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# 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 |
|---|---|---|---|---|
| **Mortality at discharge - Hospitalized patients** | 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* |
| **Mortality during follow up - Hospitalized patients** | 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 |
| **Mortality during follow up - Non-hospitalized patients** | 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 |
| **Overall Mortality** | 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<br>($n = 2101$) | Observation<br>($n = 978$) | Intervention<br>($n = 1123$) | 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<br>($n = 2101$) | Observation<br>($n = 978$) | Intervention<br>($n = 1123$) | p-value |
|---|---|---|---|---|
| **Renal Function at admission** | | | | |
| 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%) | |
| **Renal Fuction at 7 days** | | | | |
| 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 |
| Disposition | | | | |
| Sent home | 975 (46.4%) | 400 (40.9%) | 575 (51.2%) | <0.001 |
| Admitted | 1126 (53.6%) | 578 (59.1%) | 548 (48.8%) | |
| NKD | 208 (18.5%) | 125 (21.6%) | 83 (15.1%) | 0.006 |
| AKI | 518 (46.0%) | 211 (36.5%) | 307 (56.0%) | <0.001 |
| AKD | 351 (31.2%) | 208 (36.0%) | 143 (26.1%) | <0.001 |
| CKD | 49 (4.4%) | 34 (5.9%) | 15 (2.7%) | 0.012 |
| Time(hours) in health care facility in all patients | 28.69 (4.25 - 120.00) | 27.00 (3.52 - 120.78) | 31.00 (4.85 - 118.00) | 0.243 |
| Sent home | 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 |
| **Dialysis Requirement** | | | | |
| 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 |
|---|---|---|---|---|
| **Renal Recovery At 3 months** | | | | |
| 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 |
| **At 6 months** | | | | |
| 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 |
| **Overall** | | | | |
| 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%) | 714 (73.0%) | 874 (77.8%) | 0.012* |
| | | $n = 637$ | $n = 322$ | $n = 315$ | |
| | 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%) | 220 (55.0%) | 378 (65.7%) | |
| | | $n = 239$ | $n = 79$ | $n = 160$ | |
| | 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%) | 494 (85.5%) | 496 (90.5%) | |
| | | $n = 398$ | $n = 243$ | $n = 155$ | |
| | 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%) | 592 (62.2%) | 785 (76.6%) | <0.001*** |
| | | $n = 1186$ | $n = 494$ | $n = 692$ | |
| | 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%) | 140 (37.4%) | 329 (69.0%) | |
| | | $n = 449$ | $n = 138$ | $n = 311$ | |
| | 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%) | 452 (78.2%) | 456 (83.2%) | |
| | | $n = 737$ | $n = 356$ | $n = 381$ | |
| | 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 | $n = 978$ | $n = 1123$ | $n = 2101$ | |
| 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 | $n = 978$ | $n = 1123$ | $n = 2101$ | |
| 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 | $n = 978$ | $n = 1123$ | $n = 2101$ | |
| 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 | $n = 978$ | $n = 1123$ | $n = 2101$ | |
| 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 | $n = 952$ | $n = 1029$ | $n = 1981$ | |
| 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 | $n = 952$ | $n = 1031$ | $n = 1983$ | |
| 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 | $n = 952$ | $n = 1031$ | $n = 1983$ | |
| 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 | $n = 952$ | $n = 1031$ | $n = 1983$ | |
| 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 | $n = 578$ | $n = 548$ | $n = 1126$ | |
| 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 | $n = 914$ | $n = 962$ | $n = 1876$ | |
| 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 | $n = 886$ | $n = 941$ | $n = 1827$ | |
| 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%) | |
| Mortalityat 3months | $n = 868$ | $n = 909$ | $n = 1777$ | |
| 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 | $n = 836$ | $n = 889$ | $n = 1725$ | |
| 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 |
|---|---|---|---|---|
| **Renal Recovery At 3 months** | | | | |
| De novo CKD | 66/415 (15.9%) | 27/148 (18.2%) | 39/267 (14.6%) | 0.331 |
| **At 6 months** | | | | |
| De novo CKD | 37/230 (16.1%) | 21/96 (21.9%) | 16/134 (11.9%) | 0.047* |
| **Overall** | | | | |
| De novo CKD | 79/484 (16.3%) | 37/186 (19.9%) | 42/298 (14.1%) | 0.101 |

Table 8: Mortality - NKD vs. other

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

Figure 1:

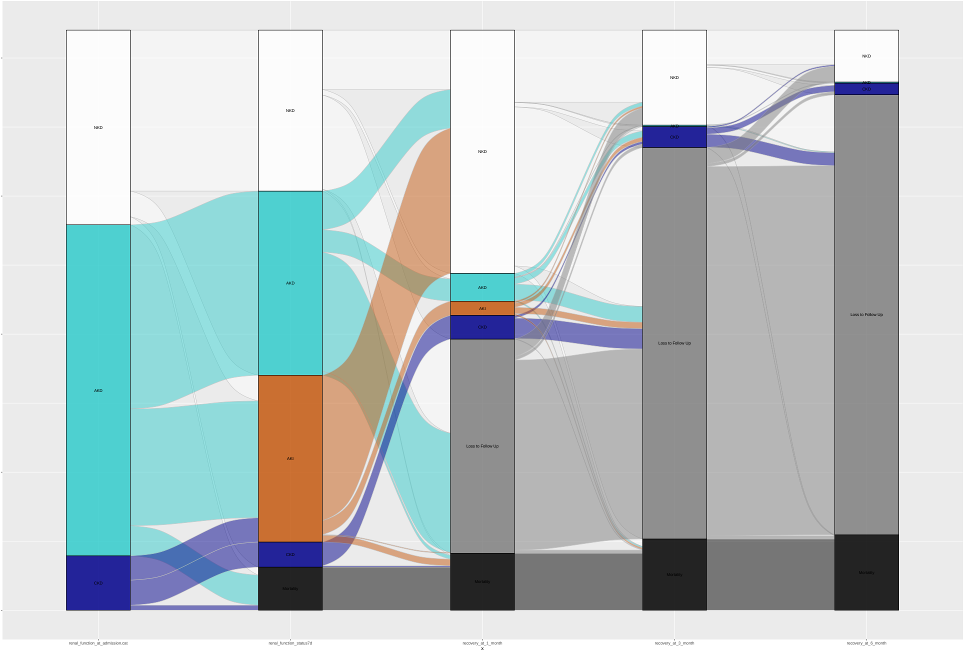

Table 9: Raw groupings of the new variables

| | Overall | Observation | Intervention |
|---|---|---|---|
| renal function at admission.cat | $n = 2101$ | $n = 978$ | $n = 1123$ |
| 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 | $n = 2101$ | $n = 978$ | $n = 1123$ |
| 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 | $n = 1189$ | $n = 515$ | $n = 674$ |
| 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 | $n = 890$ | $n = 343$ | $n = 547$ |
| 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 | $n = 786$ | $n = 313$ | $n = 473$ |
| 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:

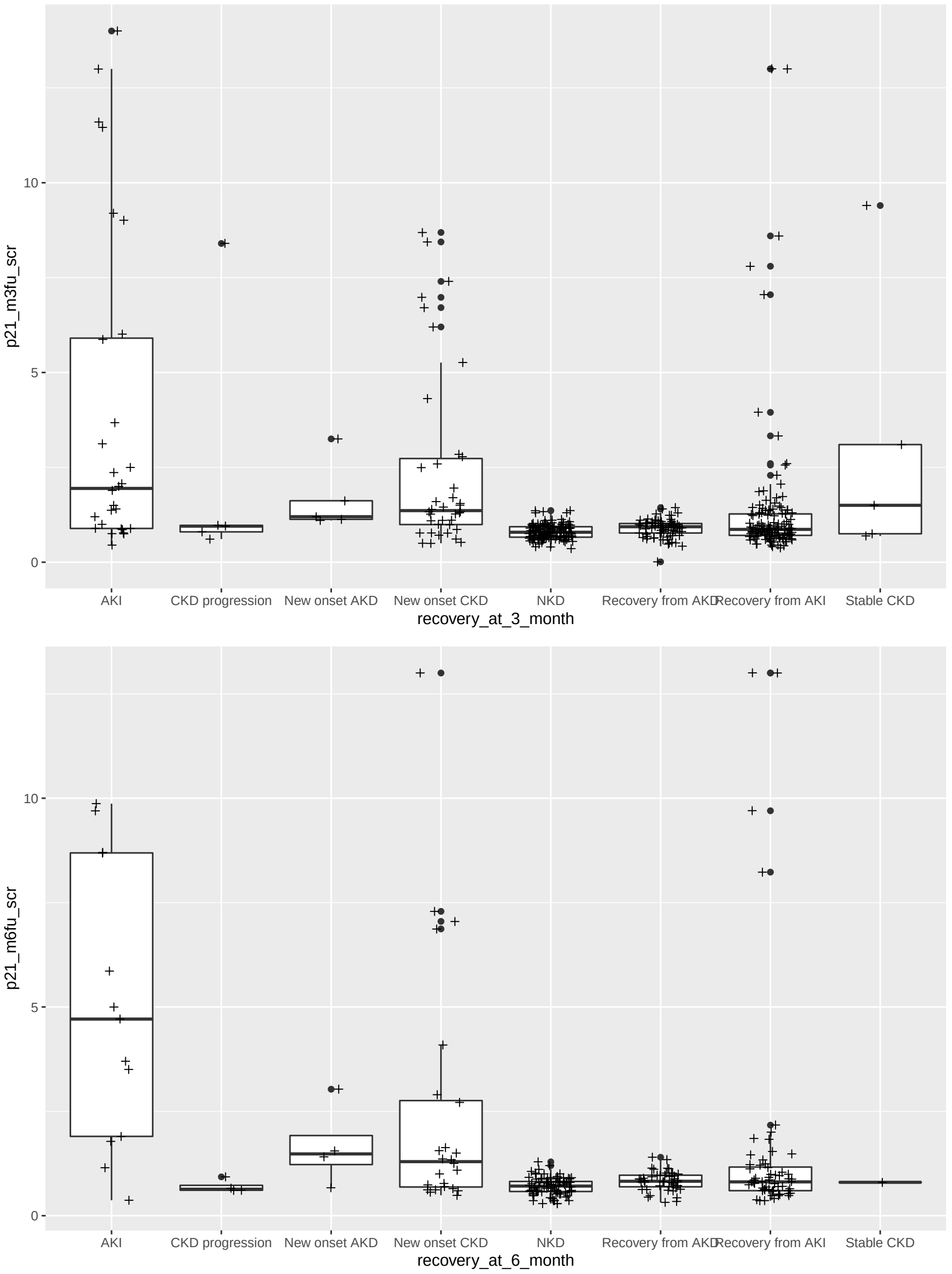
p21_m3fu_scr
0
5
10
AKI
CKD progression
New onset AKD
New onset CKD
NKD
Recovery from AKD
Recovery from AKI
Stable CKD
recovery_at_3_month
p21_m6fu_scr
0
5
10
AKI
CKD progression
New onset AKD
New onset CKD
NKD
Recovery from AKD
Recovery from AKI
Stable CKD
recovery_at_6_month

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

| | AKD | CKD | NKD | Overall | p-value |
|---|---|---|---|---|---|
| **Age** | $n = 1199$ | $n = 197$ | $n = 701$ | $n = 2097$ | |
| | 43.98 (22.15) | 54.99 (23.52) | 38.65 (19.06) | 43.23 (21.77) | <0.001*** |
| **Adult** | $n = 1199$ | $n = 197$ | $n = 701$ | $n = 2097$ | |
| Yes | 1031 (86.0%) | 173 (87.8%) | 621 (88.6%) | 1825 (87.0%) | 0.251 |
| **Female** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 612 (51.0%) | 100 (50.8%) | 405 (57.4%) | 1117 (53.2%) | 0.020* |
| **Race** | $n = 1198$ | $n = 197$ | $n = 704$ | $n = 2099$ | |
| 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%) | |
| **DM** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 146 (12.2%) | 63 (32.0%) | 47 (6.7%) | 256 (12.2%) | <0.001*** |
| **Liver** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 65 (5.4%) | 11 (5.6%) | 11 (1.6%) | 87 (4.1%) | <0.001*** |
| **Heart** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 39 (3.3%) | 29 (14.7%) | 20 (2.8%) | 88 (4.2%) | <0.001*** |
| **Lung** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 61 (5.1%) | 19 (9.6%) | 39 (5.5%) | 119 (5.7%) | 0.037* |
| **HIV** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 222 (18.5%) | 6 (3.0%) | 145 (20.6%) | 373 (17.8%) | <0.001*** |
| **Anemia** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 149 (12.4%) | 43 (21.8%) | 63 (8.9%) | 255 (12.1%) | <0.001*** |
| **Cancer** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 20 (1.7%) | 5 (2.5%) | 11 (1.6%) | 36 (1.7%) | 0.635 |
| **Hypertension** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 254 (21.2%) | 97 (49.2%) | 67 (9.5%) | 418 (19.9%) | <0.001*** |
| **Dehydration** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 902 (75.2%) | 147 (74.6%) | 484 (68.7%) | 1533 (73.0%) | 0.007** |
| **Dehydration: Diarrhea** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 335 (27.9%) | 50 (25.4%) | 215 (30.5%) | 600 (28.6%) | 0.287 |
| **Dehydration: Vomiting** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 626 (52.2%) | 95 (48.2%) | 329 (46.7%) | 1050 (50.0%) | 0.057 |
| **Dehydration: Sweating** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 78 (6.5%) | 11 (5.6%) | 70 (9.9%) | 159 (7.6%) | 0.013* |
| **Dehydration: Thirst** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 170 (14.2%) | 36 (18.3%) | 190 (27.0%) | 396 (18.8%) | <0.001*** |
| **Dehydration: Low intake** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 615 (51.3%) | 112 (56.9%) | 294 (41.7%) | 1021 (48.6%) | <0.001*** |
| **Weakness** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 1098 (91.6%) | 178 (90.4%) | 638 (90.5%) | 1914 (91.1%) | 0.675 |
| **Urinary** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 661 (55.1%) | 125 (63.5%) | 381 (54.0%) | 1167 (55.5%) | 0.057 |
| **Urinary: Oliguria** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 399 (33.3%) | 91 (46.2%) | 258 (36.6%) | 748 (35.6%) | 0.002** |
| **Urinary: Polyuria** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| 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 |
|---|---|---|---|---|---|
| **Urinary: Dysuria** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 248 (20.7%) | 36 (18.3%) | 148 (21.0%) | 432 (20.6%) | 0.697 |
