

Generalized linear models with the Generalized Estimating Equations for the VQI FBVAR Dataset

Jennifer Ci, Thu Vu, Lily Hanyi Wang

Generalized linear models with the Generalized Estimating Equations for continuous outcomes

TOTAL_LOS

Length of Stay in days calculated by DISCHARGE_DT - ADMIT_DT

TOTAL_LOS Length of Stay in days			
Characteristic	OR ¹	95% CI ¹	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	5.14	4.11, 6.43	<0.001

¹OR = Odds Ratio, CI = Confidence Interval

TOTAL_LOS Length of Stay in days			
Characteristic	OR ¹	95% CI ¹	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.79	2.99, 4.81	<0.001
AGECAT			
<50	—	—	
>79	1.91	0.88, 4.15	0.10
50-59	1.89	0.82, 4.36	0.13
60-69	1.32	0.63, 2.77	0.5
70-79	2.16	1.02, 4.55	0.043
GENDER			

¹OR = Odds Ratio, CI = Confidence Interval

	TOTAL_LOS Length of Stay in days		
Characteristic	OR ¹	95% CI ¹	p-value
female	—	—	
male	0.62	0.51, 0.75	<0.001
PREOP_SMOKING			
No	—	—	
Yes	0.99	0.76, 1.29	>0.9
PRIOR_AORSURG			
Both	—	—	
Endo	1.59	0.93, 2.71	0.091
None	1.08	0.65, 1.80	0.8
Open	1.43	0.83, 2.47	0.2
PRIOR_CHF			
No	—	—	
Yes	1.51	1.21, 1.89	<0.001
PREOP_DIALYSIS			
No	—	—	
Yes	1.87	1.10, 3.16	0.020
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.83	1.16, 2.87	0.009
Dissection	1.77	1.02, 3.06	0.041
PAU/IMH	1.94	0.90, 4.20	0.093
extent			
Juxtarenal	—	—	
No	2.10	1.72, 2.57	<0.001

¹OR = Odds Ratio, CI = Confidence Interval

ICUSTAY

ICU Stay

Characteristic	ICU Stay		
	OR ¹	95% CI ¹	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.11	2.43, 3.97	<0.001

¹OR = Odds Ratio, CI = Confidence Interval

Characteristic	ICU Stay		
	OR ¹	95% CI ¹	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.08	1.59, 2.71	<0.001
AGECAT			
<50	—	—	
>79	1.31	0.51, 3.37	0.6
50-59	1.30	0.47, 3.58	0.6
60-69	0.96	0.38, 2.42	>0.9
70-79	1.28	0.50, 3.25	0.6
GENDER			
female	—	—	
male	0.60	0.49, 0.74	<0.001
PREOP_SMOKING			
No	—	—	
Yes	1.02	0.75, 1.38	>0.9
PRIOR_AORSURG			
Both	—	—	
Endo	1.36	0.77, 2.41	0.3
None	0.75	0.43, 1.32	0.3
Open	1.31	0.72, 2.38	0.4
PRIOR_CHF			
No	—	—	

¹OR = Odds Ratio, CI = Confidence Interval

Characteristic	ICU Stay		
	OR ¹	95% CI ¹	p-value
Yes	1.21	0.93, 1.57	0.2
PREOP_DIALYSIS			
No	—	—	
Yes	1.84	1.07, 3.19	0.028
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.35	0.81, 2.25	0.3
Dissection	1.72	0.93, 3.19	0.084
PAU/IMH	1.25	0.50, 3.12	0.6
extent			
Juxtarenal	—	—	
No	2.23	1.78, 2.80	<0.001

¹OR = Odds Ratio, CI = Confidence Interval

POSTOP_HIGHCREAT

Highest Creatinine 1 - GFR reduction is $\geq 50\%$ 0 - GFR reduction is $< 50\%$

```
##
## <50% >=50%
## 3393 247
```

	GFR		
Characteristic	OR ¹	95% CI ¹	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.57	1.08, 2.29	0.018

¹OR = Odds Ratio, CI = Confidence Interval

	GFR		
Characteristic	OR ¹	95% CI ¹	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.40	0.93, 2.09	0.11
AGECAT			
<50	—	—	
>79	0.71	0.15, 3.31	0.7
50-59	1.28	0.26, 6.24	0.8
60-69	0.87	0.19, 4.01	0.9
70-79	0.80	0.17, 3.71	0.8
GENDER			
female	—	—	
male	0.65	0.49, 0.87	0.003
PREOP_SMOKING			
No	—	—	
Yes	1.25	0.80, 1.96	0.3
PRIOR_AORSURG			
Both	—	—	
Endo	1.24	0.48, 3.23	0.7
None	0.97	0.39, 2.45	>0.9

