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Statistical Analysis extra v9  
CTRI Protocol 8425-2

Recognition and Management of  
Community-Acquired Acute Kidney Injury in  
Low Resource Settings  
–The ISN 0by25 Interventional Trial  
– eGFR < 60

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## 1 Result

Table 1: Appendix Table 2

	Overall (n = 2101)	Observation (n = 978)	Intervention (n = 1123)	p-value
<b>Mortality at discharge - Hospitalized patients</b>	105/1126 (9.3%)	38/578 (6.6%)	67/548 (12.2%)	0.001**
NKD	17/208 (8.2%)	7/125 (5.6%)	10/83 (12.0%)	0.122
No AKI	86/608 (14.1%)	34/367 (9.3%)	52/241 (21.6%)	<0.001***
AKI	19/518 (3.7%)	4/211 (1.9%)	15/307 (4.9%)	0.096
stage 1	5/191 (2.6%)	1/73 (1.4%)	4/118 (3.4%)	0.651
stage 2	3/116 (2.6%)	1/41 (2.4%)	2/75 (2.7%)	1.000
stage 3	11/211 (5.2%)	2/97 (2.1%)	9/114 (7.9%)	0.068
severe AKI (stage2/3)	14/327 (4.3%)	3/138 (2.2%)	11/189 (5.8%)	0.165
Dialysis indication but not dialyzed	19/45 (42.2%)	5/15 (33.3%)	14/30 (46.7%)	0.526
Dialyzed	2/58 (3.4%)	1/31 (3.2%)	1/27 (3.7%)	1.000
AKD	59/351 (16.8%)	23/208 (11.1%)	36/143 (25.2%)	<0.001***
CKD	10/49 (20.4%)	4/34 (11.8%)	6/15 (40.0%)	0.049*
<b>Mortality during follow up - Hospitalized patients</b>	112/1021 (11.0%)	67/540 (12.4%)	45/481 (9.4%)	0.133
NKD	10/191 (5.2%)	6/118 (5.1%)	4/73 (5.5%)	1.000
No AKI	51/522 (9.8%)	35/333 (10.5%)	16/189 (8.5%)	0.540
AKI	61/499 (12.2%)	32/207 (15.5%)	29/292 (9.9%)	0.072
stage 1	13/186 (7.0%)	5/72 (6.9%)	8/114 (7.0%)	1.000
stage 2	17/113 (15.0%)	10/40 (25.0%)	7/73 (9.6%)	0.051
stage 3	31/200 (15.5%)	17/95 (17.9%)	14/105 (13.3%)	0.436
severe AKI (stage2/3)	48/313 (15.3%)	27/135 (20.0%)	21/178 (11.8%)	0.057
Dialysis indication but not dialyzed	6/26 (23.1%)	2/10 (20.0%)	4/16 (25.0%)	1.000
Dialyzed	15/56 (26.8%)	6/30 (20.0%)	9/26 (34.6%)	0.243
AKD	37/292 (12.7%)	26/185 (14.1%)	11/107 (10.3%)	0.465
CKD	4/39 (10.3%)	3/30 (10.0%)	1/9 (11.1%)	1.000
<b>Mortality during follow up - Non-hospitalized patients</b>	56/975 (5.7%)	19/400 (4.8%)	37/575 (6.4%)	0.327
NKD	9/399 (2.3%)	4/188 (2.1%)	5/211 (2.4%)	1.000
No AKI	51/865 (5.9%)	17/371 (4.6%)	34/494 (6.9%)	0.189
AKI	5/110 (4.5%)	2/29 (6.9%)	3/81 (3.7%)	0.606
stage 1	3/61 (4.9%)	2/18 (11.1%)	1/43 (2.3%)	0.205
stage 2	0/22 (0.0%)	0/5 (0.0%)	0/17 (0.0%)	1.000
stage 3	2/27 (7.4%)	0/6 (0.0%)	2/21 (9.5%)	1.000
severe AKI (stage2/3)	2/49 (4.1%)	0/11 (0.0%)	2/38 (5.3%)	1.000
Dialysis indication but not dialyzed	4/22 (18.2%)	1/7 (14.3%)	3/15 (20.0%)	1.000
Dialyzed	1/5 (20.0%)	0/1 (0.0%)	1/4 (25.0%)	1.000
AKD	32/409 (7.8%)	12/167 (7.2%)	20/242 (8.3%)	0.852
CKD	10/57 (17.5%)	1/16 (6.2%)	9/41 (22.0%)	0.253
<b>Overall Mortality</b>	273/2101 (13.0%)	124/978 (12.7%)	149/1123 (13.3%)	0.697
NKD	36/607 (5.9%)	17/313 (5.4%)	19/294 (6.5%)	0.610
No AKI	188/1473 (12.8%)	86/738 (11.7%)	102/735 (13.9%)	0.212
AKI	85/628 (13.5%)	38/240 (15.8%)	47/388 (12.1%)	0.189
stage 1	21/252 (8.3%)	8/91 (8.8%)	13/161 (8.1%)	0.817
stage 2	20/138 (14.5%)	11/46 (23.9%)	9/92 (9.8%)	0.039*
stage 3	44/238 (18.5%)	19/103 (18.4%)	25/135 (18.5%)	1.000
severe AKI (stage2/3)	64/376 (17.0%)	30/149 (20.1%)	34/227 (15.0%)	0.208
Dialysis indication but not dialyzed	29/67 (43.3%)	8/22 (36.4%)	21/45 (46.7%)	0.447
Dialyzed	18/63 (28.6%)	7/32 (21.9%)	11/31 (35.5%)	0.274
AKD	128/760 (16.8%)	61/375 (16.3%)	67/385 (17.4%)	0.699
CKD	24/106 (22.6%)	8/50 (16.0%)	16/56 (28.6%)	0.164

Table 2: Table 2 Age Section

	Overall ( <i>n</i> = 2101)	Observation ( <i>n</i> = 978)	Intervention ( <i>n</i> = 1123)	p-value
Children (<18)	272 (13.0%)	130 (13.3%)	142 (12.7%)	0.696
Mean Age	7.93 (5.69)	8.25 (5.35)	7.64 (5.98)	0.376
Adult	1825 (87.0%)	848 (86.7%)	977 (87.3%)	0.696
Mean Age	48.49 (18.06)	49.04 (18.35)	48.02 (17.80)	0.230

Table 3: Table 4

	Overall (n = 2101)	Observation (n = 978)	Intervention (n = 1123)	p-value
<b>Renal Function at admission</b>				
CKD	197 (9.4%)	80 (8.2%)	117 (10.4%)	0.094
With albuminuria	66 (3.9%)	39 (5.1%)	27 (2.9%)	
AKD	1199 (57.1%)	552 (56.4%)	647 (57.6%)	
Based on sCr alone	789 (65.8%)	338 (61.2%)	451 (69.7%)	
Based on sCr and albuminuria	218 (18.2%)	95 (17.2%)	123 (19.0%)	
Based on albuminuria alone	192 (16.0%)	119 (21.6%)	73 (11.3%)	
NKD	705 (33.6%)	346 (35.4%)	359 (32.0%)	
<b>Renal Function at 7 days</b>				
No AKI	1473 (70.1%)	738 (75.5%)	735 (65.4%)	<0.001
CKD	106 (53.8%)	50 (62.5%)	56 (47.9%)	0.058
AKD	760 (63.4%)	375 (67.9%)	385 (59.5%)	0.003
NKD	607 (86.1%)	313 (90.5%)	294 (81.9%)	0.001
AKI	628 (29.9%)	240 (24.5%)	388 (34.6%)	<0.001
Stage 1	252 (40.1%)	91 (37.9%)	161 (41.5%)	0.403
Stage 2	138 (22.0%)	46 (19.2%)	92 (23.7%)	0.198
Stage 3	238 (37.9%)	103 (42.9%)	135 (34.8%)	0.043
severe AKI (stage2/3)	376 (59.9%)	149 (62.1%)	227 (58.5%)	0.403
<b>Disposition</b>				
Sent home	975 (46.4%)	400 (40.9%)	575 (51.2%)	<0.001
<b>Admitted</b>				
NKD	1126 (53.6%)	578 (59.1%)	548 (48.8%)	
AKI	208 (18.5%)	125 (21.6%)	83 (15.1%)	0.006
AKD	518 (46.0%)	211 (36.5%)	307 (56.0%)	<0.001
CKD	351 (31.2%)	208 (36.0%)	143 (26.1%)	<0.001
Time(hours) in health care facility in all patients	49 (4.4%)	34 (5.9%)	15 (2.7%)	0.012
Sent home	28.69 (4.25 - 120.00)	27.00 (3.52 - 120.78)	31.00 (4.85 - 118.00)	0.243
Admitted	3.80 (1.00 - 6.07)	1.56 (0.21 - 5.53)	4.00 (2.00 - 6.48)	<0.001
Admitted	96.00 (46.70 - 167.13)	95.05 (29.08 - 177.35)	97.75 (49.92 - 158.95)	0.167
<b>Dialysis Requirement</b>				
Dialysis Indiction	130 (6.2%)	54 (5.5%)	76 (6.8%)	0.276
Dialyzed	63 (3.0%)	32 (3.3%)	31 (2.8%)	0.523
AKD	14 (22.2%)	11 (34.4%)	3 (9.7%)	0.027
AKI	43 (68.3%)	20 (62.5%)	23 (74.2%)	
CKD	6 (9.5%)	1 (3.1%)	5 (16.1%)	
Dialysis indication, but not dialyzed	67 (3.2%)	22 (2.2%)	45 (4.0%)	0.025
AKD	31 (46.3%)	11 (50.0%)	20 (44.4%)	0.768
AKI	21 (31.3%)	5 (22.7%)	16 (35.6%)	
CKD	12 (17.9%)	5 (22.7%)	7 (15.6%)	
NKD	3 (4.5%)	1 (4.5%)	2 (4.4%)	

Table 4: Table 6

	Overall	Observation	Intervention	p-value
<b>Renal Recovery At 3 months</b>				
Overall total recovery	344/425 (80.9%)	119/152 (78.3%)	225/273 (82.4%)	0.305
New onset AKD on NKD	5/140 (3.6%)	2/54 (3.7%)	3/86 (3.5%)	1.000
CKD progression	5/10 (50.0%)	2/4 (50.0%)	3/6 (50.0%)	1.000
New onset CKD in AKD without AKI	38/115 (33.0%)	19/45 (42.2%)	19/70 (27.1%)	0.107
New onset CKD in AKI	28/160 (17.5%)	8/49 (16.3%)	20/111 (18.0%)	1.000
<b>At 6 months</b>				
Overall total recovery	189/235 (80.4%)	73/98 (74.5%)	116/137 (84.7%)	0.066
New onset AKD on NKD	4/89 (4.5%)	2/39 (5.1%)	2/50 (4.0%)	1.000
CKD progression	4/5 (80.0%)	1/2 (50.0%)	3/3 (100.0%)	0.400
New onset CKD in AKD without AKI	24/68 (35.3%)	14/32 (43.8%)	10/36 (27.8%)	0.208
New onset CKD in AKI	13/73 (17.8%)	7/25 (28.0%)	6/48 (12.5%)	0.118
<b>Overall</b>				
Overall total recovery	398/495 (80.4%)	145/190 (76.3%)	253/305 (83.0%)	0.081
New onset AKD on NKD	7/172 (4.1%)	4/72 (5.6%)	3/100 (3.0%)	0.454
CKD progression	6/11 (54.5%)	2/4 (50.0%)	4/7 (57.1%)	1.000
New onset CKD in AKD without AKI	47/138 (34.1%)	25/61 (41.0%)	22/77 (28.6%)	0.149
New onset CKD in AKI	32/174 (18.4%)	12/53 (22.6%)	20/121 (16.5%)	0.396

Table 5: Table 5

	Overall	Observation	Intervention	P
Any fluid - all patients	1588 (75.6%) <i>n</i> = 637	714 (73.0%) <i>n</i> = 322	874 (77.8%) <i>n</i> = 315	0.012*
volume	1600.00 (1130.00 - 3000.00)	1200.00 (900.00 - 1600.00)	2500.00 (1725.00 - 3500.00)	<0.001***
Sent home	598 (61.3%) <i>n</i> = 239	220 (55.0%) <i>n</i> = 79	378 (65.7%) <i>n</i> = 160	
volume	2000.00 (1200.00 - 3000.00)	1200.00 (900.00 - 1600.00)	2500.00 (1500.00 - 3037.50)	<0.001***
Admitted	990 (87.9%) <i>n</i> = 398	494 (85.5%) <i>n</i> = 243	496 (90.5%) <i>n</i> = 155	
volume	1500.00 (1100.00 - 2500.00)	1200.00 (850.00 - 1575.00)	2500.00 (2000.00 - 3500.00)	<0.001***
IV fluid	1377 (69.7%) <i>n</i> = 1186	592 (62.2%) <i>n</i> = 494	785 (76.6%) <i>n</i> = 692	<0.001***
volume	1000.00 (1000.00 - 2000.00)	1000.00 (500.00 - 1000.00)	1500.00 (1000.00 - 2000.00)	<0.001***
Sent home	469 (55.1%) <i>n</i> = 449	140 (37.4%) <i>n</i> = 138	329 (69.0%) <i>n</i> = 311	
volume	1000.00 (1000.00 - 1500.00)	1000.00 (500.00 - 1000.00)	1000.00 (1000.00 - 2000.00)	<0.001***
Admitted	908 (80.6%) <i>n</i> = 737	452 (78.2%) <i>n</i> = 356	456 (83.2%) <i>n</i> = 381	
volume	1000.00 (1000.00 - 2000.00)	1000.00 (500.00 - 1200.00)	1500.00 (1000.00 - 2000.00)	<0.001***
PO fluid	813 (38.7%)	421 (43.0%)	392 (34.9%)	<0.001***
volume	600.00 (300.00 - 1000.00)	350.00 (200.00 - 600.00)	1000.00 (500.00 - 1500.00)	<0.001***
Sent home	316 (32.4%)	108 (27.0%)	208 (36.2%)	
volume	1000.00 (400.00 - 1500.00)	475.00 (200.00 - 1000.00)	1000.00 (500.00 - 1962.50)	<0.001***
Admitted	497 (44.1%)	313 (54.2%)	184 (33.6%)	
volume	500.00 (200.00 - 1000.00)	350.00 (200.00 - 550.00)	1000.00 (775.00 - 1200.00)	<0.001***
Diuretic use	170 (8.6%)	86 (9.0%)	84 (8.2%)	0.559

