

LDA_IGA-NTX

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§ 1

Load required packages:

```
library(ggplot2)
library(survival)
library(survminer)
library(xtable)
library(data.table)
library(readxl)
library(forcats)
library(lubridate)
library(dplyr)
```

```
#if (Sys.info()["sysname"] != "Darwin"){
#  default_theme <- theme_minimal() +
#  theme(text = element_text(family = "Decima WE", size = 15)) +
#  theme(panel.grid.major = element_line(color = "grey", size = 0.3)) +
#  theme(axis.line = element_line(color = "black", size = 0.4))
#
#} else {
#  default_theme <- theme_minimal()
#}
default_theme <- theme_minimal()
two_scale_fill <- scale_fill_manual(values=c("#69b3a2", "#404080"))
```

Read data using read_data.R scrip:

```
source("read_data.R")
```

§ 2 EDA

§ 2.1 IGA

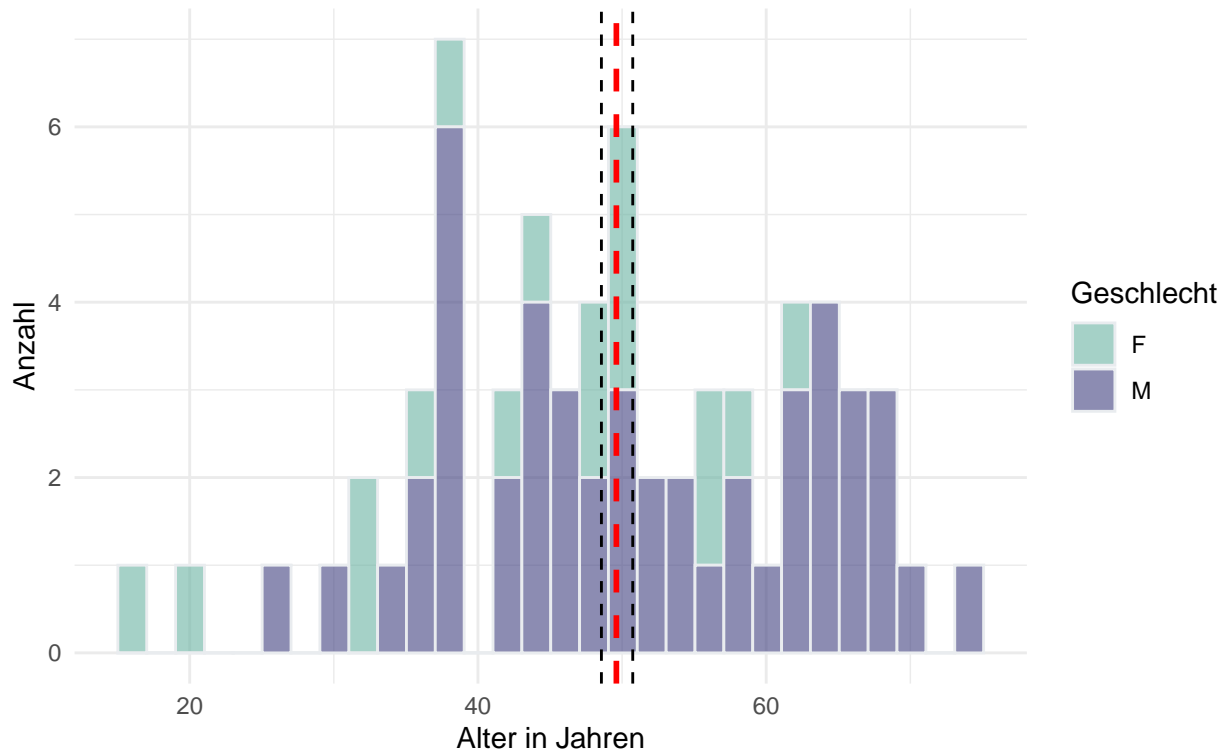
```
# follow-up (mean)
(interval(data_iga2$`T-date`, data_iga2$`T-dls`) / years(1)) %>%
  mean()

## [1] 7.728562

# age patients (yrs.)
ggplot(data = data_iga2) +
  geom_histogram(mapping = aes(x = interval(`Date of birth`, `T-date`) / years(1),