¹OR = Odds Ratio, CI = Confidence Interval

Characteristic	GFR		
	OR ¹	95% CI ¹	p-value
Open	0.94	0.34, 2.62	>0.9
PRIOR_CHF			
No	—	—	
Yes	1.13	0.79, 1.61	0.5
PREOP_DIALYSIS			
No	—	—	
Yes	0.00	0.00, 0.00	<0.001
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.33	0.10, 1.09	0.069
Dissection	0.85	0.31, 2.32	0.8
PAU/IMH	1.11	0.32, 3.90	0.9
extent			
Juxtarenal	—	—	
No	1.12	0.82, 1.53	0.5

¹OR = Odds Ratio, CI = Confidence Interval

POSTOP_INTISCH

Intestinal Ischemia

Intestinal Ischemia			
Characteristic	OR ¹	95% CI ¹	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.13	0.56, 2.26	0.7

¹OR = Odds Ratio, CI = Confidence Interval

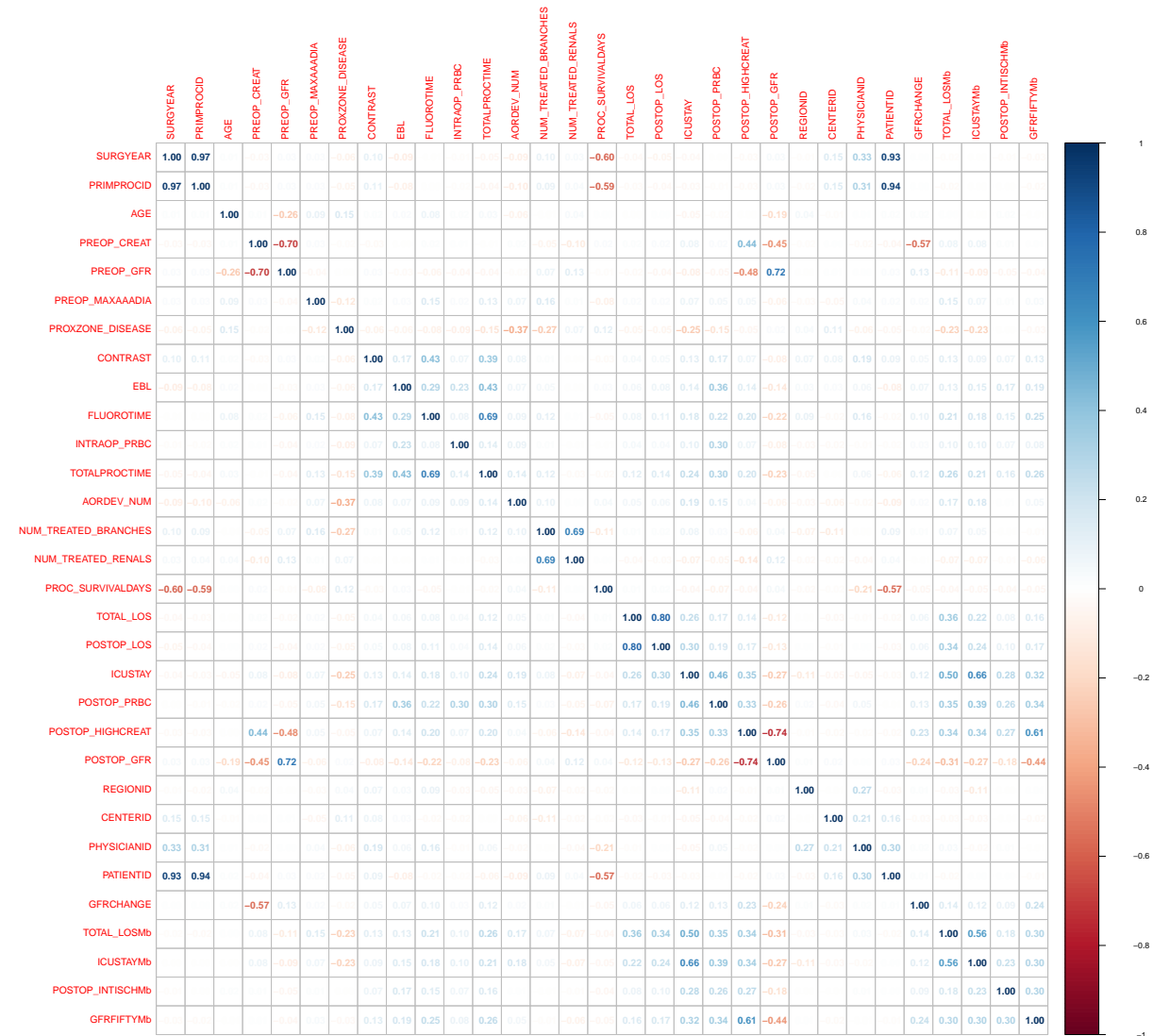
Intestinal Ischemia			
Characteristic	OR ¹	95% CI ¹	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.07	0.50, 2.30	0.9
AGECAT			
<50	—	—	
>79	0.41	0.07, 2.37	0.3
50-59	0.49	0.06, 4.15	0.5
60-69	0.36	0.06, 2.15	0.3
70-79	0.45	0.08, 2.48	0.4
GENDER			
female	—	—	
male	0.62	0.37, 1.03	0.063
PREOP_SMOKING			
No	—	—	
Yes	0.86	0.43, 1.70	0.7
PRIOR_AORSURG			
Both	—	—	
Endo	1.94	0.23, 16.6	0.5
None	1.84	0.22, 15.8	0.6
Open	1.62	0.16, 15.9	0.7
PRIOR_CHF			
No	—	—	