Table 6: Follow up at each time point

	Observation	Intervention	Overall	p-value
follow up 7d	<i>n</i> = 978	<i>n</i> = 1123	<i>n</i> = 2101	
0	143 (14.6%)	204 (18.2%)	347 (16.5%)	0.034*
1	835 (85.4%)	919 (81.8%)	1754 (83.5%)	
follow up 1m	<i>n</i> = 978	<i>n</i> = 1123	<i>n</i> = 2101	
0	352 (36.0%)	325 (28.9%)	677 (32.2%)	<0.001***
1	626 (64.0%)	798 (71.1%)	1424 (67.8%)	
follow up 3m	<i>n</i> = 978	<i>n</i> = 1123	<i>n</i> = 2101	
0	583 (59.6%)	549 (48.9%)	1132 (53.9%)	<0.001***
1	395 (40.4%)	574 (51.1%)	969 (46.1%)	
follow up 6m	<i>n</i> = 978	<i>n</i> = 1123	<i>n</i> = 2101	
0	684 (69.9%)	910 (81.0%)	1594 (75.9%)	<0.001***
1	294 (30.1%)	213 (19.0%)	507 (24.1%)	
Mortality by 7days	<i>n</i> = 952	<i>n</i> = 1029	<i>n</i> = 1981	
0	886 (90.6%)	939 (83.6%)	1825 (86.9%)	0.157
1	66 (6.7%)	90 (8.0%)	156 (7.4%)	
NA	26 (2.7%)	94 (8.4%)	120 (5.7%)	
Mortality by 1month	<i>n</i> = 952	<i>n</i> = 1031	<i>n</i> = 1983	
0	868 (88.8%)	909 (80.9%)	1777 (84.6%)	0.034*
1	84 (8.6%)	122 (10.9%)	206 (9.8%)	
NA	26 (2.7%)	92 (8.2%)	118 (5.6%)	
Mortality by 3months	<i>n</i> = 952	<i>n</i> = 1031	<i>n</i> = 1983	
0	836 (85.5%)	889 (79.2%)	1725 (82.1%)	0.325
1	116 (11.9%)	142 (12.6%)	258 (12.3%)	
NA	26 (2.7%)	92 (8.2%)	118 (5.6%)	
Mortality by 6months	<i>n</i> = 952	<i>n</i> = 1031	<i>n</i> = 1983	
0	828 (84.7%)	882 (78.5%)	1710 (81.4%)	0.392
1	124 (12.7%)	149 (13.3%)	273 (13.0%)	
NA	26 (2.7%)	92 (8.2%)	118 (5.6%)	
mortality at discharge	<i>n</i> = 578	<i>n</i> = 548	<i>n</i> = 1126	
Yes	38 (6.6%)	67 (12.2%)	105 (9.3%)	0.002**
No	540 (93.4%)	481 (87.8%)	1021 (90.7%)	
Mortality at 7days	<i>n</i> = 914	<i>n</i> = 962	<i>n</i> = 1876	
0	886 (90.6%)	939 (83.6%)	1825 (86.9%)	0.451
1	28 (2.9%)	23 (2.0%)	51 (2.4%)	
NA	64 (6.5%)	161 (14.3%)	225 (10.7%)	
Mortality at 1month	<i>n</i> = 886	<i>n</i> = 941	<i>n</i> = 1827	
0	868 (88.8%)	909 (80.9%)	1777 (84.6%)	0.099
1	18 (1.8%)	32 (2.8%)	50 (2.4%)	
NA	92 (9.4%)	182 (16.2%)	274 (13.0%)	
Mortality at 3months	<i>n</i> = 868	<i>n</i> = 909	<i>n</i> = 1777	
0	836 (85.5%)	889 (79.2%)	1725 (82.1%)	0.086
1	32 (3.3%)	20 (1.8%)	52 (2.5%)	
NA	110 (11.2%)	214 (19.1%)	324 (15.4%)	
Mortality at 6months	<i>n</i> = 836	<i>n</i> = 889	<i>n</i> = 1725	
0	828 (84.7%)	882 (78.5%)	1710 (81.4%)	0.905
1	8 (0.8%)	7 (0.6%)	15 (0.7%)	
NA	142 (14.5%)	234 (20.8%)	376 (17.9%)	

Table 7: table 6 - de novo CKD

	Overall	Observation	Intervention	p-value
<b>Renal Recovery At 3 months</b>				
De novo CKD	66/415 (15.9%)	27/148 (18.2%)	39/267 (14.6%)	0.331
<b>At 6 months</b>				
De novo CKD	37/230 (16.1%)	21/96 (21.9%)	16/134 (11.9%)	0.047*
<b>Overall</b>				
De novo CKD	79/484 (16.3%)	37/186 (19.9%)	42/298 (14.1%)	0.101

Table 8: Mortality - NKD vs. other

	NKD (n = 607)	Other (n = 1494)	Overall (n = 2101)	p-value
<b>Mortality Overall</b>				
Yes	36 (5.9%)	237 (15.9%)	273 (13.0%)	<0.001***
No	571 (94.1%)	1257 (84.1%)	1828 (87.0%)	

Figure 1:

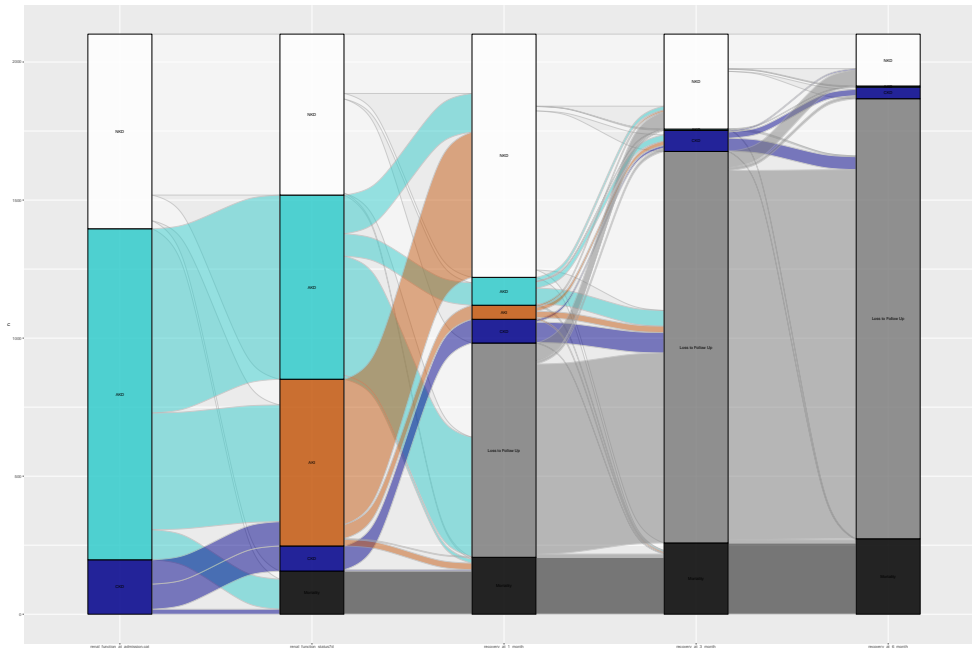




Table 9: Raw groupings of the new variables

	Overall	Observation	Intervention
renal function at admission.cat	<i>n</i> = 2101	<i>n</i> = 978	<i>n</i> = 1123
AKD	1199 (57.1%)	552 (56.4%)	647 (57.6%)
CKD	197 (9.4%)	80 (8.2%)	117 (10.4%)
NKD	705 (33.6%)	346 (35.4%)	359 (32.0%)
renal function status7d	<i>n</i> = 2101	<i>n</i> = 978	<i>n</i> = 1123
AKD	760 (36.2%)	375 (38.3%)	385 (34.3%)
AKI	628 (29.9%)	240 (24.5%)	388 (34.6%)
CKD	106 (5.0%)	50 (5.1%)	56 (5.0%)
NKD	607 (28.9%)	313 (32.0%)	294 (26.2%)
recovery at 1 month	<i>n</i> = 1189	<i>n</i> = 515	<i>n</i> = 674
AKD	83 (4.0%)	35 (3.6%)	48 (4.3%)
AKI	62 (3.0%)	23 (2.4%)	39 (3.5%)
CKD	106 (5.0%)	50 (5.1%)	56 (5.0%)
New onset AKD	20 (1.0%)	12 (1.2%)	8 (0.7%)
NKD	215 (10.2%)	109 (11.1%)	106 (9.4%)
Recovery from AKD	141 (6.7%)	69 (7.1%)	72 (6.4%)
Recovery from AKI	562 (26.7%)	217 (22.2%)	345 (30.7%)
NA	912 (43.4%)	463 (47.3%)	449 (40.0%)
recovery at 3 month	<i>n</i> = 890	<i>n</i> = 343	<i>n</i> = 547
AKI	28 (1.3%)	8 (0.8%)	20 (1.8%)
CKD progression	5 (0.2%)	2 (0.2%)	3 (0.3%)
New onset AKD	5 (0.2%)	2 (0.2%)	3 (0.3%)
New onset CKD	38 (1.8%)	19 (1.9%)	19 (1.7%)
NKD	135 (6.4%)	52 (5.3%)	83 (7.4%)
Recovery from AKD	78 (3.7%)	26 (2.7%)	52 (4.6%)
Recovery from AKI	596 (28.4%)	232 (23.7%)	364 (32.4%)
Stable CKD	5 (0.2%)	2 (0.2%)	3 (0.3%)
NA	1211 (57.6%)	635 (64.9%)	576 (51.3%)
recovery at 6 month	<i>n</i> = 786	<i>n</i> = 313	<i>n</i> = 473
AKI	13 (0.6%)	7 (0.7%)	6 (0.5%)
CKD progression	4 (0.2%)	1 (0.1%)	3 (0.3%)
New onset AKD	4 (0.2%)	2 (0.2%)	2 (0.2%)
New onset CKD	24 (1.1%)	14 (1.4%)	10 (0.9%)
NKD	85 (4.0%)	37 (3.8%)	48 (4.3%)
Recovery from AKD	44 (2.1%)	18 (1.8%)	26 (2.3%)
Recovery from AKI	611 (29.1%)	233 (23.8%)	378 (33.7%)
Stable CKD	1 (0.0%)	1 (0.1%)	0 (0.0%)
NA	1315 (62.6%)	665 (68.0%)	650 (57.9%)

Figure 2:

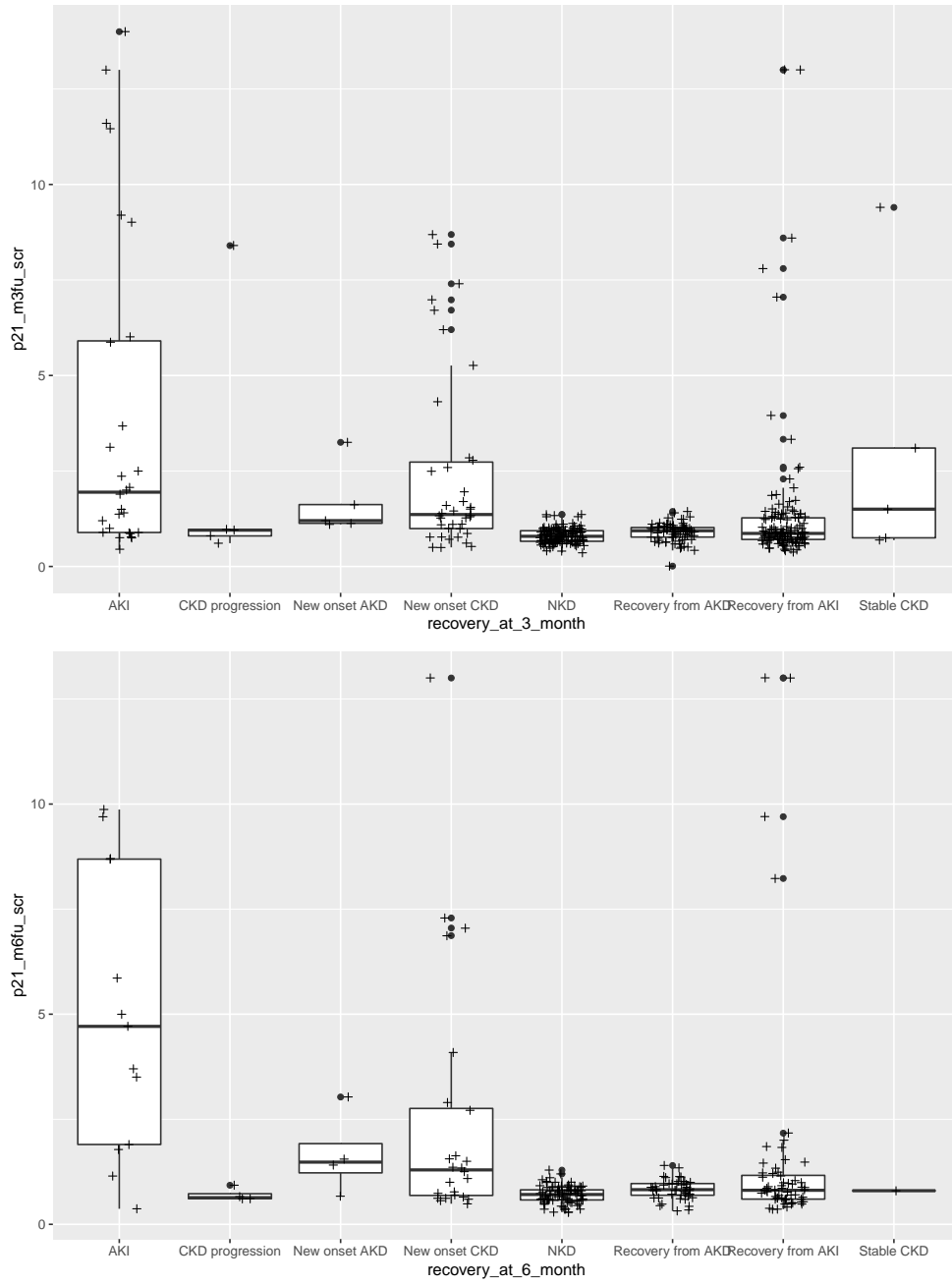


Table 10: Patient characteristics and risk factors by renal function status at enrollment.

	AKD	CKD	NKD	Overall	p-value
<b>Age</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 701	<i>n</i> = 2097	
	43.98 (22.15)	54.99 (23.52)	38.65 (19.06)	43.23 (21.77)	<0.001***
<b>Adult</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 701	<i>n</i> = 2097	
Yes	1031 (86.0%)	173 (87.8%)	621 (88.6%)	1825 (87.0%)	0.251
<b>Female</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	612 (51.0%)	100 (50.8%)	405 (57.4%)	1117 (53.2%)	0.020*
<b>Race</b>	<i>n</i> = 1198	<i>n</i> = 197	<i>n</i> = 704	<i>n</i> = 2099	
african	451 (37.6%)	26 (13.2%)	336 (47.7%)	813 (38.7%)	<0.001***
asian	615 (51.3%)	106 (53.8%)	167 (23.7%)	888 (42.3%)	
aymara	8 (0.7%)	4 (2.0%)	3 (0.4%)	15 (0.7%)	
hispanic	72 (6.0%)	39 (19.8%)	122 (17.3%)	233 (11.1%)	
middle eastern	0 (0.0%)	0 (0.0%)	1 (0.1%)	1 (0.0%)	
quechua	52 (4.3%)	22 (11.2%)	75 (10.7%)	149 (7.1%)	
<b>DM</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	146 (12.2%)	63 (32.0%)	47 (6.7%)	256 (12.2%)	<0.001***
<b>Liver</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	65 (5.4%)	11 (5.6%)	11 (1.6%)	87 (4.1%)	<0.001***
<b>Heart</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	39 (3.3%)	29 (14.7%)	20 (2.8%)	88 (4.2%)	<0.001***
<b>Lung</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	61 (5.1%)	19 (9.6%)	39 (5.5%)	119 (5.7%)	0.037*
<b>HIV</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	222 (18.5%)	6 (3.0%)	145 (20.6%)	373 (17.8%)	<0.001***
<b>Anemia</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	149 (12.4%)	43 (21.8%)	63 (8.9%)	255 (12.1%)	<0.001***
<b>Cancer</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	20 (1.7%)	5 (2.5%)	11 (1.6%)	36 (1.7%)	0.635
<b>Hypertension</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	254 (21.2%)	97 (49.2%)	67 (9.5%)	418 (19.9%)	<0.001***
<b>Dehydration</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	902 (75.2%)	147 (74.6%)	484 (68.7%)	1533 (73.0%)	0.007**
<b>Dehydration: Diarrhea</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	335 (27.9%)	50 (25.4%)	215 (30.5%)	600 (28.6%)	0.287
<b>Dehydration: Vomiting</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	626 (52.2%)	95 (48.2%)	329 (46.7%)	1050 (50.0%)	0.057
<b>Dehydration: Sweating</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	78 (6.5%)	11 (5.6%)	70 (9.9%)	159 (7.6%)	0.013*
<b>Dehydration: Thirst</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	170 (14.2%)	36 (18.3%)	190 (27.0%)	396 (18.8%)	<0.001***
<b>Dehydration: Low intake</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	615 (51.3%)	112 (56.9%)	294 (41.7%)	1021 (48.6%)	<0.001***
<b>Weakness</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	1098 (91.6%)	178 (90.4%)	638 (90.5%)	1914 (91.1%)	0.675
<b>Urinary</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	661 (55.1%)	125 (63.5%)	381 (54.0%)	1167 (55.5%)	0.057
<b>Urinary: Oliguria</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	399 (33.3%)	91 (46.2%)	258 (36.6%)	748 (35.6%)	0.002**
<b>Urinary: Polyuria</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	53 (4.4%)	4 (2.0%)	39 (5.5%)	96 (4.6%)	0.107

Table 11: Patient characteristics and risk factors by renal function status at enrollment.

