

# Logistic Regression Models with GEE for the Secondary Outcomes in the VQI FBVAR Dataset

Jennifer Ci, Thu Vu, Lily Hanyi Wang

## Variables to adjust for

*We used a correlation matrix to report the correlations between variables statistically. We also discussed with our collaborator on the choice of variables to adjust for. Here we did not report the correlation matrix.*

In the unadjusted models, we only study the differences in the secondary outcomes:

- comparing PRESENTATION

In the adjusted models, we also:

- cluster on CENTERID
- adjust for AGE CAT, GENDER, PREOP\_SMOKING, PRIOR\_AORSURG, PRIOR\_CHF, PREOP\_DIALYSIS
- adjust for PATHOLOGY, extent
- secondary outcomes: POSTOP\_CEREBROSX, POSTOP\_SPINAL\_ISCHEMIA, POSTOP\_DIALYSIS, POSTOP\_LOS, POSTOP\_COMPLICATIONS, POSTOP\_LEGEMBO, POSTOP\_RESPIRATORY, RETX\_R\_RTOR, BRANCH\_POST, TOTAL\_LOS, ICUSTAY, POSTOP\_INTISCH, POSTOP\_GFR

We use logistic regression with Generalized Estimating Equations to study the secondary outcomes, which are all categorical variables.

*To fit the models, we merge groups for the **extent**: merge “Juxtarenal AAA” with “Type 4 TAAA”; “Type 1 TAAA”, “Type 2 TAAA”, “Type 3 TAAA”, with “Type 5 TAAA”. Now **extent** is a binary variable, Juxtarenal or not.*

**TOTAL\_LOS: Length of stay in days between admission date and discharge date**

TOTAL_LOS Length of Stay in days			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	5.14	4.11, 6.43	<b>&lt;0.001</b>

<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	2.99, 4.81	<b>&lt;0.001</b>
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	0.47
70-79	2.16	1.02, 4.55	<b>0.043</b>
GENDER			
female	—	—	
male	0.62	0.51, 0.75	<b>&lt;0.001</b>
PREOP_SMOKING			
No	—	—	
Yes	0.99	0.76, 1.29	0.94
PRIOR_AORSURG			
Both	—	—	
Endo	1.59	0.93, 2.71	0.091
None	1.08	0.65, 1.80	0.76
Open	1.43	0.83, 2.47	0.20
PRIOR_CHF			
No	—	—	
Yes	1.51	1.21, 1.89	<b>&lt;0.001</b>

<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
PREOP_DIALYSIS			
No	—	—	
Yes	1.87	1.10, 3.16	<b>0.020</b>
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.83	1.16, 2.87	<b>0.009</b>
Dissection	1.77	1.02, 3.06	<b>0.041</b>
PAU/IMH extent	1.94	0.90, 4.20	0.093
Juxtarenal	—	—	
No	2.10	1.72, 2.57	<b>&lt;0.001</b>

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

## ICUSTAY: ICU Stay

ICU Stay			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.11	2.43, 3.97	<b>&lt;0.001</b>

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

ICU Stay			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.08	1.59, 2.71	<b>&lt;0.001</b>
AGECAT			
<50	—	—	
>79	1.31	0.51, 3.37	0.58
50-59	1.30	0.47, 3.58	0.62
60-69	0.96	0.38, 2.42	0.93
70-79	1.28	0.50, 3.25	0.61
GENDER			
female	—	—	
male	0.60	0.49, 0.74	<b>&lt;0.001</b>
PREOP_SMOKING			
No	—	—	
Yes	1.02	0.75, 1.38	0.92
PRIOR_AORSURG			
Both	—	—	
Endo	1.36	0.77, 2.41	0.29
None	0.75	0.43, 1.32	0.32
Open	1.31	0.72, 2.38	0.38
PRIOR_CHF			
No	—	—	
Yes	1.21	0.93, 1.57	0.17
PREOP_DIALYSIS			

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

Characteristic	ICU Stay		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
No	—	—	
Yes	1.84	1.07, 3.19	<b>0.028</b>
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.35	0.81, 2.25	0.25
Dissection	1.72	0.93, 3.19	0.084
PAU/IMH	1.25	0.50, 3.12	0.63
extent			
Juxtarenal	—	—	
No	2.23	1.78, 2.80	<b>&lt;0.001</b>

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

## Creatinine and GFR

Use POSTOP\_HIGHCREAT, Highest Creatinine, to generate corresponding GFR values.

