

LDA_IGA-NTX

Sven Morlock

28/03/2022

§ 1

Load required packages:

```
#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

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

§ 2.1 IGA

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

## [1] 7.683696

# patient death within follow up
nrow(data_iga[(`T-dls` <= (`T-date` + follow_up)) & `Pat death (0=alive, 1= dead)` == 1])

## [1] 23

# patient drop out
nrow(data_iga[(`T-dls` <= (`T-date` + follow_up)) & `Pat death (0=alive, 1= dead)` == 0])

## [1] 27

# patients with graft loss
nrow(data_iga[`graft loss (0=functionial, 1=loss)` == 1])

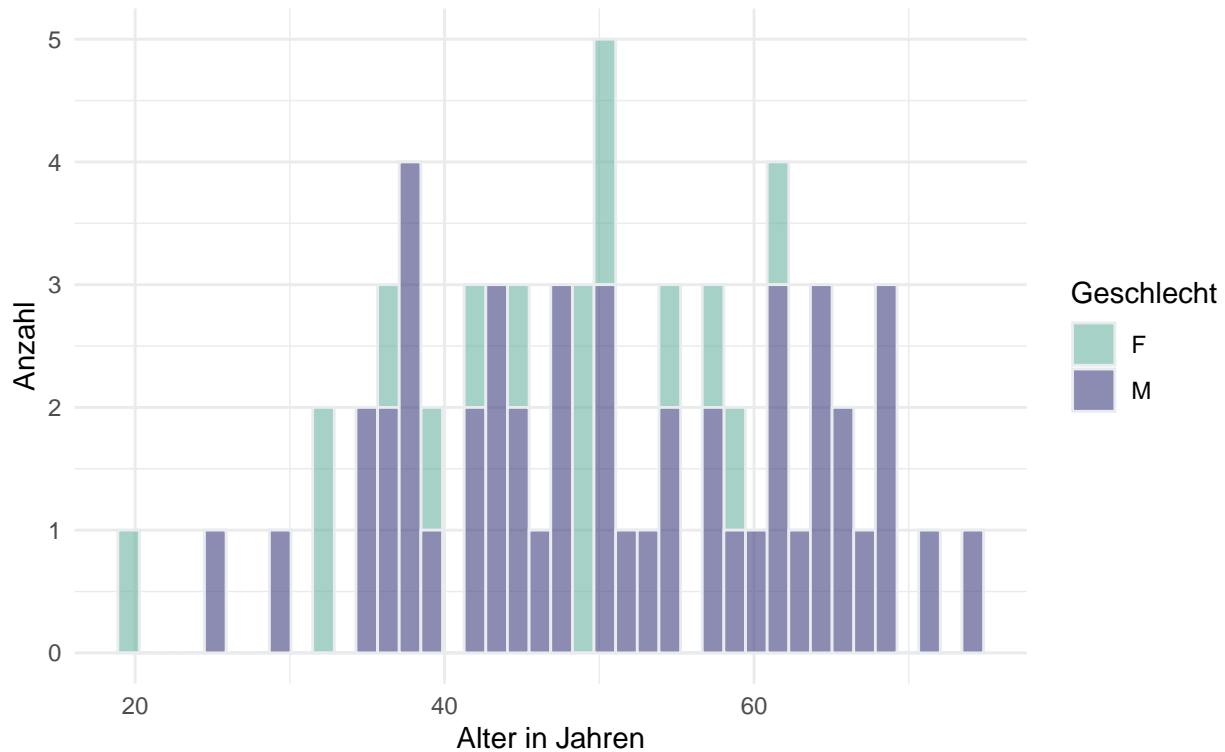
## [1] 15

# patients with graft loss within follow up period
nrow(data_iga[`graft loss date` < `T-date` + follow_up])

## [1] 14

# age patients (yrs.)
ggplot(data = data_iga) +
  geom_histogram(mapping = aes(x = interval(`Date of birth`, `T-date`) / years(1),
                                   fill = `R-sex`),
                color="#e9ecef",
                alpha=0.6,
                bins = 40) +
  two_scale_fill +
  ylab("Anzahl") +
  xlab("Alter in Jahren") +
  ggtitle("Histogram Alter in Jahren am Transplantationsdatum",
          subtitle = paste0("(IGA Patienten, n=",
                             sum(!is.na(data_iga$`Date of birth`)),
                             ")", collapse = "")) +
  labs(fill = "Geschlecht") +
  default_theme
```

Histogram Alter in Jahren am Transplantationsdatum
(IGA Patienten, n=64)