¹OR = Odds Ratio, CI = Confidence Interval

Characteristic	Intestinal Ischemia		
	OR ¹	95% CI ¹	p-value
Yes	1.05	0.53, 2.08	0.9
PREOP_DIALYSIS			
No	—	—	
Yes	0.69	0.09, 5.12	0.7
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.48	0.06, 3.66	0.5
Dissection	0.71	0.14, 3.71	0.7
PAU/IMH	1.28	0.16, 10.6	0.8
extent			
Juxtarenal	—	—	
No	0.94	0.53, 1.69	0.8

¹OR = Odds Ratio, CI = Confidence Interval

Correlation matrix



```
## $SURGMONTH
## [1] "nov" "jun" "may" "apr" "aug" "sep" "jul" "mar" "oct" "dec" "feb" "jan"
##
## $PRESENTATION
## [1] "Asymptomatic" "Symptomatic"
##
## $AGECAT
## [1] ">79" "60-69" "70-79" "<50" "50-59"
##
## $GENDER
## [1] "male" "female"
##
```

```

## $ETHNICITY
## [1] "None Hispanic or Latino" "Hispanic or Latino"
## [3] NA
##
## $RACE
## [1] "Unknown/Other"
## [2] "White"
## [3] "Black or African American"
## [4] "Asian"
## [5] "More than 1 race"
## [6] "American Indian or Alaskan Native"
## [7] "Native Hawaiian or other Pacific Islander"
##
## $TRANSFER
## [1] "No"          "Hospital"    "Rehab Unit"
##
## $PRIMARYINSURER
## [1] "Medicare"      "Commercial"  "Military/VA"    NA
## [5] "Medicaid"     "Self Pay"    "Non US Insurance"
##
## $LIVINGSTATUS
## [1] "Home"          "Nursing home" "Homeless"
##
## $PREOP_FUNCSTATUS
## [1] "Light work"    "Self care"    "Full"           "Assisted care"
## [5] NA              "Bed bound"
##
## $PRIOR_CVD
## [1] "No" "Yes"
##
## $PRIOR_CAD
## [1] "No" "Yes" NA
##
## $PRIOR_CHF
## [1] "No" "Yes"
##
## $COPD
## [1] "Yes" "No"
##
## $DIABETES
## [1] "No" "Yes"
##
## $PREOP_DIALYSIS
## [1] "No" "Yes"
##
## $HTN
## [1] "Yes" "No" NA
##
## $PREOP_SMOKING
## [1] "Yes" "No" NA
##
## $PRIOR_CABG
## [1] "No" "Yes" NA
##

