

Combined Code Near Final

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- 1 Recoding of BMI, age, LOS, gender, ethnicity...
- 2 Sepsis Defined
- 3 Parsing of APACHE Admit Diagnoses
- 4 Defining data variables: as.factor, as.character...
- 5 Medication Variable Decisions
- 6 Explanation of vital sign data variable decisions
- 7 ICU admit source recoded
- 8 ICU Type Decisions
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- 10 Physician Specialties recoded
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- 15 Checking hospital and regional level inclusion/exclusion
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- 17 Seeding/Splitting
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- 20 Setting up variables to analyze interactions
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```
Sys.setenv(TZ="America/New_York")
#install.packages("tidyverse")
#install.packages("downloader")

library(dplyr); library(Hmisc); library(ggplot2); library(sjPlot); library(tidyverse); library(dplyr); library(stringr);
library(downloader)

## 
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
## 
##     filter, lag

## The following objects are masked from 'package:base':
## 
##     intersect, setdiff, setequal, union

## Loading required package: lattice

## Loading required package: survival

## Loading required package: Formula

## Loading required package: ggplot2

## 
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:dplyr':  
##  
##     src, summarize  
  
## The following objects are masked from 'package:base':  
##  
##     format.pval, units  
  
## — Attaching packages ————— tidyverse 1.2.1 —  
  
## ✓ tibble 1.4.2      ✓ purrr  0.2.4  
## ✓ dplyr   0.8.0      ✓ stringr 1.3.0  
## ✓ readr   1.1.1      ✓forcats 0.3.0  
  
## — Conflicts ————— tidyverse_conflicts() —  
## ✘ dplyr::filter()    masks stats::filter()  
## ✘ dplyr::lag()       masks stats::lag()  
## ✘ Hmisc::src()       masks dplyr::src()  
## ✘ Hmisc::summarize() masks dplyr::summarize()  
  
setwd("~/data/EICU/teresa_sepsis/")  
spc <- read.csv("fuzzy_logic_score_first_day_v1_9_0_full.csv")  
ssd <- read.csv("sepsis_study_data_v1_9_1_full.csv")  
ap <- read.csv("apache_diagnosis_mapv2-2017-12-13.csv")  
  
setwd("~/data/EICU/teresa_sepsis/5.0/")  
ssd <- ssd %>% inner_join(spc,"patientunitstayid")  
  
summary(ssd)
```

```

## patientunitstayid exclusion_over18 exclusion_firstadmission
## Min. : 1 Min. :0.000000 Min. :0.0000
## 1st Qu.: 761960 1st Qu.:0.000000 1st Qu.:0.0000
## Median :1597616 Median :0.000000 Median :0.0000
## Mean :1647239 Mean :0.004293 Mean :0.1663
## 3rd Qu.:2628874 3rd Qu.:0.000000 3rd Qu.:0.0000
## Max. :3353271 Max. :1.000000 Max. :1.0000
##
## exclusion_yearfilter exclusion_apacheiva exclusion_vitalobservations
## Min. :0.0000 Min. :0.000 Min. :0.0000
## 1st Qu.:0.0000 1st Qu.:0.000 1st Qu.:0.0000
## Median :0.0000 Median :0.000 Median :0.0000
## Mean :0.2892 Mean :0.378 Mean :0.1026
## 3rd Qu.:1.0000 3rd Qu.:1.000 3rd Qu.:0.0000
## Max. :1.0000 Max. :1.000 Max. :1.0000
##
## exclusion_labobservations exclusion_medobservations hospitalid
## Min. :0.00000 Min. :0.00000 Min. : 1.0
## 1st Qu.:0.00000 1st Qu.:0.00000 1st Qu.:167.0
## Median :0.00000 Median :0.00000 Median :256.0
## Mean :0.02638 Mean :0.1508 Mean :257.3
## 3rd Qu.:0.00000 3rd Qu.:0.00000 3rd Qu.:365.0
## Max. :1.00000 Max. :1.00000 Max. :459.0
##
## gender age ethnicity
## : 4896 Min. : 0.00 : 47920
## Female :1309647 1st Qu.:52.00 African American: 304105
## Male :1527370 Median :65.00 Asian : 45050
## Other : 52 Mean :62.72 Caucasian :2152704
## Unknown: 556 3rd Qu.:76.00 Hispanic : 145350
## : 90.00 Native American : 25711
## NA's :2061 Other/Unknown : 121681
##
## hospital_los hospital_size hospital_type
## Min. :-6378.81 : 643295 Mode:logical
## 1st Qu.: 2.93 <100 : 141919 NA's:2842521
## Median : 5.72 100-249: 533513
## Mean : 8.94 250-500: 481826
## 3rd Qu.: 10.48 >500 :1041968
## Max. :36530.32
##
## hospital_teaching_status hospital_region
## : 554798 :632962
## f:1677818 Midwest :753120
## t: 609905 Northeast:165767
## : 94254 South :714254
## : 576418 West :576418
##
## hospital_dischargeDisposition hospital_mortality
## Home :1697524 Min. :0.00
## SNF : 320193 1st Qu.:0.00
## Death : 264032 Median :0.00
## NursingHome : 147773 Mean :0.09
## Other : 136520 3rd Qu.:0.00
## OtherExternal: 121664 Max. :1.00
## (Other) : 154815 NA's :35521
##
## hospital_mortality_ultimate hospitaladmyear hospitaldischargeyear
## Min. :0.0 Min. :1913 Min. :1987
## 1st Qu.:0.0 1st Qu.:2010 1st Qu.:2010
## Median :0.0 Median :2012 Median :2012
## Mean :0.1 Mean :2012 Mean :2012
## 3rd Qu.:0.0 3rd Qu.:2014 3rd Qu.:2014
## Max. :1.0 Max. :2016 Max. :2016
## NA's :405081
##
## icu_los icu_size icu_type
## Min. :-5.3382 Mode:logical Med-Surg ICU:1527054
## 1st Qu.: 0.8278 NA's:2842521 MICU : 248339
## Median : 1.6104 CCU-CTICU : 227460
## Mean : 2.7858 Cardiac ICU : 192048
## 3rd Qu.: 3.0500 SICU : 179514
## Max. :824.2104 Neuro ICU : 164626
## (Other) : 303480
##
## icu_admit_source icu_disch_location
## Emergency Department:1245659 Floor :1587711
## Floor : 407519 Step-Down Unit (SDU): 291173
## Operating Room : 367328 Home : 250587
## ICU to SDU : 188944 Death : 154009
## Direct Admit : 175631 Telemetry : 152891

```

```

## Recovery Room      : 109083  Other ICU          : 129053
## (Other)           : 348357  (Other)           : 277097
## icu_mortality    admitsource   dischargelocation bedcount
## Min.   :0.0000    Min.   :-1.0    Min.   :-1.0    Min.   : 1.0
## 1st Qu.:0.0000    1st Qu.: 4.0    1st Qu.: 4.0    1st Qu.: 16.0
## Median :0.0000    Median : 8.0    Median : 4.0    Median : 22.0
## Mean   :0.0542    Mean   : 5.6    Mean   : 5.1    Mean   : 26.1
## 3rd Qu.:0.0000    3rd Qu.: 8.0    3rd Qu.: 7.0    3rd Qu.: 31.0
## Max.   :1.0000    Max.   : 8.0    Max.   : 9.0    Max.   : 252.0
## NA's   :644       NA's   :405081  NA's   :405081  NA's   :405081
## readmit      apacheivava
## Min.   :0.0       Min.   : -1.0
## 1st Qu.:0.0       1st Qu.: 35.0
## Median :0.0       Median : 49.0
## Mean   :0.1       Mean   : 52.8
## 3rd Qu.:0.0       3rd Qu.: 67.0
## Max.   :1.0       Max.   :230.0
## NA's   :405081  NA's   :1010706
## apacheadmissiondx   dialysis
##                               : 321341  Min.   :0
## Infarction, acute myocardial (MI) : 108543  1st Qu.:0
## CHF, congestive heart failure   : 91037   Median :0
## Sepsis, pulmonary                : 88361   Mean   :0
## CVA, cerebrovascular accident/stroke : 82058   3rd Qu.:0
## CABG alone, coronary artery bypass grafting: 74389   Max.   :1
## (Other)                      :2076792  NA's   :405081
## aids      hepaticfailure  cirrhosis   diabetes
## Min.   :0       Min.   :0       Min.   :0       Min.   :0.0
## 1st Qu.:0      1st Qu.:0      1st Qu.:0      1st Qu.:0.0
## Median :0      Median :0      Median :0      Median :0.0
## Mean   :0      Mean   :0      Mean   :0      Mean   :0.2
## 3rd Qu.:0      3rd Qu.:0      3rd Qu.:0      3rd Qu.:0.0
## Max.   :1      Max.   :1      Max.   :1      Max.   :1.0
## NA's   :405081 NA's   :405081  NA's   :405081  NA's   :405081
## immunosuppression  leukemia    lymphoma    metastaticcancer
## Min.   :0       Min.   :0       Min.   :0       Min.   :0
## 1st Qu.:0      1st Qu.:0      1st Qu.:0      1st Qu.:0
## Median :0      Median :0      Median :0      Median :0
## Mean   :0      Mean   :0      Mean   :0      Mean   :0
## 3rd Qu.:0      3rd Qu.:0      3rd Qu.:0      3rd Qu.:0
## Max.   :1      Max.   :1      Max.   :1      Max.   :1
## NA's   :405081 NA's   :405081  NA's   :405081  NA's   :405081
## thrombolytics admissionheight admissionweight chartedweight
## Min.   :0       Min.   : 0.0    Min.   : 0.0    Min.   : 30.0
## 1st Qu.:0      1st Qu.:162.5  1st Qu.: 65.8  1st Qu.: 66.1
## Median :0      Median :170.0  Median : 79.4  Median : 80.0
## Mean   :0      Mean   :169.2  Mean   : 83.3  Mean   : 83.7
## 3rd Qu.:0      3rd Qu.:177.8  3rd Qu.: 95.8  3rd Qu.: 96.8
## Max.   :1      Max.   :720.0  Max.   :993.8  Max.   :3000.0
## NA's   :405081 NA's   :142941  NA's   :333094  NA's   :1494918
## eyes      motor        verbal     gcs
## Min.   :-1.0    Min.   :-1.0    Min.   :-1.0    Min.   :-3.0
## 1st Qu.: 3.0   1st Qu.: 6.0    1st Qu.: 3.0    1st Qu.:11.0
## Median : 4.0   Median : 6.0    Median : 5.0    Median :15.0
## Mean   : 3.3   Mean   : 5.1    Mean   : 3.8    Mean   :12.2
## 3rd Qu.: 4.0   3rd Qu.: 6.0    3rd Qu.: 5.0    3rd Qu.:15.0
## Max.   : 4.0   Max.   : 6.0    Max.   : 5.0    Max.   :15.0
## NA's   :405081 NA's   :405081  NA's   :405081  NA's   :405081
## unablegcs    urine       pao2_apache  fio2_apache
## Min.   :-1      Min.   :-11556  Min.   :-1.0   Min.   :-1.0
## 1st Qu.: 0     1st Qu.:    -1   1st Qu.: -1.0  1st Qu.: -1.0
## Median : 0     Median :     0   Median : -1.0  Median : -1.0
## Mean   : 0     Mean   :  965  Mean   : 29.5   Mean   : 12.8
## 3rd Qu.: 0     3rd Qu.: 1519  3rd Qu.: -1.0  3rd Qu.: -1.0
## Max.   : 1     Max.   :21600000 Max.   :840.0  Max.   :100.0
## NA's   :405081 NA's   :405081  NA's   :405081  NA's   :405081
## pao2fio2_apache temperature_apache respiratoryrate_apache
## Min.   : -1.0   Min.   : -1.0   Min.   : -1.0
## 1st Qu.: -1.0  1st Qu.: 36.0   1st Qu.:10.0
## Median : -1.0  Median : 36.4   Median :25.0
## Mean   : 54.9   Mean   : 32.6   Mean   :23.3
## 3rd Qu.: -1.0  3rd Qu.: 36.7   3rd Qu.:34.0
## Max.   :2847.6  Max.   :43.0    Max.   :60.0
## NA's   :405081 NA's   :405081  NA's   :405081
## heartrate_apache mbp_apache albumin_apache bilirubin_apache
## Min.   : -1.0   Min.   : -1.0   Min.   : -1.0   Min.   : -1.0
## 1st Qu.: 70.0   1st Qu.: 52.0   1st Qu.: -1.0  1st Qu.: -1.0
## Median :102.0   Median : 64.0   Median : -1.0  Median : -1.0
## Mean   : 97.1   Mean   : 82.3   Mean   : 0.5    Mean   : -0.2