| **Urinary: Hematuria** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 50 (4.2%) | 10 (5.1%) | 36 (5.1%) | 96 (4.6%) | 0.600 |
| **Infection** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 868 (72.4%) | 111 (56.3%) | 537 (76.2%) | 1516 (72.2%) | <0.001*** |
| **Infection: Malaria** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 64 (5.3%) | 2 (1.0%) | 42 (6.0%) | 108 (5.1%) | 0.019* |
| **Infection: GI** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 206 (17.2%) | 28 (14.2%) | 176 (25.0%) | 410 (19.5%) | <0.001*** |
| **Hypotension** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 285 (23.8%) | 38 (19.3%) | 136 (19.3%) | 459 (21.8%) | 0.049* |
| **Swelling: Whole** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 92 (7.7%) | 39 (19.8%) | 31 (4.4%) | 162 (7.7%) | <0.001*** |
| **Swelling: Face** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 100 (8.3%) | 15 (7.6%) | 40 (5.7%) | 155 (7.4%) | 0.098 |
| **Swelling: Lower** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 294 (24.5%) | 50 (25.4%) | 105 (14.9%) | 449 (21.4%) | <0.001*** |
| **Asthenia** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 175 (14.6%) | 39 (19.8%) | 167 (23.7%) | 381 (18.1%) | <0.001*** |
| **Dyspnea** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 209 (17.4%) | 50 (25.4%) | 76 (10.8%) | 335 (15.9%) | <0.001*** |
| **Weight loss** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 251 (20.9%) | 34 (17.3%) | 143 (20.3%) | 428 (20.4%) | 0.493 |
| **loss of appetite** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 789 (65.8%) | 112 (56.9%) | 464 (65.8%) | 1365 (65.0%) | 0.043* |
| **Pallor** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 218 (18.2%) | 47 (23.9%) | 128 (18.2%) | 393 (18.7%) | 0.150 |
| **ACEI** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 151 (12.6%) | 61 (31.0%) | 40 (5.7%) | 252 (12.0%) | <0.001*** |
| **NSAIDS** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| Yes | 154 (12.8%) | 35 (17.8%) | 112 (15.9%) | 301 (14.3%) | 0.066 |
| **Tenofovir** | $n = 1199$ | $n = 197$ | $n = 705$ | $n = 2101$ | |
| 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<br>($n = 1199$) | CKD<br>($n = 197$) | NKD<br>($n = 705$) | Overall<br>($n = 2101$) |
|---|---|---|---|---|
| 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<br>($n = 439$) | CKD<br>($n = 91$) | NKD<br>($n = 98$) |
|---|---|---|---|
| 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 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

```
library(Hmisc)
library(plyr)
library(dplyr)
library(readxl)
library(magrittr)
library(pROC)
library(lubridate)
library(xtable)
library(randomForest)
library(ROCR)
library(nnet)
library(rpart)
library(car)
library(glmnet)
library(caret)
#library(MKmisc)
library(rms)
library(scales)
library(diagram)
library(stringr)
library(stringi)
options(digit = 3, stringsAsFactors = FALSE, width = 100)
source('/Users/e4lee/Desktop/CTRI/CTRI_Functions.R')
setwd ('/Users/e4lee/Desktop/CTRI/Projects/8425_Mehta_2/Project 2/Analysis Plan/')


RE.Names <- function(x){
  dtNames <- tools::toTitleCase(tolower(gsubVec(c('\\_', '\\.'),c(' ', ' '), x)))
  dtNames <- gsubVec(c('Hops', 'Dm', 'Cad', 'Mi', 'Aki', 'Icd9', 'Hiv', 'Dg', 'Ckd', 'dm', 'Esrd', 'Mlophaty',
                       'Poisonig', 'Be ','Acei', 'Arb', 'Cni', 'Lmwh', 'Gk', 'k at', ' b', 'Gaki', 'New ', 'Age c', 'k
                            c'),
                     c('', 'DM', 'CAD', 'MI', 'AKI', 'ICD9', 'HIV', '', 'CKD', 'DM', 'ESRD', 'Miophaty',
                       'Poisoning', '', 'ACEI', 'ARB', 'CNI', 'LMWH', 'GK', 'Potassium Level at', ' B', 'gAKI', '', '
                            Age Categorized',
                       'K Categorized'),
                     dtNames, fixed = T)
  dtNames
}


#############################################
## Preliminaries                           ##
#############################################
#dat1 <- read_xlsx('/Users/e4lee/Desktop/CTRI/Projects/8425_Mehta_2/Project 2/Data/table for Euy 7feb2018.xlsx', sheet
      = 1)
dat2 <- read_xlsx('/Users/e4lee/Desktop/CTRI/Projects/8425_Mehta_2/Project 2/Data/01_11_20/table for Euy 2020 01 08.
     xlsx', sheet = 1)
dat2 <- data.frame(dat2)
dat <- dplyr::filter(dat2, p01_enrolled == 1, noscr == 0)
dat.o <- dat
dat$phase.cat <- factor(gsubVec(c(1, 2), c('Observation', 'Intervention'), dat$phase), levels = c('Observation', '
     Intervention'))


####### New data set modification ###########
## Renal function based on < 60 is now used
## The output is located in renal_function _*time*2 columns
## Reassigned column names to make the code run

dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m1fu_scr <= dat$p02_scr_us), 'recovery_at_1_month']  <- 1
dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m1fu_scr > dat$p02_scr_us), 'recovery_at_1_month'] <- 0

dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m3fu_scr <= dat$p02_scr_us), 'recovery_at_3_month']  <- 1
dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m3fu_scr > dat$p02_scr_us), 'recovery_at_3_month'] <- 0

dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m6fu_scr <= dat$p02_scr_us), 'recovery_at_6_month'] <- 1
dat[which(dat$renal_function_status7d2 == 2 & dat$p21_m6fu_scr > dat$p02_scr_us), 'recovery_at_6_month'] <- 0

dat$renal_function_at_admission.old <- dat$renal_function_at_admission
dat$renal_function_status7d.old <- dat$renal_function_status7d

dat$renal_function_at_admission <- dat$renal_function_at_admission2
dat$renal_function_status7d <- dat$renal_function_status7d2

dat$recovery_at_3_month.o <- dat$recovery_at_3_month

```

```r
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)
dat$recovery_at_3_month <- gsubVec(c(0, 1, 2, 3, 4, 5, 6, 7),
                                    c('AKI', 'Recovery from AKI', 'New onset AKD', 'Recovery from AKD', 'NKD', 'New onset CKD', 'Stable CKD', 'CKD progression'),
                                    dat$recovery_at_3_month)
dat$recovery_at_6_month <- gsubVec(c(0, 1, 2, 3, 4, 5, 6, 7),
                                    c('AKI', 'Recovery from AKI', 'New onset AKD', 'Recovery from AKD', 'NKD', 'New onset CKD', 'Stable CKD', 'CKD progression'),
                                    dat$recovery_at_6_month)
##########

#dat$Enrol_eGFR_less_60.new <- ifelse(dat$p21_enrol_gfr < 60, 1, 0)
#dat[which(dat$renal_function_at_admission == 2 & dat$proteinuria_at_enrollment == 0), 'renal_function_at_admission_AKD_by_eGFR_only'] <- 1

#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)

#dat[which(dat$renal_function_at_admission_need_change == 1), 'renal_function_at_admission'] <- 1
## Appendix Table 2 - Mortality at discharge
dat[which(is.na(dat$mortality_at_discharge)), c("mortality_at_discharge")] <- 0
dat[which(dat$final_disposition_with_mortality != 1), c("mortality_at_discharge")] <- NA
dat$mortality_at_discharge <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$mortality_at_discharge), levels = c('Yes', 'No'))
dat$renal_function_status7d <- factor(gsubVec(c(1, 2, 3, 4), c('NKD', 'AKI', 'AKD', 'CKD'), dat$renal_function_status7d), levels = c('NKD', 'AKI', 'AKD', 'CKD'))
dat$Dialysis_indication_final <- gsubVec(c(0, 1, 2), c('Not Dialyzed', 'Dialysis indication but not dialyzed', 'Dialyzed'), dat$Dialysis_indication_final)

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

dat[which(dat$renal_function_status7d != 'NKD'), 'mortality_at_discharge.NKD'] <- NA
dat[which(dat$renal_function_status7d == 'AKI'), 'mortality_at_discharge.no.aki'] <- NA
dat[which(dat$renal_function_status7d != 'AKI'), 'mortality_at_discharge.aki'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 1), 'mortality_at_discharge.stg1'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 2), 'mortality_at_discharge.stg2'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 3), 'mortality_at_discharge.stg3'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | !dat$Final_total_AKI_stage %in% c(2, 3)), 'mortality_at_discharge.stg23'] <- NA
dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'mortality_at_discharge.indi.nodia'] <- NA
dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'mortality_at_discharge.dia'] <- NA
dat[which(dat$renal_function_status7d != 'AKD'), 'mortality_at_discharge.akd'] <- NA
dat[which(dat$renal_function_status7d != 'CKD'), 'mortality_at_discharge.ckd'] <- NA


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',
                                                    'mortality_at_discharge.stg1', 'mortality_at_discharge.stg2', 'mortality_at_discharge.stg3', 'mortality_at_discharge.stg23',
                                                    'mortality_at_discharge.indi.nodia', 'mortality_at_discharge.dia', 'mortality_at_discharge.akd', 'mortality_at_discharge.ckd'),