	AKD	CKD	NKD	Overall	p-value
<b>Urinary: Dysuria</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	248 (20.7%)	36 (18.3%)	148 (21.0%)	432 (20.6%)	0.697
<b>Urinary: Hematuria</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	50 (4.2%)	10 (5.1%)	36 (5.1%)	96 (4.6%)	0.600
<b>Infection</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	868 (72.4%)	111 (56.3%)	537 (76.2%)	1516 (72.2%)	<0.001***
<b>Infection: Malaria</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	64 (5.3%)	2 (1.0%)	42 (6.0%)	108 (5.1%)	0.019*
<b>Infection: GI</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	206 (17.2%)	28 (14.2%)	176 (25.0%)	410 (19.5%)	<0.001***
<b>Hypotension</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	285 (23.8%)	38 (19.3%)	136 (19.3%)	459 (21.8%)	0.049*
<b>Swelling: Whole</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	92 (7.7%)	39 (19.8%)	31 (4.4%)	162 (7.7%)	<0.001***
<b>Swelling: Face</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	100 (8.3%)	15 (7.6%)	40 (5.7%)	155 (7.4%)	0.098
<b>Swelling: Lower</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	294 (24.5%)	50 (25.4%)	105 (14.9%)	449 (21.4%)	<0.001***
<b>Asthenia</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	175 (14.6%)	39 (19.8%)	167 (23.7%)	381 (18.1%)	<0.001***
<b>Dyspnea</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	209 (17.4%)	50 (25.4%)	76 (10.8%)	335 (15.9%)	<0.001***
<b>Weight loss</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	251 (20.9%)	34 (17.3%)	143 (20.3%)	428 (20.4%)	0.493
<b>loss of appetite</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	789 (65.8%)	112 (56.9%)	464 (65.8%)	1365 (65.0%)	0.043*
<b>Pallor</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	218 (18.2%)	47 (23.9%)	128 (18.2%)	393 (18.7%)	0.150
<b>ACEI</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	151 (12.6%)	61 (31.0%)	40 (5.7%)	252 (12.0%)	<0.001***
<b>NSAIDS</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	154 (12.8%)	35 (17.8%)	112 (15.9%)	301 (14.3%)	0.066
<b>Tenofovir</b>	<i>n</i> = 1199	<i>n</i> = 197	<i>n</i> = 705	<i>n</i> = 2101	
Yes	193 (16.1%)	6 (3.0%)	125 (17.7%)	324 (15.4%)	<0.001***

Table 12: Change in renal function status from enrollment to 7 days

	AKD (n = 1199)	CKD (n = 197)	NKD (n = 705)	Overall (n = 2101)
renal function status7d				
AKD	760 (63.4%)	0 (0.0%)	0 (0.0%)	760 (36.2%)
AKI	439 (36.6%)	91 (46.2%)	98 (13.9%)	628 (29.9%)
CKD	0 (0.0%)	106 (53.8%)	0 (0.0%)	106 (5.0%)
NKD	0 (0.0%)	0 (0.0%)	607 (86.1%)	607 (28.9%)

Table 13: Criteria for AKI at 7 days

	AKD (n = 439)	CKD (n = 91)	NKD (n = 98)
realAKI 48 7days			
0	207 (47.2%)	30 (33.0%)	24 (24.5%)
1	232 (52.8%)	61 (67.0%)	74 (75.5%)
decreaseAKI 48 7days.pure			
0	232 (52.8%)	61 (67.0%)	74 (75.5%)
1	207 (47.2%)	30 (33.0%)	24 (24.5%)

## 2 Appendix

### 2.1 Changes

The following changes were made to the data sets:

- 1/14/20
  - **recovery\_at\_3month** and **recovery\_at\_6month** have been reclassified to use the correct scr value (**p21\_m3fu\_scr** and **p21\_m6fu\_scr**)
  - **recovery\_at\_1month** was reclassified also.

Based on the new definition of  $\text{gfr} < 60$ , these patients were shown to recover from CKD.

	patient_id	recovery_at_3_month	recovery_at_6_month	sCr3month	sCr6month
148	BV3049	AKI	Recovery from AKI	1	1
731	IMW5057	AKI	Recovery from AKI	1	1
1022	INP4071	AKI	Recovery from AKI	1	1
1042	INP4094	New onset CKD	Recovery from AKD	1	1
2011	NP5159	AKI	Recovery from AKI	1	1

## 2.2 R Code

```

1 library(Hmisc)
2 library(plyr)
3 library(dplyr)
4 library(readxl)
5 library(magrittr)
6 library(pROC)
7 library(lubridate)
8 library(xtable)
9 library(randomForest)
10 library(ROCR)
11 library(nnet)
12 library(rpart)
13 library(car)
14 library(glmnet)
15 library(caret)
16 #library(MKmisc)
17 library(rms)
18 library(scales)
19 library(diagram)
20 library(stringr)
21 library(stringi)
22 options(digit = 3, stringsAsFactors = FALSE, width = 100)
23 source('/Users/e4lee/Desktop/CTRI/CTRI_Functions.R')
24 setwd('/Users/e4lee/Desktop/CTRI/Projects/8425_Mehta_2/Project 2/Analysis Plan/')
25
26
27 RE.Names <- function(x){
28   dtNames <- tools::toTitleCase(tolower(gsubVec(c('\\_', '\\.').c(' ', ' '), x)))
29   dtNames <- gsubVec(c('Hops', 'Dm', 'Cad', 'Mi', 'AKI', 'ICD9', 'Hiv', 'Dg', 'Ckd', 'dm', 'Esrd', 'Mlopathy',
30     'Poisonig', 'Be ', 'Acei', 'Arb', 'Cni', 'Lmwh', 'Gk', 'k at', ' b', 'Gaki', 'New ', 'Age c', 'k
31     c'),
32     c('', 'DM', 'CAD', 'MI', 'AKI', 'ICD9', 'HIV', '', 'CKD', 'DM', 'ESRD', 'Miopathy',
33     'Poisoning', '', 'ACEI', 'ARB', 'CNI', 'LMMH', 'GK', 'Potassium Level at', ' B', 'gAKI', '', '
34     Age Categorized',
35     'K Categorized'),
36     dtNames, fixed = T)
37 }
38
39 #####
40 ## Preliminaries ##
41 #####
42 #dat1 <- read_xlsx('/Users/e4lee/Desktop/CTRI/Projects/8425_Mehta_2/Project 2/Data/table for Euy 7feb2018.xlsx', sheet
43 = 1)
44 dat2 <- read_xlsx('/Users/e4lee/Desktop/CTRI/Projects/8425_Mehta_2/Project 2/Data/01_11_20/table for Euy 2020 01 08.
45 xlsx', sheet = 1)
46 dat2 <- data.frame(dat2)
47 dat <- dplyr::filter(dat2, p01_enrolled == 1, noscr == 0)
48 dat.o <- dat
49 dat$phase.cat <- factor(gsubVec(c(1, 2), c('Observation', 'Intervention'), dat$phase), levels = c('Observation', '
50 Intervention'))
51
52 ##### New data set modification #####
53 ## Renal function based on < 60 is now used
54 ## The output is located in renal_function_*time*2 columns
55 ## Reassigned column names to make the code run
56
57 dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m1fu_scr <= dat$p02_scr_us), 'recovery_at_1_month'] <- 1
58 dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m1fu_scr > dat$p02_scr_us), 'recovery_at_1_month'] <- 0
59
60 dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m3fu_scr <= dat$p02_scr_us), 'recovery_at_3_month'] <- 1
61 dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m3fu_scr > dat$p02_scr_us), 'recovery_at_3_month'] <- 0
62
63 dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m6fu_scr <= dat$p02_scr_us), 'recovery_at_6_month'] <- 1
64 dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m6fu_scr > dat$p02_scr_us), 'recovery_at_6_month'] <- 0
65
66 dat$renal_function_at_admission.old <- dat$renal_function_at_admission
67 dat$renal_function_status7d.old <- dat$renal_function_status7d
68
69 dat$renal_function_at_admission <- dat$renal_function_at_admission2
70 dat$renal_function_status7d <- dat$renal_function_status7d2
71
72 dat$recovery_at_3_month.o <- dat$recovery_at_3_month

```

```

72 dat$recovery_at_1_month <- gsubVec(c(0, 1, 2, 3, 4, 5, 6), c('AKI', 'Recovery from AKI', 'New onset AKD', 'Recovery
    from AKD', 'NKD', 'AKD', 'CKD'), dat$recovery_at_1_month)
73 dat$recovery_at_3_month <- gsubVec(c(0, 1, 2, 3, 4, 5, 6, 7),
74     c('AKI', 'Recovery from AKI', 'New onset AKD', 'Recovery from AKD', 'NKD', 'New
        onset CKD', 'Stable CKD', 'CKD progression'),
75     dat$recovery_at_3_month)
76 dat$recovery_at_6_month <- gsubVec(c(0, 1, 2, 3, 4, 5, 6, 7),
77     c('AKI', 'Recovery from AKI', 'New onset AKD', 'Recovery from AKD', 'NKD', 'New
        onset CKD', 'Stable CKD', 'CKD progression'),
78     dat$recovery_at_6_month)
79 #####
80
81 #dat$Enrol_eGFR_less_60.new <- ifelse(dat$p21_enrol_gfr < 60, 1, 0)
82 #dat[which(dat$renal_function_at_admission == 2 & dat$proteinuria_at_enrollment == 0), '
    renal_function_at_admission_AKD_by_eGFR_only'] <- 1
83
84 #dat$renal_function_at_admission_need_change <- ifelse(dat$renal_function_at_admission_AKD_by_eGFR_only == 1 &
    dat$Enrol_eGFR_less_60 == 0, 1, 0)
85
86 #dat[which(dat$renal_function_at_admission_need_change == 1), 'renal_function_at_admission'] <- 1
87 ## Appendix Table 2 – Mortality at discharge
88 dat[which(is.na(dat$mortality_at_discharge)), c("mortality_at_discharge")] <- 0
89 dat[which(dat$final_disposition_with_mortality != 1), c("mortality_at_discharge")] <- NA
90 dat$mortality_at_discharge <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$mortality_at_discharge), levels = c('Yes', '
    No'))
91 dat$renal_function_status7d <- factor(gsubVec(c(1, 2, 3, 4), c('NKD', 'AKI', 'AKD', 'CKD'),
    dat$renal_function_status7d), levels = c('NKD', 'AKI', 'AKD', 'CKD'))
92 dat$Dialysis_indication_final <- gsubVec(c(0, 1, 2), c('Not Dialyzed', 'Dialysis indication but not dialyzed', '
    Dialyzed'), dat$Dialysis_indication_final)
93
94 dat$mortality_at_discharge.NKD <- dat$mortality_at_discharge.no.aki <- dat$mortality_at_discharge.aki <-
    dat$mortality_at_discharge.stg1 <- dat$mortality_at_discharge.stg2 <- dat$mortality_at_discharge.stg3 <-
    dat$mortality_at_discharge.stg23 <- dat$mortality_at_discharge.indi.nodia <- dat$mortality_at_discharge.dia <-
    dat$mortality_at_discharge.akd <- dat$mortality_at_discharge.ckd <- dat$mortality_at_discharge
95
96 dat[which(dat$renal_function_status7d != 'NKD'), 'mortality_at_discharge.NKD'] <- NA
97 dat[which(dat$renal_function_status7d == 'AKI'), 'mortality_at_discharge.no.aki'] <- NA
98 dat[which(dat$renal_function_status7d != 'AKI'), 'mortality_at_discharge.aki'] <- NA
99 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 1), 'mortality_at_discharge.stg1'] <- NA
100 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 2), 'mortality_at_discharge.stg2'] <- NA
101 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 3), 'mortality_at_discharge.stg3'] <- NA
102 dat[which(dat$renal_function_status7d != 'AKI' | !dat$Final_total_AKI_stage %in% c(2, 3)), 'mortality_at_discharge.
    stg23'] <- NA
103 dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'mortality_at_discharge.indi.nodia
    '] <- NA
104 dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'mortality_at_discharge.dia'] <- NA
105 dat[which(dat$renal_function_status7d != 'AKD'), 'mortality_at_discharge.akd'] <- NA
106 dat[which(dat$renal_function_status7d != 'CKD'), 'mortality_at_discharge.ckd'] <- NA
107
108
109 app.tab2.1 <- demoTab(data = dat, group = 'phase.cat', vars = c('mortality_at_discharge', 'mortality_at_discharge.NKD
    ', 'mortality_at_discharge.no.aki', 'mortality_at_discharge.aki',
110     'mortality_at_discharge.stg1', 'mortality_at_discharge.stg2', '
        mortality_at_discharge.stg3', 'mortality_at_discharge.stg23',
111     'mortality_at_discharge.indi.nodia', 'mortality_at_discharge.dia', '
        mortality_at_discharge.akd', 'mortality_at_discharge.ckd'),
112     cat.tests = 'fisher.test', rnames = c('{\\bf Mortality at discharge – Hospitalized patients}', 'NKD', 'No AKI
        ', 'AKI', '~~~stage 1', '~~~stage 2', '~~~stage 3', '~~~severe AKI (stage2/3)',
        'Dialysis indication but not dialyzed', 'Dialyzed', 'AKD', 'CKD'))
113
114
115 rownames(app.tab2.1)[seq(2, 36, 3)] <- rownames(app.tab2.1)[seq(1, 36, 3)]
116 final <- app.tab2.1[seq(2, 36, 3), ]
117
118 size <- app.tab2.1[seq(1, 36, 3), 1:3]
119
120 dol.loc <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
121 for(i in 1:(ncol(final) - 1)){
122   for(j in 1:nrow(final)){
123     dol.loc[j, i] <- gregexpr(pattern = '\\$', final[j, i])[[1]][2]
124   }
125 }
126
127 deno.size <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
128 for(i in 1:ncol(size)){
129   for(j in 1:nrow(size)){
130     deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^]*(?=\\$)"))
131   }
132 }
133

```



```

134 for(i in 1:(ncol(final) - 1)){
135   for(j in 1:nrow(final)){
136     stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
137   }
138 }
139
140 app.tab2.d <- final
141
142
143
144 dat[which(is.na(dat$Mortality_overall)), c("patient_id", "mortality_at_discharge", 'mortality_follow_up', "
    Mortality_overall")]
145
146 dat[which(dat$mortality_at_discharge == 'Yes'), c("patient_id", "mortality_at_discharge", 'mortality_follow_up')]
147 #pc <- "bt43xx"
148 #paste(append(strsplit(pc, "")[[1]], "+", nchar(pc) - 3), collapse = "")
149
150 final %>% lapply (function(x) gregexpr(pattern = '\\$', x)[[1]][2])
151
152 #gregexpr(pattern = '\\$', final[1,1])[1][2]
153
154 ## Appendix Table 2 – Mortality during follow up – Hospitalized
155 dat$mortality_follow_up.o <- dat$mortality_follow_up
156 dat$mortality_follow_up <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$mortality_follow_up.o), levels = c('Yes', 'No')
    )
157 dat[which(dat$mortality_at_discharge == 'Yes'), "mortality_follow_up"] <- NA
158 dat[which(dat$final_disposition_with_mortality != 1), c("mortality_follow_up")] <- NA
159
160 dat$renal_function_status7d <- gsubVec(c(1, 2, 3, 4), c('NKD', 'AKI', 'AKD', 'CKD'), dat$renal_function_status7d)
161 dat$Dialysis_indication_final <- gsubVec(c(0, 1, 2), c('Not Dialyzed', 'Dialysis indication but not dialyzed', '
    Dialyzed'), dat$Dialysis_indication_final)
162
163 dat$mortality_follow_up.NKD <- dat$mortality_follow_up.no.aki <- dat$mortality_follow_up.aki <-
    dat$mortality_follow_up.stg1 <- dat$mortality_follow_up.stg2 <- dat$mortality_follow_up.stg3 <-
    dat$mortality_follow_up.stg23 <- dat$mortality_follow_up.indi.nodia <- dat$mortality_follow_up.dia <-
    dat$mortality_follow_up.akd <- dat$mortality_follow_up.ckd <- dat$mortality_follow_up
164
165 dat[which(dat$renal_function_status7d != 'NKD'), 'mortality_follow_up.NKD'] <- NA
166 dat[which(dat$renal_function_status7d == 'AKI'), 'mortality_follow_up.no.aki'] <- NA
167 dat[which(dat$renal_function_status7d != 'AKI'), 'mortality_follow_up.aki'] <- NA
168 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 1), 'mortality_follow_up.stg1'] <- NA
169 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 2), 'mortality_follow_up.stg2'] <- NA
170 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 3), 'mortality_follow_up.stg3'] <- NA
171 dat[which(dat$renal_function_status7d != 'AKI' | !dat$Final_total_AKI_stage %in% c(2, 3)), 'mortality_follow_up.stg23
    '] <- NA
172 dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'mortality_follow_up.indi.nodia']
    <- NA
173 dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'mortality_follow_up.dia'] <- NA
174 dat[which(dat$renal_function_status7d != 'AKD'), 'mortality_follow_up.akd'] <- NA
175 dat[which(dat$renal_function_status7d != 'CKD'), 'mortality_follow_up.ckd'] <- NA
176
177
178 app.tab2.2 <- demoTab(data = dat, group = 'phase.cat', vars = c('mortality_follow_up', 'mortality_follow_up.NKD', '
    mortality_follow_up.no.aki', 'mortality_follow_up.aki',
179     'mortality_follow_up.stg1', 'mortality_follow_up.stg2', '
    mortality_follow_up.stg3', 'mortality_follow_up.stg23',
180     'mortality_follow_up.indi.nodia', 'mortality_follow_up.dia', '
    mortality_follow_up.akd', 'mortality_follow_up.ckd'),
181     cat.tests = 'fisher.test', rnames = c('{\\bf Mortality during follow up – Hospitalized patients}', 'NKD', 'No
    AKI', 'AKI', '~~~stage 1', '~~~stage 2', '~~~stage 3', '~~~severe AKI (stage2/3)',
    'Dialysis indication but not dialyzed', 'Dialyzed', 'AKD', 'CKD'))
182
183
184
185 rownames(app.tab2.2)[seq(2, 36, 3)] <- rownames(app.tab2.2)[seq(1, 36, 3)]
186 final <- app.tab2.2[seq(2, 36, 3), ]
187
188 size <- app.tab2.2[seq(1, 36, 3), 1:3]
189
190 dol.loc <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
191 for(i in 1:(ncol(final) - 1)){
192   for(j in 1:nrow(final)){
193     dol.loc[j, i] <- gregexpr(pattern = '\\$', final[j, i])[1][2]
194   }
195 }
196
197 deno.size <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
198 for(i in 1:ncol(size)){
199   for(j in 1:nrow(size)){
200     deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^]*(?=\\$)"))