```

```

## $PRIOR_PCI
## [1] "No" "Yes" NA
##
## $PRIOR_ANEURREP
## [1] "No" "Yes"
##
## $STRESS
## [1] "No" "Yes" NA
##
## $PREOP_GFR_CAT
## [1] "Mildly decreased" "Normal or increased"
## [3] "Mildly to severely decreased" NA
## [5] "Severely decreased" "End-stage renal disease"
##
## $DC_ASA
## [1] "Yes" "No" NA
##
## $DC_P2Y
## [1] "No" "Yes" NA
##
## $DC_STATIN
## [1] "No" "Yes" NA
##
## $PRIOR_AORSURG
## [1] "None" "Open" "Endo" "Both"
##
## $PATHOLOGY
## [1] "Aneurysm" "Aneurysm from dissection"
## [3] "Dissection" "PAU/IMH"
##
## $URGENCY
## [1] "Elective" "Urgent" "Emergent"
##
## $PATHOLOGY_ANEURYSM_TYPE
## [1] "Degenerative, saccular" "Degenerative, fusiform"
## [3] NA "Anastomotic"
## [5] "Intercostal or visceral patch" "Prior trauma"
##
## $PATHOLOGY_DISSECT_TYPE
## [1] NA "Chronic, >30 days" "Acute, <= 30 days"
##
## $GENHIST
## [1] "None" "Non-specific" "Marfans" NA
## [5] "Ehlers-Danlos" "Loeys-Dietz"
##
## $DISTZONE_DISEASE
## [1] "10B" "9" "10R" "11L" "6" "10L" "8" "11B" "7" "11R" "5" "4"
##
## $extent
## [1] No Juxtarenal <NA>
## Levels: Juxtarenal No
##
## $ANESTHESIA
## [1] "General" "Regional" "Local"

```

```

##
## $IVUSTEE
## [1] "No"      "IVUS" "Both" "TEE"  NA
##
## $ACCESS
## [1] "Open"          "Percutaneous" NA
##
## $ARMNECK_ACCESS
## [1] "No"  "Yes"
##
## $AORDEV_CMOD
## [1] "No"  "Yes"
##
## $DEV_GTYPE
## [1] "Standard"          "Physician modified" "Custom"
##
## $ILIACDEV_END_R
## [1] "Common"          NA          "None"
## [4] "External,Intended"  "External, Unintended"
##
## $ILIACDEV_END_L
## [1] "Common"          NA          "External,Intended"
## [4] "External, Unintended" "None"
##
## $BRANCH_STAGED
## [1] "No"  "Yes" NA
##
## $BRANCH_LSUB
## [1] "No"  "Yes"
##
## $BRANCH_CELIAC
## [1] "Yes" "No"
##
## $BRANCH_SMA
## [1] "Yes" "No"
##
## $BRANCH_RRENAL
## [1] "Yes" "No"
##
## $BRANCH_LRENAL
## [1] "Yes" "No"
##
## $ANESTHESIA_GEN_TIMEEXT
## [1] "In OR"      "<12 hrs"  "12-24 hrs" ">24 hrs"  NA
##
## $POSTOP_SPINALDRAIN
## [1] "No"  "Yes" NA
##
## $lrenal
## [1] "None"          "Scallop/Fen/Branch/Chimney"
## [3] NA              "Occluded/Covered"
##
## $rrenal
## [1] "None"          "Scallop/Fen/Branch/Chimney"

```

```

## [3] NA "Occluded/Covered"
##
## $sma
## [1] "Scallop/Fen/Branch/Chimney" NA
## [3] "None" "Occluded/Covered"
##
## $celiac
## [1] "None" "Occluded/Covered"
## [3] NA "Scallop/Fen/Branch/Chimney"
##
## $lsub
## [1] NA "None"
## [3] "Scallop/Fen/Branch/Chimney" "Occluded/Covered"
##
## $OCCLUDED_RENAL
## [1] FALSE TRUE
##
## $OCCLUDED_SMA
## [1] FALSE TRUE
##
## $OCCLUDED_CELIAC
## [1] FALSE TRUE
##
## $DEAD
## [1] FALSE TRUE
##
## $AORDEV_TECHSUCC
## [1] "Yes" NA "No"
##
## $CONVTOOPEN
## [1] "No" "Yes"
##
## $LEAKATCOMP_NONE
## [1] "No" "Yes" NA
##
## $POSTOP_VASO
## [1] "No" "Yes" NA
##
## $POSTOP_GFR_CAT
## [1] "Mildly to severely decreased" "Normal or increased"
## [3] NA "Severely decreased"
## [5] "Mildly decreased" "End-stage renal disease"
##
## $POSTOP_COMPLICATIONS
## [1] "No" "Yes" NA
##
## $ACCESS_COMPLICATION
## [1] "No" NA "Yes"
##
## $POSTOP_AH
## [1] "No" "Yes" NA
##
## $POSTOP_CEREBROX
## [1] "No" "Yes" NA

