

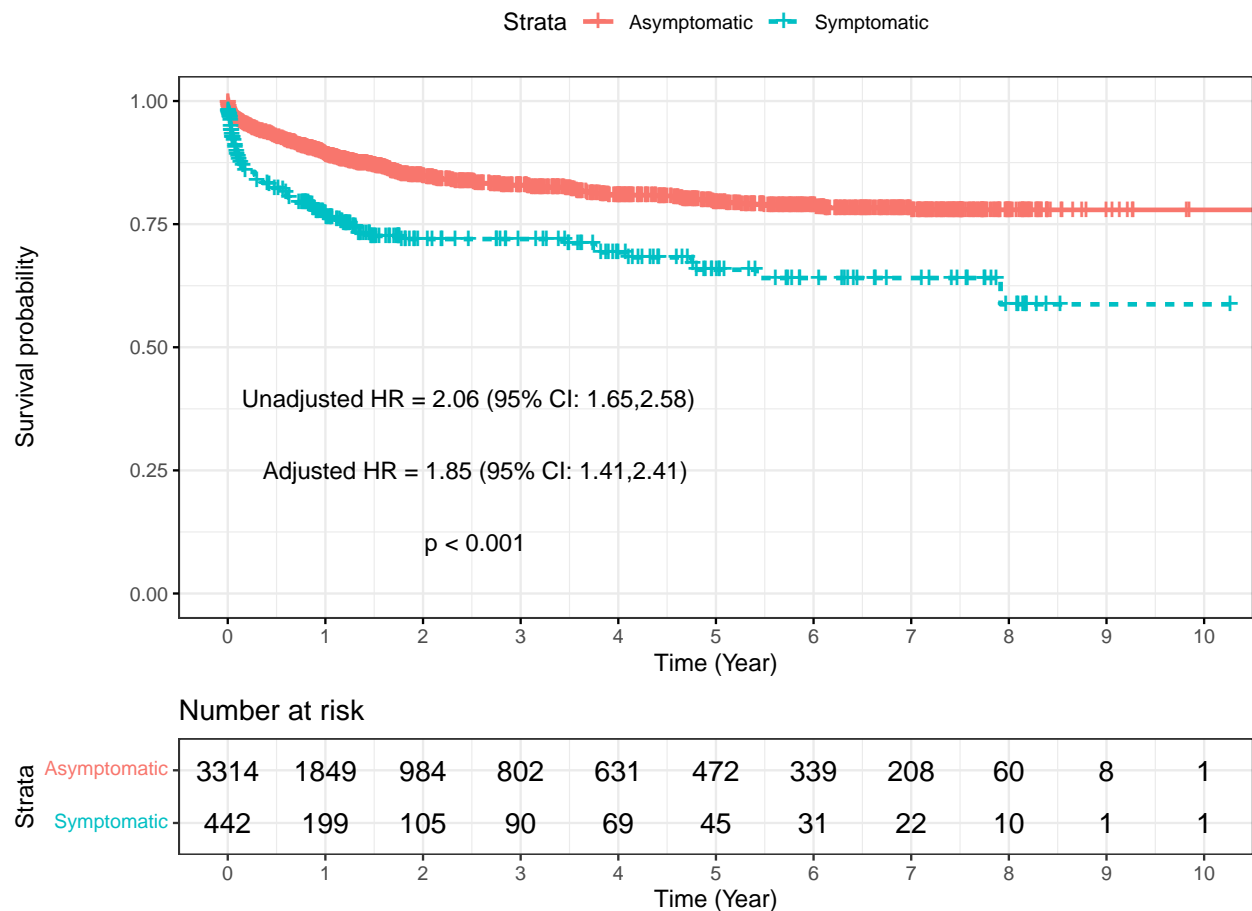
Survival Analysis for the VQI FBVAR Dataset

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Cox proportional hazards model for survival analysis

Unadjusted survival curves. Time scale changed from calendar days to calendar years. Used log rank test to produce p-value. Median survival never reached.

Any changes needed? (e.g, time scale, colors, change to at risk table, add number of censored and/or uncensored events, etc.)



Univariate (unadjusted) and Multivariate (adjusted) Cox Proportional Hazards Models. Reference group is asymptomatic patients.

Variables to adjust for:

- cluster on CENTERID
- AGECAT, GENDER, PREOP_SMOKING, PRIOR_AORSURG, PRIOR_CHF, PREOP_DIALYSIS

- PATHOLOGY, extent

In the model, we merge groups for the **extent**: merge “Juxtarenal AAA” with “Type 4 TAAA”; “Type 1 TAAA”, “Type 2 TAAA”, “Type 3 TAAA”, with “Type 5 TAAA”. Now **extent** is a binary variable, Juxtarenal or not.

