A Preprocessing analysis of clinical data 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.

In this section, we present a preprocessing analysis of clinical data.

```
## This chunk automatically generates a text .R version of this script when running within knitr.
input  = knitr::current_input()  # filename of input document
output = paste(tools::file_path_sans_ext(input), 'R', sep = '.')
knitr::purl(input,output,documentation=2,quiet=T)
# Avoid duplicate label error of knitr::purl
options(knitr.duplicate.label = 'allow')
# Code to browse the markdown file with renderized images.
knitr::opts_chunk$set(
  fig.path = "figs/render-"
)
```

1. Importing data

```
kirc_clin_raw <- read_delim("data/kirc_tcga_clinical_data.tsv", "\t",
                            escape_double = FALSE,
                            trim_ws = TRUE)
```

2. Cleaning data

Select variables based on NA count (> 50% complete is a good choice!).

```
NA_fifty <- dim(kirc_clin_raw)[1]/2

NA_sum <- colSums(is.na(kirc_clin_raw))
NA_sum <- as.data.frame(NA_sum)
NA_sum <- tibble::rownames_to_column(NA_sum, "variables")
NA_sum <- NA_sum %>%
     filter(NA_sum < NA_fifty)

kirc_clean <- kirc_clin_raw %>%
     select(one_of(NA_sum$variables))
```

Remove duplicate observations:

```
kirc_clean0 <- kirc_clean %>%
     distinct_at('Patient ID', .keep_all = TRUE)
```

Remove nuneric variables with unique observations:

```
skim(kirc_clean0)
```

Table 1: Data summary

Name	kirc_clean0
Number of rows	537
Number of columns	55
Column type frequency:	
character	43
numeric	12
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate
Study ID	0	1.00
Patient ID	0	1.00
Sample ID	0	1.00
American Joint Committee on Cancer Metastasis Stage Code	2	1.00
Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code	0	1.00
Neoplasm Disease Stage American Joint Committee on Cancer Code	3	0.99
American Joint Committee on Cancer Tumor Stage Code	0	1.00
Cancer Type	0	1.00
Cancer Type Detailed	0	1.00
Disease Free Status	99	0.82
Ethnicity Category	152	0.72
Form completion date	0	1.00
Neoplasm Histologic Grade	3	0.99
Hemoglobin level	83	0.85
Neoplasm Histologic Type Name	0	1.00
Neoadjuvant Therapy Type Administered Prior To Resection Text	0	1.00
Prior Cancer Diagnosis Occurence	0	1.00
ICD-10 Classification	0	1.00
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Histology Code	0	1.00
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Site Code	0	1.00
Informed consent verified	0	1.00
Is FFPE	0	1.00
Primary Tumor Laterality	0	1.00
Primary Lymph Node Presentation Assessment Ind-3	7	0.99
Oncotree Code	0	1.00
Overall Survival Status	0	1.00
Other Patient ID	0	1.00
Other Sample ID	0	1.00
Pathology Report File Name	0	1.00
Pathology report uuid	0	1.00
Platelet count	93	0.83
Tissue Prospective Collection Indicator	20	0.96
Race Category	7	0.99
Tissue Retrospective Collection Indicator	18	0.97
Sample Type	0	1.00
Serum calcium level	172	0.68
Sex	0	1.00
Tumor Tissue Site	0	1.00

skim_variable	n_missing	complete_rate
Tissue Source Site	0	1.00
Person Neoplasm Status	35	0.93
Vial number	0	1.00
Patient's Vital Status	3	0.99
WBC	96	0.82

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd
Diagnosis Age	0	1.00	60.59	12.15
Last Alive Less Initial Pathologic Diagnosis Date Calculated Day Value	0	1.00	0.00	0.00
Disease Free (Months)	99	0.82	40.24	31.66
Fraction Genome Altered	9	0.98	0.17	0.17
Year Cancer Initial Diagnosis	0	1.00	2006.02	2.76
Longest Dimension	35	0.93	1.66	0.66
Mutation Count	86	0.84	73.85	127.76
Overall Survival (Months)	0	1.00	44.26	32.25
Number of Samples Per Patient	0	1.00	1.00	0.04
Sample type id	0	1.00	1.00	0.00
Shortest Dimension	35	0.93	0.38	0.21
Specimen Second Longest Dimension	35	0.93	0.94	0.31

```
kirc_clean1 <-  kirc_clean0  %>%
     select(!c('Last Alive Less Initial Pathologic Diagnosis Date Calculated Day Value',
               'Number of Samples Per Patient',
               'Sample type id'))

skim(kirc_clean1)
```

Table 4: Data summary

Name	kirc_clean1
Number of rows	537
Number of columns	52
Column type frequency:	
character	43
numeric	9
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate
Study ID	0	1.00
Patient ID	0	1.00
Sample ID	0	1.00
American Joint Committee on Cancer Metastasis Stage Code	2	1.00

skim_variable	n_missing	complete_rate
Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code	0	1.00
Neoplasm Disease Stage American Joint Committee on Cancer Code	3	0.99
American Joint Committee on Cancer Tumor Stage Code	0	1.00
Cancer Type	0	1.00
Cancer Type Detailed	0	1.00
Disease Free Status	99	0.82
Ethnicity Category	152	0.72
Form completion date	0	1.00
Neoplasm Histologic Grade	3	0.99
Hemoglobin level	83	0.85
Neoplasm Histologic Type Name	0	1.00
Neoadjuvant Therapy Type Administered Prior To Resection Text	0	1.00
Prior Cancer Diagnosis Occurence	0	1.00
ICD-10 Classification	0	1.00
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Histology Code	0	1.00
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Site Code	0	1.00
Informed consent verified	0	1.00
Is FFPE	0	1.00
Primary Tumor Laterality	0	1.00
Primary Lymph Node Presentation Assessment Ind-3	7	0.99
Oncotree Code	0	1.00
Overall Survival Status	0	1.00
Other Patient ID	0	1.00
Other Sample ID	0	1.00
Pathology Report File Name	0	1.00
Pathology report uuid	0	1.00
Platelet count	93	0.83
Tissue Prospective Collection Indicator	20	0.96
Race Category	7	0.99
Tissue Retrospective Collection Indicator	18	0.97
Sample Type	0	1.00
Serum calcium level	172	0.68
Sex	0	1.00
Tumor Tissue Site	0	1.00
Tissue Source Site	0	1.00
Person Neoplasm Status	35	0.93
Vial number	0	1.00
Patient's Vital Status	3	0.99
WBC	96	0.82

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	
Diagnosis Age	0	1.00	60.59	12.15	26.00	52.00	61.00	7
Disease Free (Months)	99	0.82	40.24	31.66	-11.79	13.43	36.20	6
Fraction Genome Altered	9	0.98	0.17	0.17	0.00	0.06	0.12	
Year Cancer Initial Diagnosis	0	1.00	2006.02	2.76	1998.00	2004.00	2006.00	200
Longest Dimension	35	0.93	1.66	0.66	0.40	1.20	1.50	
Mutation Count	86	0.84	73.85	127.76	1.00	34.00	48.00	6
Overall Survival (Months)	0	1.00	44.26	32.25	0.00	18.10	38.96	6
Shortest Dimension	35	0.93	0.38	0.21	0.10	0.20	0.30	

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50
Specimen Second Longest Dimension	35	0.93	0.94	0.31	0.30	0.70	0.90

