A Preprocessing analysis of clinical data of TCGA-KIRC patients

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

In this section, the initial preprocessing is applied to clean the data and arrange following the Tidyverse philosophy. Exploratory Data Analysis summarizes their main characteristics.

```
## 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 = '.')
try(knitr::purl(input,output,documentation=2,quiet=T), silent=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/1-prep_"
)
```

1. Data importing and visualizing

```
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:

```r
kirc_clean0 %>%
     select_if(is.numeric) %>%
     skim()
```

Table 1: Data summary

Name	Piped data
Number of rows	537
Number of columns	12
Column type frequency:	
numeric	12
Group variables	None

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
Diagnosis Age	0	1.00	60.59	12.15	26.00	52.00	61.00	70.00	90.00	
Last Alive Less Initial Pathologic Diagnosis Date Calculated Day Value	0	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Disease Free (Months)	99	0.82	40.24	31.66	-11.79	13.43	36.20	60.51	133.84	
Fraction Genome Altered	9	0.98	0.17	0.17	0.00	0.06	0.12	0.21	0.95	
Year Cancer Initial Diagnosis	0	1.00	2006.02	2.76	1998.00	2004.00	2006.00	2007.00	2013.00	
Longest Dimension	35	0.93	1.66	0.66	0.40	1.20	1.50	2.00	4.00	
Mutation Count	86	0.84	73.85	127.76	1.00	34.00	48.00	65.50	1392.00	
Overall Survival (Months)	0	1.00	44.26	32.25	0.00	18.10	38.96	63.21	149.05	
Number of Samples Per Patient	0	1.00	1.00	0.04	1.00	1.00	1.00	1.00	2.00	
Sample type id	0	1.00	1.00	0.00	1.00	1.00	1.00	1.00	1.00	
Shortest Dimension	35	0.93	0.38	0.21	0.10	0.20	0.30	0.50	1.00	
Specimen Second Longest Dimension	35	0.93	0.94	0.31	0.30	0.70	0.90	1.10	2.00	

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

Remove character variables with unique observations:

```r
kirc_clean1 %>%
  select_if(is.character) %>%
  skim()
```

Table 3: Data summary

Name	Piped data
Number of rows	537
Number of columns	43

Table 3: Data summary

Column type frequency:	
character	43
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate	min	max	empty	n_unique	whitespace
Study ID	0	1.00	9	9	0	1	0
Patient ID	0	1.00	12	12	0	537	0
Sample ID	0	1.00	15	15	0	537	0
American Joint Committee on Cancer Metastasis Stage Code	2	1.00	2	2	0	3	0
Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code	0	1.00	2	2	0	3	0
Neoplasm Disease Stage American Joint Committee on Cancer Code	3	0.99	7	9	0	4	0
American Joint Committee on Cancer Tumor Stage Code	0	1.00	2	3	0	11	0
Cancer Type	0	1.00	20	20	0	1	0
Cancer Type Detailed	0	1.00	26	26	0	1	0
Disease Free Status	99	0.82	11	19	0	2	0
Ethnicity Category	152	0.72	18	22	0	2	0
Form completion date	0	1.00	6	10	0	114	0
Neoplasm Histologic Grade	3	0.99	2	2	0	5	0
Hemoglobin level	83	0.85	3	8	0	3	0
Neoplasm Histologic Type Name	0	1.00	33	33	0	1	0
Neoadjuvant Therapy Type Administered Prior To Resection Text	0	1.00	2	3	0	2	0
Prior Cancer Diagnosis Occurence	0	1.00	2	48	0	4	0
ICD-10 Classification	0	1.00	5	5	0	1	0
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Histology Code	0	1.00	6	6	0	2	0
International Classification of Diseases for Oncology, Third Edition ICD-O-3 Site Code	0	1.00	5	5	0	1	0
Informed consent verified	0	1.00	3	3	0	1	0
Is FFPE	0	1.00	2	2	0	1	0
Primary Tumor Laterality	0	1.00	4	9	0	3	0
Primary Lymph Node Presentation Assessment Ind-3	7	0.99	2	3	0	2	0
Oncotree Code	0	1.00	5	5	0	1	0
Overall Survival Status	0	1.00	6	8	0	2	0
Other Patient ID	0	1.00	36	36	0	537	0
Other Sample ID	0	1.00	36	36	0	537	0
Pathology Report File Name	0	1.00	53	53	0	537	0
Pathology report uuid	0	1.00	36	36	0	537	0
Platelet count	93	0.83	3	8	0	3	0
Tissue Prospective Collection Indicator	20	0.96	2	3	0	2	0
Race Category	7	0.99	5	25	0	3	0
Tissue Retrospective Collection Indicator	18	0.97	2	3	0	2	0
Sample Type	0	1.00	7	7	0	1	0

skim_variable	n_missing	complete_rate	min	max	empty	n_unique	whitespace
Serum calcium level	172	0.68	3	8	0	3	0
Sex	0	1.00	4	6	0	3	0
Tumor Tissue Site	0	1.00	6	6	0	1	0
Tissue Source Site	0	1.00	2	2	0	20	0
Person Neoplasm Status	35	0.93	10	10	0	2	0
Vial number	0	1.00	1	1	0	2	0
Patient's Vital Status	3	0.99	4	5	0	2	0
WBC	96	0.82	3	8	0	3	0

```
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
```

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', 'Pathol
```

Remove 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',
            lymph_stg = 'Neoplasm Disease Lymph Node Stage American Joint Committee on Cancer Code',
            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',
            mutation_cnt = 'Mutation Count',
            over_surv_mth = 'Overall Survival (Months)',
            over_surv_stt = 'Overall Survival Status',
            platelet = 'Platelet count',
            race = 'Race Category',
            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

