

# 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 <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	5.10	4.08, 6.38	<0.001

<sup>1</sup>OR = Odds Ratio, CI = Confidence Interval

	TOTAL_LOS Length of Stay in days		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.79	3.00, 4.81	<0.001
AGECAT			
<50	—	—	
>79	1.93	0.89, 4.18	0.10
50-59	1.88	0.83, 4.28	0.13
60-69	1.34	0.62, 2.87	0.5
70-79	2.20	1.03, 4.66	0.041
GENDER			

GENDER

<sup>1</sup>OR = Odds Ratio, CI = Confidence Interval

	TOTAL_LOS Length of Stay in days		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
female	—	—	
male	0.62	0.52, 0.75	<b>&lt;0.001</b>
PREOP_SMOKING			
No	—	—	
Yes	1.02	0.78, 1.33	>0.9
PRIOR_AORSURG			
Both	—	—	
Endo	1.67	0.97, 2.87	0.064
None	1.13	0.67, 1.92	0.6
Open	1.52	0.86, 2.66	0.15
PRIOR_CHF			
No	—	—	
Yes	1.50	1.19, 1.88	<b>&lt;0.001</b>
PREOP_DIALYSIS			
No	—	—	
Yes	1.75	1.02, 3.00	<b>0.042</b>
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.89	1.19, 2.99	<b>0.007</b>
Dissection	1.89	1.09, 3.28	<b>0.024</b>
PAU/IMH	1.97	0.94, 4.11	0.072
extent			
Juxtarenal	—	—	
No	2.07	1.69, 2.53	<b>&lt;0.001</b>

<sup>1</sup>OR = Odds Ratio, CI = Confidence Interval

## ICUSTAY

ICU Stay

Characteristic	ICU Stay		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.10	2.42, 3.97	<b>&lt;0.001</b>

<sup>1</sup>OR = Odds Ratio, CI = Confidence Interval

Characteristic	ICU Stay		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.10	1.60, 2.75	<b>&lt;0.001</b>
AGECAT			
<50	—	—	
>79	1.32	0.50, 3.47	0.6
50-59	1.26	0.45, 3.53	0.7
60-69	1.00	0.39, 2.57	>0.9
70-79	1.30	0.51, 3.34	0.6
GENDER			
female	—	—	
male	0.61	0.49, 0.76	<b>&lt;0.001</b>
PREOP_SMOKING			
No	—	—	
Yes	0.99	0.73, 1.34	>0.9
PRIOR_AORSURG			
Both	—	—	
Endo	1.33	0.77, 2.32	0.3
None	0.72	0.42, 1.24	0.2
Open	1.25	0.70, 2.23	0.5
PRIOR_CHF			
No	—	—	

<sup>1</sup>OR = Odds Ratio, CI = Confidence Interval

Characteristic	ICU Stay		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
Yes	1.22	0.93, 1.59	0.15
PREOP_DIALYSIS			
No	—	—	
Yes	1.96	1.12, 3.43	<b>0.019</b>
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.34	0.80, 2.23	0.3
Dissection	1.79	0.97, 3.30	0.062
PAU/IMH	1.26	0.51, 3.11	0.6
extent			
Juxtarenal	—	—	
No	2.18	1.72, 2.75	<b>&lt;0.001</b>

<sup>1</sup>OR = Odds Ratio, CI = Confidence Interval

## POSTOP\_PRBC

Transfusion # Units PRBC

	Transfusion # Units PRBC		
Characteristic	Beta	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	0.96	0.52, 1.4	<b>&lt;0.001</b>