Remove character variables with unique observations:

```
kirc_clean2 <- kirc_clean1  %>%
     select(!c('Study ID', 'Cancer Type', 'Cancer Type Detailed',
               'Neoplasm Histologic Type Name', 'ICD-10 Classification',
               'International Classification of Diseases for Oncology, Third Edition ICD-O-3 Site Code'
               'Informed consent verified', 'Is FFPE', 'Oncotree Code', 'Sample Type', 'Tumor Tissue Si

skim(kirc_clean2)
```

Table 7: Data summary

Name	kirc_clean2
Number of rows	537
Number of columns	41
_____	
Column type frequency:	
character	32
numeric	9
_____	
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate
Patient ID	0	1.00
Sample ID	0	1.00
American Joint Committee on Cancer Metastasis Stage Code	2	1.00
Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code	0	1.00
Neoplasm Disease Stage American Joint Committee on Cancer Code	3	0.99
American Joint Committee on Cancer Tumor Stage Code	0	1.00
Disease Free Status	99	0.82
Ethnicity Category	152	0.72
Form completion date	0	1.00
Neoplasm Histologic Grade	3	0.99
Hemoglobin level	83	0.85
Neoadjuvant Therapy Type Administered Prior To Resection Text	0	1.00
Prior Cancer Diagnosis Occurence	0	1.00
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Histology Code	0	1.00
Primary Tumor Laterality	0	1.00
Primary Lymph Node Presentation Assessment Ind-3	7	0.99
Overall Survival Status	0	1.00
Other Patient ID	0	1.00
Other Sample ID	0	1.00
Pathology Report File Name	0	1.00
Pathology report uuid	0	1.00
Platelet count	93	0.83
Tissue Prospective Collection Indicator	20	0.96
Race Category	7	0.99

skim_variable	n_missing	complete_rate
Tissue Retrospective Collection Indicator	18	0.97
Serum calcium level	172	0.68
Sex	0	1.00
Tissue Source Site	0	1.00
Person Neoplasm Status	35	0.93
Vial number	0	1.00
Patient's Vital Status	3	0.99
WBC	96	0.82

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	
Diagnosis Age	0	1.00	60.59	12.15	26.00	52.00	61.00	7
Disease Free (Months)	99	0.82	40.24	31.66	-11.79	13.43	36.20	6
Fraction Genome Altered	9	0.98	0.17	0.17	0.00	0.06	0.12	
Year Cancer Initial Diagnosis	0	1.00	2006.02	2.76	1998.00	2004.00	2006.00	200
Longest Dimension	35	0.93	1.66	0.66	0.40	1.20	1.50	
Mutation Count	86	0.84	73.85	127.76	1.00	34.00	48.00	6
Overall Survival (Months)	0	1.00	44.26	32.25	0.00	18.10	38.96	6
Shortest Dimension	35	0.93	0.38	0.21	0.10	0.20	0.30	
Specimen Second Longest Dimension	35	0.93	0.94	0.31	0.30	0.70	0.90	

Remove character variables with similar information - check each one!

```
table(kirc_clean2$`Overall Survival Status`, exclude = NULL)
```

```
##
## DECEASED   LIVING
##      177      360
```

```
table(kirc_clean2$`Patient's Vital Status`, exclude = NULL)
```

```
##
## Alive  Dead  <NA>
##   360   174     3
```

```
kirc_clean3 <- kirc_clean2  %>%
     select(!c('Sample ID', 'Other Patient ID', 'Other Sample ID', 'Pathology Report File Name', 'Patho

# removing other variables not directly related to patient - check each one!
kirc_clean4 <- kirc_clean3  %>%
     select(!c('Form completion date','International Classification of Diseases for Oncology, Third Edi
```

3. Changing variables names

Using snake_style

```
kirc_clean4 <- kirc_clean4 %>%
     rename(patient_id = 'Patient ID',
            age = 'Diagnosis Age',
            metastasis_stg = 'American Joint Committee on Cancer Metastasis Stage Code',
```

```
            neoplasm_ln_stg = 'Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Cod
            neoplasm_stg = 'Neoplasm Disease Stage American Joint Committee on Cancer Code',
            tumor_stg = 'American Joint Committee on Cancer Tumor Stage Code',
            disease_free_mth = 'Disease Free (Months)',
            disease_free_stt = 'Disease Free Status',
            ethnicity = 'Ethnicity Category',
            frac_genome_alter = 'Fraction Genome Altered',
            histology_grd = 'Neoplasm Histologic Grade',
            hemoglobin = 'Hemoglobin level',
            neoadj_therapy = 'Neoadjuvant Therapy Type Administered Prior To Resection Text',
            prior_cancer = 'Prior Cancer Diagnosis Occurence',
            year_diagnose = 'Year Cancer Initial Diagnosis',
            tumor_lateral = 'Primary Tumor Laterality',
            long_dim = 'Longest Dimension',
            primer_ln_ind3 = 'Primary Lymph Node Presentation Assessment Ind-3',
            mutation_cnt = 'Mutation Count',
            over_surv_mth = 'Overall Survival (Months)',
            over_surv_stt = 'Overall Survival Status',
            platelet = 'Platelet count',
            tissue_prospect = 'Tissue Prospective Collection Indicator',
            race = 'Race Category',
            tissue_retrospect = 'Tissue Retrospective Collection Indicator',
            serum_ca = 'Serum calcium level',
            gender = 'Sex',
            short_dim = 'Shortest Dimension',
            second_long_dim = 'Specimen Second Longest Dimension',
            tissue_site = 'Tissue Source Site',
            person_neoplasm_stt = 'Person Neoplasm Status',
            wbc = 'WBC')
```

4. Taming data

Use lubridate for dates

```
kirc_clean4 <- kirc_clean4 %>%
     mutate_if(is.character, as.factor) %>%
     mutate(patient_id = as.character(patient_id))
```

5. Checking NA patterns

Check distincts types of NAs: MCAR, MAR, MNAR

```
kirc_clean4  %>%
     missing_plot()
```


```
missing_glimpse(kirc_clean4)
```

```
##                                label var_type   n missing_n missing_percent
## patient_id                  patient_id    <chr> 537         0             0.0
## age                                age    <dbl> 537         0             0.0
## metastasis_stg          metastasis_stg    <fct> 535         2             0.4
## neoplasm_ln_stg        neoplasm_ln_stg    <fct> 537         0             0.0
## neoplasm_stg              neoplasm_stg    <fct> 534         3             0.6
## tumor_stg                    tumor_stg    <fct> 537         0             0.0
## disease_free_mth      disease_free_mth    <dbl> 438        99            18.4
## disease_free_stt      disease_free_stt    <fct> 438        99            18.4
## ethnicity                    ethnicity    <fct> 385       152            28.3
## frac_genome_alter    frac_genome_alter    <dbl> 528         9             1.7
## histology_grd          histology_grd    <fct> 534         3             0.6
## hemoglobin                hemoglobin    <fct> 454        83            15.5
## neoadj_therapy        neoadj_therapy    <fct> 537         0             0.0
## prior_cancer            prior_cancer    <fct> 537         0             0.0
## year_diagnose          year_diagnose    <dbl> 537         0             0.0
## tumor_lateral          tumor_lateral    <fct> 537         0             0.0
## long_dim                    long_dim    <dbl> 502        35             6.5
## primer_ln_ind3        primer_ln_ind3    <fct> 530         7             1.3
## mutation_cnt            mutation_cnt    <dbl> 451        86            16.0
## over_surv_mth          over_surv_mth    <dbl> 537         0             0.0
## over_surv_stt          over_surv_stt    <fct> 537         0             0.0
## platelet                    platelet    <fct> 444        93            17.3
## tissue_prospect      tissue_prospect    <fct> 517        20             3.7
## race                            race    <fct> 530         7             1.3
```

```
## tissue_retrospect     tissue_retrospect    <fct> 519        18             3.4
## serum_ca                       serum_ca    <fct> 365       172            32.0
## gender                           gender    <fct> 537         0             0.0
## short_dim                     short_dim    <dbl> 502        35             6.5
## second_long_dim         second_long_dim    <dbl> 502        35             6.5
## tissue_site                 tissue_site    <fct> 537         0             0.0
## person_neoplasm_stt person_neoplasm_stt    <fct> 502        35             6.5
## wbc                                 wbc    <fct> 441        96            17.9
```

