

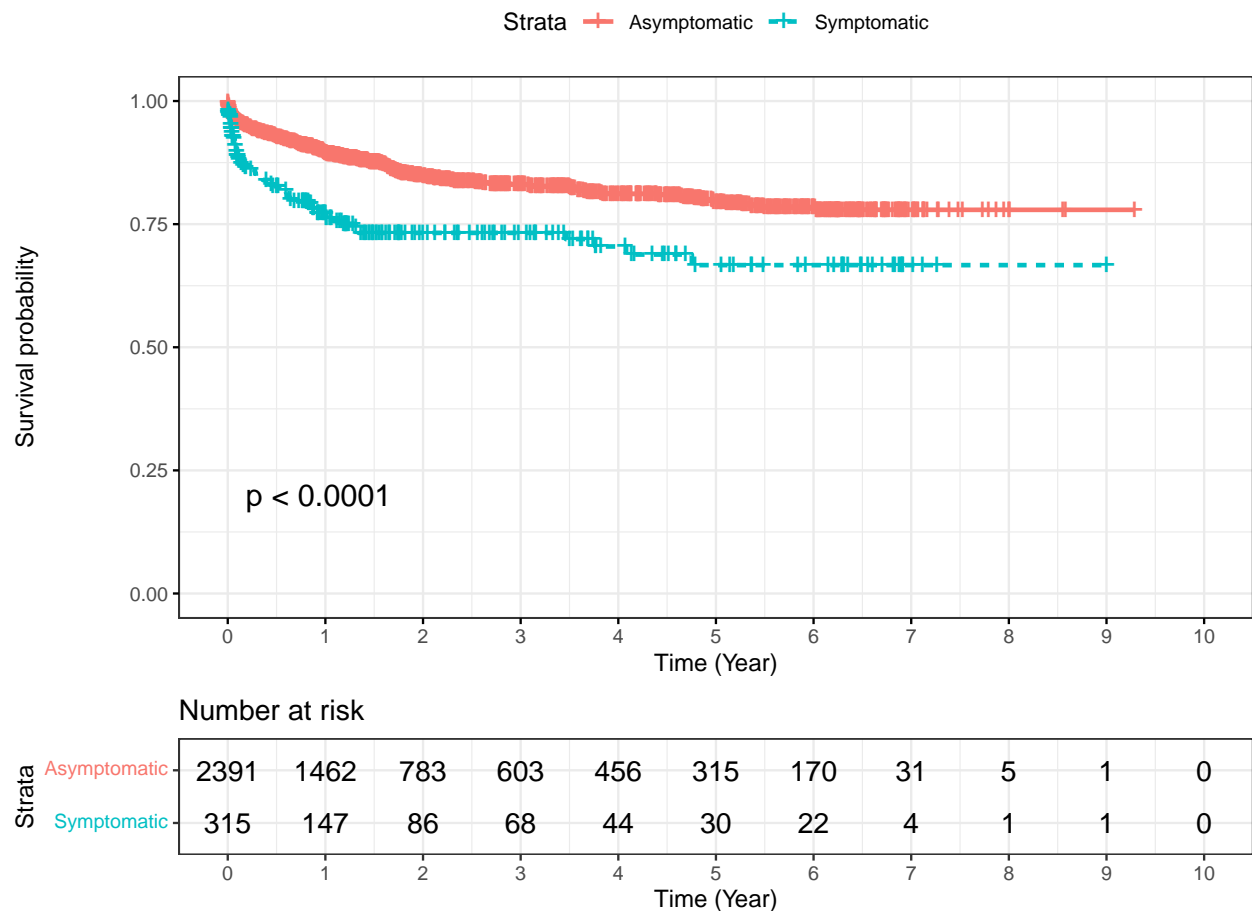
Survival Analysis for the VQI FBVAR Dataset

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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	1.99	1.53, 2.59	<0.001

¹HR = Hazard Ratio, CI = Confidence Interval

Characteristic	HR ¹	95% CI ¹	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.82	1.30, 2.54	<0.001
AGECAT			
<50	—	—	
>79	1.60	0.36, 7.02	0.5
50-59	1.51	0.37, 6.14	0.6
60-69	0.92	0.22, 3.93	>0.9
70-79	1.48	0.34, 6.51	0.6
GENDER			
female	—	—	
male	0.85	0.66, 1.10	0.2
PREOP_SMOKING			
No	—	—	
Yes	1.16	0.83, 1.63	0.4
PRIOR_AORSURG			
Both	—	—	
Endo	0.90	0.44, 1.85	0.8
None	0.53	0.28, 0.99	0.045
Open	0.50	0.26, 0.98	0.044
PRIOR_CHF			
No	—	—	
Yes	1.55	1.30, 1.83	<0.001
PREOP_DIALYSIS			

¹HR = Hazard Ratio, CI = Confidence Interval

Characteristic	HR ¹	95% CI ¹	p-value
No	—	—	
Yes	1.84	1.07, 3.16	0.028
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.47	0.23, 0.97	0.041
Dissection	0.60	0.23, 1.55	0.3
PAU/IMH	1.02	0.32, 3.29	>0.9
extent			
Juxtarenal	—	—	
No	1.38	1.05, 1.80	0.019

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_PROC = read.csv(path_thu)

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

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

ggsurvplot(fit,
            pval = TRUE,
            risk.table = TRUE,
            linetype = "strata",
            surv.median.line = "hv",
```

```

    ggtheme = theme_bw(),
    xlab = "Time (Year)",
    legend.labs = c("Asymptomatic", "Symptomatic"),
    break.time.by=1)

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()

```