<sup>1</sup>CI = Confidence Interval

	Transfusion # Units PRBC		
Characteristic	Beta	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	0.43	-0.05, 0.92	0.079
AGECAT			
<50	—	—	
>79	-0.96	-5.6, 3.7	0.7
50-59	-0.30	-5.1, 4.5	>0.9
60-69	-1.2	-5.8, 3.5	0.6
70-79	-0.89	-5.5, 3.8	0.7
GENDER			
female	—	—	
male	-0.81	-1.1, -0.49	<b>&lt;0.001</b>
PREOP_SMOKING			
No	—	—	
Yes	-0.27	-0.73, 0.20	0.3
PRIOR_AORSURG			
Both	—	—	
Endo	-0.04	-1.0, 0.92	>0.9
None	-0.32	-1.3, 0.69	0.5
Open	0.17	-0.95, 1.3	0.8
PRIOR_CHF			
No	—	—	

<sup>1</sup>CI = Confidence Interval

Characteristic	Transfusion # Units PRBC		
	Beta	95% CI <sup>1</sup>	p-value
Yes	-0.07	-0.33, 0.19	0.6
PREOP_DIALYSIS			
No	—	—	
Yes	0.73	-0.16, 1.6	0.11
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	-0.13	-1.2, 0.97	0.8
Dissection	1.2	-0.78, 3.1	0.2
PAU/IMH	0.44	-1.1, 2.0	0.6
extent			
Juxtarenal	—	—	
No	0.72	0.36, 1.1	<b>&lt;0.001</b>

<sup>1</sup>CI = Confidence Interval

## POSTOP\_HIGHCREAT

Highest Creatinine (has not updated yet)

Highest Creatinine			
Characteristic	Beta	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	0.34	0.16, 0.52	<b>&lt;0.001</b>

<sup>1</sup>CI = Confidence Interval

Highest Creatinine			
Characteristic	Beta	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	0.22	0.06, 0.37	<b>0.006</b>
AGECAT			
<50	—	—	
>79	-0.34	-0.89, 0.22	0.2
50-59	-0.12	-0.74, 0.51	0.7
60-69	-0.30	-0.85, 0.26	0.3
70-79	-0.30	-0.85, 0.25	0.3
GENDER			
female	—	—	
male	0.18	0.10, 0.26	<b>&lt;0.001</b>
PREOP_SMOKING			
No	—	—	
Yes	0.02	-0.08, 0.13	0.6
PRIOR_AORSURG			
Both	—	—	
Endo	0.28	0.03, 0.53	<b>0.030</b>
None	0.18	-0.07, 0.42	0.2
Open	0.11	-0.14, 0.36	0.4
PRIOR_CHF			
No	—	—	

<sup>1</sup>CI = Confidence Interval

Highest Creatinine			
Characteristic	Beta	95% CI <sup>1</sup>	p-value
Yes	0.16	0.07, 0.25	<0.001
PREOP_DIALYSIS			
No	—	—	
Yes	4.1	3.4, 4.9	<0.001
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	-0.16	-0.41, 0.10	0.2
Dissection	0.30	-0.10, 0.70	0.15
PAU/IMH	0.19	-0.17, 0.55	0.3
extent			
Juxtarenal	—	—	
No	0.07	-0.03, 0.16	0.2

<sup>1</sup>CI = Confidence Interval



## POSTOP\_INTISCH

Intestinal Ischemia

Intestinal Ischemia			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.14	0.56, 2.33	0.7

