

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 significant distinctions between clinical variables according to their vital status.

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

# 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

```
kirc_clinic <- read_csv("data/kirc_clinic.csv")
```

2. Taming data

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

3. Checking categorical variables

check frequency, labels and levels

```
## metastasis_stg neoplasm_ln_stg    neoplasm_stg tumor_stg
## M0 :426        N0:240            Stage I  :269    T1:275
## M1 : 79        N1: 17            Stage II : 57    T2: 69
## MX : 30        NX:280            Stage III:125   T3:182
## NA's: 2                Stage IV : 83    T4: 11
##                          NA's      : 3
##
##
##          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 prior_cancer  tumor_lateral primer_ln_ind3
## Elevated: 5      No :519      No :459      Bilateral: 1      NO :395
## Low      :263      Yes: 18      Yes: 78      Left      :253      YES :135
## Normal   :186      Right      :283      NA's: 7
## NA's      : 83
##
##
##      over_surv_stt      platelet      tissue_prospect      race
## DECEASED:177      Elevated: 38      NO :465      BLACK OR AFRICAN AMERICAN: 56
## LIVING :360      Low      : 46      YES : 52      WHITE      :466
##                                     Normal :360      NA's: 20      NA's      : 15
##                                     NA's      : 93
##
##
##      tissue_retrospect      serum_ca      gender      tissue_site      person_neoplasm_stt
## NO : 53      Elevated: 10      Female:191      A      : 79      TUMOR FREE:361
## YES :466      Low      :204      Male :346      B      :303      WITH TUMOR:141
## NA's: 18      Normal   :151      C      :127      NA's      : 35
##                                     NA's      :172      OTHERS: 28
##
##
##
##      wbc
## Elevated:164
## Low      : 9
## Normal   :268
## NA's      : 96
##
##

```

4. Checking variables

```
glimpse(kirc_clinic)
```

```

## Rows: 537
## Columns: 32
## $ patient_id      <chr> "TCGA-3Z-A93Z", "TCGA-6D-AA2E", "TCGA-A3-3306",...
## $ age              <dbl> 69, 68, 67, 66, 77, 57, 59, 57, 67, 70, 52, 51,...
## $ metastasis_stg   <fct> M0, MX, M0, M0, M0, M0, M0, M0, M0, M0, M0, M0,...
## $ neoplasm_ln_stg   <fct> N0, NX, N0, N0, N0, NX, N0, NX, N0, NX, NX, NX,...
## $ neoplasm_stg      <fct> Stage I, Stage I, Stage I, Stage III, Stage III...
## $ tumor_stg         <fct> T1, T1, T1, T3, T3, T1, T1, T2, T2, T1, T1, T1,...
## $ disease_free_mth  <dbl> 12.65, 11.89, 36.79, 47.17, 0.53, NA, NA, 49.05...
## $ disease_free_stt  <fct> DiseaseFree, DiseaseFree, DiseaseFree, DiseaseF...
## $ ethnicity         <fct> NOT HISPANIC OR LATINO, NOT HISPANIC OR LATINO,...
## $ frac_genome_alter <dbl> 0.2240, 0.0000, 0.2316, 0.0494, 0.0844, 0.0883,...
## $ histology_grd     <fct> G2, G2, G3, G3, G2, G2, G3, G3, G2, G2, G1, G2,...
## $ hemoglobin        <fct> Normal, NA, NA, NA, Normal, Low, Low, NA, NA, N...

```

```
## $ neoadj_therapy      <fct> No, No, No, No, No, No, No, No, No, No, No, No, No,...
## $ prior_cancer       <fct> No, No, No, Yes, No, No, No, No, No, No, No, No, No...
## $ year_diagnose      <dbl> 2013, 2013, 2005, 2005, 2006, 2005, 2005, 2005,...
## $ tumor_lateral      <fct> Right, Right, Left, Right, Right, Right, Right,...
## $ long_dim           <dbl> NA, NA, 0.9, 1.0, 1.2, 1.7, 2.0, 1.7, 1.5, 1.5,...
## $ primer_ln_ind3     <fct> NO, NO, NO, YES, NO, NO, NA, NO, NO, NO, NO, NO, NO...
## $ mutation_cnt       <dbl> NA, NA, NA, NA, 514, 56, 656, 577, 62, 537, 477...
## $ over_surv_mth      <dbl> 12.65, 11.89, 36.79, 47.17, 0.53, 39.13, 24.15,...
## $ over_surv_stt      <fct> LIVING, LIVING, LIVING, LIVING, LIVING, DECEASE...
## $ platelet           <fct> Normal, NA, NA, NA, NA, Normal, NA, NA, NA, NA, NA,...
## $ tissue_prospect     <fct> YES, YES, NO, NO, NO, NO, NO, NO, NO, NO, NO, NO, N...
## $ race               <fct> BLACK OR AFRICAN AMERICAN, BLACK OR AFRICAN AME...
## $ tissue_retrospect   <fct> NO, NO, YES, YES, YES, YES, YES, YES, YES, YES, YES,...
## $ serum_ca           <fct> Normal, NA, NA, NA, NA, Normal, NA, NA, NA, NA, NA,...
## $ gender             <fct> Male, Female, Male, Male, Female, Male, Male, M...
## $ short_dim          <dbl> NA, NA, 0.4, 0.6, 0.4, 0.4, 0.8, 0.8, 0.3, 0.4,...
## $ second_long_dim    <dbl> NA, NA, 0.7, 0.8, 1.0, 1.0, 0.9, 0.8, 1.0, 1.1,...
## $ tissue_site        <fct> OTHERS, OTHERS, A, A, A, A, A, A, A, A, A, A, A...
## $ person_neoplasm_stt <fct> TUMOR FREE, TUMOR FREE, NA, WITH TUMOR, TUMOR F...
## $ wbc               <fct> Normal, NA, NA, NA, Normal, NA, NA, NA, NA, NA,...
```

```
skim(kirc_clinic)
```

Table 1: Data summary

Name	kirc_clinic
Number of rows	537
Number of columns	32
Column type frequency:	
character	1
factor	22
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
neoplasm_ln_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

skim_variable	n_missing	complete_rate	ordered	n_unique	top_counts
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
primer_ln_ind3	7	0.99	FALSE	2	NO: 395, YES: 135
over_surv_stt	0	1.00	FALSE	2	LIV: 360, DEC: 177
platelet	93	0.83	FALSE	3	Nor: 360, Low: 46, Ele: 38
tissue_prospect	20	0.96	FALSE	2	NO: 465, YES: 52
race	15	0.97	FALSE	2	WHI: 466, BLA: 56
tissue_retrospect	18	0.97	FALSE	2	YES: 466, NO: 53
serum_ca	172	0.68	FALSE	3	Low: 204, Nor: 151, Ele: 10
gender	0	1.00	FALSE	2	Mal: 346, Fem: 191
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	h
age	0	1.00	60.59	12.15	26.00	52.00	61.00	70.00	90.00	
disease_free_mth	99	0.82	40.24	31.66	-11.79	13.43	36.20	60.51	133.84	
frac_genome_alter	9	0.98	0.17	0.17	0.00	0.06	0.12	0.21	0.95	
year_diagnose	0	1.00	2006.02	2.76	1998.00	2004.00	2006.00	2007.00	2013.00	
long_dim	35	0.93	1.66	0.66	0.40	1.20	1.50	2.00	4.00	
mutation_cnt	86	0.84	73.85	127.76	1.00	34.00	48.00	65.50	1392.00	
over_surv_mth	0	1.00	44.26	32.25	0.00	18.10	38.96	63.21	149.05	
short_dim	35	0.93	0.38	0.21	0.10	0.20	0.30	0.50	1.00	
second_long_dim	35	0.93	0.94	0.31	0.30	0.70	0.90	1.10	2.00	

#View(kirc_clinic)

5. Numeric variables vs. over_surv_stt

graphic visualization and t-test

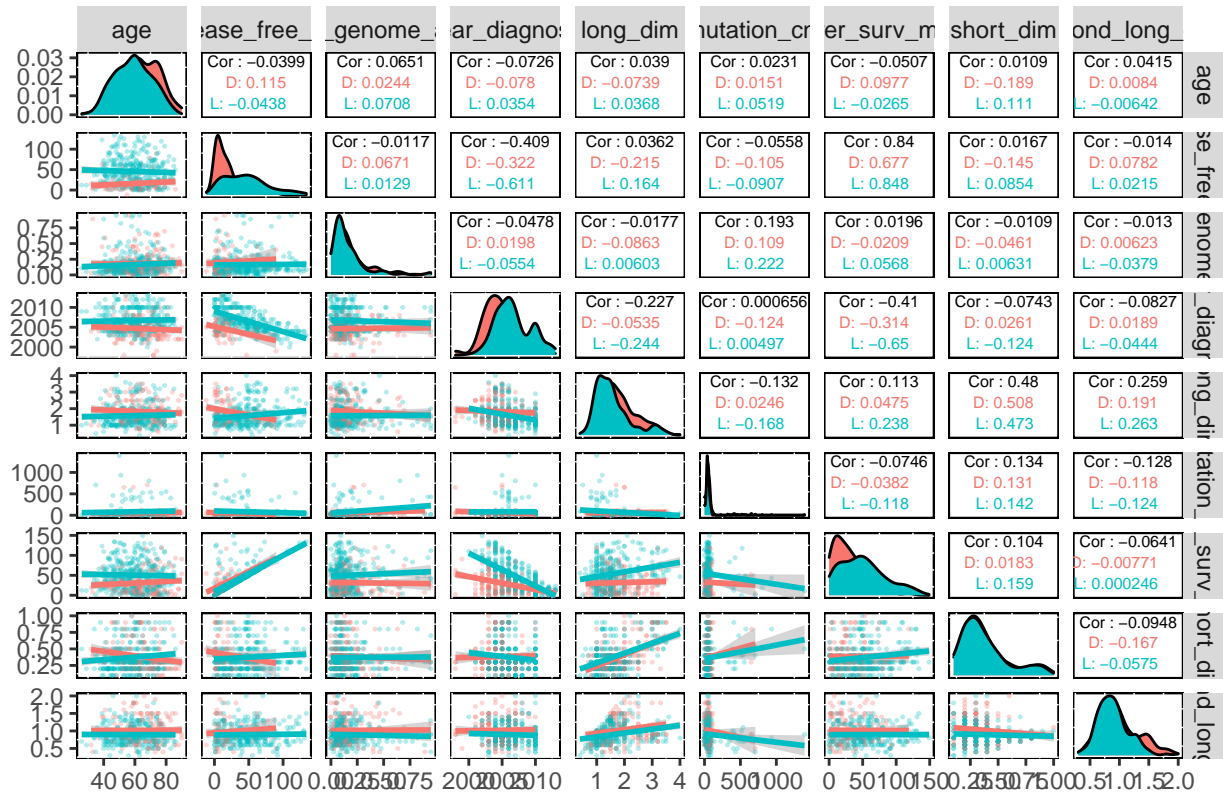
```
cols_numeric <- kirc_clinic %>% select_if(is.numeric) %>% names

kirc_clinic_numeric <- kirc_clinic %>%
  select(one_of(c(cols_numeric, "over_surv_stt")))

levels(kirc_clinic_numeric$over_surv_stt) <- c("D", "L")

ggpairs(kirc_clinic_numeric, columns = cols_numeric,
  title="Correlation matrix",
  mapping= aes(colour = over_surv_stt),
  upper = list(combo = wrap("box_no_facet", alpha=0.1),
    continuous = wrap("cor", size = 2, alignPercent = 0.8)),
  lower = list(continuous = wrap("smooth", alpha = 0.3, size=0.2) )) +
  theme(panel.background = element_rect(color = "black", size=0.5, fill="white"),
    panel.grid.major = element_blank())
```

Correlation matrix



5.1 Run multiple T-tests on over_surv_stt

Transform the data into long format

```
# Put all variables in the same column except `over_surv_stt`, the grouping variable
levels(kirc_clinic_numeric$over_surv_stt) <- c("DECEASED", "LIVING")

kirc_clinic_numeric.long <- kirc_clinic_numeric %>%
  pivot_longer(-over_surv_stt, names_to = "variables", values_to = "value")

kirc_clinic_numeric.long <- kirc_clinic_numeric.long[!is.na(kirc_clinic_numeric.long$value), ]

kirc_clinic_numeric.long$value.log <- log2(kirc_clinic_numeric.long$value+1)

## Warning: NaNs produced
kirc_clinic_numeric.long %>% sample_n(6)
```

```
## # A tibble: 6 x 4
##   over_surv_stt variables      value value.log
##   <fct>         <chr>         <dbl>     <dbl>
## 1 DECEASED     long_dim             1.7       1.43
## 2 LIVING       year_diagnose       2007       11.0
## 3 DECEASED     second_long_dim      1.5       1.32
## 4 DECEASED     year_diagnose       2002       11.0
## 5 LIVING       short_dim            0.3       0.379
```

```
## 6 LIVING      mutation_cnt      17      4.17
```

