

SNV Analysis

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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>.

library(maftools)
library(ggplot2)
library(fmsb)
library(ggpubr)
library(waffle)
library(ggradar)
library(RColorBrewer)

setwd('D:/CancerData/TCGA BRCA cBioPortal/BRCA/BRCA CNV and SNV/SNV')

#Read file
snv<-read.delim('data_mutations.txt', header = T, sep = '\t')
###Remember to use read.delim instead of read.csv since its a big file

#Select gene of interest
snv1<- filter(snv, snv$Hugo_Symbol=='BRCA1' | snv$Hugo_Symbol=='BRCA2')
snv_final<-snv1[,c(1, 5:8, 10:14, 40)]
snv_final$Variant_Classification<- gsub("_", " ", as.character(snv_final$Variant_Classification))

#Filter for BRCA
snv_BRCA1<- snv_final %>% filter(snv_final$Hugo_Symbol=='BRCA1')

#Counting variant types
snv_BRCA1_count <- snv_BRCA1 %>%
  group_by(Variant_Classification) %>% # Variable to be transformed
  count()

#Preparing data
snv_BRCA1_count<- data.frame(t(snv_BRCA1_count))
snv_BRCA1_count<-read.csv('snv_BRCA1_count.csv', row.names = 1)
colnames(snv_BRCA1_count)

## [1] "Frame.Shift.Ins"    "In.Frame.Del"       "Splice.Site"
## [4] "Frame.Shift.Del"    "Silent"              "Nonsense.Mutation"
## [7] "Missense.Mutation"

#Set Max and Minimum cutoffs
max_min <- data.frame(
  Frame.Shift.Ins = c(15, 0), In.Frame.Del = c(15, 0), Splice.Site = c(15, 0), Frame.Shift.Del= c(15, 0),
  Silent= c(15, 0), Nonsense.Mutation= c(15, 0), Missense.Mutation= c(15, 0))

#Create data frame
snv_BRCA1_count <- rbind(max_min, snv_BRCA1_count)

#Select color
col="#E7B800"

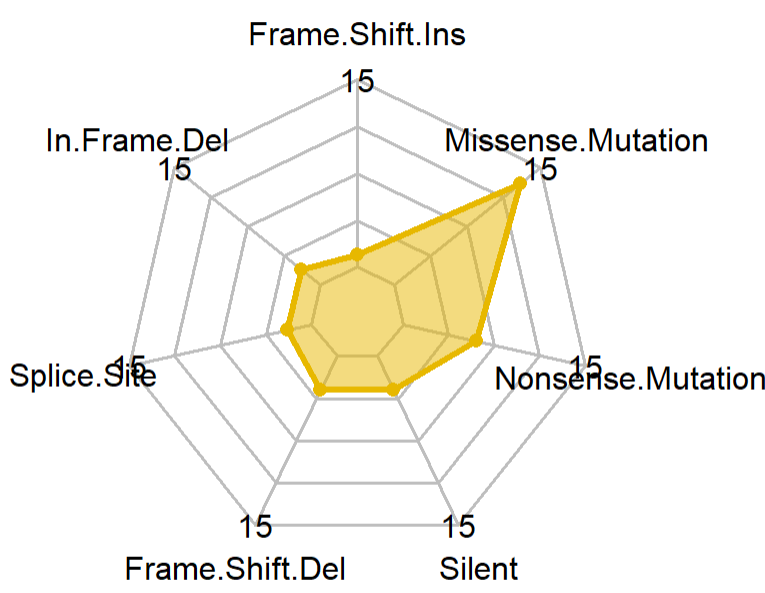
#Plot the radarplot
radarchart( snv_BRCA1_count, axistype=2,

             #custom polygon
             pcol=col, pfc=col,scales::alpha(col, 0.5), plwd=3, plty=1 ,

             #custom the grid
             cglcol="grey", cglty=1, axislabcol="black", caxislabels=seq(0,10, 15), cglwd=1.5,

