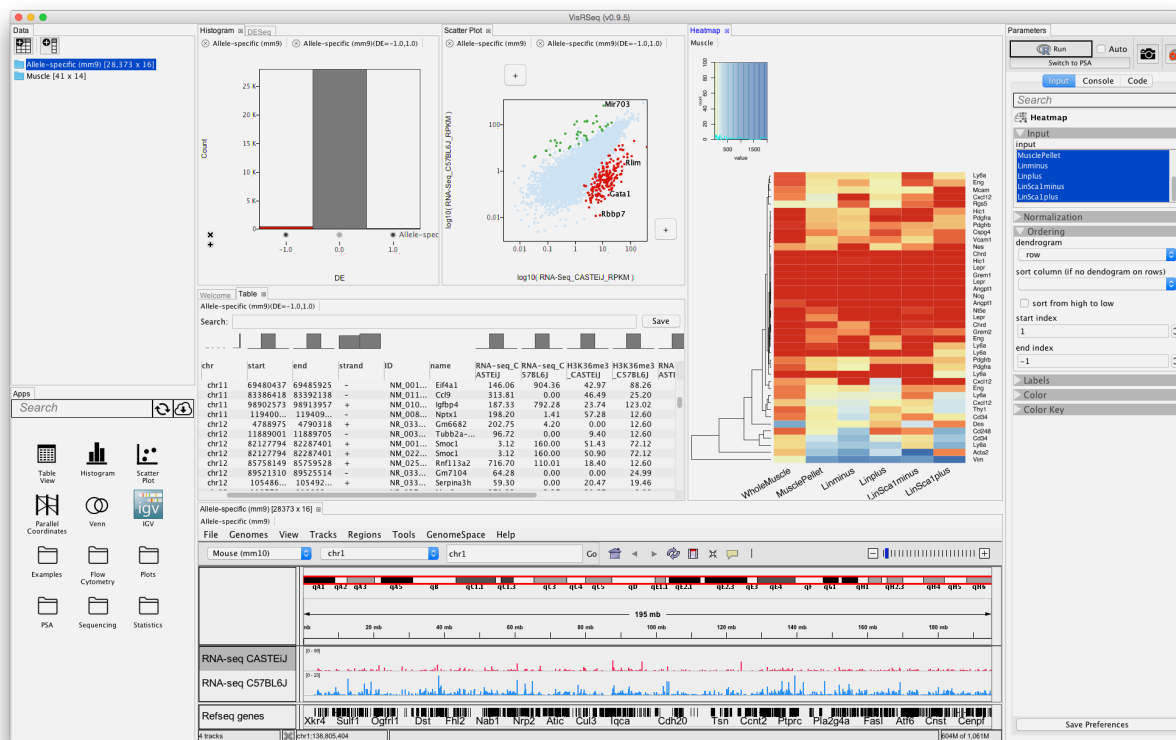
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Abstract

I will introduce the [VisRseq framework](#) and walk the participants through the quick process of creating modules called R-apps from R packages. I expect this to be specially useful for bioinformaticians and package developers that develop R-based analysis tools and would like to make them accessible to their non-programmer collaborators or to the public without having to spend significant time on creating extensive graphical user interfaces. I will walk the participants through several examples of creating diverse types of apps, from simple plotting (e.g. plots) to intermediate (e.g. clustering) to more advanced (e.g. edgeR and DEseq) packages. I will also show how several R-apps can be linked together to create more complex workflows. Participants will require having beginner/intermediate knowledge of R and a machine with R and Java installation.