        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'))

rownames(app.tab2.1)[seq(2, 36, 3)] <- rownames(app.tab2.1)[seq(1, 36, 3)]
final <- app.tab2.1[seq(2, 36, 3), ]

size <- app.tab2.1[seq(1, 36, 3), 1:3]

dol.loc <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    dol.loc[j, i] <- gregexpr(pattern ='\\$', final[j, i])[[1]][2]
  }
}

deno.size <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
for(i in 1:ncol(size)){
  for(j in 1:nrow(size)){
    deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^;]*(?=\\$)"))
  }
}

```

```r
for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
  }
}

app.tab2.d <- final



dat[which(is.na(dat$Mortality_overall)), c("patient_id", "mortality_at_discharge", 'mortality_follow_up', "Mortality_overall")]

dat[which(dat$mortality_at_discharge == 'Yes'), c("patient_id", "mortality_at_discharge", 'mortality_follow_up')]
#pc <- "bt43xx"
#paste(append(strsplit(pc, "")[[1]], "+", nchar(pc) - 3), collapse = "")

final %<>% lapply (function(x) gregexpr(pattern ='\\$', x)[[1]][2])

#gregexpr(pattern ='\\$', final[1,1])[[1]][2]

## Appendix Table 2 - Mortality during follow up - Hospitalized
dat$mortality_follow_up.o <- dat$mortality_follow_up
dat$mortality_follow_up <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$mortality_follow_up.o), levels = c('Yes', 'No'))
dat[which(dat$mortality_at_discharge == 'Yes'), "mortality_follow_up"] <- NA
dat[which(dat$final_disposition_with_mortality != 1), c("mortality_follow_up")] <- NA

dat$renal_function_status7d <- gsubVec(c(1, 2, 3, 4), c('NKD', 'AKI', 'AKD', 'CKD'), dat$renal_function_status7d)
dat$Dialysis_indication_final <- gsubVec(c(0, 1, 2), c('Not Dialyzed', 'Dialysis indication but not dialyzed', 'Dialyzed'), dat$Dialysis_indication_final)

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

dat[which(dat$renal_function_status7d != 'NKD'), 'mortality_follow_up.NKD'] <- NA
dat[which(dat$renal_function_status7d == 'AKI'), 'mortality_follow_up.no.aki'] <- NA
dat[which(dat$renal_function_status7d != 'AKI'), 'mortality_follow_up.aki'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 1), 'mortality_follow_up.stg1'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 2), 'mortality_follow_up.stg2'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 3), 'mortality_follow_up.stg3'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | !dat$Final_total_AKI_stage %in% c(2, 3)), 'mortality_follow_up.stg23'] <- NA
dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'mortality_follow_up.indi.nodia'] <- NA
dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'mortality_follow_up.dia'] <- NA
dat[which(dat$renal_function_status7d != 'AKD'), 'mortality_follow_up.akd'] <- NA
dat[which(dat$renal_function_status7d != 'CKD'), 'mortality_follow_up.ckd'] <- NA


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',
                                                 'mortality_follow_up.stg1', 'mortality_follow_up.stg2', 'mortality_follow_up.stg3', 'mortality_follow_up.stg23',
                                                 'mortality_follow_up.indi.nodia', 'mortality_follow_up.dia', 'mortality_follow_up.akd', 'mortality_follow_up.ckd'),
        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'))


rownames(app.tab2.2)[seq(2, 36, 3)] <- rownames(app.tab2.2)[seq(1, 36, 3)]
final <- app.tab2.2[seq(2, 36, 3), ]

size <- app.tab2.2[seq(1, 36, 3), 1:3]

dol.loc <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    dol.loc[j, i] <- gregexpr(pattern ='\\$', final[j, i])[[1]][2]
  }
}

deno.size <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
for(i in 1:ncol(size)){
  for(j in 1:nrow(size)){
    deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^;]*(?=\\$)"))
```

```r
  }
}

for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
  }
}

app.tab2.f <- final


## Appendix Table 2 - Mortality during follow up - Sent Home
dat$mortality_follow_up <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$mortality_follow_up.o), levels = c('Yes', 'No'))
dat[which(dat$mortality_at_discharge == 'Yes'), "mortality_follow_up"] <- NA
dat[which(dat$final_disposition_with_mortality != 2), c("mortality_follow_up")] <- NA

dat$renal_function_status7d <- gsubVec(c(1, 2, 3, 4), c('NKD', 'AKI', 'AKD', 'CKD'), dat$renal_function_status7d)
dat$Dialysis_indication_final <- gsubVec(c(0, 1, 2), c('Not Dialyzed', 'Dialysis indication but not dialyzed', 'Dialyzed'), dat$Dialysis_indication_final)

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

dat[which(dat$renal_function_status7d != 'NKD'), 'mortality_follow_up.NKD'] <- NA
dat[which(dat$renal_function_status7d == 'AKI'), 'mortality_follow_up.no.aki'] <- NA
dat[which(dat$renal_function_status7d != 'AKI'), 'mortality_follow_up.aki'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 1), 'mortality_follow_up.stg1'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 2), 'mortality_follow_up.stg2'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 3), 'mortality_follow_up.stg3'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | !dat$Final_total_AKI_stage %in% c(2, 3)), 'mortality_follow_up.stg23'] <- NA
dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'mortality_follow_up.indi.nodia'] <- NA
dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'mortality_follow_up.dia'] <- NA
dat[which(dat$renal_function_status7d != 'AKD'), 'mortality_follow_up.akd'] <- NA
dat[which(dat$renal_function_status7d != 'CKD'), 'mortality_follow_up.ckd'] <- NA


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',
                                                  'mortality_follow_up.stg1', 'mortality_follow_up.stg2', 'mortality_follow_up.stg3', 'mortality_follow_up.stg23',
                                                  'mortality_follow_up.indi.nodia', 'mortality_follow_up.dia', 'mortality_follow_up.akd', 'mortality_follow_up.ckd'),
        cat.tests = 'fisher.test', rnames = c('{\\bf Mortality during follow up - Non-hospitalized patients}', 'NKD', 'No AKI', 'AKI', '~~~stage 1', '~~~stage 2', '~~~stage 3', '~~~severe AKI (stage2/3)',
                                              'Dialysis indication but not dialyzed', 'Dialyzed', 'AKD', 'CKD'))


rownames(app.tab2.2)[seq(2, 36, 3)] <- rownames(app.tab2.2)[seq(1, 36, 3)]
final <- app.tab2.2[seq(2, 36, 3), ]

size <- app.tab2.2[seq(1, 36, 3), 1:3]

dol.loc <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    dol.loc[j, i] <- gregexpr(pattern ='\\$', final[j, i])[[1]][2]
  }
}

deno.size <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
for(i in 1:ncol(size)){
  for(j in 1:nrow(size)){
    deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^;]*(?=\\$)"))
  }
}

for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
  }
}

app.tab2.f.1 <- final
```

```

## Appendix Table 2 - Overall Mortality
dat[which(is.na(dat$Mortality_overall)), c("Mortality_overall")] <- 0
dat$Mortality_overall <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$Mortality_overall), levels = c('Yes', 'No'))
dat$renal_function_status7d <- gsubVec(c(1, 2, 3, 4), c('NKD', 'AKI', 'AKD', 'CKD'), dat$renal_function_status7d)
dat$Dialysis_indication_final <- gsubVec(c(0, 1, 2), c('Not Dialyzed', 'Dialysis indication but not dialyzed', '
     Dialyzed'), dat$Dialysis_indication_final)

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

dat[which(dat$renal_function_status7d != 'NKD'), 'Mortality_overall.NKD'] <- NA
dat[which(dat$renal_function_status7d == 'AKI'), 'Mortality_overall.no.aki'] <- NA
dat[which(dat$renal_function_status7d != 'AKI'), 'Mortality_overall.aki'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 1), 'Mortality_overall.stg1'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 2), 'Mortality_overall.stg2'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | dat$Final_total_AKI_stage != 3), 'Mortality_overall.stg3'] <- NA
dat[which(dat$renal_function_status7d != 'AKI' | !dat$Final_total_AKI_stage %in% c(2, 3)), 'Mortality_overall.stg23']
     <- NA
dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'Mortality_overall.indi.nodia'] <-
      NA
dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'Mortality_overall.dia'] <- NA
dat[which(dat$renal_function_status7d != 'AKD'), 'Mortality_overall.akd'] <- NA
dat[which(dat$renal_function_status7d != 'CKD'), 'Mortality_overall.ckd'] <- NA


app.tab2.3 <- demoTab(data = dat, group = 'phase.cat', vars = c('Mortality_overall', 'Mortality_overall.NKD', '
     Mortality_overall.no.aki', 'Mortality_overall.aki',
                                                  'Mortality_overall.stg1', 'Mortality_overall.stg2', '
                                                       Mortality_overall.stg3', 'Mortality_overall.stg23',
