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Testing the clickme package: [https://github.com/nachocab/clickme](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("clickme", "nachocab") }
```

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,
)```
2nd example: letters

```r
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.tiki.org/R_r_test10_clickme")
```

3rd example: Microarray experiment

```r
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),
```
results from a microarray experiment,