

Data Preprocessing on VQI TEVAR Dataset

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merge the datasets

Compare the data from July 2021 and September 2021. Keep the most updated ones.

There are 6 rows from LTF July data missing in September dataset. And also 6 missing from the PROC dataset.

Only received info of PROC dataset variables? No info about LTF variables?

Variables that exists in both LTF and PROC datasets are: PATIENTID, PRIMPROCID, DEAD, PROC_SURVIVALDAYS, IDE_OTHER. Merge by these variables.

3327 participants have more than one records in this dataset.

data cleaning based on inclusion, exclusion criteria

Exclusion criteria:

- PRESENTATION exclude rupture patients
- PATHOLOGY exclude groups with pathology: 4=trauma, 8 = Aortic Thrombus,9 = Other (Retired) (retired since 09/30/2014),10 = Aorto-esophageal Fistula (Retired) (retired since 09/30/2014),11 = Aorto-bronchial Fistula (Retired) (retired since 09/30/2014)
- URGENCY: exclude rupture. (elective is same to asymptomatic)
- PROXZONE_DISEASE: exclude 0 and 1
- DISTZONE_DISEASE: exclude 0
- PROXZONE_DISEASE < DISTZONE_DISEASE: disease starting point should be earlier than ending point.

Wrong data points with distal zone < proximal zone:

##	PATIENTID	PROXZONE_DISEASE	DISTZONE_DISEASE
## 1	85423	5	4
## 2	184672	3	0
## 3	188991	8	7
## 4	192399	3	0
## 5	198402	4	3
## 6	199759	4	0
## 7	251502	2	1
## 8	287173	4	1
## 9	288150	5	2
## 10	288150	5	2
## 11	290463	5	3
## 12	307868	3	2
## 13	347630	4	3
## 14	349408	9	8
## 15	375257	8	6

## 16	376442	8	6
## 17	405193	5	4
## 18	420868	5	0
## 19	443562	4	3
## 20	445629	3	2
## 21	455349	8	4
## 22	599099	2	1
## 23	603976	4	2
## 24	603976	4	2
## 25	640888	4	3
## 26	666627	3	0
## 27	666627	3	0
## 28	689701	2	1
## 29	714961	3	1
## 30	760981	4	3
## 31	793532	4	2
## 32	793634	5	2
## 33	793704	5	4
## 34	794699	5	4
## 35	801346	5	4

After excision, there are in total 15424 objectives in the final TEVAR dataset. 1995 participants have more than one records in this dataset.

Data cleaning: comorbidities changed to No/Yes scale.

What is the point of filtering `BRANCH_POST`. *Filter `BRANCH_POST` based on the same criteria?*

Patient demographic and co-morbidities

`R_CR_PRESENT`: a lot of missing values, probably because Retired December 2014.

strange unit (normally 0.7 to 1.3 mg/dL)

```
## R_CR_PRESENT
## 1 2
## 10 15
```

Operative Variables

7 variables related to details about `PRIOR_AORSURG`. *include?*

`GENHIST`, `R_GENHIST`: *merge and change to 0/1 scale?*

`DEV1_PROXZONE`: *exclude align with `PROXZONE`?*

`DEV1_GRAFTDET`: *shouldn't be included in operative variables?* This field is required if Number of Aortic Devices has one of [1, 2, 3, 4, 5, 6]. To protect the identity of the device a random number is assigned.

many variables related to details about `PATHOLOGY`. *include?*

deal with 'conditional' variables

Outcomes

long term outcomes vs procedure outcomes?

Primary (Long term) outcomes: `DEAD` and `PROC_SURVIVALDAYS`.

Cox model for estimation of hazard ratios.

Secondary (Procedure) outcomes: others

Volume Variables

Volume Variables: REGIONID, CENTERID, PHYSICIANID

how to do cluster on centers and physicians? Dr. Dansey's instructions

Report mean or median: based on outliers?