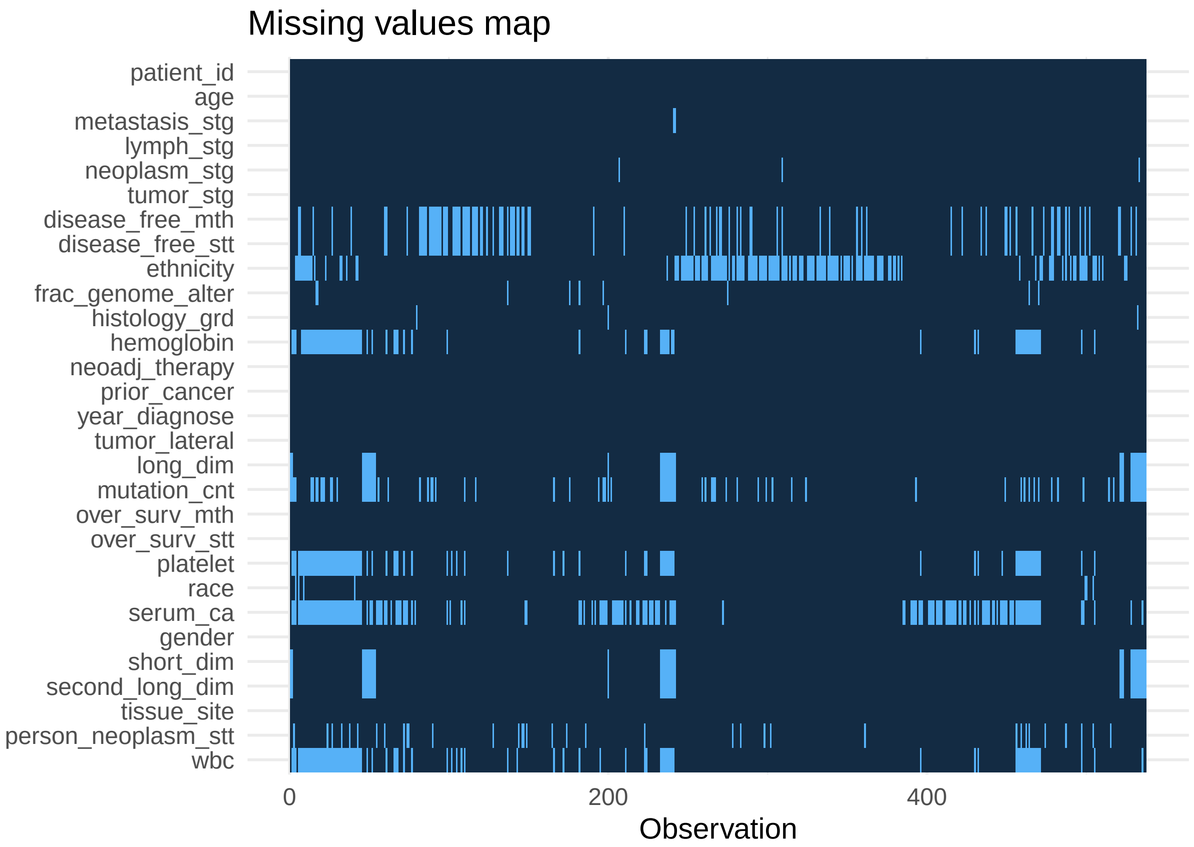
Use lubridate for dates

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

5. Checking NA patterns

Check distincts types of NAs: MCAR, MAR, MNAR

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



```r
missing_glimpse(kirc_clean4)  %>% knitr::kable(.)
```

	label	var_type	n	missing_n	missing_percent
patient_id	patient_id		537	0	0.0
age	age		537	0	0.0
metastasis_stg	metastasis_stg		535	2	0.4
lymph_stg	lymph_stg		537	0	0.0
neoplasm_stg	neoplasm_stg		534	3	0.6
tumor_stg	tumor_stg		537	0	0.0
disease_free_mth	disease_free_mth		438	99	18.4
disease_free_stt	disease_free_stt		438	99	18.4
ethnicity	ethnicity		385	152	28.3
frac_genome_alter	frac_genome_alter		528	9	1.7
histology_grd	histology_grd		534	3	0.6
hemoglobin	hemoglobin		454	83	15.5
neoadj_therapy	neoadj_therapy		537	0	0.0
prior_cancer	prior_cancer		537	0	0.0
year_diagnose	year_diagnose		537	0	0.0
tumor_lateral	tumor_lateral		537	0	0.0
long_dim	long_dim		502	35	6.5
mutation_cnt	mutation_cnt		451	86	16.0
over_surv_mth	over_surv_mth		537	0	0.0
over_surv_stt	over_surv_stt		537	0	0.0
platelet	platelet		444	93	17.3
race	race		530	7	1.3
serum_ca	serum_ca		365	172	32.0
gender	gender		537	0	0.0

	label	var_type	n	missing_n	missing_percent
short_dim	short_dim		502	35	6.5
second_long_dim	second_long_dim		502	35	6.5
tissue_site	tissue_site		537	0	0.0
person_neoplasm_stt	person_neoplasm_stt		502	35	6.5
wbc	wbc		441	96	17.9