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

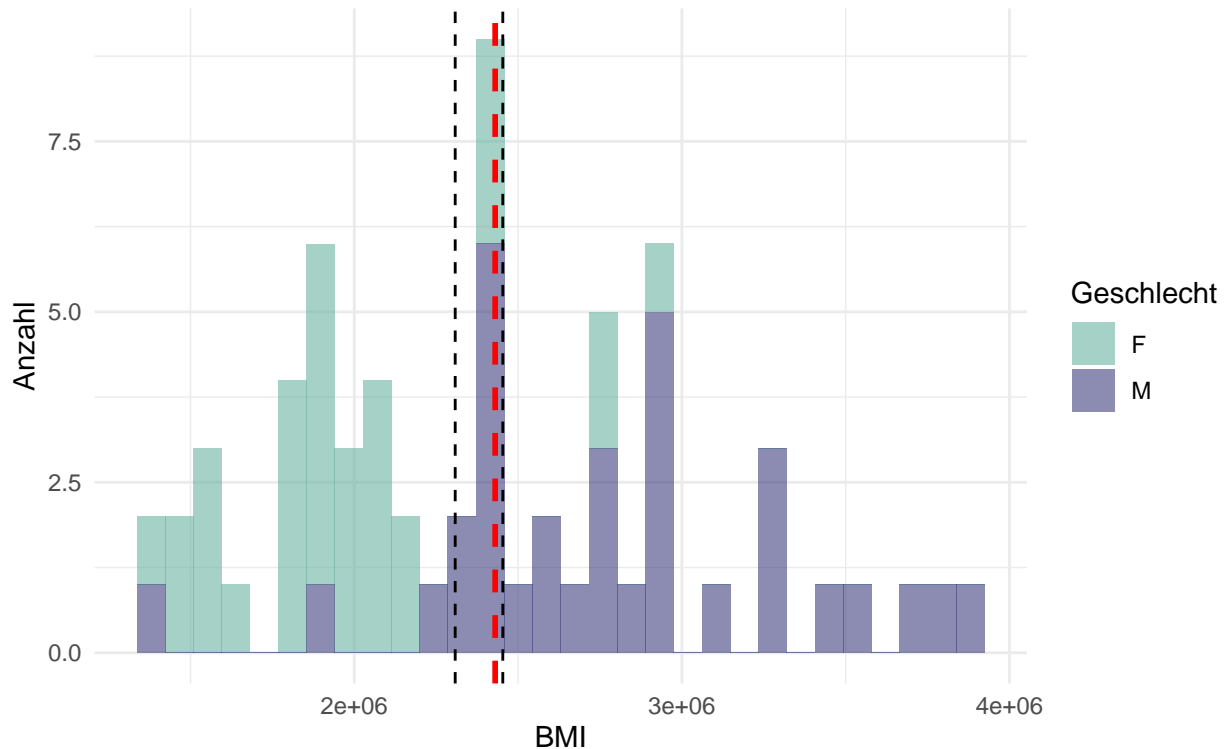
```
## F M
## 16 48
```

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

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

Histogramm BMI

(IGA Patienten, n=30)



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

```
##           Cadaver Living
## loss      0.867  0.133
## functional 0.735  0.265
```

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

```
##           Cadaver Living
## dead      0.917  0.083
## alive     0.675  0.325
```

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

```
## [1] 2400685
```

```

# HLA-mm (0-6)
## data.table of mm-A, mm-B and mm-DR
tbl_1 <- as.data.table(lapply(data_iga[, c("mm-A", "mm-B", "mm-DR")],
                               as.numeric))

## calculate mean for each column
tbl_2 <- apply(X = tbl_1,
               MARGIN = 2,
               FUN = mean, na.rm = TRUE)
round(tbl_2, 3)

```

```

## mm-A mm-B mm-DR
## 1.792 2.146 1.917

```

```

# mean of means
round(mean(tbl_2),3)

```

```

## [1] 1.951

```

```

## sum of mm-A, mm-B and mm-DR
tbl_3 <- apply(X = tbl_1,
               MARGIN = 1,
               FUN = sum, na.rm = TRUE)

# mean value
mean(tbl_3)

```

```

## [1] 4.390625

```

```

# median value
sd(tbl_3)

```

```

## [1] 2.711628

```

```

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

```

```

## Current PRA% Highest PRA%
##      5.216667      10.916667

```

```

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

```

```

## [1] 50.53125

```

```

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

```

```

## [1] 11.61224

```

```

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

```

```

## [1] 12

```

```

# standard error
sd(data_iga$`Cold ischaemic period hours`, na.rm = TRUE)

```

```
## [1] 6.330536
# living vs dead donator
cbind("Living" = nrow(data_iga[`D-type` == "Living"]),
      "Cadaver" = nrow(data_iga[`D-type` == "Cadaver"]))
)

##      Living Cadaver
## [1,]      15      49
```

