R implementation

Sleiman Bassim, PhD

October 31, 2014

1 Loaded functions:

```
source("/media/Data/Dropbox/R/01funcs.R")
#load("", .GlobalEnv)
lsos()

                        Type   Size PrettySize Rows Columns
bagging              function  23520      23 Kb   NA      NA
bagging.clas         function  24280    23.7 Kb   NA      NA
baggingTune          function  23856    23.3 Kb   NA      NA
circos.test          function  55408    54.1 Kb   NA      NA
Cols                 function   6576     6.4 Kb   NA      NA
ensemble.mean        function  24232    23.7 Kb   NA      NA
locusRMR             function  11224      11 Kb   NA      NA
model.clas           function  20680    20.2 Kb   NA      NA
model.reg            function  18528    18.1 Kb   NA      NA
modelTune.clas       function  21016    20.5 Kb   NA      NA
modelTune.reg        function  18864    18.4 Kb   NA      NA
net2Bin              function  33240    32.5 Kb   NA      NA
normDataWithin       function  21816    21.3 Kb   NA      NA
olBarplot            function  31992    31.2 Kb   NA      NA
overLapper           function  86584    84.6 Kb   NA      NA
password            character    104  104 bytes    1      NA
predict.regsubsets   function  10208      10 Kb   NA      NA
range_correlation    function  16472    16.1 Kb   NA      NA
regfit               function   9912     9.7 Kb   NA      NA
regfit.int           function  10360    10.1 Kb   NA      NA
rocplot              function   7768     7.6 Kb   NA      NA
servername          character    120  120 bytes    1      NA
set.cor              function  10712    10.5 Kb   NA      NA
set.var              function  12216    11.9 Kb   NA      NA
summarySE            function  30400    29.7 Kb   NA      NA
summarySEwithin      function  39616    38.7 Kb   NA      NA
username            character    120  120 bytes    1      NA
vennPlot             function 562632   549.4 Kb   NA      NA
visualizeNet         function  30288    29.6 Kb   NA      NA
```

1   Testing the GenePattern package

3 First thing is to install the package from the website.

```
#install.packages("full-path-to-GenePattern-R-package", type="source", repos=NULL)
```

4 Load my credentials to login to GenePattern website and use their tools locally.

```
load("keys.Rdata", .GlobalEnv)
```

5 Obtain a GPClient object which references a specific server and user.

```
require(GenePattern)
gp.client <- gp.login(servername, username, password)
```

2   Testing a dataset with some modules from GenePattern

7 Load a random dataset to preprocess it.

```
input.ds1 <- "ftp://ftp.broadinstitute.org/pub/genepattern/all_aml/all_aml_train.res"
```

8   To preprocess the dataset several modules can be invoked.

```
## not working because the servername (in the keys.Rdata) is not set correctly
#preprocess.ds1 <- run.analysis(gp.client, "PreprocessDataset", input.filename=input.ds1)
```

9   # 3   System Information

10   The version number of R and packages loaded for generating the vignette were:

```
R version 3.1.1 (2014-07-10)
Platform: x86_64-pc-linux-gnu (64-bit)

locale:
 [1] LC_CTYPE=en_CA.UTF-8        LC_NUMERIC=C
 [3] LC_TIME=en_CA.UTF-8        LC_COLLATE=en_CA.UTF-8
 [5] LC_MONETARY=en_CA.UTF-8    LC_MESSAGES=en_CA.UTF-8
 [7] LC_PAPER=en_CA.UTF-8       LC_NAME=en_CA.UTF-8
 [9] LC_ADDRESS=en_CA.UTF-8     LC_TELEPHONE=en_CA.UTF-8
[11] LC_MEASUREMENT=en_CA.UTF-8  LC_IDENTIFICATION=en_CA.UTF-8


attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods
[7] base

other attached packages:
[1] GenePattern_1.0.2 rJava_0.9-6      knitr_1.6

loaded via a namespace (and not attached):
[1] compiler_3.1.1 evaluate_0.5.5 formatR_1.0    highr_0.3
[5] stringr_0.6.2  tools_3.1.1
```