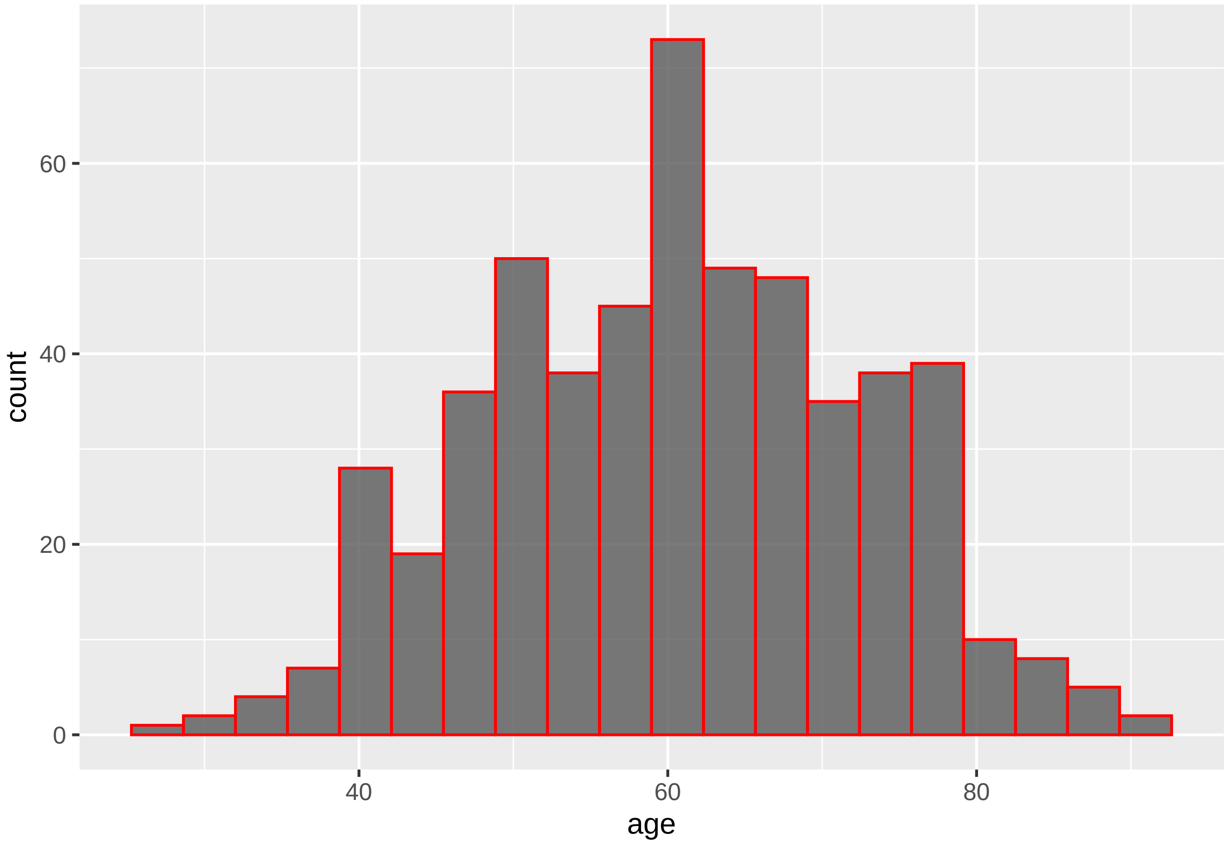
6. Checking numeric variables

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

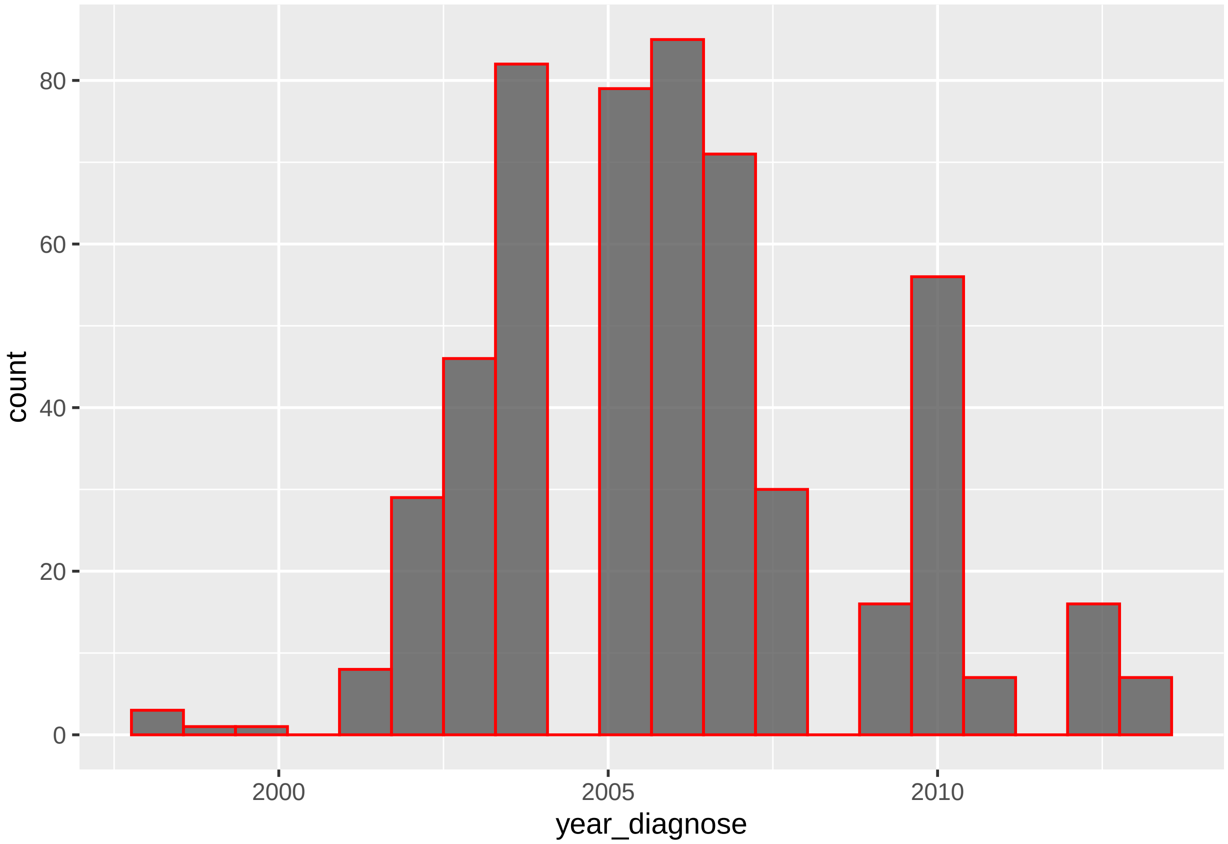
```
kirc_clean4 %>%
     select_if(is.numeric) %>%
     summary()
```

```
##       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")
```