             #custom labels
             vlce=1, title = 'BRCA1 Mutation Summary in Breast Cancer')
```

BRCA1 Mutation Summary in Breast Cancer

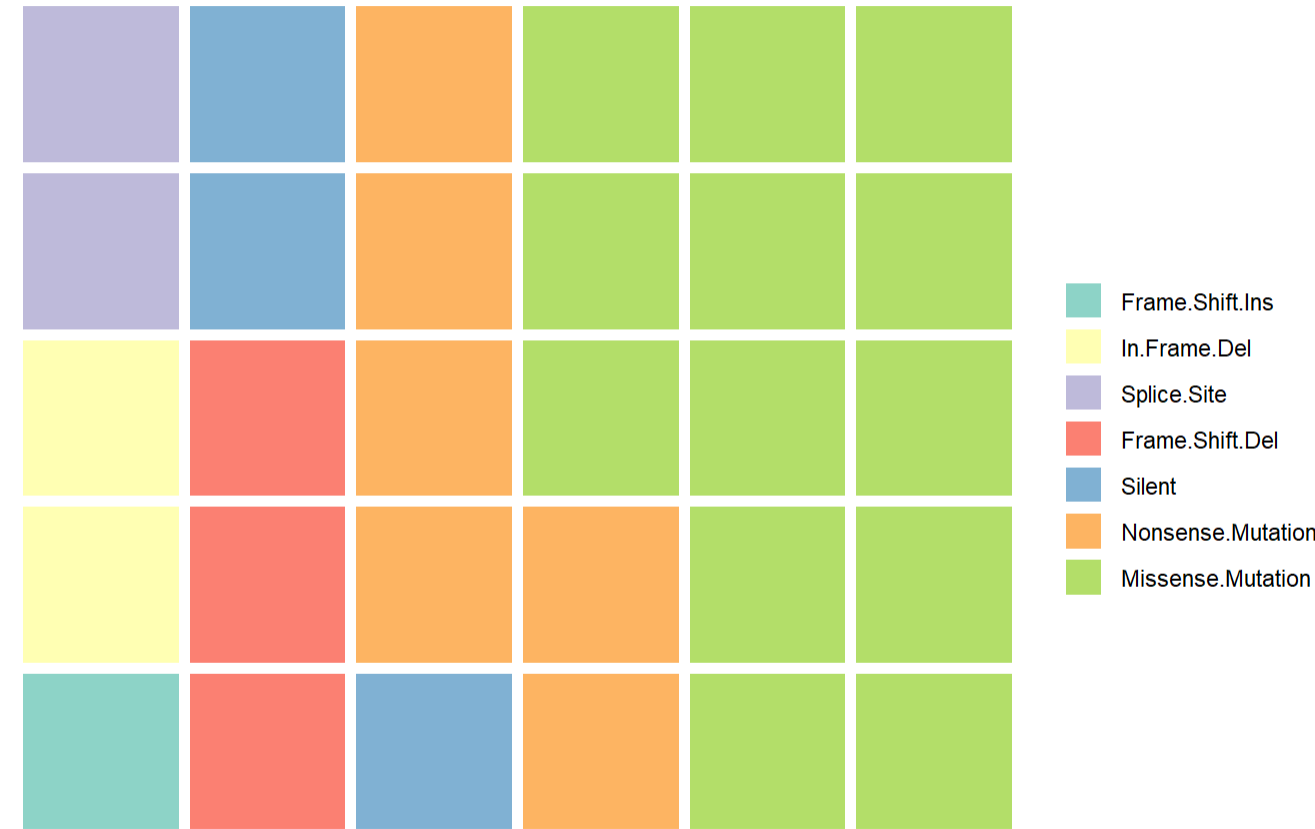


```
#Alternative way is waffle plot
BRCA1_Waffle<- c(Frame.Shift.Ins=1, In.Frame.Del=2, Splice.Site=2, Frame.Shift.Del=3, Silent=3,
  Nonsense.Mutation=6, Missense.Mutation=13)

#Select palette
pal<- brewer.pal(n=8, "Set3")

#Draw plot
waffle(BRCA1_Waffle, rows=5, colors = pal, title = 'BRCA1 Mutation Summary in Breast Cancer')
```

BRCA1 Mutation Summary in Breast Cancer



```
#Generating lollipop diagram from cBioPortal Study
#Prepare object
mutation.dat <- g3viz::getMutationsFromCbioportal("brca_tcga_pan_can_atlas_2018", "BRCA1")

## Warning in .service_validate_md5sum(api_reference_url, api_reference_md5sum): service version differs from validated version
##   service url: https://www.cbioportal.org/api/api-docs
##   observed md5sum: 008be96361f24a5c8d1cfb7f10a9c97
##   expected md5sum: 6abc321feb60da3251620743b527bab9

## Found study brca_tcga_pan_can_atlas_2018

## Found mutation data set brca_tcga_pan_can_atlas_2018_mutations

## 1066 cases in this study

###The project ID can be found here "https://github.com/cBioPortal/datahub/tree/master/public"
# "cbioportal" chart theme

#Prepare plot
plot.options <- g3Lollipop.theme(theme.name = "cbioportal",
  title.text = "BRCA1 Gene Somatic Mutation Summary in Breast Cancer",
  y.axis.label = "# of TP53 Mutations")

g3Lollipop(mutation.dat,
  gene.symbol = "BRCA1",
  btn.style = "gray", # gray-style chart download buttons
  plot.options = plot.options,
  output.filename = "BRCA1")

## Factor is set to Mutation_Class

## legend title is set to Mutation_Class
```