<sup>1</sup>OR = Odds Ratio, CI = Confidence Interval

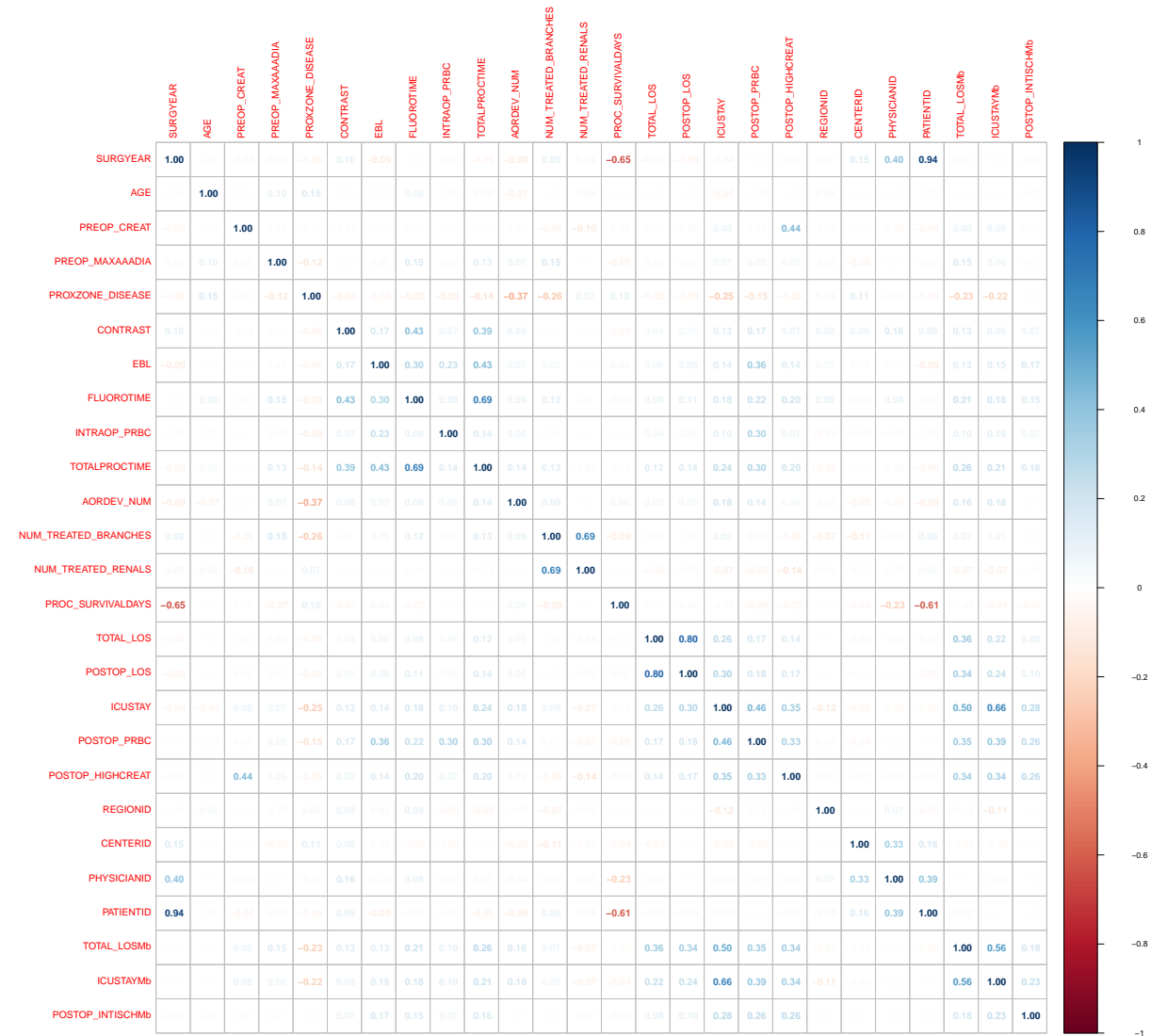
Intestinal Ischemia			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.08	0.50, 2.32	0.9
AGECAT			
<50	—	—	
>79	0.42	0.07, 2.43	0.3
50-59	0.49	0.06, 4.21	0.5
60-69	0.37	0.06, 2.20	0.3
70-79	0.45	0.08, 2.54	0.4
GENDER			
female	—	—	
male	0.62	0.37, 1.03	0.064
PREOP_SMOKING			
No	—	—	
Yes	0.86	0.43, 1.73	0.7
PRIOR_AORSURG			
Both	—	—	
Endo	1.89	0.22, 16.1	0.6
None	1.78	0.21, 15.1	0.6
Open	1.57	0.16, 15.4	0.7
PRIOR_CHF			
No	—	—	