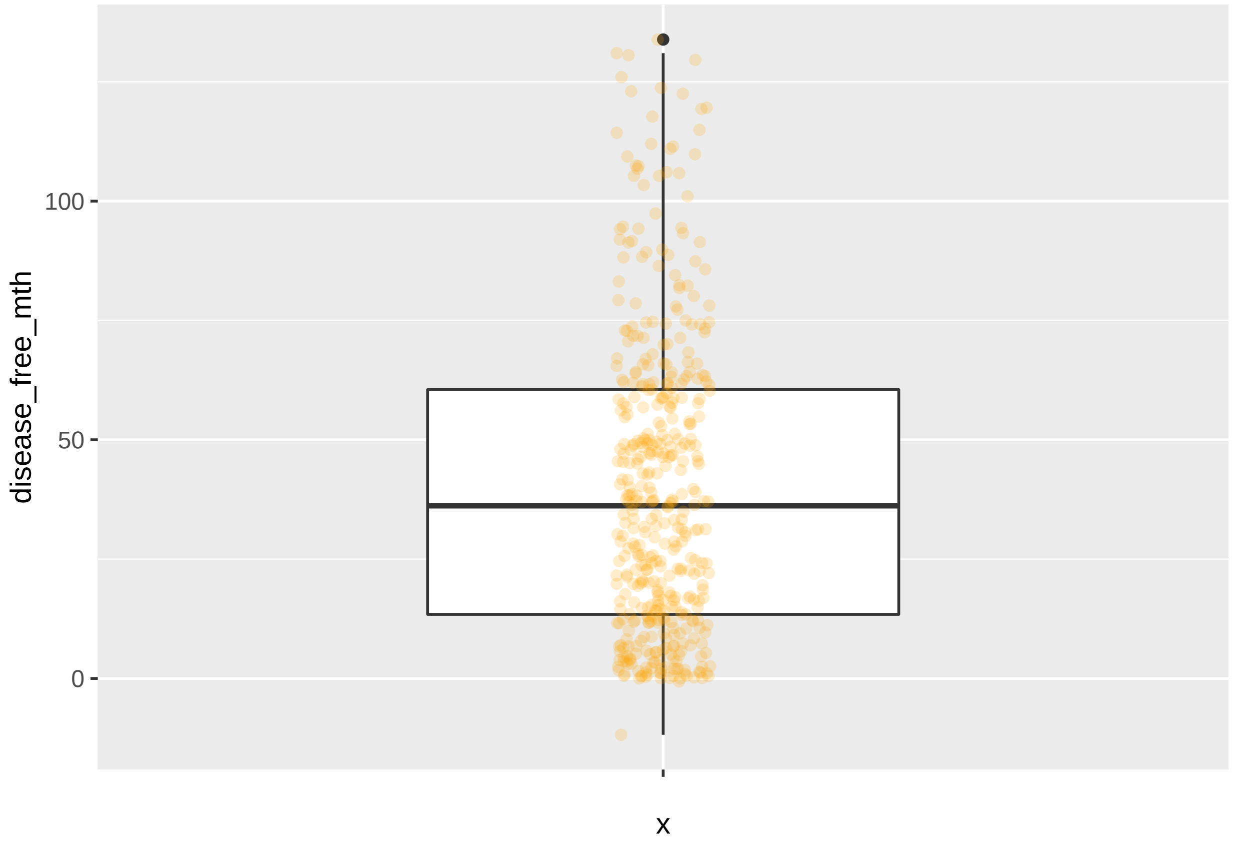
```
ggplot(kirc_clean4, aes(year_diagnose)) +
    geom_histogram(bins = 20, alpha = 0.8, color = "red")
```



```
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).
```



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

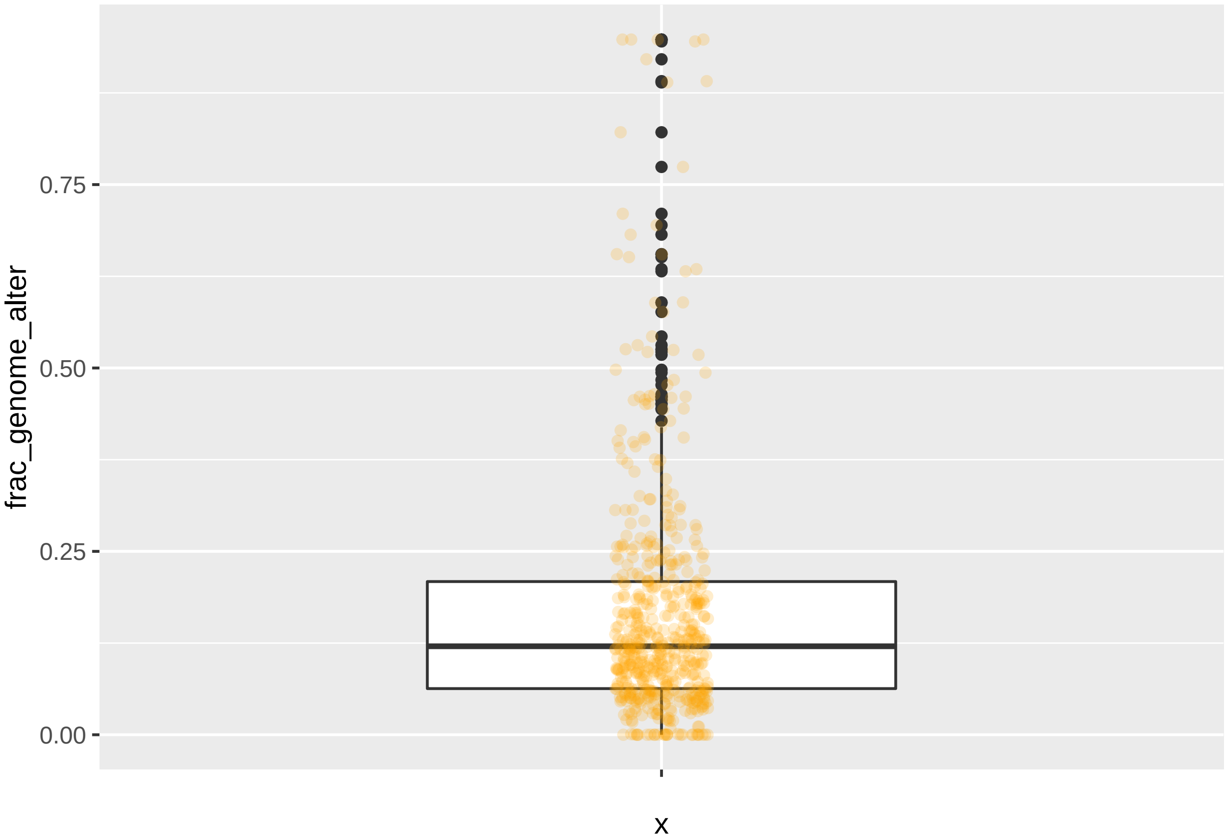
```
## $stats
## [1] -11.79  13.40  36.20  60.55 130.98
##
## $n
## [1] 438
##
## $conf
## [1] 32.6404 39.7596
##
## $out
## [1] 133.84
```

```r
# error: disease_free_mth < 0
```

```r
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).
```