Group the data by variables and compare over_surv_stt groups

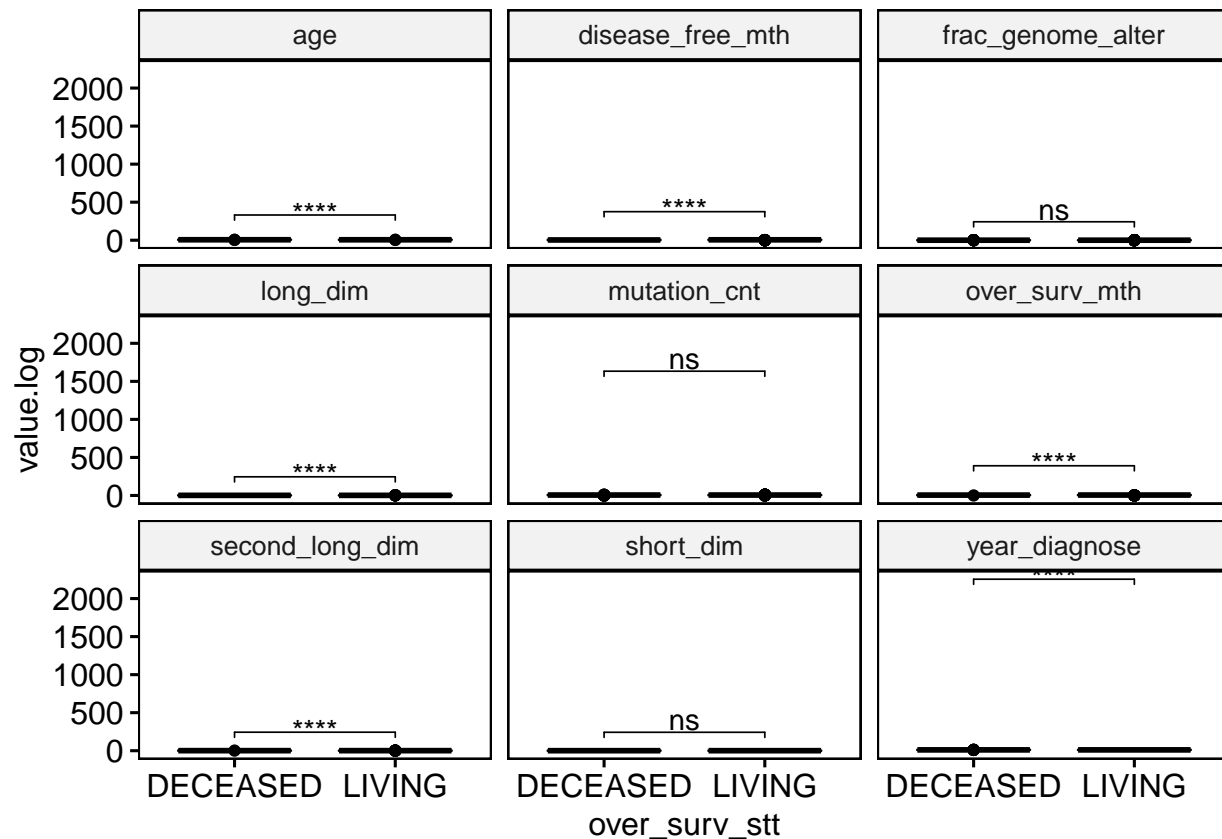
Adjust the p-values and add significance levels

```
stat.test <- kirc_clinic_numeric.long %>%
  group_by(variables) %>%
  t_test(value ~ over_surv_stt) %>%
  adjust_pvalue(method = "BH") %>%
  add_significance()
stat.test

## # A tibble: 9 x 11
##   variables .y. group1 group2   n1   n2 statistic    df      p    p.adj
##   <chr>      <chr> <chr>  <chr> <int> <int>    <dbl> <dbl>    <dbl>    <dbl>
## 1 age      value DECEA~ LIVING   177   360     4.89   348. 1.57e- 6 3.53e- 6
## 2 disease_~ value DECEA~ LIVING    78   360    -11.0   188. 5.24e-22 4.72e-21
## 3 frac_gen~ value DECEA~ LIVING   175   353     1.20   344. 2.33e- 1 2.62e- 1
## 4 long_dim value DECEA~ LIVING   173   329     4.13   363. 4.51e- 5 8.12e- 5
## 5 mutation~ value DECEA~ LIVING   153   298    -1.83   429. 6.79e- 2 8.73e- 2
## 6 over_sur~ value DECEA~ LIVING   177   360    -7.32   451. 1.17e-12 3.51e-12
## 7 second_l~ value DECEA~ LIVING   173   329     4.06   288. 6.23e- 5 9.34e- 5
## 8 short_dim value DECEA~ LIVING   173   329     0.478  345. 6.33e- 1 6.33e- 1
## 9 year_dia~ value DECEA~ LIVING   177   360    -8.90   377. 2.41e-17 1.08e-16
## # ... with 1 more variable: p.adj.signif <chr>

# Create the plot on logscale
myplot <- ggboxplot(
  kirc_clinic_numeric.long, x = "over_surv_stt", y = "value.log",
  fill = "over_surv_stt", palette = "npg", legend = "none",
  ggtheme = theme_pubr(border = TRUE)
) +
  facet_wrap(~variables)
# Add statistical test p-values
stat.test <- stat.test %>% add_xy_position(x = "over_surv_stt")
myplot + stat_pvalue_manual(stat.test, label = "p.adj.signif")

## Warning: Removed 1 rows containing non-finite values (stat_boxplot).
```



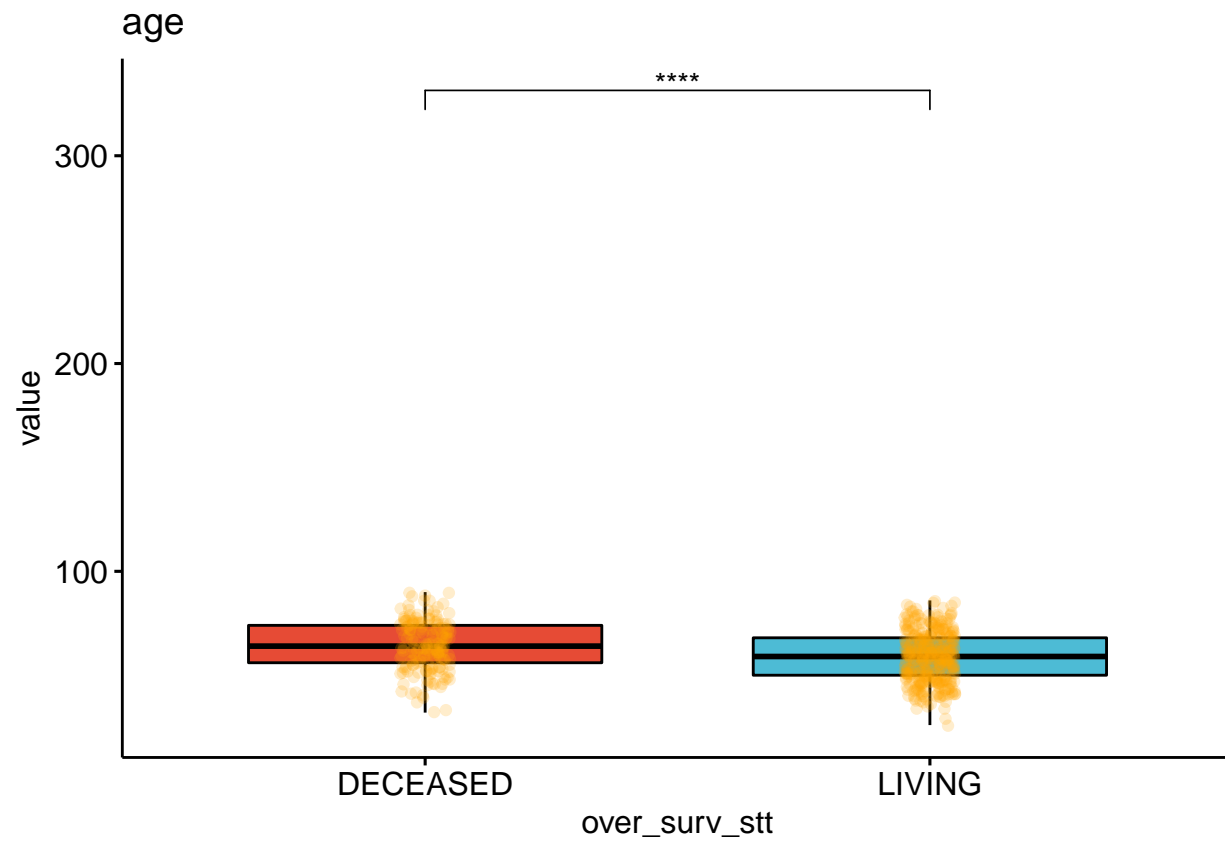
```
# Group the data by variables and do a graph for each variable
graphs <- kirc_clinic_numeric.long %>%
  group_by(variables) %>%
  doo(
    ~ggboxplot(
      data = ., x = "over_surv_stt", y = "value",
      fill = "over_surv_stt", palette = "npg", legend = "none",
      ggtheme = theme_pubr()
    ) +
    geom_jitter(width = 0.05, alpha = 0.2, color = "orange"),
    result = "plots"
  )
graphs
```

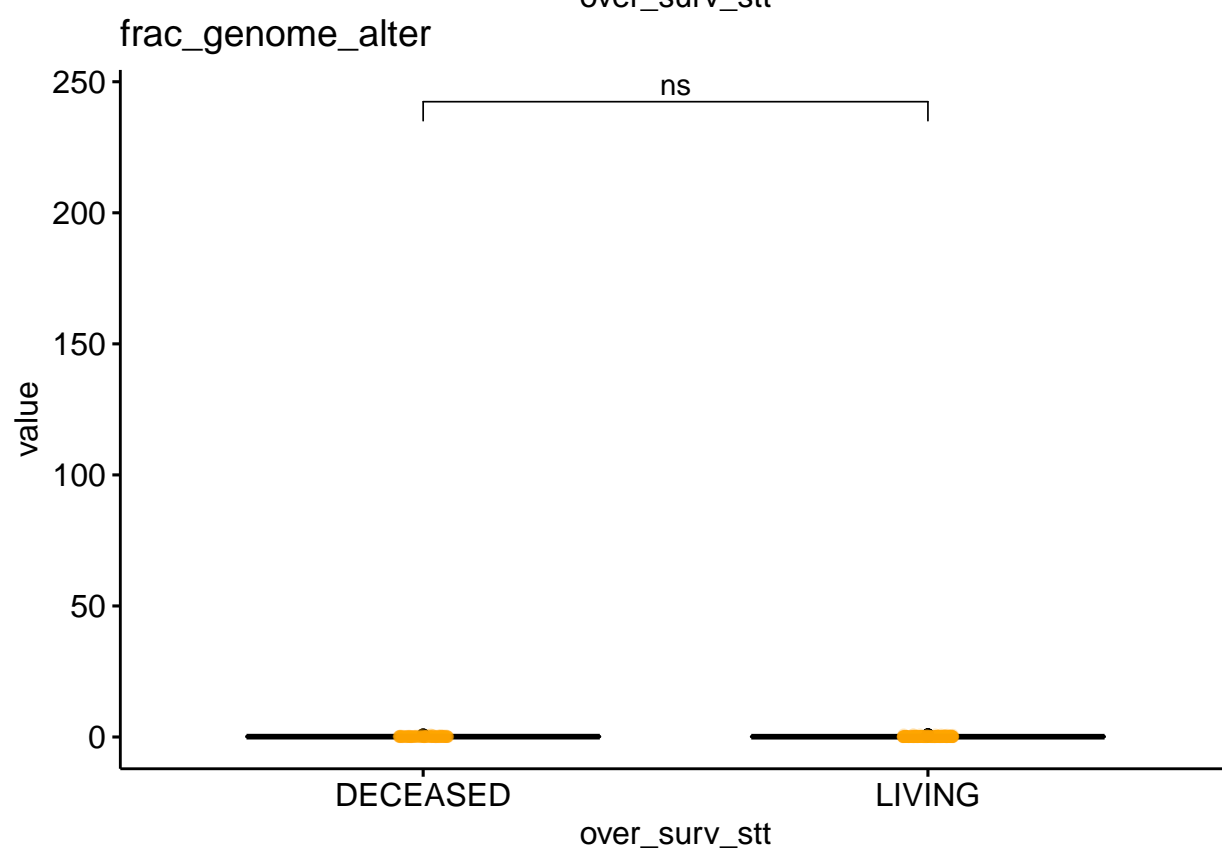
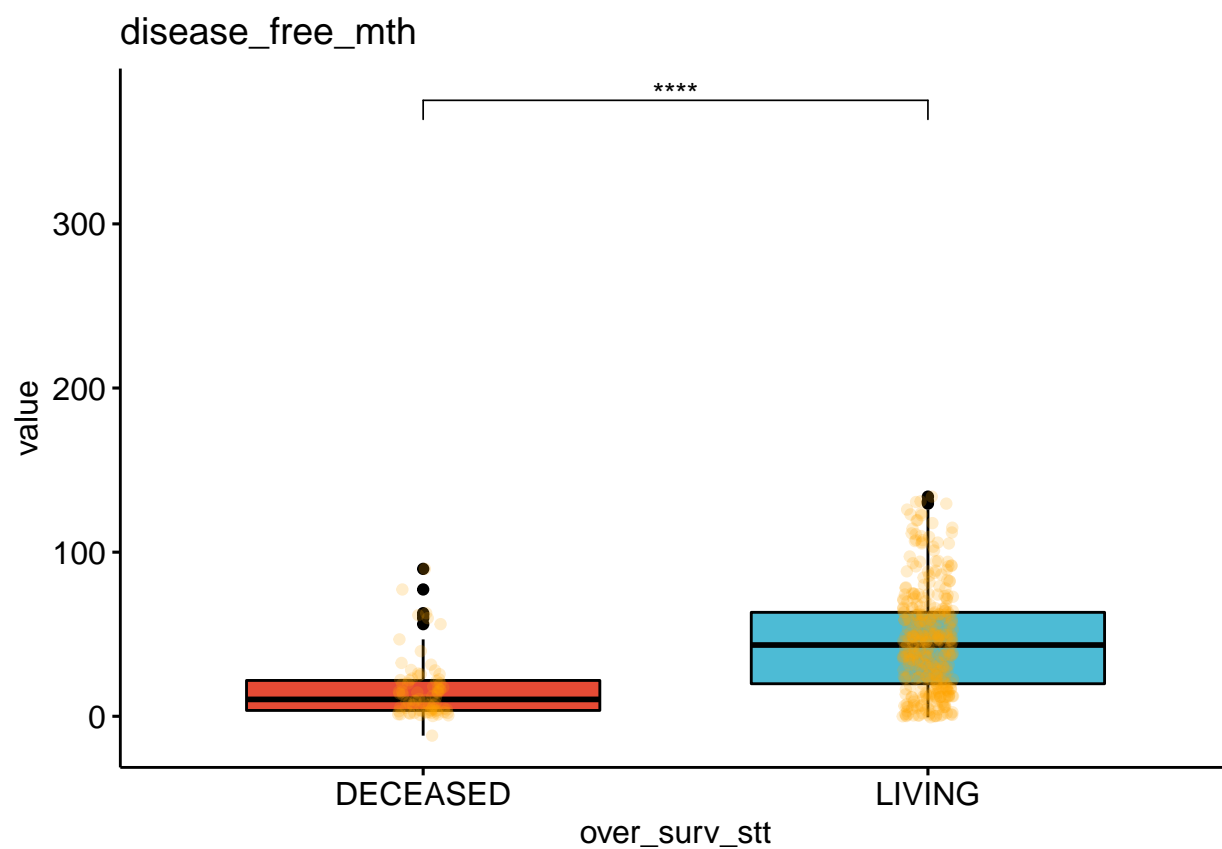
```
## # A tibble: 9 x 2
##   variables      plots
##   <chr>         <list>
## 1 age          <gg>
## 2 disease_free_mth <gg>
## 3 frac_genome_alter <gg>
## 4 long_dim      <gg>
## 5 mutation_cnt   <gg>
## 6 over_surv_mth   <gg>
## 7 second_long_dim <gg>
## 8 short_dim      <gg>
## 9 year_diagnose   <gg>
```