<sup>1</sup>OR = Odds Ratio, CI = Confidence Interval

Intestinal Ischemia			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
Yes	1.06	0.53, 2.12	0.9
PREOP_DIALYSIS			
No	—	—	
Yes	0.70	0.09, 5.20	0.7
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.51	0.07, 3.85	0.5
Dissection	0.73	0.14, 3.76	0.7
PAU/IMH	1.28	0.16, 10.5	0.8
extent			
Juxtarenal	—	—	
No	0.94	0.53, 1.68	0.8

<sup>1</sup>OR = Odds Ratio, CI = Confidence Interval

## Correlation matrix



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

```

## $ETHNICITY
## [1] "None Hispanic or Latino" "Hispanic or Latino"
## [3] NA
##
## $RACE
## [1] "Black or African American"
## [2] "White"
## [3] "Unknown/Other"
## [4] "Asian"
## [5] "American Indian or Alaskan Native"
## [6] "Native Hawaiian or other Pacific Islander"
## [7] "More than 1 race"
##
## $TRANSFER
## [1] "No"          "Hospital"    "Rehab Unit"
##
## $PRIMARYINSURER
## [1] "Medicare"      "Commercial"   NA             "Medicaid"
## [5] "Military/VA"   "Self Pay"     "Non US Insurance"
##
## $LIVINGSTATUS
## [1] "Home"          "Nursing home" "Homeless"
##
## $PREOP_FUNCSTATUS
## [1] "Full"          "Light work"   "Self care"    "Assisted care"
## [5] NA             "Bed bound"
##
## $PRIOR_CVD
## [1] "No" "Yes"
##
## $PRIOR_CAD
## [1] "No" "Yes" NA
##
## $PRIOR_CHF
## [1] "No" "Yes"
##
## $COPD
## [1] "No" "Yes"
##
## $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] "Yes" "No"
##
## $STRESS
## [1] "Yes" "No" NA
##
## $DC_ASA
## [1] "Yes" "No" NA
##
## $DC_P2Y
## [1] "No" "Yes" NA
##
## $DC_STATIN
## [1] "Yes" "No" NA
##
## $PRIOR_AORSURG
## [1] "Open" "Endo" "None" "Both"
##
## $PATHOLOGY
## [1] "Dissection" "Aneurysm from dissection"
## [3] "Aneurysm" "PAU/IMH"
##
## $URGENCY
## [1] "Elective" "Urgent" "Emergent"
##
## $PATHOLOGY_ANEURYSM_TYPE
## [1] NA "Degenerative, fusiform"
## [3] "Degenerative, saccular" "Anastomotic"
## [5] "Intercostal or visceral patch" "Prior trauma"
##
## $PATHOLOGY_DISSECT_TYPE
## [1] "Chronic, >30 days" NA "Acute, <= 30 days"
##
## $GENHIST
## [1] "None" "Non-specific" "Marfans" NA
## [5] "Loeys-Dietz" "Ehlers-Danlos"
##
## $DISTZONE_DISEASE
## [1] "9" "10B" "10L" "11B" "10R" "8" "7" "11L" "6" "5" "11R" "4"
##
## $extent
## [1] No <NA> Juxtarenal
## Levels: Juxtarenal No
##
## $ANESTHESIA
## [1] "General" "Local" "Regional"
##
## $IVUSTEE
## [1] "No" "IVUS" NA "Both" "TEE"
##
## $ACCESS

