

Lollipop Plot

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```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':  
##  
##   filter, lag
```

```
## The following objects are masked from 'package:base':  
##  
##   intersect, setdiff, setequal, union
```

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.1 --
```

```
## v ggplot2 3.4.2      v purrr   1.0.1  
## v tibble  3.2.1      v stringr 1.5.0  
## v tidyr   1.3.0      v forcats 0.5.1  
## v readr   2.1.2
```

```
## -- Conflicts ----- tidyverse_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag()    masks stats::lag()
```

```
library(g3viz)
```

```
## g3viz: visualizing gene/genome/genetics data for fun.  
##   - Pfam (v33.1)  
##   - UniProt (date: 2022/07/01)  
##  
## Any questions, please send emails to <g3viz.group@gmail.com> or post on GitHub <https://github.com/G3viz/g3viz/issues>.
```

```

setwd('E:/R-Programming-Practices/Data Visualization/Mutation Plot')

###We need to keep the CSV file in the extdata folder of the package
mutation.csv <- system.file("extdata", "snv_sample.csv", package = "g3viz")

#Prepare maf object
mut.dat <- readMAF(mutation.csv,
                   gene.symbol.col = "Hugo_Symbol",
                   variant.class.col = "Variant_Classification",
                   protein.change.col = "amino_acid_change",
                   sep = ",") # column-separator of csv file

#Creating plotting options
chart.options <- g3Lollipop.theme(theme.name = "cbioportal",
                                  title.text = "BRCA1 Gene Mutation Summary")

g3Lollipop(mut.dat,
            gene.symbol = "BRCA1",
            protein.change.col = "amino_acid_change",
            btn.style = "blue", # blue-style chart download buttons
            plot.options = chart.options,
            output.filename = "customized_plot")

```

```
## Factor is set to Mutation_Class
```

```
## legend title is set to Mutation_Class
```

[save as SVG](#)
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