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

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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.

- cluster on `CENTERID`

- adjust for `AGECAT`, `GENDER`, `PREOP_SMOKING`, `PRIOR_AORSURG`, `PRIOR_CHF`, `PREOP_DIALYSIS`

- adjust for `PATHOLOGY`, `extent`

*In the model, 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.*

- categorical 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 categorical secondary outcomes

TOTAL_LOS: Length of stay in days between admission date and discharge date

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	0.47
70-79	2.16	1.02, 4.55	**0.043**
GENDER			
female	—	—	
male	0.62	0.51, 0.75	**<0.001**
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	**<0.001**

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

Characteristic	TOTAL_LOS Length of Stay in days		
	OR[1]	95% CI[1]	p-value
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	0.58
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	**<0.001**
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			

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

	ICU Stay		
Characteristic	**OR**[1]	**95% CI**[1]	**p-value**
No	—	—	
Yes	1.84	1.07, 3.19	**0.028**
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	**<0.001**

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

Creatinine and GFR

Use `POSTOP_HIGHCREAT`, Highest Creatinine, to generate corresponding GFR values.

`GFRFIFTY`: 1 - GFR reduction is $>=50\%$; 0 - GFR reduction is $<50\%$

	GFR reduction		
Characteristic	**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

	GFR reduction		
Characteristic	**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	0.68
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	**0.006**
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			
No	—	—	

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

	GFR reduction		
Characteristic	**OR**[1]	**95% CI**[1]	**p-value**
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	**<0.001**
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

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

POSTOP_INTISCH: Post-op Intestinal Ischemia

	Intestinal Ischemia		
Characteristic	**OR[1]**	**95% CI[1]**	**p-value**
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.13	0.56, 2.26	0.74

[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	0.87
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			

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

Characteristic	OR[1]	95% CI[1]	p-value
	Intestinal Ischemia		
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

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

POSTOP_CEREBROSX: Post-op Cerebrovascular Stroke:

Also account for `ARMNECK_ACCESS`

	Post-op Cerebrovascular Stroke		
Characteristic	**OR**[1]	**95% CI**[1]	**p-value**
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.42	1.83, 6.38	**<0.001**

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

	Post-op Cerebrovascular Stroke		
Characteristic	**OR**[1]	**95% CI**[1]	**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	**0.023**
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	**0.032**

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

Characteristic	Post-op Cerebrovascular Stroke		
	OR[1]	95% CI[1]	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	**0.045**
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	**0.007**

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

POSTOP_SPINAL_ISCHEMIA: Post-op Spinal Ischemia

Also account for `POSTOP_SPINALDRAIN` and `OCCLUDED_CELIAC`

Characteristic	OR[1]	95% CI[1]	p-value
	Post-op Spinal Ischemia		
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.56	1.70, 3.86	**<0.001**

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

Characteristic	OR[1]	95% CI[1]	p-value
	Post-op Spinal Ischemia		
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.61	1.00, 2.60	**0.050**
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

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

Characteristic	OR[1]	95% CI[1]	p-value
Post-op Spinal Ischemia			
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	0.44	0.05, 3.63	0.45
extent			
Juxtarenal	—	—	
No	1.01	0.65, 1.57	0.97
POSTOP_SPINALDRAIN			
No	—	—	
Yes	19.0	11.1, 32.6	**<0.001**
OCCLUDED_CELIAC			
FALSE	—	—	
TRUE	1.57	0.83, 2.99	0.17

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

POSTOP_LOS: Length of stay in days between surgery date and discharge date

Characteristic	Length of stay in days between surgery date and discharge date		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	3.39	2.69, 4.29	**<0.001**

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

Characteristic	Length of stay in days between surgery date and discharge date		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.46	1.91, 3.17	**<0.001**
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	**<0.001**
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	**0.005**

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

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

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

POSTOP_COMPLICATIONS: Any Complications Post-op

Characteristic	Any Complications Post-op		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.74	1.37, 2.21	**<0.001**

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

Characteristic	Any Complications Post-op		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.44	1.12, 1.86	**0.004**
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	**<0.001**
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	**0.018**
PREOP_DIALYSIS			

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

| | **Any Complications Post-op** | | |
Characteristic	OR[1]	95% CI[1]	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	**<0.001**

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

RETX_R_RTOR: Re-intervention

Characteristic	Re-intervention		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.86	1.33, 2.62	**<0.001**

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

Characteristic	Re-intervention		
	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.48	1.04, 2.09	**0.029**
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	**<0.001**
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			

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

| | Re-intervention | | |
Characteristic	OR[1]	95% CI[1]	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	**0.004**

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

BRANCH_POST: Post-treatment Status of All Branches

Characteristic	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.28	1.78, 2.91	**<0.001**

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

Characteristic	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.64	1.24, 2.16	**<0.001**
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	**<0.001**
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	**0.011**
Open	0.69	0.39, 1.23	0.21
PRIOR_CHF			
No	—	—	
Yes	1.43	1.12, 1.82	**0.004**

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

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

[1]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**[1]	**95% CI**[1]	**p-value**
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.42	1.44, 4.07	**<0.001**

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

	Post-op Dialysis		
Characteristic	**OR**[1]	**95% CI**[1]	**p-value**
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.78	1.01, 3.13	**0.047**
AGECAT			
<59	—	—	
60-69	0.53	0.22, 1.27	0.16
70-79	0.40	0.17, 0.97	**0.042**
>79	0.39	0.15, 1.01	0.053
GENDER			
female	—	—	
male	0.62	0.38, 1.00	**0.049**
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	—	—	

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

| | Post-op Dialysis | | |
Characteristic	OR[1]	95% CI[1]	p-value
Yes	0.74	0.37, 1.45	0.38
PREOP_DIALYSIS			
No	—	—	
Yes	0.00	0.00, 0.00	**<0.001**
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	**<0.001**

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

POSTOP_LEGEMBO: Leg Ischemia/Embol

Characteristic	OR[1]	95% CI[1]	p-value
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	1.97	1.13, 3.46	**0.017**

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

Characteristic	OR[1]	95% CI[1]	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	**<0.001**
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	—	—	

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

Characteristic	Leg Ischemia/Embol		
	OR[1]	95% CI[1]	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

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

POSTOP_RESPIRATORY: Post-op Respiratory

Characteristic	OR[1]	95% CI[1]	p-value
Post-op Respiratory			
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.65	1.87, 3.75	**<0.001**

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

Characteristic	OR[1]	95% CI[1]	p-value
Post-op Respiratory			
PRESENTATION			
Asymptomatic	—	—	
Symptomatic	2.17	1.47, 3.21	**<0.001**
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	**0.014**
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	—	—	

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

Characteristic	Post-op Respiratory		
	OR[1]	95% CI[1]	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	**<0.001**

[1]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)
#
```

```r
# 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","

  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, co

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_BRANCHE
#    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, cors

#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)
```

```r
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, cors

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,id

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()
```

```r
## ------------- 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 = "indeper
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+PRIO

# 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_CEREBROSX1 = geeglm(POSTOP_CEREBROSX ~ PRESENTATION,
                           data=TEVAR_PROC, family=binomial(link="logit"),
                           id = CENTERID, corstr = "independence")

t1 = POSTOP_CEREBROSX1 %>%
  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_CEREBROSX2 = geeglm(POSTOP_CEREBROSX ~ 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_CEREBROSX2 %>%
  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)
```

```r
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 dat

## ------------- 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 dat
## ------------- 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,
```

```r
                    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)))
```

```r
## ------------- 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()
#
```