Code Appendix

```
knitr::opts_chunk$set(echo = FALSE,message = FALSE,warning = FALSE)
library(tidyverse)
library(table1)
library(Hmisc)
library(ggplot2)
## ----- working directories for Lily -----
wd_lily = '/Users/hanyiwang/Desktop/Comparative-analysis-of-treatments-of-CAA'
path_lily = c(
  "../data/TEVAR_International_20210712/TEVAR_International_LTF_r12_2_14_20210701.csv",
  "../data/TEVAR_International_20210712/TEVAR_International_PROC_r12_2_14_20210701.csv",
  "../data/TEVAR_International_20210901/TEVAR_International_LTF_r12_2_14_20210901.csv",
  "../data/TEVAR_International_20210901/TEVAR_International_PROC_r12_2_14_20210901.csv",
  "../data/FBVAR.csv")

## ----- working directories for Jenn -----
wd_jenn = '/Users/jennifercci/Desktop/Comparative-analysis-of-treatments-of-CAA'
path_jenn = c(
  # "/Users/jennifercci/Desktop/Comparative-analysis-of-treatments-of-CAA/TEVAR_International_20210712/TE
  # "/Users/jennifercci/Desktop/Comparative-analysis-of-treatments-of-CAA/TEVAR_International_20210712/TE
  # "/Users/jennifercci/Desktop/Comparative-analysis-of-treatments-of-CAA/TEVAR_International_20210901/TE
  # "/Users/jennifercci/Desktop/Comparative-analysis-of-treatments-of-CAA/TEVAR_International_20210901/TE

## ----- read data -----
setwd(wd_lily)
TEVAR_LTF_07 = read.csv(path_lily[1])
TEVAR_PROC_07 = read.csv(path_lily[2])
TEVAR_LTF_09 = read.csv(path_lily[3])
TEVAR_PROC_09 = read.csv(path_lily[4])

#setwd(wd_jenn)
#TEVAR_LTF_07 = read.csv(path_jenn[1])
#TEVAR_PROC_07 = read.csv(path_jenn[2])
#TEVAR_LTF_09 = read.csv(path_jenn[3])
#TEVAR_PROC_09 = read.csv(path_jenn[4])
## ----- merge July and September data -----

# find data in LTF July data but not in LTF September data by `PATIENTID`
# add these data points to the September data
TEVAR_LTF <- rbind(TEVAR_LTF_07[! TEVAR_LTF_07$PATIENTID %in% TEVAR_LTF_09$PATIENTID,],
  TEVAR_LTF_09)

# Similar for PROC data
TEVAR_PROC <-rbind(TEVAR_PROC_07[! TEVAR_PROC_07$PATIENTID %in% TEVAR_PROC_09$PATIENTID,],
  TEVAR_PROC_09)

## ----- merge LTF and PROC data-----
# same variables in LTF and PROC data
#colnames(TEVAR_PROC)[colnames(TEVAR_PROC) %in% colnames(TEVAR_LTF)]

TEVAR <- merge(TEVAR_LTF,TEVAR_PROC, all = TRUE,
  by=c("PATIENTID","PRIMPROCID","DEAD","PROC_SURVIVALDAYS","IDE_OTHER"))
```

```

# diagnosing duplicate id, decide which record to keep?
n_occur <- data.frame(table(TEVAR$PATIENTID))
#n_occur[n_occur$Freq > 1,]%>%n_distinct

TEVAR %>% filter(DISTZONE_DISEASE < PROXZONE_DISEASE) %>%
  select(PATIENTID,PROXZONE_DISEASE,DISTZONE_DISEASE)

## ----- inclusion and exclusion-----
TEVAR = TEVAR %>%
  filter(PRESENTATION !=2) %>%
  filter(PATHOLOGY %in% c(1,2,3,5,6,7)) %>%
  filter(URGENCY %in% c(1,2,3)) %>%
  filter(PROXZONE_DISEASE %in% c(2,3,4,5,6,7,8,9)) %>%
  filter(DISTZONE_DISEASE > PROXZONE_DISEASE)

n_occur <- data.frame(table(TEVAR$PATIENTID))
## ----- variables cleaning, patient demographic and co-morbidities-----
TEVAR = TEVAR %>%
  mutate(PRESENTATION = factor(PRESENTATION,levels = c(0,1),
                                labels = c('Asymptomatic','Symptomatic')))

TEVAR = TEVAR %>%
  mutate(DEAD=factor(DEAD)) %>%
  mutate(PRESENTATION = factor(PRESENTATION,levels = c(0,1),
                                labels = c('Asymptomatic','Symptomatic')))) %>%
  mutate(AGECAT = factor(AGECAT,levels = c(1,2,3,4,5,6,7),
                                labels = c('<40','40-49','50-59','60-69','70-79','80-89','>89')))) %>%
  mutate(GENDER=factor(GENDER,levels=c(1,2),
                                labels=c('male','female')))) %>%
  #mutate(SURGYEAR=factor(SURGYEAR)) %>%
  mutate(PROXZONE_DISEASE=factor(PROXZONE_DISEASE)) %>%
  mutate(URGENCY=factor(URGENCY,levels = c(1,2,3),labels = c('Elective','Urgent','Emergent')))) %>%
  mutate(PATHOLOGY=factor(PATHOLOGY,levels=c(1,2,3,5,6,7),
                                labels = c('Aneurysm','Dissection','Aneurysm from dissection','PAU',
                                              'IMH','PAU with IMH')))) %>%
  mutate(R_PREOP_AMBUL = factor(R_PREOP_AMBUL,levels = c(1,2,3,4),
                                labels=c('Amb',"Amb w/ Assistance","Wheelchair","Bedridden")))) %>%
  mutate(AGECAT = factor(AGECAT,levels = c(1,2,3,4,5,6,7),
                                labels = c('<40','40-49','50-59','60-69','70-79','80-89','>89')))) %>%