VisRseq Overview



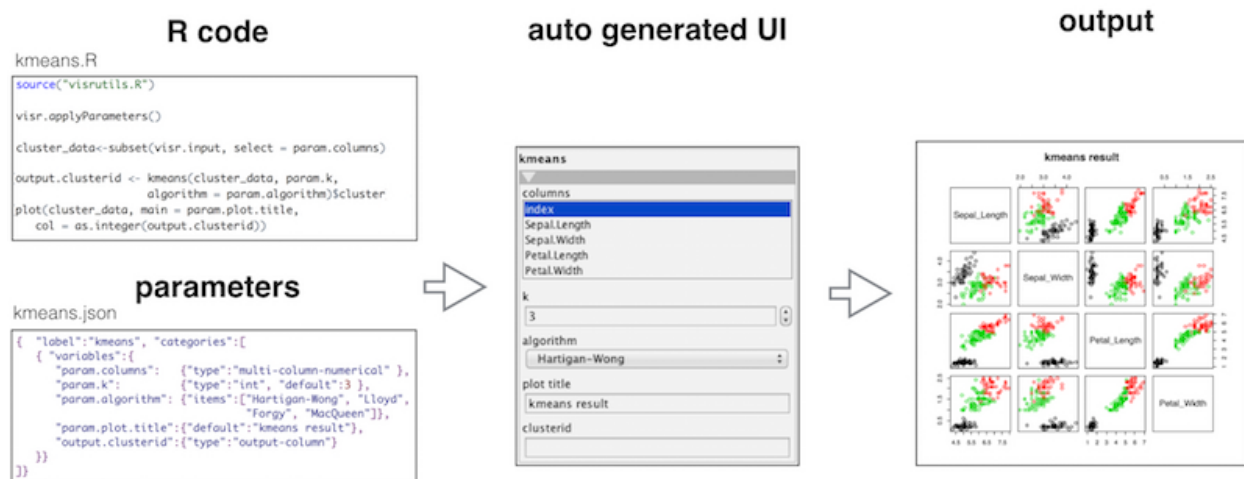
Goals for this workshop

- Learn about VisRseq framework.
- Learn how to create R-apps through several examples.

Requirements

To get the most out of this workshop you are recommended to install the latest version of VisRseq from visrseq.github.io/downloads. You can still follow the instructions and create R-apps using plain R, however you will require VisRseq to be able to run the apps and see the results.

Structure of an R-App



To create an R app you need a .R code containing the main script together with a .json specifying parameters. Each R app can have any number of “parameters“, grouped into “categories“. The .json file can be created manually or using the helper function in visrutils.R

```
source("https://raw.githubusercontent.com/hyounesy/visr-apps/master/visrutils.R")
```

which defines the following functions among other things.

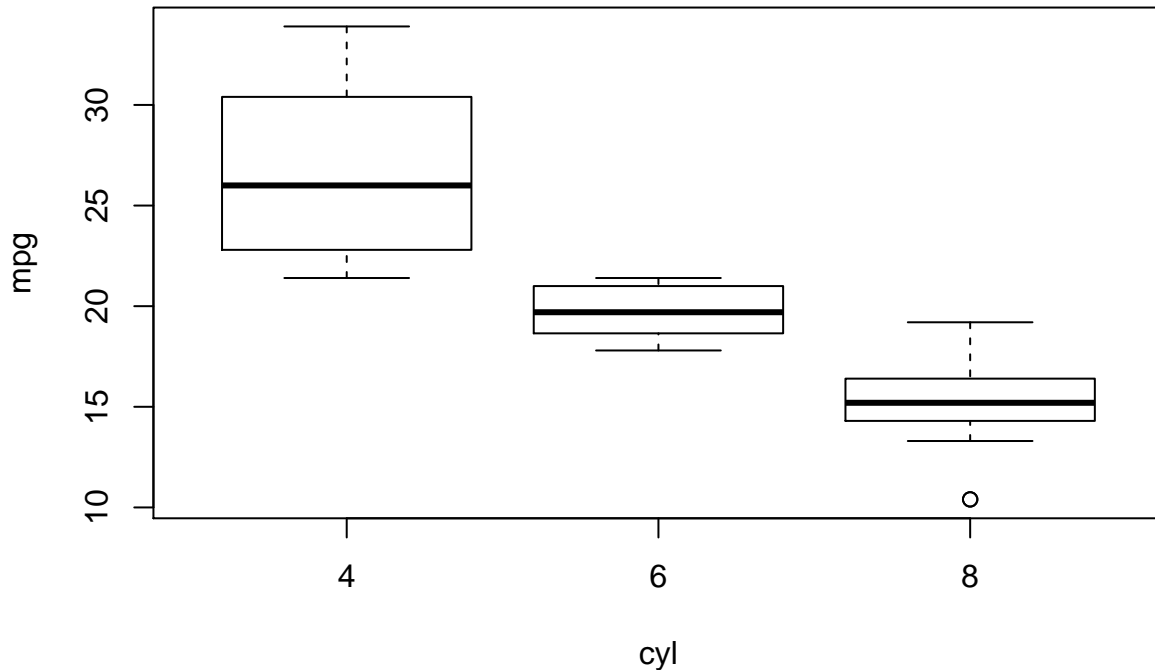
```
visr.app.start(name, info = "", debugdata = NULL)
visr.category(label, info = "")
visr.app.end(printjson = FALSE, writefile = FALSE, filename = NULL)
visr.param(name, label = NULL, info = NULL,
  default = NULL, min = NULL, max = NULL,
  items = NULL, item.labels = NULL,
  type = c("string", "character", "int", "integer", "double", "boolean", "logical", "multi-st",
    "column", "multi-column", "column-numerical", "multi-column-numerical",
    "color", "multi-color", "filename",
    "output-column", "output-multi-column", "output-table"),
  filename.mode = c("load", "save", "dir"), debugvalue = NULL)
```