§ 2.2 NTX

```
# follow_up mean
pmin(
  # follow up
  interval(data_ntx$Datum, (data_ntx$Datum + follow_up)) / years(1),
  # last seen
  interval(data_ntx$Datum, data_ntx$tdls) / years(1)
) %>%
  mean()

## [1] 7.41754
# patient death within follow up
nrow(data_ntx[`Todesdatum[NTX PatientenInformation]` < (Datum + follow_up)])

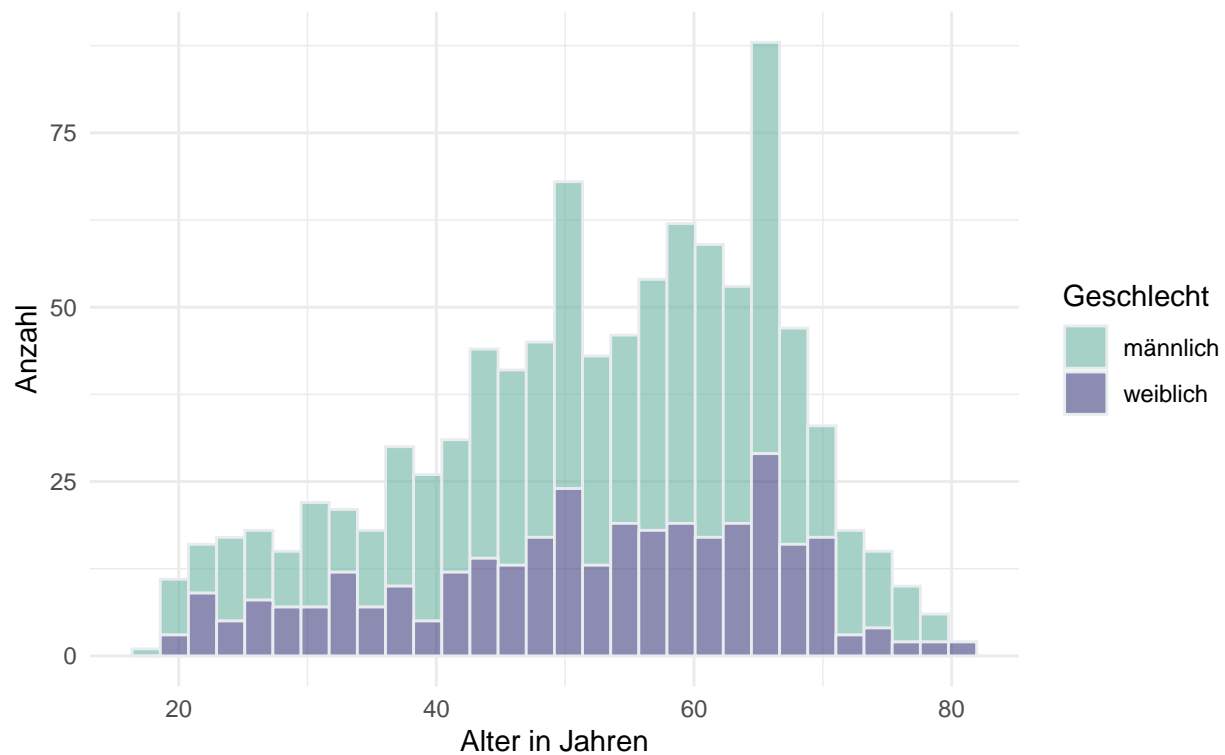
## [1] 317
# patient drop out
nrow(data_ntx[`Date last seen[NTX PatientenInformation]` <= (Datum + follow_up) & `Patienten Status[NTX
PatientenInformation]` == "2 - ohne Transplantatfunktion"]])

## [1] 370
# patients with graft loss
nrow(data_ntx[data_ntx$`TX Status[NTX PatientenInformation]` == "2 - ohne Transplantatfunktion"]])

## [1] 179
# age patients (yrs.)
ggplot(data = data_ntx) +
  geom_histogram(mapping = aes(x = R_age_Datum, fill = Geschlecht),
                 color = "#e9ecef", alpha = 0.6) +
  two_scale_fill +
  ylab("Anzahl") +
  xlab("Alter in Jahren") +
  ggtitle("Histogram Alter in Jahren am Transplantationsdatum",
          subtitle = paste0("(NTX Patienten, n=", sum(!is.na(data_ntx$R_age_Datum)),
                             ")", collapse = "")) +
  labs(fill = "Geschlecht") +
  default_theme

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

Histogram Alter in Jahren am Transplantationsdatum
(NTX Patienten, n=960)