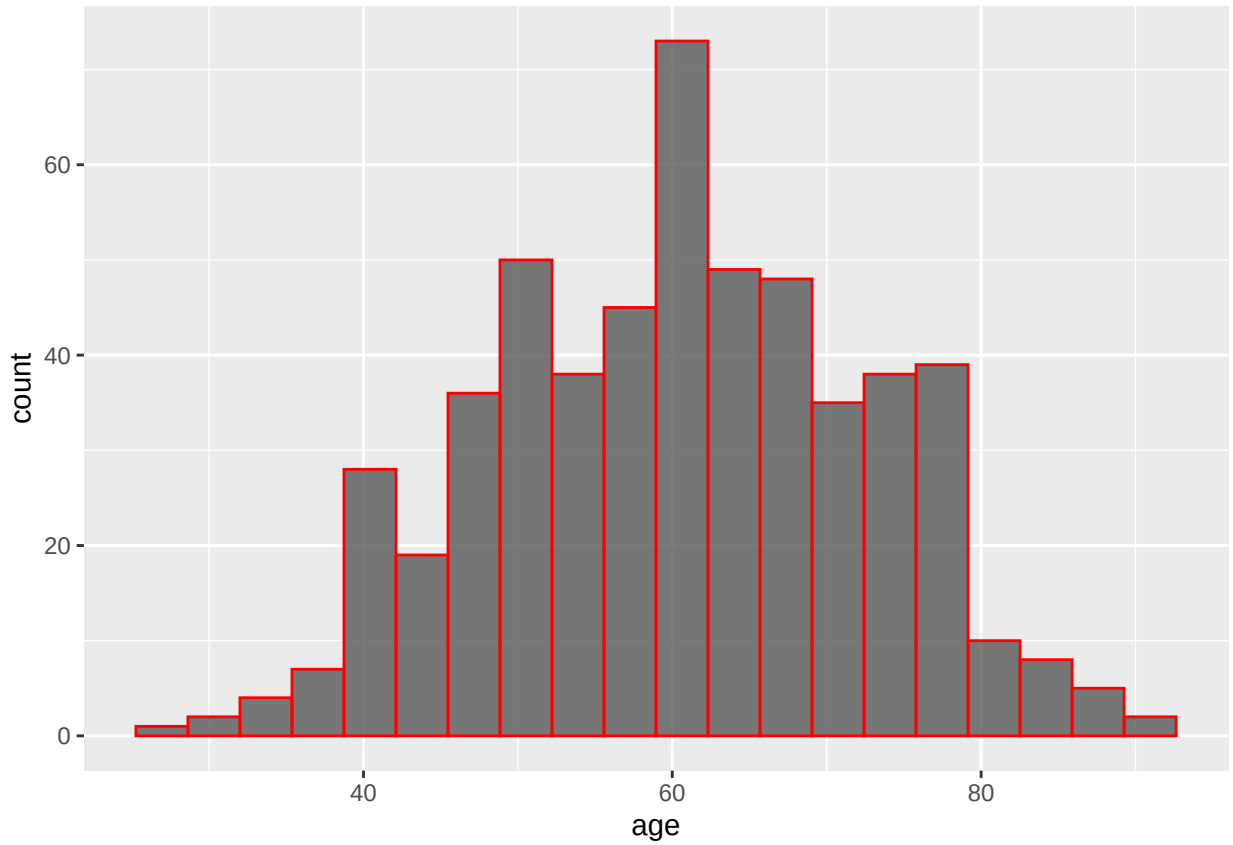
6. Checking numeric variables

Check data distribution, plausible ranges, outliers; Thinking about deleting outliers from dataset? Need to evaluate carefully each one!

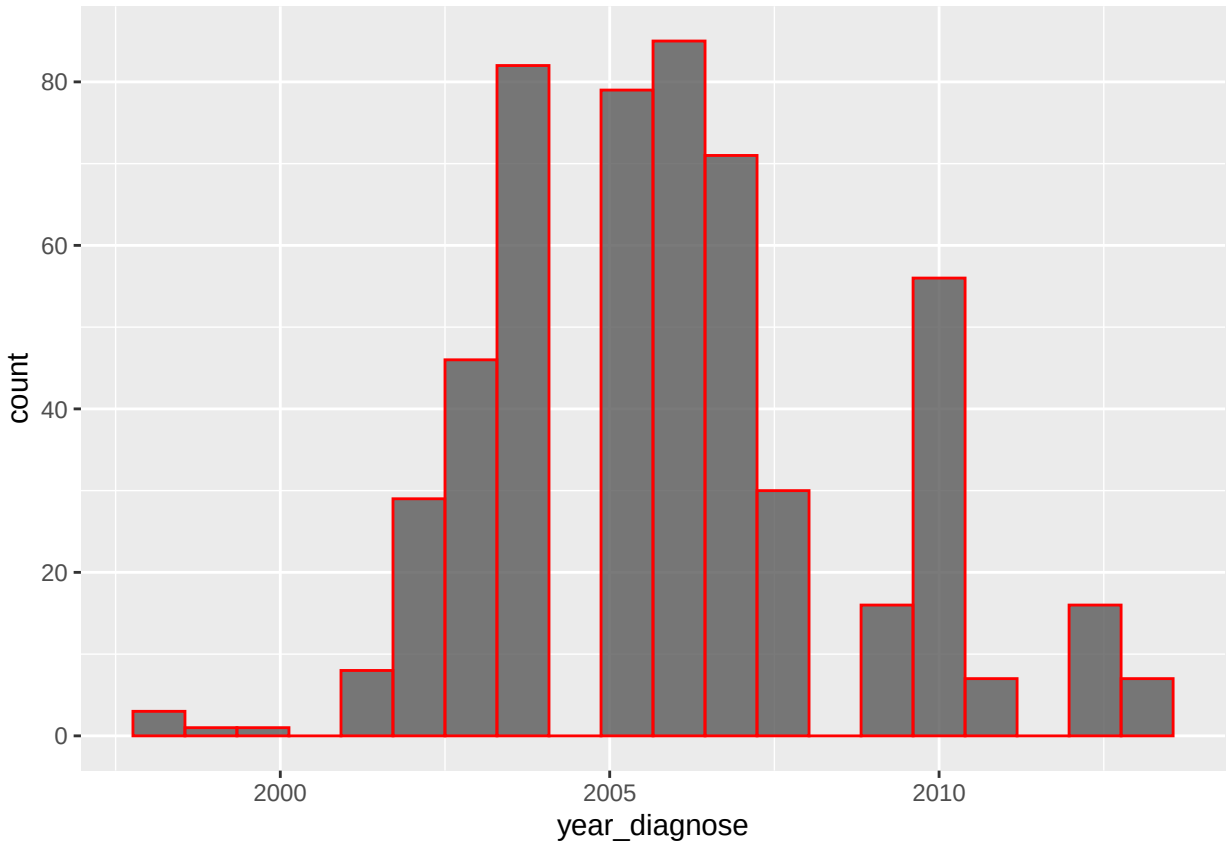
```
kirc_clean4 %>%
     select_if(is.numeric) %>%
     summary()
```

```
##       age         disease_free_mth frac_genome_alter year_diagnose
##  Min.   :26.00   Min.   :-11.79   Min.   :0.00000   Min.   :1998
##  1st Qu.:52.00   1st Qu.: 13.43   1st Qu.:0.06295   1st Qu.:2004
##  Median :61.00   Median : 36.20   Median :0.12065   Median :2006
##  Mean   :60.59   Mean   : 40.24   Mean   :0.17016   Mean   :2006
##  3rd Qu.:70.00   3rd Qu.: 60.51   3rd Qu.:0.20885   3rd Qu.:2007
##  Max.   :90.00   Max.   :133.84   Max.   :0.94770   Max.   :2013
##                  NA's   :99       NA's   :9
##     long_dim      mutation_cnt     over_surv_mth      short_dim
##  Min.   :0.400   Min.   :   1.00   Min.   :  0.00   Min.   :0.1000
##  1st Qu.:1.200   1st Qu.:  34.00   1st Qu.: 18.10   1st Qu.:0.2000
##  Median :1.500   Median :  48.00   Median : 38.96   Median :0.3000
##  Mean   :1.662   Mean   :  73.85   Mean   : 44.26   Mean   :0.3759
##  3rd Qu.:2.000   3rd Qu.:  65.50   3rd Qu.: 63.21   3rd Qu.:0.5000
##  Max.   :4.000   Max.   :1392.00   Max.   :149.05   Max.   :1.0000
##  NA's   :35      NA's   :86                         NA's   :35
##  second_long_dim
##  Min.   :0.3000
##  1st Qu.:0.7000
##  Median :0.9000
##  Mean   :0.9368
##  3rd Qu.:1.1000
##  Max.   :2.0000
##  NA's   :35
```

```
ggplot(kirc_clean4, aes(age)) +
     geom_histogram(bins = 20, alpha = 0.8, color = "red")
```