Let's get started and create our first app!

Example 1: Boxplot

Let's start simple by creating a basic app that draws a barplot. Let's first write a basic boxplot script in a file simple_boxplot.R:

```
boxplot(mtcars[["mpg"]]~mtcars[["cyl"], xlab = "cyl", ylab = "mpg")
```



Assume we would like to allow user to use their own data set and be able to specify x and y columns from their data.

We start the app definition by calling `visr.app.start` and specifying the app name. If we want be able to debug this app in R, we pass a test data set to `debugdata`. This parameter will be ignored when running the app in VisRseq. The data assigned to an app will be store in `visr.input` variable.

```
visr.app.start("Simple Boxplot", debugdata=mtcars)
```

We then add two parameters: `y` the numeric vector of data values that will be split into groups according to the parameter `group`. The parameter `y` has to be a numerical column in the input data, so we specify the `type="column-numerical"`. The parameter `group` can be any column, so we specify `type="column"`. Inorder to be able the debug the app inside the R, we also specify the values using `debugvalue`. This is optional but recommended.

```
visr.param("y", type="column-numerical", debugvalue="mpg")
visr.param("group", type="column", debugvalue="cyl")
```

This will create two parameters `visr.param.y` and `visr.param.group`. When running the script in R, they will be initialized with their corresponding `debugvalue` column names. When running the app in VisRseq, they will contain the string name of the column selected in the GUI.

We end the definition by calling `visr.app.end`. If argument `printjson == TRUE`, the json data for the app parameters will be printed to console. If argument `writefile == TRUE`, the output json will be written to a file specified by `filename` argument. If `filename` is not specified, the json file will be created at the same path of the the R script, with the same name, but `.json` extension (i.e. `simple_boxplot.json`).

```
visr.app.end(printjson=TRUE, writefile = FALSE, filename = NULL)
```