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## 3rd Qu.:119.0   3rd Qu.:120.0   3rd Qu.: 2.6   3rd Qu.: 0.5
## Max.    :220.0   Max.    :200.0   Max.    : 8.6   Max.    :72.4
## NA's    :405081  NA's    :405081  NA's    :405081  NA's    :405081
##   bun_apache   creatinine_apache glucose_apache   hematocrit_apache
## Min.     :-1.0   Min.     :-1.0   Min.     :-1.0   Min.     :-1.0
## 1st Qu.:  6.0   1st Qu.: 0.4   1st Qu.: 85.0   1st Qu.:19.6
## Median   :15.0   Median   : 0.8   Median   :118.0   Median   :29.9
## Mean     :20.2   Mean     : 1.0   Mean     :142.3   Mean     :24.8
## 3rd Qu.: 27.0   3rd Qu.: 1.4   3rd Qu.:191.0   3rd Qu.:35.9
## Max.    :255.0   Max.    :25.0   Max.    :2954.0   Max.    :93.0
## NA's    :405081  NA's    :405081  NA's    :405081  NA's    :405081
## sodium_apache paco2_apache   ph_apache   intubated_apache
## Min.     :-1     Min.     :-1.0   Min.     :-1.0   Min.     :0.0
## 1st Qu.:128    1st Qu.: -1.0  1st Qu.: -1.0  1st Qu.:0.0
## Median   :136    Median   :-1.0  Median   :-1.0  Median   :0.0
## Mean     :107    Mean     : 8.9   Mean     : 0.9   Mean     :0.1
## 3rd Qu.:140    3rd Qu.: -1.0  3rd Qu.: -1.0  3rd Qu.:0.0
## Max.    :199    Max.    :150.0   Max.    : 8.6   Max.    :1.0
## NA's    :405081  NA's    :405081  NA's    :405081  NA's    :405081
##   wbc_apache   oobintubday1_apache oobventday1_apache ventday1_apache
## Min.     :-1.0   Min.     :0.0   Min.     :0.0   Min.     :0.0
## 1st Qu.: -1.0  1st Qu.:0.0   1st Qu.:0.0   1st Qu.:0.0
## Median   : 8.2   Median   :0.0   Median   :0.0   Median   :0.0
## Mean     : 8.7   Mean     :0.2   Mean     :0.3   Mean     :0.2
## 3rd Qu.:13.2   3rd Qu.:0.0   3rd Qu.:1.0   3rd Qu.:0.0
## Max.    :199.7  Max.    :1.0   Max.    :1.0   Max.    :1.0
## NA's    :405081  NA's    :405081  NA's    :405081  NA's    :405081
##   physicianspeciality acutephysiologyscore apachescore
## :1010706   Min.     :-1.0   Min.     :-1.0   Min.     :-1.0
## internal medicine   :299354  1st Qu.: 25.0   1st Qu.: 35.0
## hospitalist   :259993  Median   :37.0   Median   :49.0
## cardiology   :166439  Mean     :41.4   Mean     :52.8
## pulmonary/CCM   :143113  3rd Qu.: 53.0   3rd Qu.: 67.0
## Specialty Not Specified:142045  Max.    :206.0   Max.    :230.0
## (Other)      :820871  NA's    :1010706  NA's    :1010706
## predictedicu mortality predictedicullos  predictedhospitalmortality
## Min.     :-1.0   Min.     :-1.0   Min.     :-1.0
## 1st Qu.: 0.0   1st Qu.: 2.0   1st Qu.: 0.0
## Median   : 0.0   Median   : 3.2   Median   : 0.0
## Mean     : 0.0   Mean     : 3.6   Mean     : 0.0
## 3rd Qu.: 0.1   3rd Qu.: 5.0   3rd Qu.: 0.1
## Max.    : 1.0   Max.    :19.9   Max.    : 1.0
## NA's    :1010706  NA's    :1010706  NA's    :1010706
## predictedhospitallos  preopmi   preopcardiaccath
## Min.     :-1.0   Min.     :0     Min.     :0
## 1st Qu.: 5.8   1st Qu.:0   1st Qu.:0
## Median   : 8.8   Median   :0   Median   :0
## Mean     : 8.9   Mean     :0   Mean     :0
## 3rd Qu.:12.0   3rd Qu.:0   3rd Qu.:0
## Max.    :224.9  Max.    :1   Max.    :1
## NA's    :1010706  NA's    :1010706  NA's    :1010706
## ptcawithin2h   graftcount   mbp_min   sbp_min
## Min.     :0.0   Min.     :1     Min.     : 1.0   Min.     : 1.0
## 1st Qu.:0.0   1st Qu.: 3   1st Qu.: 48.0  1st Qu.: 50.0
## Median   :0.0   Median   : 3   Median   : 59.0  Median   : 60.0
## Mean     :0.1   Mean     : 3   Mean     : 58.5  Mean     : 60.4
## 3rd Qu.:0.0   3rd Qu.: 3   3rd Qu.: 70.0  3rd Qu.: 71.0
## Max.    :1.0   Max.    :10   Max.    :360.0  Max.    :347.0
## NA's    :1010706  NA's    :405081  NA's    :355269  NA's    :355500
## temperature_min  temperature_max heartrate_max respiratoryrate_max
## Min.     : 0.0   Min.     : 0.1   Min.     : 5.0   Min.     : 1.0
## 1st Qu.: 35.0  1st Qu.: 37.3  1st Qu.: 91.0  1st Qu.: 24.0
## Median   :36.1   Median   : 37.8  Median   :105.0  Median   : 28.0
## Mean     :40.0   Mean     : 43.5  Mean     :106.9  Mean     : 32.1
## 3rd Qu.:36.9   3rd Qu.: 38.5  3rd Qu.:120.0 3rd Qu.: 35.0
## Max.    :137.0  Max.    :224.5  Max.    :300.0  Max.    :63017.0
## NA's    :2626885  NA's    :2626885  NA's    :308791  NA's    :461697
## heartrate_charted_max respiratoryrate_charted_max
## Min.     : 1.0   Min.     : 1.0
## 1st Qu.: 85.0   1st Qu.:20.0
## Median   : 98.0   Median   :25.0
## Mean     :100.4   Mean     :26.3
## 3rd Qu.:114.0   3rd Qu.:30.0
## Max.    :387.0   Max.    : 79.0
## NA's    :702383  NA's    :628438
## o2saturation_charted_min nibp_systolic_charted_min
## Min.     : 0.5   Min.     : 1.0
## 1st Qu.: 91.0   1st Qu.: 86.0
## Median   : 94.0   Median   : 99.0

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## Mean : 92.1          Mean : 100.6
## 3rd Qu.: 96.0        3rd Qu.: 114.0
## Max. : 100.0         Max. : 278.0
## NA's : 853531       NA's : 748024
## nibr_diastolic_charted_min nibr_mean_charted_min ibp_systolic_charted_min
## Min. : 1.0           Min. : 0.1           Min. : 1.0
## 1st Qu.: 42.0         1st Qu.: 56.0         1st Qu.: 82.0
## Median : 51.0         Median : 66.0         Median : 95.0
## Mean : 51.7           Mean : 66.8           Mean : 97.4
## 3rd Qu.: 60.0         3rd Qu.: 77.0         3rd Qu.: 111.0
## Max. : 235.0          Max. : 242.0          Max. : 390.0
## NA's : 746572         NA's : 837390         NA's : 2387420
## ibp_diastolic_charted_min ibp_mean_charted_min mbp_charted_min
## Min. : 1.0           Min. : 0.9           Min. : 0.1
## 1st Qu.: 41.0         1st Qu.: 56.0         1st Qu.: 55.0
## Median : 48.0         Median : 64.0         Median : 65.0
## Mean : 48.8           Mean : 65.4           Mean : 65.8
## 3rd Qu.: 56.0         3rd Qu.: 74.0         3rd Qu.: 76.0
## Max. : 390.0          Max. : 390.0          Max. : 359.0
## NA's : 2387543        NA's : 2360225        NA's : 743730
## sbp_charted_min temperature_charted_min temperature_charted_max
## Min. : 1.0           Min. : 20.1          Min. : 21.0
## 1st Qu.: 85.0          1st Qu.: 36.1          1st Qu.: 36.8
## Median : 98.0          Median : 36.4          Median : 37.1
## Mean : 99.1           Mean : 36.3           Mean : 37.3
## 3rd Qu.: 113.0         3rd Qu.: 36.7         3rd Qu.: 37.6
## Max. : 264.0          Max. : 48.2           Max. : 49.3
## NA's : 702587         NA's : 483953         NA's : 483953
## gcs_charted_min bilirubin_max creatinine_max lactate_min
## Min. : 3.0           Min. : 0.0           Min. : 0.0   Min. : 0.0
## 1st Qu.: 11.0          1st Qu.: 0.4          1st Qu.: 0.8   1st Qu.: 1.0
## Median : 15.0          Median : 0.7          Median : 1.0   Median : 1.5
## Mean : 12.5           Mean : 1.2           Mean : 1.6   Mean : 2.2
## 3rd Qu.: 15.0          3rd Qu.: 1.1           3rd Qu.: 1.6   3rd Qu.: 2.3
## Max. : 15.0           Max. : 198.0          Max. : 405.0   Max. : 557.0
## NA's : 1385494         NA's : 1769123        NA's : 457288   NA's : 2348514
## lactate_max pao2_min pao2_max paco2_min
## Min. : 0.0           Min. : 0.0           Min. : 0.0   Min. : -104.0
## 1st Qu.: 1.2           1st Qu.: 67.0          1st Qu.: 86.8   1st Qu.: 31.8
## Median : 1.9           Median : 84.0           Median : 126.0   Median : 37.0
## Mean : 3.0             Mean : 102.4          Mean : 169.1   Mean : 38.9
## 3rd Qu.: 3.3           3rd Qu.: 115.0          3rd Qu.: 214.0   3rd Qu.: 43.3
## Max. : 557.0          Max. : 11830.0         Max. : 31109.0   Max. : 4560.0
## NA's : 2348514         NA's : 1914680        NA's : 1914680   NA's : 1918151
## paco2_max platelet_min inr_max wbc_min
## Min. : 0.0           Min. : -99999.0        Min. : 0.0   Min. : 0.0
## 1st Qu.: 36.0          1st Qu.: 138.0         1st Qu.: 1.1   1st Qu.: 7.3
## Median : 42.9           Median : 189.0         Median : 1.3   Median : 9.9
## Mean : 45.9           Mean : 201.2          Mean : 1.6   Mean : 11.3
## 3rd Qu.: 51.0           3rd Qu.: 248.0         3rd Qu.: 1.6   3rd Qu.: 13.5
## Max. : 7572.0          Max. : 3211.0          Max. : 130.0   Max. : 813.9
## NA's : 1918151         NA's : 555601          NA's : 1836686   NA's : 551423
## wbc_max ptt_max bands_max ph_min
## Min. : 0.0           Min. : -180.0          Min. : 0.0   Min. : -7.3
## 1st Qu.: 7.9            1st Qu.: 28.9          1st Qu.: 3.0   1st Qu.: 7.3
## Median : 10.8           Median : 34.0           Median : 8.0   Median : 7.3
## Mean : 12.6           Mean : 45.3           Mean : 12.9   Mean : 7.6
## 3rd Qu.: 14.9           3rd Qu.: 46.8           3rd Qu.: 18.0   3rd Qu.: 7.4
## Max. : 346000.0          Max. : 2935.0          Max. : 6424.0   Max. : 70566.0
## NA's : 551423          NA's : 2093556         NA's : 2610683   NA's : 1926604
## basedeficit_min basedeficit_max ast_max alt_max
## Min. : -30.0          Min. : -30.0          Min. : -68.0   Min. : -645.0
## 1st Qu.: 2.4            1st Qu.: 2.4           1st Qu.: 20.0   1st Qu.: 18.0
## Median : 4.8             Median : 4.8           Median : 32.0   Median : 29.0
## Mean : 6.1               Mean : 6.1           Mean : 166.9   Mean : 105.6
## 3rd Qu.: 8.0             3rd Qu.: 8.0           3rd Qu.: 67.0   3rd Qu.: 51.0
## Max. : 405.0            Max. : 405.0          Max. : 787878.0   Max. : 474747.0
## NA's : 2698012          NA's : 2698012         NA's : 1745541   NA's : 1760955
## alp_max penicilin penicilin_anti_staph
## Min. : -154.0          Min. : 0             Min. : 0
## 1st Qu.: 59.0            1st Qu.: 0           1st Qu.: 0
## Median : 79.0             Median : 0           Median : 0
## Mean : 107.4            Mean : 0             Mean : 0
## 3rd Qu.: 111.0            3rd Qu.: 0           3rd Qu.: 0
## Max. : 868488.0           Max. : 1             Max. : 1
## NA's : 1770314          NA's : 472327         NA's : 472327
## penicilin_anti_pseudo augmentin_unasyn cephalosporin_1st_gen
## Min. : 0.0               Min. : 0             Min. : 0
## 1st Qu.: 0.0              1st Qu.: 0           1st Qu.: 0

```