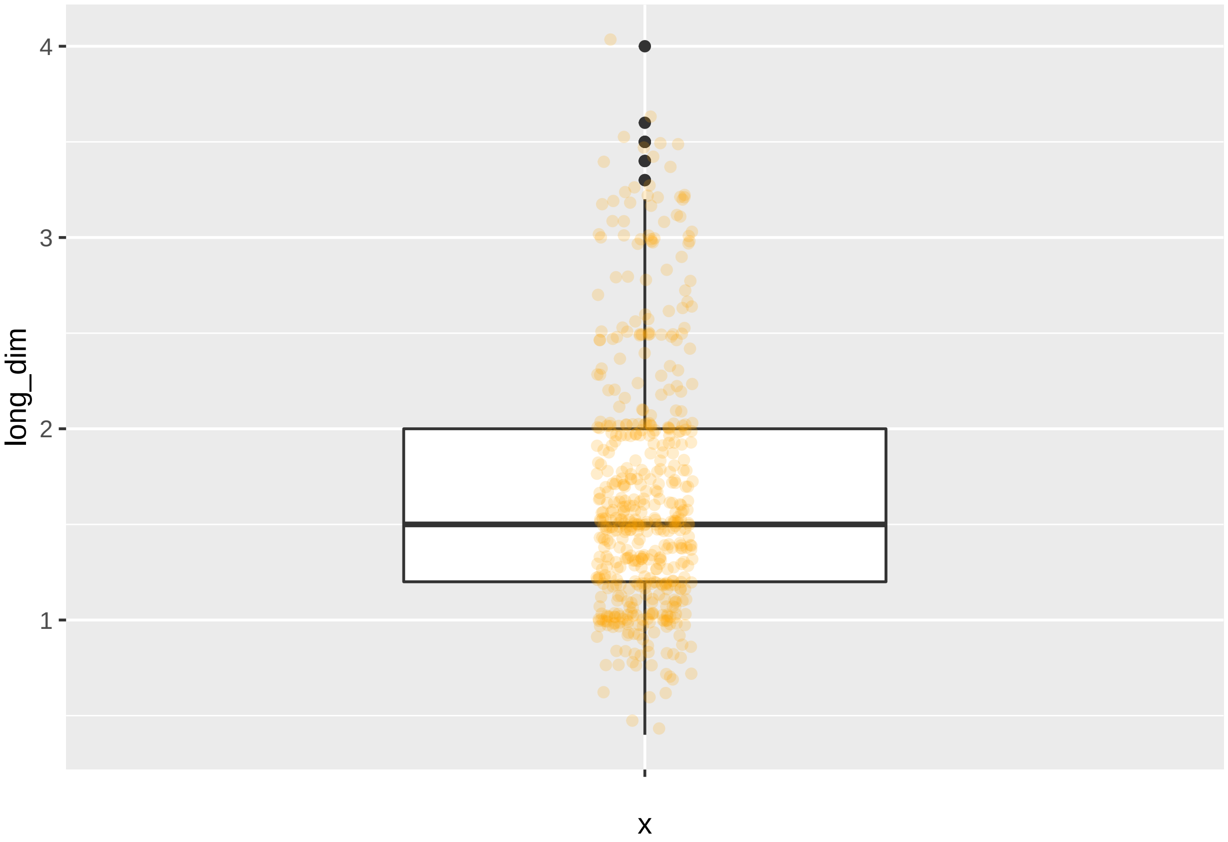
```
boxplot.stats(kirc_clean4$frac_genome_alter)
```

```
## $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).
```



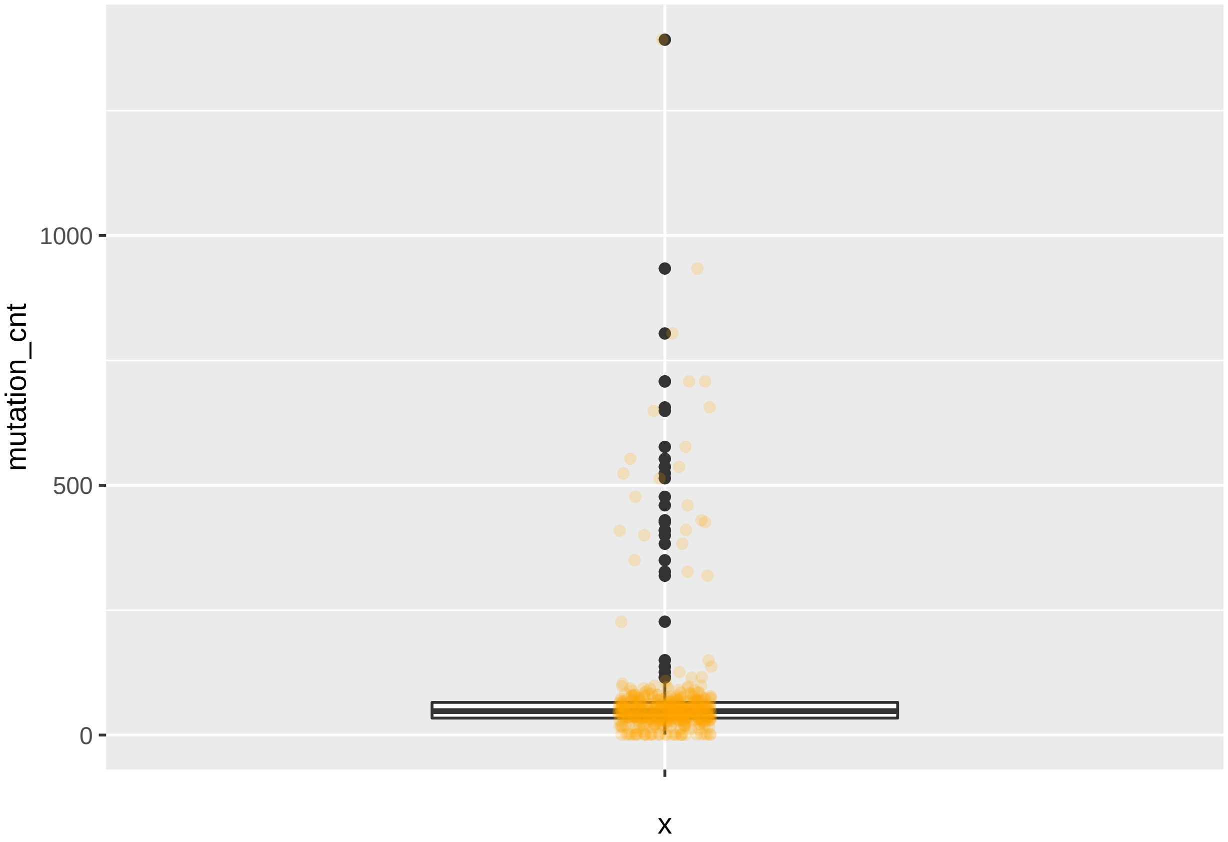
```
boxplot.stats(kirc_clean4$long_dim)
```

```
## $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).
```

