

A logistic regression analysis of TCGA-KIRC

This project contains a pipeline of clinical analysis of the Cancer Genome Atlas Kidney Renal Clear Cell Carcinoma (TCGA-KIRC) data of patients from Genomic Data Commons Data Portal and cBioPortal.

Previously, we presented a An exploratory preprocessing analysis, and a correlation analysis.

In this final section, we present a logistic regression analysis of each clinical variable weight for TCGA-KIRC.

```
# Set the packages of interest
packages = c("tidyverse","skimr","finalfit")

# if a package is installed, it will be loaded
# otherwise, the missing package(s) will be installed and loaded
package.check <- lapply(packages, FUN = function(x) {
  if (!require(x, character.only = TRUE)) {
    install.packages(x, dependencies = TRUE)
    library(x, character.only = TRUE)
  }
})

suppressMessages(library("tidyverse"))
setwd(".")
```

1. Importing data

TO DO

```
sessionInfo()

## R version 3.6.3 (2020-02-29)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 18.04.4 LTS
##
## Matrix products: default
## BLAS: /usr/lib/x86_64-linux-gnu/openblas/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/libopenblas-r0.2.20.so
##
## locale:
##  [1] LC_CTYPE=pt_BR.UTF-8      LC_NUMERIC=C
##  [3] LC_TIME=pt_BR.UTF-8      LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=pt_BR.UTF-8  LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=pt_BR.UTF-8     LC_NAME=C
##  [9] LC_ADDRESS=C             LC_TELEPHONE=C
## [11] LC_MEASUREMENT=pt_BR.UTF-8 LC_IDENTIFICATION=C
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
```

```

## other attached packages:
## [1] finalfit_1.0.1  skimr_2.1.1      forcats_0.5.0    stringr_1.4.0
## [5] dplyr_0.8.5     purrr_0.3.4      readr_1.3.1      tidyr_1.0.3
## [9] tibble_3.0.1    ggplot2_3.3.0    tidyverse_1.3.0
##
## loaded via a namespace (and not attached):
## [1] tidyselect_1.1.0 xfun_0.13        repr_1.1.0       splines_3.6.3
## [5] haven_2.2.0      lattice_0.20-41  colorspace_1.4-1 vctrs_0.3.0
## [9] generics_0.0.2   htmltools_0.4.0 base64enc_0.1-3  yaml_2.2.1
## [13] survival_3.1-12  rlang_0.4.6      pillar_1.4.4     glue_1.4.0
## [17] withr_2.2.0      DBI_1.1.0        dbplyr_1.4.3     modelr_0.1.7
## [21] readxl_1.3.1     lifecycle_0.2.0  munsell_0.5.0    gtable_0.3.0
## [25] cellranger_1.1.0 rvest_0.3.5      evaluate_0.14    knitr_1.28
## [29] fansi_0.4.1      broom_0.5.6      Rcpp_1.0.4.6     scales_1.1.1
## [33] backports_1.1.6  jsonlite_1.6.1   fs_1.4.1         hms_0.5.3
## [37] digest_0.6.25    stringi_1.4.6    grid_3.6.3       cli_2.0.2
## [41] tools_3.6.3      magrittr_1.5     mice_3.8.0       crayon_1.3.4
## [45] pkgconfig_2.0.3  Matrix_1.2-18    ellipsis_0.3.0   xml2_1.3.2
## [49] reprex_0.3.0     lubridate_1.7.8  assertthat_0.2.1 rmarkdown_2.1
## [53] httr_1.4.1       rstudioapi_0.11  boot_1.3-25      R6_2.4.1
## [57] nlme_3.1-147     compiler_3.6.3

```