```

## Median :0.0      Median :0      Median :0
## Mean   :0.1      Mean   :0      Mean   :0
## 3rd Qu.:0.0      3rd Qu.:0      3rd Qu.:0
## Max.   :1.0      Max.   :1      Max.   :1
## NA's   :472327    NA's   :472327    NA's   :472327
## cephalosporin_2nd_gen cephalosporin_3rd_gen cephalosporin_4th_5th_gen
## Min.   :0          Min.   :0.0      Min.   :0
## 1st Qu.:0          1st Qu.:0.0      1st Qu.:0
## Median :0          Median :0.0      Median :0
## Mean   :0          Mean   :0.1      Mean   :0
## 3rd Qu.:0          3rd Qu.:0.0      3rd Qu.:0
## Max.   :1          Max.   :1.0      Max.   :1
## NA's   :472327    NA's   :472327    NA's   :472327
## carbapenems       monobactam      fq        vancomycin
## Min.   :0          Min.   :0.0      Min.   :0.0
## 1st Qu.:0          1st Qu.:0.0      1st Qu.:0.0
## Median :0          Median :0.0      Median :0.0
## Mean   :0          Mean   :0.1      Mean   :0.2
## 3rd Qu.:0          3rd Qu.:0.0      3rd Qu.:0.0
## Max.   :1          Max.   :1.0      Max.   :1.0
## NA's   :472327    NA's   :472327    NA's   :472327
## amg        polymixins      linezolid      daptomycin
## Min.   :0          Min.   :0.0      Min.   :0.0
## 1st Qu.:0          1st Qu.:0.0      1st Qu.:0.0
## Median :0          Median :0.0      Median :0.0
## Mean   :0          Mean   :0.0      Mean   :0
## 3rd Qu.:0          3rd Qu.:0.0      3rd Qu.:0.0
## Max.   :1          Max.   :1.0      Max.   :1.0
## NA's   :472327    NA's   :472327    NA's   :472327
## clinda      doxycyclin      macrolides      sulfa
## Min.   :0          Min.   :0.0      Min.   :0.0
## 1st Qu.:0          1st Qu.:0.0      1st Qu.:0.0
## Median :0          Median :0.0      Median :0.0
## Mean   :0          Mean   :0.0      Mean   :0
## 3rd Qu.:0          3rd Qu.:0.0      3rd Qu.:0.0
## Max.   :1          Max.   :1.0      Max.   :1.0
## NA's   :472327    NA's   :472327    NA's   :472327
## metronidazole     nitrofurantoin    tigecycline    ceftriaxone
## Min.   :0          Min.   :0.0      Min.   :0.0
## 1st Qu.:0          1st Qu.:0.0      1st Qu.:0.0
## Median :0          Median :0.0      Median :0.0
## Mean   :0          Mean   :0.0      Mean   :0
## 3rd Qu.:0          3rd Qu.:0.0      3rd Qu.:0.0
## Max.   :1          Max.   :1.0      Max.   :1.0
## NA's   :472327    NA's   :472327    NA's   :472327
## cefotaxime        ampicillin_sulbactam    levofloxacin    moxifloxacin
## Min.   :0          Min.   :0.0      Min.   :0.0
## 1st Qu.:0          1st Qu.:0.0      1st Qu.:0.0
## Median :0          Median :0.0      Median :0.0
## Mean   :0          Mean   :0.0      Mean   :0
## 3rd Qu.:0          3rd Qu.:0.0      3rd Qu.:0.0
## Max.   :0          Max.   :1.0      Max.   :1.0
## NA's   :472327    NA's   :472327    NA's   :472327
## piperacillin_tazobactam    cefepim      meropenem
## Min.   :0          Min.   :0.0      Min.   :0.0
## 1st Qu.:0          1st Qu.:0.0      1st Qu.:0.0
## Median :0          Median :0.0      Median :0.0
## Mean   :0          Mean   :0.0      Mean   :0
## 3rd Qu.:0          3rd Qu.:0.0      3rd Qu.:0.0
## Max.   :0          Max.   :1.0      Max.   :1.0
## NA's   :472327    NA's   :472327    NA's   :472327
## imipenem         doripenem      gentamicin      tobramycin
## Min.   :0          Min.   :0.0      Min.   :0.0
## 1st Qu.:0          1st Qu.:0.0      1st Qu.:0.0
## Median :0          Median :0.0      Median :0.0
## Mean   :0          Mean   :0.0      Mean   :0
## 3rd Qu.:0          3rd Qu.:0.0      3rd Qu.:0.0
## Max.   :0          Max.   :1.0      Max.   :1.0
## NA's   :472327    NA's   :472327    NA's   :472327
## amikacin         dopamine_infusion    epinephrine_infusion
## Min.   :0          Min.   :0.0      Min.   :0.0
## 1st Qu.:0          1st Qu.:0.0      1st Qu.:0.0
## Median :0          Median :0.0      Median :0.0
## Mean   :0          Mean   :0.1      Mean   :0
## 3rd Qu.:0          3rd Qu.:0.0      3rd Qu.:0.0
## Max.   :0          Max.   :1.0      Max.   :1.0
## NA's   :472327    NA's   :2005993    NA's   :2005993
## norepinephrine_infusion    phenylephrine_infusion    vasopressin_infusion
## Min.   :0.0          Min.   :0.0      Min.   :0.0

```

```

## 1st Qu.:0.0          1st Qu.:0.0          1st Qu.:0
## Median :0.0          Median :0.0          Median :0
## Mean   :0.2          Mean   :0.1          Mean   :0
## 3rd Qu.:0.0          3rd Qu.:0.0          3rd Qu.:0
## Max.   :1.0          Max.   :1.0          Max.   :1
## NA's   :2005993      NA's   :2005993      NA's   :2005993
## milrinone_infusion heparin_infusion dopamine_medication
## Min.   :0             Min.   :0.0          Min.   :0.0
## 1st Qu.:0             1st Qu.:0.0        1st Qu.:0.0
## Median :0             Median :0.0        Median :0.0
## Mean   :0             Mean   :0.1          Mean   :0.1
## 3rd Qu.:0             3rd Qu.:0.0        3rd Qu.:0.0
## Max.   :1             Max.   :1.0          Max.   :1.0
## NA's   :2005993      NA's   :2005993      NA's   :472327
## epinephrine_medication norepinephrine_medication phenylephrine_medication
## Min.   :0             Min.   :0.0          Min.   :0.0
## 1st Qu.:0             1st Qu.:0.0        1st Qu.:0.0
## Median :0             Median :0.0        Median :0.0
## Mean   :0             Mean   :0.1          Mean   :0.1
## 3rd Qu.:0             3rd Qu.:0.0        3rd Qu.:0.0
## Max.   :1             Max.   :1.0          Max.   :1.0
## NA's   :2005993      NA's   :2005993      NA's   :472327
## vasopressin_medication milrinone_medication heparin_medication
## Min.   :0             Min.   :0           Min.   :0.0
## 1st Qu.:0             1st Qu.:0         1st Qu.:0.0
## Median :0             Median :0         Median :0.0
## Mean   :0             Mean   :0.2          Mean   :0.2
## 3rd Qu.:0             3rd Qu.:0         3rd Qu.:0.0
## Max.   :1             Max.   :1           Max.   :1.0
## NA's   :472327       NA's   :472327       NA's   :472327
## sepsis    sepsis_priority infection   infection_priority
## Min.   :0.0            Min.   :0.0          Min.   :0.0
## 1st Qu.:0.0            1st Qu.:0.0        1st Qu.:0.0
## Median :0.0            Median :0.0        Median :0.0
## Mean   :0.1            Mean   :0.2          Mean   :0.3
## 3rd Qu.:0.0            3rd Qu.:0.0        3rd Qu.:1.0
## Max.   :1.0            Max.   :3.0          Max.   :1.0
## NA's   :451180         NA's   :451180        NA's   :451180
## aidshiv   aidshiv_priority organfailure organfailure_priority
## Min.   :0             Min.   :0           Min.   :0.0
## 1st Qu.:0             1st Qu.:0         1st Qu.:0.0
## Median :0             Median :0         Median :0.0
## Mean   :0             Mean   :0.4          Mean   :0.7
## 3rd Qu.:0             3rd Qu.:0         3rd Qu.:1.0
## Max.   :1             Max.   :3           Max.   :3.0
## NA's   :451180         NA's   :451180        NA's   :451180
## altered_mental_status altered_mental_status_priority infection_apache
## Min.   :0.0            Min.   :0.0          Min.   :0.0
## 1st Qu.:0.0            1st Qu.:0.0        1st Qu.:0.0
## Median :0.0            Median :0.0        Median :0.0
## Mean   :0.1            Mean   :0.2          Mean   :0.2
## 3rd Qu.:0.0            3rd Qu.:0.0        3rd Qu.:0.0
## Max.   :1.0            Max.   :3           Max.   :1.0
## NA's   :451180         NA's   :451180        NA's   :405081
## organfailure_apache prompt_inflam   prompt_severe_sepsis
## Min.   :0.0            Min.   :0.0          Min.   :0.0
## 1st Qu.:0.0            1st Qu.:0.0        1st Qu.:0.0
## Median :0.0            Median :0.0        Median :0.0
## Mean   :0.1            Mean   :0.2          Mean   :0.1
## 3rd Qu.:0.0            3rd Qu.:0.0        3rd Qu.:0.0
## Max.   :1.0            Max.   :1           Max.   :1.0
## NA's   :405081         NA's   :2043713       NA's   :2043713
## prompt_sepsis   prompt_inflam_with_org_dys prompt_clinical_responce_req
## Min.   :0             Min.   :0           Min.   :0
## 1st Qu.:0             1st Qu.:0         1st Qu.:1
## Median :0             Median :0         Median :1
## Mean   :0             Mean   :0           Mean   :1
## 3rd Qu.:0             3rd Qu.:0         3rd Qu.:1
## Max.   :1             Max.   :1           Max.   :1
## NA's   :2043713       NA's   :2043713       NA's   :2043713
## sofa_respiration sofa_coagulation sofa_liver   sofa_cardiovascular
## Min.   :0.0000          Min.   :0.0000          Min.   :0.0000          Min.   :0
## 1st Qu.:0.0000          1st Qu.:0.0000          1st Qu.:0.0000          1st Qu.:0
## Median :0.0000          Median :0.0000          Median :0.0000          Median :1
## Mean   :0.2906          Mean   :0.3582          Mean   :0.1393          Mean   :1
## 3rd Qu.:0.0000          3rd Qu.:0.0000          3rd Qu.:0.0000          3rd Qu.:1
## Max.   :4.0000          Max.   :4.0000          Max.   :4.0000          Max.   :3
##
## sofa_cns    sofa_renal   sofa_renal_baseline sofa_liver_baseline

```

```

## Min.   :0.0000  Min.   :0.0000  Min.   :0.0000  Min.   :0.0000
## 1st Qu.:0.0000 1st Qu.:0.0000 1st Qu.:0.0000 1st Qu.:0.0000
## Median :0.0000  Median :0.0000  Median :0.0000  Median :0.0000
## Mean    :0.6754  Mean    :0.7193  Mean    :0.1244  Mean    :0.0704
## 3rd Qu.:1.0000 3rd Qu.:1.0000 3rd Qu.:0.0000 3rd Qu.:0.0000
## Max.    :4.0000  Max.    :4.0000  Max.    :4.0000  Max.    :4.0000
##
## sofa_respiration_baseline cardiovascular_baseline soi_alpha
## Min.   :0.000      Min.   :0.0000      Min.   :2.5
## 1st Qu.:0.000      1st Qu.:0.0000      1st Qu.:2.6
## Median :0.000      Median :0.0000      Median :2.8
## Mean    :0.403      Mean    :0.1942      Mean    :3.0
## 3rd Qu.:0.000      3rd Qu.:0.0000      3rd Qu.:3.1
## Max.    :2.000      Max.    :1.0000      Max.    :8.0
##                               NA's   :1172186
## soi_minutes          od_alpha        od_minutes       both_soi_alpha
## Min.   :-60.0       Min.   :1.0       Min.   :-60.0      Min.   :2.5
## 1st Qu.: 0.0       1st Qu.:1.0       1st Qu.:-60.0     1st Qu.:2.6
## Median : 45.0       Median :1.0       Median : 20.0     Median :2.9
## Mean   :196.7       Mean   :1.2       Mean   :161.3     Mean   :3.1
## 3rd Qu.:265.0       3rd Qu.:1.0       3rd Qu.:225.0    3rd Qu.:3.3
## Max.   :1440.0      Max.   :7.0       Max.   :1440.0    Max.   :9.0
## NA's   :1172186     NA's   :735024     NA's   :735024    NA's   :1523008
## both_od_alpha       both_minutes    soi_alteredmentalstatus
## Min.   :1.0       Min.   :-60.0      Min.   :0
## 1st Qu.:1.0       1st Qu.: 5.0      1st Qu.:0
## Median :1.0       Median : 80.0      Median :0
## Mean   :1.4       Mean   :243.1     Mean   :0
## 3rd Qu.:2.0       3rd Qu.:375.0    3rd Qu.:0
## Max.   :7.0       Max.   :1440.0    Max.   :1
## NA's   :1523008     NA's   :1523008    NA's   :1172186
## soi_glucose        soi_heartrate  soi_inr           soi_respiratoryrate
## Min.   :0.0       Min.   :0.0       Min.   :0.0       Min.   :0.0
## 1st Qu.:0.0       1st Qu.:0.3     1st Qu.:0.0       1st Qu.:0.4
## Median :0.9       Median :0.9       Median :0.0       Median :0.8
## Mean   :0.6       Mean   :0.7       Mean   :0.2       Mean   :0.6
## 3rd Qu.:1.0       3rd Qu.:1.0       3rd Qu.:0.0       3rd Qu.:1.0
## Max.   :1.0       Max.   :1.0       Max.   :1.0       Max.   :1.0
## NA's   :1172186     NA's   :1172186    NA's   :1172186    NA's   :1172186
## soi_temperature    soi_bands      soi_wbc           soi_lactate
## Min.   :0.0       Min.   :0.0       Min.   :0.0       Min.   :0.0
## 1st Qu.:0.0       1st Qu.:0.0     1st Qu.:0.0       1st Qu.:0.0
## Median :0.0       Median :0.0       Median :0.6       Median :0.0
## Mean   :0.2       Mean   :0.1       Mean   :0.5       Mean   :0.1
## 3rd Qu.:0.2       3rd Qu.:0.0     3rd Qu.:1.0       3rd Qu.:0.0
## Max.   :1.0       Max.   :1.0       Max.   :1.0       Max.   :1.0
## NA's   :1172186     NA's   :1172186    NA's   :1172186    NA's   :1172186
## od_liver          od_cardiovascular od_respiratory    od_kidney
## Min.   :0.0       Min.   :0.0       Min.   :0.0       Min.   :0.0
## 1st Qu.:0.0       1st Qu.:0.0     1st Qu.:0.0       1st Qu.:0.0
## Median :0.0       Median :1.0       Median :0.0       Median :0.0
## Mean   :0.1       Mean   :0.6       Mean   :0.2       Mean   :0.1
## 3rd Qu.:0.0       3rd Qu.:1.0     3rd Qu.:0.0       3rd Qu.:0.0
## Max.   :1.0       Max.   :1.0       Max.   :1.0       Max.   :1.0
## NA's   :735024     NA's   :735024    NA's   :735024    NA's   :735024
## od_lactate        od_metabolic   od_hematologic
## Min.   :0.0       Min.   :0.0       Min.   :0
## 1st Qu.:0.0       1st Qu.:0.0     1st Qu.:0
## Median :0.0       Median :0.0       Median :0
## Mean   :0.1       Mean   :0.1       Mean   :0
## 3rd Qu.:0.0       3rd Qu.:0.0     3rd Qu.:0
## Max.   :1.0       Max.   :1.0       Max.   :1
## NA's   :735024     NA's   :735024    NA's   :735024
## both_soi_alteredmentalstatus both_soi_glucose both_soi_heartrate
## Min.   :0           Min.   :0.0       Min.   :0.0
## 1st Qu.:0           1st Qu.:0.0     1st Qu.:0.3
## Median :0           Median :0.8       Median :0.9
## Mean   :0           Mean   :0.6       Mean   :0.7
## 3rd Qu.:0           3rd Qu.:1.0     3rd Qu.:1.0
## Max.   :1           Max.   :1.0       Max.   :1.0
## NA's   :1523008     NA's   :1523008    NA's   :1523008
## both_soi_inr       both_soi_respiratoryrate both_soi_temperature
## Min.   :0.0       Min.   :0.0       Min.   :0.0
## 1st Qu.:0.0       1st Qu.:0.4     1st Qu.:0.0
## Median :0.0       Median :0.8       Median :0.0
## Mean   :0.2       Mean   :0.6       Mean   :0.2
## 3rd Qu.:0.2       3rd Qu.:1.0     3rd Qu.:0.2
## Max.   :1.0       Max.   :1.0       Max.   :1.0
## NA's   :1523008     NA's   :1523008    NA's   :1523008

```