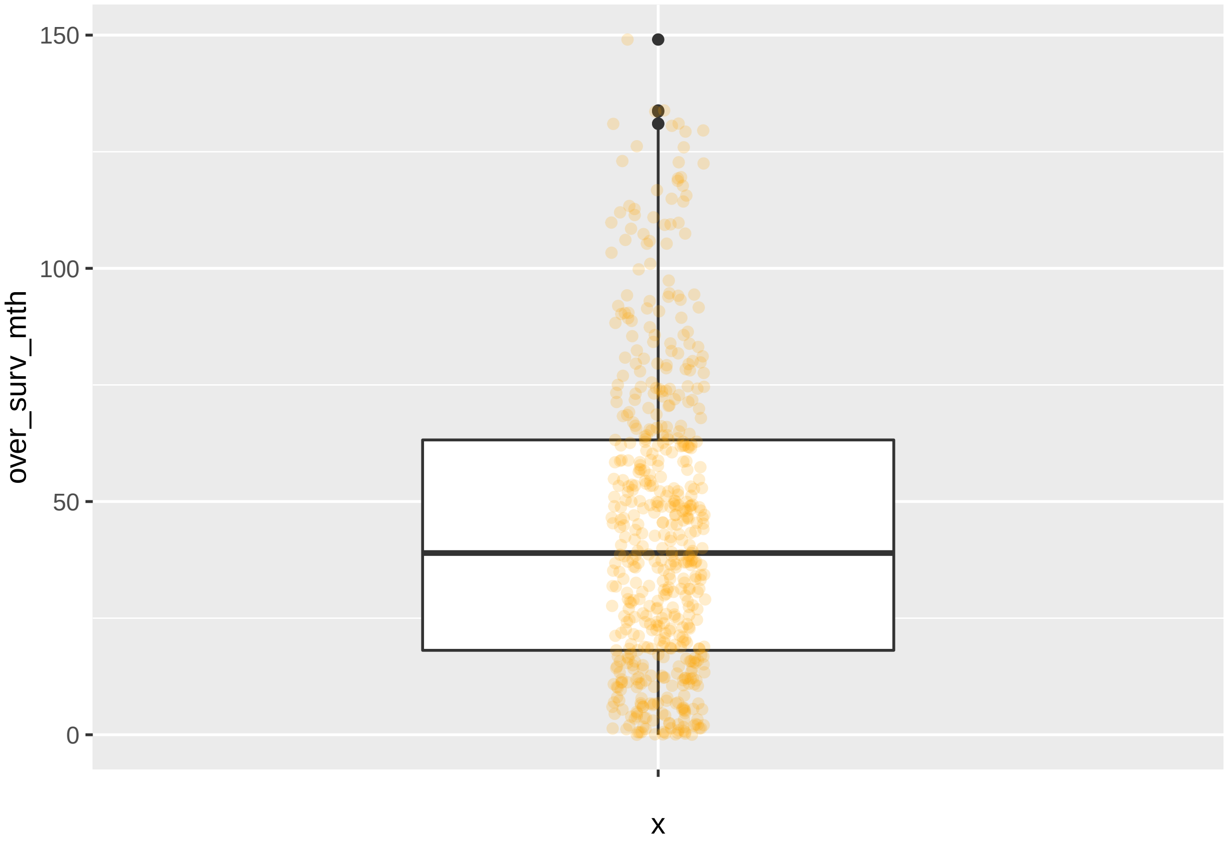
```
## Warning: Removed 86 rows containing missing values (geom_point).
```



```
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")
```



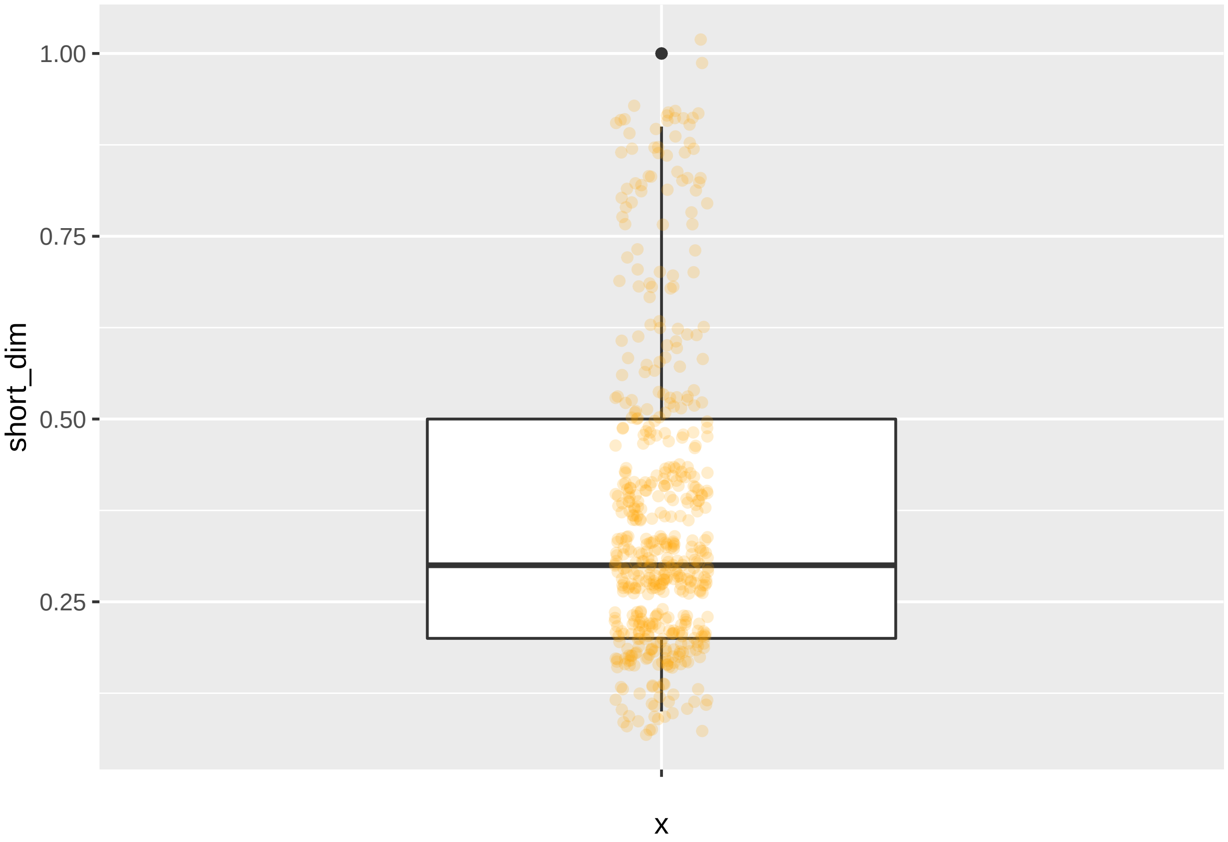
```
boxplot.stats(kirc_clean4$over_surv_mth)
```

```
## $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).
```