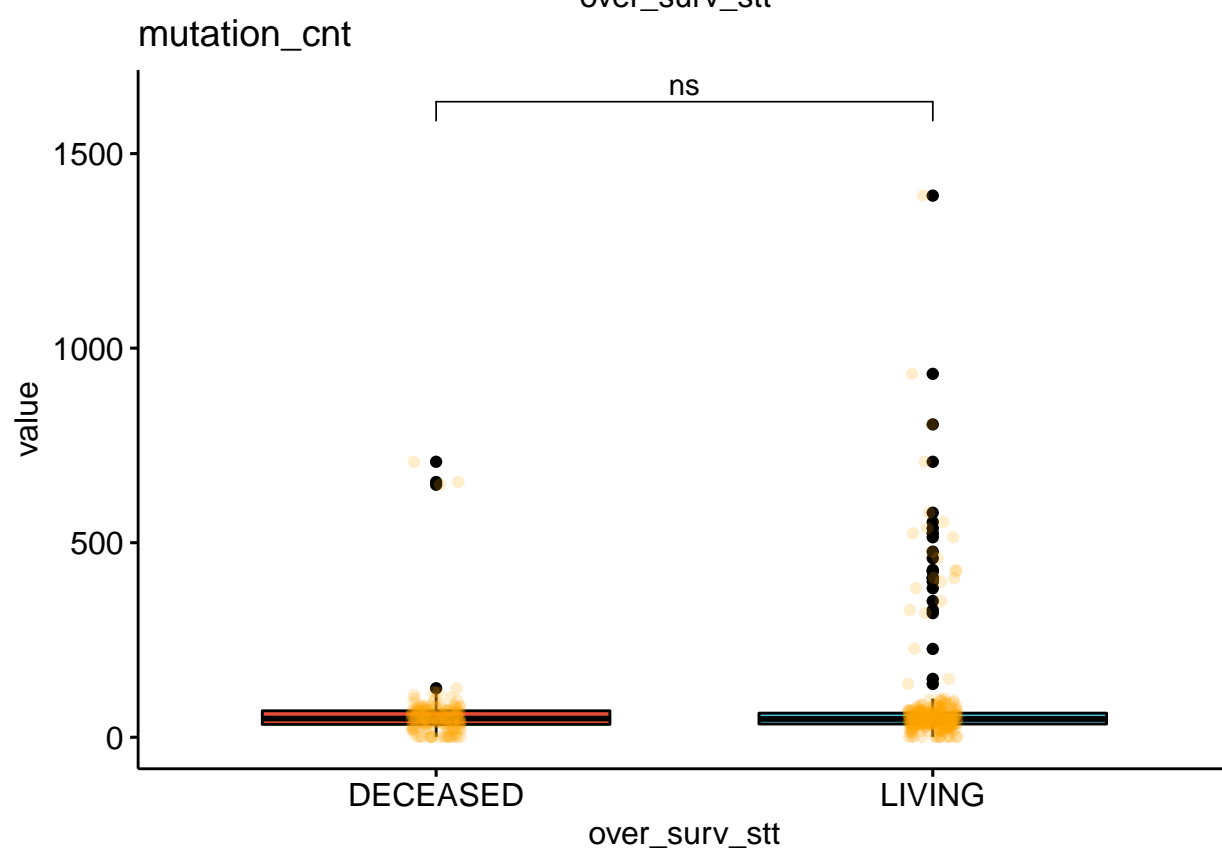
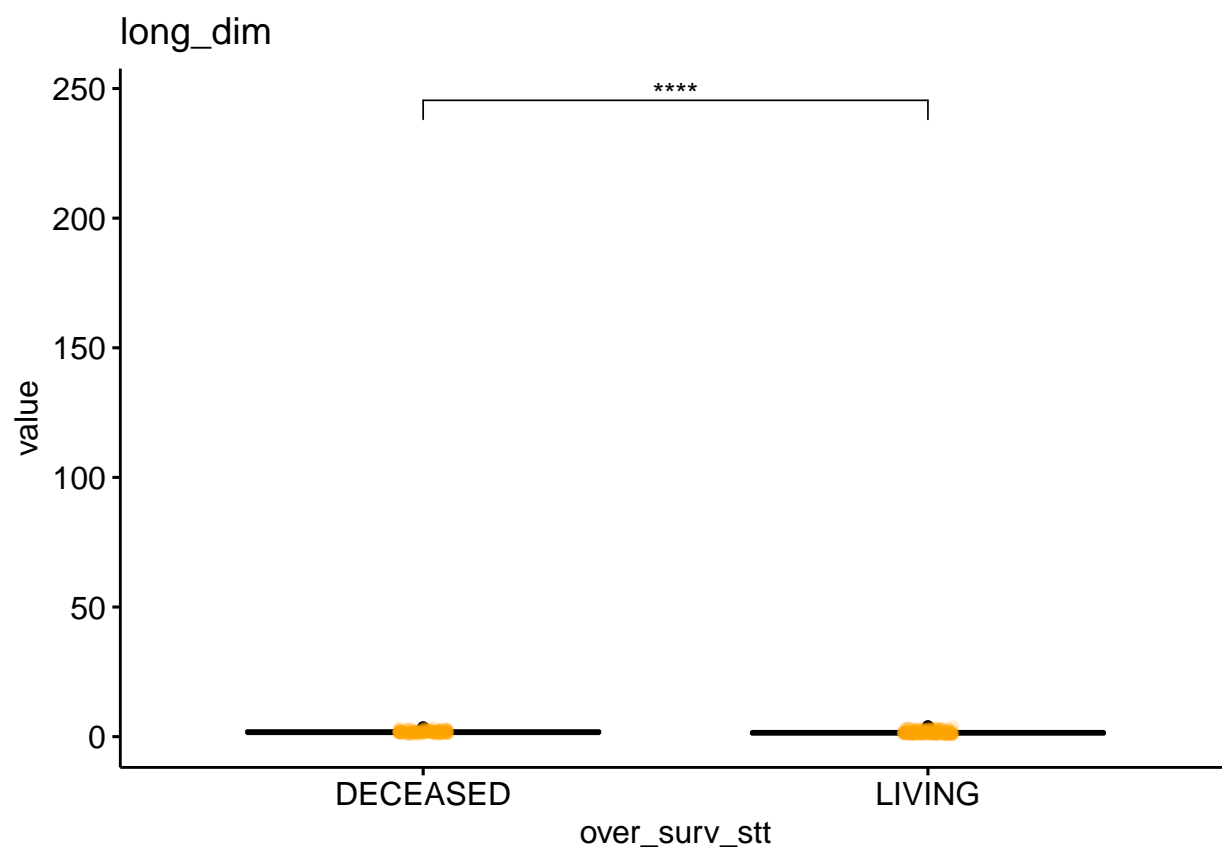
```

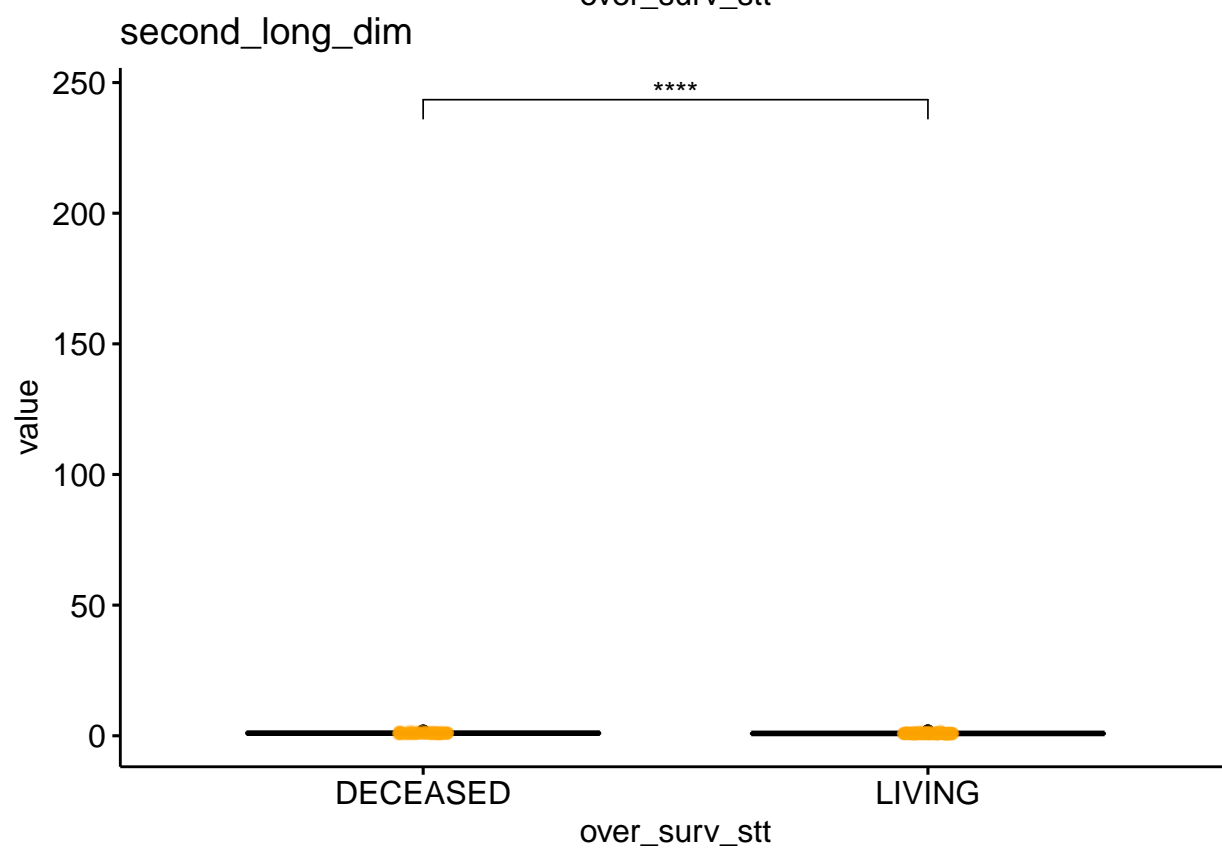
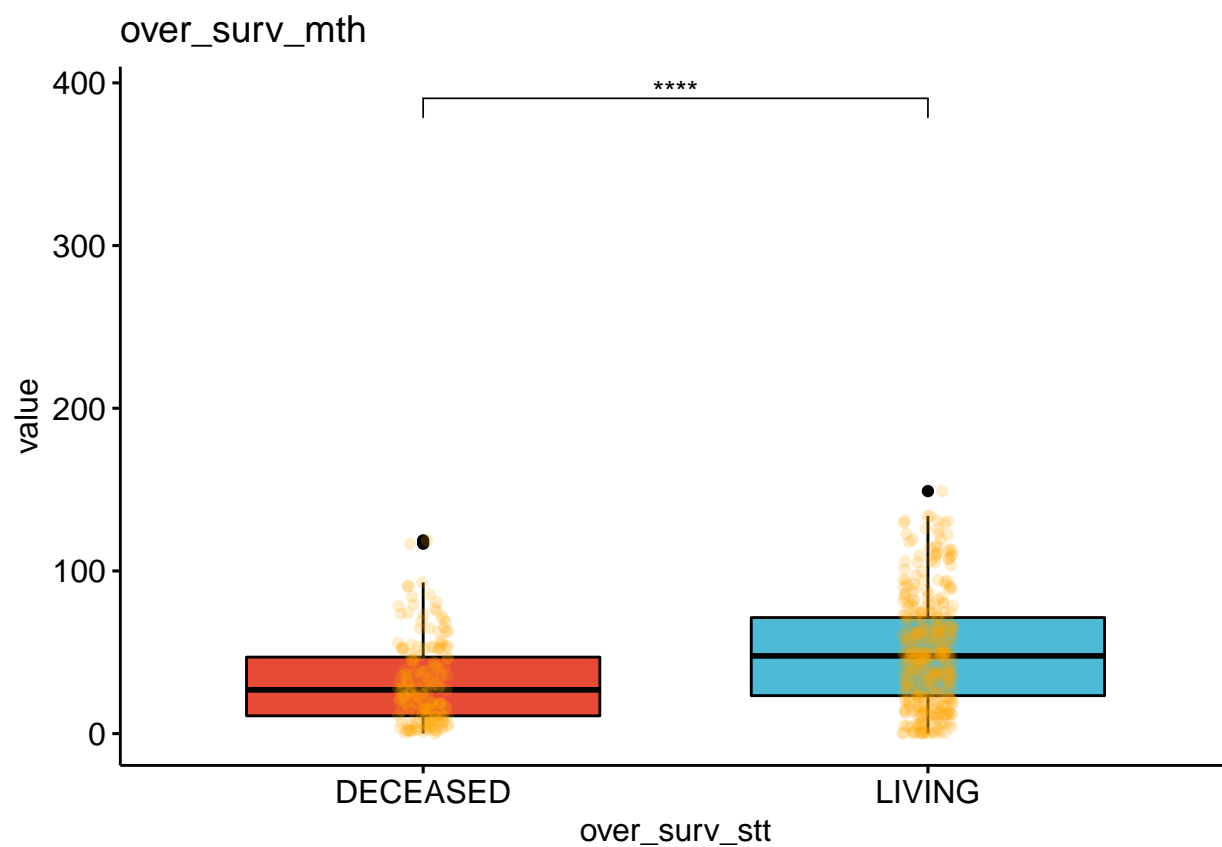
# Add statistical tests to each corresponding plot
variables <- graphs$variables