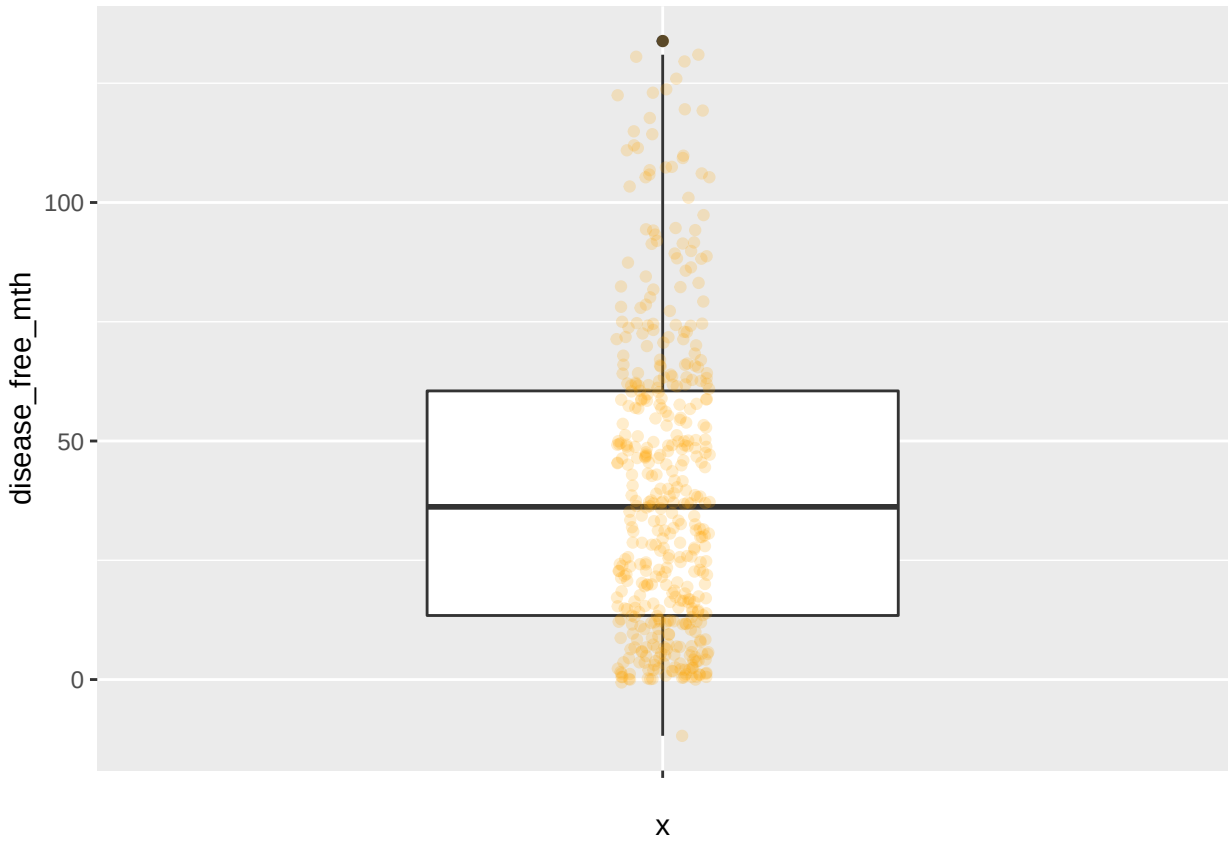

```
ggplot(kirc_clean4, aes(year_diagnose)) +
     geom_histogram(bins = 20, alpha = 0.8, color = "red")
```




```
ggplot(kirc_clean4, aes(x ='', y=disease_free_mth)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 99 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 99 rows containing missing values (geom_point).
```




```
boxplot.stats(kirc_clean4$disease_free_mth)
```

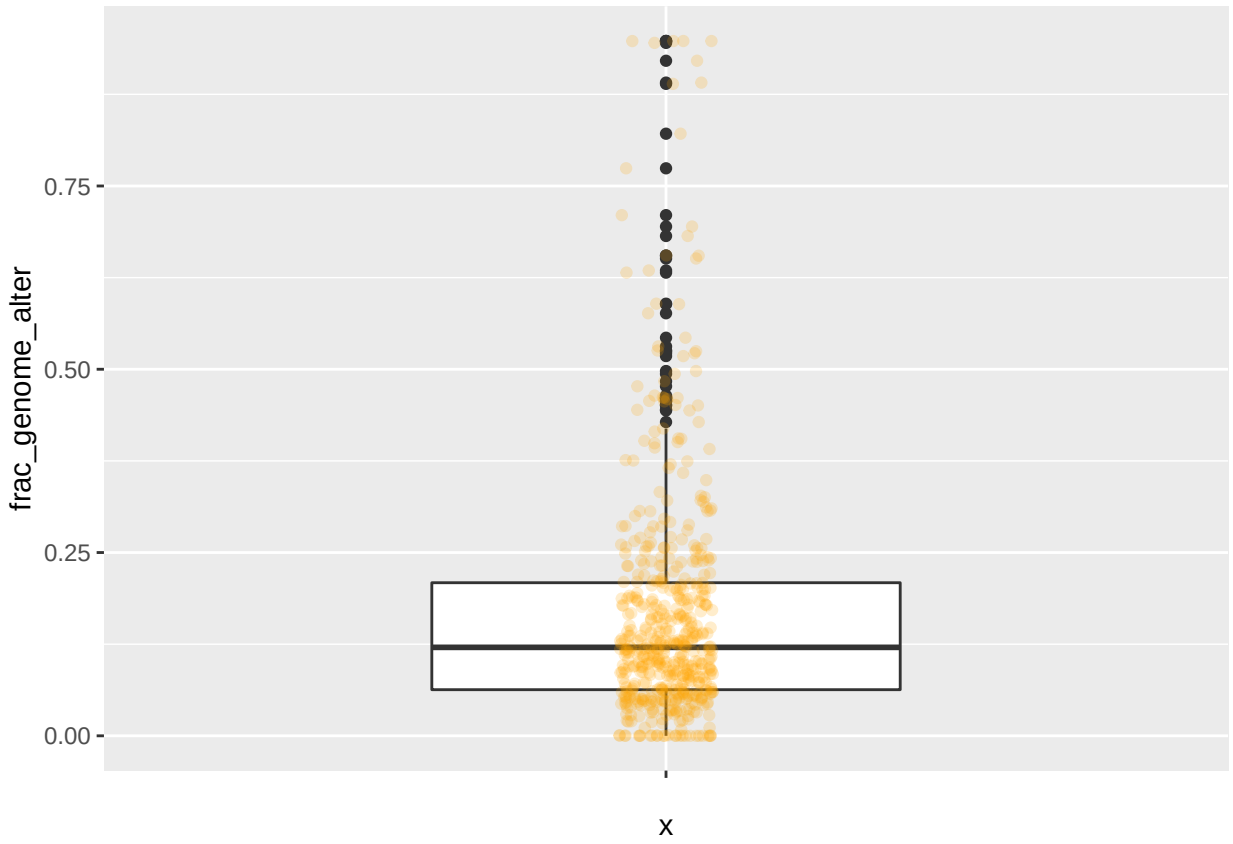
```
## $stats
## [1] -11.79  13.40  36.20  60.55 130.98
##
## $n
## [1] 438
##
## $conf
## [1] 32.6404 39.7596
##
## $out
## [1] 133.84
```

```
# filter(disease_free_mth >= 0)
```

```
ggplot(kirc_clean4, aes(x ='', y=frac_genome_alter)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 9 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 9 rows containing missing values (geom_point).
```