```

```

201 }
202 }
203
204 for(i in 1:(ncol(final) - 1)){
205   for(j in 1:nrow(final)){
206     stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
207   }
208 }
209
210 app.tab2.f <- final
211
212
213 ## Appendix Table 2 – Mortality during follow up – Sent Home
214 dat$mortality_follow_up <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$mortality_follow_up.o), levels = c('Yes', 'No')
215 )
216 dat[which(dat$mortality_at_discharge == 'Yes'), "mortality_follow_up"] <- NA
217 dat[which(dat$final_disposition_with_mortality != 2), c("mortality_follow_up")] <- NA
218
219 dat$renal_function_status7d <- gsubVec(c(1, 2, 3, 4), c('NKD', 'AKI', 'AKD', 'CKD'), dat$renal_function_status7d)
220 dat$Dialysis_indication_final <- gsubVec(c(0, 1, 2), c('Not Dialyzed', 'Dialysis indication but not dialyzed', '
221 Dialyzed'), dat$Dialysis_indication_final)
222
223 dat$mortality_follow_up.NKD <- dat$mortality_follow_up.no.aki <- dat$mortality_follow_up.aki <-
224 dat$mortality_follow_up.stg1 <- dat$mortality_follow_up.stg2 <- dat$mortality_follow_up.stg3 <-
225 dat$mortality_follow_up.stg23 <- dat$mortality_follow_up.indi.nodia <- dat$mortality_follow_up.dia <-
226 dat$mortality_follow_up.akd <- dat$mortality_follow_up.ckd <- dat$mortality_follow_up
227
228 dat[which(dat$renal_function_status7d != 'NKD'), 'mortality_follow_up.NKD'] <- NA
229 dat[which(dat$renal_function_status7d == 'AKI'), 'mortality_follow_up.no.aki'] <- NA
230 dat[which(dat$renal_function_status7d != 'AKI'), 'mortality_follow_up.aki'] <- NA
231 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 1), 'mortality_follow_up.stg1'] <- NA
232 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 2), 'mortality_follow_up.stg2'] <- NA
233 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 3), 'mortality_follow_up.stg3'] <- NA
234 dat[which(dat$renal_function_status7d != 'AKI' | !dat$Final_total_AKI_stage %in% c(2, 3)), 'mortality_follow_up.stg23
235 '] <- NA
236 dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'mortality_follow_up.indi.nodia']
237 <- NA
238 dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'mortality_follow_up.dia'] <- NA
239 dat[which(dat$renal_function_status7d != 'AKD'), 'mortality_follow_up.akd'] <- NA
240 dat[which(dat$renal_function_status7d != 'CKD'), 'mortality_follow_up.ckd'] <- NA
241
242
243 app.tab2.2 <- demoTab(data = dat, group = 'phase.cat', vars = c('mortality_follow_up', 'mortality_follow_up.NKD', '
244 mortality_follow_up.no.aki', 'mortality_follow_up.aki',
245 'mortality_follow_up.stg1', 'mortality_follow_up.stg2', '
246 mortality_follow_up.stg3', 'mortality_follow_up.stg23',
247 'mortality_follow_up.indi.nodia', 'mortality_follow_up.dia', '
248 mortality_follow_up.akd', 'mortality_follow_up.ckd'),
249 cat.tests = 'fisher.test', rnames = c('\bf Mortality during follow up – Non-hospitalized patients', 'NKD',
250 'No AKI', 'AKI', '~~~stage 1', '~~~stage 2', '~~~stage 3', '~~~severe AKI (stage2/3)',
251 'Dialysis indication but not dialyzed', 'Dialyzed', 'AKD', 'CKD'))
252
253
254
255 rownames(app.tab2.2)[seq(2, 36, 3)] <- rownames(app.tab2.2)[seq(1, 36, 3)]
256 final <- app.tab2.2[seq(2, 36, 3), ]
257
258 size <- app.tab2.2[seq(1, 36, 3), 1:3]
259
260 dol.loc <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
261 for(i in 1:(ncol(final) - 1)){
262   for(j in 1:nrow(final)){
263     dol.loc[j, i] <- gregexpr(pattern = '\\$', final[j, i])[1][2]
264   }
265 }
266
267 deno.size <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
268 for(i in 1:(ncol(size))){
269   for(j in 1:nrow(size)){
270     deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^]*(?=\\$)"))
271   }
272 }
273
274 for(i in 1:(ncol(final) - 1)){
275   for(j in 1:nrow(final)){
276     stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
277   }
278 }
279
280 app.tab2.f.1 <- final

```

```

269
270 ## Appendix Table 2 – Overall Mortality
271 dat[which(is.na(dat$Mortality_overall)), c("Mortality_overall")] <- 0
272 dat$Mortality_overall <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$Mortality_overall), levels = c('Yes', 'No'))
273 dat$renal_function_status7d <- gsubVec(c(1, 2, 3, 4), c('NKD', 'AKI', 'AKD', 'CKD'), dat$renal_function_status7d)
274 dat$Dialysis_indication_final <- gsubVec(c(0, 1, 2), c('Not Dialyzed', 'Dialysis indication but not dialyzed', '
Dialyzed'), dat$Dialysis_indication_final)
275
276 dat$Mortality_overall.NKD <- dat$Mortality_overall.no.aki <- dat$Mortality_overall.aki <- dat$Mortality_overall.stg1
<- dat$Mortality_overall.stg2 <- dat$Mortality_overall.stg3 <- dat$Mortality_overall.stg23 <-
dat$Mortality_overall.indi.nodia <- dat$Mortality_overall.dia <- dat$Mortality_overall.akd <-
dat$Mortality_overall.ckd <- dat$Mortality_overall
277
278 dat[which(dat$renal_function_status7d != 'NKD'), 'Mortality_overall.NKD'] <- NA
279 dat[which(dat$renal_function_status7d == 'AKI'), 'Mortality_overall.no.aki'] <- NA
280 dat[which(dat$renal_function_status7d != 'AKI'), 'Mortality_overall.aki'] <- NA
281 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 1), 'Mortality_overall.stg1'] <- NA
282 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 2), 'Mortality_overall.stg2'] <- NA
283 dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 3), 'Mortality_overall.stg3'] <- NA
284 dat[which(dat$renal_function_status7d != 'AKI' | !dat$Final_total_AKI_stage %in% c(2, 3)), 'Mortality_overall.stg23']
<- NA
285 dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'Mortality_overall.indi.nodia'] <-
NA
286 dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'Mortality_overall.dia'] <- NA
287 dat[which(dat$renal_function_status7d != 'AKD'), 'Mortality_overall.akd'] <- NA
288 dat[which(dat$renal_function_status7d != 'CKD'), 'Mortality_overall.ckd'] <- NA
289
290
291 app.tab2.3 <- demoTab(data = dat, group = 'phase.cat', vars = c('Mortality_overall', 'Mortality_overall.NKD', '
Mortality_overall.no.aki', 'Mortality_overall.aki',
292 'Mortality_overall.stg1', 'Mortality_overall.stg2', '
Mortality_overall.stg3', 'Mortality_overall.stg23',
293 'Mortality_overall.indi.nodia', 'Mortality_overall.dia', '
Mortality_overall.akd', 'Mortality_overall.ckd'),
294 cat.tests = 'fisher.test', rnames = c('{\\bf Overall Mortality}', 'NKD', 'No AKI', 'AKI', '~~~stage 1', '~~~
stage 2', '~~~stage 3', '~~~severe AKI (stage2/3)',
'Dialysis indication but not dialyzed', 'Dialyzed', 'AKD', 'CKD'))
295
296
297
298 rownames(app.tab2.3)[seq(2, 36, 3)] <- rownames(app.tab2.3)[seq(1, 36, 3)]
299 final <- app.tab2.3[seq(2, 36, 3), ]
300
301 size <- app.tab2.3[seq(1, 36, 3), 1:3]
302
303 dol.loc <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
304 for(i in 1:(ncol(final) - 1)){
305   for(j in 1:nrow(final)){
306     dol.loc[j, i] <- gregexpr(pattern = '\\$', final[j, i])[[1]][2]
307   }
308 }
309
310 deno.size <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
311 for(i in 1:ncol(size)){
312   for(j in 1:nrow(size)){
313     deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^;]*(?=\\$)"))
314   }
315 }
316
317 for(i in 1:(ncol(final) - 1)){
318   for(j in 1:nrow(final)){
319     stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
320   }
321 }
322
323 app.tab2.o <- final
324
325 app.tab2 <- rbind(app.tab2.d, app.tab2.f, app.tab2.f.1, app.tab2.o)
326 app.tab2 <- app.tab2[, c(3, 1, 2, 4)]
327 colnames(app.tab2)[1:3] <- c("\\begin{tabular}{c}Overall\\\\ (\\$n = 2101\\$) \\end{tabular}", "\\begin{tabular}{c}
Observation\\\\ (\\$n = 978\\$) \\end{tabular}",
"\\begin{tabular}{c}Intervention\\\\ (\\$n = 1123\\$) \\end{tabular}")
328
329
330 ### Table 2
331
332
333 dat$p01_age_child <- dat$p01_age_adult <- dat$p01_age
334 dat$p01_is_child <- factor(gsubVec(c(0, 1), c('Yes', 'No'), dat$p01_is_adult), levels = c('Yes', 'No'))
335 dat$p01_is_adult <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$p01_is_adult), levels = c('Yes', 'No'))
336

```

```

337 dat[which(dat$p01_is_adult == 'No'), 'p01_age.adult'] <- NA
338 dat[which(dat$p01_is_adult == 'Yes'), 'p01_age.child'] <- NA
339
340 tab2 <- demoTab(vars = c('p01_is_child', 'p01_age.child', 'p01_is_adult', 'p01_age.adult'), group = 'phase.cat', data
  = dat, cat.tests = 'fisher.test')
341 tab2 <- tab2[c(2, 5, 7, 10), ]
342 rownames(tab2) <- c('Children (<18)', '~~~ Mean Age', 'Adult', '~~~ Mean Age')
343 tab2 <- tab2[, c(3, 1, 2, 4)]
344 colnames(tab2)[1:3] <- c("\begin{tabular}{c}Overall\\\\ ($n = 2101$) \\\end{tabular}", "\begin{tabular}{c}Observation
  \\\ ($n = 978$) \\\end{tabular}",
345 "\begin{tabular}{c}Intervention\\\\ ($n = 1123$) \\\end{tabular}")
346 ## 4 patients with unknwn age/age group
347 dat[which(is.na(dat$p01_is_adult)), c('patient_id', 'p01_is_adult', 'p01_age')]
348
349
350 ## Table 4
351
352 table(dat$eGFR_less_than75_at_enrol)
353 dat$Enrol_eGFR_less_60.new <- ifelse(dat$p21_enrol_gfr < 60, 2, 0)
354
355 table(dat$proteinuria_at_enrollment)
356 #dat$eGFR_less_than75_at_enrol.new <- as.numeric(gsub(1, 2, dat$Enrol_eGFR_less_60.new))
357 dat[which(is.na(dat$Enrol_eGFR_less_60.new)), 'Enrol_eGFR_less_60.new'] <- 0
358 dat$akd_cause_enrol <- dat$Enrol_eGFR_less_60.new + dat$proteinuria_at_enrollment
359 dat$akd_cause_enrol <- factor(gsubVec(c(0, 1, 2, 3), c(NA, 'Based on albuminuria alone', 'Based on sCr alone', 'Based
  on sCr and albuminuria'), dat$akd_cause_enrol),
360 levels = c('Based on sCr alone', 'Based on sCr and albuminuria', 'Based on albuminuria
  alone'))
361
362 adm.overall <- fisher.test(dat$renal_function_at_admission, dat$phase.cat)
363
364 dat$ckd_adm <- dat$akd_adm <- dat$NKD_adm <- dat$renal_function_at_admission
365
366 dat[which(dat$renal_function_at_admission != 1), 'NKD_adm'] <- 0
367 dat[which(dat$renal_function_at_admission != 2), 'akd_adm'] <- 1
368 dat[which(dat$renal_function_at_admission != 3), 'ckd_adm'] <- 1
369 dat[which(dat$renal_function_at_admission != 2), 'akd_cause_enrol'] <- NA
370
371 dat$ckd_adm_alb <- dat$ckd_adm
372 dat[which(dat$renal_function_at_admission != 3), 'ckd_adm_alb'] <- NA
373 dat[which(dat$proteinuria_at_enrollment != 1), 'ckd_adm_alb'] <- 1
374
375 dat$NKD_adm <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$NKD_adm), levels = c('Yes', 'No'))
376 dat$akd_adm <- factor(gsubVec(c(1, 2), c('No', 'Yes'), dat$akd_adm), levels = c('Yes', 'No'))
377 dat$ckd_adm <- factor(gsubVec(c(1, 3), c('No', 'Yes'), dat$ckd_adm), levels = c('Yes', 'No'))
378 dat$ckd_adm_alb <- factor(gsubVec(c(1, 3), c('No', 'Yes'), dat$ckd_adm_alb), levels = c('Yes', 'No'))
379
380
381 tab4.1 <- demoTab(vars = c('ckd_adm', 'ckd_adm_alb', 'akd_adm', 'akd_cause_enrol', 'NKD_adm'), group = 'phase.cat',
  data = dat,
382 rnames = c('CKD', '~~~ With albuminuria', 'AKD', 'AKD_base', 'NKD'), cat.tests = 'fisher.test')
383 rownames(tab4.1)[c(2, 5, 8, 15)] <- rownames(tab4.1)[c(1, 4, 7, 14)]
384 tab4.1 <- tab4.1[c(2, 5, 8, 11, 12, 13, 15), ]
385 tab4.1[c(1, 2, 3, 7), 4] <- ''
386 tab4.1[4, 4] <- pvalFormat(adm.overall$p.value)
387
388 dat$ckd_7d <- dat$akd_7d <- dat$NKD_7d <- dat$aki_7d <- dat$renal_function_status7d
389
390 dat[which(dat$renal_function_status7d != 'NKD'), 'NKD_7d'] <- 'No'
391 dat[which(dat$renal_function_at_admission != 1), 'NKD_7d'] <- NA
392 dat[which(dat$renal_function_status7d != 'AKD'), 'akd_7d'] <- 'No'
393 dat[which(dat$renal_function_at_admission != 2), 'akd_7d'] <- NA
394 dat[which(dat$renal_function_status7d != 'CKD'), 'ckd_7d'] <- 'No'
395 dat[which(dat$renal_function_at_admission != 3), 'ckd_7d'] <- NA
396 dat[which(dat$renal_function_status7d != 'AKI'), 'aki_7d'] <- 'No'
397
398 dat$NKD_7d <- factor(gsubVec(c('NKD'), c('Yes'), dat$NKD_7d), levels = c('Yes', 'No'))
399 dat$akd_7d <- factor(gsubVec(c('AKD'), c('Yes'), dat$akd_7d), levels = c('Yes', 'No'))
400 dat$ckd_7d <- factor(gsubVec(c('CKD'), c('Yes'), dat$ckd_7d), levels = c('Yes', 'No'))
401 dat$aki_7d <- factor(gsubVec(c('AKI'), c('Yes'), dat$aki_7d), levels = c('Yes', 'No'))
402 dat$noaki_7d <- factor(dat$aki_7d, levels = c('No', 'Yes'))
403
404 dat$aki_7d.mod <- dat$aki_7d
405 dat[which(dat$aki_7d == 'No'), 'aki_7d.mod'] <- NA
406 dat$aki_7d_stg1 <- dat$aki_7d_stg2 <- dat$aki_7d_stg3 <- dat$aki_7d_stg23 <- dat$aki_7d.mod
407 dat[which(dat$renal_function_status7d == 'AKI' & dat$Final_total_AKI_stage != 1), 'aki_7d_stg1'] <- 'No'
408 dat[which(dat$renal_function_status7d == 'AKI' & dat$Final_total_AKI_stage != 2), 'aki_7d_stg2'] <- 'No'
409 dat[which(dat$renal_function_status7d == 'AKI' & dat$Final_total_AKI_stage != 3), 'aki_7d_stg3'] <- 'No'
410 dat[which(dat$renal_function_status7d == 'AKI' & !dat$Final_total_AKI_stage %in% c(2, 3)), 'aki_7d_stg23'] <- 'No'