```

```

## [1] "Percutaneous" NA "Open"
##
## $ARMNECK_ACCESS
## [1] "No" "Yes"
##
## $AORDEV_CMED
## [1] "Yes" "No"
##
## $DEV_GTYPE
## [1] "Physician modified" "Standard" "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] "Yes" "No" NA
##
## $BRANCH_LSUB
## [1] "Yes" "No"
##
## $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] "Yes" "No"
##
## $lrenal
## [1] "Scallop/Fen/Branch/Chimney" "None"
## [3] "Occluded/Covered" NA
##
## $rrenal
## [1] "Scallop/Fen/Branch/Chimney" "None"
## [3] "Occluded/Covered" NA
##
## $sma
## [1] "Scallop/Fen/Branch/Chimney" NA
## [3] "None" "Occluded/Covered"

```

```

##
## $celiac
## [1] "Scallop/Fen/Branch/Chimney" "None"
## [3] NA "Occluded/Covered"
##
## $lsub
## [1] NA "Scallop/Fen/Branch/Chimney"
## [3] "Occluded/Covered" "None"
##
## $OCCLUDED_RENAL
## [1] FALSE TRUE
##
## $OCCLUDED_SMA
## [1] FALSE TRUE
##
## $OCCLUDED_CELIAC
## [1] FALSE TRUE
##
## $DEAD
## [1] FALSE TRUE
##
## $AORDEV_TECHSUCC
## [1] "Yes" "No" NA
##
## $CONVTOOPEN
## [1] "No" "Yes"
##
## $LEAKATCOMP_NONE
## [1] NA "Yes" "No"
##
## $POSTOP_VASO
## [1] "No" "Yes" NA
##
## $POSTOP_COMPLICATIONS
## [1] "No" "Yes" NA
##
## $ACCESS_COMPLICATION
## [1] "No" "Yes" NA
##
## $POSTOP_AH
## [1] "No" "Yes"
##
## $POSTOP_CEREBROX
## [1] "No" "Yes" NA
##
## $POSTOP_RESPIRATORY
## [1] "No" "Yes"
##
## $POSTOP_DIALYSIS
## [1] "No" NA "Yes"
##
## $POSTOP_ARMEMBO
## [1] "No" "Yes"
##