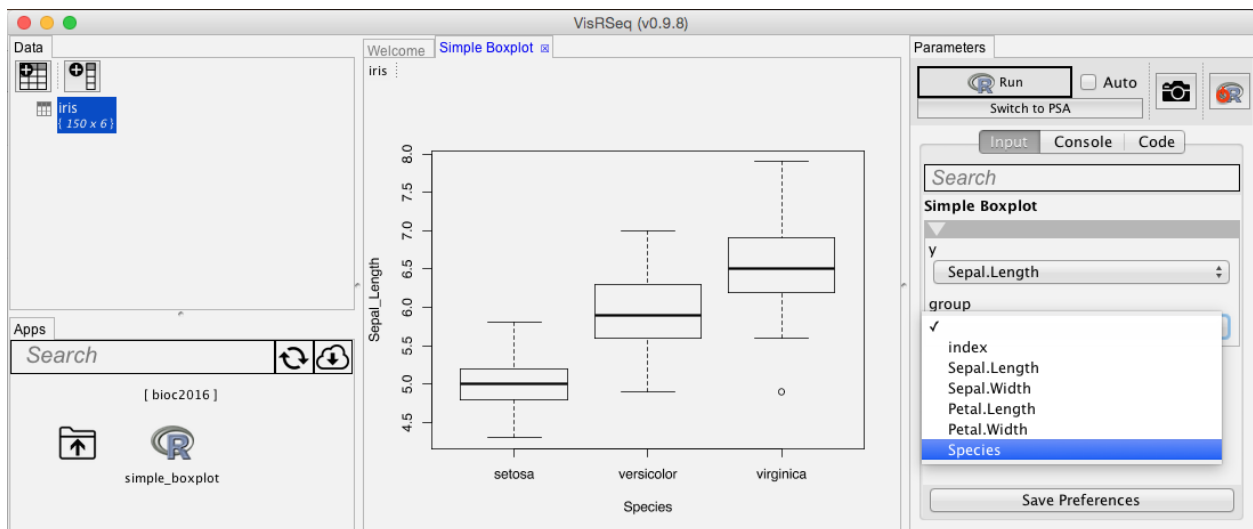
```
## {
##   "label": "Simple Boxplot",
##   "info": "",
##   "categories": [ {
##     "label": "",
##     "info": "",
##     "variables": {
##       "visr.param.y": {
##         "type": "column-numerical"
##       },
##       "visr.param.group": {
##         "type": "column"
##       }
##     }
##   }
## }
## ]
## }
```

We now have the json file. So we just have to modify our original R script to use the correct parameter names.

```
visr.applyParameters()
```

```
boxplot(visr.input[[visr.param.y]]~visr.input[[visr.param.group]], xlab = visr.param.group, ylab = visr
```

Done! now if we place the `simple_boxplot.R` and `simple_boxplot.json` inside `VisRseq/visr/srcR` and hit the **Refresh** icon above the apps pane, we will have our first custom app in VisRseq. For demonstration purpose here we have used the app to draw a boxplot for the iris dataset.



here is the complete source code for `simple_boxplot.R` app:

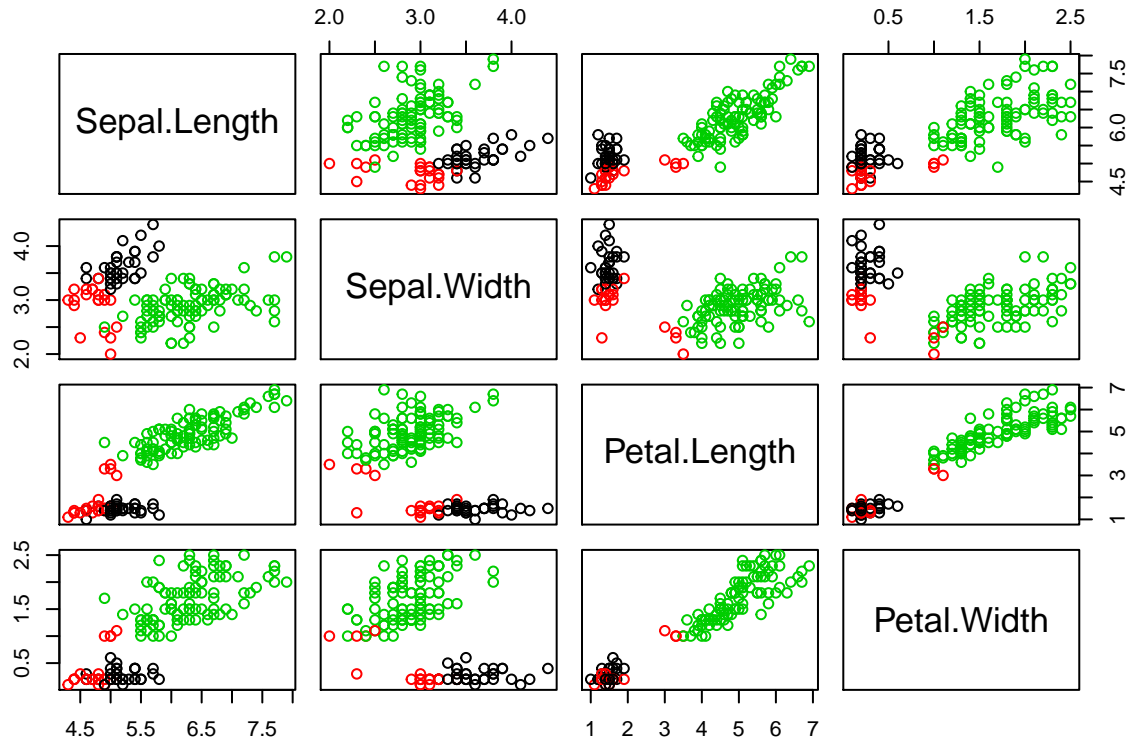
```
source("visrutils.R")
visr.app.start("Simple Boxplot", debugdata=mtcars)
visr.param("y", type="column-numerical", debugvalue="mpg")
visr.param("group", type="column", debugvalue="cyl")
visr.app.end(printjson=TRUE, writefile = FALSE, filename = NULL)
visr.applyParameters()
```

```
boxplot(visr.input[[visr.param.y]]~visr.input[[visr.param.group]], xlab = visr.param.group, ylab = visr
```

Example 2: Kmeans

We will now make something more interesting. A kmeans clustering app. Like the previous example, we will start with a R script for kmeans clustering.

```
input <- iris
columns <- c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")
cluster_data <- subset(input, select = columns)
clusterid <- kmeans(cluster_data, centers = 3)$cluster
plot(cluster_data, col = as.integer(clusterid))
```