                                fill = `R-sex`),
                color="#e9ecef",
                alpha=0.6) +
  two_scale_fill +
  # median age total
  geom_vline(aes(xintercept = median(
    interval(`Date of birth`, `T-date`) / years(1))
  ), size = 1.0, color = "red", linetype = "dashed") +
  # median age F
  geom_vline(aes(xintercept = median(
    interval(`Date of birth`, `T-date`) / years(1))
  ), data = data_iga2[`R-sex` == "F"], linetype = "dashed") +
  # median M
  geom_vline(aes(xintercept = median(
    interval(`Date of birth`, `T-date`) / years(1))
  ), data = data_iga2[`R-sex` == "M"], linetype = "dashed") +
  ylab("Anzahl") +
  xlab("Alter in Jahren") +
  ggtitle("Histogram Alter in Jahren am Transplantationsdatum",
          subtitle = paste0("(IGA Patienten, n=",
                              sum(!is.na(data_iga2$`Date of birth`)),
                              ")", collapse = "")) +
  labs(fill = "Geschlecht") +
  default_theme

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram Alter in Jahren am Transplantationsdatum (IGA Patienten, n=65)

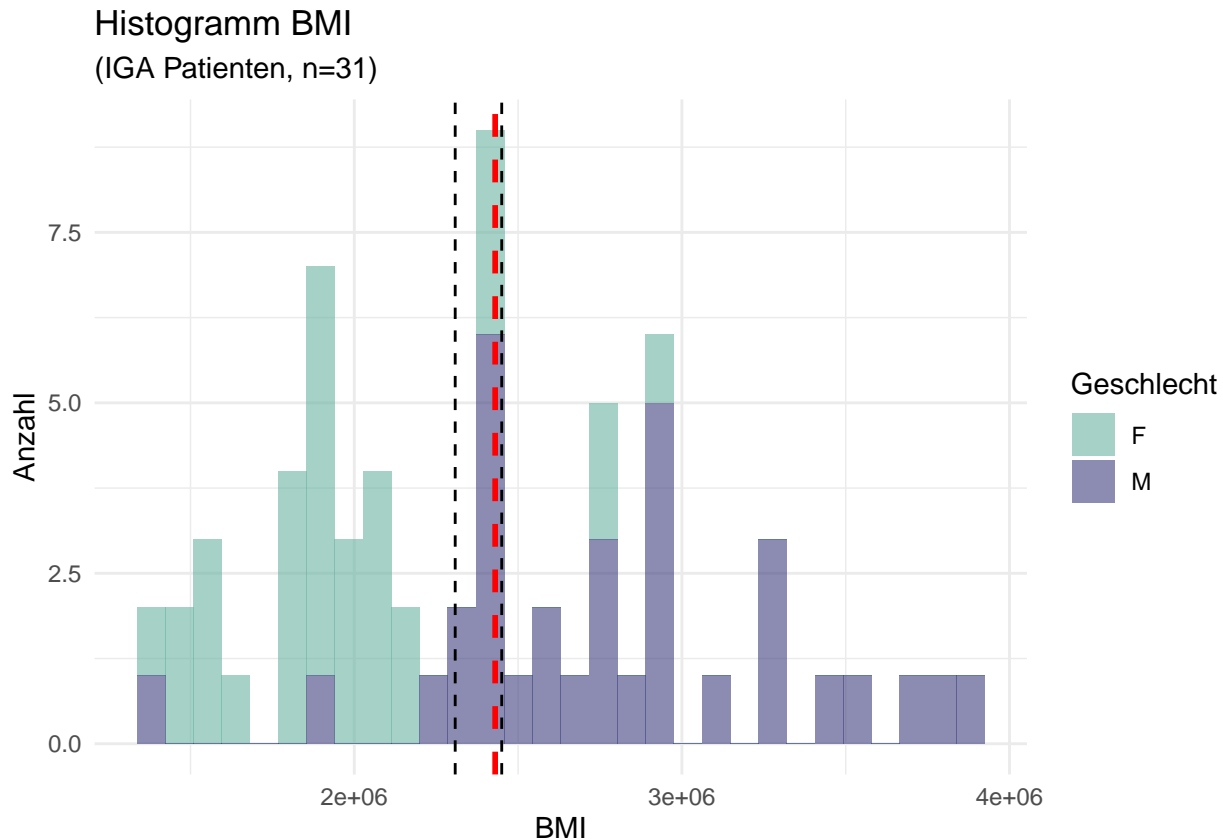