```

```

411
412
413 tab4.2 <- demoTab(vars = c('noaki_7d', 'ckd_7d', 'akd_7d', 'NKD_7d', 'aki_7d', 'aki_7d_stg1', 'aki_7d_stg2', '
aki_7d_stg3', 'aki_7d_stg23'), group = 'phase.cat', data = dat,
414 rnames = c('No AKI', 'CKD', 'AKD', 'NKD', 'AKI', '~~~ Stage 1', '~~~ Stage 2', '~~~ Stage 3', '~~~
severe AKI (stage2/3)'), cat.tests = 'fisher.test')
415
416 rownames(tab4.2)[seq(2, 27, 3)] <- rownames(tab4.2)[seq(1, 27, 3)]
417 tab4.2 <- tab4.2[seq(2, 27, 3), ]
418
419
420 dat$final_disposition_cat <- factor(gsubVec(c(1, 2), c('Admitted', 'Sent home'), dat$final_disposition_with_mortality)
, levels = c('Sent home', 'Admitted'))
421
422 dat$ckd_dis <- dat$akd_dis <- dat$NKD_dis <- dat$aki_dis <- dat$renal_function_status7d
423
424 dat[which(dat$renal_function_status7d != 'NKD'), 'NKD_dis'] <- 'No'
425 dat[which(dat$renal_function_status7d != 'AKD'), 'akd_dis'] <- 'No'
426 dat[which(dat$renal_function_status7d != 'CKD'), 'ckd_dis'] <- 'No'
427 dat[which(dat$renal_function_status7d != 'AKI'), 'aki_dis'] <- 'No'
428
429 dat$NKD_dis <- factor(gsubVec(c('NKD'), c('Yes'), dat$NKD_dis), levels = c('Yes', 'No'))
430 dat$akd_dis <- factor(gsubVec(c('AKD'), c('Yes'), dat$akd_dis), levels = c('Yes', 'No'))
431 dat$ckd_dis <- factor(gsubVec(c('CKD'), c('Yes'), dat$ckd_dis), levels = c('Yes', 'No'))
432 dat$aki_dis <- factor(gsubVec(c('AKI'), c('Yes'), dat$aki_dis), levels = c('Yes', 'No'))
433
434 dat$Time_between_screening_and_discharge.new <- dat$Time_between_screening_and_discharge
435 dat[which(dat$Time_between_screening_and_discharge < 0), 'Time_between_screening_and_discharge.new'] <- NA
436
437 #####
438 dat$p01_rec_dtime <- as.numeric(dat$p01_rec_dtime)
439 dat[["p01_rec_dtime"]] <-
440 as.POSIXct(dat[["p01_rec_dtime"]] * (60*60*24)
441 , origin="1899-12-30"
442 , tz="UTC")
443
444 dat$p05_rec_dtime <- as.numeric(dat$p05_rec_dtime)
445 dat[["p05_rec_dtime"]] <-
446 as.POSIXct(dat[["p05_rec_dtime"]] * (60*60*24)
447 , origin="1899-12-30"
448 , tz="UTC")
449
450 dat$p05_rec_dtime - dat$p01_rec_dtime
451 dat$Time_between_screening_and_discharge.new <- as.numeric(difftime(dat$p05_rec_dtime, dat$p01_rec_dtime, units="hours
"))
452 #####
453 dat[which(dat$Time_between_screening_and_discharge.new < 0), 'Time_between_screening_and_discharge.new'] <- NA
454 dat$Time_between_screening_and_discharge.new.home <- dat$Time_between_screening_and_discharge.new.adm <-
dat$Time_between_screening_and_discharge.new
455
456 dat[which(dat$final_disposition_cat != 'Admitted'), 'Time_between_screening_and_discharge.new.adm'] <- NA
457 dat[which(dat$final_disposition_cat != 'Sent home'), 'Time_between_screening_and_discharge.new.home'] <- NA
458
459 dat[which(dat$final_disposition_cat != 'Admitted'), c('ckd_dis', 'aki_dis', 'akd_dis', 'NKD_dis')] <- NA
460
461
462 time.all <- wilcox.test(dat[which(dat$phase.cat == 'Observation'), 'Time_between_screening_and_discharge.new'], dat[
which(dat$phase.cat == 'Intervention'), 'Time_between_screening_and_discharge.new'])
463
464 kruskal.test(dat$Time_between_screening_and_discharge.new, dat$phase.cat)
465
466 time.home <- wilcox.test(dat[which(dat$phase.cat == 'Observation'), 'Time_between_screening_and_discharge.new.home'],
dat[which(dat$phase.cat == 'Intervention'), 'Time_between_screening_and_discharge.new.home'])
467
468 time.adm <- wilcox.test(dat[which(dat$phase.cat == 'Observation'), 'Time_between_screening_and_discharge.new.adm'],
dat[which(dat$phase.cat == 'Intervention'), 'Time_between_screening_and_discharge.new.adm'])
469
470
471 tab4.3 <- demoTab(vars = c('final_disposition_cat', 'NKD_dis', 'aki_dis', 'akd_dis', 'ckd_dis', '
Time_between_screening_and_discharge.new', 'Time_between_screening_and_discharge.new.home', '
Time_between_screening_and_discharge.new.adm'), group = 'phase.cat', data = dat,
472 rnames = c('Disposition', '~~~ NKD', '~~~ AKI', '~~~ AKD', '~~~ CKD', 'Time(hours) in health care
facility in all patients', '~~~ Sent home', '~~~ Admitted'),
473 cent.funs = rep(c('median'), 100), var.funs = rep(c('quantile'), 100), cat.tests = 'fisher.test')
474 rownames(tab4.3)[c(seq(5, 15, 3), 17, 19, 21)] <- rownames(tab4.3)[c(seq(4, 15, 3), 16, 18, 20)]
475 tab4.3 <- tab4.3[c(1:3, c(seq(5, 15, 3), 17, 19, 21)), ]
476 rownames(tab4.3)[c(2, 3)] <- gsub('~~~', '', rownames(tab4.3)[c(2, 3)])
477 tab4.3[1, ] <- ''
478

```

```

479 tab4.3[8, 4] <- pvalFormat(time.all$p.value)
480 tab4.3[9, 4] <- pvalFormat(time.home$p.value)
481 tab4.3[10, 4] <- pvalFormat(time.adm$p.value)
482
483 dat$dialysis_indi <- dat$dialysis_dialyze <- dat$Dialysis_indication_final
484 dat$indi_7d <- dat$dialy_7d <- dat$renal_function_status7d
485
486 dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'dialysis_indi'] <- 0
487 dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'dialysis_dialyze'] <- 0
488 dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'indi_7d'] <- NA
489 dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'dialy_7d'] <- NA
490
491 dat$dialysis_was_indicateyn <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$dialysis_was_indicateyn), levels = c('Yes',
'No'))
492 dat$dialysis_dialyze <- factor(gsubVec(c(0, 'Dialyzed'), c('No', 'Yes'), dat$dialysis_dialyze), levels = c('Yes', 'No
'))
493 dat$dialysis_indi <- factor(gsubVec(c(0, 'Dialysis indication but not dialyzed'), c('No', 'Yes'), dat$dialysis_indi),
levels = c('Yes', 'No'))
494
495 tab4.4 <- demoTab(vars = c('dialysis_was_indicateyn', 'dialysis_dialyze', 'dialy_7d', 'dialysis_indi', 'indi_7d'),
group = 'phase.cat', data = dat, show.na = FALSE,
496 rnames = c('Dialysis Indiction', 'Dialyzed', 'dia_status', 'Dialysis indication, but not dialyzed',
'indi_status'), cat.tests = 'fisher.test')
497 rownames(tab4.4)[c(2, 5, 12)] <- rownames(tab4.4)[c(1, 4, 11)]
498 tab4.4 <- tab4.4[c(2, 5, 8, 9, 10, 12, 15, 16, 17, 18), ]
499
500 tab4 <- rbind(tab4.1, tab4.2, tab4.3, tab4.4)
501 tab4 <- tab4[, c(3, 1, 2, 4)]
502 colnames(tab4)[1:3] <- c("\begin{tabular}{c}Overall\\\\ ($n = 2101$) \\end{tabular}", "\begin{tabular}{c}Observation
\\\\ ($n = 978$) \\end{tabular}",
503 "\begin{tabular}{c}Intervention\\\\ ($n = 1123$) \\end{tabular}")
504
505
506
507 ## Table 6
508 # dat$CKD_cat_3month_prog <- dat$CKD_cat_enrollment_gfr - dat$CKD_cat_m3fu_gfr
509 # dat[which(dat$CKD_cat_3month_prog > 0), 'CKD_cat_3month_prog'] <- 0
510 # dat[which(dat$CKD_cat_3month_prog < 0), 'CKD_cat_3month_prog'] <- 1
511 dat[, 'CKD_cat_3month_prog'] <- NA
512 dat[which(dat$recovery_at_3_month == 'CKD progression' & dat$sCr3month == 1), 'CKD_cat_3month_prog'] <- 'Yes'
513 dat[which(dat$recovery_at_3_month == 'Stable CKD' & dat$sCr3month == 1), 'CKD_cat_3month_prog'] <- 'No'
514 dat$CKD_cat_3month_prog <- factor(dat$CKD_cat_3month_prog, levels = c('Yes', 'No'))
515
516 #
517 # dat$CKD_cat_6month_prog <- dat$CKD_cat_enrollment_gfr - dat$CKD_cat_m6fu_gfr
518 # dat[which(dat$CKD_cat_6month_prog > 0), 'CKD_cat_6month_prog'] <- 0
519 # dat[which(dat$CKD_cat_6month_prog < 0), 'CKD_cat_6month_prog'] <- 1
520 # dat[which(dat$renal_function_status7d != 'CKD'), 'CKD_cat_6month_prog'] <- NA
521 # dat$CKD_cat_6month_prog <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$CKD_cat_6month_prog), levels = c('Yes', 'No
'))
522 #
523 dat[, 'CKD_cat_6month_prog'] <- NA
524 dat[which(dat$recovery_at_6_month == 'CKD progression' & dat$sCr6month == 1), 'CKD_cat_6month_prog'] <- 'Yes'
525 dat[which(dat$recovery_at_6_month == 'Stable CKD' & dat$sCr6month == 1), 'CKD_cat_6month_prog'] <- 'No'
526 dat$CKD_cat_6month_prog <- factor(dat$CKD_cat_6month_prog, levels = c('Yes', 'No'))
527
528
529 # dat$Recovery_at_3months_bin <- gsub(1, 0, dat$NRecovery_at_3month)
530 # dat$Recovery_at_6months_bin <- gsub(1, 0, dat$NRecovery_at_6month)
531 # dat$Recovery_at_3months_bin <- factor(gsubVec(c(0, 2), c('No', 'Yes'), dat$Recovery_at_3months_bin), levels = c('Yes
', 'No'))
532 # dat$Recovery_at_6months_bin <- factor(gsubVec(c(0, 2), c('No', 'Yes'), dat$Recovery_at_6months_bin), levels = c('Yes
', 'No'))
533
534 dat[which(!is.na(dat$recovery_at_3_month) & dat$sCr3month == 1), 'Recovery_at_3months_bin'] <- 'No'
535 dat[which(dat$recovery_at_3_month %in% c('NKD', 'Recovery from AKD', 'Recovery from AKI') & dat$sCr3month == 1), '
Recovery_at_3months_bin'] <- 'Yes'
536
537 dat[which(!is.na(dat$recovery_at_6_month) & dat$sCr6month == 1), 'Recovery_at_6months_bin'] <- 'No'
538 dat[which(dat$recovery_at_6_month %in% c('NKD', 'Recovery from AKD', 'Recovery from AKI') & dat$sCr6month == 1), '
Recovery_at_6months_bin'] <- 'Yes'
539
540 dat$Recovery_at_3months_bin <- factor(dat$Recovery_at_3months_bin, levels = c('Yes', 'No'))
541 dat$Recovery_at_6months_bin <- factor(dat$Recovery_at_6months_bin, levels = c('Yes', 'No'))
542
543 dat$eGFR3months_60 <- ifelse(dat$p21_m3fu_gfr >= 60, 1, 0)
544 dat$eGFR6months_60 <- ifelse(dat$p21_m6fu_gfr >= 60, 1, 0)
545
546 #table(dat$eGFR3months_60, dat$recovery_at_3_month)