```

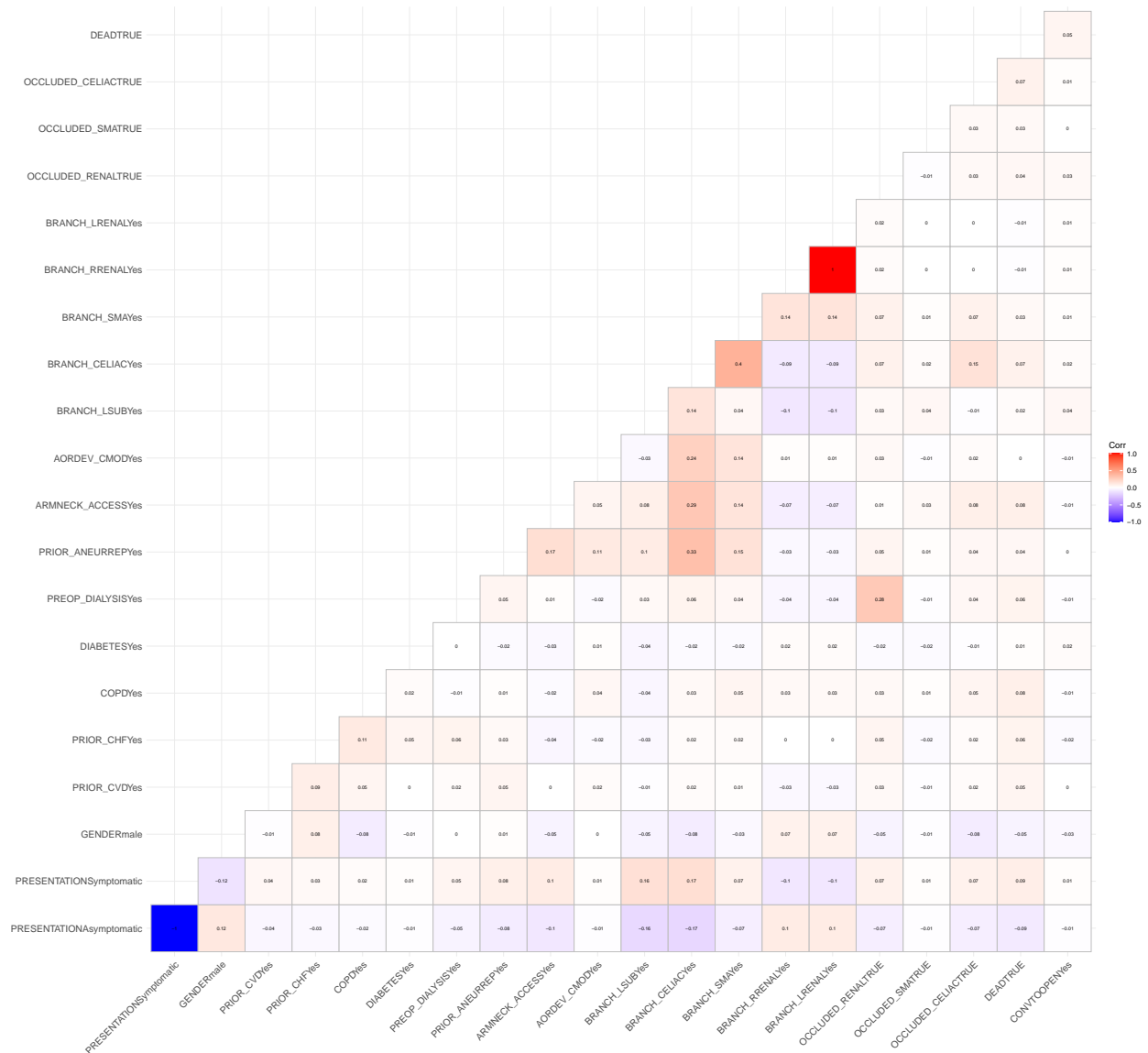
```

##
## $POSTOP_RESPIRATORY
## [1] "No" "Yes" NA
##
## $POSTOP_DIALYSIS
## [1] "No" "Yes" NA
##
## $POSTOP_ARMEMBO
## [1] "No" "Yes" NA
##
## $POSTOP_LEGEMBO
## [1] "No" "Yes" NA
##
## $POSTOP_LEGCOMPART
## [1] "No" "Yes" NA
##
## $POSTOP_INTISCH
## [1] "No" "Yes" NA
##
## $POSTOP_RENALISCH
## [1] "No" "Yes" NA
##
## $POSTOP_SPINAL_ISCHEMIA
## [1] "No" "Yes" NA
##
## $RETX_R_RTOR
## [1] "No" "Yes" NA
##
## $DC_STATUS
## [1] "Rehab Unit" "Nursing Home" "Home" "Other Hospital"
## [5] "Dead" NA "Homeless"
##
## $BRANCH_POST
## [1] "No" "Yes" NA
##
## $TOTAL_LOSM
## [1] "<=7" ">7" NA
##
## $ICUSTAYM
## [1] "<=4" ">4" NA
##
## $GFRFIFTY
## [1] "<50%" ">=50%" NA

##          SURGMONTH          PRESENTATION          AGECAT
##              12              2              5
##          GENDER          ETHNICITY          RACE
##              2              3              7
##          TRANSFER          PRIMARYINSURER          LIVINGSTATUS
##              3              7              3
##          PREOP_FUNCSTATUS          PRIOR_CVD          PRIOR_CAD
##              6              2              3
##          PRIOR_CHF          COPD          DIABETES
##              2              2              2