```
## both_soi_bands both_soi_wbc both_soi_lactate both_od_liver
## Min. :0.0 Min. :0.0 Min. :0.0 Min. :0.0
## 1st Qu.:0.0 1st Qu.:0.0 1st Qu.:0.0 1st Qu.:0.0
## Median :0.0 Median :0.7 Median :0.0 Median :0.0
## Mean :0.1 Mean :0.6 Mean :0.2 Mean :0.2
## 3rd Qu.:0.0 3rd Qu.:1.0 3rd Qu.:0.0 3rd Qu.:0.0
## Max. :1.0 Max. :1.0 Max. :1.0 Max. :1.0
## NA's :1523008 NA's :1523008 NA's :1523008 NA's :1523008
## both_od_cardiovascular both_od_respiratory both_od_kidney
## Min. :0.0 Min. :0.0 Min. :0.0
## 1st Qu.:0.0 1st Qu.:0.0 1st Qu.:0.0
## Median :1.0 Median :0.0 Median :0.0
## Mean :0.5 Mean :0.2 Mean :0.1
## 3rd Qu.:1.0 3rd Qu.:0.0 3rd Qu.:0.0
## Max. :1.0 Max. :1.0 Max. :1.0
## NA's :1523008 NA's :1523008 NA's :1523008
## both_od_lactate both_od_metabolic both_od_hematologic
## Min. :0.0 Min. :0.0 Min. :0
## 1st Qu.:0.0 1st Qu.:0.0 1st Qu.:0
## Median :0.0 Median :0.0 Median :0
## Mean :0.2 Mean :0.2 Mean :0
## 3rd Qu.:0.0 3rd Qu.:0.0 3rd Qu.:0
## Max. :1.0 Max. :1.0 Max. :1
## NA's :1523008 NA's :1523008 NA's :1523008
```

```
colnames(ssd)
```

```

## [1] "patientunitstayid"
## [3] "exclusion_firstadmission"
## [5] "exclusion_apacheiva"
## [7] "exclusion_labobservations"
## [9] "hospitalid"
## [11] "age"
## [13] "hospital_los"
## [15] "hospital_type"
## [17] "hospital_region"
## [19] "hospital_mortality"
## [21] "hospitaladmityear"
## [23] "icu_los"
## [25] "icu_type"
## [27] "icu_disch_location"
## [29] "admitsource"
## [31] "bedcount"
## [33] "apacheiva"
## [35] "dialysis"
## [37] "hepatictfailure"
## [39] "diabetes"
## [41] "leukemia"
## [43] "metastaticcancer"
## [45] "admissionheight"
## [47] "chartedweight"
## [49] "motor"
## [51] "gcs"
## [53] "urine"
## [55] "fio2_apache"
## [57] "temperature_apache"
## [59] "heartrate_apache"
## [61] "albumin_apache"
## [63] "bun_apache"
## [65] "glucose_apache"
## [67] "sodium_apache"
## [69] "ph_apache"
## [71] "wbc_apache"
## [73] "oobventday1_apache"
## [75] "physicianspeciality"
## [77] "apachescore"
## [79] "predictediculos"
## [81] "predictedhospitallos"
## [83] "preopcardiacath"
## [85] "graftcount"
## [87] "sbp_min"
## [89] "temperature_max"
## [91] "respiratoryrate_max"
## [93] "respiratoryrate_charted_max"
## [95] "nibp_systolic_charted_min"
## [97] "nibp_mean_charted_min"
## [99] "ibp_diastolic_charted_min"
## [101] "mbp_charted_min"
## [103] "temperature_charted_min"
## [105] "gcs_charted_min"
## [107] "creatinine_max"
## [109] "lactate_max"
## [111] "pao2_max"
## [113] "paco2_max"
## [115] "inr_max"
## [117] "wbc_max"
## [119] "bands_max"
## [121] "basedeficit_min"
## [123] "ast_max"
## [125] "alp_max"
## [127] "penicillin_anti_staph"
## [129] "augmentin_unasyn"
## [131] "cephalosporin_2nd_gen"
## [133] "cephalosporin_4th_5th_gen"
## [135] "monobactam"
## [137] "vancomycin"
## [139] "polymixins"
## [141] "dapto"
## [143] "doxycyclin"
## [145] "sulfa"
## [147] "nitrofurantoin"
## [149] "ceftriaxone"
## [151] "ampicillin_sulbactam"
## [153] "moxifloxacin"
## [155] "cefepim"
## [157] "meropenem"
## [159] "linezolid"
## [161] "clinda"
## [163] "macrolides"
## [165] "metronidazole"
## [167] "tigecycline"
## [169] "cefotaxime"
## [171] "levofloxacin"
## [173] "piperacillin_tazobactam"
## [175] "meropenem"
## [177] "penicillin"
## [179] "penicillins"
## [181] "cephalosporin_1st_gen"
## [183] "cephalosporin_3rd_gen"
## [185] "carbapenems"
## [187] "fq"
## [189] "amg"
## [191] "cefotaxime"
## [193] "ceftriaxone"
## [195] "ampicillin_sulbactam"
## [197] "moxifloxacin"
## [199] "piperacillin_tazobactam"
## [201] "meropenem"
## [203] "penicillin"
## [205] "penicillins"
## [207] "cephalosporin_1st_gen"
## [209] "cephalosporin_3rd_gen"
## [211] "carbapenems"
## [213] "fq"
## [215] "amg"
## [217] "cefotaxime"
## [219] "ceftriaxone"
## [221] "ampicillin_sulbactam"
## [223] "moxifloxacin"
## [225] "piperacillin_tazobactam"
## [227] "meropenem"
## [229] "penicillin"
## [231] "penicillins"
## [233] "cephalosporin_1st_gen"
## [235] "cephalosporin_3rd_gen"
## [237] "carbapenems"
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## [1457] "cephalosporin_3rd_gen"
## [1459] "carbapenems"
## [1461] "fq"
## [1463] "amg"
## [1465] "cefotaxime"
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## [1473] "piperacillin_tazobactam"
## [1475] "meropenem"
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## [1499] "piperacillin_tazobactam"
## [1501] "meropenem"
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## [1515] "amg"
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```

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## [187] "organfailure_apache"
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## [199] "sofa_renal_baseline"
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## [207] "both_soi_alpha"
## [209] "both_minutes"
## [211] "soi_glucose"
## [213] "soi_inr"
## [215] "soi_temperature"
## [217] "soi_wbc"
## [219] "od_liver"
## [221] "od_respiratory"
## [223] "od_lactate"
## [225] "od_hematologic"
## [227] "both_soi_glucose"
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## [231] "both_soi_temperature"
## [233] "both_soi_wbc"
## [235] "both_od_liver"
## [237] "both_od_respiratory"
## [239] "both_od_lactate"
## [241] "both_od_hematologic"

```

```
nrow(ssd)
```

```
## [1] 2842521
```

1 Recoding of BMI, age, LOS, gender, ethnicity...

```

ssd <- ssd %>% mutate(patientweight = ifelse (is.na (chartedweight), (admissionweight),chartedweight))

ssd$BMI <- ssd$patientweight/((ssd$admissionheight/100)^2)
ssd$BMI_Ranges <- cut(ssd$BMI, c(0, 18.5, 25, 35, 200))
ssd <- ssd %>% mutate (BMI_Ranges=as.factor(if_else(is.na(BMI_Ranges),"Other/Unknown", as.character(BMI_Ranges))))
summary(ssd$BMI_Ranges, useNA = "ifany")

```

	(0,18.5]	(18.5,25]	(25,35]	(35,200]	Other/Unknown
##	128213	753213	1191774	453265	316056

```
table(ssd$BMI_Ranges,useNA = "ifany")
```

	(0,18.5]	(18.5,25]	(25,35]	(35,200]	Other/Unknown
##	128213	753213	1191774	453265	316056

```
ssd$age_Ranges <- cut(ssd$age, c(0, 25, 35, 45, 55, 65, 75, 85, 100))
table(ssd$age_Ranges,useNA = "ifany")
```

```
##  
##   (0,25]  (25,35]  (35,45]  (45,55]  (55,65]  (65,75]  (75,85]  (85,100]  
##   105109    141150    215032    421325    585296    621393    526359    224233  
##   <NA>  
##   2624
```

```
ssd %>% filter(is.na(age_Ranges)) %>% select(-age_Ranges, -age)
```

```
##      age_Ranges age
## 1          <NA>  NA
## 2          <NA>   0
## 3          <NA>  NA
## 4          <NA>  NA
## 5          <NA>  NA
## 6          <NA>  NA
## 7          <NA>  NA
## 8          <NA>  NA
## 9          <NA>  NA
## 10         <NA>  NA
## 11         <NA>  NA
## 12         <NA>  NA
## 13         <NA>  NA
## 14         <NA>  NA
## 15         <NA>  NA
## 16         <NA>  NA
## 17         <NA>  NA
## 18         <NA>  NA
## 19         <NA>   0
## 20         <NA>  NA
## 21         <NA>  NA
## 22         <NA>  NA
## 23         <NA>  NA
## 24         <NA>  NA
## 25         <NA>  NA
## 26         <NA>  NA
## 27         <NA>  NA
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## 29         <NA>  NA
## 30         <NA>  NA
## 31         <NA>  NA
## 32         <NA>  NA
## 33         <NA>  NA
## 34         <NA>   0
## 35         <NA>   0
## 36         <NA>  NA
## 37         <NA>  NA
## 38         <NA>  NA
## 39         <NA>   0
## 40         <NA>  NA
## 41         <NA>  NA
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## 2449 <NA> NA
## 2450 <NA> NA
## 2451 <NA> NA
## 2452 <NA> NA
## 2453 <NA> 0
## 2454 <NA> NA
## 2455 <NA> NA
## 2456 <NA> 0
## 2457 <NA> NA
## 2458 <NA> NA
## 2459 <NA> NA
## 2460 <NA> NA
## 2461 <NA> NA
## 2462 <NA> NA
## 2463 <NA> 0
## 2464 <NA> 0
## 2465 <NA> 0
## 2466 <NA> 0
## 2467 <NA> 0
## 2468 <NA> NA
## 2469 <NA> 0
## 2470 <NA> NA
## 2471 <NA> NA
## 2472 <NA> NA
## 2473 <NA> NA
## 2474 <NA> NA
## 2475 <NA> NA
## 2476 <NA> NA
## 2477 <NA> NA
## 2478 <NA> NA
## 2479 <NA> NA
## 2480 <NA> NA
## 2481 <NA> NA
## 2482 <NA> NA
## 2483 <NA> NA
## 2484 <NA> NA
## 2485 <NA> NA
## 2486 <NA> NA
## 2487 <NA> 0
## 2488 <NA> NA
## 2489 <NA> NA
## 2490 <NA> NA
## 2491 <NA> NA
## 2492 <NA> 0
## 2493 <NA> NA
## 2494 <NA> NA
## 2495 <NA> NA
## 2496 <NA> NA
## 2497 <NA> 0
## 2498 <NA> NA
## 2499 <NA> 0
## 2500 <NA> 0
## 2501 <NA> NA
## 2502 <NA> 0
## 2503 <NA> NA
## 2504 <NA> 0
## 2505 <NA> NA
## 2506 <NA> NA
## 2507 <NA> NA
## 2508 <NA> 0
## 2509 <NA> NA
## 2510 <NA> NA
## 2511 <NA> 0
## 2512 <NA> 0
## 2513 <NA> 0
## 2514 <NA> 0
## 2515 <NA> NA
## 2516 <NA> 0
## 2517 <NA> 0
## 2518 <NA> 0
## 2519 <NA> 0
## 2520 <NA> NA
## 2521 <NA> NA
## 2522 <NA> NA
## 2523 <NA> NA
## 2524 <NA> NA
## 2525 <NA> NA
## 2526 <NA> NA
```

