GenVisR: Installation instructions

Note: Due to pdf conversion software it may be difficult to copy-paste from this document. A version of this document has been made available here that solves these issues:

Installation Instructions

GenVisR is an R package available via Bioconductor (version 3.3) and GitHub. GenVisR currently resides on the development branch of Bioconductor and will be included on the release branch at the next Bioconductor release cycle (April 2016). To install GenVisR from the Bioconductor development branch it is necessary to install the R and bioconductor development versions. Alternatively, the package can be installed directly from the GenVisR GitHub repository. Briefly, the steps for both options are as follows:

A) Install from Bioconductor (Option 1)

Note: Requires R version 3.3.0 (devel), full instructions can be found here: http://bioconductor.org/packages/devel/bioc/html/GenVisR.html

1. Install R-devel (version 3.3.0), OS-specific installation instructions can be found at: http://bioconductor.org/developers/how-to/useDevel/

2. Install the latest BiocInstaller

```
# Repeat the command below until R says there is no package for
# 'BiocInstaller' to remove
remove.packages("BiocInstaller")

# Install the current version
source("https://bioconductor.org/biocLite.R")
BiocInstaller::biocValid()
```

3. Install GenVisR

```
source("https://bioconductor.org/biocLite.R")
biocLite("GenVisR")
```

B) Install from GitHub (Option 2)

note: Requires R version 3.2.3, full instructions can be found here: https://github.com/griffithlab/GenVisR

1. Install the devtools package from CRAN

```
install.packages("devtools")
```

2. Install Bioconductor dependencies

```
source("http://bioconductor.org/biocLite.R")
biocLite(c("AnnotationDbi", "biomaRt", "Biostrings", "GenomicFeatures", "GenomicRanges",
    "Rsamtools"))
```

3. Install GenVisR

```
devtools::install_github("griffithlab/GenVisR")
```

Examples

For a brief introduction to core functions with examples please refer to the GenVisR vignette available at:
http://bioconductor.org/packages/devel/bioc/html/GenVisR.html

A selection of R code used to make the figures in the manuscript is provided below. Please increase the size of the graphics device to avoid grob collisions.

```
# Load the GenVisR package
library(GenVisR)
```

Figure 1A

```
# brcaMAF is a maf file loaded with GenVisR Take the preloaded maf file and
# restrict to just PIK3CA
data <- brcaMAF[brcaMAF$Hugo_Symbol == "PIK3CA", c("Hugo_Symbol", "amino_acid_change_WU",
    "trv_type_WU")]

# Add in the ensembl transcript id
data <- as.data.frame(cbind(data, "ENST00000263967"))
colnames(data) <- c("gene", "amino_acid_change", "trv_type", "transcript_name")

# Call lolliplot
lolliplot(data, fillCol = "trv_type")
```

Figure 1B

```
# Call Waterfall
waterfall(brcaMAF, plotGenes = c("PIK3CA", "TP53", "USH2A", "MLL3", "BRCA1"))
```

Figure 1E

```
# Randomly generate data representing sequence coverage for a set of
# experiments
x <- matrix(sample(1e+05, 500), nrow = 50, ncol = 10, dimnames = list(0:49,
    paste0("Sample", 1:10)))

# Call covbars
covBars(x)
```