  mutate(GENDER=factor(GENDER,levels=c(1,2),labels=c('male','female')))) %>%
  mutate(ETHNICITY = factor(ETHNICITY,levels=c(0,1),
                                labels = c('None Hispanic or Latino','Hispanic or Latino')))) %>%
  mutate(RACE=factor(RACE,levels = c(5,3,2,1,4,6,7),
                                labels = c('White','Black or African American','Asian',
                                              'American Indian or Alaskan Native',
                                              'Native Hawaiian or other Pacific Islander','More than 1 race',
                                              'Unknown/Other')))) %>%
  mutate(TRANSFER=factor(TRANSFER,levels = c(0,1,2),labels = c('No','Hospital','Rehab Unit')))) %>%
  mutate(PRIMARYINSURER=factor(PRIMARYINSURER,levels=c(1,2,3,4,5,6),
                                labels = c('Medicare','Medicaid','Commercial','Military/VA',
                                              'Non US Insurance','Self Pay')))) %>%
  mutate(LIVINGSTATUS=factor(LIVINGSTATUS,levels=c(1,2,3),

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        labels=c('Home','Nursing home','Homeless')) %>%
mutate(PREOP_FUNCSTATUS=factor(PREOP_FUNCSTATUS,levels = c(0,1,2,3,4),
        labels = c('Full','Light work','Self care','Assisted care',
        'Bed bound')) %>%
mutate(PRIOR_CVD = factor(PRIOR_CVD,levels =c(0,1,2,3),labels = c('No','Yes','Yes','Yes')) %>%
mutate(PRIOR_CAD = factor(PRIOR_CAD,levels =c(0,1,2,3,4,5),
        labels = c('No','Yes','Yes','Yes','Yes','Yes')) %>%
mutate(PRIOR_CHF = factor(PRIOR_CHF,levels =c(0,1,2,3,4),
        labels = c('No','Yes','Yes','Yes','Yes')) %>%
mutate(COPD = factor(COPD,levels = c(0,1,2,3),labels = c('No','Yes','Yes','Yes')) %>%
mutate(DIABETES=factor(DIABETES,levels = c(0,1,2,3),labels = c('No','Yes','Yes','Yes')) %>%
mutate(PREOP_DIALYSIS=factor(PREOP_DIALYSIS,levels=c(0,1,2),labels=c('No','Yes','Yes')) %>%
mutate(HTN=factor(HTN,levels = c(0,1,2,3),labels = c('No','Yes','Yes','Yes')) %>%
mutate(PREOP_SMOKING=factor(PREOP_SMOKING,levels=c(0,1,2),labels=c('No','Yes','Yes')) %>%
mutate(PRIOR_CABG = factor(PRIOR_CABG,levels = c(0,1,2),labels = c('No','Yes','Yes')) %>%
mutate(PRIOR_PCI = factor(PRIOR_PCI,levels = c(0,1,2),labels = c('No','Yes','Yes')) %>%
mutate(PRIOR_ANEURREP = factor(PRIOR_ANEURREP,levels =c(0,1,2,3,4,5),
        labels = c('No','Yes','Yes','Yes','Yes','Yes')) %>%
mutate(STRESS = factor(STRESS,levels =c(0,1,2,3,4),
        labels = c('No','Yes','Yes','Yes','Yes')) %>%
mutate(DC_ASA = factor(DC_ASA,levels = c(0,1,2,3),labels = c('No','Yes','No','No')) %>%
mutate(DC_P2Y = factor(DC_P2Y,levels =c(0,1,2,3,4,5,6,7),
        labels = c('No','Yes','Yes','Yes','Yes','Yes','No','No')) %>%
mutate(DC_STATIN = factor(DC_STATIN,levels = c(0,1,2,3),labels = c('No','Yes','No','No'))

## ----- variables cleaning, operative variables-----

TEVAR = TEVAR %>%
mutate(PRIOR_AORSURG=factor(PRIOR_AORSURG,levels=c(0,1,2,3,4),
        labels=c('None','Open','Endo','Both','Other')) %>%
mutate(PRIOR_AORSURG_OPENLOC1=factor(PRIOR_AORSURG_OPENLOC1,
        levels=c(0,1),labels=c('No','Yes')) %>%
mutate(PRIOR_AORSURG_OPENLOC2=factor(PRIOR_AORSURG_OPENLOC2,
        levels=c(0,1),labels=c('No','Yes')) %>%
mutate(PRIOR_AORSURG_OPENLOC3=factor(PRIOR_AORSURG_OPENLOC3,
        levels=c(0,1),labels=c('No','Yes')) %>%
mutate(PRIOR_AORSURG_OPENLOC4=factor(PRIOR_AORSURG_OPENLOC4,
        levels=c(0,1),labels=c('No','Yes')) %>%
mutate(PRIOR_AORSURG_ENDOLOC1=factor(PRIOR_AORSURG_ENDOLOC1,
        levels=c(0,1),labels=c('No','Yes')) %>%
mutate(PRIOR_AORSURG_ENDOLOC2=factor(PRIOR_AORSURG_ENDOLOC2,
        levels=c(0,1),labels=c('No','Yes')) %>%
mutate(PRIOR_AORSURG_ENDOLOC3=factor(PRIOR_AORSURG_ENDOLOC3,
        levels=c(0,1),labels=c('No','Yes')) %>%
mutate(PRIOR_AORSURG_ENDOLOC4=factor(PRIOR_AORSURG_ENDOLOC4,
        levels=c(0,1),labels=c('No','Yes')) %>%
mutate(PATHOLOGY=factor(PATHOLOGY,levels=c(1,2,3,5,6,7),
        labels = c('Aneurysm','Dissection','Aneurysm from dissection','PAU',
        'IMH','PAU with IMH')) %>%
mutate(URGENCY=factor(URGENCY,levels = c(1,2,3),labels = c('Elective','Urgent','Emergent')) %>%
mutate(PATHOLOGY_ANEURYSM_TYPE=
        factor(PATHOLOGY_ANEURYSM_TYPE,levels = c(1,2,3,4,5),
        labels = c('Degenerative, fusiform','Degenerative, saccular','Anastomotic',