```
## 2527 <NA> 0
## 2528 <NA> NA
## 2529 <NA> 0
## 2530 <NA> NA
## 2531 <NA> NA
## 2532 <NA> NA
## 2533 <NA> NA
## 2534 <NA> 0
## 2535 <NA> NA
## 2536 <NA> NA
## 2537 <NA> 0
## 2538 <NA> NA
## 2539 <NA> 0
## 2540 <NA> NA
## 2541 <NA> 0
## 2542 <NA> 0
## 2543 <NA> NA
## 2544 <NA> NA
## 2545 <NA> 0
## 2546 <NA> 0
## 2547 <NA> NA
## 2548 <NA> 0
## 2549 <NA> NA
## 2550 <NA> NA
## 2551 <NA> NA
## 2552 <NA> NA
## 2553 <NA> 0
## 2554 <NA> 0
## 2555 <NA> NA
## 2556 <NA> NA
## 2557 <NA> 0
## 2558 <NA> 0
## 2559 <NA> NA
## 2560 <NA> 0
## 2561 <NA> NA
## 2562 <NA> 0
## 2563 <NA> NA
## 2564 <NA> 0
## 2565 <NA> NA
## 2566 <NA> NA
## 2567 <NA> NA
## 2568 <NA> NA
## 2569 <NA> 0
## 2570 <NA> 0
## 2571 <NA> 0
## 2572 <NA> NA
## 2573 <NA> 0
## 2574 <NA> 0
## 2575 <NA> NA
## 2576 <NA> NA
## 2577 <NA> NA
## 2578 <NA> NA
## 2579 <NA> NA
## 2580 <NA> 0
## 2581 <NA> NA
## 2582 <NA> NA
## 2583 <NA> NA
## 2584 <NA> 0
## 2585 <NA> NA
## 2586 <NA> NA
## 2587 <NA> 0
## 2588 <NA> 0
## 2589 <NA> 0
## 2590 <NA> 0
## 2591 <NA> NA
## 2592 <NA> NA
## 2593 <NA> NA
## 2594 <NA> NA
## 2595 <NA> 0
## 2596 <NA> 0
## 2597 <NA> NA
## 2598 <NA> NA
## 2599 <NA> 0
## 2600 <NA> NA
## 2601 <NA> NA
## 2602 <NA> NA
## 2603 <NA> 0
## 2604 <NA> 0
## 2605 <NA> 0
```

```
## 2606 <NA> 0
## 2607 <NA> NA
## 2608 <NA> NA
## 2609 <NA> NA
## 2610 <NA> NA
## 2611 <NA> 0
## 2612 <NA> NA
## 2613 <NA> NA
## 2614 <NA> 0
## 2615 <NA> NA
## 2616 <NA> 0
## 2617 <NA> 0
## 2618 <NA> NA
## 2619 <NA> NA
## 2620 <NA> NA
## 2621 <NA> NA
## 2622 <NA> NA
## 2623 <NA> NA
## 2624 <NA> NA
```

```
summary(ssd$hospital_los, useNA = "ifany")
```

```
## Min. 1st Qu. Median Mean 3rd Qu. Max.
## -6378.81 2.93 5.72 8.94 10.48 36530.32
```

```
ssd$hospitalLOS_Ranges <- cut(ssd$hospital_los, c(0, 1, 3, 5, 10, 20, 30, 60, 90, 150, 999))
table(ssd$hospitalLOS_Ranges,useNA = "ifany")
```

```
##
## (0,1] (1,3] (3,5] (5,10] (10,20] (20,30] (30,60]
## 150460 582206 529927 820698 507248 143837 85601
## (60,90] (90,150] (150,999] <NA>
## 12058 4741 2364 3381
```

```
summary(ssd$icu_los, useNA = "ifany")
```

```
## Min. 1st Qu. Median Mean 3rd Qu. Max.
## -5.3382 0.8278 1.6104 2.7858 3.0500 824.2104
```

```
ssd$icuLOS_Ranges <- cut(ssd$icu_los, c(0, 1, 3, 5, 10, 20, 30, 60, 999))
table(ssd$icuLOS_Ranges,useNA = "ifany")
```

```
##
## (0,1] (1,3] (3,5] (5,10] (10,20] (20,30] (30,60] (60,999]
## 928888 1168923 352746 247099 99566 20292 8379 886
## <NA>
## 15742
```

```
summary(ssd$ethnicity, useNA = "ifany")
```

	African American	Asian	Caucasian
##	47920	304105	2152704
##	Hispanic	Native American	Other/Unknown
##	145350	25711	121681

```
ssd <- ssd %>% mutate(ethnicity2=recode_factor(ethnicity,
`Caucasian` = "Caucasian",
`African American` = "African American",
`Hispanic` = "Hispanic",
`Asian` = "Asian",
`Native American` = "Native American",
`Other/Unknown` = "Other/Unknown",
.default = "Other/Unknown"))

summary(ssd$ethnicity2, useNA = "ifany")
```

	Caucasian	African American	Hispanic	Asian
##	2152704	304105	145350	45050
##	Native American	Other/Unknown		
##	25711	169601		

```

summary(ssd$gender, useNA = "ifany")

##      Female     Male   Other Unknown
## 4896 1309647 1527370      52      556

ssd <- ssd %>% mutate(gender2=recode_factor(gender,
                                              `Male` = "Male",
                                              `Female` = "Female",
                                              `Other` = "Other/Unknown",
                                              `Unknown` = "Other/Unknown",
                                              .default = "Other/Unknown"))

summary(ssd$gender2, useNA = "ifany")

##      Male      Female Other/Unknown
## 1527370    1309647      5504

ssd<- ssd%>%mutate(hospital_mortality=as.factor(hospital_mortality), hospital_mortality_ultimate=as.factor(hospital_mortality_ultimate), icu_mortality=as.factor(icu_mortality))

ssd <- ssd%>%mutate(hospital_region=as.factor(hospital_region))
summary(ssd$hospital_region)

##      Midwest Northeast     South      West
## 632962    753120   165767   714254   576418

ssd <- ssd %>% mutate(hospital_region2=recode_factor(hospital_region, 'Midwest' = "Midwest", 'Northeast' = "Northeast", 'South' = "South", 'West' = "West", .default = "Unknown"))

summary(ssd$hospital_region2)

##      Midwest Northeast     South      West Unknown
## 753120    165767   714254   576418   632962

```

2 Sepsis Defined

We defined positive for sepsis (in-hospital sepsis) as having either a severe sepsis or septic shock diagnosis or having an infection and an acute organ failure diagnosis in the medical record during a 24-hour period starting from the documented ICU admission date and time. Patients with no diagnoses in the diagnoses

```

ssd<- ssd %>% mutate(sepsis_outcome = (sepsis >0 | (infection >0 & organfailure >0)))
summary(ssd$sepsis_outcome)

##      Mode    FALSE     TRUE    NA's
## logical 1906183  485158  451180

table(ssd$sepsis_outcome, useNA = "ifany")

##
##      FALSE     TRUE    <NA>
## 1906183  485158  451180

```

3 Parsing of APACHE Admit Diagnoses

Parsing of APACHE admission diagnoses into organ system grouper with sepsis diagnoses in separate category. 25 diagnoses were categorized as Undefined with 16 transplant diagnoses and 9 of various other non-specific nature.

```

parse_dx <- function(x) {
  sp <- str_split(as.character(x), "\\| ")
  idx <- sapply(sp,length)
  out <- sapply(1:length(idx),function(v) { return(sp[[v]][idx[v]])})
  return(out)
}

ap <- ap %>% mutate(new_apdx =parse_dx(admitxpath)) %>% group_by(new_apdx) %>% mutate(n=row_number()) %>% ungroup()
nrow(ap)

```

```

## [1] 448

colnames(ap)

## [1] "group"           "post.operative" "code"          "dx"
## [5] "number"          "admitdiagnosis" "admitxpath"    "numobs"
## [9] "possible.group" "X"             "new_apdx"      "n"

ssd_j <- ssd %>% left_join(ap%>%filter(n==1)%>%select(-n),by=c("apacheheadmissiondx"="new_apdx"))

## Warning: Column `apacheheadmissiondx`/`new_apdx` joining factor and character
## vector, coercing into character vector

nrow(ssd_j)

## [1] 2842521

if(nrow(ssd_j)==nrow(ssd)) {ssd <- ssd_j;rm(ssd_j)}
nrow(ssd)

## [1] 2842521

summary(ssd$group, useNA = "ifany")

##          Cardiovascular      Gastrointestinal
##                 839352                  266781
##          Gynaecological      Hematological
##                   6754                  18705
##          Metabolic Muscoskeletal/Skin disease
##                  193873                  35740
##          Neurological   Other medical disorders
##                  323997                      0
##          Renal/Genitourinary      Respiratory
##                  61926                  381474
##          Sepsis                  Trauma
##                  571651                  111731
##          Undefined                NA's
##                  21389                  9148

ssd<-ssd%>%mutate(group=droplevels(group))
summary(ssd$group, useNA = "ifany")

##          Cardiovascular      Gastrointestinal
##                 839352                  266781
##          Gynaecological      Hematological
##                   6754                  18705
##          Metabolic Muscoskeletal/Skin disease
##                  193873                  35740
##          Neurological   Renal/Genitourinary
##                  323997                  61926
##          Respiratory            Sepsis
##                  381474                  571651
##          Trauma                  Undefined
##                  111731                  21389
##          NA's                     9148

```

4 Defining data variables: as.factor, as.character...

```
ssd <- ssd %>% mutate(dialysis=as.factor(dialysis),
  aids=as.factor(aids),
  hepaticfailure=as.factor(hepaticfailure|
    cirrhosis),
  diabetes=as.factor(diabetes),
  immunosuppression=as.factor(imunosuppression),
  leukemia=as.factor(leukemia),
  lymphoma=as.factor(lymphoma),
  metastaticcancer=as.factor(metastaticcancer),
  thrombolytics=as.factor(thrombolytics),
  cardiovascular_baseline=as.factor(cardiovascular_baseline))

ssd <- ssd %>% mutate(hospitaldischargeyear=as.character(hospitaldischargeyear))
ssd$hospitaldischargeyear[ssd$hospitaldischargeyear<=2010] <- "-2010"
ssd$hospitaldischargeyear[ssd$hospitaldischargeyear>=2015] <- "2015-16"
summary(ssd$hospitaldischargeyear)
```

```
##      Length     Class      Mode
## 2842521 character character
```

```
ssd <- ssd %>% mutate(hospital_mortality=as.factor(hospital_mortality), hospital_mortality_ultimate=as.factor(hospital_mortality_ultimate), icu_mortality=as.factor(icu_mortality))
```

5 Medication Variable Decisions

Organ dysfunction criteria are met or ignored when certain medications are present. For example, when warfarin and heparin are present lab values associated with coagulopathies (INR and aPTT) are ignored. Vasopressors are generally ordered for a patient with evidence of hypotension, hypoperfusion, or shock. In this study, patients without activity in the medication tables were excluded. Medication data related to continuous infusions are found in one of two places; the medication table which indicates a medication as being ordered or in the nurse charted table indicating starting and/or titrating a continuous infusion. In the early years many ICUs used the TeleICU EHR (also known as eCareManager) as a clinical documentation system. Overtime as hospitals began to implement more comprehensive EHR solutions nurse charting was interfaced in many but not all ICUs. This is consistent with other studies using the eRI complete dataset.

```
ssd$dopamine_infusion[is.na(ssd$dopamine_infusion)]<-0
ssd$dopamine_medication[is.na(ssd$dopamine_medication)]<-0
ssd$epinephrine_infusion[is.na(ssd$epinephrine_infusion)]<-0
ssd$epinephrine_medication[is.na(ssd$epinephrine_medication)]<-0
ssd$norepinephrine_infusion[is.na(ssd$norepinephrine_infusion)]<-0
ssd$norepinephrine_medication[is.na(ssd$norepinephrine_medication)]<-0
ssd$milrinone_infusion[is.na(ssd$milrinone_infusion)]<-0
ssd$milrinone_medication[is.na(ssd$milrinone_medication)]<-0
ssd$phenylephrine_infusion[is.na(ssd$phenylephrine_infusion)]<-0
ssd$phenylephrine_medication[is.na(ssd$phenylephrine_medication)]<-0
```

```
nrow(ssd)
```

```
## [1] 2842521
```

6 Explanation of vital sign data variable decisions

Vital Sign (VS) data can come from several sources within the dataset. When multiple VS data sources were available within a single patient chart data were selected in this order 1) Charted/validated nurse 2) If no charted VS data were available then by vital signs interfaced from bedside monitor (unvalidated) were used 3) Non-invasive blood pressure (NIBP) data were selected over invasive blood pressure (IBP) data if both were present on the same patient. NIBP readings tend to have less variation than IBP readings. 4) APACHE VS variables are the worst reading from normal based on APACHE data collection methods.