                                                  'Mortality_overall.indi.nodia', 'Mortality_overall.dia', '
                                                       Mortality_overall.akd', 'Mortality_overall.ckd'),
        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'))


rownames(app.tab2.3)[seq(2, 36, 3)] <- rownames(app.tab2.3)[seq(1, 36, 3)]
final <- app.tab2.3[seq(2, 36, 3), ]

size <- app.tab2.3[seq(1, 36, 3), 1:3]

dol.loc <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    dol.loc[j, i] <- gregexpr(pattern ='\\$', final[j, i])[[1]][2]
  }
}

deno.size <- matrix(rep(NA, 36), nrow = 12, ncol = 3)
for(i in 1:ncol(size)){
  for(j in 1:nrow(size)){
    deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^;]*(?=\\$)"))
  }
}

for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
  }
}

app.tab2.o <- final

app.tab2 <- rbind(app.tab2.d, app.tab2.f, app.tab2.f.1, app.tab2.o)
app.tab2 <- app.tab2[, c(3, 1, 2, 4)]
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}")

### Table 2


dat$p01_age.child <- dat$p01_age.adult <- dat$p01_age
dat$p01_is_child <- factor(gsubVec(c(0, 1), c('Yes', 'No'), dat$p01_is_adult), levels = c('Yes', 'No'))
dat$p01_is_adult <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$p01_is_adult), levels = c('Yes', 'No'))

```

```r
dat[which(dat$p01_is_adult == 'No'), 'p01_age.adult'] <- NA
dat[which(dat$p01_is_adult == 'Yes'), 'p01_age.child'] <- NA

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')
tab2 <- tab2[c(2, 5, 7, 10), ]
rownames(tab2) <- c('Children (<18)', '~~~ Mean Age', 'Adult', '~~~ Mean Age')
tab2 <- tab2[, c(3, 1, 2, 4)]
colnames(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}")
## 4 patients with unkown age/age group
dat[which(is.na(dat$p01_is_adult)), c('patient_id', 'p01_is_adult', 'p01_age')]


## Table 4

table(dat$eGFR_less_than75_at_enrol)
dat$Enrol_eGFR_less_60.new <- ifelse(dat$p21_enrol_gfr < 60, 2, 0)

table(dat$proteinuria_at_enrollment)
#dat$eGFR_less_than75_at_enrol.new <- as.numeric(gsub(1, 2, dat$Enrol_eGFR_less_60.new))
dat[which(is.na(dat$Enrol_eGFR_less_60.new)), 'Enrol_eGFR_less_60.new'] <- 0
dat$akd_cause_enrol <- dat$Enrol_eGFR_less_60.new + dat$proteinuria_at_enrollment
dat$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),
                              levels = c('Based on sCr alone', 'Based on sCr and albuminuria', 'Based on albuminuria alone'))

adm.overall <- fisher.test(dat$renal_function_at_admission, dat$phase.cat)

dat$ckd_adm <- dat$akd_adm <- dat$NKD_adm <- dat$renal_function_at_admission

dat[which(dat$renal_function_at_admission != 1), 'NKD_adm'] <- 0
dat[which(dat$renal_function_at_admission != 2), 'akd_adm'] <- 1
dat[which(dat$renal_function_at_admission != 3), 'ckd_adm'] <- 1
dat[which(dat$renal_function_at_admission != 2), 'akd_cause_enrol'] <- NA

dat$ckd_adm_alb <- dat$ckd_adm
dat[which(dat$renal_function_at_admission != 3), 'ckd_adm_alb'] <- NA
dat[which(dat$proteinuria_at_enrollment != 1), 'ckd_adm_alb'] <- 1

dat$NKD_adm <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$NKD_adm), levels = c('Yes', 'No'))
dat$akd_adm <- factor(gsubVec(c(1, 2), c('No', 'Yes'), dat$akd_adm), levels = c('Yes', 'No'))
dat$ckd_adm <- factor(gsubVec(c(1, 3), c('No', 'Yes'), dat$ckd_adm), levels = c('Yes', 'No'))
dat$ckd_adm_alb <- factor(gsubVec(c(1, 3), c('No', 'Yes'), dat$ckd_adm_alb), levels = c('Yes', 'No'))


tab4.1 <- demoTab(vars = c('ckd_adm', 'ckd_adm_alb', 'akd_adm', 'akd_cause_enrol', 'NKD_adm'), group = 'phase.cat', data = dat,
                  rnames= c('CKD', '~~~ With albuminuria', 'AKD', 'AKD_base', 'NKD'), cat.tests = 'fisher.test')
rownames(tab4.1)[c(2, 5, 8, 15)] <- rownames(tab4.1)[c(1, 4, 7, 14)]
tab4.1 <- tab4.1[c(2, 5, 8, 11, 12, 13, 15), ]
tab4.1[c(1, 2, 3, 7), 4] <- ''
tab4.1[4, 4] <- pvalFormat(adm.overall$p.value)

dat$ckd_7d <- dat$akd_7d <- dat$NKD_7d <- dat$aki_7d <- dat$renal_function_status7d

dat[which(dat$renal_function_status7d != 'NKD'), 'NKD_7d'] <- 'No'
dat[which(dat$renal_function_at_admission != 1), 'NKD_7d'] <- NA
dat[which(dat$renal_function_status7d != 'AKD'), 'akd_7d'] <- 'No'
dat[which(dat$renal_function_at_admission != 2), 'akd_7d'] <- NA
dat[which(dat$renal_function_status7d != 'CKD'), 'ckd_7d'] <- 'No'
dat[which(dat$renal_function_at_admission != 3), 'ckd_7d'] <- NA
dat[which(dat$renal_function_status7d != 'AKI'), 'aki_7d'] <- 'No'

dat$NKD_7d <- factor(gsubVec(c('NKD'), c('Yes'), dat$NKD_7d), levels = c('Yes', 'No'))
dat$akd_7d <- factor(gsubVec(c('AKD'), c('Yes'), dat$akd_7d), levels = c('Yes', 'No'))
dat$ckd_7d <- factor(gsubVec(c('CKD'), c('Yes'), dat$ckd_7d), levels = c('Yes', 'No'))
dat$aki_7d <- factor(gsubVec(c('AKI'), c('Yes'), dat$aki_7d), levels = c('Yes', 'No'))
dat$noaki_7d <- factor(dat$aki_7d, levels = c('No', 'Yes'))

dat$aki_7d.mod <- dat$aki_7d
dat[which(dat$aki_7d == 'No'), 'aki_7d.mod'] <- NA
dat$aki_7d_stg1 <- dat$aki_7d_stg2 <- dat$aki_7d_stg3 <- dat$aki_7d_stg23 <- dat$aki_7d.mod
dat[which(dat$renal_function_status7d == 'AKI' & dat$Final_total_AKI_stage != 1), 'aki_7d_stg1'] <- 'No'
dat[which(dat$renal_function_status7d == 'AKI' & dat$Final_total_AKI_stage != 2), 'aki_7d_stg2'] <- 'No'
dat[which(dat$renal_function_status7d == 'AKI' & dat$Final_total_AKI_stage != 3), 'aki_7d_stg3'] <- 'No'
dat[which(dat$renal_function_status7d == 'AKI' & !dat$Final_total_AKI_stage %in% c(2, 3)), 'aki_7d_stg23'] <- 'No'
```

```r


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,
                  rnames = c('No AKI', 'CKD', 'AKD', 'NKD', 'AKI', '~~~ Stage 1', '~~~ Stage 2', '~~~ Stage 3', '~~~ severe AKI (stage2/3)'), cat.tests = 'fisher.test')

rownames(tab4.2)[seq(2, 27, 3)] <- rownames(tab4.2)[seq(1, 27, 3)]
tab4.2 <- tab4.2[seq(2, 27, 3), ]


dat$final_disposition_cat <- factor(gsubVec(c(1, 2), c('Admitted', 'Sent home'), dat$final_disposition_with_mortality), levels = c('Sent home', 'Admitted'))

dat$ckd_dis <- dat$akd_dis <- dat$NKD_dis <- dat$aki_dis <- dat$renal_function_status7d

dat[which(dat$renal_function_status7d != 'NKD'), 'NKD_dis'] <- 'No'
dat[which(dat$renal_function_status7d != 'AKD'), 'akd_dis'] <- 'No'
dat[which(dat$renal_function_status7d != 'CKD'), 'ckd_dis'] <- 'No'
dat[which(dat$renal_function_status7d != 'AKI'), 'aki_dis'] <- 'No'

dat$NKD_dis <- factor(gsubVec(c('NKD'), c('Yes'), dat$NKD_dis), levels = c('Yes', 'No'))
dat$akd_dis <- factor(gsubVec(c('AKD'), c('Yes'), dat$akd_dis), levels = c('Yes', 'No'))
dat$ckd_dis <- factor(gsubVec(c('CKD'), c('Yes'), dat$ckd_dis), levels = c('Yes', 'No'))
dat$aki_dis <- factor(gsubVec(c('AKI'), c('Yes'), dat$aki_dis), levels = c('Yes', 'No'))

dat$Time_between_screening_and_discharge.new <- dat$Time_between_screening_and_discharge
dat[which(dat$Time_between_screening_and_discharge < 0), 'Time_between_screening_and_discharge.new'] <- NA

###################
dat$p01_rec_dtime <- as.numeric(dat$p01_rec_dtime)
dat[["p01_rec_dtime"]] <-
  as.POSIXct(dat[["p01_rec_dtime"]] * (60*60*24)
    , origin="1899-12-30"
    , tz="UTC")

dat$p05_rec_dtime <- as.numeric(dat$p05_rec_dtime)
dat[["p05_rec_dtime"]] <-
  as.POSIXct(dat[["p05_rec_dtime"]] * (60*60*24)
    , origin="1899-12-30"
    , tz="UTC")

dat$p05_rec_dtime - dat$p01_rec_dtime
dat$Time_between_screening_and_discharge.new <- as.numeric(difftime(dat$p05_rec_dtime, dat$p01_rec_dtime, units="hours"))
#######################
dat[which(dat$Time_between_screening_and_discharge.new < 0), 'Time_between_screening_and_discharge.new'] <- NA
dat$Time_between_screening_and_discharge.new.home <- dat$Time_between_screening_and_discharge.new.adm <- dat$Time_between_screening_and_discharge.new

dat[which(dat$final_disposition_cat != 'Admitted'), 'Time_between_screening_and_discharge.new.adm'] <- NA
dat[which(dat$final_disposition_cat != 'Sent home'), 'Time_between_screening_and_discharge.new.home'] <- NA

dat[which(dat$final_disposition_cat != 'Admitted'), c('ckd_dis', 'aki_dis', 'akd_dis', 'NKD_dis')] <- NA


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'])

kruskal.test(dat$Time_between_screening_and_discharge.new, dat$phase.cat)

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'])

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'])


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,
                  rnames= c('Disposition', '~~~ NKD', '~~~ AKI','~~~ AKD','~~~ CKD', 'Time(hours) in health care facility in all patients', '~~~ Sent home', '~~~ Admitted'),
                  cent.funs = rep(c('median'), 100), var.funs = rep(c('quantile'), 100), cat.tests = 'fisher.test')
rownames(tab4.3)[c(seq(5, 15, 3), 17, 19, 21)] <- rownames(tab4.3)[c(seq(4, 15, 3), 16, 18, 20)]
tab4.3 <- tab4.3[c(1:3, c(seq(5, 15, 3), 17, 19, 21)), ]
rownames(tab4.3)[c(2, 3)] <- gsub('~~~~', '', rownames(tab4.3)[c(2, 3)])
tab4.3[1, ] <- ''

```

```r