```
# male sex
summary(data_ntx$Geschlecht)
```

```
## männlich weiblich
##      627      333
```

```
# BMI (mean.)
## NO DATA AVAILABLE
```

```
# deceased D.
# living D.
## NO DATA AVAILABLE
```

```
# HLA-mm
## NO DATA AVAILABLE
```

```
# PPR
## NO DATA AVAILABLE
```

```
# living vs dead donator
## NO DATA AVAILABLE
```

§ 3 Kaplan-Meier

§ 3.1 IGA

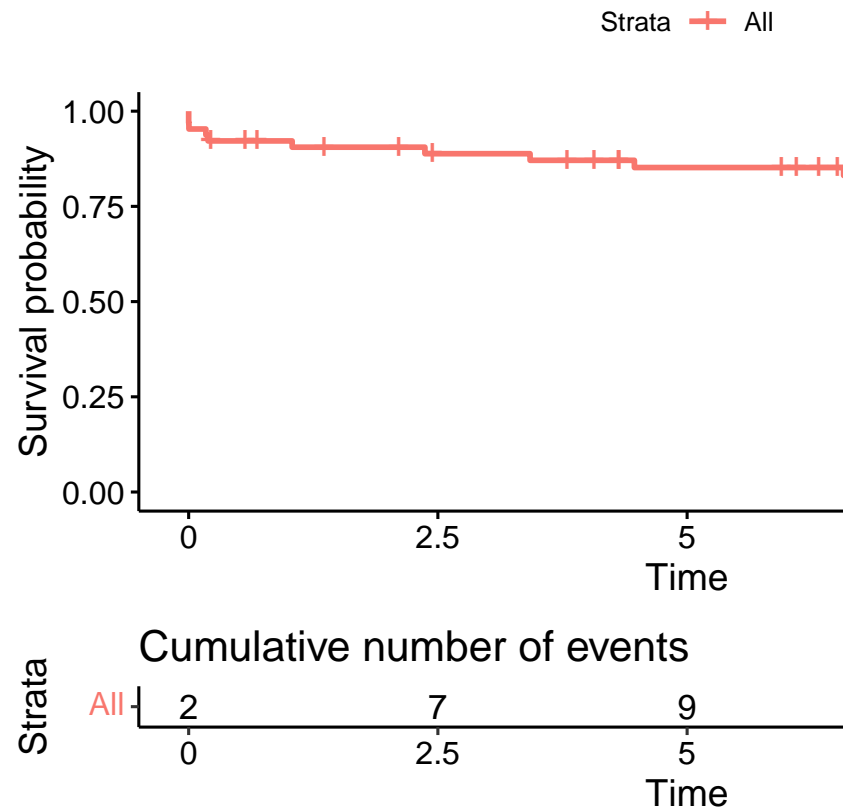
```
# functions in survival and survminer package need numeric-type input
data_iga[, time_date_biopsy := interval(`T-date`, `date of biopsy`) / years(1)]
data_iga[, time_t_dls := interval(`T-date`, `T-dls`) / years(1)]
data_iga[, time_date_birth := interval(`T-date`, `Date of birth`) / years(1)]
data_iga[, time_graft_loss := interval(`T-date`, `graft loss date`) / years(1)]
data_iga[, 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_iga <- data_iga %>%
  mutate(status_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_iga <- data_iga %>%
  mutate(status = 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 = status_date,
                                     event = status, type = "right") ~ 1,
                      data = data_iga)
ggsurvplot(model_iga_1,
            conf.int = FALSE,
            cumevents = TRUE)
```

Overall kaplan-Meier curve (no stratification)

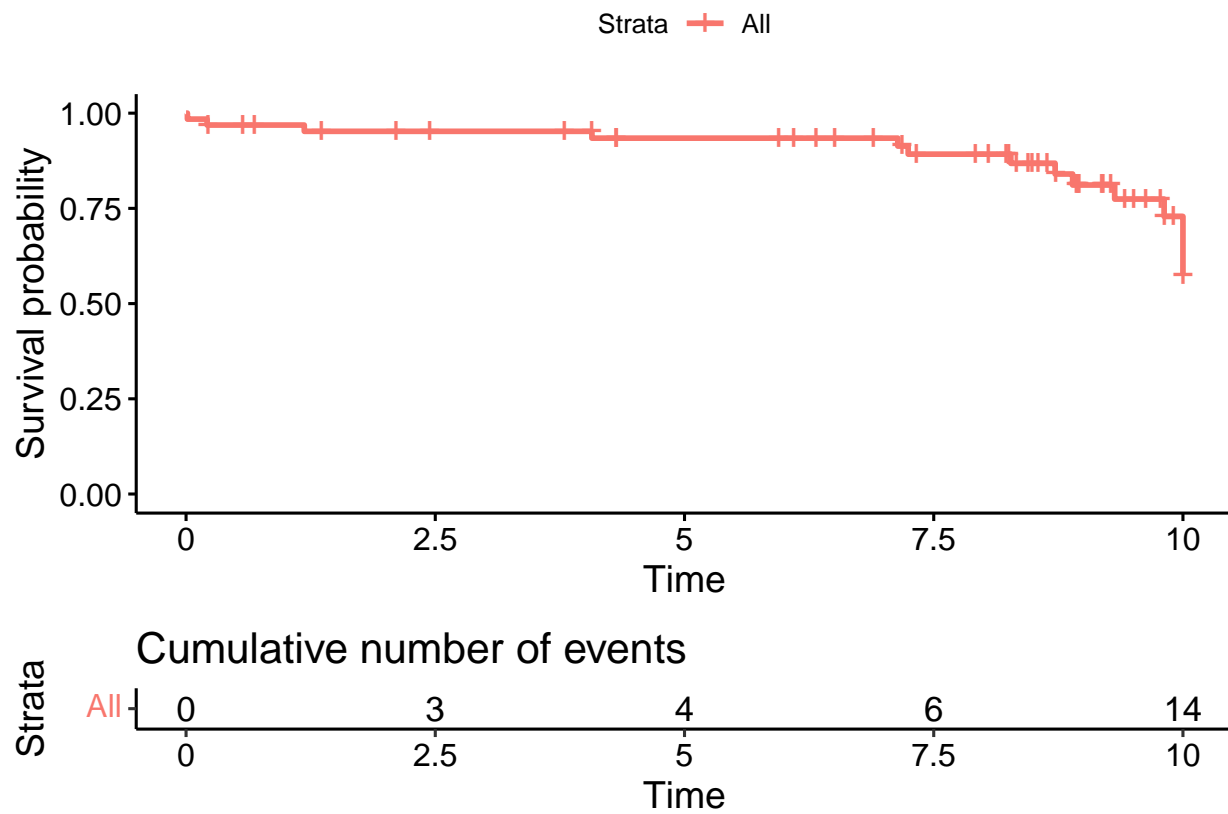
§ 3.1.2

- 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 transplantation).