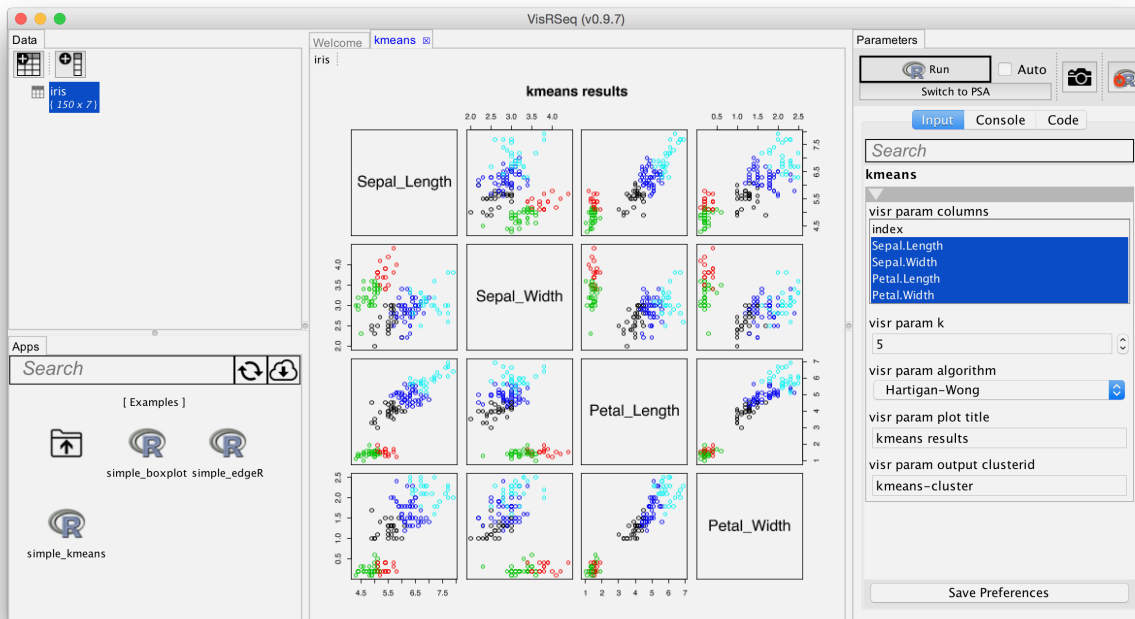
```
# start parameter definition
visr.app.start("Simple Kmeans", debugdata = iris)
visr.category("clustering parameters")
visr.param("columns", type = "multi-column-numerical",
           debugvalue = c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width"))
visr.param("k", default = 3)
visr.param("algorithm", items = c("Hartigan-Wong", "Lloyd", "Forgy", "MacQueen"))
visr.category("output")
visr.param("plot.title", default = "kmeans results")
visr.param("output.clusterid", type = "output-column")
visr.app.end(printjson=TRUE)
```

```
## {
##   "label": "Simple Kmeans",
##   "info": "",
##   "categories": [ {
##     "label": "clustering parameters",
##     "info": "",
```

```
## "variables": {
##   "visr.param.columns": {
##     "type": "multi-column-numerical"
##   },
##   "visr.param.k": {
##     "type": "int",
##     "default": 3
##   },
##   "visr.param.algorithm": {
##     "type": "string",
##     "items": [ "Hartigan-Wong", "Lloyd", "Forgy", "MacQueen" ]
##   }
## },
## {
##   "label": "output",
##   "info": "",
##   "variables": {
##     "visr.param.plot.title": {
##       "type": "string",
##       "default": "kmeans results"
##     },
##     "visr.param.output.clusterid": {
##       "type": "output-column"
##     }
##   }
## }
## }]
```