tab4.3[8, 4] <- pvalFormat(time.all$p.value)
tab4.3[9, 4] <- pvalFormat(time.home$p.value)
tab4.3[10, 4] <- pvalFormat(time.adm$p.value)

dat$dialysis_indi <- dat$dialysis_dialyze <- dat$Dialysis_indication_final
dat$indi_7d <- dat$dialy_7d <- dat$renal_function_status7d

dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'dialysis_indi'] <- 0
dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'dialysis_dialyze'] <- 0
dat[which(dat$Dialysis_indication_final != 'Dialysis indication but not dialyzed'), 'indi_7d'] <- NA
dat[which(dat$Dialysis_indication_final != 'Dialyzed'), 'dialy_7d'] <- NA

dat$dialysis_was_indicateyn <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$dialysis_was_indicateyn), levels = c('Yes', 'No'))
dat$dialysis_dialyze <- factor(gsubVec(c(0, 'Dialyzed'), c('No', 'Yes'), dat$dialysis_dialyze), levels = c('Yes', 'No'))
dat$dialysis_indi <- factor(gsubVec(c(0, 'Dialysis indication but not dialyzed'), c('No', 'Yes'), dat$dialysis_indi), levels = c('Yes', 'No'))

tab4.4 <- demoTab(vars = c('dialysis_was_indicateyn', 'dialysis_dialyze', 'dialy_7d', 'dialysis_indi','indi_7d'), group = 'phase.cat', data = dat, show.na = FALSE,
                  rnames = c('Dialysis Indiction', 'Dialyzed', 'dia_status', 'Dialysis indication, but not dialyzed', 'indi_status'), cat.tests = 'fisher.test')
rownames(tab4.4)[c(2, 5, 12)] <- rownames(tab4.4)[c(1, 4, 11)]
tab4.4 <- tab4.4[c(2, 5, 8, 9, 10, 12, 15, 16, 17, 18), ]

tab4 <- rbind(tab4.1, tab4.2, tab4.3, tab4.4)
tab4 <- tab4[, c(3, 1, 2, 4)]
colnames(tab4)[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}")



## Table 6
# dat$CKD_cat_3month_prog <- dat$CKD_cat_enrollment_gfr - dat$CKD_cat_m3fu_gfr
# dat[which(dat$CKD_cat_3month_prog > 0), 'CKD_cat_3month_prog'] <- 0
# dat[which(dat$CKD_cat_3month_prog < 0), 'CKD_cat_3month_prog'] <- 1
dat[, 'CKD_cat_3month_prog'] <- NA
dat[which(dat$recovery_at_3_month == 'CKD progression' & dat$sCr3month == 1), 'CKD_cat_3month_prog'] <- 'Yes'
dat[which(dat$recovery_at_3_month == 'Stable CKD' & dat$sCr3month == 1), 'CKD_cat_3month_prog'] <- 'No'
dat$CKD_cat_3month_prog <-  factor(dat$CKD_cat_3month_prog, levels = c('Yes', 'No'))

#
# dat$CKD_cat_6month_prog <- dat$CKD_cat_enrollment_gfr - dat$CKD_cat_m6fu_gfr
# dat[which(dat$CKD_cat_6month_prog > 0), 'CKD_cat_6month_prog'] <- 0
# dat[which(dat$CKD_cat_6month_prog < 0), 'CKD_cat_6month_prog'] <- 1
# dat[which(dat$renal_function_status7d != 'CKD'), 'CKD_cat_6month_prog'] <- NA
# dat$CKD_cat_6month_prog <-  factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$CKD_cat_6month_prog), levels = c('Yes', 'No'))
#
dat[, 'CKD_cat_6month_prog'] <- NA
dat[which(dat$recovery_at_6_month == 'CKD progression' & dat$sCr6month == 1), 'CKD_cat_6month_prog'] <- 'Yes'
dat[which(dat$recovery_at_6_month == 'Stable CKD' & dat$sCr6month == 1), 'CKD_cat_6month_prog'] <- 'No'
dat$CKD_cat_6month_prog <-  factor(dat$CKD_cat_6month_prog, levels = c('Yes', 'No'))


# dat$Recovery_at_3months_bin <- gsub(1, 0, dat$NRecovery_at_3month)
# dat$Recovery_at_6months_bin <- gsub(1, 0, dat$NRecovery_at_6month)
# dat$Recovery_at_3months_bin <- factor(gsubVec(c(0, 2), c('No', 'Yes'), dat$Recovery_at_3months_bin), levels = c('Yes', 'No'))
# dat$Recovery_at_6months_bin <- factor(gsubVec(c(0, 2), c('No', 'Yes'), dat$Recovery_at_6months_bin), levels = c('Yes', 'No'))

dat[which(!is.na(dat$recovery_at_3_month) & dat$sCr3month == 1), 'Recovery_at_3months_bin'] <- 'No'
dat[which(dat$recovery_at_3_month %in% c('NKD', 'Recovery from AKD', 'Recovery from AKI') & dat$sCr3month == 1), 'Recovery_at_3months_bin'] <- 'Yes'

dat[which(!is.na(dat$recovery_at_6_month) & dat$sCr6month == 1), 'Recovery_at_6months_bin'] <- 'No'
dat[which(dat$recovery_at_6_month %in% c('NKD', 'Recovery from AKD', 'Recovery from AKI') & dat$sCr6month == 1), 'Recovery_at_6months_bin'] <- 'Yes'

dat$Recovery_at_3months_bin <- factor(dat$Recovery_at_3months_bin, levels = c('Yes', 'No'))
dat$Recovery_at_6months_bin <- factor(dat$Recovery_at_6months_bin, levels = c('Yes', 'No'))

dat$eGFR3months_60 <- ifelse(dat$p21_m3fu_gfr >= 60, 1, 0)
dat$eGFR6months_60 <- ifelse(dat$p21_m6fu_gfr >= 60, 1, 0)

#table(dat$eGFR3months_60, dat$recovery_at_3_month)
```

```r

dat$onset.NKD.3mon <- NA
dat[which(dat$renal_function_status7d == 'NKD' & dat$recovery_at_3_month == 'NKD' & dat$sCr3month == 1), 'onset.NKD.3mon'] <- 'No'
dat[which(dat$renal_function_status7d == 'NKD' & dat$recovery_at_3_month == 'New onset AKD' & dat$sCr3month == 1), 'onset.NKD.3mon'] <- 'Yes'

dat$onset.aki.3mon <- NA
dat[which(dat$renal_function_status7d == 'AKI' & dat$recovery_at_3_month %in% c('Recovery from AKI') & dat$sCr3month == 1), 'onset.aki.3mon'] <- 'No'
dat[which(dat$renal_function_status7d == 'AKI' & dat$recovery_at_3_month == 'AKI' & dat$sCr3month == 1), 'onset.aki.3mon'] <- 'Yes'

dat$onset.akd.3mon <- NA
dat[which(dat$renal_function_status7d == 'AKD' & dat$recovery_at_3_month == 'Recovery from AKD' & dat$sCr3month == 1), 'onset.akd.3mon'] <- 'No'
dat[which(dat$renal_function_status7d == 'AKD' & dat$recovery_at_3_month == 'New onset CKD' & dat$sCr3month == 1), 'onset.akd.3mon'] <- 'Yes'

dat$onset.NKD.6mon <- NA
dat[which(dat$renal_function_status7d == 'NKD' & dat$recovery_at_6_month == 'NKD' & dat$sCr6month == 1), 'onset.NKD.6mon'] <- 'No'
dat[which(dat$renal_function_status7d == 'NKD' & dat$recovery_at_6_month == 'New onset AKD' & dat$sCr6month == 1), 'onset.NKD.6mon'] <- 'Yes'

dat$onset.aki.6mon <- NA
dat[which(dat$renal_function_status7d == 'AKI' & dat$recovery_at_6_month == 'Recovery from AKI' & dat$sCr6month == 1), 'onset.aki.6mon'] <- 'No'
dat[which(dat$renal_function_status7d == 'AKI' & dat$recovery_at_6_month == 'AKI'  & dat$sCr6month == 1), 'onset.aki.6mon'] <- 'Yes'

dat$onset.akd.6mon <- NA
dat[which(dat$renal_function_status7d == 'AKD' & dat$recovery_at_6_month == 'Recovery from AKD' & dat$sCr6month == 1), 'onset.akd.6mon'] <- 'No'
dat[which(dat$renal_function_status7d == 'AKD' & dat$recovery_at_6_month == 'New onset CKD' & dat$sCr6month == 1), 'onset.akd.6mon'] <- 'Yes'

dat$denovo.ckd.3mon <- NA
dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & !is.na(dat$recovery_at_3_month) & dat$sCr3month == 1), 'denovo.ckd.3mon'] <-'No'
dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & dat$recovery_at_3_month == 'New onset CKD' & dat$sCr3month == 1), 'denovo.ckd.3mon'] <- 'Yes'
dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & dat$onset.aki.3mon == 'Yes' & dat$sCr3month == 1), 'denovo.ckd.3mon'] <- 'Yes'

dat$denovo.ckd.6mon <- NA
dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & !is.na(dat$recovery_at_6_month) & dat$sCr6month == 1), 'denovo.ckd.6mon'] <-'No'
dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & dat$recovery_at_6_month == 'New onset CKD' & dat$sCr6month == 1), 'denovo.ckd.6mon'] <- 'Yes'
dat[which(dat$renal_function_status7d %in% c('NKD', 'AKI', 'AKD') & dat$onset.aki.6mon == 'Yes' & dat$sCr6month == 1), 'denovo.ckd.6mon'] <- 'Yes'

dat$denovo.ckd_overall <- dat$denovo.ckd.3mon
dat[which(dat$denovo.ckd.6mon == 'Yes'), 'denovo.ckd_overall'] <- 'Yes'
dat[which(dat$denovo.ckd.6mon == 'No'), 'denovo.ckd_overall'] <- 'No'

test <- dat[which(dat$recovery_at_3_month == 'AKI'), ]

plot(test$p02_scr_us, test$sCr3month)

change <- c('onset.NKD.3mon', 'onset.akd.3mon', 'onset.aki.3mon', 'onset.NKD.6mon', 'onset.akd.6mon', 'onset.aki.6mon')
dat[,change] %<>% lapply (function(x) factor(x, levels = c('Yes', 'No')))

dat$Recovery_overall <- dat$Recovery_at_3months_bin
dat[which(dat$Recovery_at_6months_bin == 'Yes'), 'Recovery_overall'] <- 'Yes'
dat[which(dat$Recovery_at_6months_bin == 'No'), 'Recovery_overall'] <- 'No'

dat$onset.NKD_overall <- dat$onset.NKD.3mon
dat[which(dat$onset.NKD.6mon == 'Yes'), 'onset.NKD_overall'] <- 'Yes'
dat[which(dat$onset.NKD.6mon == 'No'), 'onset.NKD_overall'] <- 'No'

dat$onset.aki_overall <- dat$onset.aki.3mon
dat[which(dat$onset.aki.6mon == 'Yes'), 'onset.aki_overall'] <- 'Yes'
dat[which(dat$onset.aki.6mon == 'No'), 'onset.aki_overall'] <- 'No'

dat$onset.akd_overall <- dat$onset.akd.3mon
dat[which(dat$onset.akd.6mon == 'Yes'), 'onset.akd_overall'] <- 'Yes'
```

```r
dat[which(dat$onset.akd.6mon == 'No'), 'onset.akd_overall'] <- 'No'

dat$CKD_cat_overall <- dat$CKD_cat_3month_prog
dat[which(dat$CKD_cat_6month_prog == 'Yes'), 'CKD_cat_overall'] <- 'Yes'
dat[which(dat$CKD_cat_6month_prog == 'No'), 'CKD_cat_overall'] <- 'No'

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')

rownames(tab6)[seq(2, 45, 3)] <- rownames(tab6)[seq(1, 45, 3)]
final <- tab6[seq(2, 45, 3), ]

size <- tab6[seq(1, 45, 3), 1:3]

dol.loc <- matrix(rep(NA, 45), nrow = 15, ncol = 3)
for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    dol.loc[j, i] <- gregexpr(pattern ='\\$', final[j, i])[[1]][2]
  }