```
# male sex
summary(data_iga2$`R-sex`)
```

```
## F M
## 17 48
```

```
# BMI (mean.)
ggplot(data = data_iga2) +
  geom_histogram(mapping = aes(`D-weight` * (`D-height`)^2,
                                fill = `D-sex`),
                alpha = 0.6) +
  two_scale_fill +
  # median BMI total
  geom_vline(aes(xintercept = median(`D-weight` * (`D-height`)^2)),
            size = 1.0, color = "red", linetype = "dashed") +
  # median BMI F
  geom_vline(aes(xintercept = median(`D-weight` * (`D-height`)^2),
                data = data_iga2[`R-sex` == "F"], linetype = "dashed") +
  # median BMI M
  geom_vline(aes(xintercept = median(`D-weight` * (`D-height`)^2),
                data = data_iga2[`R-sex` == "M"], linetype = "dashed") +
  ylab("Anzahl") +
  xlab("BMI") + # Einheit???
  ggtitle("Histogramm BMI", subtitle = paste0("(IGA Patienten, n=",
                                                sum(!is.na(data_iga2$`R-height`)),
                                                ")", collapse = "")) +
  labs(fill = "Geschlecht") +
  default_theme
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
# deceased D.
# living D.
tbl_1 <- summary(data_iga2[`graft loss (0=functionial, 1=loss)` == 1]`D-type`)
tbl_1 <- round(tbl_1 / sum(tbl_1), 3)
tbl_2 <- summary(data_iga2[`graft loss (0=functionial, 1=loss)` == 0]`D-type`)
tbl_2 <- round(tbl_2 / sum(tbl_2), 3)
rbind("loss" = tbl_1, "functional" = tbl_2)
```

```
##          Cadaver Living
## loss      0.867  0.133
## functional 0.740  0.260
```

```
tbl_1 <- summary(data_iga2[`Pat death (0=alive, 1= dead)` == 1]`D-type`)
tbl_1 <- round(tbl_1 / sum(tbl_1), 3)
tbl_2 <- summary(data_iga2[`Pat death (0=alive, 1= dead)` == 0]`D-type`)
tbl_2 <- round(tbl_2 / sum(tbl_2), 3)
rbind("dead" = tbl_1, "alive" = tbl_2)
```

```
##          Cadaver Living
## dead      0.917  0.083
## alive     0.683  0.317
```

```
# BMI (mean.)
mean(data_iga2$`D-weight` * (data_iga2$`D-height`)^2)
```

```
## [1] 2393290
```

```
# HLA-mm (0-6)
tbl_1 <- as.data.table(lapply(data_iga2[, c("mm-A", "mm-B", "mm-DR")],
                             as.numeric))
tbl_2 <- apply(X = tbl_1,
               MARGIN = 2, # for each column
               FUN = mean, na.rm = TRUE)

round(tbl_2, 3)
```

```
## mm-A mm-B mm-DR
## 1.776 2.143 1.918
```

```
round(mean(tbl_2),3)
```

```
## [1] 1.946
```

```
tbl_2 <- apply(X = tbl_1,
               MARGIN = 1, # for each row
               FUN = sum, na.rm = TRUE)
mean(tbl_2)
```

```
## [1] 4.4
```

```
# PRA current (mean)
# PRA highest (mean)
data_iga2[, c("Current PRA%", "Highest PRA%")] %>%
  apply(MARGIN = 2,
        FUN = mean, na.rm = TRUE)
```

```
## Current PRA% Highest PRA%
##      5.163934      10.786885
```

```
# age donor (mean.)
mean(data_iga2$`D-age`)
```

```
## [1] 50.33846
```

```
# cold-ischemia time (hours)
mean(data_iga2$`Cold ischaemic period hours`, na.rm = TRUE)
```