```
visr.applyParameters()
```

```
cluster_data<-subset(visr.input, select = visr.param.columns)
visr.param.output.clusterid <- kmeans(cluster_data, visr.param.k, algorithm = visr.param.algorithm)$clu
plot(cluster_data, main = visr.param.plot.title, col = as.integer(visr.param.output.clusterid))
```



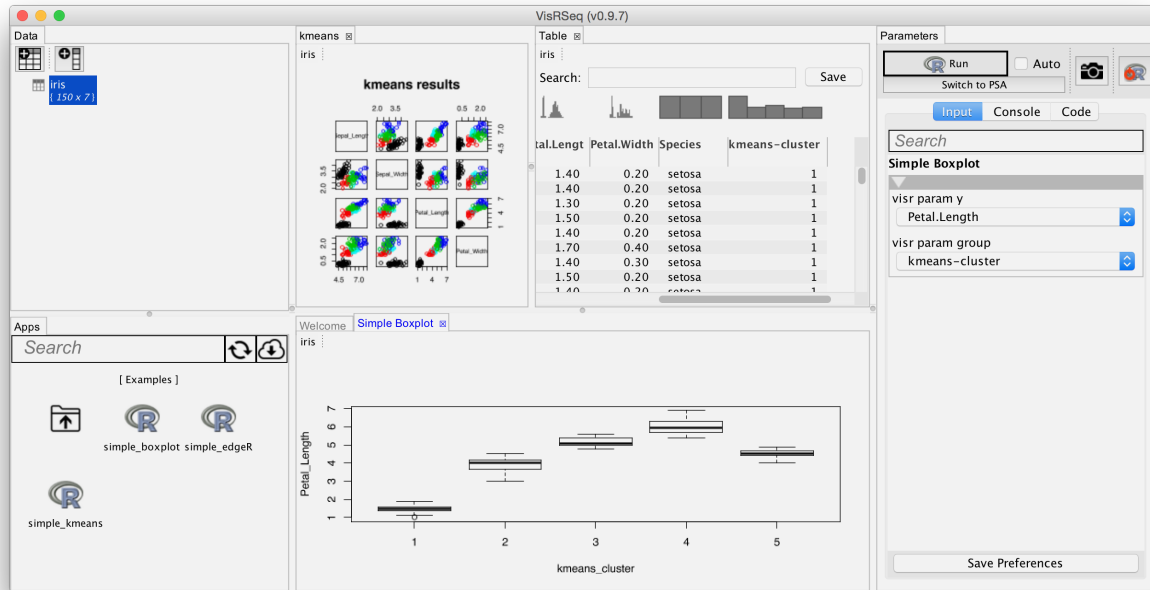
here is the complete source code for `simple_kmeans.R` app:

```
# start parameter definition
visr.app.start("Simple Kmeans", debugdata = iris)
visr.category("clustering parameters")
visr.param("columns", type = "multi-column-numerical",
           debugvalue = c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width"))
visr.param("k", default = 3)
visr.param("algorithm", items = c("Hartigan-Wong", "Lloyd", "Forgy", "MacQueen"))
visr.category("output")
visr.param("plot.title", default = "kmeans results")
visr.param("output.clusterid", type = "output-column")
visr.app.end(printjson=TRUE)

visr.applyParameters()

cluster_data<-subset(visr.input, select = visr.param.columns)
visr.param.output.clusterid <- kmeans(cluster_data, visr.param.k, algorithm = visr.param.algorithm)$cluster
plot(cluster_data, main = visr.param.plot.title, col = as.integer(visr.param.output.clusterid))
```