```

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        'Prior trauma','Intercostal or visceral patch')) %>%
mutate(PATHOLOGY_DISSECT_TYPE=
  factor(PATHOLOGY_DISSECT_TYPE,levels = c(1,2),
    labels = c('Acute, <= 30 days','Chronic, >30 daysr')) %>%
mutate(GENHIST = factor(GENHIST,levels = c(0,1,2,3,4,5),
  labels = c('No','Yes','Yes','Yes','Yes','Yes')) %>%
mutate(R_GENHIST = factor(R_GENHIST,levels = c(0,1,2,3),labels = c('No','Yes','Yes','Yes')) %>%
mutate(Genetic=GENHIST) %>% #####
mutate(PROXZONE_DISEASE=factor(PROXZONE_DISEASE)) %>%
mutate(DISTZONE_DISEASE=
  factor(DISTZONE_DISEASE, levels = c(0:15),
    labels = c(0,1,2,3,4,5,6,7,8,9,'10R','10L','10B','11R','11L','11B')) %>%
mutate(ANESTHESIA=factor(ANESTHESIA,levels = c(1,2,3),labels = c('Local','Regional','General')) %>%
mutate(IVUSTEE=factor(IVUSTEE,levels = c(0:5),labels = c('No','IVUS','TEE','Both','No','IVUS')) %>%
mutate(ACCESS_R=factor(ACCESS_R,levels = c(0,1,2,3,4,5),
  labels = c('None','Percutaneous femoral','Open femoral, transverse',
    'Open femoral, vertical','Open femoral, failed percutaneous',
    'Iliac, via retroperitoneal')) %>%
mutate(ACCESS_L=factor(ACCESS_L,levels = c(0,1,2,3,4,5),
  labels = c('None','Percutaneous femoral','Open femoral, transverse',
    'Open femoral, vertical','Open femoral, failed percutaneous',
    'Iliac, via retroperitoneal')) %>%
mutate(ARMNECK_ACCESS=factor(ARMNECK_ACCESS,levels =c(0,1,2,3),
  labels = c('No','For branch treatment',
    'For femoral-brachial wire','For both')) %>%
mutate(ARMNECK_ACCESS_LOC=factor(ARMNECK_ACCESS_LOC,levels =c(1:7),
  labels = c('Right arm','Left arm','Right axillary',
    'Left axillary','Right carotid',
    'Left carotid','Multiple')) %>%

mutate(AORDEV_NUM=factor(AORDEV_NUM)) %>%
mutate(AORDEV_CMOD=factor(AORDEV_CMOD,levels=c(0,1),labels=c('No','Yes')) %>%
mutate(STAGEDAORTRT=factor(STAGEDAORTRT,levels=c(0,1),labels=c('No','Yes')) %>%
mutate(DEV1_GTYPE=factor(DEV1_GTYPE,levels=c(1,2,3),
  labels=c('Standard','Custom','Physician modified')) %>%
mutate(DEV2_GTYPE=factor(DEV2_GTYPE,levels=c(1,2,3),
  labels=c('Standard','Custom','Physician modified')) %>%
mutate(DEV3_GTYPE=factor(DEV3_GTYPE,levels=c(1,2,3),
  labels=c('Standard','Custom','Physician modified')) %>%
mutate(DEV1_PROXZONE=factor(DEV1_PROXZONE)) %>%
mutate(DEV2_PROXZONE=factor(DEV2_PROXZONE)) %>%
mutate(DEV3_PROXZONE=factor(DEV3_PROXZONE)) %>%
mutate(DEV4_PROXZONE=factor(DEV4_PROXZONE)) %>%
mutate(DEV5_PROXZONE=factor(DEV5_PROXZONE)) %>%
mutate(DEV6_PROXZONE=factor(DEV6_PROXZONE)) %>%
mutate(DEV1_DISTZONE= factor(DEV1_DISTZONE, levels = c(0:15),
  labels = c(0,1,2,3,4,5,6,7,8,9,'10R','10L',
    '10B','11R','11L','11B')) %>%
mutate(DEV2_DISTZONE= factor(DEV2_DISTZONE, levels = c(0:15),
  labels = c(0,1,2,3,4,5,6,7,8,9,'10R','10L',
    '10B','11R','11L','11B')) %>%
mutate(DEV3_DISTZONE= factor(DEV3_DISTZONE, levels = c(0:15),
  labels = c(0,1,2,3,4,5,6,7,8,9,'10R','10L',
    '10B','11R','11L','11B')) %>%