GFRFIFTY: 1 - GFR reduction is  $\geq 50\%$ ; 0 - GFR reduction is  $< 50\%$

Also adjust for PREOP\_GFR\_CAT and TREATED\_RENALS

GFR reduction			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.57	1.08, 2.29	<b>0.018</b>

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

GFR reduction			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.35	0.90, 2.02	0.15
AGECAT			
<50	—	—	
>79	0.72	0.15, 3.43	0.68
50-59	1.33	0.27, 6.48	0.73
60-69	0.91	0.20, 4.24	0.91
70-79	0.82	0.17, 3.87	0.81
GENDER			
female	—	—	
male	0.67	0.50, 0.89	<b>0.006</b>
PREOP_SMOKING			
No	—	—	
Yes	1.27	0.81, 2.00	0.29
PRIOR_AORSURG			
Both	—	—	
Endo	1.36	0.52, 3.53	0.53
None	1.04	0.41, 2.61	0.94
Open	0.99	0.36, 2.76	0.99
PRIOR_CHF			

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

Characteristic	GFR reduction		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
No	—	—	
Yes	1.08	0.76, 1.54	0.66
PREOP_GFR_CAT			
End-stage renal disease	—	—	
Mildly decreased	1.83	0.23, 14.4	0.56
Mildly to severely decreased	2.51	0.32, 19.7	0.38
Normal or increased	2.12	0.27, 16.9	0.48
Severely decreased	2.08	0.24, 18.3	0.51
TREATED_RENALS			
No	—	—	
Yes	0.54	0.39, 0.73	<b>&lt;0.001</b>
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.33	0.10, 1.09	0.068
Dissection	0.85	0.31, 2.33	0.76
PAU/IMH	1.21	0.35, 4.23	0.77
extent			
Juxtarenal	—	—	
No	1.12	0.82, 1.54	0.47

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

## POSTOP\_INTISCH: Post-op Intestinal Ischemia

	Intestinal Ischemia		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.13	0.56, 2.26	0.74

<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	1.07	0.50, 2.30	0.87
AGECAT			
<50	—	—	
>79	0.41	0.07, 2.37	0.32
50-59	0.49	0.06, 4.15	0.51
60-69	0.36	0.06, 2.15	0.26
70-79	0.45	0.08, 2.48	0.36
GENDER			
female	—	—	
male	0.62	0.37, 1.03	0.063
PREOP_SMOKING			
No	—	—	
Yes	0.86	0.43, 1.70	0.66
PRIOR_AORSURG			
Both	—	—	
Endo	1.94	0.23, 16.6	0.55
None	1.84	0.22, 15.8	0.58
Open	1.62	0.16, 15.9	0.68
PRIOR_CHF			
No	—	—	
Yes	1.05	0.53, 2.08	0.89
PREOP_DIALYSIS			

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



Intestinal Ischemia			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
No	—	—	
Yes	0.69	0.09, 5.12	0.71
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.48	0.06, 3.66	0.48
Dissection	0.71	0.14, 3.71	0.69
PAU/IMH	1.28	0.16, 10.6	0.82
extent			
Juxtarenal	—	—	
No	0.94	0.53, 1.69	0.85

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

## POSTOP\_CEREBROSX: Post-op Cerebrovascular Stroke:

Also account for ARMNECK\_ACCESS

Post-op Cerebrovascular Stroke			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.42	1.83, 6.38	<b>&lt;0.001</b>

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

Post-op Cerebrovascular Stroke			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.81	0.91, 3.60	0.091
AGECAT			
<50	—	—	
>79	0.51	0.08, 3.29	0.48
50-59	0.79	0.13, 4.95	0.81
60-69	0.23	0.04, 1.45	0.12
70-79	0.62	0.11, 3.46	0.58
GENDER			
female	—	—	
male	0.49	0.26, 0.90	<b>0.023</b>
PREOP_SMOKING			
No	—	—	
Yes	0.73	0.34, 1.58	0.43
PRIOR_AORSURG			
Both	—	—	
Endo	1.20	0.24, 6.05	0.83
None	1.39	0.28, 6.92	0.69
Open	0.95	0.15, 5.88	0.95
PRIOR_CHF			
No	—	—	
Yes	2.14	1.07, 4.31	<b>0.032</b>

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

Post-op Cerebrovascular Stroke			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PREOP_DIALYSIS			
No	—	—	
Yes	1.97	0.46, 8.55	0.36
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	3.44	1.03, 11.6	<b>0.045</b>
Dissection	2.56	0.57, 11.5	0.22
PAU/IMH	1.46	0.21, 10.2	0.70
extent			
Juxtarenal	—	—	
No	1.44	0.68, 3.04	0.34
ARMNECK_ACCESS			
No	—	—	
Yes	2.31	1.26, 4.25	<b>0.007</b>

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

## POSTOP\_SPINAL\_ISCHEMIA: Post-op Spinal Ischemia

Also account for POSTOP\_SPINALDRAIN and OCCLUDED\_CELIAC

Post-op Spinal Ischemia			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.56	1.70, 3.86	<b>&lt;0.001</b>

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

Post-op Spinal Ischemia			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.61	1.00, 2.60	<b>0.050</b>
AGECAT			
<50	—	—	
>79	2.19	0.27, 17.7	0.46
50-59	1.99	0.23, 17.3	0.53
60-69	1.63	0.21, 13.0	0.64
70-79	2.13	0.27, 16.6	0.47
GENDER			
female	—	—	
male	0.88	0.58, 1.36	0.58
PREOP_SMOKING			
No	—	—	
Yes	1.22	0.64, 2.32	0.55
PRIOR_AORSURG			
Both	—	—	
Endo	1.23	0.52, 2.95	0.64
None	1.46	0.63, 3.40	0.37
Open	1.47	0.60, 3.63	0.40
PRIOR_CHF			
No	—	—	
Yes	1.06	0.61, 1.83	0.84