Chaining apps When running kmeans inside VisRseq on a test data, the result of the clustering will be stored in a new column specified by output cluster id. We can preview this new column in a table view app, or even better we can now use that with the boxplot app we created earlier.



Example 3: Differential expression analysis using edgeR

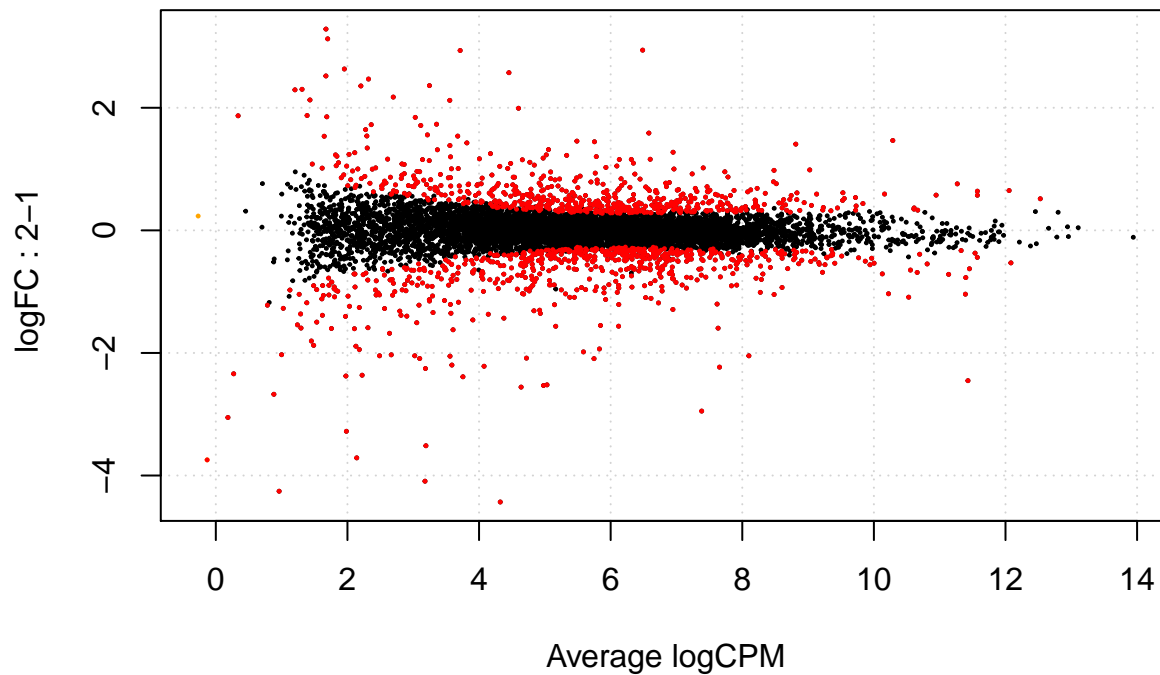
```
library("edgeR", quietly=T)
countdata = read.table("https://raw.githubusercontent.com/hyounesy/bioc2016.visrseq/master/data/counts.")
x <- countdata
head(x)
```

```
##          CT.PA.1 CT.PA.2 KD.PA.3 KD.PA.4 CT.SI.5 KD.SI.6 CT.SI.7
## FBgn0000008      76      71      87      68      137      115      82
## FBgn0000017    3498    3087    3029    3264    7014    4322    3926
## FBgn0000018     240     306     288     307     613     528     485
## FBgn0000032     611     672     694     757    1479    1361    1351
## FBgn0000042   40048   49144   70574   72850   97565   95760   99372
## FBgn0000043   15910   18194   31086   34085   34171   42389   29671
```

```
group1 <- c("CT.PA.1", "CT.PA.2")
group2 <- c("KD.PA.3", "KD.PA.4")
groups <- factor(c(rep(1, length(group1)), rep(2, length(group2)))) # c(1, 1, 2, 2)
# create edgeR's container for RNA-seq count data
y <- DGEList(counts=x[, c(group1, group2)], group = groups)
# estimate normalization factors
y <- calcNormFactors(y)
# estimate tagwise dispersion (simple design)
y <- estimateCommonDisp(y)
y <- estimateTagwiseDisp(y)
# test for differential expression using classic edgeR approach
et <- exactTest(y)
# total number of DE genes in each direction
is.de <- decideTestsDGE(et, adjust.method = "BH", p.value = 0.05, lfc = 0)
```



```
# The log-fold change for each gene is plotted against the average abundance
plotSmea(y, de.tags=rownames(y)[is.de!=0])
```



```
## edgeR parameters
#countdata = read.table("https://raw.githubusercontent.com/hyounesy/bioc2016.visrseq/master/data/counts")
visr.app.start("edgeR", debugdata = countdata)
visr.param("group1", type = "multi-column-numerical", debugvalue = c("CT.PA.1", "CT.PA.2"))
visr.param("group2", type = "multi-column-numerical", debugvalue = c("KD.PA.3", "KD.PA.4"))
visr.param("output.de", label = "DE clusters", type = "output-column")
visr.app.end(printjson=TRUE, writefile=T)
```

```
## {
##   "label": "edgeR",
##   "info": "",
##   "categories": [ {
##     "label": "",
##     "info": "",
##     "variables": {
##       "visr.param.group1": {
##         "type": "multi-column-numerical"
##       },
##       "visr.param.group2": {
##         "type": "multi-column-numerical"
##       },
##       "visr.param.output.de": {
##         "label": "DE clusters",
##         "type": "output-column"
##       }
##     }
##   }
## }
## }
```

```
visr.applyParameters()
```

```
## edgeR code
library("edgeR")
x <- visr.input
groups <- factor(c(rep(1, length(visr.param.group1)), rep(2, length(visr.param.group2)))) # c(1, 1, 2,
# create edgeR's container for RNA-seq count data
y <- DGEList(counts=x[, c(visr.param.group1, visr.param.group2)], group = groups)
# estimate normalization factors
y <- calcNormFactors(y)
# estimate tagwise dispersion (simple design)
y <- estimateCommonDisp(y)
y <- estimateTagwiseDisp(y)
# test for differential expression using classic edgeR approach
et <- exactTest(y)
# total number of DE genes in each direction
is.de <- decideTestsDGE(et, adjust.method = "BH", p.value = 0.05, lfc = 0)
# export the results to VisRseq
visr.param.output.de <- as.factor(is.de)
# The log-fold change for each gene is plotted against the average abundance
plotSmeas(y, de.tags = rownames(y)[is.de != 0])
```