```
ssd <- ssd %>% mutate(c_temp_min = ifelse(is.na(temperature_chARTed_min), ifelse(is.na(temperature_min), ifelse(temperature_apache == -1, NA, temperature_apache), temperature_min), temperature_chARTed_min))
summary(ssd$c_temp_min)
```

```
##      Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
##      0.1   36.1   36.4  36.4   36.7 108.3 319848
```

```
ssd <- ssd %>% mutate(c_temp_max = ifelse(is.na(temperature_chARTed_max), ifelse(is.na(temperature_max), ifelse(temperature_apache == -1, NA, temperature_apache), temperature_max), temperature_chARTed_max))
summary(ssd$c_temp_max)
```

```
##      Min. 1st Qu. Median Mean 3rd Qu. Max. NA's
##      0.1   36.8   37.1  37.3   37.6 112.6 319848
```

```

ssd <- ssd %>% mutate(c_HR_max =ifelse (is.na (heartrate_charted_max),ifelse(is.na(heartrate_max), ifelse(heartrate_apache==1, NA, heartrate_apache), heartrate_max),heartrate_charted_max))
summary(ssd$c_HR_max)

##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
##      1.0    86.0   99.0 101.4 115.0 387.0 112042

ssd <- ssd %>% mutate(c_resp_max =ifelse (is.na (respiratoryrate_charted_max),ifelse(is.na(respiratoryrate_max), ifelse(respiratoryrate_apache==1, NA, respiratoryrate_apache), respiratoryrate_max),respiratoryrate_charted_max))
summary(ssd$c_resp_max)

##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
##      1.00   21.00  25.00 26.98 30.00 200.00 134725

ssd <- ssd %>% mutate(c_sbp_min =ifelse (is.na (sbp_charted_min), ifelse(is.na(ibp_systolic_charted_min),nibp_systolic_charted_min, ibp_systolic_charted_min), sbp_charted_min))
summary(ssd$c_sbp_min)

##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
##      1.0    85.0   98.0  99.1 113.0 264.0 702587

ssd <- ssd %>% mutate(c_sbp_min =ifelse(is.na(c_sbp_min),(sbp_min),c_sbp_min))
summary(ssd$c_sbp_min)

##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
##      1.00   75.00  92.00 92.01 109.00 347.00 198922

ssd <- ssd %>% mutate(c_mbp_min =ifelse (is.na (nibp_mean_charted_min),ifelse(is.na(ibp_mean_charted_min), ifelse(mbp_apache==1, NA, mbp_apache), ibp_mean_charted_min),nibp_mean_charted_min))
summary(ssd$c_mbp_min)

##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
##      0.13   56.00   66.00 70.12  78.00 359.00 250116

ssd %>% filter(is.na (nibp_systolic_charted_min))%>%select(c_sbp_min,ibp_systolic_charted_min)%>%head()

##      c_sbp_min ibp_systolic_charted_min
## 1          NA                  NA
## 2          NA                  NA
## 3          NA                  NA
## 4          NA                  NA
## 5          NA                  NA
## 6          NA                  NA

ssd %>% filter(is.na (nibp_mean_charted_min))%>%select(c_mbp_min,ibp_mean_charted_min)%>%head()

##      c_mbp_min ibp_mean_charted_min
## 1          NA                  NA
## 2          NA                  NA
## 3          NA                  NA
## 4          NA                  NA
## 5          NA                  NA
## 6          NA                  NA

```

7 ICU admit source recoded

Combined the 14 unique choices for source of admission into 6 like categories. NAs were coded as "Other".

```
table(ssd$icu_admit_source, useNA = "ifany")
```

```
##          Acute Care/Floor      Chest Pain Center
##      67402             27695           9943
## Direct Admit Emergency Department      Emergency Room
##      175631            1245659            149
##      Floor                ICU        ICU to SDU
##      407519            31038          188944
## Observation     Operating Room       Other
##      118              367328            65
## Other Hospital      Other ICU        PACU
##      65765            85071           8412
## Recovery Room Step-Down Unit (SDU)
##      109083            52699
```

```
ssd <- ssd %>% mutate(icu_admit_source2=recode_factor(icu_admit_source,
  ~Acute Care/Floor` = "Floor",
  ~Chest Pain Center` = "OR/Proc Area",
  ~Direct Admit` = "Direct Admit",
  ~Emergency Department` = "Emergency Department",
  ~Floor` = "Floor",
  ~ICU` = "Other",
  ~ICU to SDU` = "Step-Down Unit",
  ~Observation` = "Other",
  ~Operating Room` = "OR/Proc Area",
  ~Other` = "Other",
  ~Other Hospital` = "Direct Admit",
  ~Other ICU` = "Other",
  ~PACU` = "OR/Proc Area",
  ~Recovery Room` = "OR/Proc Area",
  ~Step-Down Unit (SDU)` = "Step-Down Unit",
  .default = "Other"))

table(ssd$icu_admit_source2,useNA = "ifany")
```

```
##          Floor      OR/Proc Area      Direct Admit
##      435214            494766           241396
## Emergency Department      Other      Step-Down Unit
##      1245659            183843           241643
```

8 ICU Type Decisions

It appears that the names of ICUs have changed over time within the dataset and the names selected by the vendor do not clearly distinguish the type of ICU. We decided to not use the ICU type in Table 1 or in the models for this reason.

```
ssd <- ssd %>% mutate(icu_type2=recode_factor(icu_type,
  ~Burn-Trauma ICU` = "Trauma ICU",
  ~Cardiac ICU` = "Cardiac Care ICU",
  ~CCU-CTICU` = "Cardiac/Surgical Care ICU",
  ~CCU` = "Cardiac Care ICU",
  ~CSICU` = "Cardiac/Surgical Care ICU",
  ~CTICU` = "Cardiac/Surgical Care ICU",
  ~Med-Surg ICU` = "Medical/Surgical ICU",
  ~MICU` = "Medical ICU",
  ~Mobile ICU` = "Other ICU",
  ~Neuro ICU` = "Neuro ICU",
  ~PACU` = "Other ICU",
  ~SICU` = "Surgical ICU",
  ~Trauma ICU` = "Trauma ICU",
  ~Vent ICU` = "Other ICU",
  ~VICU` = "Other ICU",
  ~Virtual ICU` = "Other ICU",
  .default = "Other ICU"))

table(ssd$icu_type2, useNA = "ifany")
```

```
##          Trauma ICU      Cardiac Care ICU
##      36823             192048
## Cardiac/Surgical Care ICU      Medical/Surgical ICU
##      437527            1527054
##      Medical ICU        Other ICU
##      248339            56590
##      Neuro ICU         Surgical ICU
##      164626            179514
```

```
table(ssd$hospital_size, useNA = "ifany")
```

```
##          <100 100-249 250-500    >500
## 643295 141919 533513 481826 1041968
```

9 Discharge locations recoded

Combined the 18 unique discharge locations into 7 like categories. NAs were coded as "Other".

```
ssd <- ssd %>% mutate(icu_disch_location2=recode_factor(icu_disch_location,
`Acute Care/Floor` = "Floor",
`Death` = "Death",
`Floor` = "Floor",
`Home` = "Home",
`Nursing Home` = "SNF/Rehab",
`ICU` = "Other",
`Other ICU` = "Other",
`Observation` = "Other",
`Operating Room` = "Other",
`Other` = "Other",
`Other External` = "Other",
`Other Internal` = "Floor",
`Other Hospital` = "Other Hospital",
`Other ICU (CABG)` = "Other",
`Rehabilitation` = "SNF/Rehab",
`Skilled Nursing Facility` = "SNF/Rehab",
`Step-Down Unit (SDU)` = "Step-Down Unit",
`Telemetry` = "Floor",
.default = "Other"))

table(ssd$icu_disch_location2,useNA = "ifany")
```

```
##        Floor      Death     Home   SNF/Rehab      Other
## 1850937 154009 250587 34591 202328
## Other Hospital Step-Down Unit
##      58896 291173
```

10 Physician Specialties recoded

Combined the 48 unique physician specialties into 2 categories (Critical Care or Specialty-Other). Initial analyses in the subset suggested that there was a difference between Critical Care and all other categories. There were no NAs in the subset. There were 17 in the subset categorized as "unknown"; we coded these as "Specialty-Other".

```
table(ssd$physicianspeciality,useNA = "ifany")
```

```

##                                     allergy/immunology
##          1010706                               590
##      anesthesiology                         anesthesiology/CCM
##          1463                                7519
##      cardiology                            critical care medicine (CCM)
##          166439                               140776
##      dermatology                           emergency medicine
##          35                                    8121
##      endocrinology                          ethics
##          1536                                 13
##      family practice                        gastroenterology
##          85320                                6617
##      hematology                            hematology/oncology
##          525                                    3898
##      hospitalist                           infectious disease
##          259993                               2934
##      internal medicine                      nephrology
##          299354                               15389
##      neurology                             nurse
##          25726                                73
##      nurse practitioner                     obstetrics/gynecology
##          59                                    7244
##      oncology                             ophthalmology
##          7213                                  200
##      orthopedics                           other
##          8931                                24891
##      otolaryngology                        pain management
##          5658                                 21
##      pharmacist                           physical medicine/rehab
##          11                                    208
##      psychiatry                            pulmonary
##          378                                    71676
##      pulmonary/CCM                          radiology
##          143113                               1964
##      respiratory therapist                  rheumatology
##          10                                    98
##      Specialty Not Specified              surgery-cardiac
##          142045                               73447
##      surgery-critical care                 surgery-general
##          5883                                106574
##      surgery-neuro                          surgery-oral
##          52257                                253
##      surgery-orthopedic                    surgery-otolaryngology head & neck
##          2551                                267
##      surgery-pediatric                     surgery-plastic
##          20                                    1531
##      surgery-transplant                   surgery-trauma
##          2237                                29323
##      surgery-vascular                     unknown
##          31142                                80353
##      urology                                5936
##
```

```

ssd <- ssd %>% mutate (physicianSpeciality2= droplevels(recode_factor(physicianspeciality,`critical care medicine (CCM)`= "Critical Care",`anesthesiology/CCM`= "Critical Care",`anesthesiology`= "Critical Care",`surgery-critical care` = "Critical Care",`surgery-trauma` = "Critical Care",`surgery-transplant` = "Speciality-Other",`surgery-orthopedic` = "Speciality-Other",`surgery-general` = "Speciality-Other",`surgery-oral` = "Speciality-Other",`surgery-pediatric` = "Speciality-Other",`surgery-otolaryngology head & neck` = "Speciality-Other",`surgery-cardiac` = "Critical Care",`neurology` = "Speciality-Other",`cardiology` = "Speciality-Other",`surgery-neuro` = "Speciality-Other",`surgery-plastic` = "Speciality-Other",`surgery-vascular` = "Speciality-Other",`oncology` = "Speciality-Other",`hematology` = "Speciality-Other",`hematology/oncology` = "Speciality-Other",`family practice` = "Speciality-Other",`internal medicine` = "Speciality-Other",`Specialty Not Specified` = "Speciality-Other",`urology` = "Speciality-Other",`orthopedics` = "Speciality-Other",`nephrology` = "Speciality-Other",`allergy/immunology` = "Speciality-Other",`dermatology` = "Speciality-Other",`endocrinology` = "Speciality-Other",`ethics` = "Speciality-Other",`emergency medicine` = "Speciality-Other",`gastroenterology` = "Speciality-Other",`obstetrics/gynecology` = "Speciality-Other",`nurse practitioner` = "Speciality-Other",`nurse` = "Speciality-Other",`ophthalmology` = "Speciality-Other",`respiratory therapist` = "Speciality-Other",`other` = "Speciality-Other",`specialty other` = "Speciality-Other",`radiology` = "Speciality-Other",`rheumatology` = "Speciality-Other",`rheumatology` = "Speciality-Other",`infectious disease` = "Speciality-Other",`otolaryngology` = "Speciality-Other",`physical medicine/rehab` = "Speciality-Other",`psychiatry` = "Speciality-Other",`unknown` = "Speciality-Other",`pulmonary` = "Critical Care",`pharmacist` = "Speciality-Other",`Medicine-General` = "Speciality-Other",`pain management` = "Speciality-Other",`pulmonary/CCM` = "Critical Care",`hospitalist` = "Speciality-Other", .default = "Speciality-Other"))

```

```
table(ssd$physicianSpeciality2,useNA = "ifany")
```

```
##  
##      Critical Care Speciality-Other  
##          473200          2369321
```

11 Explanation of Fuzzy Logic SIRS/OD, SIRS, SOFA, qSOFA

The sepsis Fuzzy Logic variables are broken up into Fuzzy Logic Systemic Inflammatory Response Syndrome (SIRs) and Fuzzy Logic organ dysfunction (OD). Baseline Sequential Organ Failure Assessment (SOFA) scores were assigned for three chronic health conditions using the same methodology as the ANZICS study: patients with chronic respiratory received 2 baseline points, and chronic hepatic and renal organ failure received 4 baseline points. For cardiovascular as a comorbid condition we used documented past medical history of myocardial infarction, congestive heart failure, and angina. The following comorbid conditions (also used for baseline SOFA scoring) were defined as: 1) for respiratory we used documented past medical history of COPD, respiratory failure, restrictive pulmonary disease, sarcoidosis, status post lung transplant, or abnormal pulmonary function tests; 2) for renal we used documented past medical history of dialysis; 3) for liver we used documented past medical history of hepatic failure or cirrhosis

SOFA organ dysfunction scoring was assigned per SOFA score definitions.

Note: We made a cut for SOFA Change but will need to review this in full dataset. See partition section.