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

Characteristic	Post-op Spinal Ischemia		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PREOP_DIALYSIS			
No	—	—	
Yes	1.16	0.48, 2.83	0.75
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.98	0.43, 2.25	0.96
Dissection	1.08	0.36, 3.26	0.89
PAU/IMH extent	0.44	0.05, 3.63	0.45
Juxtarenal	—	—	
No	1.01	0.65, 1.57	0.97
POSTOP_SPINALDRAIN			
No	—	—	
Yes	19.0	11.1, 32.6	<b>&lt;0.001</b>
OCCLUDED_CELIAC			
FALSE	—	—	
TRUE	1.57	0.83, 2.99	0.17

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

POSTOP\_LOS: Length of stay in days between surgery date and discharge date

	Length of stay in days between surgery date and discharge date		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.39	2.69, 4.29	<b>&lt;0.001</b>

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

	Length of stay in days between surgery date and discharge date		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.46	1.91, 3.17	<b>&lt;0.001</b>
AGECAT			
<50	—	—	
>79	2.28	0.88, 5.88	0.089
50-59	1.93	0.72, 5.21	0.19
60-69	1.55	0.60, 3.96	0.36
70-79	2.49	0.98, 6.35	0.055
GENDER			
female	—	—	
male	0.62	0.50, 0.75	<b>&lt;0.001</b>
PREOP_SMOKING			
No	—	—	
Yes	0.97	0.74, 1.28	0.82
PRIOR_AORSURG			
Both	—	—	
Endo	1.26	0.73, 2.19	0.41
None	0.96	0.57, 1.62	0.88
Open	1.36	0.76, 2.41	0.30
PRIOR_CHF			
No	—	—	
Yes	1.41	1.11, 1.80	<b>0.005</b>

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

Characteristic	Length of stay in days between surgery date and discharge date		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PREOP_DIALYSIS			
No	—	—	
Yes	1.74	1.00, 3.00	<b>0.048</b>
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.59	0.96, 2.63	0.069
Dissection	1.96	1.11, 3.45	<b>0.020</b>
PAU/IMH extent	1.82	0.90, 3.67	0.094
Juxtarenal	—	—	
No	1.97	1.60, 2.44	<b>&lt;0.001</b>

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

# POSTOP\_COMPLICATIONS: Any Complications Post-op

	Any Complications Post-op		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.74	1.37, 2.21	<b>&lt;0.001</b>

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

	Any Complications Post-op		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.44	1.12, 1.86	<b>0.004</b>
AGECAT			
<50	—	—	
>79	1.17	0.46, 2.97	0.74
50-59	1.29	0.49, 3.42	0.61
60-69	0.97	0.39, 2.41	0.94
70-79	1.32	0.53, 3.31	0.55
GENDER			
female	—	—	
male	0.65	0.54, 0.78	<b>&lt;0.001</b>
PREOP_SMOKING			
No	—	—	
Yes	1.01	0.79, 1.31	0.91
PRIOR_AORSURG			
Both	—	—	
Endo	0.95	0.56, 1.60	0.84
None	1.00	0.60, 1.65	0.99
Open	1.41	0.82, 2.42	0.21
PRIOR_CHF			
No	—	—	
Yes	1.28	1.04, 1.58	<b>0.018</b>
PREOP_DIALYSIS			

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



Characteristic	Any Complications Post-op		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
No	—	—	
Yes	1.25	0.73, 2.15	0.41
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.32	0.82, 2.12	0.26
Dissection	0.94	0.51, 1.73	0.84
PAU/IMH	0.77	0.35, 1.70	0.52
extent			
Juxtarenal	—	—	
No	1.47	1.21, 1.78	<b>&lt;0.001</b>

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

# RETX\_R\_RTOR: Re-intervention

	Re-intervention		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.86	1.33, 2.62	<b>&lt;0.001</b>

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

	Re-intervention		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.48	1.04, 2.09	<b>0.029</b>
AGECAT			
<50	—	—	
>79	0.95	0.28, 3.27	0.93
50-59	1.41	0.38, 5.19	0.60
60-69	0.70	0.20, 2.44	0.58
70-79	0.94	0.28, 3.14	0.92
GENDER			
female	—	—	
male	0.59	0.45, 0.78	<b>&lt;0.001</b>
PREOP_SMOKING			
No	—	—	
Yes	1.29	0.81, 2.05	0.28
PRIOR_AORSURG			
Both	—	—	
Endo	0.95	0.43, 2.09	0.90
None	1.01	0.47, 2.16	0.99
Open	0.67	0.27, 1.63	0.37
PRIOR_CHF			
No	—	—	
Yes	1.21	0.86, 1.72	0.27
PREOP_DIALYSIS			