```
data_iga <- data_iga %>%
  mutate(status_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
  ))

model_iga_2 <- survfit(formula = Surv(time = status_date,
                                     event = status, type = "right") ~ 1,
                      data = data_iga)

ggsurvplot(model_iga_2,
            conf.int = FALSE,
            cumevents = TRUE)
```



§ 3.1.3

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

§ 3.2 IGA

§ 3.2.1

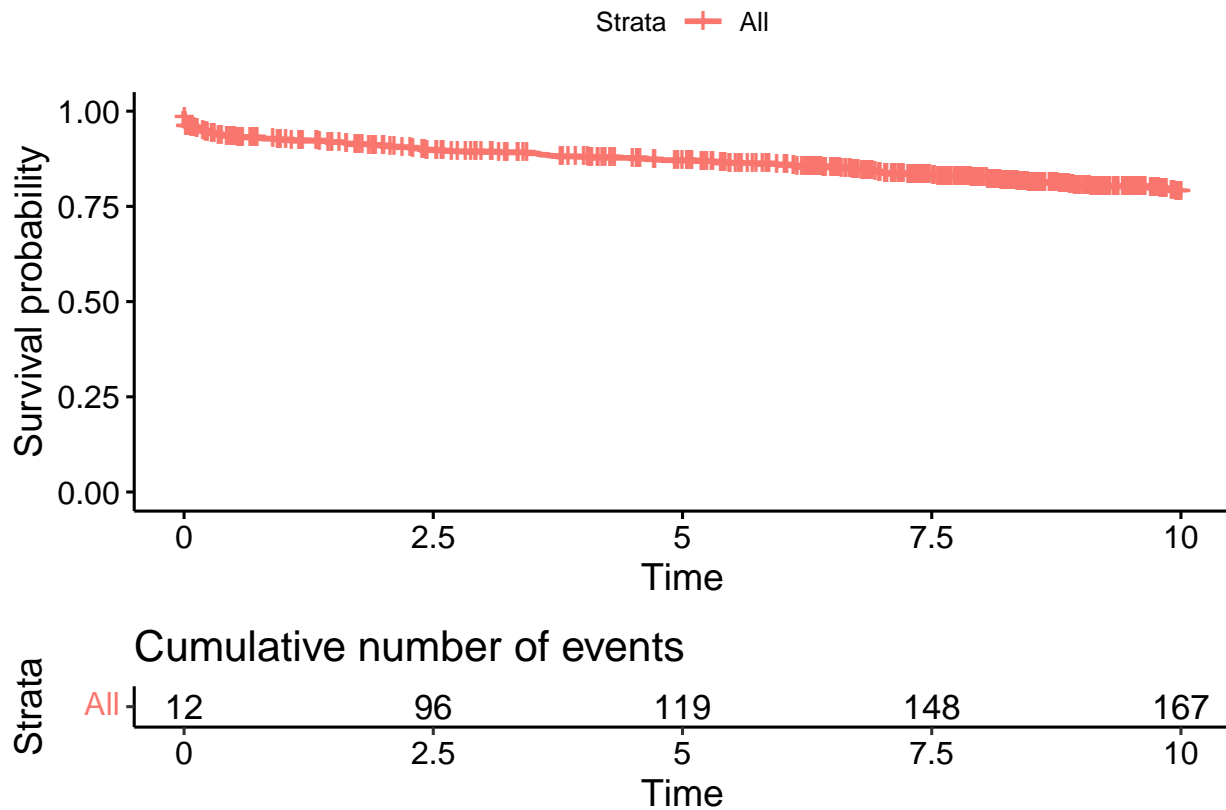
- Event: TX Status[NTX PatientenInformation]
- Censoring scheme: -if TX Status[NTX PatientenInformation] within follow up period then then event
 - if died within follow up and before no graft loss then censored
 - if last seen within follow up and before no graft loss then censored
 - if graft loss after follow up then censored
- Time period: 10 years after Datum

```
data_ntx <- data_ntx %>%
  mutate(status_date = case_when(
    ## patient experienced graft loss
    !is.na(Transplantatfunktionsende) & Transplantatfunktionsende <= (Datum + follow_up) ~ interval(Datum, Transplantatfunktionsende),
    ## patient died within follow up
    `Todesdatum[NTX PatientenInformation]` < (Datum + follow_up) ~ interval(Datum, `Todesdatum[NTX PatientenInformation]`),
    ## patient last seen within follow up
    `Date last seen[NTX PatientenInformation]` < (Datum + follow_up) ~ interval(Datum, `Date last seen[NTX PatientenInformation]`),
    ## else follow up
    TRUE ~ interval(Datum, (Datum + follow_up)) / years(1)
  )
)

data_ntx <- data_ntx %>%
  mutate(status = case_when(
    ## patient experienced graft loss
    !is.na(Transplantatfunktionsende) & Transplantatfunktionsende <= (Datum + follow_up) ~ 1,
    ## patient died within follow up
    `Todesdatum[NTX PatientenInformation]` < (Datum + follow_up) ~ 0,
    ## patient last seen within follow up
    `Date last seen[NTX PatientenInformation]` < (Datum + follow_up) ~ 0,
    ## else follow up
    TRUE ~ 0
  )
)

model_ntx_1 <- survfit(formula = Surv(time = status_date,
                                     event = status, type = "right") ~ 1,
                      data = data_ntx)

ggsurvplot(model_ntx_1,
            conf.int = FALSE,
            cumevents = TRUE)
```



§ 3.2.2

- Event: patient died within follow up period
- Censoring scheme:
 - patient died within follow up then event
 - patient dropped from study within follow up then censored