```
## [1] 11.61224
```

```
median(data_iga2$`Cold ischaemic period hours`, na.rm = TRUE)
```

```
## [1] 12
```

§ 2.2 NTX

§ 3 Kaplan-Meier

```
follow_up <- years(10)
```

§ 3.1 IGA

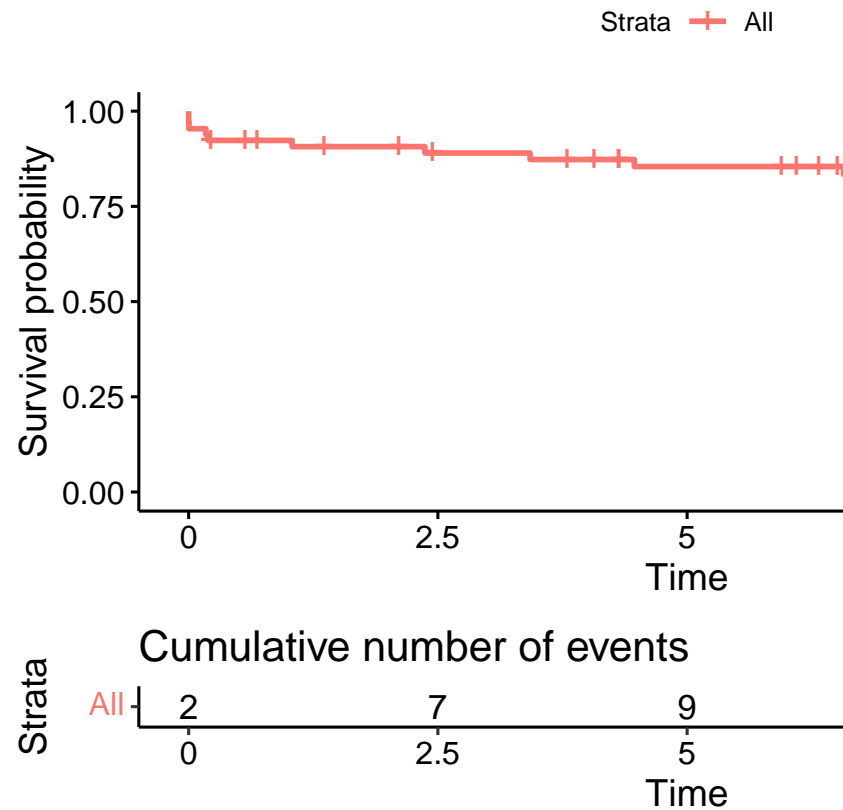
```
# functions in survival and surminer package need numeric-type input
data_iga2[, time_date_biopsy := interval(`T-date`, `date of biopsy`) / years(1)]
data_iga2[, time_t_dls := interval(`T-date`, `T-dls`) / years(1)]
data_iga2[, time_date_birth := interval(`T-date`, `Date of birth`) / years(1)]
data_iga2[, time_graft_loss := interval(`T-date`, `graft loss date`) / years(1)]
data_iga2[, time_date_follow_up := interval(`T-date`, `T-date` + follow_up) / years(1)]
```

§ 3.1.1

- Event:
 - graft-loss within the follow up period.
- Censoring scheme:
 - if `graft loss date` after follow up period, censored by end of follow up.
 - if `T-dls` (date last seen) within follow up period, censored by `T-dls`.
- Time period:
 - 10 years after `T-date` (kidney transplantaion).

```
data_iga2 <- data_iga2 %>%
  mutate(censor_date = case_when(
    ## graft-loss within follow up period
    !is.na(`graft loss date`) & `graft loss date` < `T-date` + follow_up ~ time_graft_loss,
    ## graft-loss after follow up period
    !is.na(`graft loss date`) & `graft loss date` > `T-date` + follow_up ~ time_date_follow_up,
    ## no graft-loss and last seen within follow up
    is.na(`graft loss date`) & !is.na(`T-dls`) & `T-dls` < `T-date` + follow_up ~ time_t_dls,
    ## no graft-loss and last seen after follow up
    is.na(`graft loss date`) & !is.na(`T-dls`) & `T-dls` > `T-date` + follow_up ~ time_date_follow_up,
    ## no graft loss and no last seen
    is.na(`graft loss date`) & is.na(`T-dls`) ~ time_date_follow_up
  )
)
data_iga2 <- data_iga2 %>%
  mutate(event = case_when(
    ## graft-loss within follow up period
    !is.na(`graft loss date`) & `graft loss date` < `T-date` + follow_up ~ 1,
    ## else censored
    TRUE ~ 0,
  )
)
```

