Testing the clickme package: https://github.com/nachocab/clickme

Try zooming in and out in the figures below, click the Show names button, hover over points, filter by point names in the search box

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Installation

RR Code

```
r <- getOption("repos")
r["CRAN"] <- "http://ftp.heanet.ie/mirrors/cran.r-project.org/"
options(repos=r)

if(!require(devtools)){ install.packages("devtools",
repos="http://ftp.heanet.ie/mirrors/cran.r-project.org/") }
require("devtools")
if(!require(clickme)){ install_github("nachocab/clickme") }
```

1st example: rnorm(100)

RR Code

```
require(clickme)
options(clickme_output_path = getwd() )
clickme("points",
                rnorm(100),
        title = "Testing Clickme with rnorm(100)",
                height = 300, width = 300,
                file_name = "clickme1.html")$iframe(width = 800,
                        relative_path = "./temp/cache/R_r_test10_clickme")
# try zooming in and out, click the Show names button, hover over points
```

2nd example: letters

RR Code

```
require(clickme)
options(clickme_output_path = getwd() )
# fancy
n <- 500
clickme("points",
        x = rbeta(n, 1, 10), y = rbeta(n, 1, 10),
        names = sample(letters, n, r = T),
        color_groups = sample(LETTERS[1:3], n, r = T),
        title = "Testing Clickme with letters",
                height = 300, width = 300,
                file_name = "clickme2.html")$iframe(width = 800,
                        relative_path = "./temp/cache/R_r_test10_clickme")
```

3rd example: Microarray experiment

RR Code

```
require(clickme)
options(clickme_output_path = getwd() )
data(microarray)
clickme("points", x = microarray$significance, y = microarray$logFC,
        color_groups = ifelse(microarray$adj.P.Val < 1e-4, "Significant", "Noise"),
        names = microarray$gene_name,
        xlab = "Significance (-log10)", ylab = "Fold-change (log2)",
        extra = list(Probe = microarray$probe_name),
        title = "Results from a Microarray experiment",
                height = 300, width = 300,
                file_name = "clickme3.html")$iframe(width = 800,
                        relative_path = "./temp/cache/R_r_test10_clickme")
```