```

```

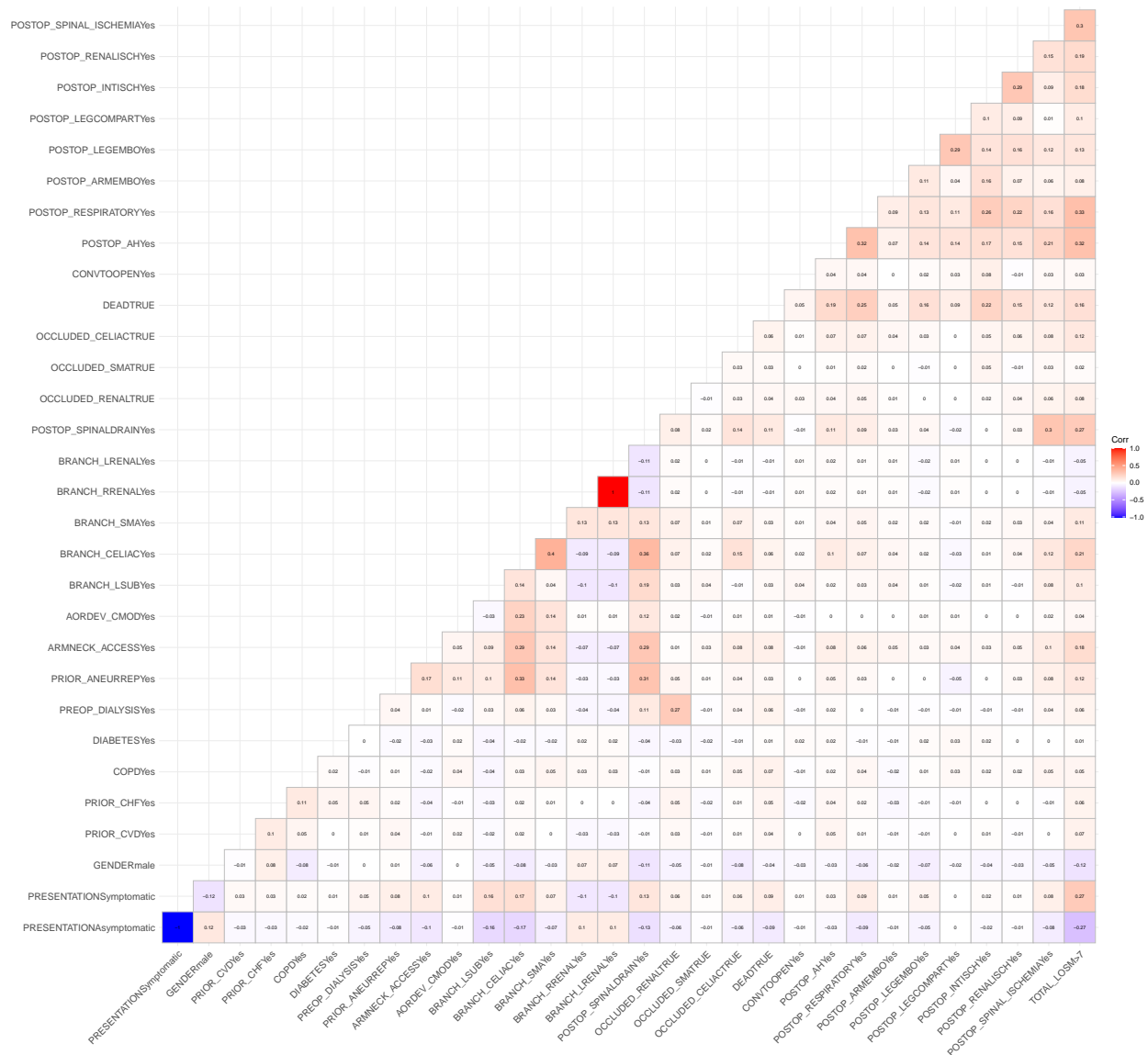
## $POSTOP_LEGEMBO
## [1] "No" "Yes"
##
## $POSTOP_LEGCOMPART
## [1] "No" "Yes"
##
## $POSTOP_INTISCH
## [1] "No" "Yes"
##
## $POSTOP_RENALISCH
## [1] "No" "Yes"
##
## $POSTOP_SPINAL_ISCHEMIA
## [1] "No" "Yes"
##
## $RETX_R_RTOR
## [1] "No" "Yes" NA
##
## $DC_STATUS
## [1] "Home" "Dead" "Rehab Unit" "Nursing Home"
## [5] "Other Hospital" NA "Homeless"
##
## $BRANCH_POST
## [1] "No" "Yes" NA
##
## $TOTAL_LOSM
## [1] "<=7" ">7"
##
## $ICUSTAYM
## [1] "<=4" ">4" 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 DC_ASA DC_P2Y
## 3 3 3
## DC_STATIN PRIOR_AORSURG PATHOLOGY
## 3 4 4
## URGENCY PATHOLOGY_ANEURYSM_TYPE PATHOLOGY_DISSECT_TYPE
## 3 6 3
## GENHIST DISTZONE_DISEASE extent
## 6 12 3
## ANESTHESIA IVUSTEE ACCESS