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mutate(DEV4_DISTZONE= factor(DEV4_DISTZONE, levels = c(0:15),
                           labels = c(0,1,2,3,4,5,6,7,8,9,'10R','10L',
                                       '10B','11R','11L','11B')))) %>%
mutate(DEV5_DISTZONE= factor(DEV5_DISTZONE, levels = c(0:15),
                           labels = c(0,1,2,3,4,5,6,7,8,9,'10R','10L',
                                       '10B','11R','11L','11B')))) %>%
mutate(DEV6_DISTZONE= factor(DEV6_DISTZONE, levels = c(0:15),
                           labels = c(0,1,2,3,4,5,6,7,8,9,'10R','10L',
                                       '10B','11R','11L','11B')))) %>%
mutate(ILIACDEV_END_R= factor(ILIACDEV_END_R, levels = c(0,1,2,3),
                           labels = c('None','Common',
                                       'External,Intended','External, Unintended')))) %>%
mutate(ILIACDEV_END_L= factor(ILIACDEV_END_L, levels = c(0,1,2,3),
                           labels = c('None','Common',
                                       'External,Intended','External, Unintended')))) %>%
mutate(BRANCH_STAGED=factor(BRANCH_STAGED,levels=c(0,1),labels=c('No','Yes')))) %>%
mutate(BRANCH_LSUB=factor(BRANCH_LSUB,levels=c(0,1),labels=c('No','Yes')))) %>%
mutate(BRANCH_CELIAC=factor(BRANCH_CELIAC,levels=c(0,1),labels=c('No','Yes')))) %>%
mutate(BRANCH_SMA=factor(BRANCH_SMA,levels=c(0,1),labels=c('No','Yes')))) %>%
mutate(BRANCH_RRENAL=factor(BRANCH_RRENAL,levels=c(0,1),labels=c('No','Yes')))) %>%
mutate(BRANCH_LRENAL=factor(BRANCH_LRENAL,levels=c(0,1),labels=c('No','Yes')))) %>%
mutate(BRANCH_INNO_POST=factor(BRANCH_INNO_POST,levels=c(1,2,3),
                           labels=c('Patent','Stenosis/Partial Coverage > 50%','Occluded')))) %>%
mutate(BRANCH_LSUB_VERTPAT=
  factor(BRANCH_LSUB_VERTPAT,levels=c(1:7),
        labels=c('Patent bilat','Patent bilat, L dominant','Patent bilat, R dominant',
                  'Occluded L, patent R','Occluded R, patent L','Occluded bilat',
                  'Not imaged')))) %>%
mutate(ANESTHESIA_GEN_TIMEEXT=factor(ANESTHESIA_GEN_TIMEEXT,levels=c(1,2,4,5),
                           labels=c('In OR','<12 hrs','12-24 hrs','>24 hrs')))) %>%
mutate(POSTOP_SPINALDRAIN=factor(POSTOP_SPINALDRAIN,levels=c(0,1,2,3),
                           labels=c('None','Pre-op','Post-op, prophylactic',
                                     'Post-op for spinal ischemia')))) %>%
mutate(R_CELIAC=factor(R_CELIAC,levels=c(0:9),
                           labels=c('Patent, no intervention','Chronically Occluded',
                                     'Purposely Occluded','De-branch','Stent Only','Chimney',
                                     'Fen/scallop Only','Stented-fen',
                                     'Fenestrated Stentgraft Branch (Branched TEVAR)',
                                     'Side-arm Stent-graft Branch')))) %>%

mutate(R_GRFTCONFIG=factor(R_GRFTCONFIG,levels=c(1,2,3),
                           labels=c('Standard','Plus Bare Stent','Branched/fenestrated')))) %>%
mutate(R_LT_RENAL=factor(R_LT_RENAL,levels=c(0:9),
                           labels=c('Patent, no intervention','Chronically Occluded',
                                     'Purposely Occluded','De-branch','Stent Only','Chimney',
                                     'Fen/scallop Only','Stented-fen',
                                     'Fenestrated Stentgraft Branch (Branched TEVAR)',
                                     'Side-arm Stent-graft Branch')))) %>%
mutate(R_PRATTZONE=factor(R_PRATTZONE)) %>%
mutate(R_RT_RENAL=factor(R_RT_RENAL,levels=c(0:9),
                           labels=c('Patent, no intervention','Chronically Occluded',
                                     'Purposely Occluded','De-branch','Stent Only','Chimney',
                                     'Fen/scallop Only','Stented-fen',

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        'Fenestrated Stentgraft Branch (Branched TEVAR)',
        'Side-arm Stent-graft Branch')) %>%
mutate(R_SMA=factor(R_SMA,levels=c(0:9),
        labels=c('Patent, no intervention','Chronically Occluded',
        'Purposely Occluded','De-branch','Stent Only','Chimney',
        'Fen/scallop Only','Stented-fen',
        'Fenestrated Stentgraft Branch (Branched TEVAR)',
        'Side-arm Stent-graft Branch')) %>%
mutate(R_SPINAL_DRAIN=factor(R_SPINAL_DRAIN,levels=c(0,1,2),
        labels=c('No Drain','Pre-op Drain','Post-op Drain'))))