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

Characteristic	Re-intervention		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
No	—	—	
Yes	0.75	0.31, 1.81	0.52
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	1.68	0.88, 3.19	0.12
Dissection	0.64	0.23, 1.78	0.39
PAU/IMH	1.77	0.70, 4.47	0.23
extent			
Juxtarenal	—	—	
No	1.56	1.15, 2.12	<b>0.004</b>

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

# BRANCH\_POST: Post-treatment Status of All Branches

Post-treatment Status of All Branches			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.28	1.78, 2.91	<b>&lt;0.001</b>

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

Post-treatment Status of All Branches			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.64	1.24, 2.16	<b>&lt;0.001</b>
AGECAT			
<50	—	—	
>79	0.78	0.32, 1.90	0.58
50-59	1.00	0.39, 2.58	>0.99
60-69	0.95	0.40, 2.27	0.91
70-79	0.90	0.38, 2.14	0.81
GENDER			
female	—	—	
male	0.47	0.39, 0.58	<b>&lt;0.001</b>
PREOP_SMOKING			
No	—	—	
Yes	1.08	0.79, 1.48	0.63
PRIOR_AORSURG			
Both	—	—	
Endo	0.79	0.46, 1.35	0.38
None	0.52	0.31, 0.86	<b>0.011</b>
Open	0.69	0.39, 1.23	0.21
PRIOR_CHF			
No	—	—	
Yes	1.43	1.12, 1.82	<b>0.004</b>

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

Characteristic	Post-treatment Status of All Branches		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PREOP_DIALYSIS			
No	—	—	
Yes	7.90	4.70, 13.3	<b>&lt;0.001</b>
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.77	0.43, 1.37	0.37
Dissection	1.57	0.90, 2.74	0.12
PAU/IMH extent	0.45	0.16, 1.24	0.12
Juxtarenal	—	—	
No	1.56	1.25, 1.93	<b>&lt;0.001</b>

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

For the following variables, we need to merge age group “<50” and “50-59” so that there’s no 0 patients on one level.

## POSTOP\_DIALYSIS: Post-op Dialysis

Also account for OCCLUDED\_RENAL

	Post-op Dialysis		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.42	1.44, 4.07	<b>&lt;0.001</b>

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

	Post-op Dialysis		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.78	1.01, 3.13	<b>0.047</b>
AGECAT			
<59	—	—	
60-69	0.53	0.22, 1.27	0.16
70-79	0.40	0.17, 0.97	<b>0.042</b>
>79	0.39	0.15, 1.01	0.053
GENDER			
female	—	—	
male	0.62	0.38, 1.00	<b>0.049</b>
PREOP_SMOKING			
No	—	—	
Yes	1.31	0.60, 2.86	0.49
PRIOR_AORSURG			
Both	—	—	
Endo	1.04	0.26, 4.10	0.95
None	0.82	0.22, 3.04	0.76
Open	0.58	0.12, 2.80	0.50
PRIOR_CHF			
No	—	—	

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

Characteristic	Post-op Dialysis		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
Yes	0.74	0.37, 1.45	0.38
PREOP_DIALYSIS			
No	—	—	
Yes	0.00	0.00, 0.00	<b>&lt;0.001</b>
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.33	0.04, 2.96	0.32
Dissection	1.74	0.52, 5.82	0.37
PAU/IMH	2.33	0.51, 10.6	0.27
extent			
Juxtarenal	—	—	
No	0.99	0.58, 1.70	0.98
OCCLUDED_RENAL			
FALSE	—	—	
TRUE	4.82	2.33, 9.95	<b>&lt;0.001</b>

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

# POSTOP\_LEGEMBO: Leg Ischemia/Embol

	Leg Ischemia/Embol		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.97	1.13, 3.46	<b>0.017</b>

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

	Leg Ischemia/Embol		
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.74	0.94, 3.22	0.078
AGECAT			
<59	—	—	
60-69	0.80	0.28, 2.27	0.68
70-79	0.80	0.29, 2.23	0.67
>79	0.67	0.23, 2.00	0.48
GENDER			
female	—	—	
male	0.43	0.28, 0.67	<b>&lt;0.001</b>
PREOP_SMOKING			
No	—	—	
Yes	2.61	0.98, 6.96	0.056
PRIOR_AORSURG			
Both	—	—	
Endo	139,944,960,652,840		
None	162,086,767,451,715		
Open	288,216,346,513,340		
PRIOR_CHF			
No	—	—	
Yes	0.85	0.44, 1.64	0.63
PREOP_DIALYSIS			
No	—	—	

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



Characteristic	Leg Ischemia/Embol		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
Yes	0.58	0.08, 4.19	0.59
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.87	0.20, 3.86	0.86
Dissection	0.60	0.08, 4.59	0.62
PAU/IMH	2.28	0.49, 10.6	0.29
extent			
Juxtarenal	—	—	
No	1.01	0.61, 1.66	0.98