```
ssd <- ssd %>% mutate (sofa_respiration_baseline2=as.factor(if_else(is.na(sofa_respiration_baseline),FALSE, as.logical(sofa_respiration_baseline))))  
  
ssd <- ssd %>% mutate (sofa_renal_baseline2=as.factor(if_else(is.na(sofa_renal_baseline),FALSE, as.logical(sofa_renal_baseline))))  
  
ssd <- ssd %>% mutate (sofa_liver_baseline2=as.factor(if_else(is.na(sofa_liver_baseline),FALSE, as.logical(sofa_liver_baseline))))  
  
ssd <- ssd %>% mutate(SOFA_Change = (sofa_respiration*(sofa_respiration_baseline!=2) + sofa_coagulation + sofa_liver*(sofa_liver_baseline !=4) + sofa_cardiovascular + sofa_cns + sofa_renal*(sofa_renal_baseline!=4)))  
  
ssd <- ssd %>% mutate(SOFA_Positive = SOFA_Change >=2)  
  
summary(ssd$SOFA_Positive)
```

```
##      Mode      FALSE      TRUE  
## logical  1141836 1700685
```

```
table(ssd$SOFA_Positive,useNA = "ifany")
```

```
##  
##      FALSE      TRUE  
## logical  1141836 1700685
```

```
ssd <- ssd %>% mutate(SOFA_Score = (sofa_respiration + sofa_coagulation + sofa_liver + sofa_cardiovascular + sofa_cns + sofa_renal))  
  
ssd <- ssd %>% mutate(SOFA_Positive2 = SOFA_Score >=2)  
summary(ssd$SOFA_Positive2)
```

```
##      Mode      FALSE      TRUE  
## logical  1092979 1749542
```

```
table(ssd$SOFA_Positive2,useNA = "ifany")
```

```
##  
##      FALSE      TRUE  
## logical  1092979 1749542
```

```
ssd <- ssd %>% mutate(GCS_qSOFA = (gcs !=-3& (gcs<15)),  
                      BP_qSOFA = (c_sbp_min <=100),  
                      Resp_qSOFA = (c_resp_max >=22))  
  
ssd <- ssd %>% mutate(qSOFA_total = (if_else(is.na(GCS_qSOFA),FALSE,GCS_qSOFA) + if_else(is.na(BP_qSOFA),FALSE, BP_qSOFA) + if_else(is.na(Resp_qSOFA),FALSE,Resp_qSOFA)))  
  
ssd <- ssd %>% mutate(qSOFA_Positive = qSOFA_total >=2)  
  
summary(ssd$qSOFA_Positive)
```

```

##      Mode   FALSE    TRUE
## logical 1236207 1606314

table(ssd$SOFA_Positive,useNA = "ifany")

##      Mode   FALSE    TRUE
## logical 1236207 1606314

ssd <- ssd %>% mutate(temp_SIRS = c_temp_max >38 | c_temp_min<36,
                       wbc_SIRS = if_else(is.na(wbc_min) & is.na(wbc_max),bands_max>=10,if_else(is.na(bands_max),wbc_max>12 | wbc_min<4,if_else(!is.na(wbc_min)&!is.na(wbc_max)&!is.na(bands_max),wbc_max>12 | wbc_min<4 | bands_max>=10,NA))),
                       resp_SIRS = if_else(is.na(c_resp_max), paco2_min <32, if_else(is.na(paco2_min), c_resp_max>20, if_else(!is.na(c_resp_max)&!is.na(paco2_min), c_resp_max>20 | paco2_min<32, NA))),
                       HR_SIRS = c_HR_max >90)

ssd <- ssd %>% mutate(SIRS_total = (if_else(is.na(temp_SIRS),FALSE, temp_SIRS) + if_else(is.na(wbc_SIRS),FALSE, wbc_SIRS) + if_else(is.na(resp_SIRS),FALSE,resp_SIRS) + if_else(is.na(HR_SIRS), FALSE, HR_SIRS)))

table(ssd$SIRS_total,useNA = "ifany")

##      0      1      2      3      4
## 310612 593666 954052 724089 260102

ssd <- ssd %>% mutate(SIRS_Positive = SIRS_total >=2)

table(ssd$SIRS_Positive,useNA = "ifany")

##      Mode   FALSE    TRUE
## logical 904278 1938243

ssd <- ssd %>% mutate(StickyMinutes = if_else (soi_minutes >= od_minutes, soi_minutes, od_minutes))

ssd <- ssd %>% mutate(FuzzyTotal1 = (if_else(is.na(soi_alpha), 0, 1) + if_else(is.na(od_alpha), 0,1)))

### HERE

table(ssd$FuzzyTotal1,useNA = "ifany")

##      0      1      2
## 487388 932434 1422699

summary(ssd$FuzzyTotal1, useNA = "ifany")

##      Min. 1st Qu. Median     Mean 3rd Qu.     Max.
## 0.000  1.000  2.000  1.329  2.000  2.000

#ssd %>% filter(patientunitstayid == 141289)

nrow(ssd)

## [1] 2842521

ssd <- ssd %>% mutate(SimultaneousMinutes = !is.na (both_minutes))

summary(ssd$SimultaneousMinutes)

##      Mode   FALSE    TRUE
## logical 1523008 1319513

```

```
ssd <- ssd %>% mutate(SepsisFuzzyLogicPositive= !is.na (both_soi_alpha + both_od_alpha))

table(ssd$SepsisFuzzyLogicPositive,useNA = "ifany")

## 
##   FALSE     TRUE
## 1523008 1319513

ssd <- ssd%>% mutate(SepsisFuzzyLogicPositive2 = SimultaneousMinutes)
```

12 Inclusion/Exclusion Criteria

The designs and findings from several previous studies using the complete dataset were used identify inclusion and exclusion criteria that would best support decision-making related to missingness and generalizability. To reduce introduction of missingness, patients where no evidence of interfaces or documentation for laboratory, vital sign, medication, and diagnosis related data existed, were excluded (convenience sample). Other similar large data studies made decisions related to imputation to deal with missingness. Limitations of imputation techniques include underestimation of standard errors/overestimation of test statistics, different imputation methods can produce different estimates and some methods can produce different estimates every time they are used on the same dataset, some require specialized software, and some can only be used for linear and log-linear models. Improper handling of missing data can compromise the validity of a study's results or inferences. Because of the sheer number of cases within the complete dataset, as well as the subset, the researcher was not concerned about losing power. Secondly, patients that show no activity in laboratory, vital sign, medication, and diagnosis tables are not missing data at random but are likely missing because of a lack of interface between hospital information systems and the eCareManager system. Imputing on these cases may introduce the bias that is trying to be avoided Given these reasons a decision was made in advance to exclude cases with no activity in the tables forementioned. Table 1 "Exclusion versus Inclusion Demographic, Severity of Illness, Diagnostic and Sepsis Outcome Date" compares excluded versus included patients.

```
table(ssd$exclusion_yearfilter)
```

```
## 
##      0      1
## 2020489 822032
```

```
table(ssd$exclusion_over18)
```

```
## 
##      0      1
## 2830319 12202
```

```
table(!is.na(ssd$age))
```

```
## 
##   FALSE     TRUE
## 2061 2840460
```

```
table(ssd$exclusion_firstadmission)
```

```
## 
##      0      1
## 2369682 472839
```

```
table(ssd$exclusion_apacheiva)
```

```
## 
##      0      1
## 1768014 1074507
```

```
table(ssd$exclusion_vitalobservations)
```

```
## 
##      0      1
## 2550796 291725
```

```
table(ssd$exclusion_labobservations)
```

```

##          0          1
## 2767549    74972

table(ssd$exclusion_medobservations)

##          0          1
## 2413821   428700

ssd_incl <- ssd %>% filter(exclusion_yearfilter==0)
nrow(ssd_incl)

## [1] 2020489

ssd_incl <- ssd_incl %>% filter(exclusion_over18==0 & !is.na(age))
nrow(ssd_incl)

## [1] 2011652

ssd_incl <- ssd_incl %>% filter(exclusion_firstadmission==0)
nrow(ssd_incl)

## [1] 1666917

ssd_incl <- ssd_incl %>% filter(exclusion_apacheiva==0)
nrow(ssd_incl)

## [1] 1162680

ssd_incl <- ssd_incl %>% filter(exclusion_vitalobservations==0)
nrow(ssd_incl)

## [1] 1073088

ssd_incl <- ssd_incl %>% filter(exclusion_labobservations==0)
nrow(ssd_incl)

## [1] 1068937

ssd_incl <- ssd_incl %>% filter(exclusion_medobservations==0)
nrow(ssd_incl)

## [1] 929538

```

Cases with no activity in the diagnosis table were excluded. Using a binary classification process positive for sepsis (in-hospital sepsis) was defined by having either a severe sepsis or septic shock diagnosis or having an infection and an acute organ failure diagnosis in the medical record during a 24-hour period starting from ICU admission date and time.

```

ssd_incl$hasDiagnosisCodes <- (!is.na(ssd_incl$sepsis)& !is.na(ssd_incl$organfailure)& !is.na(ssd_incl$infection))

ssd_incl <- ssd_incl %>% filter(hasDiagnosisCodes)

nrow(ssd_incl)

## [1] 912509

```

13 Preparation of data variables for Table 1

"Exclusion versus Inclusion Demographic, Severity of Illness, Diagnostic and Sepsis Outcome Date" compares excluded versus included patients.

```
ssd$hasDiagnosisCodes <- (!is.na(ssd$sepsis) & !is.na(ssd$organfailure) & !is.na(ssd$infection))
table(ssd$hasDiagnosisCodes, useNA = "ifany")
```

```
##  
##   FALSE      TRUE  
##  451180 2391341
```

```
ssd$inclusiongroup <- 1
ssd$inclusiongroup [ssd$exclusion_over18==1] <- 0
ssd$inclusiongroup [ssd$exclusion_firstadmission==1] <- 0
ssd$inclusiongroup [ssd$exclusion_apacheiva==1] <- 0
ssd$inclusiongroup [ssd$exclusion_yearfilter==1] <- 0
ssd$inclusiongroup [ssd$exclusion_vitalobservations==1] <- 0
ssd$inclusiongroup [ssd$exclusion_labobservations==1] <- 0
ssd$inclusiongroup [ssd$exclusion_medobservations==1] <- 0
ssd$inclusiongroup [!ssd$hasDiagnosisCodes] <- 0
summary(ssd$inclusiongroup, UseNA = "ifany")
```

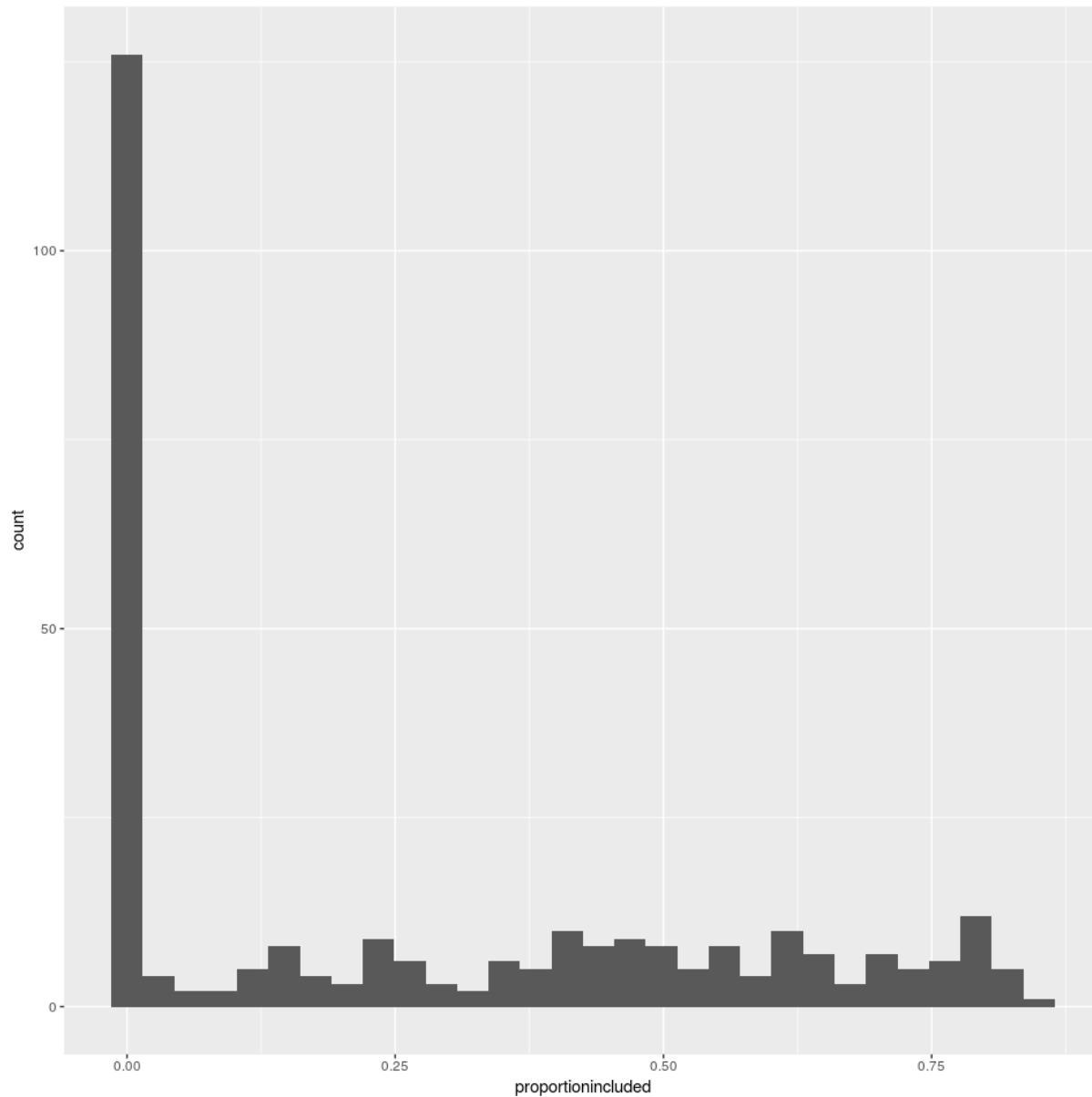
```
##      Min. 1st Qu. Median    Mean 3rd Qu.    Max.
##  0.000  0.000  0.000   0.321  1.000  1.000
```