```

```

547
548 dat$onset.NKD.3mon <- NA
549 dat[which(dat$renal_function_status7d == 'NKD' & dat$recovery_at_3_month == 'NKD' & dat$sCr3month == 1), 'onset.NKD.3
mon'] <- 'No'
550 dat[which(dat$renal_function_status7d == 'NKD' & dat$recovery_at_3_month == 'New onset AKD' & dat$sCr3month == 1), '
onset.NKD.3mon'] <- 'Yes'
551
552 dat$onset.aki.3mon <- NA
553 dat[which(dat$renal_function_status7d == 'AKI' & dat$recovery_at_3_month %in% c('Recovery from AKI') & dat$sCr3month
== 1), 'onset.aki.3mon'] <- 'No'
554 dat[which(dat$renal_function_status7d == 'AKI' & dat$recovery_at_3_month == 'AKI' & dat$sCr3month == 1), 'onset.aki.3
mon'] <- 'Yes'
555
556 dat$onset.akd.3mon <- NA
557 dat[which(dat$renal_function_status7d == 'AKD' & dat$recovery_at_3_month == 'Recovery from AKD' & dat$sCr3month == 1),
'onset.akd.3mon'] <- 'No'
558 dat[which(dat$renal_function_status7d == 'AKD' & dat$recovery_at_3_month == 'New onset CKD' & dat$sCr3month == 1), '
onset.akd.3mon'] <- 'Yes'
559
560 dat$onset.NKD.6mon <- NA
561 dat[which(dat$renal_function_status7d == 'NKD' & dat$recovery_at_6_month == 'NKD' & dat$sCr6month == 1), 'onset.NKD.6
mon'] <- 'No'
562 dat[which(dat$renal_function_status7d == 'NKD' & dat$recovery_at_6_month == 'New onset AKD' & dat$sCr6month == 1), '
onset.NKD.6mon'] <- 'Yes'
563
564 dat$onset.aki.6mon <- NA
565 dat[which(dat$renal_function_status7d == 'AKI' & dat$recovery_at_6_month == 'Recovery from AKI' & dat$sCr6month == 1),
'onset.aki.6mon'] <- 'No'
566 dat[which(dat$renal_function_status7d == 'AKI' & dat$recovery_at_6_month == 'AKI' & dat$sCr6month == 1), 'onset.aki.6
mon'] <- 'Yes'
567
568 dat$onset.akd.6mon <- NA
569 dat[which(dat$renal_function_status7d == 'AKD' & dat$recovery_at_6_month == 'Recovery from AKD' & dat$sCr6month == 1),
'onset.akd.6mon'] <- 'No'
570 dat[which(dat$renal_function_status7d == 'AKD' & dat$recovery_at_6_month == 'New onset CKD' & dat$sCr6month == 1), '
onset.akd.6mon'] <- 'Yes'
571
572 dat$denovo.ckd.3mon <- NA
573 dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & !is.na(dat$recovery_at_3_month) & dat$sCr3month ==
1), 'denovo.ckd.3mon'] <- 'No'
574 dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & dat$recovery_at_3_month == 'New onset CKD' &
dat$sCr3month == 1), 'denovo.ckd.3mon'] <- 'Yes'
575 dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & dat$onset.aki.3mon == 'Yes' & dat$sCr3month == 1),
'denovo.ckd.3mon'] <- 'Yes'
576
577 dat$denovo.ckd.6mon <- NA
578 dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & !is.na(dat$recovery_at_6_month) & dat$sCr6month ==
1), 'denovo.ckd.6mon'] <- 'No'
579 dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & dat$recovery_at_6_month == 'New onset CKD' &
dat$sCr6month == 1), 'denovo.ckd.6mon'] <- 'Yes'
580 dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & dat$onset.aki.6mon == 'Yes' & dat$sCr6month == 1),
'denovo.ckd.6mon'] <- 'Yes'
581
582 dat$denovo.ckd_overall <- dat$denovo.ckd.3mon
583 dat[which(dat$denovo.ckd.6mon == 'Yes'), 'denovo.ckd_overall'] <- 'Yes'
584 dat[which(dat$denovo.ckd.6mon == 'No'), 'denovo.ckd_overall'] <- 'No'
585
586 test <- dat[which(dat$recovery_at_3_month == 'AKI'), ]
587
588 plot(test$p02_scr_us, test$sCr3month)
589
590 change <- c('onset.NKD.3mon', 'onset.akd.3mon', 'onset.aki.3mon', 'onset.NKD.6mon', 'onset.akd.6mon', 'onset.aki.6mon
')
591 dat[,change] %>% lapply (function(x) factor(x, levels = c('Yes', 'No')))
592
593 dat$Recovery_overall <- dat$Recovery_at_3months_bin
594 dat[which(dat$Recovery_at_6months_bin == 'Yes'), 'Recovery_overall'] <- 'Yes'
595 dat[which(dat$Recovery_at_6months_bin == 'No'), 'Recovery_overall'] <- 'No'
596
597 dat$onset.NKD_overall <- dat$onset.NKD.3mon
598 dat[which(dat$onset.NKD.6mon == 'Yes'), 'onset.NKD_overall'] <- 'Yes'
599 dat[which(dat$onset.NKD.6mon == 'No'), 'onset.NKD_overall'] <- 'No'
600
601 dat$onset.aki_overall <- dat$onset.aki.3mon
602 dat[which(dat$onset.aki.6mon == 'Yes'), 'onset.aki_overall'] <- 'Yes'
603 dat[which(dat$onset.aki.6mon == 'No'), 'onset.aki_overall'] <- 'No'
604
605 dat$onset.akd_overall <- dat$onset.akd.3mon
606 dat[which(dat$onset.akd.6mon == 'Yes'), 'onset.akd_overall'] <- 'Yes'

```

```

607 dat[which(dat$onset.akd.6mon == 'No'), 'onset.akd_overall'] <- 'No'
608
609 dat$CKD_cat_overall <- dat$CKD_cat_3month_prog
610 dat[which(dat$CKD_cat_6month_prog == 'Yes'), 'CKD_cat_overall'] <- 'Yes'
611 dat[which(dat$CKD_cat_6month_prog == 'No'), 'CKD_cat_overall'] <- 'No'
612
613 tab6 <- demoTab(vars = c('Recovery_at_3months_bin', 'onset.NKD.3mon', 'CKD_cat_3month_prog', 'onset.akd.3mon', 'onset.
aki.3mon', 'Recovery_at_6months_bin', 'onset.NKD.6mon', 'CKD_cat_6month_prog', 'onset.akd.6mon', 'onset.aki.6mon
', 'Recovery_overall', 'onset.NKD_overall', 'CKD_cat_overall', 'onset.akd_overall', 'onset.aki_overall'), group =
'phase.cat', data = dat, show.na = FALSE, rnames = c('Overall total recovery', 'New onset AKD on NKD', 'CKD
progression', 'New onset CKD in AKD without AKI', 'New onset CKD in AKI', 'Overall total recovery', 'New onset
AKD on NKD', 'CKD progression', 'New onset CKD in AKD without AKI', 'New onset CKD in AKI', 'Overall total
recovery', 'New onset AKD on NKD', 'CKD progression', 'New onset CKD in AKD without AKI', 'New onset CKD in AKI')
, cat.tests = 'fisher.test')
614
615 rownames(tab6)[seq(2, 45, 3)] <- rownames(tab6)[seq(1, 45, 3)]
616 final <- tab6[seq(2, 45, 3), ]
617
618 size <- tab6[seq(1, 45, 3), 1:3]
619
620 dol.loc <- matrix(rep(NA, 45), nrow = 15, ncol = 3)
621 for(i in 1:(ncol(final) - 1)){
622   for(j in 1:nrow(final)){
623     dol.loc[j, i] <- gregexpr(pattern = '\\$', final[j, i])[[1]][2]
624   }
625 }
626
627 deno.size <- matrix(rep(NA, 45), nrow = 15, ncol = 3)
628 for(i in 1:ncol(size)){
629   for(j in 1:nrow(size)){
630     deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^;]*(?=\\$)"))
631   }
632 }
633
634 for(i in 1:(ncol(final) - 1)){
635   for(j in 1:nrow(final)){
636     stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
637   }
638 }
639
640 tab6 <- final[, c(3, 1, 2, 4)]
641
642 dat$na.rec.3mon <- dat$na.rec.6mon <- 'FALSE'
643 dat[which(is.na(dat$NRecovery_at_3month)), 'na.rec.3mon'] <- 'TRUE'
644 dat[which(is.na(dat$NRecovery_at_6month)), 'na.rec.6mon'] <- 'TRUE'
645
646 dat[which(dat$na.rec.3mon == 'TRUE' & dat$na.rec.6mon == 'FALSE'), c("patient_id", "NRecovery_at_3month", '
NRecovery_at_6month')]
647
648 dat[which(dat$na.rec.3mon == 'TRUE' & dat$na.rec.6mon == 'FALSE'), c("patient_id")]
649
650
651
652
653 #####
654 dat$Recovery_at_1months_bin <- gsub(1, 0, dat$NRecovery_at_1month)
655 dat$Recovery_at_1months_bin <- factor(gsubVec(c(0, 2), c('No', 'Yes'), dat$Recovery_at_1months_bin), levels = c('Yes',
'No'))
656
657 dat$renal_function_at_admission
658 dat$eGFR1month
659
660 dat$new.ckd.1month <- dat$eGFR1month
661
662 dat[which(dat$renal_function_at_admission == 3), 'new.ckd.1month'] <- NA
663
664 dat$follow_up_7
665
666 dat$final_disposition_cat.7d <- dat$final_disposition_cat
667 dat[which(dat$follow_up_7 == 0), 'final_disposition_cat.7d'] <- NA
668
669 dat$follow_up_7 <- as.character(dat$follow_up_7)
670 demoTab(vars = 'follow_up_7', group = 'final_disposition_cat', data = dat)
671 demoTab(vars = 'follow_up_7', group = 'phase.cat', data = dat)
672
673
674 table(dat$p21_m1fu_scr)
675
676

```



```

677 dat$scr1month.new <- 'Yes'
678 dat[which(is.na(dat$p21_m1fu_scr)), 'scr1month.new'] <- 'No'
679
680 dat$screnrol.new <- 'Yes'
681 dat[which(is.na(dat$p21_enrol_scr)), 'screnrol.new'] <- 'No'
682
683 table(dat$scr1month.new, dat$renal_function_at_admission)
684
685 dat$scr1month.new.aki <- dat$scr1month.new
686 dat[which(dat$renal_function_status7d != 'AKI'), 'scr1month.new.aki'] <- NA
687
688 dat$aki_scr.1mon <- dat$scr1month.new.aki
689 dat[which(dat$scr1month.new.aki == 'No'), 'aki_scr.1mon'] <- NA
690
691 dat$kidney_recovery.1mon <- NA
692 dat[which(!is.na(dat$p21_m1fu_scr/dat$p21_enrol_scr)), 'kidney_recovery.1mon'] <- 'No'
693 dat[which(dat$p21_m1fu_scr/dat$p21_enrol_scr <= 1), 'kidney_recovery.1mon'] <- 'Yes'
694
695 dat$Mortality_by_6months <- as.character(dat$Mortality_by_6months)
696 table(dat$Mortality_by_6months, dat$renal_function_status7d)
697 demoTab(vars = 'Mortality_by_6months', data = dat, group = 'renal_function_status7d')
698
699 dat$renal_function_at_admission.cat <- gsubVec(c(1, 2, 3), c('NKD', 'AKD', 'CKD'), dat$renal_function_at_admission)
700 demoTab(vars = 'renal_function_at_admission.cat', group = 'renal_function_status7d', data = dat)
701 demoTab(vars = 'renal_function_status7d', group = 'renal_function_at_admission.cat', data = dat)
702
703 epCr <- function(sex, race, age){
704   s <- ifelse(sex == 1, 1, 0.742)
705   r <- ifelse(race == 2, 1.21, 1)
706   a <- age^(-0.203)
707   epcr <- (75/(s * r * a * 186))^(1/1.154)
708   return(epcr)
709 }
710 dat$p01_gender
711 dat$p01_race
712 dat$p01_age
713
714 dat$gender <- gsubVec(c('female', 'male'), c(0, 1), dat$p01_gender)
715 dat$race <- gsub('african', '2', dat$p01_race)
716
717 dat$epcr <- mapply(epCr, dat$gender, dat$race, dat$p01_age)
718
719 dat$kidney_recovery.1mon <- NA
720 dat[which(!is.na(dat$p21_m1fu_scr/dat$epcr)), 'kidney_recovery.1mon'] <- 'No'
721 dat[which(dat$p21_m1fu_scr/dat$epcr <= 1), 'kidney_recovery.1mon'] <- 'Yes'
722
723
724 table(dat$screnrol.new, dat$proteinuria_at_enrollment)
725
726 toString(sprintf("%s", colnames(dat)[which(grepl('p21', colnames(dat))]))))
727
728 jj <- dat[which(complete.cases(dat[, c('p21_enrol_visit_seq', 'p21_enrol_visit_type', 'p21_enrol_rec_date', '
p21_enrol_scr', 'p21_enrol_gfr', 'proteinuria_at_enrollment')]))], ]
729
730 change <- c('f7days', 'f1month', 'f3months', 'f6months')
731 dat[,change] %<=>% lapply (function(x) as.character(x))
732
733 tab.fu <- demoTab(vars = c('f7days', 'f1month', 'f3months', 'f6months'), group = 'final_disposition_cat', data = dat,
cat.tests = 'fisher.test')
734 #jWrite(tab.fu, 'follow_up.csv')
735
736 demoTab('Mortality_overall', group = 'renal_function_status7d', data = dat, cat.tests = 'fisher.test')
737
738 a <- glm('Mortality_overall ~ renal_function_status7d', data = dat, family = 'binomial')
739 summary(a)
740
741 demoTab(vars = c('Mortality_by_6months'), group = 'final_disposition_cat', data = dat, show.na = FALSE, cat.tests = '
fisher.test')
742
743 dat$AKI_stage_2_3 <- gsubVec(c(0, 1, 2, 3), c('None and one', 'None and one', 'two and three', 'two and three'),
dat$AKI_staging)
744
745 demoTab(vars = c('Mortality_overall'), group = 'AKI_stage_2_3', data = dat, cat.tests = 'fisher.test')
746
747 #dat[which(is.na(dat$fluid_therapy)), 'fluid_therapy'] <- 0
748 dat[which(is.na(dat$fluid_therapy_POandIVat_initial_evaluation)), 'fluid_therapy_POandIVat_initial_evaluation'] <- 0
749
750 dat$fluid_therapy_POandIVat_initial_evaluation.cat <- factor(gsubVec(c(0, 1), c('No', 'Yes'),
dat$fluid_therapy_POandIVat_initial_evaluation), levels = c('Yes', 'No'))

```

```

751 dat$fluid_therapy_POandIV_during_admission.cat <- factor(gsubVec(c(0, 1), c('No', 'Yes'),
752   dat$fluid_therapy_POandIV_during_admission), levels = c('Yes', 'No'))
753 dat$p05_ip_interventions__diuretic_therapy.cat <- factor(gsubVec(c(0, 1), c('No', 'Yes'),
754   dat$p05_ip_interventions__diuretic_therapy), levels = c('Yes', 'No'))
755 dat$p05_ip_interventions__fluid_therapy_iv.cat <- factor(gsubVec(c(0, 1), c('No', 'Yes'),
756   dat$p05_ip_interventions__fluid_therapy_iv), levels = c('Yes', 'No'))
757 dat$t02_fluid_therapy_oral.cat <- factor(gsubVec(c(0, 1), c('No', 'Yes'), ifelse(is.na(dat$t02_fluid_therapy_oral), 0,
758   1)), levels = c('Yes', 'No'))
759 #dat$overall_fluid <- dat$fluid_therapy + dat$fluid_therapy_POandIVat_initial_evaluation # Fluid Therapy covers PO and
760   IV fluid mentioned at 'fluid_therapy_POandIVat_initial_evaluation'
761
762 all <- demoTab(vars = c('fluid_therapy_POandIV_during_admission.cat', '
763   total_volume_fluid_therapy_POandIVat_initial_evaluation'), data = dat, group = 'phase.cat', con.tests = 'kruskal.
764   test',
765   cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
766 all <- all[c(2, 4, 5), ]
767
768 all.s <- demoTab(vars = c('total_volume_fluid_therapy_POandIVat_initial_evaluation'), data = dat[which(
769   dat$final_disposition_cat == 'Sent home'), ], group = 'phase.cat', con.tests = 'kruskal.test',
770   cent.funs = c('median'), var.funs = c('quantile'))
771 all.s <- rbind(paste('$', as.numeric(str_extract(colnames(all.s), "(?<=\\=)[^;]*(?=\\$)")), '$', sep = ''), all.s)
772 all.s[1, 4] <- ''
773 all.a <- demoTab(vars = c('total_volume_fluid_therapy_POandIVat_initial_evaluation'), data = dat[which(
774   dat$final_disposition_cat == 'Admitted'), ], group = 'phase.cat', con.tests = 'kruskal.test',
775   cent.funs = c('median'), var.funs = c('quantile'))
776 all.a <- rbind(paste('$', as.numeric(str_extract(colnames(all.a), "(?<=\\=)[^;]*(?=\\$)")), '$', sep = ''), all.a)
777 all.a[1, 4] <- ''
778
779 all.s <- demoTab(vars = c('fluid_therapy_POandIV_during_admission.cat', '
780   total_volume_fluid_therapy_POandIVat_initial_evaluation'), data = dat[which(dat$final_disposition_cat == 'Sent
781   home'), ], group = 'phase.cat', con.tests = 'kruskal.test',
782   cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
783 all.s <- all.s[c(2, 4, 5), ]
784 all.a <- demoTab(vars = c('fluid_therapy_POandIV_during_admission.cat', '
785   total_volume_fluid_therapy_POandIVat_initial_evaluation'), data = dat[which(dat$final_disposition_cat == '
786   Admitted'), ], group = 'phase.cat', con.tests = 'kruskal.test',
787   cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
788 all.a <- all.a[c(2, 4, 5), ]
789
790 tab.all <- rbind(all, all.s, all.a)
791 rownames(tab.all) <- c('Any fluid - all patients', '', '', 'Sent home', '', '', 'Admitted', '', '')
792 tab.all[c(4, 7), 4] <- ''
793
794 all <- demoTab(vars = c('p05_ip_interventions__fluid_therapy_iv.cat', 't02_fluid_therapy_iv_amount'), data = dat,
795   group = 'phase.cat', con.tests = 'kruskal.test',
796   cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
797 all <- all[c(2, 4, 5), ]
798
799 all.s <- demoTab(vars = c('t02_fluid_therapy_iv_amount'), data = dat[which(dat$final_disposition_cat == 'Sent home'),
800   ], group = 'phase.cat', con.tests = 'kruskal.test',
801   cent.funs = c('median'), var.funs = c('quantile'), rnames = 'Sent home')
802 all.s <- rbind(paste('$', as.numeric(str_extract(colnames(all.s), "(?<=\\=)[^;]*(?=\\$)")), '$', sep = ''), all.s)
803 all.s[1, 4] <- ''
804 all.a <- demoTab(vars = c('t02_fluid_therapy_iv_amount'), data = dat[which(dat$final_disposition_cat == 'Admitted'),
805   ], group = 'phase.cat', con.tests = 'kruskal.test',
806   cent.funs = c('median'), var.funs = c('quantile'), rnames = 'Admitted')
807 all.a <- rbind(paste('$', as.numeric(str_extract(colnames(all.a), "(?<=\\=)[^;]*(?=\\$)")), '$', sep = ''), all.a)
808 all.a[1, 4] <- ''
809
810 all.s <- demoTab(vars = c('p05_ip_interventions__fluid_therapy_iv.cat', 't02_fluid_therapy_iv_amount'), data = dat[
811   which(dat$final_disposition_cat == 'Sent home'), ], group = 'phase.cat', con.tests = 'kruskal.test',
812   cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
813 all.s <- all.s[c(2, 4, 5), ]
814 all.a <- demoTab(vars = c('p05_ip_interventions__fluid_therapy_iv.cat', 't02_fluid_therapy_iv_amount'), data = dat[
815   which(dat$final_disposition_cat == 'Admitted'), ], group = 'phase.cat', con.tests = 'kruskal.test',
816   cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
817 all.a <- all.a[c(2, 4, 5), ]
818
819 tab.iv <- rbind(all, all.s, all.a)
820 rownames(tab.iv) <- c('IV fluid', '', '', 'Sent home', '', '', 'Admitted', '', '')
821 tab.iv[c(4, 7), 4] <- ''
822
823 all <- demoTab(vars = c('t02_fluid_therapy_oral.cat', 't02_fluid_therapy_oral'), data = dat, group = 'phase.cat', con.