```
model_iga_1 <- survfit(formula = Surv(time = censor_date,
                                     event = event, type = "right") ~ 1,
                      data = data_iga2)
ggsurvplot(model_iga_1,
            conf.int = FALSE,
            cumevents = TRUE)
```



Overall kaplan-Meier curve (no stratification)

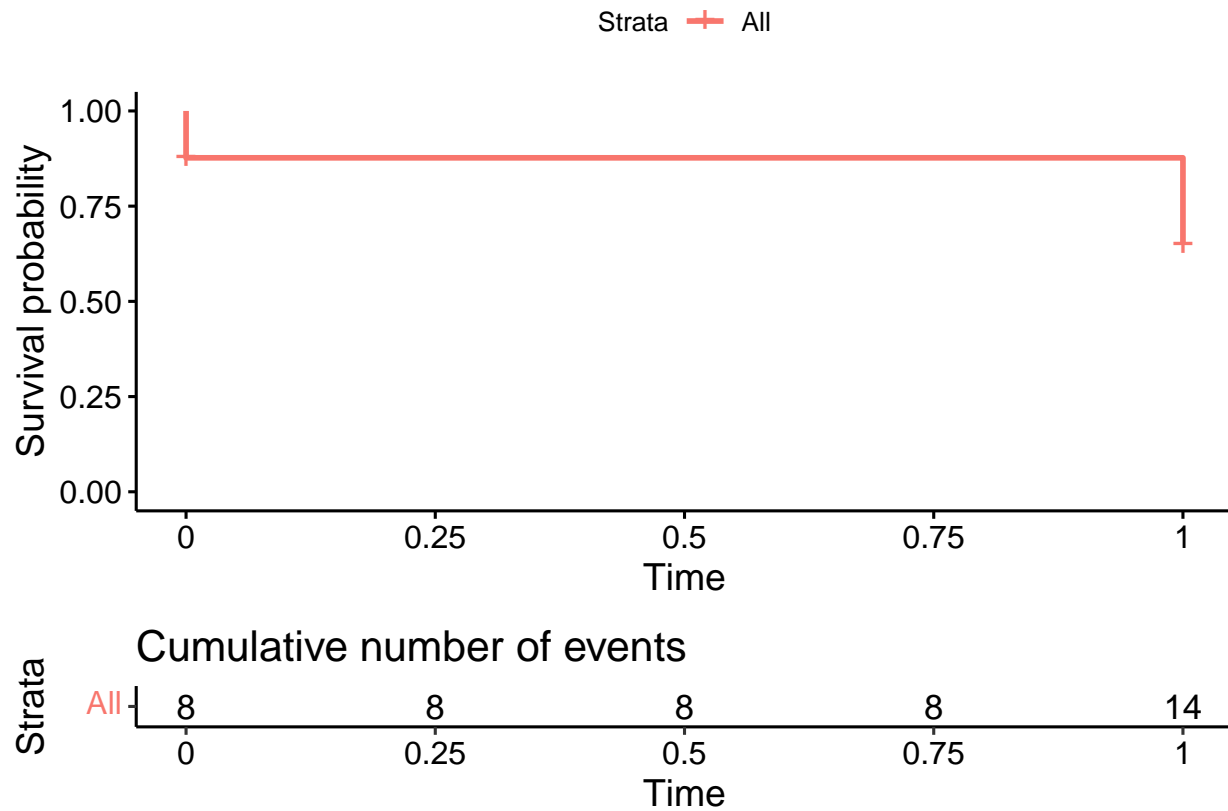
§ 3.1.2

- Event:
 - T-dls & 'Pat death (0=alive, 1= dead) (patient death).
- Censoring scheme:
 - T-dls (date last seen) within follow up period.
- Time period:
 - 10 years after T-date (kidney transplantaion).

```
data_iga2 <- data_iga2 %>%
  mutate(censor_date = case_when(
    ## patient death and death date within follow up
    (`Pat death (0=alive, 1= dead)` == 1) & `T-dls` < `T-date` + follow_up ~ time_t_dls,
    ## patient dead but after follow up
    (`Pat death (0=alive, 1= dead)` == 1) & `T-dls` > `T-date` + follow_up ~ time_date_follow_up,
    ## patient not death but dropped within follow up
    (`Pat death (0=alive, 1= dead)` == 0) & `T-dls` < `T-date` + follow_up ~ time_t_dls,
    ## patient not death but dropped after follow up
    (`Pat death (0=alive, 1= dead)` == 0) & `T-dls` > `T-date` + follow_up ~ time_date_follow_up,
    ## NOTE: T-dls never NA
  )
)
data_iga2 <- data_iga2 %>%
  mutate(censor_date = case_when(
    ##
    (`Pat death (0=alive, 1= dead)` == 1) & `T-dls` < `T-date` + follow_up ~ 1,
    ## else
    TRUE ~ 0
  )
)
```

```
))
```

```
model_iga_2 <- survfit(formula = Surv(time = censor_date,  
                                     event = event, type = "right")~ 1,  
                      data = data_iga2)  
ggsurvplot(model_iga_2,  
           conf.int = FALSE,  
           cumevents = TRUE)
```



§ 3.1.3

- Event: graft loss and death
- Censoring scheme:
- Time period: