

Chart themes of g3viz

The g3viz package contains 8 ready-to-use chart schemes: *default*, *blue*, *simple*, *cbioportal*, *nature*, *nature2*, *ggplot2*, and *dark*.

- Load data

```
# Retrieve TP53 mutation data of the MSK-IMPACT study from cBioPortal
mutation.dat <- getMutationsFromCbioportal("msk_impact_2017", "TP53")
#> Found study msk_impact_2017
#> Found mutation data set msk_impact_2017_mutations
#> 10945 cases in this study
```

1 *default* theme

```
g3Lollipop(mutation.dat,
  plot.options =
    g3Lollipop.theme(theme.name = "default",
                      title.text = "TP53 gene mutation (default theme)",
                      y.axis.label = "# of TP53 mutations",
                      legend.title = "Mutation_Class"),
  btn.style = "blue",
  gene.symbol = "TP53",
  output.filename = "default_theme")
#> Factor is set to Mutation_Class
```

2 *blue* theme

```
g3Lollipop(mutation.dat,
  plot.options =
    g3Lollipop.theme(theme.name = "blue",
                      title.text = "TP53 gene mutation (blue theme)",
                      y.axis.label = "# of TP53 mutations",
                      legend.title = "Mutation_Class"),
  btn.style = "blue",
  gene.symbol = "TP53",
  output.filename = "blue_theme")
#> Factor is set to Mutation_Class
```

3 *simple* theme

```
g3Lollipop(mutation.dat,
  plot.options =
    g3Lollipop.theme(theme.name = "simple",
                      title.text = "TP53 gene mutation (simple theme)",
                      y.axis.label = "# of TP53 mutations",
```

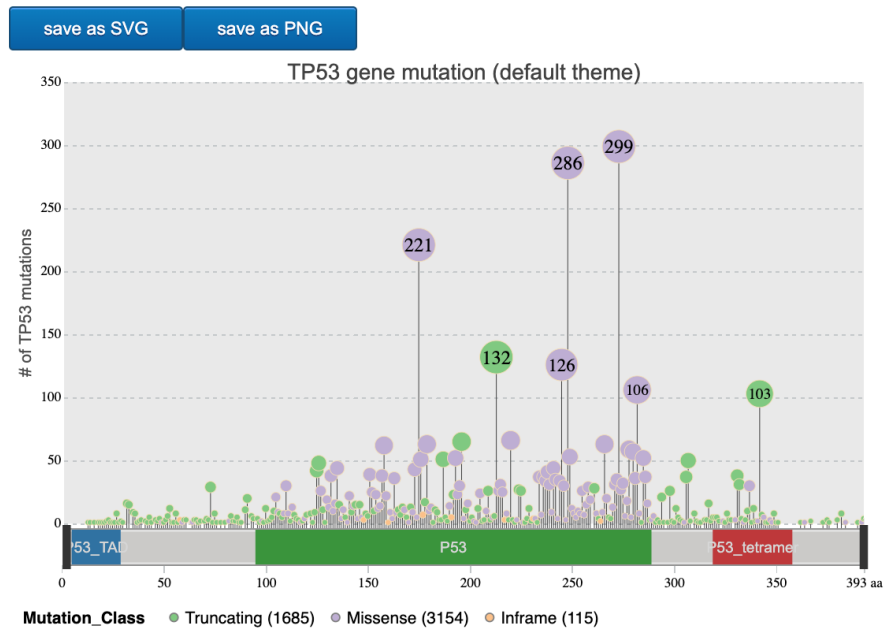


Figure 1: g3viz lollipop-diagram with default theme

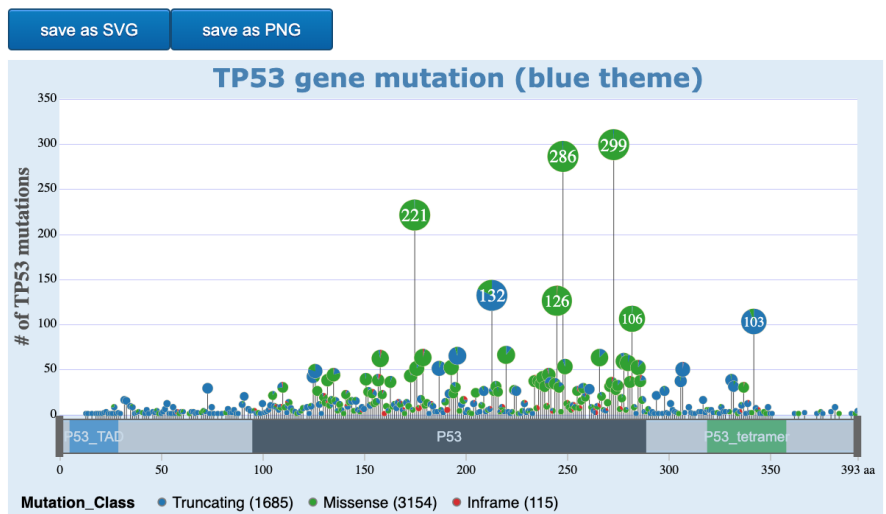


Figure 2: g3viz lollipop-diagram with blue theme

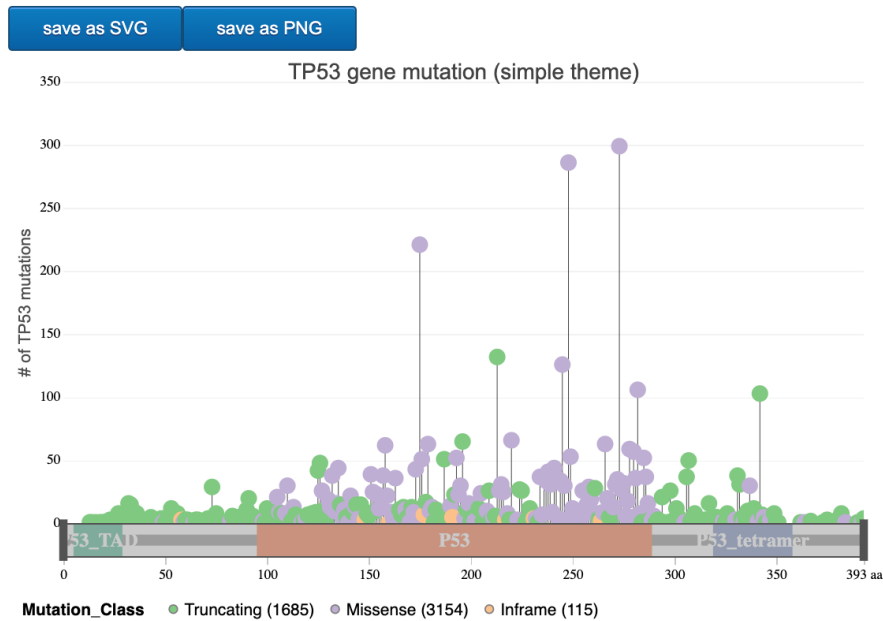


Figure 3: g3viz lollipop-diagram with simple theme

```

                                legend.title = "Mutation_Class"),
  btn.style = "blue",
  gene.symbol = "TP53",
  output.filename = "simple_theme")
#> Factor is set to Mutation_Class

```

4 cbiportal theme

```

g3Lollipop(mutation.dat,
  plot.options =
    g3Lollipop.theme(theme.name = "cbiportal",
                      title.text = "TP53 gene mutation (cBioPortal theme)",
                      y.axis.label = "# of TP53 mutations",
                      legend.title = "Mutation_Class"),
  btn.style = "blue",
  gene.symbol = "TP53",
  output.filename = "cbiportal_theme")
#> Factor is set to Mutation_Class

```

5 nature theme

```

g3Lollipop(mutation.dat,
  plot.options =
    g3Lollipop.theme(theme.name = "nature",
                      title.text = "TP53 gene mutation (nature theme)",
                      y.axis.label = "# of TP53 mutations",

```

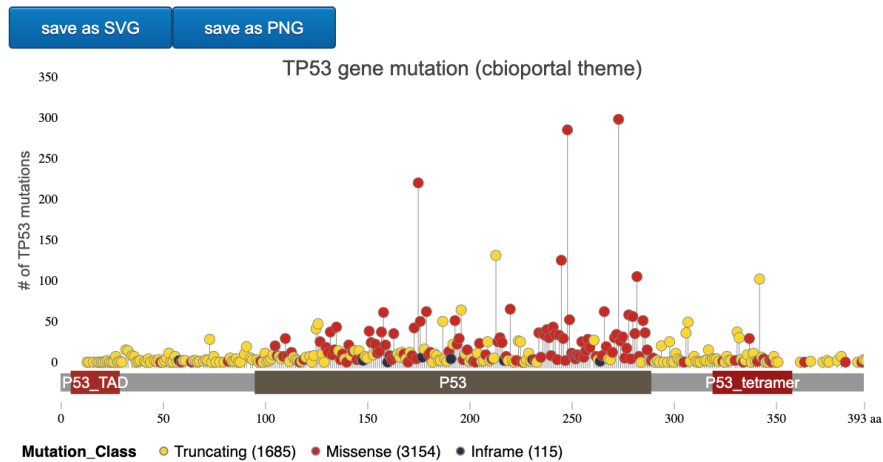


Figure 4: g3viz lollipop-diagram with cBioPortal theme

```

                                legend.title = "Mutation_Class"),
  btn.style = "blue",
  gene.symbol = "TP53",
  output.filename = "nature_theme")
#> Factor is set to Mutation_Class

```

6 nature2 theme

```

g3Lollipop(mutation.dat,
  plot.options =
    g3Lollipop.theme(theme.name = "nature2",
                      title.text = "TP53 gene mutation (nature2 theme)",
                      y.axis.label = "# of TP53 mutations",
                      legend.title = "Mutation_Class"),
  btn.style = "blue",
  gene.symbol = "TP53",
  output.filename = "nature2_theme")
#> Factor is set to Mutation_Class

```

7 ggplot2 theme

```

g3Lollipop(mutation.dat,
  plot.options =
    g3Lollipop.theme(theme.name = "ggplot2",
                      title.text = "TP53 gene mutation (ggplot2 theme)",
                      y.axis.label = "# of TP53 mutations",
                      legend.title = "Mutation_Class"),
  btn.style = "blue",
  gene.symbol = "TP53",
  output.filename = "ggplot2_theme")
#> Factor is set to Mutation_Class

