

A correlation analysis of clinical variables of TCGA-KIRC patients

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 an exploratory preprocessing analysis. In this section, we present a correlation analysis with t-test and ANOVA test to investigate significative distinctions between clinical variables according to their vital status.

1. Importing data

```
# Update the variables
# explanatory = c("Age", "Metastasis_Stage", "Neoplasm_Lymph_Stage", "Neoplasm_Stage", "Tumor_Stage", "Disease_Free_Status", "Fraction_Genome_Altered", "Histologic_Grade", "Neoadjuvant_Therapy", "Primary_Lymph_Ind3", "Overall_Surv_Status", "Platelet_count", "Sex", "Shortest_Dim", "Person_Neoplasm_Status", "Patient_Vital_Status")
#
# dependent = "Peak"
#
# dados %>%
#   summary_factorlist(dependent, explanatory, p = TRUE, na_include = TRUE,
#   column = FALSE) -> t
```

Further analysis

- A logistic regression analysis of each clinical variable weight.

```
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-p-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
```