```
data_ntx <- data_ntx %>%
  mutate(status_date = case_when(
    ## patient died within follow up
    `Todesdatum[NTX PatientenInformation]` <= (Datum + follow_up) ~ interval(Datum, `Todesdatum[NTX Pat
    ## patient died after follow up
    `Todesdatum[NTX PatientenInformation]` > (Datum + follow_up) ~ interval(Datum, (Datum + follow_up))
    ## patient dropped within follow up
    `Date last seen[NTX PatientenInformation]` <= (Datum + follow_up) ~ interval(Datum, `Date last seen
    ## patient dropped after follow up
    `Date last seen[NTX PatientenInformation]` > (Datum + follow_up) ~ interval(Datum, (Datum + follow_u
  )
)

data_ntx <- data_ntx %>%
  mutate(status = case_when(
    ## patient died within follow up
    `Todesdatum[NTX PatientenInformation]` <= (Datum + follow_up) ~ 1,
    ## patient died after follow up
    `Todesdatum[NTX PatientenInformation]` > (Datum + follow_up) ~ 0,
    ## patient dropped within follow up
```

```

`Date last seen[NTX PatientenInformation]` <= (Datum + follow_up) ~ 0,
## patient dropped after follow up
`Date last seen[NTX PatientenInformation]` > (Datum + follow_up) ~ 0
)
)

```

```

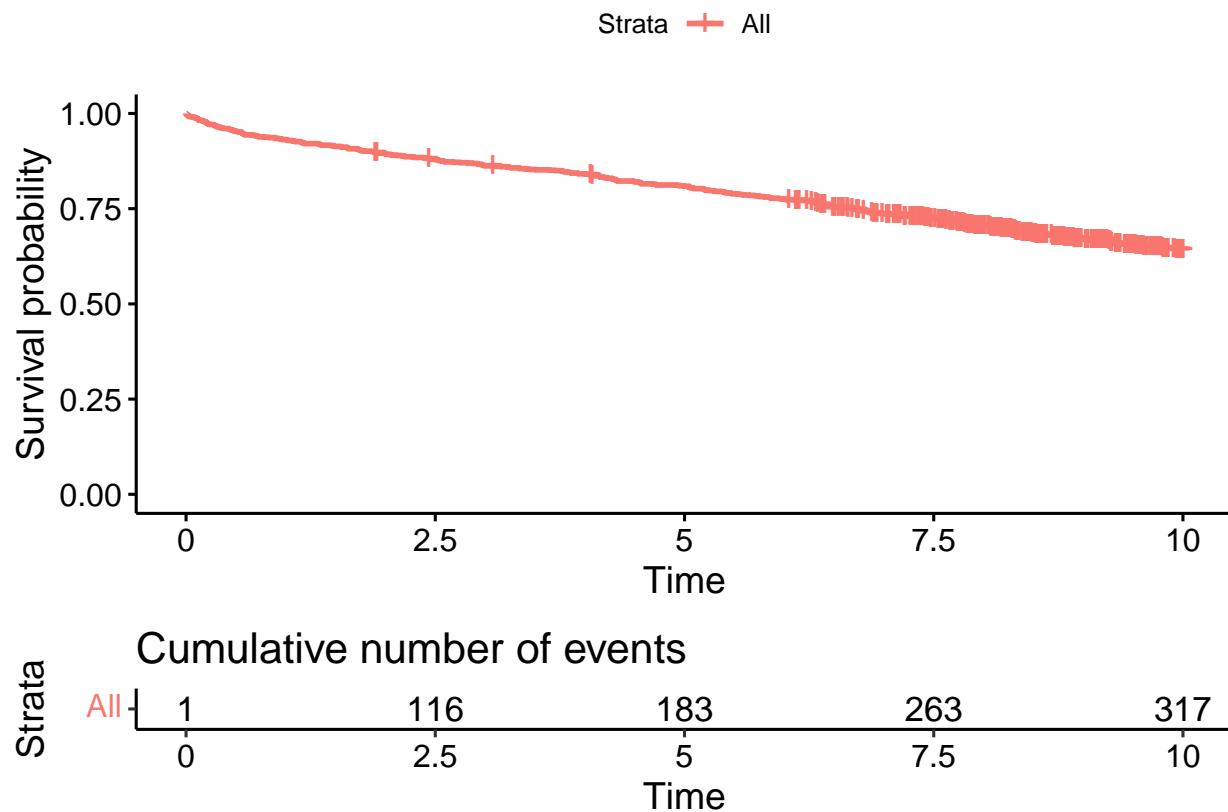
model_ntx_2 <- survfit(Surv(time = status_date, event = status,
                           type = "right") ~ 1, data = data_ntx)

```