for(i in 1:length(variables)){
  graph.i <- graphs$plots[[i]] +
    labs(title = variables[i]) +
    stat_pvalue_manual(stat.test[i, ], label = "p.adj.signif")
  print(graph.i)
}

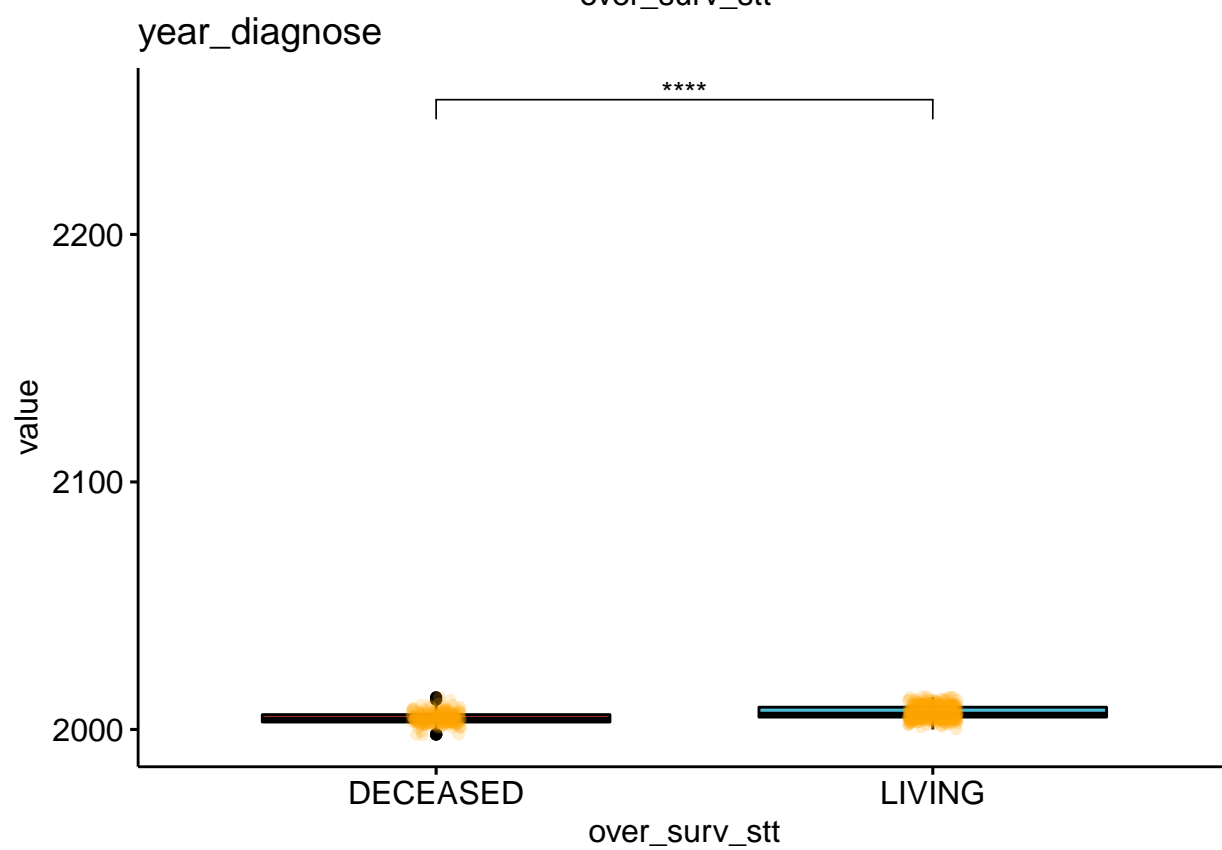
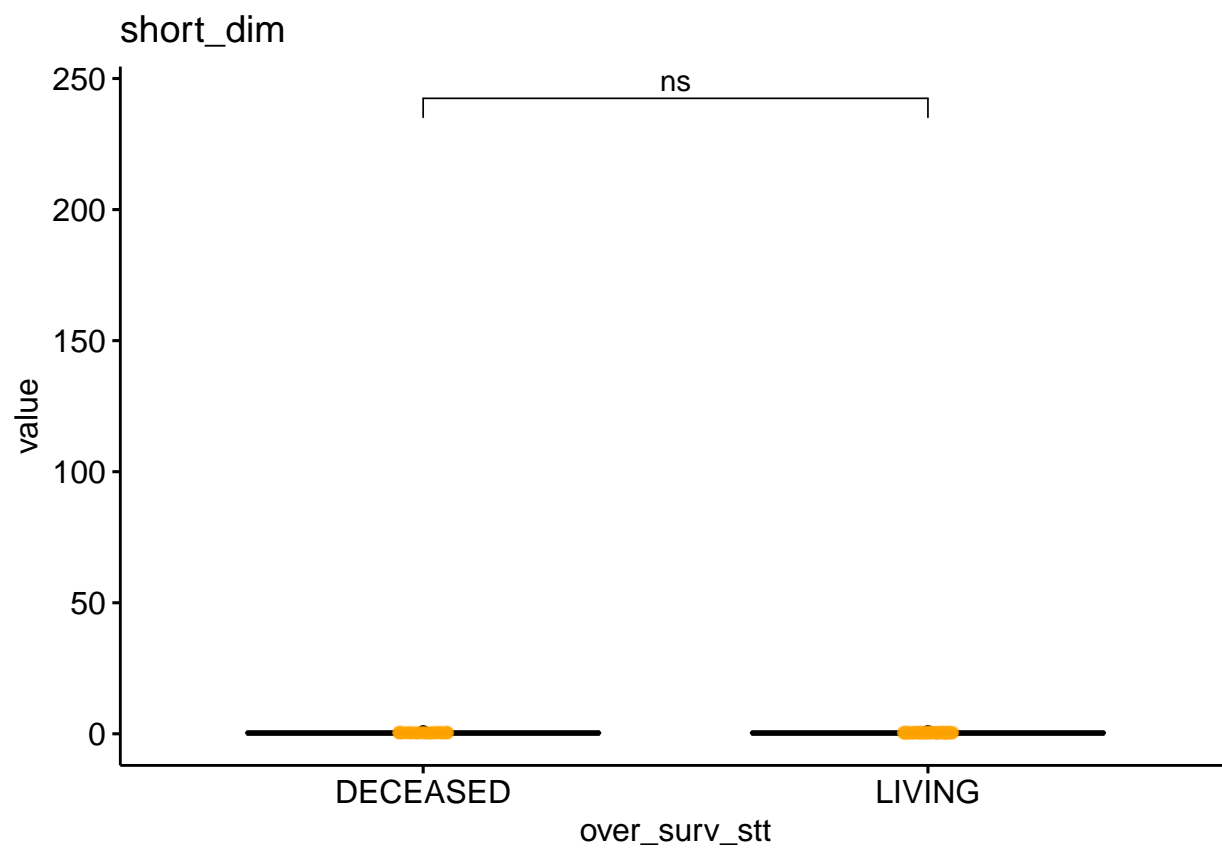
```