```

##	PREOP_DIALYSIS	HTN	PREOP_SMOKING
##	2	3	3
##	PRIOR_CABG	PRIOR_PCI	PRIOR_ANEURREP
##	3	3	2
##	STRESS	PREOP_GFR_CAT	DC_ASA
##	3	6	3
##	DC_P2Y	DC_STATIN	PRIOR_AORSURG
##	3	3	4
##	PATHOLOGY	URGENCY	PATHOLOGY_ANEURYSM_TYPE
##	4	3	6
##	PATHOLOGY_DISSECT_TYPE	GENHIST	DISTZONE_DISEASE
##	3	6	12
##	extent	ANESTHESIA	IVUSTEE
##	3	3	5
##	ACCESS	ARMNECK_ACCESS	AORDEV_CMED
##	3	2	2
##	DEV_GTYPE	ILIACDEV_END_R	ILIACDEV_END_L
##	3	5	5
##	BRANCH_STAGED	BRANCH_LSUB	BRANCH_CELIAC
##	3	2	2
##	BRANCH_SMA	BRANCH_RRENAL	BRANCH_LRENAL
##	2	2	2
##	ANESTHESIA_GEN_TIMEEXT	POSTOP_SPINALDRAIN	lrenal
##	5	3	4
##	rrenal	sma	celiac
##	4	4	4
##	lsub	OCCLUDED_RENAL	OCCLUDED_SMA
##	4	2	2
##	OCCLUDED_CELIAC	DEAD	AORDEV_TECHSUCC
##	2	2	3
##	CONVTOOPEN	LEAKATCOMP_NONE	POSTOP_VASO
##	2	3	3
##	POSTOP_GFR_CAT	POSTOP_COMPLICATIONS	ACCESS_COMPLICATION
##	6	3	3
##	POSTOP_AH	POSTOP_CEREBROX	POSTOP_RESPIRATORY
##	3	3	3
##	POSTOP_DIALYSIS	POSTOP_ARMEMBO	POSTOP_LEGEMBO
##	3	3	3
##	POSTOP_LEGCOMPART	POSTOP_INTISCH	POSTOP_RENALISCH
##	3	3	3
##	POSTOP_SPINAL_ISCHEMIA	RETX_R_RTOR	DC_STATUS
##	3	3	7
##	BRANCH_POST	TOTAL_LOSM	ICUSTAYM
##	3	3	3
##	GFRFIFTY		
##	3		



```
## 'data.frame': 3757 obs. of 20 variables:
## $ PRESENTATION : chr "Asymptomatic" "Asymptomatic" "Symptomatic" "Symptomatic" ...
## $ GENDER : chr "male" "male" "male" "male" ...
## $ PRIOR_CVD : chr "No" "Yes" "No" "Yes" ...
## $ PRIOR_CHF : chr "No" "No" "No" "No" ...
## $ COPD : chr "Yes" "Yes" "No" "No" ...
## $ DIABETES : chr "No" "No" "Yes" "Yes" ...
## $ PREOP_DIALYSIS : chr "No" "No" "No" "No" ...
## $ PRIOR_ANEURREP : chr "No" "Yes" "No" "No" ...
## $ ARMNECK_ACCESS : chr "No" "No" "No" "No" ...
## $ AORDEV_CMODYes : chr "No" "Yes" "Yes" "Yes" ...
## $ BRANCH_LSUB : chr "No" "No" "No" "No" ...
## $ BRANCH_CELIAC : chr "Yes" "Yes" "No" "Yes" ...
## $ BRANCH_SMA : chr "Yes" "Yes" "Yes" "Yes" ...
```



```

## $ BRANCH_RRENAL : chr "Yes" "Yes" "Yes" "Yes" ...
## $ BRANCH_LRENAL : chr "Yes" "Yes" "Yes" "Yes" ...
## $ OCCLUDED_RENAL : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
## $ OCCLUDED_SMA : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
## $ OCCLUDED_CELIAC: logi FALSE TRUE FALSE FALSE FALSE FALSE ...
## $ DEAD : logi FALSE FALSE FALSE FALSE TRUE FALSE ...
## $ CONVTOOPEN : chr "No" "No" "No" "No" ...

