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

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Generalized linear models with the Generalized Estimating Equations for continuous outcomes

TOTAL_LOS

Length of Stay in days calculated by DISCHARGE_DT - ADMIT_DT

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

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	OR[1]	95% CI[1]	p-value
	TOTAL_LOS Length of Stay in days		
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			

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	**TOTAL_LOS Length of Stay in days**		
	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**

[1]OR = Odds Ratio, CI = Confidence Interval

ICUSTAY

ICU Stay

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

[1]OR = Odds Ratio, CI = Confidence Interval

	ICU Stay		
Characteristic	**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	—	—	

[1]OR = Odds Ratio, CI = Confidence Interval

	ICU Stay		
Characteristic	**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**

[1]OR = Odds Ratio, CI = Confidence Interval

POSTOP_HIGHCREAT

Highest Creatinine 1 - GFR reduction is >=50% 0 - GFR reduction is <50%

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

[1]OR = Odds Ratio, CI = Confidence Interval

Characteristic	GFR		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.35	0.90, 2.02	0.15
AGECAT			
<50	—	—	
>79	0.72	0.15, 3.43	0.7
50-59	1.33	0.27, 6.48	0.7
60-69	0.91	0.20, 4.24	>0.9
70-79	0.82	0.17, 3.87	0.8
GENDER			
female	—	—	
male	0.67	0.50, 0.89	**0.006**
PREOP_SMOKING			
No	—	—	
Yes	1.27	0.81, 2.00	0.3
PRIOR_AORSURG			
Both	—	—	
Endo	1.36	0.52, 3.53	0.5
None	1.04	0.41, 2.61	>0.9
Open	0.99	0.36, 2.76	>0.9
PRIOR_CHF			
No	—	—	

[1]OR = Odds Ratio, CI = Confidence Interval

	GFR		
Characteristic	**OR**[1]	**95% CI**[1]	**p-value**
Yes	1.08	0.76, 1.54	0.7
PREOP_GFR_CAT			
End-stage renal disease	—	—	
Mildly decreased	1.83	0.23, 14.4	0.6
Mildly to severely decreased	2.51	0.32, 19.7	0.4
Normal or increased	2.12	0.27, 16.9	0.5
Severely decreased	2.08	0.24, 18.3	0.5
TREATED_RENALS			
No	—	—	
Yes	0.54	0.39, 0.73	**<0.001**
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.33	0.10, 1.09	0.068
Dissection	0.85	0.31, 2.33	0.8
PAU/IMH	1.21	0.35, 4.23	0.8
extent			
Juxtarenal	—	—	
No	1.12	0.82, 1.54	0.5

[1]OR = 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

[1]OR = 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	—	—	

[1]OR = 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

[1]OR = Odds Ratio, CI = Confidence Interval

Correlation matrix
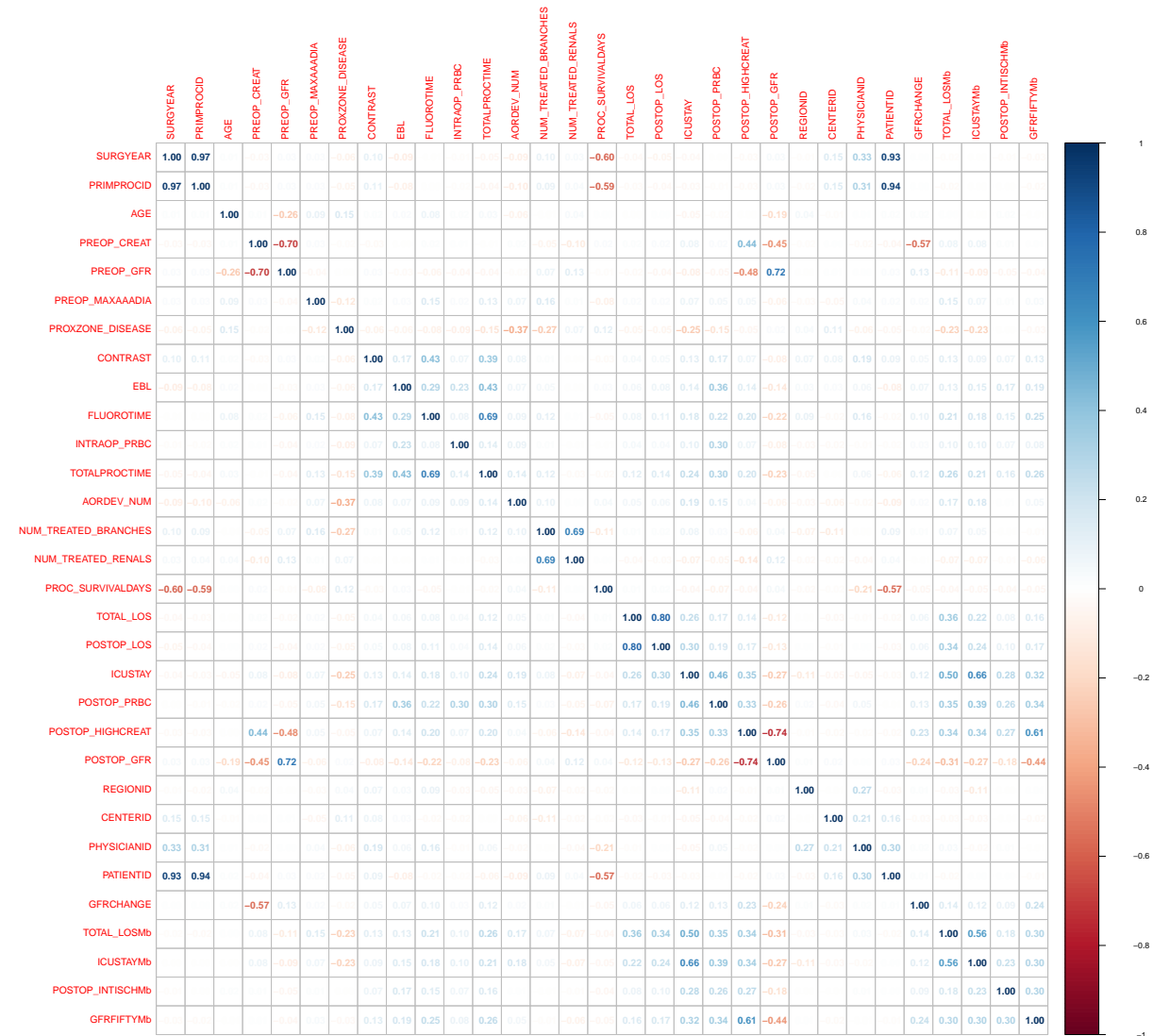

```
## $SURGMONTH
##  [1] "nov" "jun" "may" "apr" "aug" "sep" "jul" "mar" "oct" "dec" "feb" "jan"
##
## $PRESENTATION
## [1] "Asymptomatic" "Symptomatic"
##
## $AGECAT
## [1] ">79"   "60-69" "70-79" "<50"   "50-59"
##
## $GENDER
## [1] "male"   "female"
##
```

```
## $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" "Severely decreased"
## [5] NA                            "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] "Mildly decreased"             "Severely decreased"
## [5] "End-stage renal disease"      NA
##
## $POSTOP_COMPLICATIONS
## [1] "No"  "Yes" NA
##
## $ACCESS_COMPLICATION
## [1] "No"  NA    "Yes"
##
## $POSTOP_AH
## [1] "No"  "Yes" NA
##
## $POSTOP_CEREBROSX
## [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     
## 
## $TREATED_RENALS
## [1] "No"  "Yes"


##            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_CMOD
##                        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_CEREBROSX      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          TREATED_RENALS
##                        3                       2
```
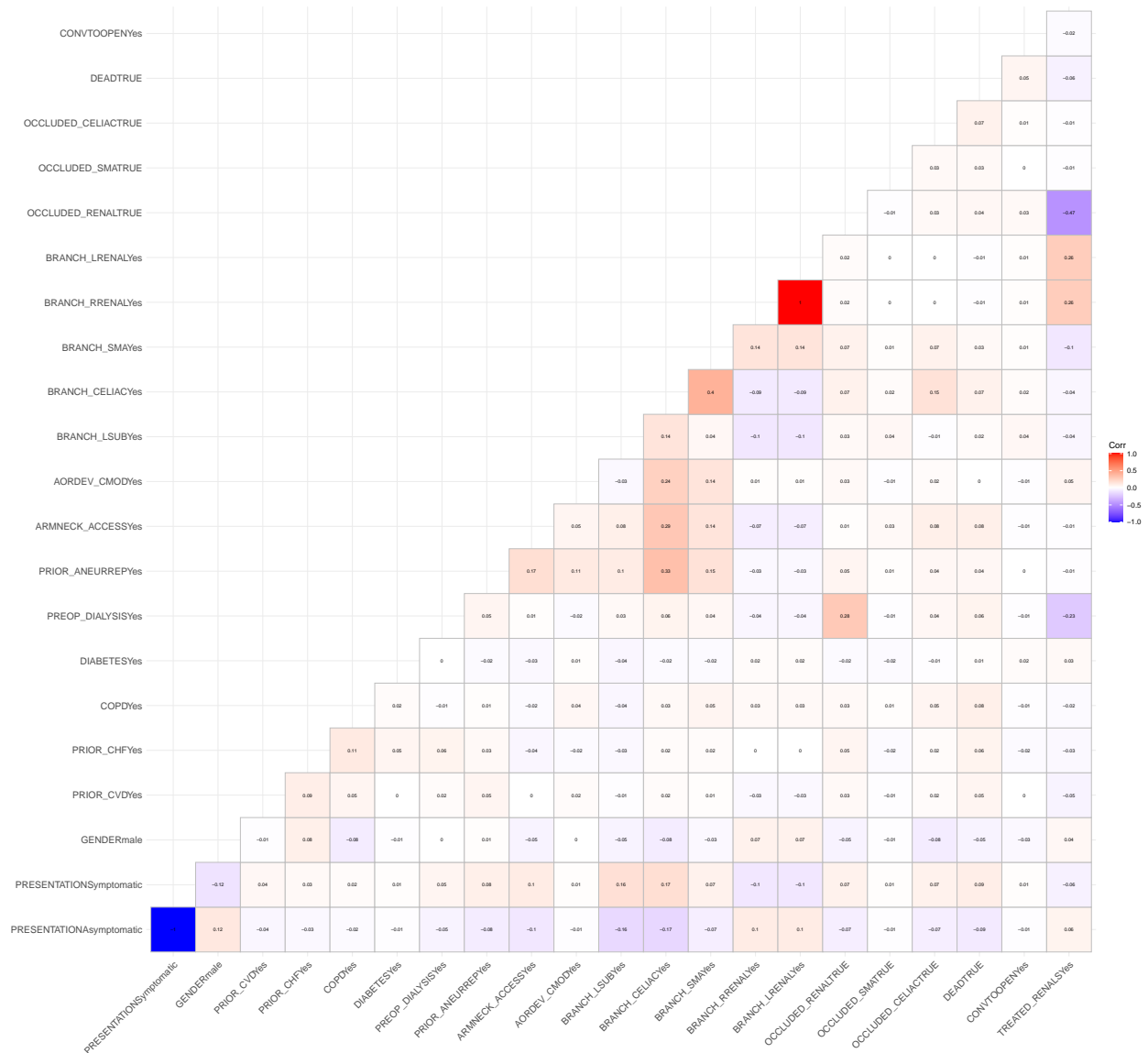
```
## 'data.frame':    3757 obs. of  21 variables:
##  $ PRESENTATION   : chr  "Asymptomatic" "Asymptomatic" "Symptomatic" "Symptomatic" ...
##  $ GENDER         : chr  "male" "male" "male" "male" ...
##  $ PRIOR_CVD      : chr  "No" "Yes" "No" "Yes" ...
##  $ PRIOR_CHF      : chr  "No" "No" "No" "No" ...
##  $ 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_CMOD    : 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" ...
```

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```
##  $ 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" ...
##  $ TREATED_RENALS : chr  "No" "Yes" "Yes" "Yes" ...
```

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 %>%
```

```r
  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))),
TREATED_RENALS = (ifelse(NUM_TREATED_RENALS<1, "No",
                     ifelse(NUM_TREATED_RENALS>=1, "Yes",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$GFRFIFTYMb <- as.numeric(PROC$GFRFIFTY != "<50%")
#PROC%>% select(GFRFIFTY,GFRFIFTYMb)

#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$TOTAL_LOSMb)
#PROC%>% select(ICUSTAYM,ICUSTAY,ICUSTAYMb)
#PROC%>% select(POSTOP_INTISCH,POSTOP_INTISCHMb)
#check the GFR
#a<-PROC%>% filter(is.na(PREOP_GFR_CAT))%>% select(PREOP_CREAT,POSTOP_HIGHCREAT, PREOP_GFR,PREOP_GFR_CA
#table(PROC$extent)

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

#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, cors

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_DIALYS
            , data=PROCNM, family=binomial(link="logit"),id = CENTERID, corstr = "independence")
```

```r
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

#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+PRE
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, corst

#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()


#table(PROCNM$PREOP_GFR_CAT)


#adjusted
GFR2<-geeglm(GFRFIFTYMb ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_GFR_CAT
            , 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 = "independe
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+PRI
                         , 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 =

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

```r
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_
                        , data=PROCNM,family=binomial(link="logit"), id = CENTERID, corstr = "independen
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), 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)
```