}

deno.size <- matrix(rep(NA, 45), nrow = 15, ncol = 3)
for(i in 1:ncol(size)){
  for(j in 1:nrow(size)){
    deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^;]*(?=\\$)"))
  }
}

for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
  }
}

tab6 <- final[, c(3, 1, 2, 4)]

dat$na.rec.3mon <- dat$na.rec.6mon <- 'FALSE'
dat[which(is.na(dat$NRecovery_at_3month)), 'na.rec.3mon'] <- 'TRUE'
dat[which(is.na(dat$NRecovery_at_6month)), 'na.rec.6mon'] <- 'TRUE'

dat[which(dat$na.rec.3mon == 'TRUE' & dat$na.rec.6mon == 'FALSE'), c("patient_id", 'NRecovery_at_3month', 'NRecovery_at_6month')]

dat[which(dat$na.rec.3mon == 'TRUE' & dat$na.rec.6mon == 'FALSE'), c("patient_id")]




####################################
dat$Recovery_at_1months_bin <- gsub(1, 0, dat$NRecovery_at_1month)
dat$Recovery_at_1months_bin <- factor(gsubVec(c(0, 2), c('No', 'Yes'), dat$Recovery_at_1months_bin), levels = c('Yes', 'No'))

dat$renal_function_at_admission
dat$eGFR1month

dat$new.ckd.1month <- dat$eGFR1month

dat[which(dat$renal_function_at_admission == 3), 'new.ckd.1month'] <- NA

dat$follow_up_7

dat$final_disposition_cat.7d <- dat$final_disposition_cat
dat[which(dat$follow_up_7 == 0), 'final_disposition_cat.7d'] <- NA

dat$follow_up_7 <- as.character(dat$follow_up_7)
demoTab(vars = 'follow_up_7', group = 'final_disposition_cat', data = dat)
demoTab(vars = 'follow_up_7', group = 'phase.cat', data = dat)


table(dat$p21_m1fu_scr)

```

```
dat$scr1month.new <- ’Yes’
dat[which(is.na(dat$p21_m1fu_scr)), ’scr1month.new’] <- ’No’

dat$screnrol.new <- ’Yes’
dat[which(is.na(dat$p21_enrol_scr)), ’screnrol.new’] <- ’No’

table(dat$scr1month.new, dat$renal_function_at_admission)

dat$scr1month.new.aki <- dat$scr1month.new
dat[which(dat$renal_function_status7d != ’AKI’), ’scr1month.new.aki’] <- NA

dat$aki.scr.1mon <- dat$scr1month.new.aki
dat[which(dat$scr1month.new.aki == ’No’), ’aki.scr.1mon’] <- NA

dat$kidney.recovery.1mon <- NA
dat[which(!is.na(dat$p21_m1fu_scr/dat$p21_enrol_scr)), ’kidney.recovery.1mon’] <- ’No’
dat[which(dat$p21_m1fu_scr/dat$p21_enrol_scr <= 1), ’kidney.recovery.1mon’] <- ’Yes’

dat$Mortality_by_6months <- as.character(dat$Mortality_by_6months)
table(dat$Mortality_by_6months, dat$renal_function_status7d)
demoTab(vars = ’Mortality_by_6months’, data = dat, group = ’renal_function_status7d’)

dat$renal_function_at_admission.cat <- gsubVec(c(1, 2, 3), c(’NKD’, ’AKD’, ’CKD’), dat$renal_function_at_admission)
demoTab(vars = ’renal_function_at_admission.cat’, group = ’renal_function_status7d’, data = dat)
demoTab(vars = ’renal_function_status7d’, group = ’renal_function_at_admission.cat’, data = dat)

epCr <- function(sex, race, age){
  s <- ifelse(sex == 1, 1, 0.742)
  r <- ifelse(race ==2, 1.21, 1)
  a <- age^(-0.203)
  epcr <- (75/(s * r* a* 186))^(-1/1.154)
  return(epcr)
}
dat$p01_gender
dat$p01_race
dat$p01_age

dat$gender <- gsubVec(c(’female’, ’male’), c(0, 1), dat$p01_gender)
dat$race <- gsub(’african’, ’2’, dat$p01_race)

dat$epcr <- mapply(epCr, dat$gender, dat$race, dat$p01_age)

dat$kidney.recovery.1mon <- NA
dat[which(!is.na(dat$p21_m1fu_scr/dat$epcr)), ’kidney.recovery.1mon’] <- ’No’
dat[which(dat$p21_m1fu_scr/dat$epcr <= 1), ’kidney.recovery.1mon’] <- ’Yes’


table(dat$screnrol.new, dat$proteinuria_at_enrollment)

toString(sprintf("’%s’", colnames(dat)[which(grepl(’p21’, colnames(dat)))]))

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’)])), ]

change <- c(’f7days’, ’f1month’, ’f3months’, ’f6months’)
dat[,change] %<>% lapply (function(x) as.character(x))

tab.fu <- demoTab(vars = c(’f7days’, ’f1month’, ’f3months’, ’f6months’), group = ’final_disposition_cat’, data = dat,
     cat.tests = ’fisher.test’)
#jWrite(tab.fu, ’follow_up.csv’)

demoTab(’Mortality_overall’, group = ’renal_function_status7d’, data = dat, cat.tests = ’fisher.test’)

a <- glm(’Mortality_overall ~ renal_function_status7d’, data = dat, family = ’binomial’)
summary(a)

demoTab(vars = c(’Mortality_by_6months’), group = ’final_disposition_cat’, data = dat, show.na = FALSE, cat.tests = ’
     fisher.test’)

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)

demoTab(vars = c(’Mortality_overall’), group = ’AKI_stage_2_3’, data = dat, cat.tests = ’fisher.test’)

#dat[which(is.na(dat$fluid_therapy)), ’fluid_therapy’] <- 0
dat[which(is.na(dat$fluid_therapy_POandIVat_initial_evaluation)), ’fluid_therapy_POandIVat_initial_evaluation’] <- 0

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’))
```

```r
dat$fluid_therapy_POandIV_during_admission.cat <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$fluid_therapy_POandIV_during_admission), levels = c('Yes', 'No'))
dat$p05_ip_interventions__diuretic_therapy.cat <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$p05_ip_interventions__diuretic_therapy), levels = c('Yes', 'No'))
dat$p05_ip_interventions__fluid_therapy_iv.cat <- factor(gsubVec(c(0, 1), c('No', 'Yes'), dat$p05_ip_interventions__fluid_therapy_iv), levels = c('Yes', 'No'))
dat$t02_fluid_therapy_oral.cat <- factor(gsubVec(c(0, 1), c('No', 'Yes'), ifelse(is.na(dat$t02_fluid_therapy_oral), 0, 1)), levels = c('Yes', 'No'))
#dat$overall_fluid <- dat$fluid_therapy + dat$fluid_therapy_POandIVat_initial_evaluation # Fluid Therapy covers PO and IV fluid mentioned at 'fluid_therapy_POandIVat_initial_evaluation


 all <- demoTab(vars = c('fluid_therapy_POandIV_during_admission.cat', 'total_volume_fluid_therapy_POandIVat_initial_evaluation'), data = dat, group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
 all <- all[c(2, 4, 5), ]

 all.s <- demoTab(vars = c('total_volume_fluid_therapy_POandIVat_initial_evaluation'), data = dat[which(dat$final_disposition_cat == 'Sent home'), ], group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('median'), var.funs = c('quantile'))
 all.s <- rbind(paste('$', as.numeric(str_extract(colnames(all.s), "(?<=\\=)[^;]*(?=\\$)")), '$', sep = ''), all.s)
 all.s[1, 4] <- ''
 all.a <- demoTab(vars = c('total_volume_fluid_therapy_POandIVat_initial_evaluation'), data = dat[which(dat$final_disposition_cat == 'Admitted'), ], group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('median'), var.funs = c('quantile'))
 all.a <- rbind(paste('$', as.numeric(str_extract(colnames(all.a), "(?<=\\=)[^;]*(?=\\$)")), '$', sep = ''), all.a)
 all.a[1, 4] <- ''


 all.s <- demoTab(vars = c('fluid_therapy_POandIV_during_admission.cat', 'total_volume_fluid_therapy_POandIVat_initial_evaluation'), data = dat[which(dat$final_disposition_cat == 'Sent home'), ], group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
 all.s <- all.s[c(2, 4, 5), ]
 all.a <- demoTab(vars = c('fluid_therapy_POandIV_during_admission.cat', 'total_volume_fluid_therapy_POandIVat_initial_evaluation'), data = dat[which(dat$final_disposition_cat == 'Admitted'), ], group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
 all.a <- all.a[c(2, 4, 5), ]


tab.all <- rbind(all, all.s, all.a)
rownames(tab.all) <- c('Any fluid - all patients', '', '', 'Sent home', '', '', 'Admitted', '', '')
tab.all[c(4, 7), 4] <- ''

 all <- demoTab(vars = c('p05_ip_interventions__fluid_therapy_iv.cat', 't02_fluid_therapy_iv_amount'), data = dat, group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
 all <- all[c(2, 4, 5), ]

 all.s <- demoTab(vars = c('t02_fluid_therapy_iv_amount'), data = dat[which(dat$final_disposition_cat == 'Sent home'), ], group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('median'), var.funs = c('quantile'), rnames = 'Sent home')
 all.s <- rbind(paste('$', as.numeric(str_extract(colnames(all.s), "(?<=\\=)[^;]*(?=\\$)")), '$', sep = ''), all.s)
 all.s[1, 4] <- ''
 all.a <- demoTab(vars = c('t02_fluid_therapy_iv_amount'), data = dat[which(dat$final_disposition_cat == 'Admitted'), ], group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('median'), var.funs = c('quantile'), rnames = 'Admitted')
 all.a <- rbind(paste('$', as.numeric(str_extract(colnames(all.a), "(?<=\\=)[^;]*(?=\\$)")), '$', sep = ''), all.a)
 all.a[1, 4] <- ''

 all.s <- demoTab(vars = c('p05_ip_interventions__fluid_therapy_iv.cat', 't02_fluid_therapy_iv_amount'), data = dat[which(dat$final_disposition_cat == 'Sent home'), ], group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
 all.s <- all.s[c(2, 4, 5), ]
 all.a <- demoTab(vars = c('p05_ip_interventions__fluid_therapy_iv.cat', 't02_fluid_therapy_iv_amount'), data = dat[which(dat$final_disposition_cat == 'Admitted'), ], group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
 all.a <- all.a[c(2, 4, 5), ]


tab.iv <- rbind(all, all.s, all.a)
rownames(tab.iv) <- c('IV fluid', '', '', 'Sent home', '', '', 'Admitted', '', '')
tab.iv[c(4, 7), 4] <- ''



 all <- demoTab(vars = c('t02_fluid_therapy_oral.cat', 't02_fluid_therapy_oral'), data = dat, group = 'phase.cat', con.