# 0"0.None" 1"1.Scallop/Fen/Branch" 2"2.Occluded/Covered" 3"3.Chimney"
TEVAR<-TEVAR %>% mutate(lrenal = ifelse(BRANCH_LRENAL_TRT %in% c(0,6,7), 0,
        ifelse(BRANCH_LRENAL_TRT %in% c(9,10,11,12,13,14), 1,
        ifelse(BRANCH_LRENAL_TRT %in% c(1,2,3,4), 2,
        ifelse(BRANCH_LRENAL_TRT == 8, 3,NA))))),
        rrenal = ifelse(BRANCH_RRENAL_TRT %in% c(0,6,7), 0,
        ifelse(BRANCH_LRENAL_TRT %in% c(9,10,11,12,13,14), 1,
        ifelse(BRANCH_LRENAL_TRT %in% c(1,2,3,4), 2,
        ifelse(BRANCH_LRENAL_TRT == 8, 3,NA))))),
        sma = ifelse(BRANCH_SMA_TRT %in% c(0,6,7), 0,
        ifelse(BRANCH_SMA_TRT %in% c(9,10,11,12,13,14), 1,
        ifelse(BRANCH_SMA_TRT %in% c(1,2,3,4), 2,
        ifelse(BRANCH_SMA_TRT == 8,3,NA))))),
        celiac = ifelse(BRANCH_CELIAC_TRT %in% c(0,6,7), 0,
        ifelse(BRANCH_CELIAC_TRT %in% c(9,10,11,12,13,14), 1,
        ifelse(BRANCH_CELIAC_TRT %in% c(1,2,3,4), 2,
        ifelse(BRANCH_CELIAC_TRT == 8,3,NA))))),
        lsub = ifelse(BRANCH_LSUB_TRT %in% c(0,6,7), 0,
        ifelse(BRANCH_LSUB_TRT %in% c(9,10,11,12,13,14), 1,
        ifelse(BRANCH_LSUB_TRT %in% c(1,2,3,4), 2,
        ifelse(BRANCH_LSUB_TRT == 8,3,NA))))),
        )

# drop missing data
TEVAR = TEVAR %>% filter(lrenal %in% c(1,2,3)
        |rrenal %in% c(1,2,3)
        |celiac %in% c(1,2,3)
        |lsub %in% c(1,2,3)
        |sma %in% c(1,2,3))

## ----- variables cleaning, outcomes-----
TEVAR = TEVAR %>%
        mutate(DEAD=factor(DEAD)) %>%
        mutate(AORDEV_TECHSUCC=factor(AORDEV_TECHSUCC,levels=c(0,1),labels=c('No','Yes')) %>%
        mutate(CONVTOOPEN=factor(CONVTOOPEN,levels=c(0,1),labels=c('No','Yes')) %>%
        mutate(R_ENDOLEAK_AT_COMPLETION=
        factor(R_ENDOLEAK_AT_COMPLETION,levels=c(0:4),
        labels=c('No','Attachment Site (type I)','Branch (type II)',
        'Mid Graft (type III)','Indeterminate')) %>%
        mutate(BRANCH_LSUB_POST=factor(BRANCH_LSUB_POST,levels=c(1,2,3),

```

