# Survival Analysis for the VQI FBVAR Dataset

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### Variables to adjust for

In the unadjusted model, we studied only the differences in the outcomes:

• comparing PRESENTATION

In the adjusted models, we also:

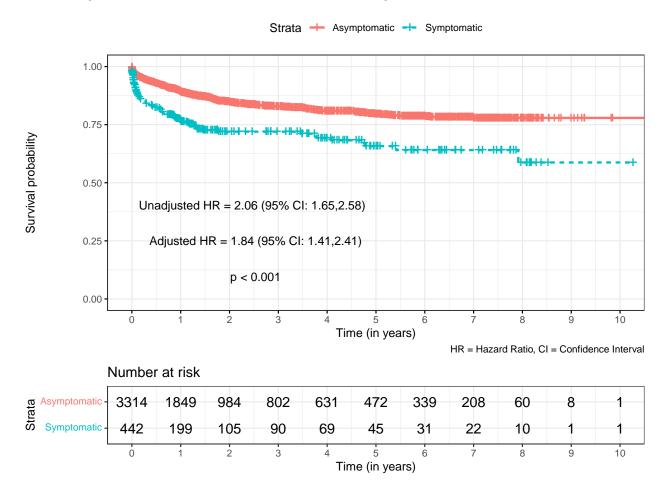
- cluster on CENTERID
- adjust for AGECAT, GENDER, PREOP\_SMOKING, PRIOR\_AORSURG, PRIOR\_CHF, PREOP\_DIALYSIS
- adjust for PATHOLOGY, extent
- primary outcome: All-cause mortality
- secondary outcome: Time-to-first reintervention for patients with long-term follow-up

For the outcomes described below, Kaplan-Meier curves were produced grouped by presentation, asymptomatic and symptomatic.

For the primary outcome only, we fitted a univariate Cox proportional hazards model and a multivariate stratified Cox proportional hazards model stratifying on sex.

To fit the models, 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.

## Primary Outcome: All-Cause Mortality



Due to violating the proportional-hazards assumption, the multivariate Cox proportional-hazards model was stratified on sex to resolve this issue.

	All-Cause Mortality				
Characteristic	$\mathrm{HR}^1$	$95\%~\mathrm{CI}^1$	p-value		
PRESENTATION					
Asymptomatic		_			
Symptomatic	2.06	1.65,  2.58	< 0.001		

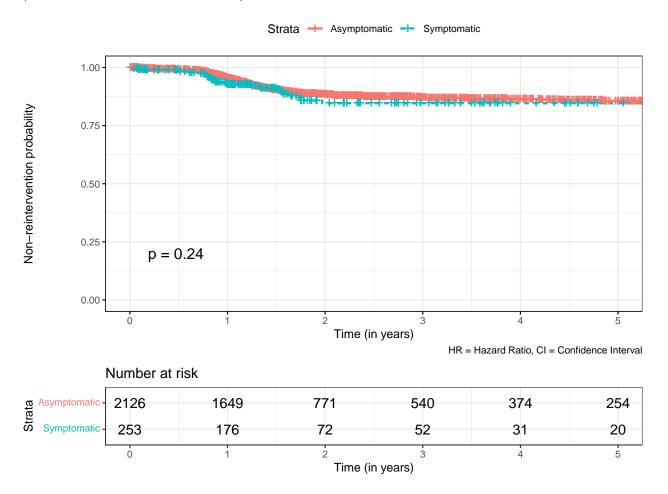
 $<sup>^{1}\</sup>mathrm{HR}=\mathrm{Hazard}$  Ratio,  $\mathrm{CI}=\mathrm{Confidence}$  Interval

	All-Cause Mortality				
Characteristic	$HR^1$	$95\%$ CI $^1$	p-value		
PRESENTATION					
Asymptomatic	_	_			
Symptomatic	1.84	1.41,  2.41	< 0.001		
$^{1}\mathrm{HR}=\mathrm{Hazard}$ Ratio, $\mathrm{CI}=\mathrm{Confidence}$ Interval					

Characteristic	All-Cause Mortality			
	${ m HR}^1$	$95\%~\mathrm{CI}^1$	p-value	
AGECAT				
< 50				
>79	2.18	0.52, 9.12	0.28	
50-59	2.30	0.57, 9.24	0.24	
60-69	1.42	0.36,  5.56	0.61	
70-79	2.02	0.50,  8.25	0.33	
PREOP_SMOKING				
No	_	_		
Yes	1.12	0.85,  1.48	0.42	
PRIOR_AORSURG				
Both	_	_		
Endo	0.90	0.50,1.62	0.72	
None	0.59	0.36,  0.98	0.040	
Open	0.63	0.34, 1.16	0.14	
PRIOR_CHF				
No	_			
Yes	1.57	1.32,  1.87	< 0.001	
PREOP_DIALYSIS				
No		_		
Yes	1.61	1.00,  2.58	0.050	
PATHOLOGY				
Aneurysm		_		
Aneurysm from dissection	0.52	0.31,0.87	0.013	
Dissection	0.49	0.20,1.19	0.12	
PAU/IMH	1.00	0.37,  2.73	>0.99	
extent				
Juxtarenal	_	_		
No	1.39	1.10, 1.76	0.006	