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

## POSTOP\_RESPIRATORY: Post-op Respiratory

Post-op Respiratory			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.65	1.87, 3.75	<b>&lt;0.001</b>

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

Post-op Respiratory			
Characteristic	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.17	1.47, 3.21	<b>&lt;0.001</b>
AGECAT			
<59	—	—	
60-69	0.94	0.44, 1.98	0.86
70-79	1.06	0.50, 2.25	0.87
>79	0.94	0.42, 2.06	0.87
GENDER			
female	—	—	
male	0.66	0.47, 0.92	<b>0.014</b>
PREOP_SMOKING			
No	—	—	
Yes	1.08	0.68, 1.72	0.75
PRIOR_AORSURG			
Both	—	—	
Endo	0.59	0.27, 1.30	0.19
None	0.55	0.26, 1.16	0.11
Open	0.67	0.28, 1.60	0.36
PRIOR_CHF			
No	—	—	
Yes	1.23	0.82, 1.84	0.31
PREOP_DIALYSIS			
No	—	—	

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

Characteristic	Post-op Respiratory		
	OR <sup>1</sup>	95% CI <sup>1</sup>	p-value
Yes	0.78	0.27, 2.23	0.64
PATHOLOGY			
Aneurysm	—	—	
Aneurysm from dissection	0.60	0.23, 1.55	0.29
Dissection	0.83	0.29, 2.38	0.73
PAU/IMH	1.14	0.33, 4.02	0.83
extent			
Juxtarenal	—	—	
No	1.74	1.25, 2.41	<b>&lt;0.001</b>

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

### POSTOP\_PRBC: Transfusion # Units PRBC

We don't include this variable in the final report.

## Code Appendix

```
knitr::opts_chunk$set(echo = FALSE,message = FALSE,warning = FALSE)
library(tidyverse)
library(table1)
library(dplyr)
library(geepack)
library(gtsummary)
library(broom.mixed)
## ----- working directories for Lily -----
wd_lily = '/Users/hanyiwang/Desktop/Comparative-analysis-of-treatments-of-CAA'
path_lily = c("../data/TEVAR_PROC.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")

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

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

# ### ----- Correlation matrix -----
# 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)
## ----- modify dataset -----
TEVAR_PROC = TEVAR_PROC %>%
  mutate(extent = factor(extent, levels = c("Juxtarenal AAA", "Type 1 TAAA", "Type 2 TAAA", "Type 3 TAAA", "Type 4 TAAA")))

mutate(GFRCHANGE = (PREOP_GFR-POSTOP_GFR)/PREOP_GFR) %>%
mutate(GFRFIFTY = (ifelse(GFRCHANGE<0.5, "<50%",
                          ifelse(GFRCHANGE>=0.5, ">=50%", NA)))) %>%
mutate(TREATED_RENALS = (ifelse(NUM_TREATED_RENALS<1, "No",
                                ifelse(NUM_TREATED_RENALS>=1, "Yes", NA)))) %>%

mutate(TOTAL_LOS = case_when(TOTAL_LOS>7 ~ '>7',
                             TOTAL_LOS<=7 ~ '<=7')) %>%
mutate(ICUSTAY = case_when(ICUSTAY>4 ~ '>4',
                           ICUSTAY<=4 ~ '<=4')) %>%
mutate(POSTOP_LOS = case_when(POSTOP_LOS>7 ~ '>7',
                              POSTOP_LOS<=7 ~ '<=7')) %>%

mutate(TOTAL_LOS = as.numeric(TOTAL_LOS != "<=7") ) %>%
mutate(ICUSTAY = as.numeric(ICUSTAY != "<=4") ) %>%
mutate(POSTOP_LOS = as.numeric(POSTOP_LOS != "<=7") ) %>%

mutate(POSTOP_INTISCH = as.numeric(POSTOP_INTISCH == "Yes")) %>%
mutate(POSTOP_CEREBROSX = as.numeric(POSTOP_CEREBROSX == "Yes")) %>%
mutate(POSTOP_SPINAL_ISCHEMIA = as.numeric(POSTOP_SPINAL_ISCHEMIA == "Yes")) %>%
mutate(POSTOP_DIALYSIS = as.numeric(POSTOP_DIALYSIS == "Yes")) %>%
mutate(POSTOP_COMPLICATIONS = as.numeric(POSTOP_COMPLICATIONS == "Yes")) %>%
mutate(POSTOP_LEGEMBO = as.numeric(POSTOP_LEGEMBO == "Yes")) %>%
mutate(POSTOP_RESPIRATORY = as.numeric(POSTOP_RESPIRATORY == "Yes")) %>%
mutate(RETX_R_RTOR = as.numeric(RETX_R_RTOR == "Yes")) %>%
mutate(BRANCH_POST = as.numeric(BRANCH_POST == "Yes")) %>%
mutate(GFRFIFTY = as.numeric(GFRFIFTY != "<50%") )

# remove missing values
TEVAR_PROC = subset(TEVAR_PROC, !is.na(extent))

## ----- change class of variables -----
names <- c('CENTERID', 'AGECAT', 'GENDER', 'PREOP_SMOKING', 'PRIOR_AORSURG', 'PRIOR_CHF', 'PREOP_DIALYSIS')
TEVAR_PROC[,names] <- lapply(TEVAR_PROC[,names] , factor)

## ----- Length of stay in days between admission date and discharge date -----

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

## ----- unadjusted -----
LOS1<-geeglm(TOTAL_LOS~ PRESENTATION, data=TEVAR_PROC, family=binomial(link="logit"), id = CENTERID, covariates=AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS)

t1<-LOS1 %>%
tbl_regression(exponentiate=TRUE,
```

```

        tidy_fun = broom.mixed::tidy,
        pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
bold_p(t = 0.05)

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

## ----- adjusted -----
LOS2<-geeglm(TOTAL_LOS ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+
, data=TEVAR_PROC, family=binomial(link="logit"),id = CENTERID, corstr = "independence")
t2<-LOS2 %>%
tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner = "**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()
## ----- ICU Stay -----

## ----- unadjusted -----
ICU1<-geeglm(ICUSTAY~ PRESENTATION, data=TEVAR_PROC, 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,
pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
bold_p(t = 0.05)

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

## ----- adjusted -----
ICU2<-geeglm(ICUSTAY ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+
, family=binomial(link="logit"), data=TEVAR_PROC, id = CENTERID, corstr = "independence")
t2<- ICU2 %>%tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
bold_p(t = 0.05)

```

```

tbl_merge(tbls = list(t2),tab_spanner = "**ICU Stay**")%>%as_flex_table()
# ## ----- Creatinine -----
# ## ----- unadjusted -----
# POSTOP_HIGHCREAT1<-geeglm(POSTOP_HIGHCREAT ~ PRESENTATION, data=TEVAR_PROC,id = CENTERID, corstr = "i
#
# t1<-POSTOP_HIGHCREAT1 %>%
#   tbl_regression(tidy_fun = broom.mixed::tidy,
#                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
#   bold_p(t = 0.05)
#
# tbl_merge(tbls = list(t1),tab_spanner = "**Highest Creatinine**")%>%as_flex_table()
#
# ## ----- adjusted -----
# POSTOP_HIGHCREAT2<-geeglm(POSTOP_HIGHCREAT ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+P
#   , data=TEVAR_PROC, id = CENTERID, corstr = "independence")
# t2<- POSTOP_HIGHCREAT2 %>%
#   tbl_regression(tidy_fun = broom.mixed::tidy,
#                 pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
#   bold_p(t = 0.05)
# tbl_merge(tbls = list(t2),tab_spanner = "**Highest Creatinine**")%>%as_flex_table()

## ----- GFR reduction -----
#table(PROC$GFRFIFTY)

## ----- unadjusted -----
GFR1<-geeglm(GFRFIFTY~ PRESENTATION, data=TEVAR_PROC, family=binomial(link="logit"), id = CENTERID, cor
t1<-GFR1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

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

## ----- adjusted -----
GFR2<-geeglm(GFRFIFTY ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+PREOP_GFR_CAT+
  , family=binomial(link="logit"), data=TEVAR_PROC, id = CENTERID, corstr = "independence")
t2<- GFR2 %>%
  tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
                pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

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

## ----- Post-op Intestinal Ischemia -----
## ----- unadjusted -----
POSTOP_INTISCH1<-geeglm(POSTOP_INTISCH ~ PRESENTATION, family=binomial(link="logit"), data=TEVAR_PROC,i
t1<-POSTOP_INTISCH1 %>%tbl_regression(exponentiate=TRUE,tidy_fun = broom.mixed::tidy,
  pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

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

```

```

## ----- adjusted -----
POSTOP_INTISCH2<-geeglm(POSTOP_INTISCH ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_C
, data=TEVAR_PROC,family=binomial(link="logit"), id = CENTERID, corstr = "independe
t2<- POSTOP_INTISCH2 %>%tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)
tbl_merge(tbls = list(t2), tab_spanner = "**Intestinal Ischemia**")%>%as_flex_table()

# model<-geeglm(as.numeric(POSTOP_DIALYSIS)~PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_C
# 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
## ----- Post-op Cerebrovascular Stroke -----
## ----- unadjusted -----
POSTOP_CEREBROX1 = geeglm(POSTOP_CEREBROX ~ PRESENTATION,
data=TEVAR_PROC, family=binomial(link="logit"),
id = CENTERID, corstr = "independence")

t1 = POSTOP_CEREBROX1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1), tab_spanner = "**Post-op Cerebrovascular Stroke**")%>%as_flex_table()

## ----- adjusted -----
POSTOP_CEREBROX2 = geeglm(POSTOP_CEREBROX ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent+ARMNECK_ACCESS,
family=binomial(link="logit"), data=TEVAR_PROC,
id = CENTERID, corstr = "independence")

t2 = POSTOP_CEREBROX2 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2), tab_spanner = "**Post-op Cerebrovascular Stroke**")%>%as_flex_table()
## ----- Post-op Spinal Ischemia -----
## ----- unadjusted -----
POSTOP_SPINAL_ISCHEMIA1 = geeglm(POSTOP_SPINAL_ISCHEMIA ~ PRESENTATION,
data=TEVAR_PROC,family=binomial(link="logit"),
id = CENTERID, corstr = "independence")

t1 = POSTOP_SPINAL_ISCHEMIA1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

```



```

tbl_merge(tbls = list(t1),tab_spanner = "**Post-op Spinal Ischemia**")%>%as_flex_table()

## ----- adjusted -----
POSTOP_SPINAL_ISCHEMIA2 = geeglm(POSTOP_SPINAL_ISCHEMIA ~ PRESENTATION+AGECAT+GENDER+
                                PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+
                                PREOP_DIALYSIS+PATHOLOGY+extent+
                                POSTOP_SPINALDRAIN+OCCLUDED_CELIAC,
                                family=binomial(link="logit"), data=TEVAR_PROC,
                                id = CENTERID, corstr = "independence")

t2 = POSTOP_SPINAL_ISCHEMIA2 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner = "**Post-op Spinal Ischemia**")%>%as_flex_table()

## ----- Length of stay in days between surgery date and discharge date -----
## ----- unadjusted -----
POSTOP_LOS1 = geeglm(POSTOP_LOS~ PRESENTATION,
                    data=TEVAR_PROC, family=binomial(link="logit"),
                    id = CENTERID, corstr = "independence")
# summary(POSTOP_LOS1)

t1 = POSTOP_LOS1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner = "**Length of stay in days between surgery date and discharge date**")%>%as_flex_table()

## ----- adjusted -----
POSTOP_LOS2 = geeglm(POSTOP_LOS ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
                    PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
                    family=binomial(link="logit"), data=TEVAR_PROC,
                    id = CENTERID, corstr = "independence")

t2 = POSTOP_LOS2 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner = "**Length of stay in days between surgery date and discharge date**")%>%as_flex_table()

## ----- Any Complications Post-op -----
## ----- unadjusted -----
POSTOP_COMPLICATIONS1 = geeglm(POSTOP_COMPLICATIONS~ PRESENTATION,
                              data=TEVAR_PROC, family=binomial(link="logit"),
                              id = CENTERID, corstr = "independence")

t1 = POSTOP_COMPLICATIONS1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,

```

```

        pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner = "**Any Complications Post-op**")%>%as_flex_table()

## ----- adjusted -----
POSTOP_COMPLICATIONS2 = geeglm(POSTOP_COMPLICATIONS ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
    PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
    family=binomial(link="logit"), data=TEVAR_PROC,
    id = CENTERID, corstr = "independence")

t2 = POSTOP_COMPLICATIONS2 %>%
tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
    pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner = "**Any Complications Post-op**")%>%as_flex_table()
## ----- Re-intervention -----
## ----- unadjusted -----
RETX_R_RTOR1 = geeglm(RETX_R_RTOR~ PRESENTATION,
    data=TEVAR_PROC, family=binomial(link="logit"),
    id = CENTERID, corstr = "independence")
# summary(POSTOP_LOS1)

t1 = RETX_R_RTOR1 %>%
tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
    pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
bold_p(t = 0.05)

tbl_merge(tbls = list(t1),tab_spanner = "**Re-intervention**")%>%as_flex_table()

## ----- adjusted -----
RETX_R_RTOR2 = geeglm(RETX_R_RTOR ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
    PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
    family=binomial(link="logit"), data=TEVAR_PROC,
    id = CENTERID, corstr = "independence")

t2 = RETX_R_RTOR2 %>%
tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
    pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
bold_p(t = 0.05)

tbl_merge(tbls = list(t2),tab_spanner = "**Re-intervention**")%>%as_flex_table()
## ----- Post-treatment Status of All Branches -----
## ----- unadjusted -----
BRANCH_POST1 = geeglm(BRANCH_POST~ PRESENTATION,
    data=TEVAR_PROC, family=binomial(link="logit"),
    id = CENTERID, corstr = "independence")
# summary(POSTOP_LOS1)

t1 = BRANCH_POST1 %>%
tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
    pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%