```

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(dplyr)

## ----- 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 = '/Users/jennifer-ci/Desktop/stlp new laptop/Capstone/Comparative-analysis-of-treatments-of-CAA'
path_jenn = c("TEVAR_PROC.csv")

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

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

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

#find duplicate participants
#n_occur <- data.frame(table(PROC$PATIENTID))
#n_occur[n_occur$Freq > 1,]

#PROC[PROC$PATIENTID %in% n_occur$Var1[n_occur$Freq > 1],]

# setwd(wd_thu)
# FBVAR = read.csv(path_thu)

library(geepack)
library(gtsummary)

PROC = 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'))
#change to bianry variables
PROC = PROC %>% mutate(
TOTAL_LOSM = (ifelse(TOTAL_LOS>7, ">7",
                     ifelse( TOTAL_LOS<=7, "<=7", NA))),
ICUSTAYM = (ifelse(ICUSTAY>4, ">4",
                  ifelse(ICUSTAY<=4, "<=4", NA))),
GFRCHANGE=(PROC$PREOP_GFR - PROC$POSTOP_GFR)/PROC$PREOP_GFR,
GFRFIFTY = (ifelse(GFRCHANGE>=0.5, ">=50%",
                  ifelse( GFRCHANGE<0.5, "<50%", NA))))

PROC$TOTAL_LOSMb <- as.numeric(PROC$TOTAL_LOSM != "<=7")
PROC$ICUSTAYMb <- as.numeric(PROC$ICUSTAYM != "<=4")
PROC$POSTOP_INTISCHMb<-as.numeric(PROC$POSTOP_INTISCH != "No")
PROC$GFRFIFTYb <- as.numeric(PROC$GFRFIFTY != "<50%")
#PROC%>% select(GFRFIFTY, GFRFIFTYb)

#PROC[PROC$PATIENTID %in%c('510979', '558643', '259097', '603199', '246350', '598705', '554182'),]

#check the variables
#PROC%>% select(TOTAL_LOSM, TOTAL_LOS, TOTAL_LOSMb)
#class(PROC$TOTAL_LOSMb)
#PROC%>% select(ICUSTAYM, ICUSTAY, ICUSTAYMb)
#PROC%>% select(POSTOP_INTISCH, POSTOP_INTISCHMb)

#table(PROC$extent)

#remove missing values
PROCNM<-subset(PROC, !is.na(extent))

#PROCNM[is.na(PROCNM) | PROCNM=="Inf"] = NA
# repeated patients, need id, geeglm needs complete data, extent is not complete
#unadjusted

LOS1<-geeglm(TOTAL_LOSMb~ PRESENTATION, data=PROCNM, family=binomial(link="logit"), id = CENTERID, corstr="independence")
t1<-LOS1 %>%tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1), tab_spanner = "**TOTAL_LOS Length of Stay in days**")%>%as_flex_table()

#adjusted
LOS2<-geeglm(TOTAL_LOSMb ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS,
              data=PROCNM, family=binomial(link="logit"), id = CENTERID, corstr = "independence")
t2<-LOS2 %>%tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)

```

```

tbl_merge(tbls = list(t2),tab_spanner = "**TOTAL_LOS Length of Stay in days**")%>%as_flex_table()

#the difference in mean number of sessions attended comparing treatment to control

#adjust<-c('PRESENTATION','AGECAT', 'GENDER', 'PREOP_SMOKING','PRIOR_AORSURG', 'PRIOR_CHF','PATHOLOGY',
#PROC %>%
#   tbl_uvregression(
#     y = TOTAL_LOS,
#     x = PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PATHOLOGY+NUM_TREATED_BRANCHES,
#     method = geepack::geeglm,
#     method.args = list(id = X+CENTERID, corstr = "independence"),
#     include = all_of(adjust)
#   ) %>%
#   as_kable()

#unadjusted
ICU1<-geeglm(ICUSTAYMb~ PRESENTATION, data=PROCNM, family=binomial(link="logit"), id = CENTERID, corstr="independence")

#summary(LOS2)
#summary(ICU1)

#ICU1<-geeglm(ICUSTAY ~ PRESENTATION, data=PROCNM,id = CENTERID, corstr = "independence")
t1<-ICU1 %>%tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner = "**ICU Stay**")%>%as_flex_table()

