

Dear Shixiang Wang,

The problem is with the UCSCXenaShiny version 1.1.10 in Windows RStudio.

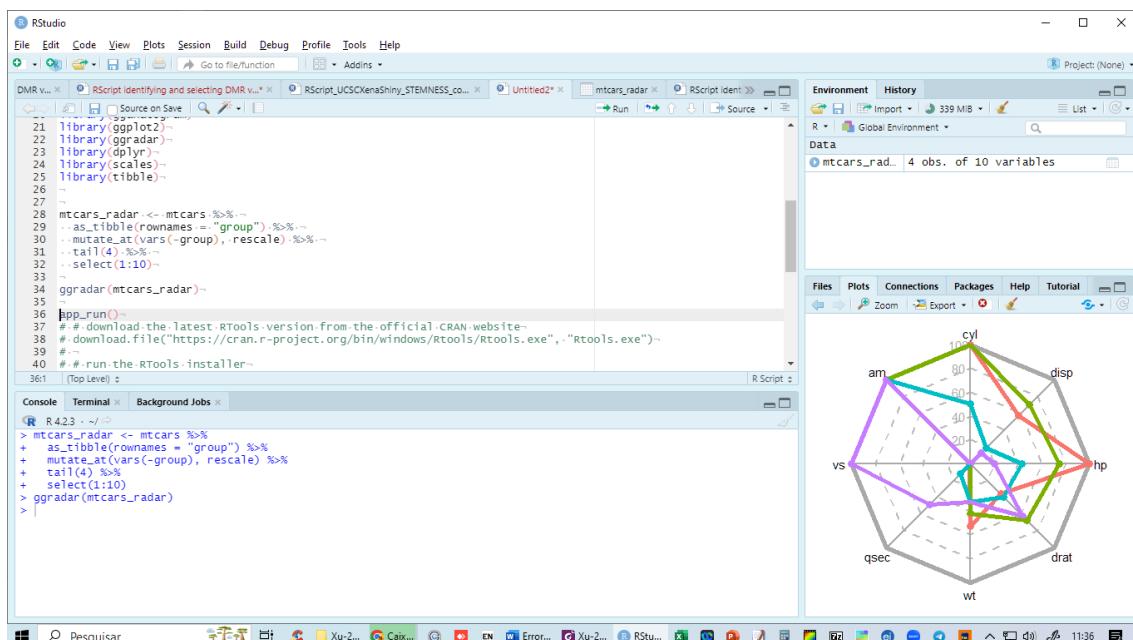
The hiplot, <https://hiplot.cn/advance/ucsc-xena-shiny>, is version 1.1.9, and it does work ok, but the error I get is with v1.1.10.

As you suggested, I uninstalled R.4.2.3, UCSCXena vs 1.1.10, ggradar.

I Reinstalled R.4.2.3, UCSCXena vs 1.1.10 from CRAN, and "ricardo-bion/ggradar" from github with dependencies.

The ggradar in RStudio is working and plotting, tested with the code:

```
mtcars_radar <- mtcars %>%
  as_tibble(rownames = "group") %>%
  mutate_at(vars(-group), rescale) %>%
  tail(4) %>%
  select(1:10)
ggradar(mtcars_radar)
```



But, it does not plot using the UCSCXenaShiny v.1.1.10, Example code:

```
## To generate a radar plot, uncomment the following code
p = vis_gene_stemness_cor()
```

```

Gene = ``MT-ATP8`` + `MT-ATP6` + `MT-CO1` + `MT-CO2` + `MT-CO3` + `MT-
CYB` + `MT-ND1` + `MT-ND2` + `MT-ND3` + `MT-ND4L` + `MT-ND4` + `MT-
ND5` + `MT-ND6`,
cor_method = "spearman",
data_type = "mRNA",
Plot = "TRUE"
)
pdata <- p$data %>%
  dplyr::mutate(cor = round(cor, digits = 3), p.value = round(p.value,
  digits = 3))
df <- pdata %>%
  select(cor, cancer) %>%
  pivot_wider(names_from = cancer, values_from = cor)
df$gene <- "Gene signature"
df<-df[,c(34,1:33)]
ggradar::ggradar(
  df[1, ],
  font.radar = "sans",
  values.radar = c("-1", "0", "1"),
  grid.min = -1, grid.mid = 0, grid.max = 1,
  # Background and grid lines
  background.circle.colour = "white",
  gridline.mid.colour = "grey",
  # Polygons
  group.line.width = 1,
  group.point.size = 3,
  group.colours = "# 00AFBB",
) + theme(plot.title = element_text(hjust = .5))

```

It generates the error message and it does no plot:

```
Error in ggradar::ggradar(df[1, ], font.radar = "sans", values.radar =
c("-1", :
  unused arguments (font.radar = "sans", values.radar = c("-1", "0",
"1"), grid.min = -1, grid.mid = 0, grid.max = 1,
background.circle.colour = "white", gridline.mid.colour = "grey",
group.line.width = 1, group.point.size = 3, group.colours = "# 00AFBB")
```

The same error message remains in the app_run()

C:/Users/Enrique Medina/AppData/Local/R/win-library/4.2/UCSCXenaShiny/shinyapp - Shiny
http://127.0.0.1:7590 | Open in Browser |

Xena Shiny Home Repository General Analysis Quick PanCan Analysis Global Setting Help Developers

Select a genomic profile:
 mRNA Expression
 Transcript Expression
 DNA Methylation
 Protein Expression
 miRNA Expression
 Copy Number Variation

Error: unused arguments (font.radar = "sans", values.radar = c("-1", "0", "1"), grid.min = -1, grid.mid = 0, grid.max = 1, background.circle.colour = "white", gridline.mid.colour = "grey", group.line.width = 1, group.point.size = 3, group.colours = "#00AFBB", plot.title = paste0(input\$Pancan_search, " ", input\$profile, " ", input\$type, " "))

Input a gene or formula (as signature)
MYOC

Select a feature
stemness

Select Correlation method
spearman

Height

Go!

NOTES:
1. The data query may take some time based on your network. Wait until a plot shows

Pesquisar

```
devtools::install_github("ricardo-bion/ggradar",
                        dependencies = TRUE, force = TRUE)
```

Could you please advise on how to correct the error message.

Thank you.

Enrique Medina-Acosta