```

```

bold_p(t = 0.05)

tbl_merge(tbls = list(t1), tab_spanner = "**Post-treatment Status of All Branches**") %>% as_flex_table()

## ----- adjusted -----
BRANCH_POST2 = geeglm(BRANCH_POST ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
  PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
  family=binomial(link="logit"), data=TEVAR_PROC,
  id = CENTERID, corstr = "independence")

t2 = BRANCH_POST2 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
    pvalue_fun = function(x) style_pvalue(x, digits = 2)) %>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2), tab_spanner = "**Post-treatment Status of All Branches**") %>% as_flex_table()

## ----- modify dataset -----
TEVAR_PROC = TEVAR_PROC %>%
  mutate(AGECAT = factor(AGECAT, levels = c('<50', '50-59', '60-69', '70-79', '>79'),
    labels = c('<59', '<59', '60-69', '70-79', '>79')))

## ----- Post-op Dialysis -----
# table1(~ AGECAT | factor(POSTOP_DIALYSIS), data=subset(TEVAR_PROC, !is.na(POSTOP_DIALYSIS)))

## ----- unadjusted -----
POSTOP_DIALYSIS1 = geeglm(POSTOP_DIALYSIS ~ PRESENTATION,
  data=TEVAR_PROC, family=binomial(link="logit"),
  id = CENTERID, corstr = "independence")

t1 = POSTOP_DIALYSIS1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
    pvalue_fun = function(x) style_pvalue(x, digits = 2)) %>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1), tab_spanner = "**Post-op Dialysis**") %>% as_flex_table()

## ----- adjusted -----
POSTOP_DIALYSIS2 = geeglm(POSTOP_DIALYSIS ~ PRESENTATION+AGECAT+GENDER+
  PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+
  PREOP_DIALYSIS+PATHOLOGY+extent+
  OCCLUDED_RENAL,
  family=binomial(link="logit"), data=TEVAR_PROC,
  id = CENTERID, corstr = "independence")

t2 = POSTOP_DIALYSIS2 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
    pvalue_fun = function(x) style_pvalue(x, digits = 2)) %>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2), tab_spanner = "**Post-op Dialysis**") %>% as_flex_table()

## ----- Leg Ischemia/Emboli -----
# table1(~ AGECAT | factor(POSTOP_LEGEMBO), data=subset(TEVAR_PROC, !is.na(POSTOP_LEGEMBO)))

```

```

## ----- unadjusted -----
POSTOP_LEGEMBO1 = geeglm(POSTOP_LEGEMBO~ PRESENTATION,
                        data=TEVAR_PROC, family=binomial(link="logit"),
                        id = CENTERID, corstr = "independence")
# summary(POSTOP_LOS1)

t1 = POSTOP_LEGEMBO1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1), tab_spanner = "**Leg Ischemia/Embol**")%>%as_flex_table()

## ----- adjusted -----
POSTOP_LEGEMBO2 = geeglm(POSTOP_LEGEMBO ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
                        PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
                        family=binomial(link="logit"), data=TEVAR_PROC,
                        id = CENTERID, corstr = "independence")

t2 = POSTOP_LEGEMBO2 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2), tab_spanner = "**Leg Ischemia/Embol**")%>%as_flex_table()
## ----- Post-op Respiratory -----
# table1(~ AGECAT | factor(POSTOP_RESPIRATORY), data=subset(TEVAR_PROC, !is.na(POSTOP_RESPIRATORY)))

## ----- unadjusted -----
POSTOP_RESPIRATORY1 = geeglm(POSTOP_RESPIRATORY~ PRESENTATION,
                        data=TEVAR_PROC, family=binomial(link="logit"),
                        id = CENTERID, corstr = "independence")

t1 = POSTOP_RESPIRATORY1 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t1), tab_spanner = "**Post-op Respiratory**")%>%as_flex_table()

## ----- adjusted -----
POSTOP_RESPIRATORY2 = geeglm(POSTOP_RESPIRATORY ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+
                        PRIOR_AORSURG+PRIOR_CHF+PREOP_DIALYSIS+PATHOLOGY+extent,
                        family=binomial(link="logit"), data=TEVAR_PROC,
                        id = CENTERID, corstr = "independence")

t2 = POSTOP_RESPIRATORY2 %>%
  tbl_regression(exponentiate=TRUE, tidy_fun = broom.mixed::tidy,
                pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
  bold_p(t = 0.05)

tbl_merge(tbls = list(t2), tab_spanner = "**Post-op Respiratory**")%>%as_flex_table()
# ## ----- Transfusion # Units PRBC -----

```

```

# ## ----- unadjusted -----
# POSTOP_PRBC1<-geeglm(POSTOP_PRBC ~ PRESENTATION, data=TEVAR_PROC, id = CENTERID, corstr = "independenc
# t1<-POSTOP_PRBC1 %>%tbl_regression(tidy_fun = broom.mixed::tidy,
#                               pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
#   bold_p(t = 0.05)
#
# tbl_merge(tbls = list(t1), tab_spanner = "**Transfusion # Units PRBC**")%>%as_flex_table()
#
# ## ----- adjusted -----
# POSTOP_PRBC2<-geeglm(POSTOP_PRBC ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+P
#
# POSTOP_PRBC2<-geeglm(POSTOP_PRBC ~ PRESENTATION+AGECAT+GENDER+PREOP_SMOKING+PRIOR_AORSURG+PRIOR_CHF+P
#
# t2<- POSTOP_PRBC2 %>%tbl_regression(tidy_fun = broom.mixed::tidy,
#                               pvalue_fun = function(x) style_pvalue(x, digits = 2))%>%
#   bold_p(t = 0.05)
# tbl_merge(tbls = list(t2), tab_spanner = "**Transfusion # Units PRBC**")%>%as_flex_table()
#

```