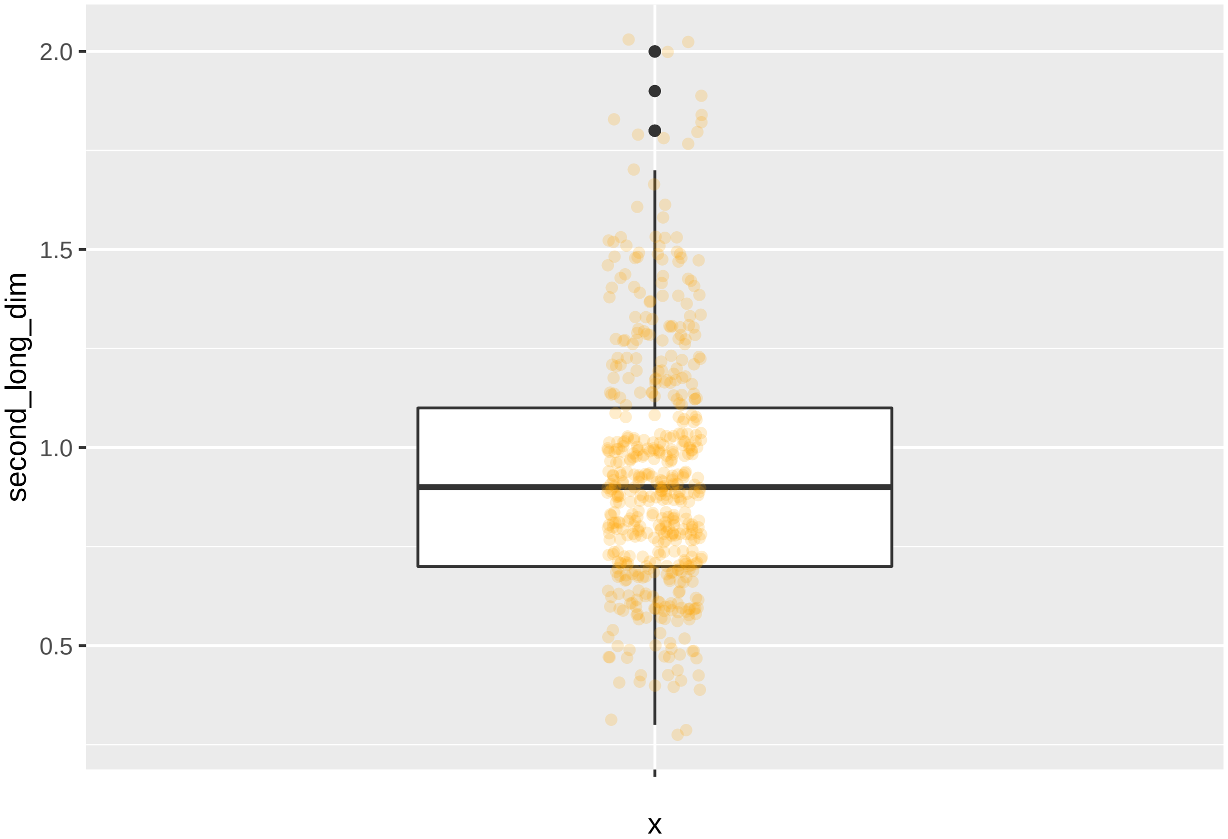
```
boxplot.stats(kirc_clean4$short_dim)
```

```
## $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 lymph_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
##
##
##
##   over_surv_stt     platelet                          race         serum_ca
##  DECEASED:177   Elevated: 38   ASIAN                    :  8   Elevated: 10
##  LIVING  :360   Low     : 46   BLACK OR AFRICAN AMERICAN: 56   Low     :204
##                 Normal  :360   WHITE                    :466   Normal  :151
##                 NA's    : 93   NA's                     :  7   NA's    :172
##
##
##
##     gender     tissue_site  person_neoplasm_stt       wbc
##  Female:191   BP     :142   TUMOR FREE:361      Elevated:164
##  Male  :345   B0     :107   WITH TUMOR:141      Low     :  9
##  MALE  :  1   CJ     : 71   NA's      : 35      Normal  :268
##               A3     : 52                       NA's    : 96
##               CZ     : 40
##               B8     : 33
##               (Other): 92
```

```
# agregating levels
kirc_clin <- 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_clin <- kirc_clin %>%
     mutate(prior_cancer = fct_collapse(prior_cancer,
               Yes = c('Yes', 'Yes, History of Prior Malignancy', 'Yes, History of Synchronous/Bilatera
kirc_clin <- kirc_clin %>%
     mutate(gender = fct_collapse(gender, Male = c('MALE', 'Male')))

kirc_clin <- kirc_clin %>%
     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')))

# changing level names
kirc_clin <- kirc_clin %>%
     mutate(ethnicity = fct_recode(ethnicity, 'hispanic/latino'='HISPANIC OR LATINO', 'not hispanic/lati
            race = fct_recode(race, Asian='ASIAN', 'Black/African.american'='BLACK OR AFRICAN AMERICAN'
            person_neoplasm_stt = fct_recode(person_neoplasm_stt, Tumor.Free='TUMOR FREE', With.Tumor='


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

