# Table of Contents

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Table of contents</td>
<td>2</td>
</tr>
<tr>
<td><strong>Installation</strong></td>
<td>2</td>
</tr>
<tr>
<td>1st example: rnorm(100)</td>
<td>2</td>
</tr>
<tr>
<td>2nd example: letters</td>
<td>3</td>
</tr>
<tr>
<td>3rd example: Microarray experiment</td>
<td>3</td>
</tr>
</tbody>
</table>
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

Table of contents

- Installation
- 1st example: rnorm(100)
- 2nd example: letters
- 3rd example: Microarray experiment

Installation

RR Code

```r
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

```r
require(clickme)
options(clickme_output_path = getwd())
clickme("points",
rnorm(100),
title = "Testing Clickme with rnorm(100)",
height = 300, width = 300,
```
2nd example: letters

RR Code

```r
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

RR Code

```r
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,