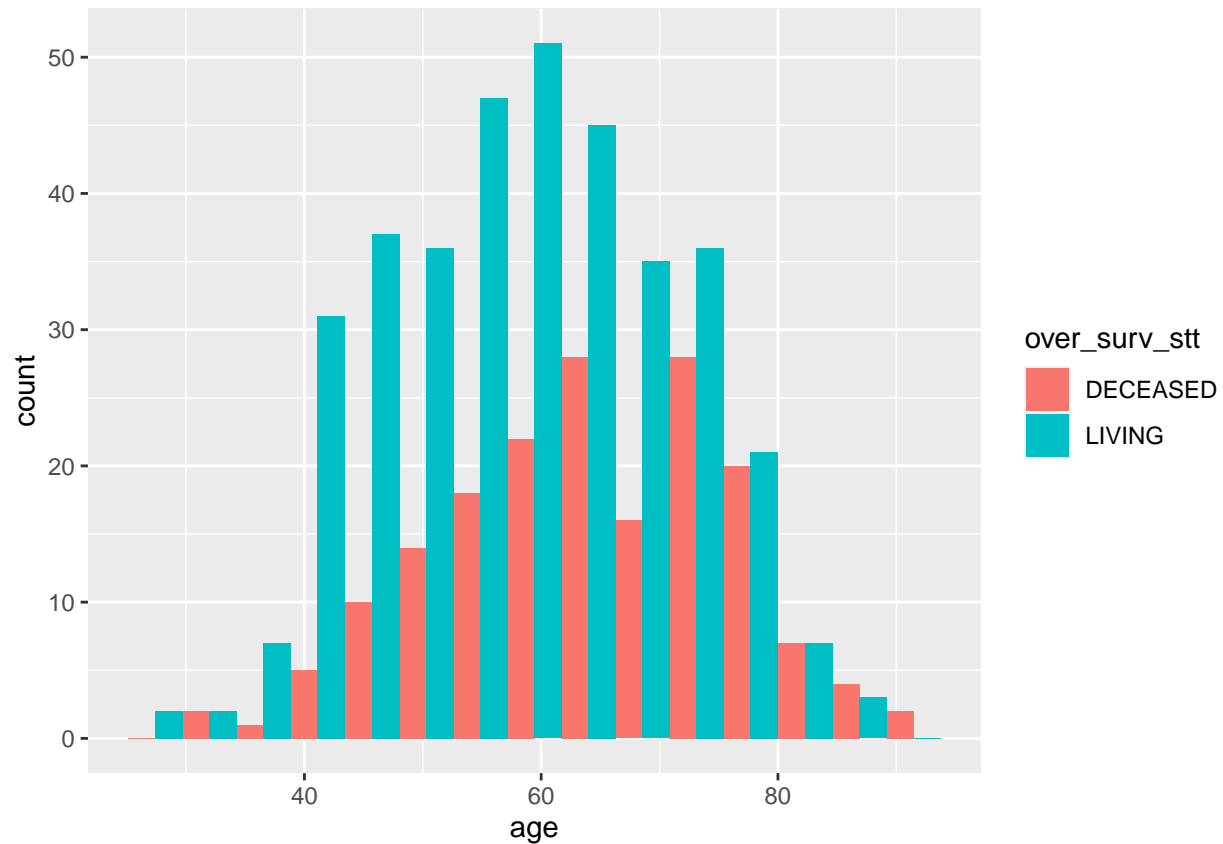








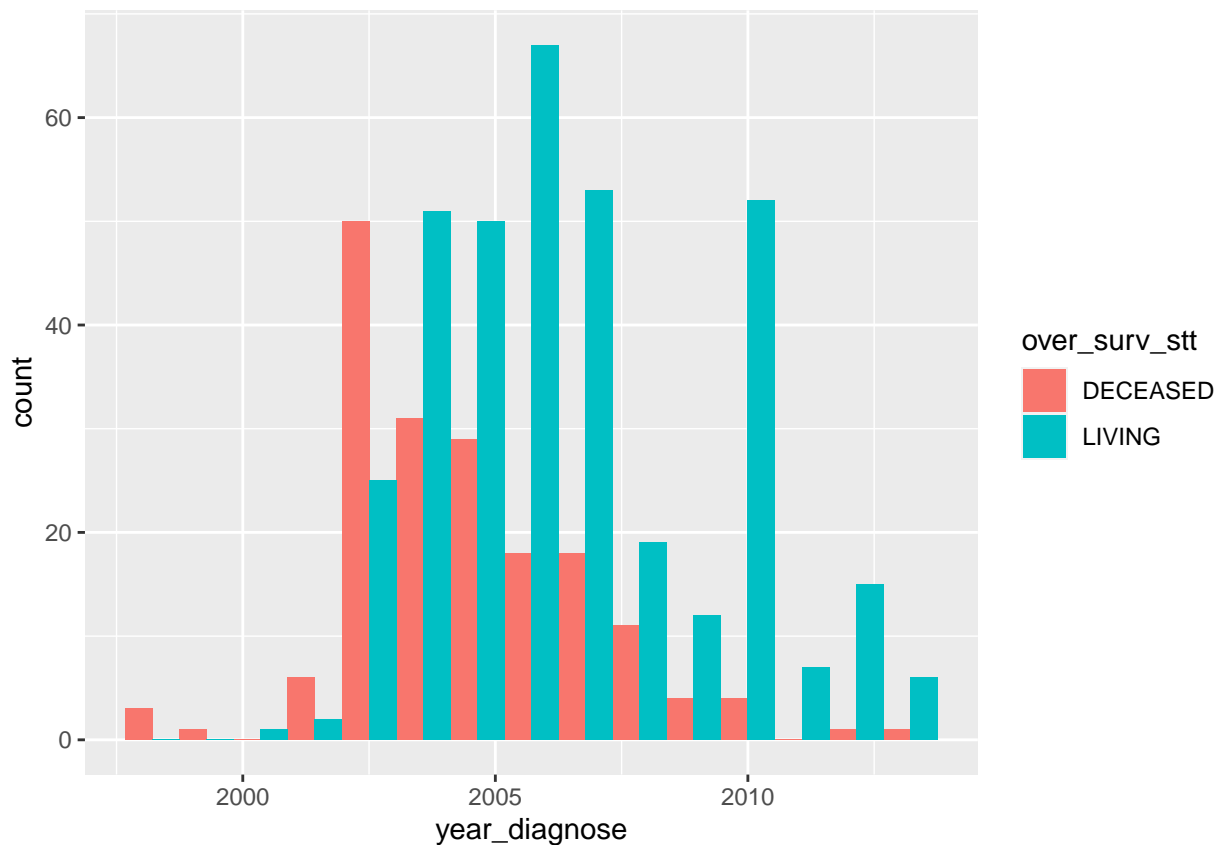
```
ggplot(kirc_clinic, aes(age, fill= over_surv_stt)) +  
  geom_histogram(bins = 15, position = "dodge")
```



```
t.test(kirc_clinic$age ~ kirc_clinic$over_surv_stt)
```

```
##  
## Welch Two Sample t-test  
##  
## data: kirc_clinic$age by kirc_clinic$over_surv_stt  
## t = 4.887, df = 348.17, p-value = 1.565e-06  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 3.196986 7.503485  
## sample estimates:  
## mean in group DECEASED mean in group LIVING  
## 64.18079 58.83056
```

```
ggplot(kirc_clinic, aes(year_diagnose, fill= over_surv_stt)) +  
  geom_histogram(bins = 15, position = "dodge")
```

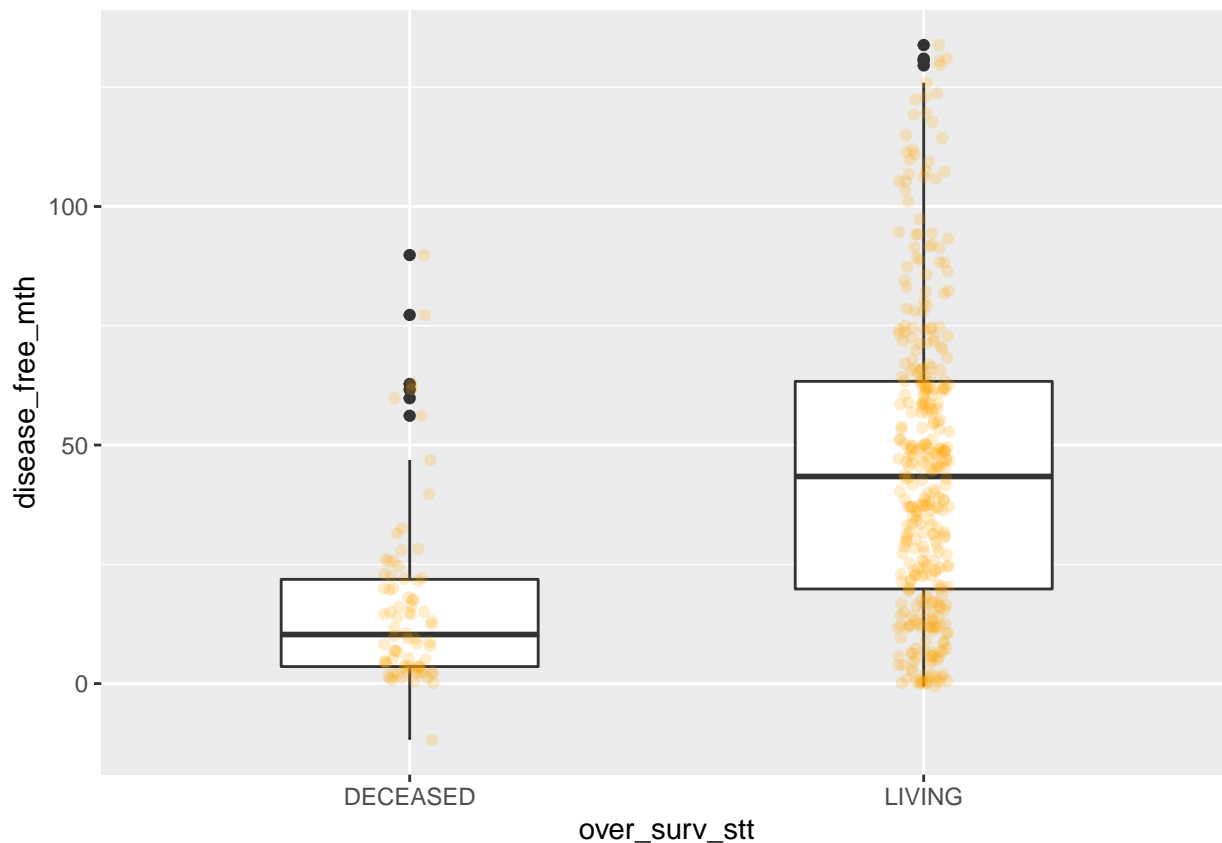


```
t.test(kirc_clinic$year_diagnose ~ kirc_clinic$over_surv_stt)
```

```
##
## Welch Two Sample t-test
##
## data: kirc_clinic$year_diagnose by kirc_clinic$over_surv_stt
## t = -8.898, df = 377.09, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -2.510367 -1.601685
## sample estimates:
## mean in group DECEASED mean in group LIVING
## 2004.638 2006.694
```

```
ggplot(kirc_clinic, aes(x=over_surv_stt, 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).
```

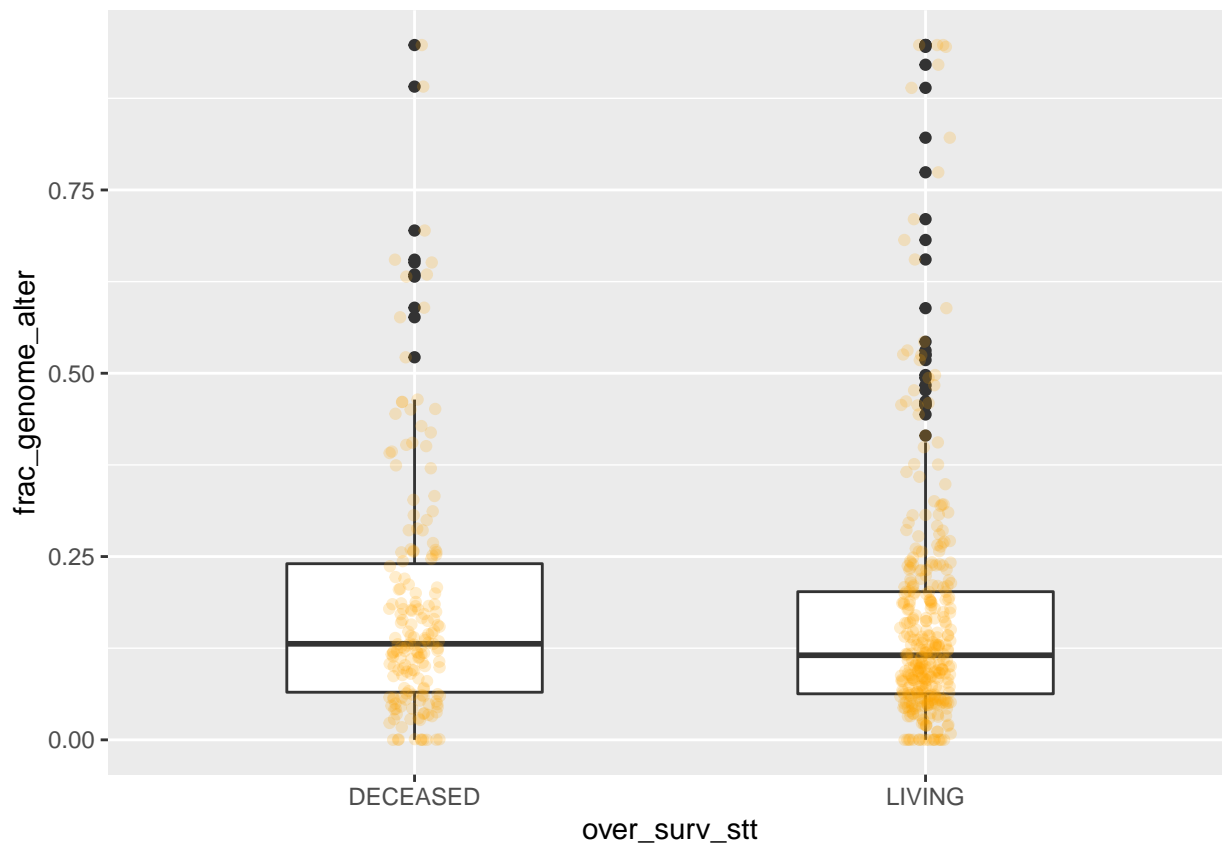


```
t.test(kirc_clinic$disease_free_mth ~ kirc_clinic$over_surv_stt)
```

```
##
## Welch Two Sample t-test
##
## data: kirc_clinic$disease_free_mth by kirc_clinic$over_surv_stt
## t = -10.985, df = 188.22, p-value < 2.2e-16
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -34.63580 -24.08972
## sample estimates:
## mean in group DECEASED mean in group LIVING
## 16.10846 45.47122
```

```
ggplot(kirc_clinic, aes(x=over_surv_stt, 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).
```

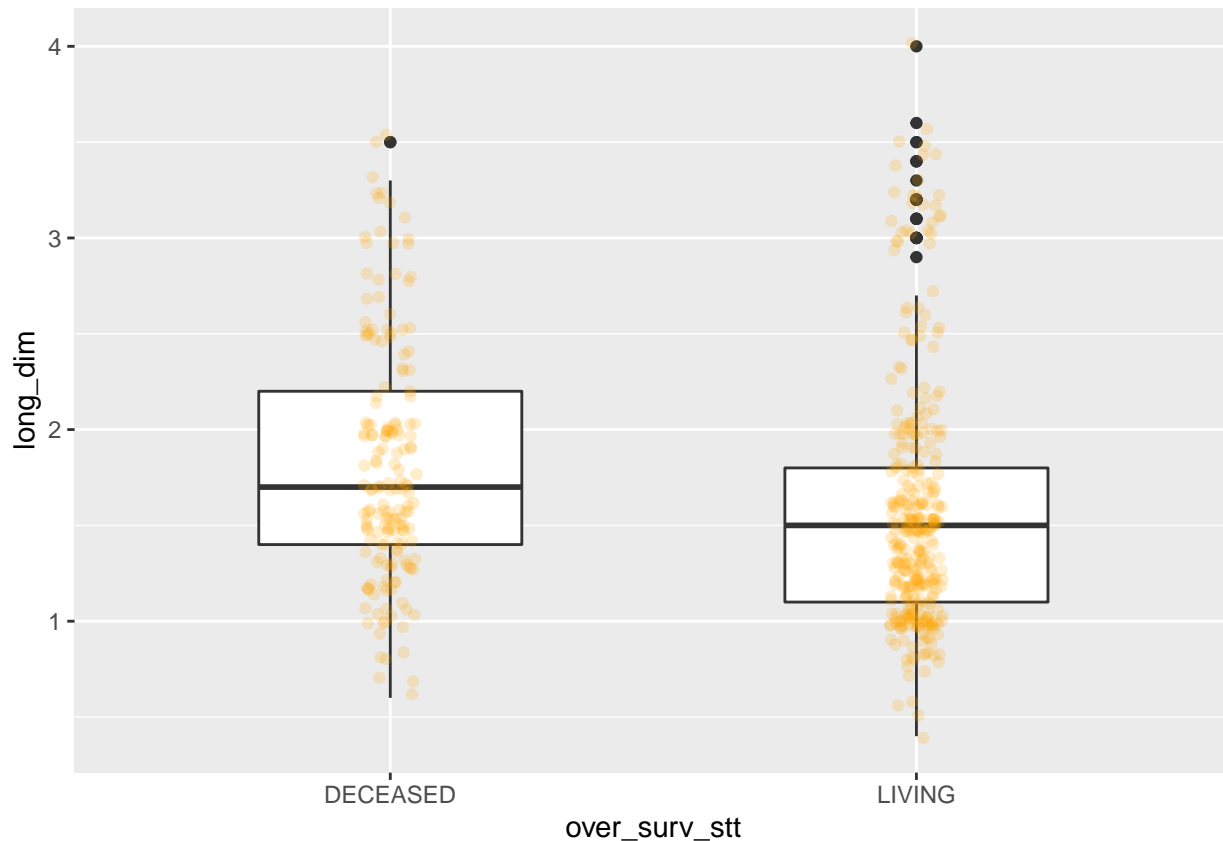


```
t.test(kirc_clinic$frac_genome_alter ~ kirc_clinic$over_surv_stt)
```

```
##
## Welch Two Sample t-test
##
## data: kirc_clinic$frac_genome_alter by kirc_clinic$over_surv_stt
## t = 1.196, df = 343.6, p-value = 0.2325
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.01199882 0.04923234
## sample estimates:
## mean in group DECEASED mean in group LIVING
## 0.1826051 0.1639884
```

```
ggplot(kirc_clinic, aes(x=over_surv_stt, 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).
```

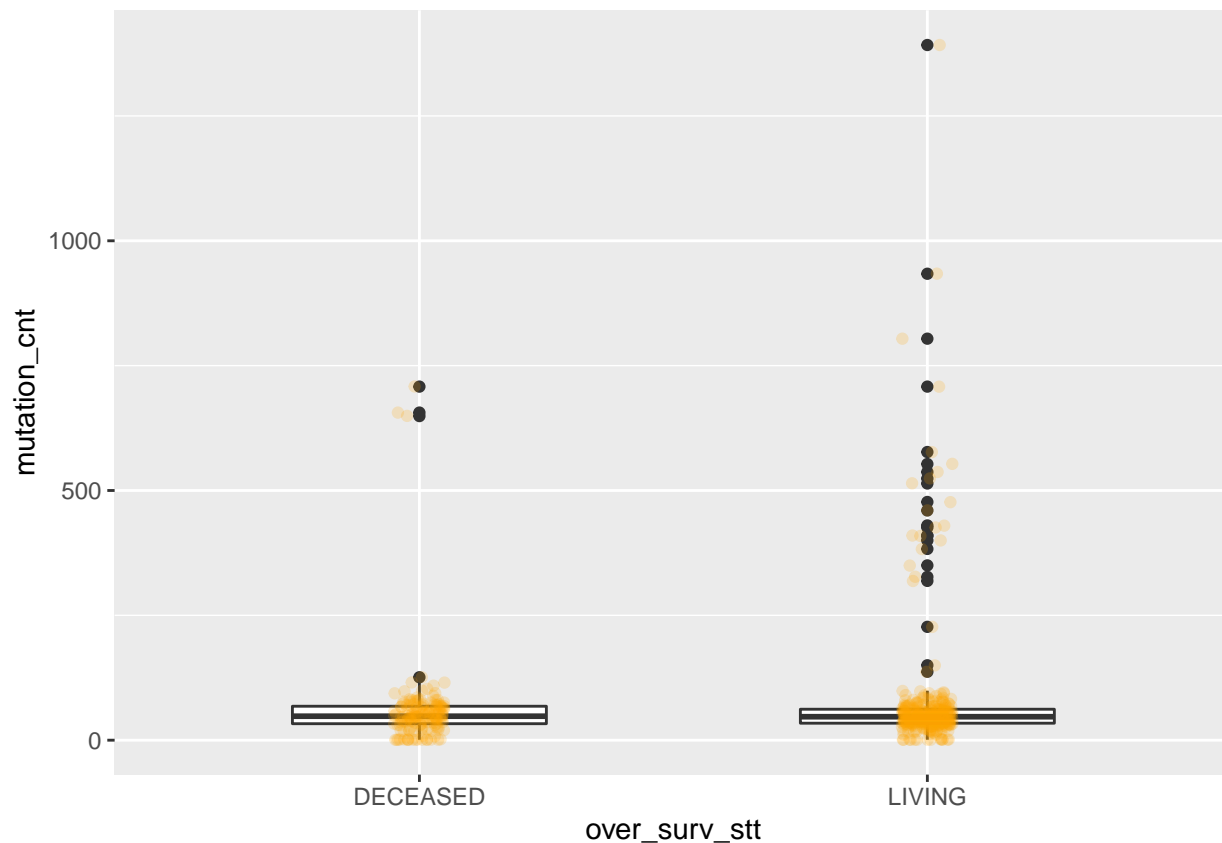



```
t.test(kirc_clinic$long_dim ~ kirc_clinic$over_surv_stt)
```

```
##
##  Welch Two Sample t-test
##
## data:  kirc_clinic$long_dim by kirc_clinic$over_surv_stt
## t = 4.1297, df = 363.45, p-value = 4.51e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.1295804 0.3651751
## sample estimates:
## mean in group DECEASED    mean in group LIVING
##           1.824277           1.576900
```

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

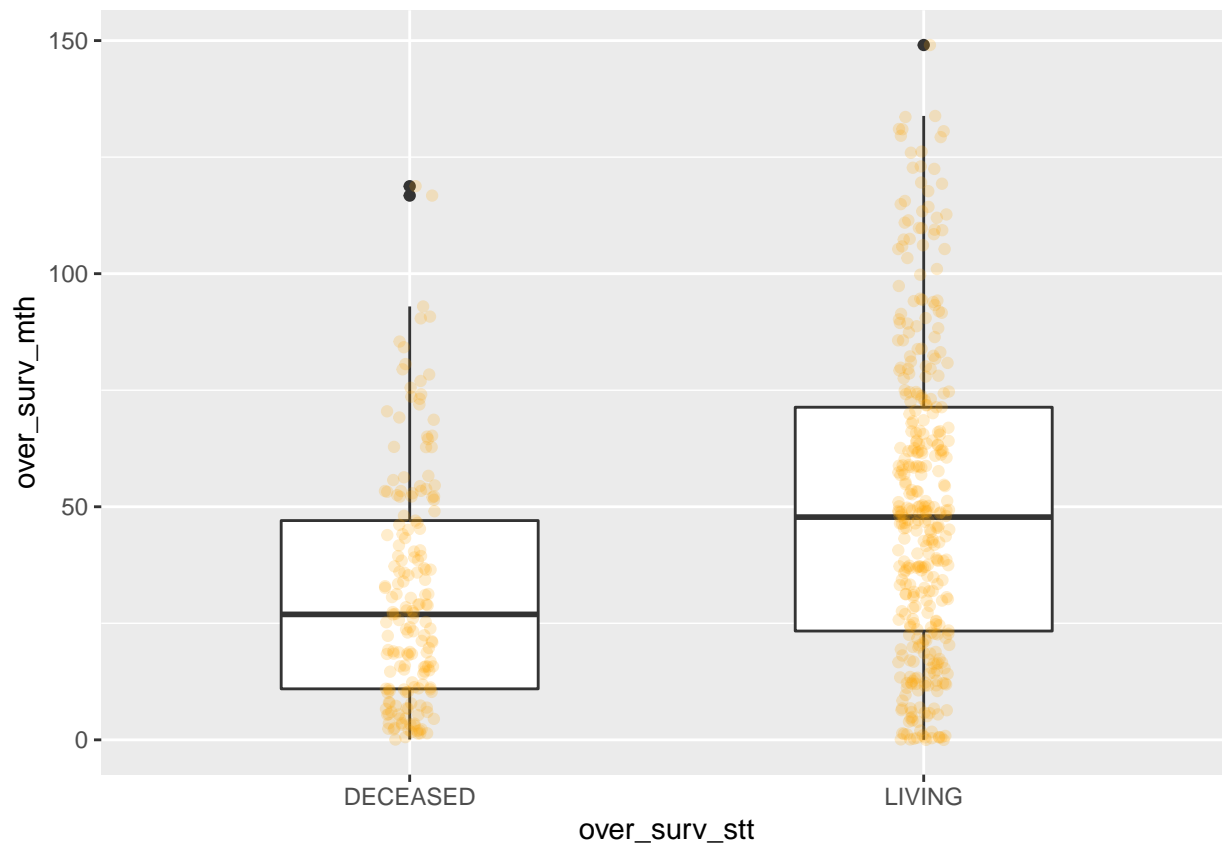
```
## Warning: Removed 86 rows containing non-finite values (stat_boxplot).
## Warning: Removed 86 rows containing missing values (geom_point).
```



```
t.test(kirc_clinic$mutation_cnt ~ kirc_clinic$over_surv_stt)
```

```
##
##  Welch Two Sample t-test
##
## data:  kirc_clinic$mutation_cnt by kirc_clinic$over_surv_stt
## t = -1.8306, df = 428.83, p-value = 0.06786
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -41.980661  1.492307
## sample estimates:
## mean in group DECEASED    mean in group LIVING
##           60.47059           80.71477
```

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

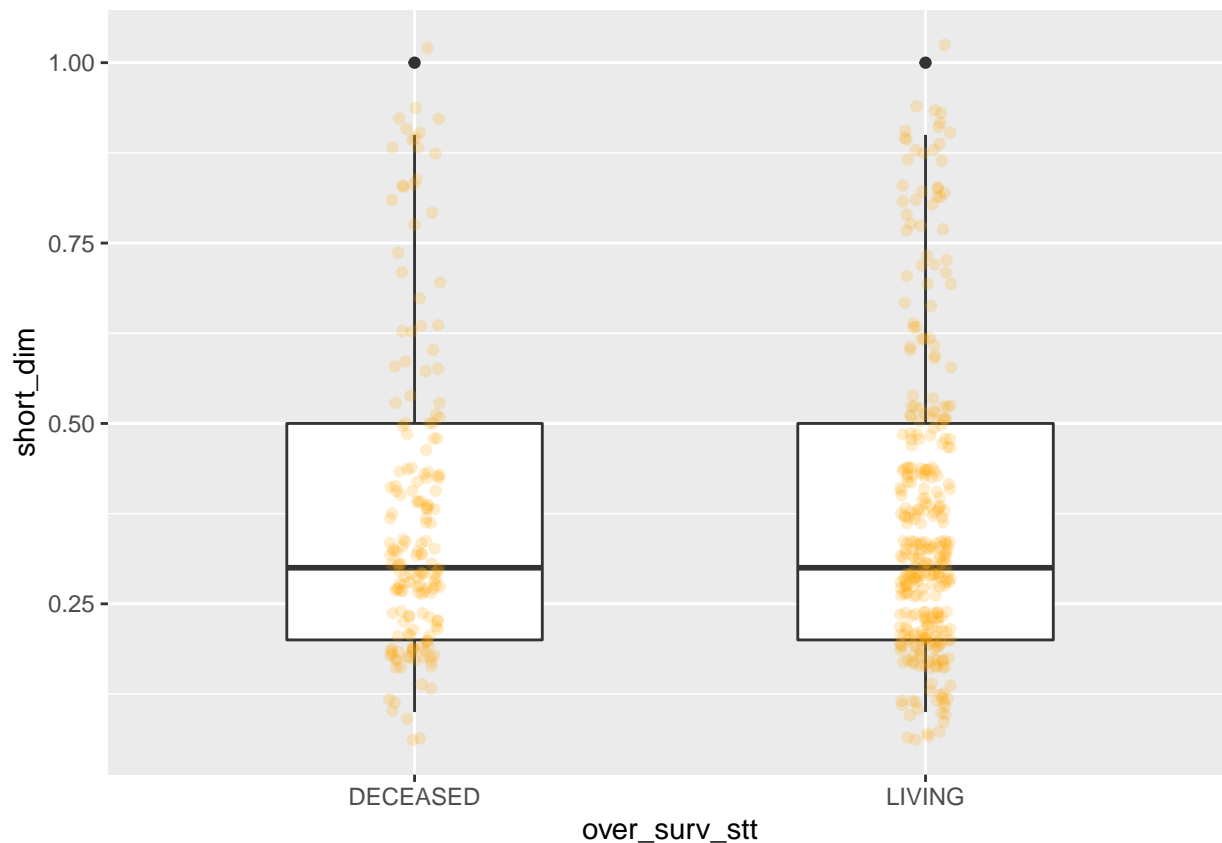


```
t.test(kirc_clinic$over_surv_mth ~ kirc_clinic$over_surv_stt)
```

```
##
## Welch Two Sample t-test
##
## data: kirc_clinic$over_surv_mth by kirc_clinic$over_surv_stt
## t = -7.3172, df = 450.92, p-value = 1.169e-12
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -23.99320 -13.83372
## sample estimates:
## mean in group DECEASED mean in group LIVING
## 31.57734 50.49081
```

```
ggplot(kirc_clinic, aes(x=over_surv_stt, 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).
```



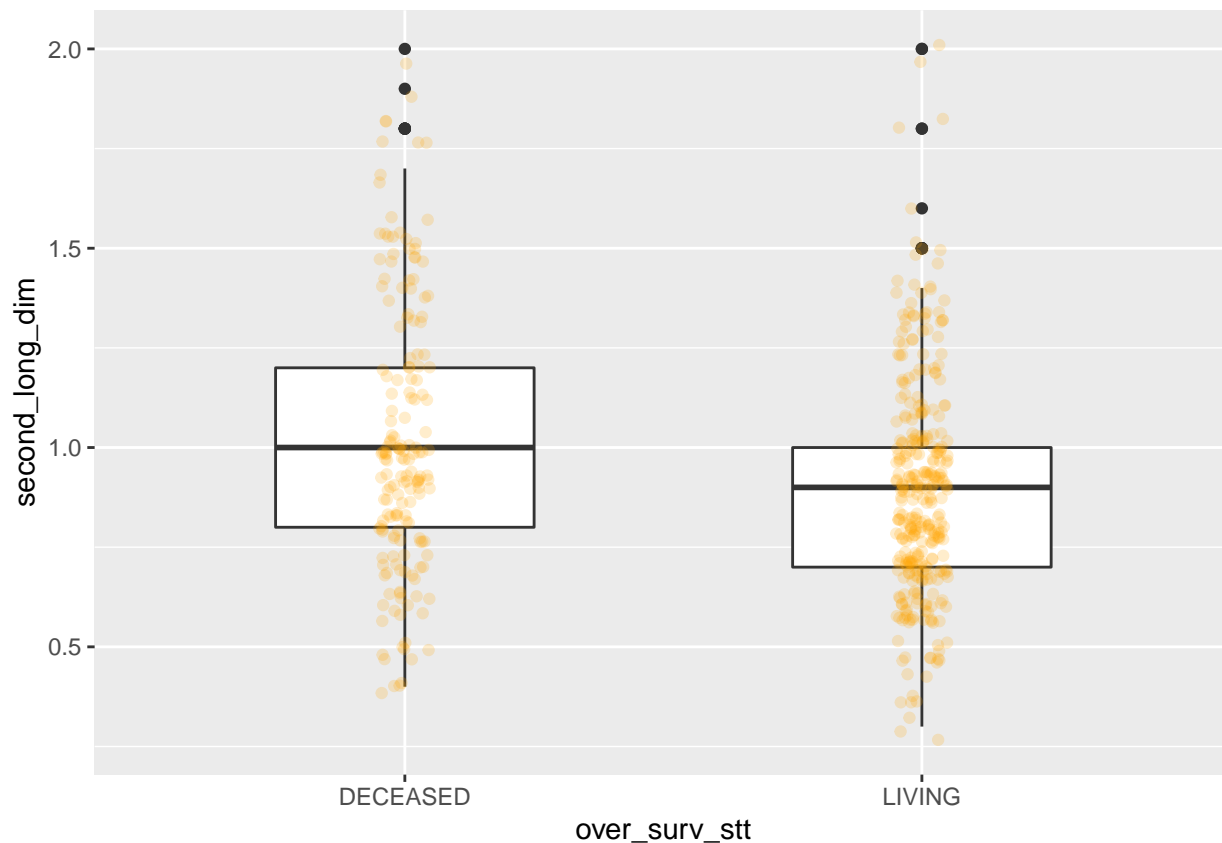
```
t.test(kirc_clinic$short_dim ~ kirc_clinic$over_surv_stt)
```

```
##
##  Welch Two Sample t-test
##
## data:  kirc_clinic$short_dim by kirc_clinic$over_surv_stt
## t = 0.47841, df = 344.68, p-value = 0.6327
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.02935985  0.04823295
## sample estimates:
## mean in group DECEASED    mean in group LIVING
##          0.3820809          0.3726444
```

```
ggplot(kirc_clinic, aes(x=over_surv_stt, 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).
```



```
t.test(kirc_clinic$second_long_dim ~ kirc_clinic$over_surv_stt)
```

```
##
## Welch Two Sample t-test
##
## data: kirc_clinic$second_long_dim by kirc_clinic$over_surv_stt
## t = 4.0639, df = 287.92, p-value = 6.231e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  0.06333111 0.18229322
## sample estimates:
## mean in group DECEASED mean in group LIVING
##          1.0173410          0.8945289
# fazer uma table com as variaveis dependentes, independente e p-valores
```

4. Categorical variables vs. over_surv_stt

Tabulation and chi-square test

```
# talvez isso possa sair uma vez que ja tem a mesma analise com tablefit
kirc_clinic %>%
  select_if(is.factor) %>%
  summary()
```

```
## metastasis_stg neoplasm_ln_stg neoplasm_stg tumor_stg
## M0 :426 N0:240 Stage I :269 T1:275
```

```

## M1 : 79      N1: 17      Stage II : 57      T2: 69
## MX : 30      NX:280     Stage III:125    T3:182
## NA's: 2      Stage IV : 83    T4: 11
##              NA's      : 3
##
##              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      prior_cancer      tumor_lateral      primer_ln_ind3
## Elevated: 5      No :519      No :459      Bilateral: 1      NO :395
## Low      :263      Yes: 18      Yes: 78      Left      :253      YES :135
## Normal   :186      Right      :283      NA's: 7
## NA's      : 83
##
##      over_surv_stt      platelet      tissue_prospect      race
## DECEASED:177      Elevated: 38      NO :465      BLACK OR AFRICAN AMERICAN: 56
## LIVING :360      Low      : 46      YES : 52      WHITE      :466
##              Normal :360      NA's: 20      NA's      : 15
##              NA's      : 93
##
##      tissue_retrospect      serum_ca      gender      tissue_site      person_neoplasm_stt
## NO : 53      Elevated: 10      Female:191      A      : 79      TUMOR FREE:361
## YES :466      Low      :204      Male :346      B      :303      WITH TUMOR:141
## NA's: 18      Normal :151      C      :127      NA's      : 35
##              NA's      :172      OTHERS: 28
##
##
##      wbc
## Elevated:164
## Low      : 9
## Normal   :268
## NA's      : 96
##
##
t_metas_stg <- table(kirc_clinic$metastasis_stg, kirc_clinic$over_surv_stt, exclude = NULL)
t_metas_stg <- addmargins(round(100*prop.table(t_metas_stg)))
t_metas_stg

##
##      DECEASED      LIVING      Sum
## M0      20      59      79
## M1      12      3      15
## MX      1      5      6
## <NA>      0      0      0
## Sum      33      67      100

```

```
chisq.test(x = kirc_clinic$metastasis_stg, y = kirc_clinic$over_surv_stt)

##
## Pearson's Chi-squared test
##
## data: kirc_clinic$metastasis_stg and kirc_clinic$over_surv_stt
## X-squared = 99.343, df = 2, p-value < 2.2e-16

t_lymph <- table(kirc_clinic$neoplasm_ln_stg, kirc_clinic$over_surv_stt, exclude = NULL)
t_lymph <- addmargins(round(100*prop.table(t_lymph)))
t_lymph
```

```
##
##      DECEASED LIVING Sum
## NO          16      29  45
## N1           2       1   3
## NX          15      37  52
## Sum         33      67 100
```

```
chisq.test(x = kirc_clinic$neoplasm_ln_stg, y = kirc_clinic$over_surv_stt)
```

```
##
## Pearson's Chi-squared test
##
## data: kirc_clinic$neoplasm_ln_stg and kirc_clinic$over_surv_stt
## X-squared = 13.989, df = 2, p-value = 0.0009169

t_neop <- table(kirc_clinic$neoplasm_stg, kirc_clinic$over_surv_stt, exclude = NULL)
t_neop <- addmargins(round(100*prop.table(t_neop)))
t_neop
```

```
##
##      DECEASED LIVING Sum
## Stage I         8      42  50
## Stage II        2       8  10
## Stage III       9      14  23
## Stage IV      12       3  15
## <NA>            0       0   0
## Sum           31      67  98
```

```
chisq.test(x = kirc_clinic$neoplasm_stg, y = kirc_clinic$over_surv_stt)
```

```
##
## Pearson's Chi-squared test
##
## data: kirc_clinic$neoplasm_stg and kirc_clinic$over_surv_stt
## X-squared = 123.9, df = 3, p-value < 2.2e-16

t_tumor <- table(kirc_clinic$tumor_stg, kirc_clinic$over_surv_stt, exclude = NULL)
t_tumor <- addmargins(round(100*prop.table(t_tumor)))
t_tumor
```

```
##
##      DECEASED LIVING Sum
## T1          9      42  51
## T2          4       9  13
## T3         18      16  34
```

```
##      T4          2      0      2
##      Sum         33     67    100
```

```
chisq.test(x = kirc_clinic$tumor_stg, y = kirc_clinic$over_surv_stt)
```

```
##
## Pearson's Chi-squared test
##
## data: kirc_clinic$tumor_stg and kirc_clinic$over_surv_stt
## X-squared = 76.345, df = 3, p-value < 2.2e-16
```

```
t_free <- table(kirc_clinic$disease_free_stt, kirc_clinic$over_surv_stt, exclude = NULL)
t_free <- addmargins(round(100*prop.table(t_free)))
t_free
```

```
##
##              DECEASED LIVING Sum
## DiseaseFree           0      58  58
## Recurred/Progressed    15       9  24
## <NA>                   18       0  18
## Sum                   33      67 100
```

```
chisq.test(x = kirc_clinic$disease_free_stt, y = kirc_clinic$over_surv_stt)
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: kirc_clinic$disease_free_stt and kirc_clinic$over_surv_stt
## X-squared = 228.22, df = 1, p-value < 2.2e-16
```

```
t_prior <- table(kirc_clinic$prior_cancer, kirc_clinic$over_surv_stt, exclude = NULL)
t_prior <- addmargins(round(100*prop.table(t_prior)))
t_prior
```

```
##
##          DECEASED LIVING Sum
## No          28      57  85
## Yes          4      10  14
## Sum         32      67  99
```

```
chisq.test(x = kirc_clinic$prior_cancer, y = kirc_clinic$over_surv_stt)
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: kirc_clinic$prior_cancer and kirc_clinic$over_surv_stt
## X-squared = 0.0993, df = 1, p-value = 0.7527
```

```
t_neo <- table(kirc_clinic$neoadj_therapy, kirc_clinic$over_surv_stt, exclude = NULL)
t_neo <- addmargins(round(100*prop.table(t_neo)))
t_neo
```

```
##
##          DECEASED LIVING Sum
## No          31      66  97
## Yes          2       1   3
## Sum         33      67 100
```



```

chisq.test(x = kirc_clinic$neoadj_therapy, y = kirc_clinic$over_surv_stt)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: kirc_clinic$neoadj_therapy and kirc_clinic$over_surv_stt
## X-squared = 3.31, df = 1, p-value = 0.06886

t_platelet <- table(kirc_clinic$platelet, kirc_clinic$over_surv_stt, exclude = NULL)
t_platelet <- addmargins(round(100*prop.table(t_platelet)))
t_platelet

##
##              DECEASED LIVING Sum
## Elevated          6         1   7
## Low                4         5   9
## Normal            20        47  67
## <NA>                4        14  18
## Sum               34        67 101

chisq.test(x = kirc_clinic$platelet, y = kirc_clinic$over_surv_stt)

##
## Pearson's Chi-squared test
##
## data: kirc_clinic$platelet and kirc_clinic$over_surv_stt
## X-squared = 37.32, df = 2, p-value = 7.871e-09

t_prospect <- table(kirc_clinic$tissue_prospect, kirc_clinic$over_surv_stt, exclude = NULL)
t_prospect <- addmargins(round(100*prop.table(t_prospect)))
t_prospect

##
##              DECEASED LIVING Sum
## NO              31         55  86
## YES              0          9   9
## <NA>              1          3   4
## Sum             32         67  99

chisq.test(x = kirc_clinic$tissue_prospect, y = kirc_clinic$over_surv_stt)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: kirc_clinic$tissue_prospect and kirc_clinic$over_surv_stt
## X-squared = 20.87, df = 1, p-value = 4.914e-06

t_race <- table(kirc_clinic$race, kirc_clinic$over_surv_stt, exclude = NULL)
t_race <- addmargins(round(100*prop.table(t_race)))
t_race

##
##              DECEASED LIVING Sum
## BLACK OR AFRICAN AMERICAN      2      8  10
## WHITE                          30     56  86
## <NA>                             1      2   3
## Sum                           33     66  99

```

```
chisq.test(x = kirc_clinic$race, y = kirc_clinic$over_surv_stt)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: kirc_clinic$race and kirc_clinic$over_surv_stt
## X-squared = 4.6232, df = 1, p-value = 0.03154

t_retros <- table(kirc_clinic$tissue_retrospect, kirc_clinic$over_surv_stt, exclude = NULL)
t_retros <- addmargins(round(100*prop.table(t_retros)))
t_retros

##
##          DECEASED LIVING Sum
## NO              0      9   9
## YES             31     55  86
## <NA>             1      2   3
## Sum             32     66  98

chisq.test(x = kirc_clinic$tissue_retrospect, y = kirc_clinic$over_surv_stt)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: kirc_clinic$tissue_retrospect and kirc_clinic$over_surv_stt
## X-squared = 21.295, df = 1, p-value = 3.938e-06

t_ca <- table(kirc_clinic$serum_ca, kirc_clinic$over_surv_stt, exclude = NULL)
t_ca <- addmargins(round(100*prop.table(t_ca)))
t_ca

##
##          DECEASED LIVING Sum
## Elevated         2      0   2
## Low              12     26  38
## Normal           12     17  29
## <NA>              7     25  32
## Sum              33     68 101

chisq.test(x = kirc_clinic$serum_ca, y = kirc_clinic$over_surv_stt)

##
## Pearson's Chi-squared test
##
## data: kirc_clinic$serum_ca and kirc_clinic$over_surv_stt
## X-squared = 14.877, df = 2, p-value = 0.0005883

t_gender <- table(kirc_clinic$gender, kirc_clinic$over_surv_stt, exclude = NULL)
t_gender <- addmargins(round(100*prop.table(t_gender)))
t_gender

##
##          DECEASED LIVING Sum
## Female        12     23  35
## Male          21     44  65
## Sum           33     67 100
```

```
chisq.test(x = kirc_clinic$gender, y = kirc_clinic$over_surv_stt)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: kirc_clinic$gender and kirc_clinic$over_surv_stt
## X-squared = 0.087745, df = 1, p-value = 0.7671

t_site <- table(kirc_clinic$tissue_site, kirc_clinic$over_surv_stt, exclude = NULL)
t_site <- addmargins(round(100*prop.table(t_site)))
t_site

##
##          DECEASED LIVING Sum
## A              2      13  15
## B             21      36  57
## C              9      15  24
## OTHERS         1       4   5
## Sum           33      68 101

chisq.test(x = kirc_clinic$tissue_site, y = kirc_clinic$over_surv_stt)

##
## Pearson's Chi-squared test
##
## data: kirc_clinic$tissue_site and kirc_clinic$over_surv_stt
## X-squared = 19.861, df = 3, p-value = 0.0001814

t_neop_st <- table(kirc_clinic$person_neoplasm_stt, kirc_clinic$over_surv_stt, exclude = NULL)
t_neop_st <- addmargins(round(100*prop.table(t_neop_st)))
t_neop_st

##
##          DECEASED LIVING Sum
## TUMOR FREE      11      57  68
## WITH TUMOR      20       7  27
## <NA>             3       4   7
## Sum            34      68 102

chisq.test(x = kirc_clinic$person_neoplasm_stt, y = kirc_clinic$over_surv_stt)

##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: kirc_clinic$person_neoplasm_stt and kirc_clinic$over_surv_stt
## X-squared = 157.06, df = 1, p-value < 2.2e-16

t_wbc <- table(kirc_clinic$wbc, kirc_clinic$over_surv_stt, exclude = NULL)
t_wbc <- addmargins(round(100*prop.table(t_wbc)))
t_wbc

##
##          DECEASED LIVING Sum
## Elevated       9      22  31
## Low            1       1   2
## Normal        19      31  50
## <NA>           4      14  18
```

```
##      Sum          33      68 101
chisq.test(x = kirc_clinic$wbc, y = kirc_clinic$over_surv_stt)

##
## Pearson's Chi-squared test
##
## data:  kirc_clinic$wbc and kirc_clinic$over_surv_stt
## X-squared = 9.0853, df = 2, p-value = 0.01065
```

7. FinalFit

summarise variables/factors by a categorical variable

```
explanatory <- names(kirc_clinic %>%
  select(-over_surv_stt) %>%
  select_if(is.factor))
dependent <- 'over_surv_stt'

table_fit <- kirc_clinic %>%
  summary_factorlist(dependent, explanatory, p=TRUE, add_dependent_label=TRUE)
table_fit
```

```
## Dependent: over_surv_stt
## metastasis_stg
## M0 110 (62.1) 316 (88.3)
## M1 64 (36.2) 15 (4.2)
## MX 3 (1.7) 27 (7.5)
## neoplasm_ln_stg
## N0 85 (48.0) 155 (43.1)
## N1 12 (6.8) 5 (1.4)
## NX 80 (45.2) 200 (55.6)
## neoplasm_stg
## Stage I 45 (25.6) 224 (62.6)
## Stage II 13 (7.4) 44 (12.3)
## Stage III 51 (29.0) 74 (20.7)
## Stage IV 67 (38.1) 16 (4.5)
## tumor_stg
## T1 50 (28.2) 225 (62.5)
## T2 21 (11.9) 48 (13.3)
## T3 96 (54.2) 86 (23.9)
## T4 10 (5.6) 1 (0.3)
## disease_free_stt Recurred/Progressed 78 (100.0) 49 (13.6)
## DiseaseFree 311 (86.4)
## ethnicity
## HISPANIC OR LATINO 3 (2.2) 23 (9.2)
## NOT HISPANIC OR LATINO 132 (97.8) 227 (90.8)
## histology_grd
## G2 45 (25.4) 185 (51.8)
## G3 74 (41.8) 133 (37.3)
## G4 57 (32.2) 21 (5.9)
## GX 1 (0.6) 4 (1.1)
## G1 14 (3.9)
## hemoglobin
## Elevated 3 (1.8) 2 (0.7)
## Low 118 (72.0) 145 (50.0)
## Normal 43 (26.2) 143 (49.3)
## neoadj_therapy
## No 167 (94.4) 352 (97.8)
## Yes 10 (5.6) 8 (2.2)
## prior_cancer
## No 153 (86.4) 306 (85.0)
## Yes 24 (13.6) 54 (15.0)
## tumor_lateral
## Left 98 (55.4) 155 (43.1)
```

##		Right	79 (44.6)	204 (56.7)
##		Bilateral		1 (0.3)
##	primer_ln_ind3	NO	120 (68.2)	275 (77.7)
##		YES	56 (31.8)	79 (22.3)
##	platelet	Elevated	30 (19.0)	8 (2.8)
##		Low	20 (12.7)	26 (9.1)
##		Normal	108 (68.4)	252 (88.1)
##	tissue_prospect	NO	169 (98.8)	296 (85.5)
##		YES	2 (1.2)	50 (14.5)
##	race	BLACK OR AFRICAN AMERICAN	11 (6.3)	45 (12.9)
##		WHITE	163 (93.7)	303 (87.1)
##	tissue_retrospect	NO	2 (1.2)	51 (14.7)
##		YES	169 (98.8)	297 (85.3)
##	serum_ca	Elevated	9 (6.6)	1 (0.4)
##		Low	66 (48.2)	138 (60.5)
##		Normal	62 (45.3)	89 (39.0)
##	gender	Female	65 (36.7)	126 (35.0)
##		Male	112 (63.3)	234 (65.0)
##	tissue_site	A	11 (6.2)	68 (18.9)
##		B	112 (63.3)	191 (53.1)
##		C	49 (27.7)	78 (21.7)
##		OTHERS	5 (2.8)	23 (6.4)
##	person_neoplasms_stt	TUMOR FREE	57 (35.2)	304 (89.4)
##		WITH TUMOR	105 (64.8)	36 (10.6)
##	wbc	Elevated	46 (29.5)	118 (41.4)
##		Low	6 (3.8)	3 (1.1)
##		Normal	104 (66.7)	164 (57.5)
##	p			
##	<0.001			
##				
##				
##	0.001			
##				
##				
##	<0.001			
##				
##				
##	<0.001			
##				
##				
##	<0.001			
##				
##	0.017			
##				
##	<0.001			
##				
##				
##	<0.001			
##				
##				

```
## 0.069
##
## 0.753
##
## 0.023
##
##
## 0.024
##
## <0.001
##
##
## <0.001
##
## 0.032
##
## <0.001
##
## 0.001
##
##
## 0.767
##
## <0.001
##
##
## <0.001
##
## 0.011
##
##
```

```
warnings()
```

```
#knitr::kable(table_fit, row.names=FALSE, align=c("l", "l", "r", "r", "r"))
```

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-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] GGally_1.5.0    ggpubr_0.3.0    rstatix_0.5.0    finalfit_1.0.1
## [5] skimr_2.1.1     forcats_0.5.0   stringr_1.4.0    dplyr_0.8.5
## [9] purrr_0.3.4     readr_1.3.1     tidyr_1.0.3      tibble_3.0.1
## [13] ggplot2_3.3.0   tidyverse_1.3.0
##
## loaded via a namespace (and not attached):
## [1] nlme_3.1-147      fs_1.4.1          lubridate_1.7.8    RColorBrewer_1.1-2
## [5] httr_1.4.1        ggsci_2.9          repr_1.1.0         tools_3.6.3
## [9] backports_1.1.6   utf8_1.1.4         R6_2.4.1           DBI_1.1.0
## [13] mgcv_1.8-31       colorspace_1.4-1   withr_2.2.0        tidyselect_1.1.0
## [17] curl_4.3          compiler_3.6.3     cli_2.0.2          rvest_0.3.5
## [21] mice_3.8.0        xml2_1.3.2         labeling_0.3       scales_1.1.1
## [25] digest_0.6.25     foreign_0.8-76     rmarkdown_2.1      rio_0.5.16
## [29] base64enc_0.1-3   pkgconfig_2.0.3    htmltools_0.4.0    dbplyr_1.4.3
## [33] highr_0.8         rlang_0.4.6        readxl_1.3.1       rstudioapi_0.11
## [37] generics_0.0.2    farver_2.0.3       jsonlite_1.6.1     zip_2.0.4
## [41] car_3.0-7         magrittr_1.5        Matrix_1.2-18      Rcpp_1.0.4.6
## [45] munsell_0.5.0     fansi_0.4.1        abind_1.4-5        lifecycle_0.2.0
## [49] stringi_1.4.6     yaml_2.2.1         carData_3.0-3      plyr_1.8.6
## [53] grid_3.6.3        crayon_1.3.4       lattice_0.20-41    haven_2.2.0
## [57] splines_3.6.3     hms_0.5.3          knitr_1.28         pillar_1.4.4
## [61] boot_1.3-25       ggsignif_0.6.0     reprex_0.3.0       glue_1.4.0
## [65] evaluate_0.14     data.table_1.12.8  modelr_0.1.7       vctrs_0.3.0
## [69] cellranger_1.1.0  gtable_0.3.0       reshape_0.8.8      assertthat_0.2.1
## [73] xfun_0.13         openxlsx_4.1.5     broom_0.5.6        survival_3.1-12
## [77] ellipsis_0.3.0

```