```
##  metastasis_stg lymph_stg    neoplasm_stg tumor_stg            disease_free_stt
##  M0  :426       N0:240    Stage I  :269   T1:275    DiseaseFree        :311
##  M1  : 79       N1: 17    Stage II : 57   T2: 69    Recurred/Progressed:127
##  MX  : 30       NX:280    Stage III:125   T3:182    NA's               : 99
##  NA's:  2                 Stage IV : 83   T4: 11
##                           NA's     :  3
##
##                ethnicity   histology_grd    hemoglobin  neoadj_therapy
##  hispanic/latino    : 26   G1  : 14      Elevated:  5   No :519
##  not hispanic/latino:359   G2  :230      Low     :263   Yes: 18
##  NA's               :152   G3  :207      Normal  :186
##                            G4  : 78      NA's    : 83
##                            GX  :  5
##                            NA's:  3
##  prior_cancer   tumor_lateral  over_surv_stt     platelet
##  No :459      Bilateral:  1   DECEASED:177   Elevated: 38
##  Yes: 78      Left     :253   LIVING  :360   Low     : 46
##               Right    :283                  Normal  :360
##                                              NA's    : 93
##
##
##                      race        serum_ca      gender    tissue_site
##  Asian                 :  8   Elevated: 10   Female:191   OTHERS: 28
##  Black/African.american: 56   Low     :204   Male  :346   A     : 79
##  White                 :466   Normal  :151                B     :303
##  NA's                  :  7   NA's    :172                C     :127
##
##
##  person_neoplasm_stt      wbc
##  Tumor.Free:361      Elevated:164
##  With.Tumor:141      Low     :  9
##  NA's      : 35      Normal  :268
##                      NA's    : 96
##
##
```

8. Correcting and checking again

```
# month values < 0
kirc_clin$disease_free_mth[kirc_clin$disease_free_mth == -11.79] <- 11.79
kirc_clin$disease_free_mth[kirc_clin$disease_free_mth == -0.62] <- 0.62

skim(kirc_clin)
```

Table 6: Data summary

Name	kirc_clin
Number of rows	537
Number of columns	29
Column type frequency:	
character	1
factor	19
numeric	9
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate	min	max	empty	n_unique	whitespace
patient_id	0	1	12	12	0	537	0

Variable type: factor

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
metastasis_stg	2	1.00	FALSE	3	M0: 426, M1: 79, MX: 30
lymph_stg	0	1.00	FALSE	3	NX: 280, N0: 240, N1: 17
neoplasm_stg	3	0.99	FALSE	4	Sta: 269, Sta: 125, Sta: 83, Sta: 57
tumor_stg	0	1.00	FALSE	4	T1: 275, T3: 182, T2: 69, T4: 11
disease_free_stt	99	0.82	FALSE	2	Dis: 311, Rec: 127
ethnicity	152	0.72	FALSE	2	not: 359, his: 26
histology_grd	3	0.99	FALSE	5	G2: 230, G3: 207, G4: 78, G1: 14
hemoglobin	83	0.85	FALSE	3	Low: 263, Nor: 186, Ele: 5
neoadj_therapy	0	1.00	FALSE	2	No: 519, Yes: 18
prior_cancer	0	1.00	FALSE	2	No: 459, Yes: 78
tumor_lateral	0	1.00	FALSE	3	Rig: 283, Lef: 253, Bil: 1
over_surv_stt	0	1.00	FALSE	2	LIV: 360, DEC: 177
platelet	93	0.83	FALSE	3	Nor: 360, Low: 46, Ele: 38
race	7	0.99	FALSE	3	Whi: 466, Bla: 56, Asi: 8
serum_ca	172	0.68	FALSE	3	Low: 204, Nor: 151, Ele: 10
gender	0	1.00	FALSE	2	Mal: 346, Fem: 191

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
tissue_site	0	1.00	FALSE	4	B: 303, C: 127, A: 79, OTH: 28
person_neoplasm_stt	35	0.93	FALSE	2	Tum: 361, Wit: 141
wbc	96	0.82	FALSE	3	Nor: 268, Ele: 164, Low: 9

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	his
age	0	1.00	60.59	12.15	26.0	52.00	61.00	70.00	90.00	
disease_free_mth	99	0.82	40.30	31.58	0.0	13.43	36.20	60.51	133.84	
frac_genome_alter	9	0.98	0.17	0.17	0.0	0.06	0.12	0.21	0.95	
year_diagnose	0	1.00	2006.02	2.76	1998.0	2004.00	2006.00	2007.00	2013.00	
long_dim	35	0.93	1.66	0.66	0.4	1.20	1.50	2.00	4.00	
mutation_cnt	86	0.84	73.85	127.76	1.0	34.00	48.00	65.50	1392.00	
over_surv_mth	0	1.00	44.26	32.25	0.0	18.10	38.96	63.21	149.05	
short_dim	35	0.93	0.38	0.21	0.1	0.20	0.30	0.50	1.00	
second_long_dim	35	0.93	0.94	0.31	0.3	0.70	0.90	1.10	2.00	

9. Saving dataset

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

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

Further analysis

- Comparison and Hyphotesis test
- Logistic Regression Model

```
sessionInfo()
```

```
## R version 4.0.3 (2020-10-10)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 18.04.5 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_1.0.2  skimr_2.1.2     forcats_0.5.0   stringr_1.4.0
##  [5] dplyr_1.0.2     purrr_0.3.4     readr_1.4.0     tidyr_1.1.2
##  [9] tibble_3.0.3    ggplot2_3.3.2   tidyverse_1.3.0
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.5       lubridate_1.7.9  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_1.1.10 reprex_0.3.0     evaluate_0.14
## [13] highr_0.8        httr_1.4.2       pillar_1.4.6     rlang_0.4.7
## [17] readxl_1.3.1     rstudioapi_0.11  blob_1.2.1       Matrix_1.2-18
## [21] rmarkdown_2.4    labeling_0.3     splines_4.0.3    munsell_0.5.0
## [25] broom_0.7.1      compiler_4.0.3   modelr_0.1.8     xfun_0.18
## [29] pkgconfig_2.0.3  base64enc_0.1-3  htmltools_0.5.0  tidyselect_1.1.0
## [33] fansi_0.4.1      crayon_1.3.4     dbplyr_1.4.4     withr_2.3.0
## [37] grid_4.0.3       jsonlite_1.7.1   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_1.5.3    farver_2.0.3     fs_1.5.0         mice_3.11.0
## [49] xml2_1.3.2       ellipsis_0.3.1   generics_0.0.2   vctrs_0.3.4
## [53] boot_1.3-25      tools_4.0.3      glue_1.4.2       hms_0.5.3
## [57] survival_3.2-7   yaml_2.2.1       colorspace_1.4-1 rvest_0.3.6
## [61] knitr_1.30       haven_2.3.1
```