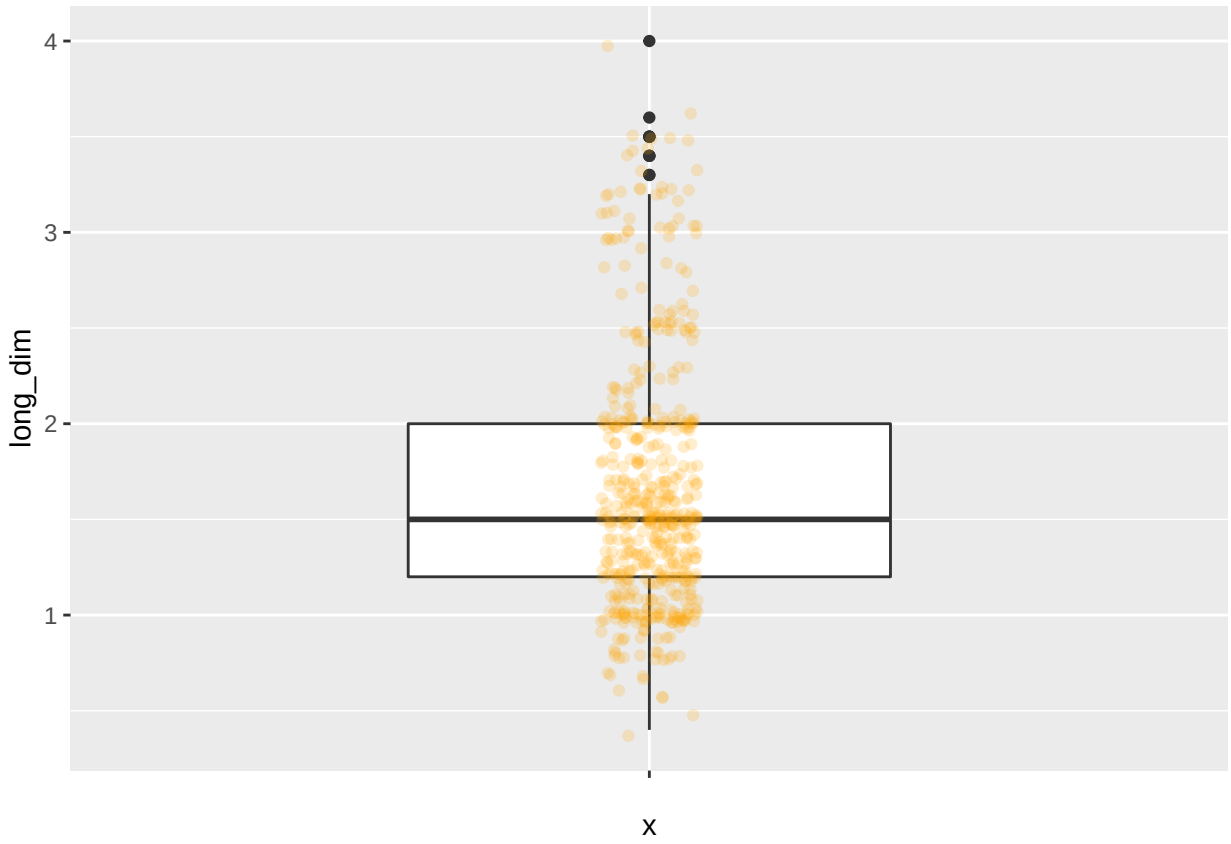

```
boxplot.stats(kirc_clean4$frac_genome_alter)
```

```
## $stats
## [1] 0.00000 0.06290 0.12065 0.20920 0.42800
##
## $n
## [1] 528
##
## $conf
## [1] 0.1105903 0.1307097
##
## $out
##  [1] 0.8213 0.6552 0.4608 0.9477 0.5888 0.9208 0.7741 0.4837 0.9477 0.4610
## [11] 0.6549 0.6511 0.5180 0.8910 0.8893 0.9477 0.5246 0.4568 0.4937 0.9477
## [21] 0.4438 0.6947 0.5218 0.4768 0.4593 0.4447 0.9452 0.6347 0.5311 0.4562
## [31] 0.4617 0.5256 0.6318 0.5430 0.4506 0.5764 0.7102 0.4641 0.5894 0.4976
## [41] 0.4513 0.6818
```

```
ggplot(kirc_clean4, aes(x ='', y=long_dim)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 35 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 35 rows containing missing values (geom_point).
```



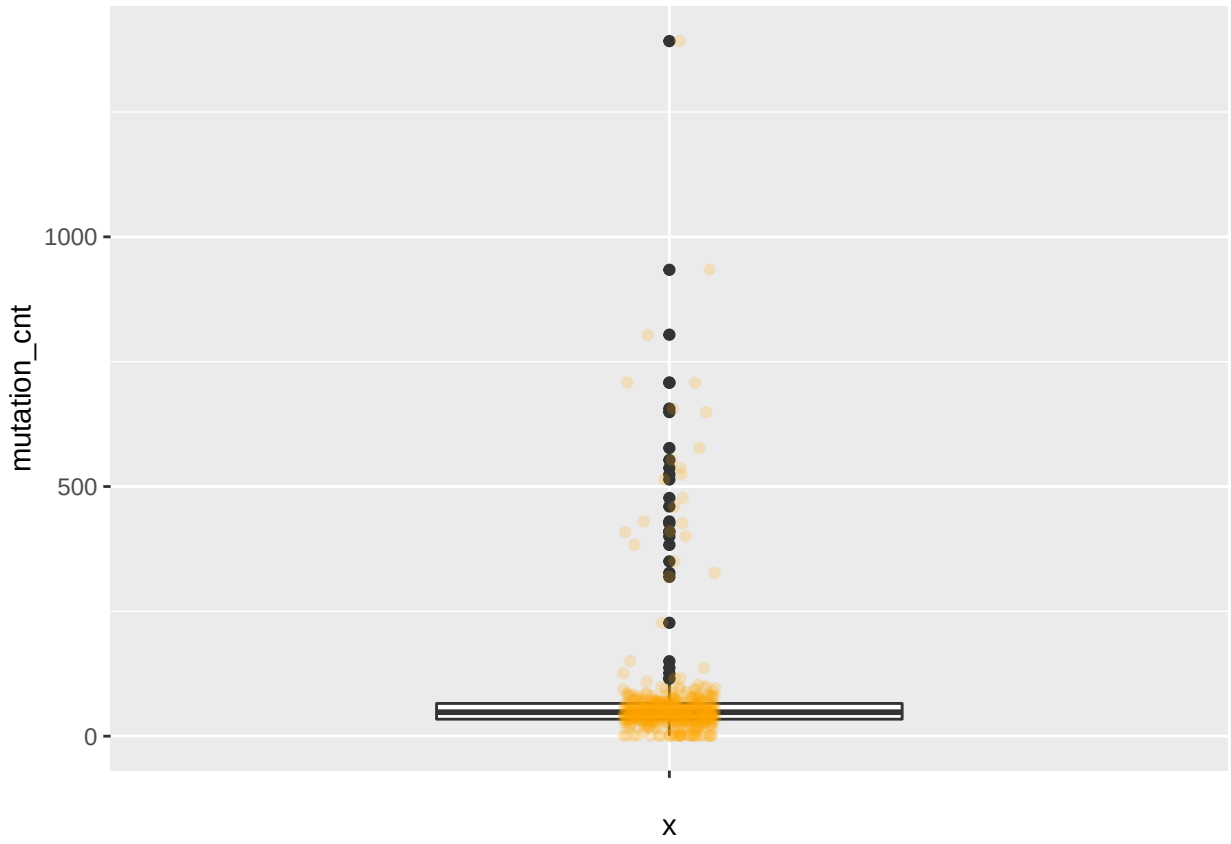

```
boxplot.stats(kirc_clean4$long_dim)
```

```
## $stats
## [1] 0.4 1.2 1.5 2.0 3.2
##
## $n
## [1] 502
##
## $conf
## [1] 1.443585 1.556415
##
## $out
##  [1] 3.3 4.0 3.3 3.5 3.4 3.5 3.5 3.4 3.4 3.5 3.6
```

```
ggplot(kirc_clean4, aes(x ='', y=mutation_cnt)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 86 rows containing non-finite values (stat_boxplot).
```

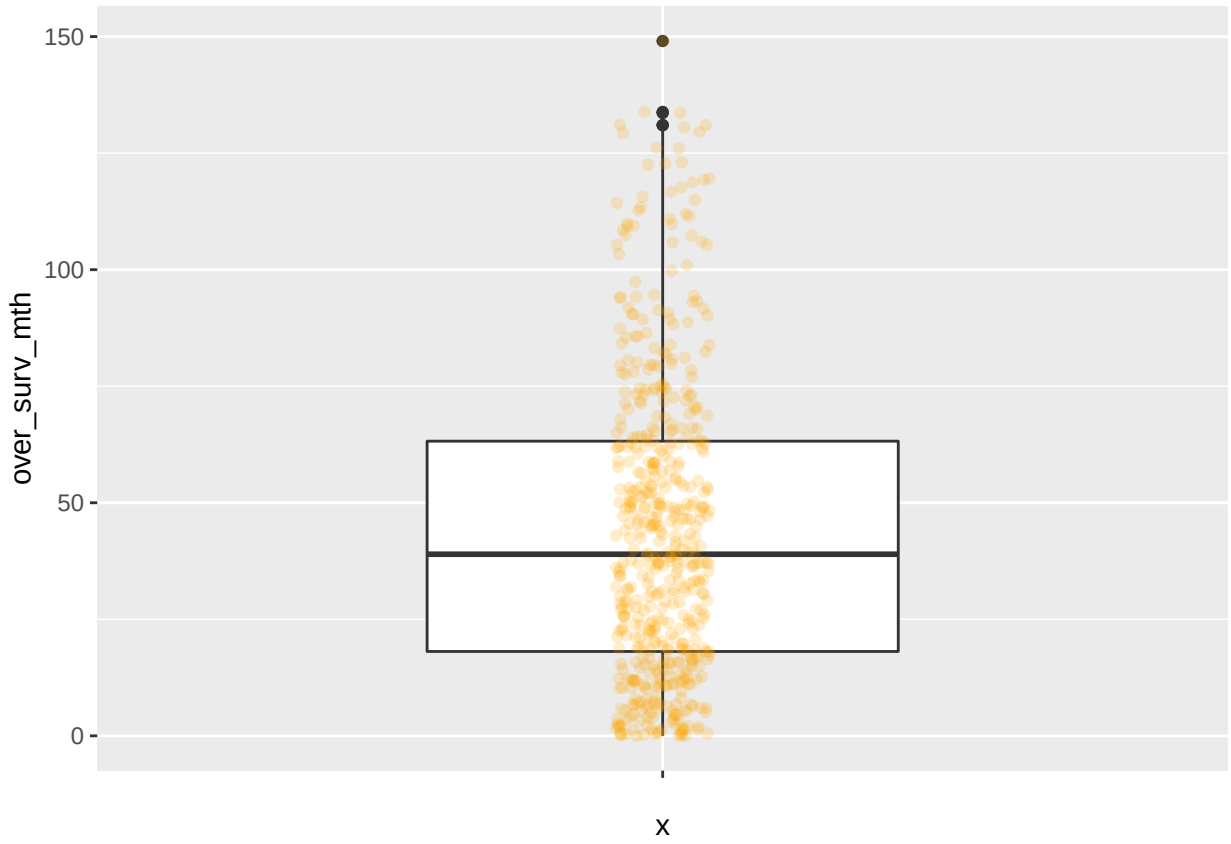
```
## Warning: Removed 86 rows containing missing values (geom_point).
```




```
boxplot.stats(kirc_clean4$mutation_cnt)
```

```
## $stats
## [1]   1.0  34.0  48.0  65.5 109.0
##
## $n
## [1] 451
##
## $conf
## [1] 45.65642 50.34358
##
## $out
##  [1]  514  656  577  537  477  150  137  708 1392  460  327  934  409  383  804
## [16]  319  524  426  227  553  400  350  410  430  708  649  126  116  115
```

```
ggplot(kirc_clean4, aes(x ='', y=over_surv_mth)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```



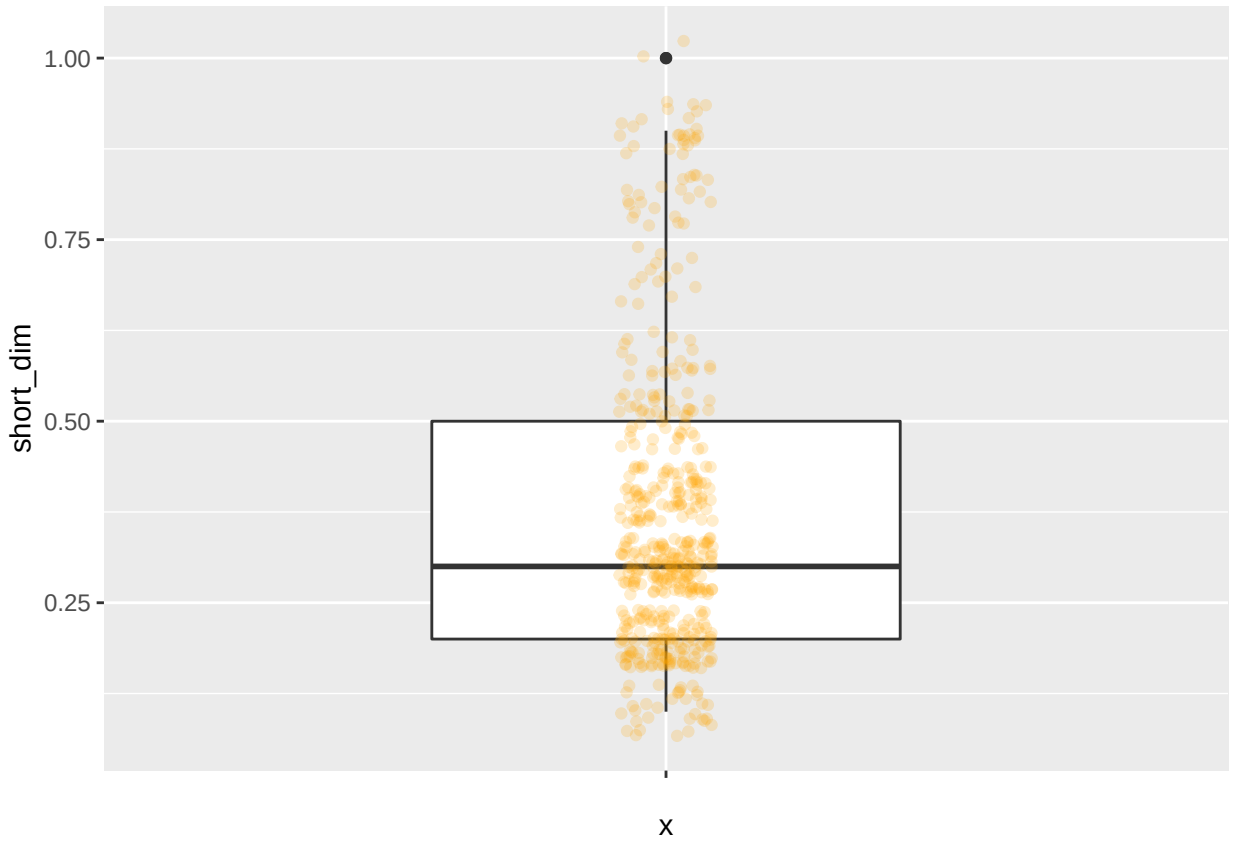