```

ggsurvplot(model_ntx_2,
            conf.int = FALSE,
            cumevents = TRUE)

```



§ 4 Cox regression

§ 4.1 IGA

- Event:
 - graft loss within follow up
- Censoring scheme:
 - if patient dropped within follow up, then censored by time dropped
 - if patient experienced graft loss after follow up, then censored by follow up end
 - if patient experienced death within follow up, then censored by death date else by follow up end

```
data_iga <- data_iga %>%
  ## censor/event date
  mutate(status_date = case_when(
    ## patient dropped during follow up
    (`T-dls` <= `T-date` + follow_up) ~ `T-dls`,
    ## patient experienced graft loss but after follow up
    ((!is.na(`graft loss date`)) & (`graft loss date` > `T-date` + follow_up)) ~ `T-date` + follow_up,
    ## patient experienced graft loss within follow up
    ((!is.na(`graft loss date`)) & (`graft loss date` <= `T-date` + follow_up)) ~ `graft loss date`,
    ## patient experienced no graft loss within follow up, neither dropped
    (is.na(`graft loss date`) & (`T-dls` > `T-date` + follow_up)) ~ `T-date` + follow_up
  )) %>%
  ## status indicator
  mutate(status = case_when(
    ## patient dropped during follow up
    (`T-dls` <= `T-date` + follow_up) ~ 0,
    ## patient experienced graft loss but after follow up
    ((!is.na(`graft loss date`)) & (`graft loss date` > `T-date` + follow_up)) ~ 0,
    ## patient experienced graft loss within follow up
    ((!is.na(`graft loss date`)) & (`graft loss date` <= `T-date` + follow_up)) ~ 1,
    ## patient experienced no graft loss within follow up, neither dropped
    (is.na(`graft loss date`) & (`T-dls` > `T-date` + follow_up)) ~ 0
  ))
```

```
data_iga <- data_iga %>%
  ## censor/event date
  mutate(status_date = case_when(
    ## if graft loss within follow up
    `graft loss date` <= `T-date` + follow_up ~ `graft loss date`,
    ## else
    TRUE ~ `T-dls`
  )) %>%
  ## censor/event indicator
  mutate(status = case_when(
    ## if graft loss within follow up
    data_iga$`graft loss date` <= data_iga$`T-date` + follow_up ~ 1,
    ## else
    TRUE ~ 0
  ))

model_iga_cox <- coxph(formula = Surv(time = as.numeric(status_date),
                                     event = status) ~ R_age_Tdate +
  ##
  data_iga$`D-age` +
```

```

data_iga$`D-sex` +
data_iga$`R-sex`,
data = data_iga)
summary(model_iga_cox)

## Call:
## coxph(formula = Surv(time = as.numeric(status_date), event = status) ~
##       R_age_Tdate + data_iga$`D-age` + data_iga$`D-sex` + data_iga$`R-sex`,
##       data = data_iga)
##
##      n= 64, number of events= 14
##
##              coef exp(coef) se(coef)      z Pr(>|z|)
## R_age_Tdate    -0.01826   0.98191  0.02425 -0.753   0.4516
## data_iga$`D-age`  0.04152   1.04240  0.02932  1.416   0.1567
## data_iga$`D-sex`M -1.68067   0.18625  0.66215 -2.538   0.0111 *
## data_iga$`R-sex`M -0.40765   0.66521  0.60625 -0.672   0.5013
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##              exp(coef) exp(-coef) lower .95 upper .95
## R_age_Tdate         0.9819      1.0184   0.93633   1.0297
## data_iga$`D-age`     1.0424      0.9593   0.98419   1.1041
## data_iga$`D-sex`M    0.1862      5.3692   0.05087   0.6819
## data_iga$`R-sex`M    0.6652      1.5033   0.20273   2.1827
##
## Concordance= 0.753 (se = 0.057 )
## Likelihood ratio test= 11.3 on 4 df,  p=0.02
## Wald test               = 8.54 on 4 df,  p=0.07
## Score (logrank) test = 10.34 on 4 df,  p=0.04
cox.zph(model_iga_cox)

```

```

##              chisq df    p
## R_age_Tdate      0.00117  1 0.97
## data_iga$`D-age` 0.13570  1 0.71
## data_iga$`D-sex` 0.03163  1 0.86
## data_iga$`R-sex` 0.48064  1 0.49
## GLOBAL           0.56464  4 0.97

```

all p-values are relatively large, therefore the Null hypothesis of proportional hazards can not be rejected

\$ 4.2 NTX

```

data_ntx <- data_ntx %>%
  mutate(status_date = case_when(
    ## patient died within follow up
    `Todesdatum[NTX PatientenInformation]` <= (Datum + follow_up) ~ interval(Datum, `Todesdatum[NTX PatientenInformation]`),
    ## patient died after follow up
    `Todesdatum[NTX PatientenInformation]` > (Datum + follow_up) ~ interval(Datum, Datum + follow_up),
    ## patient dropped within follow up
    `Date last seen[NTX PatientenInformation]` <= (Datum + follow_up) ~ interval(Datum, `Date last seen[NTX PatientenInformation]`),
    ## patient dropped after follow up
    `Date last seen[NTX PatientenInformation]` > (Datum + follow_up) ~ interval(Datum, Datum + follow_up)
  ))

```