```

                                labels=c('Patent','Stenosis/Partial Coverage > 50%','Occluded')))) %>%
mutate(BRANCH_CELIAC_POST=factor(BRANCH_CELIAC_POST,levels=c(1,2,3),
                                labels=c('Patent','Stenosis/Partial Coverage > 50%','Occluded')))) %>%
mutate(BRANCH_SMA_POST=factor(BRANCH_SMA_POST,levels=c(1,2,3),
                                labels=c('Patent','Stenosis/Partial Coverage > 50%','Occluded')))) %>%
mutate(BRANCH_RRENAL_POST=factor(BRANCH_RRENAL_POST,levels=c(1,2,3),
                                labels=c('Patent','Stenosis/Partial Coverage > 50%','Occluded')))) %>%
mutate(BRANCH_LRENAL_POST=factor(BRANCH_LRENAL_POST,levels=c(1,2,3),
                                labels=c('Patent','Stenosis/Partial Coverage > 50%','Occluded')))) %>%
mutate(BRANCH_RCOMILI_POST=factor(BRANCH_RCOMILI_POST,levels=c(1,2,3),
                                labels=c('Patent','Stenosis/Partial Coverage > 50%','Occluded')))) %>%
mutate(BRANCH_LCOMILI_POST=factor(BRANCH_LCOMILI_POST,levels=c(1,2,3),
                                labels=c('Patent','Stenosis/Partial Coverage > 50%','Occluded')))) %>%
mutate(POSTOP_VASO=factor(POSTOP_VASO,levels=c(0,1,2,3),labels=c('No','Yes','Yes','Yes')) %>%
mutate(POSTOP_COMPLICATIONS=factor(POSTOP_COMPLICATIONS,levels=c(0,1),labels=c('No','Yes')) %>%
mutate(R_POSTOP_HEMATOMA=factor(R_POSTOP_HEMATOMA,levels=c(0,1,2,3,4),
                                labels=c('No','Minor','Transfusion','Thrombin injection',
                                           'Surgical Rx')))) %>%
mutate(R_POSTOP_SITEOCC=factor(R_POSTOP_SITEOCC,levels=c(0:5),
                                labels=c('No','Medical Rx','Interventional Rx','Surgical Rx',
                                           'Stenosis','Occlusion')))) %>%
mutate(POSTOP_MI=factor(POSTOP_MI,levels=c(0,1,2),
                                labels=c('No','Troponin only','EKG or clinical')))) %>%
mutate(POSTOP_DYSRHYTHMIA=factor(POSTOP_DYSRHYTHMIA,levels=c(0,1),labels=c('No','Yes')) %>%
mutate(POSTOP_CHF=factor(POSTOP_CHF,levels=c(0,1),labels=c('No','Yes')) %>%
mutate(POSTOP_RESPIRATORY=factor(POSTOP_RESPIRATORY,levels = c(0:3),
                                labels = c('No','Yes','Yes','Yes')) %>%
mutate(POSTOP_DIALYSIS=factor(POSTOP_DIALYSIS,levels = c(0:2),
                                labels = c('No','Yes','Yes')) %>%
mutate(POSTOP_ARMEMBO=factor(POSTOP_ARMEMBO,levels = c(0:5),
                                labels = c('No','Yes','Yes','Yes','Yes','Yes')) %>%
mutate(POSTOP_LEGEMBO=factor(POSTOP_LEGEMBO,levels = c(0:5),
                                labels = c('No','Yes','Yes','Yes','Yes','Yes')) %>%
mutate(POSTOP_LEGCOMPART=factor(POSTOP_LEGCOMPART,levels = c(0:4),
                                labels = c('No','Yes','Yes','Yes','Yes')) %>%
mutate(R_POSTOP_BOWELISCH=factor(R_POSTOP_BOWELISCH,levels = c(0:2),labels = c('No','Yes','Yes')) %>%
mutate(POSTOP_RENALISCH=factor(POSTOP_RENALISCH,levels = c(0:3),
                                labels = c('No','Yes','Yes','Yes')) %>%
mutate(R_POSTOP_SSI=factor(R_POSTOP_SSI,levels = c(0:4),labels = c('No','Yes','Yes','Yes','Yes')) %>%
mutate(POSTOP_SPINAL_ISCHEMIA=factor(POSTOP_SPINAL_ISCHEMIA,levels = c(0:2),
                                labels = c('No','Yes','Yes')) %>%
mutate(RETX=factor(RETX,levels = c(0:2),labels = c('No','Yes','Yes')) %>%
mutate(DC_STATUS=factor(DC_STATUS,levels = c(1:6),
                                labels = c('Home','Rehab Unit','Nursing Home',
                                           'Dead','Other Hospital','Homeless')) %>%
mutate(R_LE_ISCH=factor(R_LE_ISCH,levels = c(0,1),labels = c('No','Yes')) %>%
mutate(R_POSTOP_RENAL=factor(R_POSTOP_RENAL,levels = c(0:5),
                                labels = c('No','Yes','Yes','Yes','Yes','Yes')) %>%
mutate(R_RTOR=factor(R_RTOR,levels = c(0:5),labels = c('No','Yes','Yes','Yes','Yes','Yes'))))

## ----- variables cleaning, volume variables-----
TEVAR = TEVAR %>%

```

```

mutate(REGIONID=factor(REGIONID)) %>%
mutate(CENTERID=factor(CENTERID)) %>%
mutate(PHYSICIANID=factor(PHYSICIANID))