```
boxplot.stats(kirc_clean4$over_surv_mth)
```

```
## $stats
## [1]   0.00  18.10  38.96  63.21 130.55
##
## $n
## [1] 537
##
## $conf
## [1] 35.88431 42.03569
##
## $out
## [1] 133.84 149.05 131.04 130.98 133.61
```

```
ggplot(kirc_clean4, aes(x ='', y=short_dim)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 35 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 35 rows containing missing values (geom_point).
```



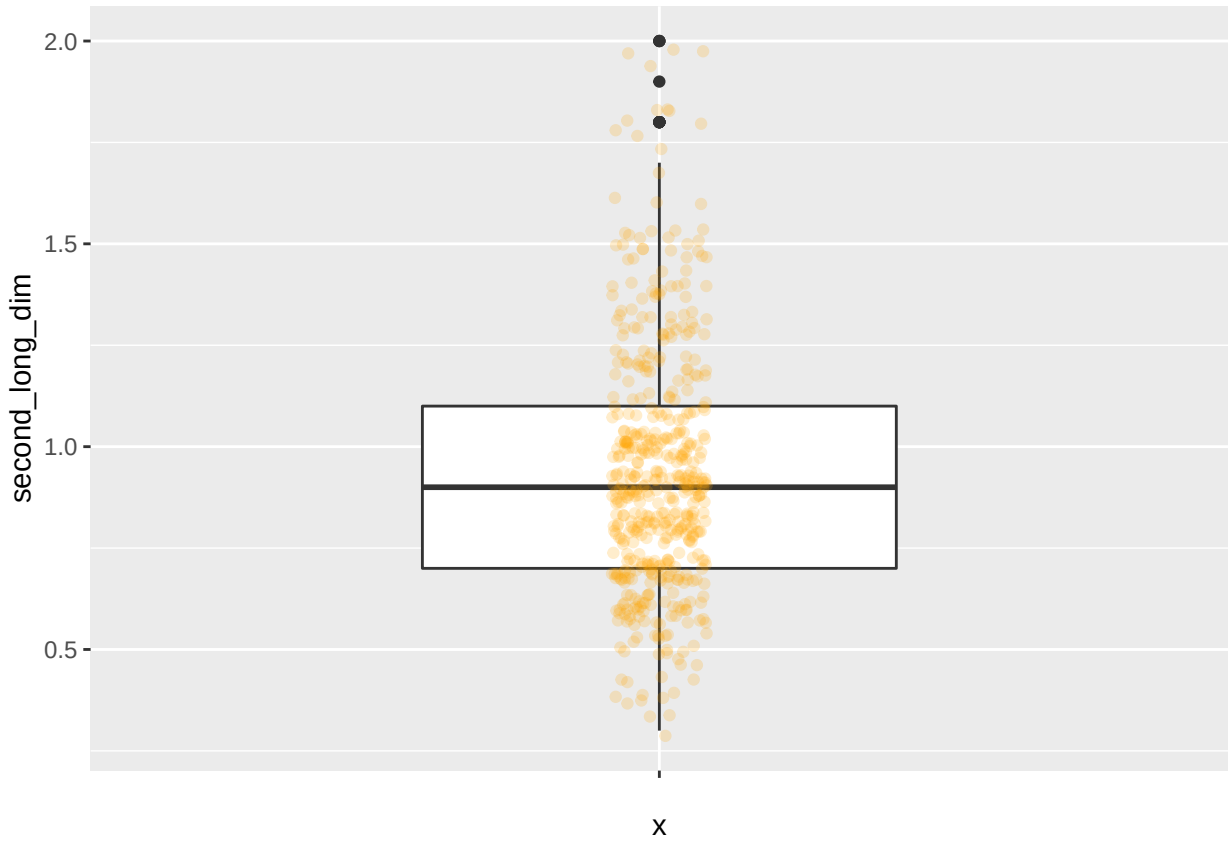

```
boxplot.stats(kirc_clean4$short_dim)
```

```
## $stats
## [1] 0.1 0.2 0.3 0.5 0.9
##
## $n
## [1] 502
##
## $conf
## [1] 0.2788443 0.3211557
##
## $out
## [1] 1 1
```

```
ggplot(kirc_clean4, aes(x ='', y=second_long_dim)) +
     geom_boxplot(width = .5) +
     geom_jitter(width = 0.05, alpha = 0.2, color = "orange")
```

```
## Warning: Removed 35 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 35 rows containing missing values (geom_point).
```




```
boxplot.stats(kirc_clean4$second_long_dim)
```

```
## $stats
## [1] 0.3 0.7 0.9 1.1 1.7
##
## $n
## [1] 502
##
## $conf
## [1] 0.8717925 0.9282075
##
## $out
##  [1] 1.8 2.0 1.8 1.9 1.8 2.0 2.0 1.8 1.8 1.8 1.8
```

7. Checking categorical variables

Check frequency, lables and levels

```
kirc_clean4 %>%
     select_if(is.factor) %>%
     summary()
```

```
##  metastasis_stg neoplasm_ln_stg    neoplasm_stg   tumor_stg
##  M0  :426       N0:240          Stage I  :269   T1a    :142
##  M1  : 79       N1: 17          Stage II : 57   T3a    :122
##  MX  : 30       NX:280          Stage III:125   T1b    :111
##  NA's:  2                       Stage IV : 83   T2     : 55
```