```

```r
     tests = 'kruskal.test',
        cent.funns = c('', 'median'), var.funs = c('', 'quantile'), rnames = 'Any fluid - all patients')
all <- all[c(2, 5), ]

all.s <- demoTab(vars = c('t02_fluid_therapy_oral'), data = dat[which(dat$final_disposition_cat == 'Sent home'), ],
     group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('median'), var.funs = c('quantile'), rnames = 'Sent home')
all.s <- rbind(paste('$', as.numeric(str_extract(colnames(all.s), "(?<=\\=)[^;]*(?=\\$)")), '$', sep = ''), all.s)
all.s[1, 4] <- ''
all.a <- demoTab(vars = c('t02_fluid_therapy_oral'), data = dat[which(dat$final_disposition_cat == 'Admitted'), ],
     group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('median'), var.funs = c('quantile'), rnames = 'Admitted')
all.a <- rbind(paste('$', as.numeric(str_extract(colnames(all.a), "(?<=\\=)[^;]*(?=\\$)")), '$', sep = ''), all.a)
all.a[1, 4] <- ''

all.s <- demoTab(vars = c('t02_fluid_therapy_oral.cat', 't02_fluid_therapy_oral'), data = dat[which(
     dat$final_disposition_cat == 'Sent home'), ], group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
all.s <- all.s[c(2, 5), ]
all.a <- demoTab(vars = c('t02_fluid_therapy_oral.cat', 't02_fluid_therapy_oral'), data = dat[which(
     dat$final_disposition_cat == 'Admitted'), ], group = 'phase.cat', con.tests = 'kruskal.test',
        cent.funs = c('', 'median'), var.funs = c('', 'quantile'))
all.a <- all.a[c(2, 5), ]


tab.po <- rbind(all, all.s, all.a)
rownames(tab.po) <- c('PO fluid', '', 'Sent home', '', 'Admitted', '')
tab.po[c(3, 5), 4] <- ''



all <- demoTab(vars = c('p05_ip_interventions__diuretic_therapy.cat'), data = dat, group = 'phase.cat', con.tests = '
     kruskal.test',
        cent.funs = c('', 'median'), var.funs = c('', 'quantile'), rnames = 'Diuretic use')
tab.d <- all[c(1, 2), ]
rownames(tab.d) <- c('Diuretic use', '')

tab5 <- rbind(tab.all, tab.iv, tab.po, tab.d)
tab5 <- cbind(tab5, 'a' = c('', '', 'volume', '', '', 'volume', '', '', 'volume', '', '', 'volume', '', '', 'volume',
     '', '', 'volume', '', 'volume', '', 'volume', '', 'volume', '', ''))

tab5 <- tab5[, c(5, 3, 1, 2, 4)]

#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')

colnames(tab5) <- c("", "Overall", "Observation",
                              "Intervention", 'P')

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')
dat[,change] %<>% lapply (function(x) as.character(x))

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'),
                 group = 'phase.cat', data = dat,
                 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'))

table(dat$scr1month.new)

## Mortality at

dat$Mortality_at_7days <- dat$Mortality_by_7days
dat$Mortality_at_1month <- dat$Mortality_by_1month
dat$Mortality_at_3months <- dat$Mortality_by_3months
dat$Mortality_at_6months <- dat$Mortality_by_6months

dat[which(dat$mortality_at_discharge == 'Yes'), 'Mortality_at_7days'] <- NA
dat[which(dat$Mortality_by_7days == 1), c('Mortality_at_1month', 'Mortality_at_3months', 'Mortality_at_6months')] <-
     NA
dat[which(dat$Mortality_by_1month == 1), c('Mortality_at_3months', 'Mortality_at_6months')] <- NA
dat[which(dat$Mortality_by_3months == 1), c('Mortality_at_6months')] <- NA


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',
                    'mortality_at_discharge', 'Mortality_at_7days', 'Mortality_at_1month', 'Mortality_at_3months', '
                         Mortality_at_6months'),
```

```r
                  group = 'phase.cat', data = dat,
                  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',
                             'mortality at discharge', 'Mortality at 7days', 'Mortality at 1month', 'Mortalityat 3 months', 'Mortality at 6months'))


change <- c('denovo.ckd.3mon', 'denovo.ckd.6mon', 'denovo.ckd_overall')
dat[,change] %<>% lapply (function(x) factor(x, levels = c('Yes', 'No')))

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')

rownames(tab6.ext)[seq(2, 9, 3)] <- rownames(tab6.ext)[seq(1, 9, 3)]
final <- tab6.ext[seq(2, 9, 3), ]

size <- tab6.ext[seq(1, 9, 3), 1:3]

dol.loc <- matrix(rep(NA, 9), nrow = 15, ncol = 3)
for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    dol.loc[j, i] <- gregexpr(pattern ='\\$', final[j, i])[[1]][2]
  }
}

deno.size <- matrix(rep(NA, 9), nrow = 15, ncol = 3)
for(i in 1:ncol(size)){
  for(j in 1:nrow(size)){
    deno.size[j, i] <- as.numeric(str_extract(size[j, i], "(?<=\\=)[^;]*(?=\\$)"))
  }
}

for(i in 1:(ncol(final) - 1)){
  for(j in 1:nrow(final)){
    stri_sub(final[j, i], dol.loc[j, i], dol.loc[j, i] - 1) <- paste('/', deno.size[j, i], sep = '')
  }
}

tab6.ext <- final[, c(3, 1, 2, 4)]


dat$p21_enrol_scr
dat$p21_m1fu_scr

dat$recovery_1month_enrollment_scr <- ifelse(dat$p21_m1fu_scr <= dat$p21_enrol_scr, 'Yes', 'No')

dat$renal_function_status7d_scr <- dat$renal_function_status7d

dat[which(dat$scr1month.new != 'Yes'), 'renal_function_status7d_scr'] <- NA

table(dat$recovery_1month_enrollment_scr, dat$renal_function_status7d_scr)

demoTab(vars = 'recovery_1month_enrollment_scr', data = dat, group = 'renal_function_status7d_scr', show.na = FALSE)

dat$eGFR_less_than75_at_1month.ch <- as.character(dat$eGFR_less_than75_at_1month)

demoTab(vars = 'eGFR_less_than75_at_1month.ch', data = dat, group = 'renal_function_status7d_scr' , show.na = FALSE)

head(dat[, c("p21_enrol_scr", "p21_m1fu_scr", "recovery_1month_enrollment_scr")])

demoTab(vars = 'kidney.recovery.1mon', data = dat, group = 'renal_function_status7d_scr')

table(dat$dialysis_at_1month, dat$renal_function_status7d_scr, dat$eGFR_less_than75_at_1month.ch)


## KDIGO and Decline

dat$realAKI_48_7days

dat$decreaseAKI_48_7days

dat$decreaseAKI_48_7days.pure <- dat$decreaseAKI_48_7days

dat[which(dat$realAKI_48_7days == 1), "decreaseAKI_48_7days.pure"] <- 0

change <- c('realAKI_48_7days', 'decreaseAKI_48_7days.pure')
dat[,change] %<>% lapply (function(x) as.character(x))

demoTab(vars = c('realAKI_48_7days', 'decreaseAKI_48_7days.pure'), group = 'renal_function_at_admission.cat', data =
```

```
    dat)

dat$renal_function_at_admission.cat.aki.at.7d.only <- dat$renal_function_at_admission.cat
dat[which(dat$renal_function_status7d != 'AKI'), 'renal_function_at_admission.cat.aki.at.7d.only'] <- NA

demoTab(vars = c('realAKI_48_7days', 'decreaseAKI_48_7days.pure'), group = 'renal_function_at_admission.cat.aki.at.7d.
    only', data = dat)

dat$in_hospital_mortality
dat$time_in_health_care_facility_less_than_24hours

table(dat$in_hospital_mortality, dat$time_in_health_care_facility_less_than_24hours)


demoTab(vars = c('renal_function_status7d'), group = 'renal_function_at_admission.cat', data = dat)


## 11/27/19
## Identify patients who would not be classified as AKD if cut off is <60 instead of <75
dat$p21_enrol_gfr
dat$Enrol_eGFR_less_60

dat$renal_function_at_admission.cat
dat$proteinuria_at_enrollment

dat$AKD_at_admission

dat$AKD_at_adm_by_egfr_only <- NA
dat[which(dat$akd_adm == 'Yes'), 'AKD_at_adm_by_egfr_only'] <- 1
dat[which(dat$proteinuria_at_enrollment == 1), 'AKD_at_adm_by_egfr_only'] <- NA

#table(dat$AKD_at_adm_by_egfr_only, dat$eGFR_less_than75_at_enrol.new)

table(dat$AKD_at_adm_by_egfr_only, dat$Enrol_eGFR_less_60) # 7 missing

dat$Enrol_eGFR_less_60.new <- ifelse(dat$p21_enrol_gfr < 60, 1, 0)

table(dat$AKD_at_adm_by_egfr_only, dat$Enrol_eGFR_less_60.new)
#       0   1
#   1 193 789
## 193 patients will no longer be classified as AKD if the cut off was lowered

dat$renal_function_status7d_NKD_vs <- gsubVec(c('AKD', 'AKI', 'CKD'), c('Other', 'Other', 'Other'),
    dat$renal_function_status7d)

ext.tab <- demoTab(vars = 'Mortality_overall', group = 'renal_function_status7d_NKD_vs', data = dat, cat.tests = '
    fisher.test',
                   rnames = c('Mortality Overall'))


dat$renal_function_status7d_NKD_vs
dat$eGFR1month
dat$eGFR_less_than75_at_1month.ch

table(dat$renal_function_at_admission.cat, dat$eGFR_less_than75_at_1month)

table(dat$renal_function_status7d_scr)

demoTab(vars = 'eGFR_less_than75_at_1month.ch', data = dat, group = 'renal_function_status7d_scr' , show.na = FALSE)

dat$p21_m1fu_scr

dat$eGFR_less_than75_at_1month.new <- ifelse(dat$p21_m1fu_gfr < 75, 'Yes', 'No')

demoTab(vars = 'eGFR_less_than75_at_1month.new', data = dat, group = 'renal_function_status7d_scr' , show.na = FALSE)

dat[which(dat$renal_function_status7d_scr == 'NKD' & is.na(dat$eGFR_less_than75_at_1month.new)), c("p21_m1fu_gfr", "
    p21_m1fu_scr")]

###12/11/19 Additional Request

dat$onset.NKD.3mon.75 <- NA
dat[which(dat$renal_function_status7d == 'NKD' & dat$eGFR_less_than75_at_3month == 0), 'onset.NKD.3mon.75'] <- 'No'
dat[which(dat$renal_function_status7d == 'NKD' & dat$eGFR_less_than75_at_3month == 1), 'onset.NKD.3mon.75'] <- 'Yes'

dat$eGFR_less_than75_at_6month <- ifelse(dat$p21_m6fu_gfr < 75, 1, 0)

dat$onset.NKD.6mon.75 <- NA
dat[which(dat$renal_function_status7d == 'NKD' & dat$eGFR_less_than75_at_6month == 0), 'onset.NKD.6mon.75'] <- 'No'
```

```r
dat[which(dat$renal_function_status7d == 'NKD' & dat$eGFR_less_than75_at_6month == 1), 'onset.NKD.6mon.75'] <- 'Yes'

table(dat$onset.NKD.3mon, dat$onset.NKD.3mon.75)

table(dat$renal_function_status_1month, dat$onset.NKD.3mon)

dat$renal_function_status_1month.chr <- factor(gsubVec(c(1, 2, 3), c('NKD', 'AKD', 'CKD'),
     dat$renal_function_status_1month), levels = c('NKD', 'AKD', 'CKD'))

table(dat$renal_function_status_1month.chr, dat$onset.NKD.3mon)

dat[which(dat$onset.NKD.3mon == 'Yes'), 'renal_function_status_1month.chr']
dat[which(dat$onset.NKD.3mon == 'Yes'), 'renal_function_status_1month']

# dat$renal_function_at_admission.cat
# dat$renal_function_status7d
# dat$renal_function_status_1month.chr
# dat$renal_function_status_3month

library(tidyr)
library(data.table)
dat$renal_function_status_3month.chr <- gsubVec(c(1, 2, 3), c('NKD', 'AKD', 'CKD'), dat$renal_function_status_3month)