Characteristic	HR ¹	95% CI ¹	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.06	1.65, 2.58	<0.001

¹HR = Hazard Ratio, CI = Confidence Interval

Characteristic	HR ¹	95% CI ¹	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.85	1.41, 2.41	<0.001
AGECAT			
<50	—	—	
>79	2.11	0.51, 8.72	0.3
50-59	2.22	0.56, 8.80	0.3
60-69	1.38	0.36, 5.31	0.6
70-79	1.96	0.49, 7.89	0.3
GENDER			
female	—	—	
male	0.79	0.63, 0.97	0.027
PREOP_SMOKING			
No	—	—	
Yes	1.12	0.85, 1.48	0.4
PRIOR_AORSURG			
Both	—	—	
Endo	0.90	0.50, 1.62	0.7
None	0.59	0.36, 0.98	0.040
Open	0.63	0.35, 1.16	0.14
PRIOR_CHF			
No	—	—	
Yes	1.58	1.32, 1.88	<0.001
PREOP_DIALYSIS			

¹HR = Hazard Ratio, CI = Confidence Interval

Characteristic	HR ¹	95% CI ¹	p-value
No	—	—	
Yes	1.61	1.00, 2.60	0.051
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.51	0.30, 0.86	0.012
Dissection	0.48	0.20, 1.16	0.10
PAU/IMH	1.01	0.37, 2.78	>0.9
extent			
Juxtarenal	—	—	
No	1.40	1.11, 1.77	0.005

¹HR = Hazard Ratio, CI = Confidence Interval

Code Appendix

```
knitr::opts_chunk$set(echo = FALSE,message = FALSE,warning = FALSE)
knitr::opts_chunk$set(fig.width=20, fig.height=20)

library(tidyverse)
library(table1)
library(survival)
library(Hmisc)
library(ggplot2)
library(ggpubr)
library(corrplot)
library(caret)
library(survminer)
library(knitr)
library(kableExtra)
library(gtsummary)
library(flextable)

## ----- working directories for Lily -----
wd_lily = '/Users/hanyiwang/Desktop/Comparative-analysis-of-treatments-of-CAA'
path_lily = c("../data/FBVAR.csv")

## ----- working directories for Jenn -----
# wd_jenn =
# path_jenn =

## ----- working directories for Thu -----
wd_thu = '/Users/thuvu/Desktop/Comparative-analysis-of-treatments-of-CAA'
path_thu = c("TEVAR_PROC.csv")

## ----- read data -----
# setwd(wd_lily)
# FBVAR = read.csv(path_lily)

# setwd(wd_jenn)
# FBVAR = read.csv(path_jenn)

setwd(wd_thu)
TEVAR_PROC1 = read.csv(path_thu)

## Omitting patients with negative survival days
TEVAR_PROC <- subset(TEVAR_PROC1, PROC_SURVIVALDAYS>=0)

## Survival analysis
tte <- TEVAR_PROC %>% with(Surv(PROC_SURVIVALDAYS/365, DEAD))

# compute survival curves
fit <- survfit(tte ~ PRESENTATION, data=TEVAR_PROC)

ggsurv <- ggsurvplot(fit,
  risk.table = TRUE,
```

```

    linetype = "strata",
    surv.median.line = "hv",
    ggtheme = theme_bw(),
    xlab = "Time (Year)",
    legend.labs = c("Asymptomatic", "Symptomatic"),
    break.time.by=1)

ggsurv$plot <- ggsurv$plot +
  annotate(
    "text",
    x = 2.5, y = 0.25,
    label = "Unadjusted HR = 2.06 (95% CI: 1.65,2.58)
\n Adjusted HR = 1.85 (95% CI: 1.41,2.41)
\n p < 0.001",
    size = 4
  )

ggsurv

TEVAR_PROC = TEVAR_PROC %>%
  mutate(extent = factor(extent, levels = c("Juxtarenal AAA", "Type 1 TAAA", "Type 2 TAAA",
    "Type 3 TAAA", "Type 4 TAAA", "Type 5 TAAA"),
    labels = c('Juxtarenal', 'No', 'No', 'No', 'Juxtarenal', 'No'))

# Unadjusted survival model
mod.cox1 <- coxph(tte ~ PRESENTATION, data=TEVAR_PROC)

# Adjusted survival model
mod.cox2 <- coxph(tte ~ PRESENTATION + cluster(CENTERID) + AGECAT + GENDER +
  PREOP_SMOKING + PRIOR_AORSURG + PRIOR_CHF +
  PREOP_DIALYSIS + PATHOLOGY + extent ,
  data=TEVAR_PROC)

t1 <- mod.cox1 %>% tbl_regression(exponentiate = TRUE)
t2 <- mod.cox2 %>% tbl_regression(exponentiate = TRUE)

t1 %>% as_flex_table()
t2 %>% as_flex_table()

```