```

```

      tests = 'kruskal.test',
812     cent.funs = c('', 'median'), var.funs = c('', 'quantile'), rnames = 'Any fluid - all patients')
813 all <- all[c(2, 5), ]
814
815 all.s <- demoTab(vars = c('t02_fluid_therapy_oral'), data = dat[which(dat$final_disposition_cat == 'Sent home'), ],
      group = 'phase.cat', con.tests = 'kruskal.test',
816     cent.funs = c('median'), var.funs = c('quantile'), rnames = 'Sent home')
817 all.s <- rbind(paste('$', as.numeric(str_extract(colnames(all.s), "(?<=\\=)[^:]*(?=\\$)")), '$', sep = ''), all.s)
818 all.s[1, 4] <- ''
819 all.a <- demoTab(vars = c('t02_fluid_therapy_oral'), data = dat[which(dat$final_disposition_cat == 'Admitted'), ],
      group = 'phase.cat', con.tests = 'kruskal.test',
820     cent.funs = c('median'), var.funs = c('quantile'), rnames = 'Admitted')
821 all.a <- rbind(paste('$', as.numeric(str_extract(colnames(all.a), "(?<=\\=)[^:]*(?=\\$)")), '$', sep = ''), all.a)
822 all.a[1, 4] <- ''
823
824 all.s <- demoTab(vars = c('t02_fluid_therapy_oral.cat', 't02_fluid_therapy_oral'), data = dat[which(
      dat$final_disposition_cat == 'Sent home'), ], group = 'phase.cat', con.tests = 'kruskal.test',
825     cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
826 all.s <- all.s[c(2, 5), ]
827 all.a <- demoTab(vars = c('t02_fluid_therapy_oral.cat', 't02_fluid_therapy_oral'), data = dat[which(
      dat$final_disposition_cat == 'Admitted'), ], group = 'phase.cat', con.tests = 'kruskal.test',
828     cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
829 all.a <- all.a[c(2, 5), ]
830
831
832 tab.po <- rbind(all, all.s, all.a)
833 rownames(tab.po) <- c('PO fluid', '', 'Sent home', '', 'Admitted', '')
834 tab.po[c(3, 5), 4] <- ''
835
836
837
838 all <- demoTab(vars = c('p05_ip_interventions__diuretic_therapy.cat'), data = dat, group = 'phase.cat', con.tests = '
      kruskal.test',
839     cent.funs = c('', 'median'), var.funs = c('', 'quantile'), rnames = 'Diuretic use')
840 tab.d <- all[c(1, 2), ]
841 rownames(tab.d) <- c('Diuretic use', '')
842
843 tab5 <- rbind(tab.all, tab.iv, tab.po, tab.d)
844 tab5 <- cbind(tab5, 'a' = c('', '', 'volume', '', '', 'volume', '', '', 'volume', '', '', 'volume',
      '', '', 'volume', '', 'volume', '', 'volume', '', 'volume', '', ''))
845
846 tab5 <- tab5[, c(5, 3, 1, 2, 4)]
847
848 #colnames(tab5) <- c("", "\\begin{tabular}{c}Overall\\\\\\ ($n = 2101$) \\end{tabular}", "\\begin{tabular}{c}Observation
      \\\\\\ ($n = 978$) \\end{tabular}", "\\begin{tabular}{c}Intervention\\\\\\ ($n = 1123$) \\end{tabular}", 'P')
849
850 colnames(tab5) <- c("", "Overall", "Observation",
851     "Intervention", 'P')
852
853 change <- c('follow_up_7', 'follow_up_1m', 'follow_up_3m', 'follow_up_6m', 'Mortality_by_7days', 'Mortality_by_1month',
      'Mortality_by_3months', 'Mortality_by_6months')
854 dat[,change] %>% lapply (function(x) as.character(x))
855
856 tab.fu <- demoTab(c('follow_up_7', 'follow_up_1m', 'follow_up_3m', 'follow_up_6m', 'Mortality_by_7days', '
      Mortality_by_1month', 'Mortality_by_3months', 'Mortality_by_6months'),
857     group = 'phase.cat', data = dat,
858     rnames = c('follow up 7d', 'follow up 1m', 'follow up 3m', 'follow up 6m', 'Mortality by 7days', '
      Mortality by 1month', 'Mortality by 3months', 'Mortality by 6months'))
859
860 table(dat$scr1month.new)
861
862 ## Mortality at
863
864 dat$Mortality_at_7days <- dat$Mortality_by_7days
865 dat$Mortality_at_1month <- dat$Mortality_by_1month
866 dat$Mortality_at_3months <- dat$Mortality_by_3months
867 dat$Mortality_at_6months <- dat$Mortality_by_6months
868
869 dat[which(dat$mortality_at_discharge == 'Yes'), 'Mortality_at_7days'] <- NA
870 dat[which(dat$Mortality_by_7days == 1), c('Mortality_at_1month', 'Mortality_at_3months', 'Mortality_at_6months')] <-
      NA
871 dat[which(dat$Mortality_by_1month == 1), c('Mortality_at_3months', 'Mortality_at_6months')] <- NA
872 dat[which(dat$Mortality_by_3months == 1), c('Mortality_at_6months')] <- NA
873
874
875 tab.mor <- demoTab(c('follow_up_7', 'follow_up_1m', 'follow_up_3m', 'follow_up_6m', 'Mortality_by_7days', '
      Mortality_by_1month', 'Mortality_by_3months', 'Mortality_by_6months',
876     'mortality_at_discharge', 'Mortality_at_7days', 'Mortality_at_1month', 'Mortality_at_3months', '
      Mortality_at_6months'),

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877     group = 'phase.cat', data = dat,
878     rnames = c('follow up 7d', 'follow up 1m', 'follow up 3m', 'follow up 6m', 'Mortality by 7days', '
      Mortality by 1month', 'Mortality by 3months', 'Mortality by 6months',
879     'mortality at discharge', 'Mortality at 7days', 'Mortality at 1month', 'Mortalityat 3
      months', 'Mortality at 6months')
880
881
882 change <- c('denovo.ckd.3mon', 'denovo.ckd.6mon', 'denovo.ckd_overall')
883 dat[,change] %<>% lapply (function(x) factor(x, levels = c('Yes', 'No')))
884
885 tab6.ext <- demoTab(vars = c('denovo.ckd.3mon', 'denovo.ckd.6mon', 'denovo.ckd_overall'), group = 'phase.cat', data =
      dat, show.na = FALSE, rnames = c('De novo CKD', 'De novo CKD', 'De novo CKD'), cat.tests = 'fisher.test')
886
887 rownames(tab6.ext)[seq(2, 9, 3)] <- rownames(tab6.ext)[seq(1, 9, 3)]
888 final <- tab6.ext[seq(2, 9, 3), ]
889
890 size <- tab6.ext[seq(1, 9, 3), 1:3]
891
892 dol.loc <- matrix(rep(NA, 9), nrow = 15, ncol = 3)
893 for(i in 1:(ncol(final) - 1)){
894   for(j in 1:nrow(final)){
895     dol.loc[j, i] <- gregexpr(pattern = '\\$', final[j, i])[[1]][2]
896   }
897 }
898
899 deno.size <- matrix(rep(NA, 9), nrow = 15, ncol = 3)
900 for(i in 1:(ncol(size))){
901   for(j in 1:nrow(size)){
902     deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^;]*(?=\\$)"))
903   }
904 }
905
906 for(i in 1:(ncol(final) - 1)){
907   for(j in 1:nrow(final)){
908     stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
909   }
910 }
911
912 tab6.ext <- final[, c(3, 1, 2, 4)]
913
914
915 dat$p21_enrol_scr
916 dat$p21_m1fu_scr
917
918 dat$recovery_1month_enrollment_scr <- ifelse(dat$p21_m1fu_scr <= dat$p21_enrol_scr, 'Yes', 'No')
919
920 dat$renal_function_status7d_scr <- dat$renal_function_status7d
921
922 dat[which(dat$scr1month.new != 'Yes'), 'renal_function_status7d_scr'] <- NA
923
924 table(dat$recovery_1month_enrollment_scr, dat$renal_function_status7d_scr)
925
926 demoTab(vars = 'recovery_1month_enrollment_scr', data = dat, group = 'renal_function_status7d_scr', show.na = FALSE)
927
928 dat$eGFR_less_than75_at_1month.ch <- as.character(dat$eGFR_less_than75_at_1month)
929
930 demoTab(vars = 'eGFR_less_than75_at_1month.ch', data = dat, group = 'renal_function_status7d_scr', show.na = FALSE)
931
932 head(dat[, c("p21_enrol_scr", "p21_m1fu_scr", "recovery_1month_enrollment_scr")])
933
934 demoTab(vars = 'kidney.recovery.1mon', data = dat, group = 'renal_function_status7d_scr')
935
936 table(dat$dialysis_at_1month, dat$renal_function_status7d_scr, dat$eGFR_less_than75_at_1month.ch)
937
938
939 ## KDIGO and Decline
940
941 dat$realAKI_48_7days
942
943 dat$decreaseAKI_48_7days
944
945 dat$decreaseAKI_48_7days.pure <- dat$decreaseAKI_48_7days
946
947 dat[which(dat$realAKI_48_7days == 1), "decreaseAKI_48_7days.pure"] <- 0
948
949 change <- c('realAKI_48_7days', 'decreaseAKI_48_7days.pure')
950 dat[,change] %<>% lapply (function(x) as.character(x))
951
952 demoTab(vars = c('realAKI_48_7days', 'decreaseAKI_48_7days.pure'), group = 'renal_function_at_admission.cat', data =

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    dat)
953
954 dat$renal_function_at_admission.cat.aki.at.7d.only <- dat$renal_function_at_admission.cat
955 dat[which(dat$renal_function_status7d != 'AKI'), 'renal_function_at_admission.cat.aki.at.7d.only'] <- NA
956
957 demoTab(vars = c('renalAKI_48_7days', 'decreaseAKI_48_7days.pure'), group = 'renal_function_at_admission.cat.aki.at.7d.
    only', data = dat)
958
959 dat$in_hospital_mortality
960 dat$time_in_health_care_facility_less_than_24hours
961
962 table(dat$in_hospital_mortality, dat$time_in_health_care_facility_less_than_24hours)
963
964
965 demoTab(vars = c('renal_function_status7d'), group = 'renal_function_at_admission.cat', data = dat)
966
967
968 ## 11/27/19
969 ## Identify patients who would not be classified as AKD if cut off is <60 instead of <75
970 dat$p21_enrol_gfr
971 dat$Enrol_eGFR_less_60
972
973 dat$renal_function_at_admission.cat
974 dat$proteinuria_at_enrollment
975
976 dat$AKD_at_admission
977
978 dat$AKD_at_adm_by_egfr_only <- NA
979 dat[which(dat$akd_adm == 'Yes'), 'AKD_at_adm_by_egfr_only'] <- 1
980 dat[which(dat$proteinuria_at_enrollment == 1), 'AKD_at_adm_by_egfr_only'] <- NA
981
982 #table(dat$AKD_at_adm_by_egfr_only, dat$eGFR_less_than75_at_enrol.new)
983
984 table(dat$AKD_at_adm_by_egfr_only, dat$Enrol_eGFR_less_60) # 7 missing
985
986 dat$Enrol_eGFR_less_60.new <- ifelse(dat$p21_enrol_gfr < 60, 1, 0)
987
988 table(dat$AKD_at_adm_by_egfr_only, dat$Enrol_eGFR_less_60.new)
989 #      0      1
990 # 1 193 789
991 ## 193 patients will no longer be classified as AKD if the cut off was lowered
992
993 dat$renal_function_status7d_NKD_vs <- gsubVec(c('AKD', 'AKI', 'CKD'), c('Other', 'Other', 'Other'),
    dat$renal_function_status7d)
994
995 ext.tab <- demoTab(vars = 'Mortality_overall', group = 'renal_function_status7d_NKD_vs', data = dat, cat.tests = '
    fisher.test',
    rnames = c('Mortality Overall'))
996
997
998
999 dat$renal_function_status7d_NKD_vs
1000 dat$eGFR1month
1001 dat$eGFR_less_than75_at_1month.ch
1002
1003 table(dat$renal_function_at_admission.cat, dat$eGFR_less_than75_at_1month)
1004
1005 table(dat$renal_function_status7d_scr)
1006
1007 demoTab(vars = 'eGFR_less_than75_at_1month.ch', data = dat, group = 'renal_function_status7d_scr', show.na = FALSE)
1008
1009 dat$p21_m1fu_scr
1010
1011 dat$eGFR_less_than75_at_1month.new <- ifelse(dat$p21_m1fu_gfr < 75, 'Yes', 'No')
1012
1013 demoTab(vars = 'eGFR_less_than75_at_1month.new', data = dat, group = 'renal_function_status7d_scr', show.na = FALSE)
1014
1015 dat[which(dat$renal_function_status7d_scr == 'NKD' & is.na(dat$eGFR_less_than75_at_1month.new)), c("p21_m1fu_gfr", "
    p21_m1fu_scr")]
1016
1017 ###12/11/19 Additional Request
1018
1019 dat$onset.NKD.3mon.75 <- NA
1020 dat[which(dat$renal_function_status7d == 'NKD' & dat$eGFR_less_than75_at_3month == 0), 'onset.NKD.3mon.75'] <- 'No'
1021 dat[which(dat$renal_function_status7d == 'NKD' & dat$eGFR_less_than75_at_3month == 1), 'onset.NKD.3mon.75'] <- 'Yes'
1022
1023 dat$eGFR_less_than75_at_6month <- ifelse(dat$p21_m6fu_gfr < 75, 1, 0)
1024
1025 dat$onset.NKD.6mon.75 <- NA
1026 dat[which(dat$renal_function_status7d == 'NKD' & dat$eGFR_less_than75_at_6month == 0), 'onset.NKD.6mon.75'] <- 'No'

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1027 dat[which(dat$renal_function_status7d == 'NKD' & dat$eGFR_less_than75_at_6month == 1), 'onset.NKD.6mon.75'] <- 'Yes'
1028
1029 table(dat$onset.NKD.3mon, dat$onset.NKD.3mon.75)
1030
1031 table(dat$renal_function_status_1month, dat$onset.NKD.3mon)
1032
1033 dat$renal_function_status_1month.chr <- factor(gsubVec(c(1, 2, 3), c('NKD', 'AKD', 'CKD'),
1034       dat$renal_function_status_1month), levels = c('NKD', 'AKD', 'CKD'))
1035
1036 table(dat$renal_function_status_1month.chr, dat$onset.NKD.3mon)
1037
1038 dat[which(dat$onset.NKD.3mon == 'Yes'), 'renal_function_status_1month.chr']
1039 dat[which(dat$onset.NKD.3mon == 'Yes'), 'renal_function_status_1month']
1040
1041 # dat$renal_function_at_admission.cat
1042 # dat$renal_function_status7d
1043 # dat$renal_function_status_1month.chr
1044 # dat$renal_function_status_3month
1045
1046 library(tidyr)
1047 library(data.table)
1048 dat$renal_function_status_3month.chr <- gsubVec(c(1, 2, 3), c('NKD', 'AKD', 'CKD'), dat$renal_function_status_3month)
1049 dat$renal_function_status_1month.chr <- as.character(dat$renal_function_status_1month.chr)
1050 dat[which(is.na(dat$renal_function_status_1month.chr)), ]
1051
1052 #dat[, .N, by=.(renal_function_at_admission.cat, renal_function_status7d, renal_function_status_1month.chr,
1053       renal_function_status_3month)]
1054
1055 library(tidyverse)
1056
1057 sankey1 <- dat %>% count(renal_function_at_admission.cat, renal_function_status7d)
1058 colnames(sankey1) <- c("source", "target", "value")
1059
1060 sankey1$source <- gsubVec(c('NKD', 'AKD', 'CKD'), c(0, 1, 2), sankey1$source)
1061 sankey1$target <- gsubVec(c('NKD', 'AKD', 'AKI', 'CKD'), c(3, 4, 5, 6), sankey1$target)
1062
1063 sankey2 <- dat %>% count(renal_function_status7d, renal_function_status_1month.chr)
1064 colnames(sankey2) <- c("source", "target", "value")
1065 sankey2[is.na(sankey2)] = "NA"
1066
1067 sankey2$source <- gsubVec(c('NKD', 'AKD', 'AKI', 'CKD'), c(3, 4, 5, 6), sankey2$source)
1068 sankey2$target <- gsubVec(c('NKD', 'AKD', 'CKD', 'NA'), c(7, 8, 9, 10), sankey2$target)
1069
1070 sankey3 <- dat %>% count(renal_function_status_1month.chr, renal_function_status_3month.chr)
1071 colnames(sankey3) <- c("source", "target", "value")
1072 sankey3[is.na(sankey3)] = "NA"
1073
1074 sankey3$source <- gsubVec(c('NKD', 'AKD', 'CKD', 'NA'), c(7, 8, 9, 10), sankey3$source)
1075 sankey3$target <- gsubVec(c('NKD', 'AKD', 'CKD', 'NA'), c(11, 12, 13, 14), sankey3$target)
1076
1077 sankey.tot <- data.frame(rbind(sankey1, sankey2, sankey3))
1078
1079 change <- c('source', 'target', 'value')
1080 sankey.tot[,change] %>% lapply(function(x) as.numeric(x))
1081
1082 sankey.tot <- arrange(sankey.tot, source, target)
1083
1084 nodes = data.frame("name" =
1085   c("NKD",
1086     "AKD",
1087     "CKD",
1088     "NKD",
1089     "AKD",
1090     "AKI",
1091     "CKD",
1092     "NKD",
1093     "AKD",
1094     "CKD",
1095     "NA",
1096     "NKD",
1097     "AKD",
1098     "CKD",
1099     "NA"))
1100
1101 nodes1 = data.frame("name" =
1102   c("NKD",
1103     "AKD",
1104     "CKD",
1105     "NKD",