dat$renal_function_status_1month.chr <- as.character(dat$renal_function_status_1month.chr)
dat[which(is.na(dat$renal_function_status_1month.chr)), ]

#dat[, .N, by=.(renal_function_at_admission.cat, renal_function_status7d, renal_function_status_1month.chr,
     renal_function_status_3month)]

library(tidyverse)

sankey1 <- dat %>% count(renal_function_at_admission.cat, renal_function_status7d)
colnames(sankey1) <- c("source", "target", "value")

sankey1$source <- gsubVec(c('NKD', 'AKD', 'CKD'), c(0, 1, 2), sankey1$source)
sankey1$target <- gsubVec(c('NKD', 'AKD', 'AKI', 'CKD'), c(3, 4, 5, 6), sankey1$target)

sankey2 <- dat %>% count(renal_function_status7d, renal_function_status_1month.chr)
colnames(sankey2) <- c("source", "target", "value")
sankey2[is.na(sankey2)] = "NA"

sankey2$source <- gsubVec(c('NKD', 'AKD', 'AKI', 'CKD'), c(3, 4, 5, 6), sankey2$source)
sankey2$target <- gsubVec(c('NKD', 'AKD', 'CKD', 'NA'), c(7, 8, 9, 10), sankey2$target)

sankey3 <- dat %>% count(renal_function_status_1month.chr, renal_function_status_3month.chr)
colnames(sankey3) <- c("source", "target", "value")
sankey3[is.na(sankey3)] = "NA"

sankey3$source <- gsubVec(c('NKD', 'AKD', 'CKD', 'NA'), c(7, 8, 9, 10), sankey3$source)
sankey3$target <- gsubVec(c('NKD', 'AKD', 'CKD', 'NA'), c(11, 12, 13, 14), sankey3$target)

sankey.tot <- data.frame(rbind(sankey1, sankey2, sankey3))

change <- c('source', 'target', 'value')
sankey.tot[,change] %<>% lapply (function(x) as.numeric(x))

sankey.tot <- arrange(sankey.tot, source, target)

nodes = data.frame("name" =
 c("NKD",
 "AKD",
 "CKD",
 "NKD",
 "AKD",
 "AKI",
 "CKD",
 "NKD",
 "AKD",
 "CKD",
 "NA",
 "NKD",
 "AKD",
 "CKD",
 "NA"))

nodes1 = data.frame("name" =
 c("NKD",
 "AKD",
 "CKD",
 "NKD",
```

```
 "AKD",
 "AKI",
 "CKD"))

library(networkD3)

require(RColorBrewer)

match(sankey.tot$source, nodes$name)

f <- function(pal) brewer.pal(brewer.pal.info[pal, "maxcolors"], pal)
cols <- f("Set1")

nodes[which(nodes$name == "NKD"), 'color'] <- '#FFFFFF'
nodes[which(nodes$name == "AKD"), 'color'] <- '33CCCC'   #'#87CEEB' skyblue
nodes[which(nodes$name == "CKD"), 'color'] <- '#00008B'
nodes[which(nodes$name == "AKI"), 'color'] <- 'C55A11'
nodes[which(nodes$name == "NA"), 'color'] <- '#808080'
nodes[which(nodes$name == "NA"), 'color'] <- '#000000'

sankey.1 <- as.data.frame(sankey1)

sankeyNetwork(Links = sankey.1, Nodes = nodes1,
 Source = "source", Target = "target",
 Value = "value", NodeID = "name")

library(plotly)

p <- plot_ly(
    type = "sankey",
    orientation = "h",

    node = list(
      label = nodes$name,
      color = nodes$color,
      pad = 15,
      thickness = 20,
      line = list(
        color = "black",
        width = 0.5
      )
    ),

    link = list(
      source = sankey.tot$source,
      target = sankey.tot$target,
      value =  sankey.tot$value
    )
  ) %>%
  layout(
    font = list(
      size = 10
    )
)
print(p)

if (!require("processx")) install.packages("processx")

orca(p, "sankey.pdf")



#mytable <- xtabs( ~ Enrol_eGFR_less_60.new + eGFR_less_than75_at_enrol.new + renal_function_at_admission.cat, data = dat)


library(gmodels)


#CrossTable(dat$Enrol_eGFR_less_60.new, dat$eGFR_less_than75_at_enrol.new, dat$renal_function_at_admission.cat)


#devtools::install_github("erblast/easyalluvial")



#library(magrittr)
#change <- c('renal_function_at_admission.cat', 'renal_function_status7d', 'renal_function_status_1month.chr', 'renal_function_status_3month.chr')
```

```r
#dat[,change] %<>% lapply(function(x) as.character(x))




# library(easyalluvial)
# alluvial_wide( dplyr::select(dat, admission = renal_function_at_admission.cat, '7day' = renal_function_status7d,
#                               '1month' = renal_function_status_1month.chr, '2month' = renal_function_status_3month.chr),
#               fill_by = 'first_variable', auto_rotate_xlabs = FALSE)

library(ggalluvial)
library(tidyverse)
dat.g <- dat

dat.g[which(dat.g$sCr3month == 0), 'recovery_at_3_month'] <- NA
dat.g[which(dat.g$sCr6month == 0), 'recovery_at_6_month'] <- NA

dat.g$renal_function_status7d <- gsub('NKD', 'NKD', dat.g$renal_function_status7d)
dat.g[which(dat.g$Mortality_by_7days == 1), 'renal_function_status7d'] <- 'Mortality'
dat.g[which(is.na(dat.g$renal_function_status7d)), 'renal_function_status7d'] <- 'Loss to Follow Up'

dat.g[which(dat.g$Mortality_by_1month == 1), 'recovery_at_1_month'] <- 'Mortality'
dat.g[which(is.na(dat.g$recovery_at_1_month)), 'recovery_at_1_month'] <- 'Loss to Follow Up'

dat.g[which(dat.g$Mortality_by_3months == 1), 'recovery_at_3_month'] <- 'Mortality'
dat.g[which(is.na(dat.g$recovery_at_3_month)), 'recovery_at_3_month'] <- 'Loss to Follow Up'

dat.g[which(dat.g$Mortality_by_6months == 1), 'recovery_at_6_month'] <- 'Mortality'
dat.g[which(is.na(dat.g$recovery_at_6_month)), 'recovery_at_6_month'] <- 'Loss to Follow Up'

dat.g[which(dat.g$recovery_at_1_month == 'New onset AKD'), 'recovery_at_1_month'] <- 'AKD'
dat.g[which(dat.g$recovery_at_1_month == 'Recovery from AKD'), 'recovery_at_1_month'] <- 'NKD'
dat.g[which(dat.g$recovery_at_1_month == 'Recovery from AKI'), 'recovery_at_1_month'] <- 'NKD'

dat.g[which(dat.g$recovery_at_3_month == 'New onset AKD'), 'recovery_at_3_month'] <- 'AKD'
dat.g[which(dat.g$recovery_at_3_month == 'Recovery from AKD'), 'recovery_at_3_month'] <- 'NKD'
dat.g[which(dat.g$recovery_at_3_month == 'Recovery from AKI'), 'recovery_at_3_month'] <- 'NKD'
dat.g[which(dat.g$recovery_at_3_month %in% c('CKD progression', 'New onset CKD', 'Stable CKD')), 'recovery_at_3_month'] <- 'CKD'
dat.g[which(dat.g$renal_function_status7d == 'AKI' & dat.g$recovery_at_3_month == 'AKI'), 'recovery_at_3_month'] <- 'CKD'

dat.g[which(dat.g$recovery_at_6_month == 'New onset AKD'), 'recovery_at_6_month'] <- 'AKD'
dat.g[which(dat.g$recovery_at_6_month == 'Recovery from AKD'), 'recovery_at_6_month'] <- 'NKD'
dat.g[which(dat.g$recovery_at_6_month == 'Recovery from AKI'), 'recovery_at_6_month'] <- 'NKD'
dat.g[which(dat.g$recovery_at_6_month %in% c('CKD progression', 'New onset CKD', 'Stable CKD')), 'recovery_at_6_month'] <- 'CKD'
dat.g[which(dat.g$renal_function_status7d == 'AKI' & dat.g$recovery_at_6_month == 'AKI'), 'recovery_at_6_month'] <- 'CKD'

dat.g$renal_function_at_admission.cat <- factor(levels = c('NKD', 'AKD', 'AKI', 'CKD', 'Loss to Follow Up', 'Mortality'), dat.g$renal_function_at_admission.cat)
dat.g$renal_function_status7d <- factor(levels = c('NKD', 'AKD', 'AKI', 'CKD', 'Mortality'), dat.g$renal_function_status7d)
dat.g$recovery_at_1_month <- factor(levels = c('NKD', 'AKD', 'AKI', 'CKD', 'Loss to Follow Up', 'Mortality'), dat.g$recovery_at_1_month)
dat.g$recovery_at_3_month <- factor(levels = c('NKD', 'AKD', 'AKI', 'CKD', 'Loss to Follow Up', 'Mortality'), dat.g$recovery_at_3_month)
dat.g$recovery_at_6_month <- factor(levels = c('NKD', 'AKD', 'AKI', 'CKD', 'Loss to Follow Up', 'Mortality'), dat.g$recovery_at_6_month)

count.dat <- dat.g %>% count(renal_function_at_admission.cat, renal_function_status7d, recovery_at_1_month, recovery_at_3_month, recovery_at_6_month)

nodes[which(nodes$name == "NKD"), 'color'] <- '#FFFFFF'
nodes[which(nodes$name == "AKD"), 'color'] <- '33CCCC'  #'#87CEEB' skyblue
nodes[which(nodes$name == "CKD"), 'color'] <- '#00008B'
nodes[which(nodes$name == "AKI"), 'color'] <- 'C55A11'
nodes[which(nodes$name == "NA"), 'color'] <- '#808080'
nodes[which(nodes$name == "NA"), 'color'] <- '#000000'

ggplot(as.data.frame(count.dat),
       aes(y = n, axis1 = renal_function_at_admission.cat, axis2 = renal_function_status7d,
           axis3 = recovery_at_1_month, axis4 = recovery_at_3_month, axis5 = recovery_at_6_month)) +
  geom_alluvium(aes(fill = renal_function_at_admission.cat)) +
  geom_stratum() +
  geom_text(stat = "stratum", infer.label = TRUE) +
  scale_fill_manual(values = c("#FFFFFF", "#33CCCC", '#C55A11', "#00008B", '#808080', '#000000'))
```

```



dRG.long <- to_lodes_form(count.dat,
                          axes = 1:5,
                           id = "Cohort")

p <- ggplot(dRG.long,
       aes(x = x, stratum = stratum, alluvium = Cohort,
           y = n,
           fill = stratum, label = stratum)) +
  scale_x_discrete(expand = c(.1, .1)) +
  geom_flow(color = ’darkgray’) +
  geom_stratum(alpha = 0.85) +
  geom_text(stat = "stratum", size = 3) +
  #geom_text(aes(x = stratum), dRG.long, col = ’white’) +
  theme(legend.position = "none") +
  scale_fill_manual(values = c("#FFFFFF", "#33CCCC", ’#C55A11’, "#00008B", ’#808080’, ’#000000’))


pdf(’alluvial.pdf’, height = 20, width = 30)
print(p)
dev.off()


raw.tab <- demoTab(vars = c(’renal_function_at_admission.cat’, ’renal_function_status7d’, ’recovery_at_1_month’, ’
     recovery_at_3_month’, ’recovery_at_6_month’), data = dat, group = ’phase.cat’)

rownames(raw.tab) <- gsub(’\\_’, ’ ’, rownames(raw.tab))


dat[which(dat.g$recovery_at_6_month == ’NKD’ & dat.g$recovery_at_3_month == ’CKD’), c("patient_id", "
     recovery_at_3_month", "recovery_at_6_month", "sCr3month", "sCr6month")]

dat[which(is.na(dat$recovery_at_3_month) & dat$sCr3month == 1), c("patient_id", "recovery_at_3_month", "sCr3month", ’
     p21_m3fu_scr’, "renal_function_status7d2", "p02_scr_us", "Mortality_by_3months", "p21_m3fu_gfr", "
     p21_m1fu_gfr_original")]

dat[which(is.na(dat$recovery_at_6_month) & dat$sCr6month == 1), c("patient_id", "recovery_at_6_month", "sCr6month", ’
     p21_m6fu_scr’, "renal_function_status7d2", "p02_scr_us", "Mortality_by_6months", "p21_m6fu_gfr", "
     p21_m1fu_gfr_original")]


pdf(’box_plot.pdf’, height = 6, width = 9)
p <- ggplot(dat[complete.cases(dat$recovery_at_3_month), ], aes(x = recovery_at_3_month, y = p21_m3fu_scr)) +
  geom_boxplot() + geom_jitter(shape=3, position=position_jitter(0.2))
p

p <- ggplot(dat[complete.cases(dat$recovery_at_6_month), ], aes(x = recovery_at_6_month, y = p21_m6fu_scr)) +
  geom_boxplot() + geom_jitter(shape=3, position=position_jitter(0.2))
p
dev.off()
```