```
##                                NA's     :  3   T3b    : 53
##                                               T1     : 22
##                                               (Other): 32
##             disease_free_stt                  ethnicity   histology_grd
##  DiseaseFree        :311     HISPANIC OR LATINO    : 26   G1  : 14
##  Recurred/Progressed:127     NOT HISPANIC OR LATINO:359   G2  :230
##  NA's               : 99     NA's                  :152   G3  :207
##                                                           G4  : 78
##                                                           GX  :  5
##                                                           NA's:  3
##
##     hemoglobin  neoadj_therapy
##  Elevated:  5   No :519
##  Low     :263   Yes: 18
##  Normal  :186
##  NA's    : 83
##
##
##
##                                          prior_cancer   tumor_lateral
##  No                                            :459   Bilateral:  1
##  Yes                                           : 72   Left     :253
##  Yes, History of Prior Malignancy              :  2   Right    :283
##  Yes, History of Synchronous/Bilateral Malignancy:  4
##
##
##
##  primer_ln_ind3  over_surv_stt     platelet   tissue_prospect
##  NO  :395        DECEASED:177   Elevated: 38   NO  :465
##  YES :135        LIVING  :360   Low     : 46   YES : 52
##  NA's:  7                       Normal  :360   NA's: 20
##                                 NA's    : 93
##
##
##
##                          race     tissue_retrospect     serum_ca      gender
##  ASIAN                     :  8   NO  : 53          Elevated: 10   Female:191
##  BLACK OR AFRICAN AMERICAN: 56   YES :466          Low     :204   Male  :345
##  WHITE                     :466   NA's: 18          Normal  :151   MALE  :  1
##  NA's                      :  7                     NA's    :172
##
##
##
##   tissue_site  person_neoplasm_stt       wbc
##  BP     :142   TUMOR FREE:361      Elevated:164
##  B0     :107   WITH TUMOR:141      Low     :  9
##  CJ     : 71   NA's      : 35      Normal  :268
##  A3     : 52                       NA's    : 96
##  CZ     : 40
##  B8     : 33
##  (Other): 92
```

```
# agregating levels
kirc_clinic <- kirc_clean4 %>%
```

```
    mutate(tumor_stg = fct_collapse(tumor_stg,
                            T1 = c('T1', 'T1a', 'T1b'),
                            T2 = c('T2', 'T2a', 'T2b'),
                            T3 = c('T3', 'T3a', 'T3b', 'T3c')))

kirc_clinic <- kirc_clinic %>%
    mutate(prior_cancer = fct_collapse(prior_cancer,
              Yes = c('Yes', 'Yes, History of Prior Malignancy', 'Yes, History of Synchronous/Bilateral

kirc_clinic <- kirc_clinic %>%
    mutate(gender = fct_collapse(gender, Male = c('MALE', 'Male')))

kirc_clinic <- kirc_clinic %>%
    mutate(tissue_site = fct_collapse(tissue_site,
                          A = c('A3', 'AK', 'AS'),
                          B = c('B0', 'B2', 'B4', 'B8', 'BP'),
                          C = c('CJ', 'CW', 'CZ'),
                          OTHERS = c('G6', 'GK', 'MM', 'MW',
                                     '3Z', '6D', 'DV', 'EU', 'T7')))

# droping levels
kirc_clinic <- kirc_clinic %>%
    mutate(race = fct_recode(race, NULL = 'ASIAN'))

# kirc_clinic <- kirc_clinic %>%
#     mutate(race = fct_drop(race, only = 'ASIAN'))

# recoding levels
# OBS: It can be donne latter, for regression analysis
#
# kirc_clinic <- kirc_clinic %>%
#     mutate(gender = fct_recode(gender, '1'='Male', '2'='Female'))
#
# kirc_clinic <- kirc_clinic %>%
#     mutate(gender = if_else(gender %in% c('Male', 'Female'), 1, 0))
```

```
# table(kirc_clinic$metastasis_stg, exclude = NULL)
# table(kirc_clinic$neoplasm_ln_stg, exclude = NULL)
# table(kirc_clinic$neoplasm_stg, exclude = NULL)
# table(kirc_clinic$tumor_stg, exclude = NULL)
# table(kirc_clinic$disease_free_stt, exclude = NULL)
# table(kirc_clinic$ethnicity, exclude = NULL)
# table(kirc_clinic$histology_grd, exclude = NULL)
# table(kirc_clinic$hemoglobin, exclude = NULL)
# table(kirc_clinic$neoadj_therapy, exclude = NULL)
# table(kirc_clinic$prior_cancer, exclude = NULL)
# table(kirc_clinic$tumor_lateral, exclude = NULL)
# table(kirc_clinic$primer_ln_ind3, exclude = NULL)
# table(kirc_clinic$platelet, exclude = NULL)
# table(kirc_clinic$tissue_prospect, exclude = NULL)
# table(kirc_clinic$race, exclude = NULL)
# table(kirc_clinic$tissue_retrospect, exclude = NULL)
# table(kirc_clinic$serum_ca, exclude = NULL)
# table(kirc_clinic$gender, exclude = NULL)
```

```
# table(kirc_clinic$tissue_site, exclude = NULL)
# table(kirc_clinic$person_neoplasm_stt, exclude = NULL)
# table(kirc_clinic$wbc, exclude = NULL)
```

8. Saving dataset

```
write_csv(kirc_clinic, path = "data/kirc_clinic.csv")

rm(kirc_clean4, kirc_clean3, kirc_clean2, kirc_clean1, kirc_clean0, kirc_clean, NA_sum, NA_fifty)
```

Further analysis

- A correlation analysis with t-test and ANOVA checking significant distinction between variables acording their vital status.
- 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/libopenblasp-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] Rcpp_1.0.4.6     lubridate_1.7.8  lattice_0.20-41  assertthat_0.2.1
##  [5] digest_0.6.25    utf8_1.1.4       R6_2.4.1         cellranger_1.1.0
##  [9] repr_1.1.0       backports_1.1.6  reprex_0.3.0     evaluate_0.14
## [13] httr_1.4.1       highr_0.8        pillar_1.4.4     rlang_0.4.6
## [17] readxl_1.3.1     rstudioapi_0.11  Matrix_1.2-18    rmarkdown_2.1
## [21] labeling_0.3     splines_3.6.3    munsell_0.5.0    broom_0.5.6
## [25] compiler_3.6.3   modelr_0.1.7     xfun_0.13        pkgconfig_2.0.3
## [29] base64enc_0.1-3  htmltools_0.4.0  tidyselect_1.1.0 fansi_0.4.1
## [33] crayon_1.3.4     dbplyr_1.4.3     withr_2.2.0      grid_3.6.3
```

```
## [37] nlme_3.1-147     jsonlite_1.6.1   gtable_0.3.0     lifecycle_0.2.0
## [41] DBI_1.1.0        magrittr_1.5     scales_1.1.1     cli_2.0.2
## [45] stringi_1.4.6    farver_2.0.3     fs_1.4.1         mice_3.8.0
## [49] xml2_1.3.2       ellipsis_0.3.0   generics_0.0.2   vctrs_0.3.0
## [53] boot_1.3-25      tools_3.6.3      glue_1.4.0       hms_0.5.3
## [57] survival_3.1-12  yaml_2.2.1       colorspace_1.4-1 rvest_0.3.5
## [61] knitr_1.28       haven_2.2.0
```