```

)
)

data_ntx <- data_ntx %>%
  mutate(status = case_when(
    ## patient died within follow up
    `Todesdatum[NTX PatientenInformation]` <= (Datum + follow_up) ~ 1,
    ## patient died after follow up
    `Todesdatum[NTX PatientenInformation]` > (Datum + follow_up) ~ 0,
    ## patient dropped within follow up
    `Date last seen[NTX PatientenInformation]` <= (Datum + follow_up) ~ 0,
    ## patient dropped after follow up
    `Date last seen[NTX PatientenInformation]` > (Datum + follow_up) ~ 0
  )
)

model_ntx_cox <- coxph(formula = Surv(time = status_date, event = status) ~ R_age_Datum +
  Geschlecht + `TX Status[NTX PatientenInformation]`,
  data = data_ntx)

## Warning in coxph.fit(X, Y, istrat, offset, init, control, weights = weights, :
## Loglik converged before variable 4 ; coefficient may be infinite.

summary(model_ntx_cox)

## Call:
## coxph(formula = Surv(time = status_date, event = status) ~ R_age_Datum +
##   Geschlecht + `TX Status[NTX PatientenInformation]`, data = data_ntx)
##
##   n= 960, number of events= 317
##
##                                     coef
## R_age_Datum                        6.693e-02
## Geschlechtweiblich                -2.412e-01
## `TX Status[NTX PatientenInformation]`2 - ohne Transplantatfunktion  7.966e-01
## `TX Status[NTX PatientenInformation]`2- ohne Transplantatfunktion -1.385e+01
##                                     exp(coef)
## R_age_Datum                        1.069e+00
## Geschlechtweiblich                7.857e-01
## `TX Status[NTX PatientenInformation]`2 - ohne Transplantatfunktion  2.218e+00
## `TX Status[NTX PatientenInformation]`2- ohne Transplantatfunktion  9.645e-07
##                                     se(coef)
## R_age_Datum                        5.395e-03
## Geschlechtweiblich                1.224e-01
## `TX Status[NTX PatientenInformation]`2 - ohne Transplantatfunktion  1.308e-01
## `TX Status[NTX PatientenInformation]`2- ohne Transplantatfunktion  1.086e+03
##                                     z
## R_age_Datum                        12.406
## Geschlechtweiblich                -1.971
## `TX Status[NTX PatientenInformation]`2 - ohne Transplantatfunktion  6.089
## `TX Status[NTX PatientenInformation]`2- ohne Transplantatfunktion -0.013
##                                     Pr(>|z|)
## R_age_Datum                        < 2e-16 ***
## Geschlechtweiblich                0.0487 *

```



```
## `TX Status[NTX PatientenInformation]`2 - ohne Transplantatfunktion 1.14e-09 ***
## `TX Status[NTX PatientenInformation]`2- ohne Transplantatfunktion 0.9898
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
##                                     exp(coef)
## R_age_Datum                        1.069e+00
## Geschlechtweiblich                7.857e-01
## `TX Status[NTX PatientenInformation]`2 - ohne Transplantatfunktion 2.218e+00
## `TX Status[NTX PatientenInformation]`2- ohne Transplantatfunktion 9.645e-07
##                                     exp(-coef)
## R_age_Datum                        9.353e-01
## Geschlechtweiblich                1.273e+00
## `TX Status[NTX PatientenInformation]`2 - ohne Transplantatfunktion 4.509e-01
## `TX Status[NTX PatientenInformation]`2- ohne Transplantatfunktion 1.037e+06
##                                     lower .95
## R_age_Datum                        1.0580
## Geschlechtweiblich                0.6182
## `TX Status[NTX PatientenInformation]`2 - ohne Transplantatfunktion 1.7163
## `TX Status[NTX PatientenInformation]`2- ohne Transplantatfunktion 0.0000
##                                     upper .95
## R_age_Datum                        1.0806
## Geschlechtweiblich                0.9987
## `TX Status[NTX PatientenInformation]`2 - ohne Transplantatfunktion 2.8663
## `TX Status[NTX PatientenInformation]`2- ohne Transplantatfunktion Inf
##
## Concordance= 0.716 (se = 0.015 )
## Likelihood ratio test= 211.1 on 4 df, p=<2e-16
## Wald test              = 176.5 on 4 df, p=<2e-16
## Score (logrank) test = 189.1 on 4 df, p=<2e-16
```

```
cox.zph(model_ntx_cox)
```

```
##                                     chisq df    p
## R_age_Datum                        3.600  1 0.058
## Geschlecht                        0.336  1 0.562
## `TX Status[NTX PatientenInformation]` 0.641  2 0.726
## GLOBAL                            4.301  4 0.367
```

```
## all p-values are relatively large, therefore the Null hypothesis of proportional hazards can not be
```