```



##	3	5	3
##	ARMNECK_ACCESS	AORDEV_CMED	DEV_GTYPE
##	2	2	3
##	ILIACDEV_END_R	ILIACDEV_END_L	BRANCH_STAGED
##	5	5	3
##	BRANCH_LSUB	BRANCH_CELIAC	BRANCH_SMA
##	2	2	2
##	BRANCH_RRENAL	BRANCH_LRENAL	ANESTHESIA_GEN_TIMEEXT
##	2	2	5
##	POSTOP_SPINALDRAIN	lrenal	rrenal
##	2	4	4
##	sma	celiac	lsab
##	4	4	4
##	OCCLUDED_RENAL	OCCLUDED_SMA	OCCLUDED_CELIAC
##	2	2	2
##	DEAD	AORDEV_TECHSUCC	CONVTOOPEN
##	2	3	2
##	LEAKATCOMP_NONE	POSTOP_VASO	POSTOP_COMPLICATIONS
##	3	3	3
##	ACCESS_COMPLICATION	POSTOP_AH	POSTOP_CEREBROX
##	3	2	3
##	POSTOP_RESPIRATORY	POSTOP_DIALYSIS	POSTOP_ARMEMBO
##	2	3	2
##	POSTOP_LEGEMBO	POSTOP_LEGCOMPART	POSTOP_INTISCH
##	2	2	2
##	POSTOP_RENALISCH	POSTOP_SPINAL_ISCHEMIA	RETX_R_RTOR
##	2	2	3
##	DC_STATUS	BRANCH_POST	TOTAL_LOSM
##	7	3	2
##	ICUSTAYM		
##	3		



```
## 'data.frame': 3744 obs. of 30 variables:
## $ PRESENTATION : chr "Asymptomatic" "Asymptomatic" "Asymptomatic" "Asymptomatic" ...
## $ GENDER : chr "male" "male" "female" "male" ...
## $ PRIOR_CVD : chr "No" "Yes" "No" "No" ...
## $ PRIOR_CHF : chr "No" "Yes" "No" "No" ...
## $ COPD : chr "No" "Yes" "No" "No" ...
## $ DIABETES : chr "No" "Yes" "No" "No" ...
## $ PREOP_DIALYSIS : chr "No" "No" "No" "No" ...
## $ PRIOR_ANEURREP : chr "Yes" "Yes" "No" "No" ...
## $ ARMNECK_ACCESS : chr "No" "No" "No" "No" ...
## $ AORDEV_CMODYes : chr "Yes" "Yes" "Yes" "Yes" ...
## $ BRANCH_LSUB : chr "Yes" "No" "No" "No" ...
## $ BRANCH_CELIAC : chr "Yes" "Yes" "Yes" "Yes" ...
## $ BRANCH_SMA : chr "Yes" "Yes" "Yes" "Yes" ...
```

```

## $ BRANCH_RENAL      : chr "Yes" "Yes" "Yes" "Yes" ...
## $ BRANCH_LRENAL     : chr "Yes" "Yes" "Yes" "Yes" ...
## $ POSTOP_SPINALDRAIN : chr "Yes" "Yes" "No" "No" ...
## $ OCCLUDED_RENAL    : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
## $ OCCLUDED_SMA      : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
## $ OCCLUDED_CELIAC   : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
## $ DEAD              : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
## $ CONVTOOPEN        : chr "No" "No" "No" "No" ...
## $ POSTOP_AH         : chr "No" "No" "No" "No" ...
## $ POSTOP_RESPIRATORY : chr "No" "No" "No" "No" ...
## $ POSTOP_ARMEMBO     : chr "No" "No" "No" "No" ...
## $ POSTOP_LEGEMBO     : chr "No" "No" "No" "No" ...
## $ POSTOP_LEGCOMPART  : chr "No" "No" "No" "No" ...
## $ POSTOP_INTISCH     : chr "No" "No" "No" "No" ...
## $ POSTOP_RENALISCH   : chr "No" "No" "No" "No" ...
## $ POSTOP_SPINAL_ISCHEMIA: chr "No" "No" "No" "No" ...
## $ TOTAL_LOSM        : chr "<=7" "<=7" "<=7" "<=7" ...

```

## 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/jenniferCi/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 binary 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))))

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")

#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()

#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()

#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_INTISCH,
                           , 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)
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_INTISCH,
                           , 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_INTISCH,
                 data=PROCNM,family=binomial(link="logit"), id = CENTERID, corstr = "independence")

#model<-geeglm(outcome~predictor+confounder, family=binomial(link = "logit"),
#data=na.omit(data), corstr='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)

```