#adjusted
ICU2<-geeglm(ICUSTAYMb ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS,
  , family=binomial(link="logit"), data=PROCNM, id = CENTERID, corstr = "independence")
t2<- ICU2 %>%tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner = "**ICU Stay**")%>%as_flex_table()
## POSTOP_PRBC
#Transfusion # Units PRBC
#unadjusted
POSTOP_PRBC1<-geeglm(POSTOP_PRBC ~ PRESENTATION, data=PROCNM,id = CENTERID, corstr = "independence")
t1<-POSTOP_PRBC1 %>%tbl_regression(tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner = "**Transfusion # Units PRBC**")%>%as_flex_table()

#adjusted
POSTOP_PRBC2<-geeglm(POSTOP_PRBC ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS,
  , family=binomial(link="logit"), data=PROCNM, id = CENTERID, corstr = "independence")
t2<- POSTOP_PRBC2 %>%tbl_regression(tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)
tbl_merge(tbls = list(t2),tab_spanner = "**Transfusion # Units PRBC**")%>%as_flex_table()

```

```

table(PROC$GFRFIFTY)

#unadjusted
GFR1<-geeglm(GFRFIFTYmb~ PRESENTATION, data=PROCNM, family=binomial(link="logit"), id = CENTERID, corstr="independence")

#summary(LOS2)
#summary(ICU1)

#ICU1<-geeglm(ICUSTAY ~ PRESENTATION, data=PROCNM,id = CENTERID, corstr = "independence")
t1<-GFR1 %>%tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner = "**GFR**")%>%as_flex_table()

#adjusted
GFR2<-geeglm(GFRFIFTYmb ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS,
  , family=binomial(link="logit"), data=PROCNM, id = CENTERID, corstr = "independence")
t2<- GFR2 %>%tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner = "**GFR**")%>%as_flex_table()

#unadjusted
POSTOP_HIGHCREAT1<-geeglm(POSTOP_HIGHCREAT ~ PRESENTATION, data=PROCNM,id = CENTERID, corstr = "independence")
t1<-POSTOP_HIGHCREAT1 %>%tbl_regression(tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner = "**Highest Creatinine**")%>%as_flex_table()

#adjusted
POSTOP_HIGHCREAT2<-geeglm(POSTOP_HIGHCREAT ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS,
  , data=PROCNM, id = CENTERID, corstr = "independence")
t2<- POSTOP_HIGHCREAT2 %>%tbl_regression(tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)
tbl_merge(tbls = list(t2),tab_spanner = "**Highest Creatinine**")%>%as_flex_table()

#unadjusted
POSTOP_INTISCH1<-geeglm(POSTOP_INTISCHMb ~ PRESENTATION, family=binomial(link="logit"), data=PROCNM,id = CENTERID, corstr="independence")

t1<-POSTOP_INTISCH1 %>%tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner = "**Intestinal Ischemia**")%>%as_flex_table()

#adjusted
POSTOP_INTISCH2<-geeglm(POSTOP_INTISCHMb ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS,
  , data=PROCNM,family=binomial(link="logit"), id = CENTERID, corstr = "independence")

```

```

t2<- POSTOP_INTISCH2 %>%tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy)%>%
  bold_p(t = 0.05)
tbl_merge(tbls = list(t2), tab_spanner = "**Intestinal Ischemia**")%>%as_flex_table()

#model<-geeglm(as.numeric(POSTOP_DIALYSIS)~PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR,

#model<-geeglm(outcome~predictor+confounder, family=binomial(link = "logit"),
#data=na.omit(data), constr='ar1', id=id, std.err="san.se")
#TOTAL_LOS

#ICUSTAY
#POSTOP_PRBC
#POSTOP_HIGHCREAT

#POSTOP_INTISCH

library(corrplot)
library(tidyverse)
library(caret)
library(ggcorrplot)

matrix <- PROC %>%
  select_if(is.numeric) %>% subset(., select = -1)%>%
  cor(., use = "complete")

corrplot(matrix, method="number")

#select dataset that column are not numeric
matrix <- PROC %>% select_if(negate(is.numeric))

# find out the variables
lapply(matrix[,], unique)
sapply(lapply(matrix, unique), length)

#select if more than one variable
y<-matrix %>%select_if(function(col) length(unique(col))==2)

# Convert all columns to factor
data3 <- as.data.frame(unclass(y),
  stringsAsFactors = TRUE)

model.matrix(~0 +., data=data3) %>%
  cor(use="pairwise.complete.obs") %>%

```

```
ggcorrplot(show.diag = F, type="lower", lab=TRUE, lab_size=2)
```

```
str(y)
```