 $<sup>\</sup>overline{^{1}}$ HR = Hazard Ratio, CI = Confidence Interval

# Secondary Outcome: Long-term Follow-up First Reintervention (time-to-event outcome)



#### 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(survival)
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")
path_thu1 = c("LT 2.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)
LTF = read.csv(path_thu1)
### Primary Outcome: All-Cause Mortality
# omitting patients with negative survival days
TEVAR_PROC <- subset(TEVAR_PROC1, PROC_SURVIVALDAYS>=0)
# create survival object, time-to-event
# converted days to years
tte <- TEVAR_PROC %>% with(Surv(PROC_SURVIVALDAYS/365, DEAD))
# compute survival curves
fit <- survfit(tte ~ PRESENTATION, data=TEVAR_PROC)</pre>
# plotting KM curves
ggsurv <- ggsurvplot(fit,</pre>
          risk.table = TRUE,
          linetype = "strata",
```

```
surv.median.line = "hv",
           ggtheme = theme_bw(),
           xlab = "Time (in years)",
           legend.labs = c("Asymptomatic", "Symptomatic"),
           break.time.by=1,
           caption="HR = Hazard Ratio, CI = Confidence Interval")
ggsurv$plot <- ggsurv$plot +</pre>
 annotate(
    "text",
    x = 2.5, y = 0.25,
    label = "Unadjusted HR = 2.06 (95% CI: 1.65,2.58)
    \n Adjusted HR = 1.84 (95% CI: 1.41,2.41)
    n p < 0.001",
   size = 4
  )
ggsurv
# changing extent into a binary variable
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)</pre>
# Adjusted survival model
mod.cox2 <- coxph(tte ~ PRESENTATION + cluster(CENTERID) + AGECAT + strata(GENDER) +
                    PREOP_SMOKING + PRIOR_AORSURG + PRIOR_CHF +
                    PREOP_DIALYSIS + PATHOLOGY + extent ,
                  data=TEVAR_PROC)
t1 <- mod.cox1 %>%
  tbl_regression(exponentiate = TRUE,
                 tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2)) %>%
  bold p(t = 0.05)
tbl_merge(tbls = list(t1),tab_spanner ="**All-Cause Mortality**") %%
  as_flex_table()
t2 <- mod.cox2 %>%
  tbl_regression(exponentiate = TRUE,
                 tidy_fun = broom.mixed::tidy,
                 pvalue_fun = function(x) style_pvalue(x, digits = 2)) %>%
  bold_p(t = 0.05)
tbl_merge(tbls = list(t2),tab_spanner ="**All-Cause Mortality**") %%
  as_flex_table()
### Secondary Outcome: Long-term Follow-up First Reintervention
### (time-to-event outcome)
# filtering the LTF dataset to only include FEVAR procedures
```

```
t <- as.data.frame(table(TEVAR_PROC1$PRIMPROCID))</pre>
LTF_merge <- LTF[LTF$PRIMPROCID %in% t$Var1,]</pre>
# replacing all missing in number of reinterventions with O
LTF_merge$total_reint[is.na(LTF_merge$total_reint)] <- 0
# creating event variable, binary re-intervention
# 1 = had at least 1 reintervention, 0 = had 0 reinterventions
LTF_merge$retx_bin <- ifelse(LTF_merge$total_reint>=1, 1, 0)
# creating time variable (in days)
LTF_merge$time <- ifelse(LTF_merge$retx_bin==1,
                         LTF_merge$first_reint_time, LTF_merge$new_surv)
# omitting patients with negative survival days
LTF_merge <- subset(LTF_merge, time>=0)
# merging proc and ltf datasets on procedure ID
LTF_comb <- merge(LTF_merge, TEVAR_PROC1, by = "PRIMPROCID")
# create survival object, time-to-event
# converted days to years
tte1 <- LTF_comb %>% with(Surv(time/365, retx_bin))
# compute survival curves
fit1 <- survfit(tte1~PRESENTATION, data=LTF comb)</pre>
# plotting KM curves
ggsurvplot(
 fit1,
 pval = TRUE,
 risk.table = TRUE,
 linetype = "strata",
 ggtheme = theme_bw(),
 legend.labs = c("Asymptomatic", "Symptomatic"),
 xlab = "Time (in years)",
 ylab = "Non-reintervention probability",
 break.time.by = 1,
 xlim = c(0,5),
  caption = "HR = Hazard Ratio, CI = Confidence Interval"
```