```

```

1104 "AKD",
1105 "AKI",
1106 "CKD"))
1107
1108 library(networkD3)
1109
1110 require(RColorBrewer)
1111
1112 match(sanke$tot$source, nodes$name)
1113
1114 f <- function(pal) brewer.pal(brewer.pal.info[pal, "maxcolors"], pal)
1115 cols <- f("Set1")
1116
1117 nodes[which(nodes$name == "NKD"), 'color'] <- '#FFFFFF'
1118 nodes[which(nodes$name == "AKD"), 'color'] <- '#33CCCC' #'#87CEEB' skyblue
1119 nodes[which(nodes$name == "CKD"), 'color'] <- '#00008B'
1120 nodes[which(nodes$name == "AKI"), 'color'] <- '#C5A111'
1121 nodes[which(nodes$name == "NA"), 'color'] <- '#808080'
1122 nodes[which(nodes$name == "NA"), 'color'] <- '#000000'
1123
1124 sankey.1 <- as.data.frame(sanke1)
1125
1126 sankeyNetwork(Links = sankey.1, Nodes = nodes1,
1127 Source = "source", Target = "target",
1128 Value = "value", NodeID = "name")
1129
1130 library(plotly)
1131
1132 p <- plot_ly(
1133   type = "sankey",
1134   orientation = "h",
1135
1136   node = list(
1137     label = nodes$name,
1138     color = nodes$color,
1139     pad = 15,
1140     thickness = 20,
1141     line = list(
1142       color = "black",
1143       width = 0.5
1144     )
1145   ),
1146
1147   link = list(
1148     source = sankey$tot$source,
1149     target = sankey$tot$target,
1150     value = sankey$tot$value
1151   )
1152 ) %>%
1153 layout(
1154   font = list(
1155     size = 10
1156   )
1157 )
1158 print(p)
1159
1160 if (!require("processx")) install.packages("processx")
1161
1162orca(p, "sankey.pdf")
1163
1164
1165
1166 #mytable <- xtabs( ~ Enrol_eGFR_less_60.new + eGFR_less_than75_at_enrol.new + renal_function_at_admission.cat, data =
1167   dat)
1168
1169 library(gmodels)
1170
1171
1172 #CrossTable(dat$Enrol_eGFR_less_60.new, dat$eGFR_less_than75_at_enrol.new, dat$renal_function_at_admission.cat)
1173
1174
1175 #devtools::install_github("erblast/easyalluvial")
1176
1177
1178
1179 #library(magrittr)
1180 #change <- c('renal_function_at_admission.cat', 'renal_function_status7d', 'renal_function_status_1month.chr', '
1181   renal_function_status_3month.chr')

```

```

1181 #dat[,change] %>% lapply (function(x) as.character(x))
1182
1183
1184
1185
1186 # library(easyalluvial)
1187 # alluvial_wide( dplyr::select(dat, admission = renal_function_at_admission.cat, '7day' = renal_function_status7d ,
1188 #                             '1month' = renal_function_status_1month.chr, '2month' = renal_function_status_3month.
1189 #                             chr),
1190 #               fill_by = 'first_variable', auto_rotate_xlabs = FALSE)
1191
1192 library(ggalluvial)
1193 library(tidyverse)
1194 dat.g <- dat
1195 dat.g[which(dat.g$Cr3month == 0), 'recovery_at_3_month'] <- NA
1196 dat.g[which(dat.g$Cr6month == 0), 'recovery_at_6_month'] <- NA
1197
1198 dat.g$renal_function_status7d <- gsub('NKD', 'NKD', dat.g$renal_function_status7d)
1199 dat.g[which(dat.g$Mortality_by_7days == 1), 'renal_function_status7d'] <- 'Mortality'
1200 dat.g[which(is.na(dat.g$renal_function_status7d)), 'renal_function_status7d'] <- 'Loss to Follow Up'
1201
1202 dat.g[which(dat.g$Mortality_by_1month == 1), 'recovery_at_1_month'] <- 'Mortality'
1203 dat.g[which(is.na(dat.g$recovery_at_1_month)), 'recovery_at_1_month'] <- 'Loss to Follow Up'
1204
1205 dat.g[which(dat.g$Mortality_by_3months == 1), 'recovery_at_3_month'] <- 'Mortality'
1206 dat.g[which(is.na(dat.g$recovery_at_3_month)), 'recovery_at_3_month'] <- 'Loss to Follow Up'
1207
1208 dat.g[which(dat.g$Mortality_by_6months == 1), 'recovery_at_6_month'] <- 'Mortality'
1209 dat.g[which(is.na(dat.g$recovery_at_6_month)), 'recovery_at_6_month'] <- 'Loss to Follow Up'
1210
1211 dat.g[which(dat.g$recovery_at_1_month == 'New onset AKD'), 'recovery_at_1_month'] <- 'AKD'
1212 dat.g[which(dat.g$recovery_at_1_month == 'Recovery from AKD'), 'recovery_at_1_month'] <- 'NKD'
1213 dat.g[which(dat.g$recovery_at_1_month == 'Recovery from AKI'), 'recovery_at_1_month'] <- 'NKD'
1214
1215 dat.g[which(dat.g$recovery_at_3_month == 'New onset AKD'), 'recovery_at_3_month'] <- 'AKD'
1216 dat.g[which(dat.g$recovery_at_3_month == 'Recovery from AKD'), 'recovery_at_3_month'] <- 'NKD'
1217 dat.g[which(dat.g$recovery_at_3_month == 'Recovery from AKI'), 'recovery_at_3_month'] <- 'NKD'
1218 dat.g[which(dat.g$recovery_at_3_month %in% c('CKD progression', 'New onset CKD', 'Stable CKD')), 'recovery_at_3_month
1219 ] <- 'CKD'
1220
1221 dat.g[which(dat.g$renal_function_status7d == 'AKI' & dat.g$recovery_at_3_month == 'AKI'), 'recovery_at_3_month'] <- '
1222 CKD'
1223
1224 dat.g[which(dat.g$recovery_at_6_month == 'New onset AKD'), 'recovery_at_6_month'] <- 'AKD'
1225 dat.g[which(dat.g$recovery_at_6_month == 'Recovery from AKD'), 'recovery_at_6_month'] <- 'NKD'
1226 dat.g[which(dat.g$recovery_at_6_month == 'Recovery from AKI'), 'recovery_at_6_month'] <- 'NKD'
1227 dat.g[which(dat.g$recovery_at_6_month %in% c('CKD progression', 'New onset CKD', 'Stable CKD')), 'recovery_at_6_month
1228 ] <- 'CKD'
1229
1230 dat.g[which(dat.g$renal_function_status7d == 'AKI' & dat.g$recovery_at_6_month == 'AKI'), 'recovery_at_6_month'] <- '
1231 CKD'
1232
1233 dat.g$renal_function_at_admission.cat <- factor(levels = c('NKD', 'AKD', 'AKI', 'CKD', 'Loss to Follow Up', 'Mortality
1234 '), dat.g$renal_function_at_admission.cat)
1235
1236 dat.g$renal_function_status7d <- factor(levels = c('NKD', 'AKD', 'AKI', 'CKD', 'Mortality'), dat.
1237 g$renal_function_status7d)
1238
1239 dat.g$recovery_at_1_month <- factor(levels = c('NKD', 'AKD', 'AKI', 'CKD', 'Loss to Follow Up', 'Mortality'), dat.
1240 g$recovery_at_1_month)
1241
1242 dat.g$recovery_at_3_month <- factor(levels = c('NKD', 'AKD', 'AKI', 'CKD', 'Loss to Follow Up', 'Mortality'), dat.
1243 g$recovery_at_3_month)
1244
1245 dat.g$recovery_at_6_month <- factor(levels = c('NKD', 'AKD', 'AKI', 'CKD', 'Loss to Follow Up', 'Mortality'), dat.
1246 g$recovery_at_6_month)
1247
1248 count.dat <- dat.g %>% count(renal_function_at_admission.cat, renal_function_status7d, recovery_at_1_month,
1249 recovery_at_3_month, recovery_at_6_month)
1250
1251
1252 nodes[which(nodes$name == "NKD"), 'color'] <- '#FFFFFF'
1253 nodes[which(nodes$name == "AKD"), 'color'] <- '#33CCCC' #'87CEEB' skyblue
1254 nodes[which(nodes$name == "CKD"), 'color'] <- '#00008B'
1255 nodes[which(nodes$name == "AKI"), 'color'] <- '#C55A11'
1256 nodes[which(nodes$name == "NA"), 'color'] <- '#808080'
1257 nodes[which(nodes$name == "NA"), 'color'] <- '#000000'
1258
1259 ggplot(as.data.frame(count.dat),
1260        aes(y = n, axis1 = renal_function_at_admission.cat, axis2 = renal_function_status7d,
1261            axis3 = recovery_at_1_month, axis4 = recovery_at_3_month, axis5 = recovery_at_6_month)) +
1262  geom_alluvium(aes(fill = renal_function_at_admission.cat)) +
1263  geom_stratum() +
1264  geom_text(stat = "stratum", infer.label = TRUE) +
1265  scale_fill_manual(values = c("#FFFFFF", "#33CCCC", "#C55A11", "#00008B", "#808080", "#000000"))

```



```

1249
1250
1251
1252 dRG.long <- to_lodes_form(count.dat ,
1253                          axes = 1:5,
1254                          id = "Cohort")
1255
1256 p <- ggplot(dRG.long ,
1257            aes(x = x, stratum = stratum , alluvium = Cohort ,
1258              y = n,
1259              fill = stratum, label = stratum)) +
1260   scale_x_discrete(expand = c(.1, .1)) +
1261   geom_flow(color = 'darkgray') +
1262   geom_stratum(alpha = 0.85) +
1263   geom_text(stat = "stratum", size = 3) +
1264   #geom_text(aes(x = stratum), dRG.long, col = 'white') +
1265   theme(legend_position = "none") +
1266   scale_fill_manual(values = c("#FFFFFF", "#33CCCC", "#C55A11", "#00008B", "#808080", "#000000"))
1267
1268
1269 pdf('alluvial.pdf', height = 20, width = 30)
1270 print(p)
1271 dev.off()
1272
1273
1274 raw.tab <- demoTab(vars = c('renal_function_at_admission.cat', 'renal_function_status7d', 'recovery_at_1_month', '
1275   recovery_at_3_month', 'recovery_at_6_month'), data = dat, group = 'phase.cat')
1276
1277 rownames(raw.tab) <- gsub('\\_', ' ', rownames(raw.tab))
1278
1279 dat[which(dat.g$recovery_at_6_month == 'NKD' & dat.g$recovery_at_3_month == 'CKD'), c("patient_id", "
1280   recovery_at_3_month", "recovery_at_6_month", "sCr3month", "sCr6month")]
1281
1282 dat[which(is.na(dat$recovery_at_3_month) & dat$sCr3month == 1), c("patient_id", "recovery_at_3_month", "sCr3month", '
1283   p21_m3fu_scr', "renal_function_status7d2", "p02_scr_us", "Mortality_by_3months", "p21_m3fu_gfr", "
1284   p21_m1fu_gfr_original")]
1285
1286 dat[which(is.na(dat$recovery_at_6_month) & dat$sCr6month == 1), c("patient_id", "recovery_at_6_month", "sCr6month", '
1287   p21_m6fu_scr', "renal_function_status7d2", "p02_scr_us", "Mortality_by_6months", "p21_m6fu_gfr", "
1288   p21_m1fu_gfr_original")]
1289
1290
1291 pdf('box_plot.pdf', height = 6, width = 9)
1292 p <- ggplot(dat[complete.cases(dat$recovery_at_3_month), ], aes(x = recovery_at_3_month, y = p21_m3fu_scr)) +
1293   geom_boxplot() + geom_jitter(shape=3, position=position_jitter(0.2))
1294 p
1295
1296 p <- ggplot(dat[complete.cases(dat$recovery_at_6_month), ], aes(x = recovery_at_6_month, y = p21_m6fu_scr)) +
1297   geom_boxplot() + geom_jitter(shape=3, position=position_jitter(0.2))
1298 p
1299 dev.off()

```