```

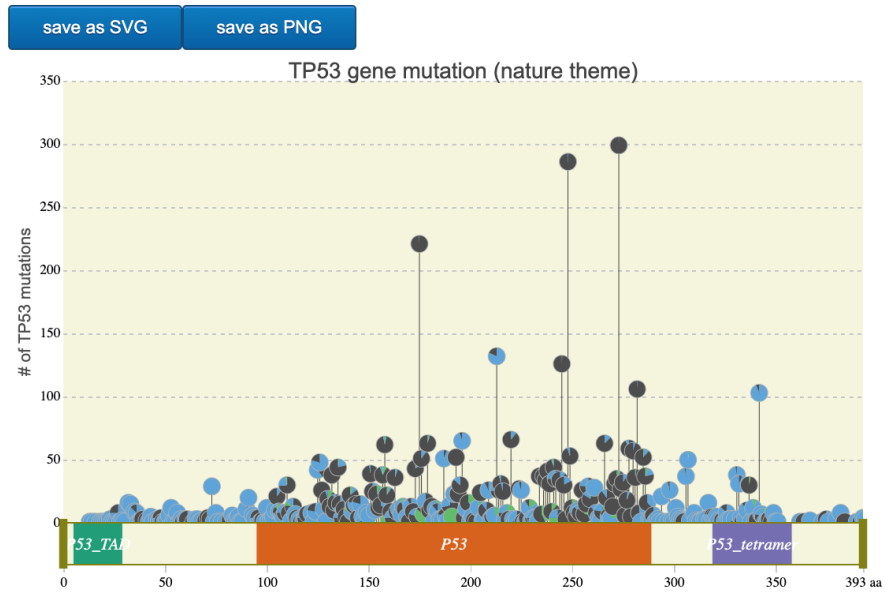


Figure 5: g3viz lollipop-diagram with nature theme

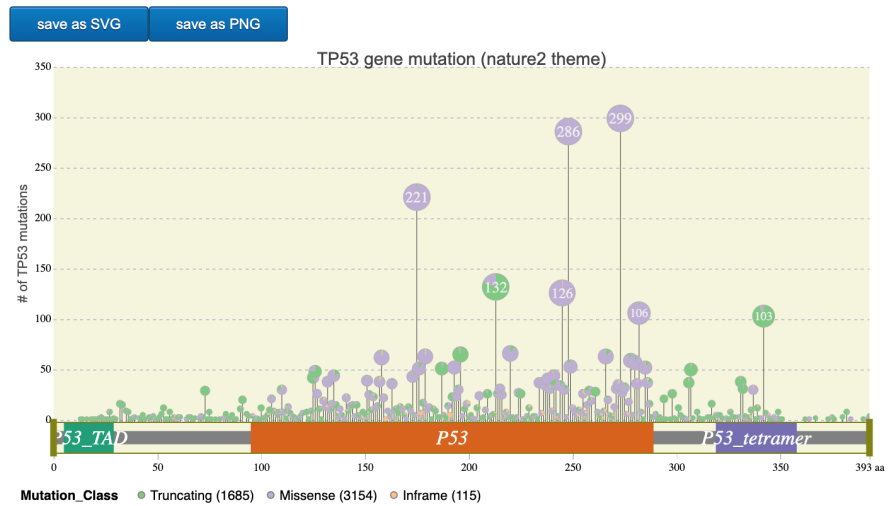


Figure 6: g3viz lollipop-diagram with nature2 theme

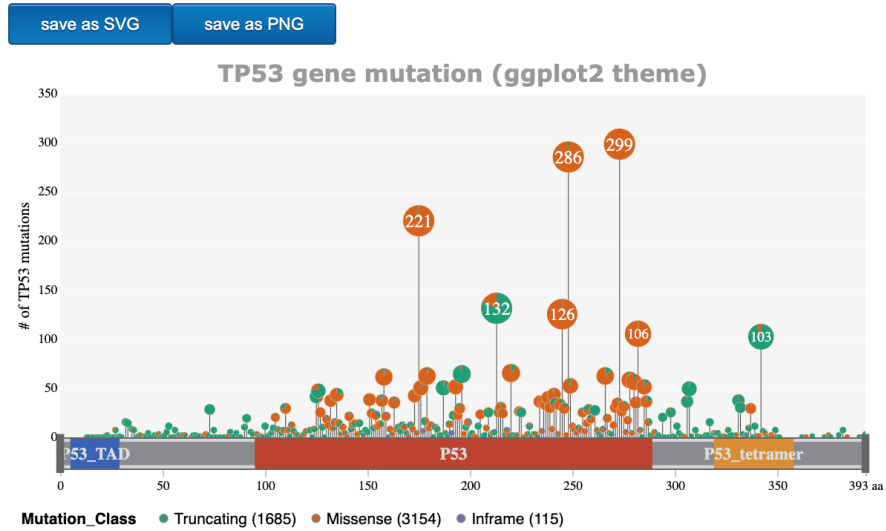


Figure 7: g3viz lollipop-diagram with ggplot2 theme

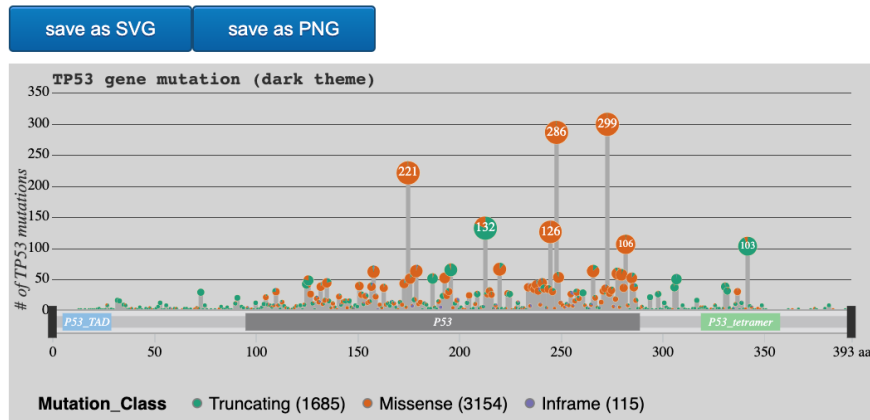


Figure 8: g3viz lollipop-diagram with dark theme

8 *dark* theme

```
g3Lollipop(mutation.dat,
  plot.options =
    g3Lollipop.theme(theme.name = "dark",
      title.text = "TP53 gene mutation (dark theme)",
      y.axis.label = "# of TP53 mutations",
      legend.title = "Mutation_Class"),
  btn.style = "blue",
  gene.symbol = "TP53",
  output.filename = "dark_theme")
#> Factor is set to Mutation_Class
```