## ----- select only variables we need-----
FBVAR = TEVAR %>% select(
  # population of interest
  PRESENTATION,
  # Patient demographic and co-morbidities
  R_PREOP_AMBUL,AGE,AGECAT,GENDER,ETHNICITY,RACE,TRANSFER,PRIMARYINSURER,
  LIVINGSTATUS,PREOP_FUNCSTATUS,PRIOR_CVD,PRIOR_CAD,PRIOR_CHF,COPD,DIABETES,
  PREOP_DIALYSIS,HTN,PREOP_SMOKING,PRIOR_CABG,PRIOR_PCI,PRIOR_ANEURREP,STRESS,
  PREOP_CREAT,DC_ASA,DC_P2Y,DC_STATIN,R_CR_PRESENT,
  lrenal,rrenal,sma,celiac,lsub,
  #operative variables
  PRIOR_AORSURG,PRIOR_AORSURG_OPENLOC1,PRIOR_AORSURG_OPENLOC2,PRIOR_AORSURG_OPENLOC3,
  PRIOR_AORSURG_OPENLOC4,PRIOR_AORSURG_ENDOLOC1,PRIOR_AORSURG_ENDOLOC2,
  PRIOR_AORSURG_ENDOLOC3,PRIOR_AORSURG_ENDOLOC4,PATHOLOGY,PREOP_MAXAAADIA,URGENCY,
  PATHOLOGY_ANEURYSM_TYPE,PATHOLOGY_DISSECT_TYPE,PATHOLOGY_DISSECT_ONSET_DAYS,
  Genetic,
  PROXZONE_DISEASE,DISTZONE_DISEASE,ANESTHESIA,CONTRAST,EBL,FLUOROTIME,INTRAOP_PRBC,
  TOTALPROCTIME,IVUSTEE,ACCESS_R,ACCESS_L,LRGST_SHEATH_SIZE_R,
  LRGST_SHEATH_SIZE_L,ARMNECK_ACCESS,ARMNECK_ACCESS_LOC,AORDEV_NUM,
  AORDEV_CMED,AORDEV_TECHSUCC,CONVTOOPEN,R_ENDOLEAK_AT_COMPLETION,
  STAGEDAORTRT,DEV1_GTYPE,DEV2_GTYPE,DEV3_GTYPE,DEV1_PROXZONE,
  DEV2_PROXZONE,DEV3_PROXZONE,DEV4_PROXZONE,DEV5_PROXZONE,DEV6_PROXZONE,
  DEV1_DISTZONE,DEV2_DISTZONE,DEV3_DISTZONE,DEV4_DISTZONE,DEV5_DISTZONE,
  DEV6_DISTZONE,DEV1_GRAFTDET,ILIACDEV_END_R,ILIACDEV_END_L,BRANCH_STAGED,BRANCH_LSUB,
  BRANCH_CELIAC,BRANCH_SMA,BRANCH_RRENAL,BRANCH_LRENAL,
  BRANCH_INNO_POST,BRANCH_LSUB_POST,BRANCH_CELIAC_POST,BRANCH_SMA_POST,
  BRANCH_RRENAL_POST,BRANCH_LRENAL_POST,BRANCH_RCOMILI_POST,BRANCH_LCOMILI_POST,
  BRANCH_LSUB_VERTPAT,ANESTHESIA_GEN_TIMEEXT,ICUSTAY,POSTOP_PRBC,POSTOP_SPINALDRAIN,
  POSTOP_VASO,POSTOP_HIGHCREAT,POSTOP_COMPLICATIONS,R_POSTOP_HEMATOMA,R_POSTOP_SITEOCC,
  POSTOP_MI,POSTOP_DYSRHYTHMIA,POSTOP_CHF,POSTOP_CEREBROX,POSTOP_RESPIRATORY,
  POSTOP_DIALYSIS,POSTOP_ARMEMBO,POSTOP_LEGEMBO,POSTOP_LEGCOMPART,POSTOP_INTISCH,
  R_POSTOP_BOWELISCH,POSTOP_RENALISCH,R_POSTOP_SSI,POSTOP_SPINAL_ISCHEMIA,RETX,DC_STATUS,
  DC_ASA,DC_P2Y,DC_STATIN,R_CELIAC,R_CR_PRESENT,R_DISTATTZONE,R_GDPROXIMAL,R_GRFTCONFIG,
  R_LE_ISCH,R_LT_RENAL,R_PRATTZONE,R_POSTOP_RENAL,R_RT_RENAL,R_RTOR,R_SMA,R_SPINAL_DRAIN,
  # outcomes
  DEAD,PROC_SURVIVALDAYS,TOTAL_LOS,POSTOP_LOS,AORDEV_TECHSUCC,CONVTOOPEN,
  R_ENDOLEAK_AT_COMPLETION,BRANCH_LSUB_POST,BRANCH_CELIAC_POST,BRANCH_SMA_POST,
  BRANCH_RRENAL_POST,BRANCH_LRENAL_POST,BRANCH_RCOMILI_POST,BRANCH_LCOMILI_POST,ICUSTAY,
  POSTOP_PRBC,POSTOP_VASO,POSTOP_HIGHCREAT,POSTOP_COMPLICATIONS,R_POSTOP_HEMATOMA,
  R_POSTOP_SITEOCC,POSTOP_MI,POSTOP_DYSRHYTHMIA,POSTOP_CHF,POSTOP_CEREBROX,POSTOP_RESPIRATORY,
  POSTOP_DIALYSIS,POSTOP_ARMEMBO,POSTOP_LEGEMBO,POSTOP_LEGCOMPART,POSTOP_INTISCH,
  R_POSTOP_BOWELISCH,POSTOP_RENALISCH,R_POSTOP_SSI,POSTOP_SPINAL_ISCHEMIA,RETX,
  DC_STATUS,R_LE_ISCH,R_POSTOP_RENAL,R_RTOR,
  # clustering
  REGIONID,CENTERID,PHYSICIANID
)

```

```
## ----- variables labels-----  
#var.labels = c(AGE="Age (years)", AGECAT="Age (category)")  
#label(FBVAR) = as.list(var.labels[match(names(FBVAR), names(var.labels))])  
  
## ----- store as new dataset 'FBVAR' to ensure easier access for modelling-----  
write.csv(FBVAR,path_lily[5])  
TEVAR %>%  
  filter(! is.na(TEVAR$R_CR_PRESENT)) %>%  
  select(R_CR_PRESENT) %>%table()
```