```
table(ssd$inclusiongroup, useNA = "ifany")
```

```
##  
##      0      1  
## 1930007 912514
```

```
ssd %>% group_by(hospitalid) %>% summarise(n=n(), numberincluded=sum(inclusiongroup), numberexcluded=sum(inclusiongroup==0), proportionincluded=numberincluded/n) %>% filter(n>100) %>% ggplot(aes(proportionincluded)) + geom_histogram()
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
ssd %>%group_by(hospitalid)%>%summarise(n=n(), numberincluded=sum(inclusiongroup), numberexcluded=sum(inclusiongroup==0), proportionincluded=numberincluded/n)%>%filter(n>100 & proportionincluded<.05)
```

```
## # A tibble: 130 x 5
##   hospitalid     n numberincluded numberexcluded proportionincluded
##       <int> <int>      <dbl>        <int>            <dbl>
## 1         1    6840        0.        6840            0.
## 2         3    1702        0.        1702            0.
## 3         4    9705        0.        9705            0.
## 4         5     722        0.        722             0.
## 5         6    1768        0.        1768            0.
## 6         7    1164        0.        1164            0.
## 7         8    5523        0.        5523            0.
## 8         9    6087        0.        6087            0.
## 9        12    3538        0.        3538            0.
## 10        13     566        0.        566             0.
## # ... with 120 more rows
```

```
ssd %>%filter(hospitalid==207)%>%select(contains("exclusion_"),icu_type)%>%summary
```

```

## exclusion_over18 exclusion_firstadmission exclusion_yearfilter
## Min. :0           Min. :0.00000           Min. :0.00000
## 1st Qu.:0          1st Qu.:0.00000        1st Qu.:0.00000
## Median :0          Median :0.00000        Median :0.00000
## Mean   :0          Mean   :0.3363         Mean   :0.07171
## 3rd Qu.:0          3rd Qu.:1.00000        3rd Qu.:0.00000
## Max.  :0           Max.  :1.00000         Max.  :1.00000
##
## exclusion_apacheiva exclusion_vitalobservations exclusion_labobservations
## Min. :0.00000      Min. :0.00000      Min. :0.00000
## 1st Qu.:0.00000    1st Qu.:0.00000    1st Qu.:0.00000
## Median :1.00000    Median :0.00000    Median :0.00000
## Mean   :0.6921     Mean   :0.04839     Mean   :0.03725
## 3rd Qu.:1.00000    3rd Qu.:0.00000    3rd Qu.:0.00000
## Max.  :1.00000     Max.  :1.00000     Max.  :1.00000
##
## exclusion_medobservations           icu_type
## Min. :0.00000      Med-Surg ICU      :5712
## 1st Qu.:1.00000    Mobile ICU       : 33
## Median :1.00000    Burn-Trauma ICU   : 0
## Mean   :0.8019      Cardiac ICU      : 0
## 3rd Qu.:1.00000    Cardiovascular ICU: 0
## Max.  :1.00000     CCU-CTICU       : 0
##                      (Other)          : 0

```

```
ssd %>%filter(hospitalid==207)%>%select(contains("exclusion_"),icu_type, hasDiagnosisCodes)%>%summary
```

```

## exclusion_over18 exclusion_firstadmission exclusion_yearfilter
## Min. :0           Min. :0.00000           Min. :0.00000
## 1st Qu.:0          1st Qu.:0.00000        1st Qu.:0.00000
## Median :0          Median :0.00000        Median :0.00000
## Mean   :0          Mean   :0.3363         Mean   :0.07171
## 3rd Qu.:0          3rd Qu.:1.00000        3rd Qu.:0.00000
## Max.  :0           Max.  :1.00000         Max.  :1.00000
##
## exclusion_apacheiva exclusion_vitalobservations exclusion_labobservations
## Min. :0.00000      Min. :0.00000      Min. :0.00000
## 1st Qu.:0.00000    1st Qu.:0.00000    1st Qu.:0.00000
## Median :1.00000    Median :0.00000    Median :0.00000
## Mean   :0.6921     Mean   :0.04839     Mean   :0.03725
## 3rd Qu.:1.00000    3rd Qu.:0.00000    3rd Qu.:0.00000
## Max.  :1.00000     Max.  :1.00000     Max.  :1.00000
##
## exclusion_medobservations           icu_type     hasDiagnosisCodes
## Min. :0.00000      Med-Surg ICU      :5712      Mode :logical
## 1st Qu.:1.00000    Mobile ICU       : 33       FALSE:3625
## Median :1.00000    Burn-Trauma ICU   : 0        TRUE :2120
## Mean   :0.8019      Cardiac ICU      : 0
## 3rd Qu.:1.00000    Cardiovascular ICU: 0
## Max.  :1.00000     CCU-CTICU       : 0
##                      (Other)          : 0

```

```
summary(ssd$c_sbp_min, useNA = "ifany")
```

```

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max. NA's
##   1.00  75.00  92.00  92.01 109.00 347.00 198922

```

```
summary(ssd_incl$c_sbp_min, useNA = "ifany")
```

```

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max. NA's
##   1.00  78.00  92.00  92.14 107.00 256.00 184

```

```
summary(ssd$c_mbp_min, useNA = "ifany")
```

```

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max. NA's
##   0.13  56.00  66.00  70.12  78.00 359.00 250116

```

```
summary(ssd_incl$c_mbp_min, useNA = "ifany")
```

```

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.
##   0.13  54.00  64.00  66.76  75.00 287.00

```

```

summary(ssd$c_temp_max, useNA = "ifany")

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
##   0.1    36.8   37.1   37.3   37.6  112.6  319848

summary(ssd_incl$c_temp_max, useNA = "ifany")

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
##   0.10   36.90  37.17  37.32  37.60 111.20  17387

summary(ssd$c_temp_min, useNA = "ifany")

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
##   0.1    36.1   36.4   36.4   36.7  108.3  319848

summary(ssd_incl$c_temp_min, useNA = "ifany")

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
##   0.10   36.10  36.40  36.29  36.70 101.00  17387

summary(ssd$c_resp_max, useNA = "ifany")

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
##   1.00   21.00  25.00  26.98  30.00 200.00 134725

summary(ssd_incl$c_resp_max, useNA = "ifany")

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.
##   1.00   22.00  26.00  28.01  31.00 199.00

summary(ssd$c_HR_max, useNA = "ifany")

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.   NA's
##   1.0    86.0   99.0  101.4  115.0 387.0  112042

summary(ssd_incl$c_HR_max, useNA = "ifany")

##   Min. 1st Qu. Median   Mean 3rd Qu.   Max.
##   5.0    87.0  101.0  102.9  116.0 379.0

```

14 Table 1 Exclusion versus Inclusion

Demographic, Severity of Illness, Diagnostic, and Mortality Outcome Data

```

varsTable1compare <- c("age", "gender2", "ethnicity2", "BMI_Ranges", "icu_admit_source2", "physicianSpeciality2",
"hospitaldischargeyear", "hospital_teaching_status", "hospital_size", "hospital_region2", "dialysis", "aids", "hep
aticfailure", "diabetes", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa
_respiration_baseline2", "cardiovascular_baseline", "SIRS_Positive", "qSOFA_Positive", "SOFA_Positive", "SepsisFuz
zyLogicPositive", "apacheiva", "hospital_mortality_ultimate", "icu_mortality", "hospital_los", "icu_los", "sepsis_
outcome", "group")

library(tableone); library(survival); library(dplyr); library(Hmisc); library(ggplot2); library(sjPlot)

if(!( "tableone" %in% rownames(installed.packages()))){
  install.packages("tableone")
}

Table1IncludeExclude <- CreateTableOne(data=ssd ,vars=varsTable1compare,strata="inclusiongroup",test=TRUE, includ
eNA=TRUE
) %>% print(nonnnormal= c("icu_mortality", "hospital_mortality_ultimate", "sepsis_outcome", "hospital_teaching_ stat
us"),minMax=TRUE,
  printToggle      = FALSE,
  showAllLevels   = TRUE,
  cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="Exclusion versus Inclusion Demographic, Severity of Illness, Diagnostic, and Outcome Dat
a")

```

15 Checking hospital and regional level inclusion/exclusion

Review changes to hospital IDs due to inclusion/exclusion criteria. Hospital ID is the unique name of a hospital within the dataset. This analysis will review how many hospitals are dropped from the analyses. Hospitals that did not build interfaces between hospital information systems and the eCareManager system will be at highest risk of having patients excluded from this study. Review of regional data (included in Demographic, Severity of Illness, Diagnostic Tables) will allow readers to visualize if populations within certain region are under-represented.

```

ssd %>% mutate(inStudy = exclusion_yearfilter==0 & exclusion_over18==0 & exclusion_firstadmission==0 & exclusion_
apacheiva==0 & exclusion_vitalobservations==0 & exclusion_labobservations==0 & exclusion_medobservations==0) %>%
group_by(hospitalid) %>% summarise(n=n(),n_study=sum(inStudy),propInstudy=n_study/n)

```

```

## # A tibble: 334 x 4
##   hospitalid     n n_study propInstudy
##       <int> <int>    <int>      <dbl>
## 1          1   6840      0      0.
## 2          3   1702      0      0.
## 3          4   9705      0      0.
## 4          5    722      0      0.
## 5          6   1768      0      0.
## 6          7   1164      0      0.
## 7          8   5523      0      0.
## 8          9   6087      0      0.
## 9         12   3538      0      0.
## 10         13    566      0      0.
## # ... with 324 more rows

```

```

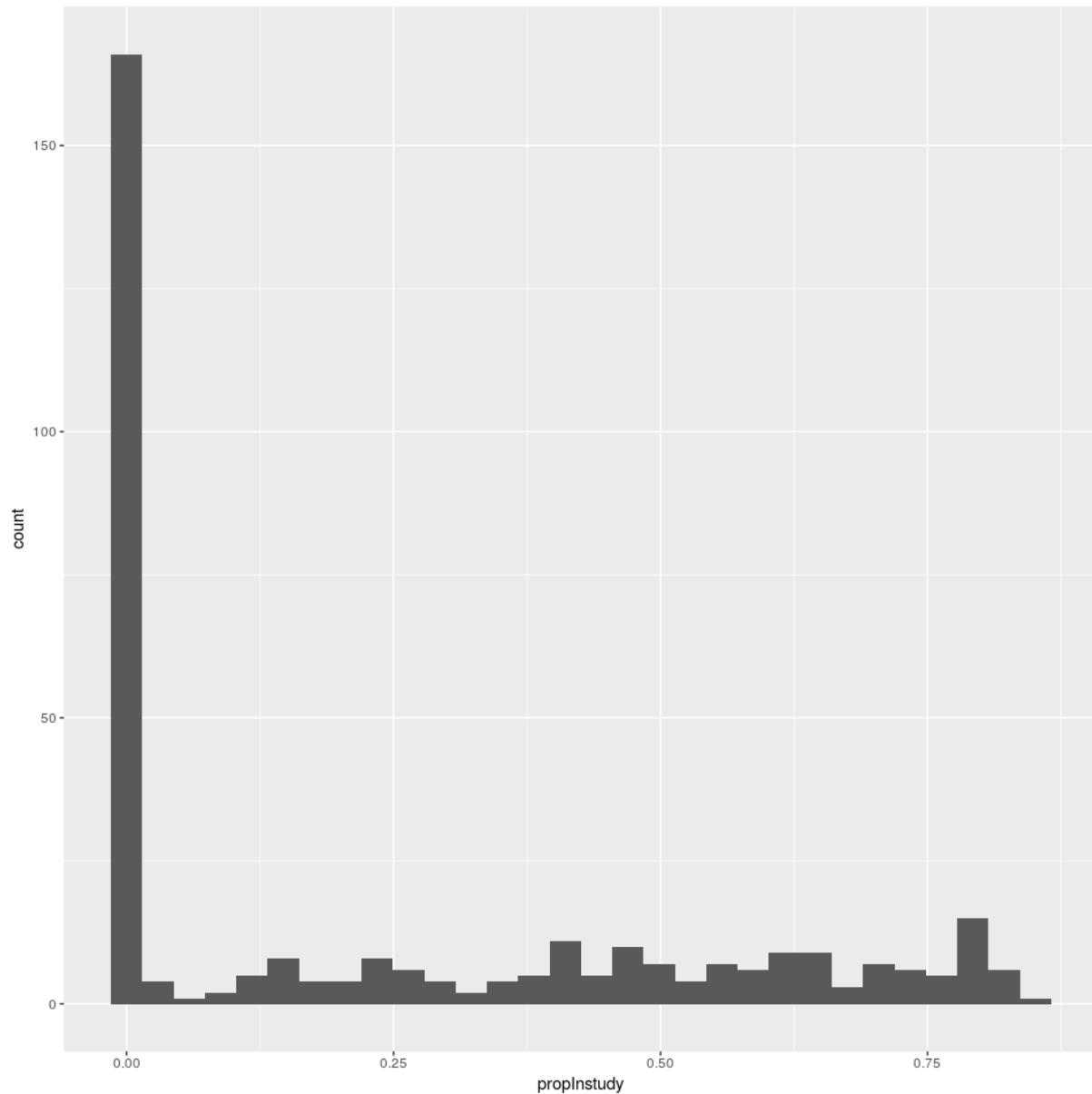
ssd %>% mutate(inStudy = exclusion_yearfilter==0 & exclusion_over18==0 & exclusion_firstadmission==0 & exclusion_
apacheiva==0 & exclusion_vitalobservations==0 & exclusion_labobservations==0 & exclusion_medobservations==0) %>%
group_by(hospitalid) %>% summarise(n=n(),n_study=sum(inStudy),propInstudy=n_study/n) %>% ggplot(aes(propInstudy))
+ geom_histogram()

```

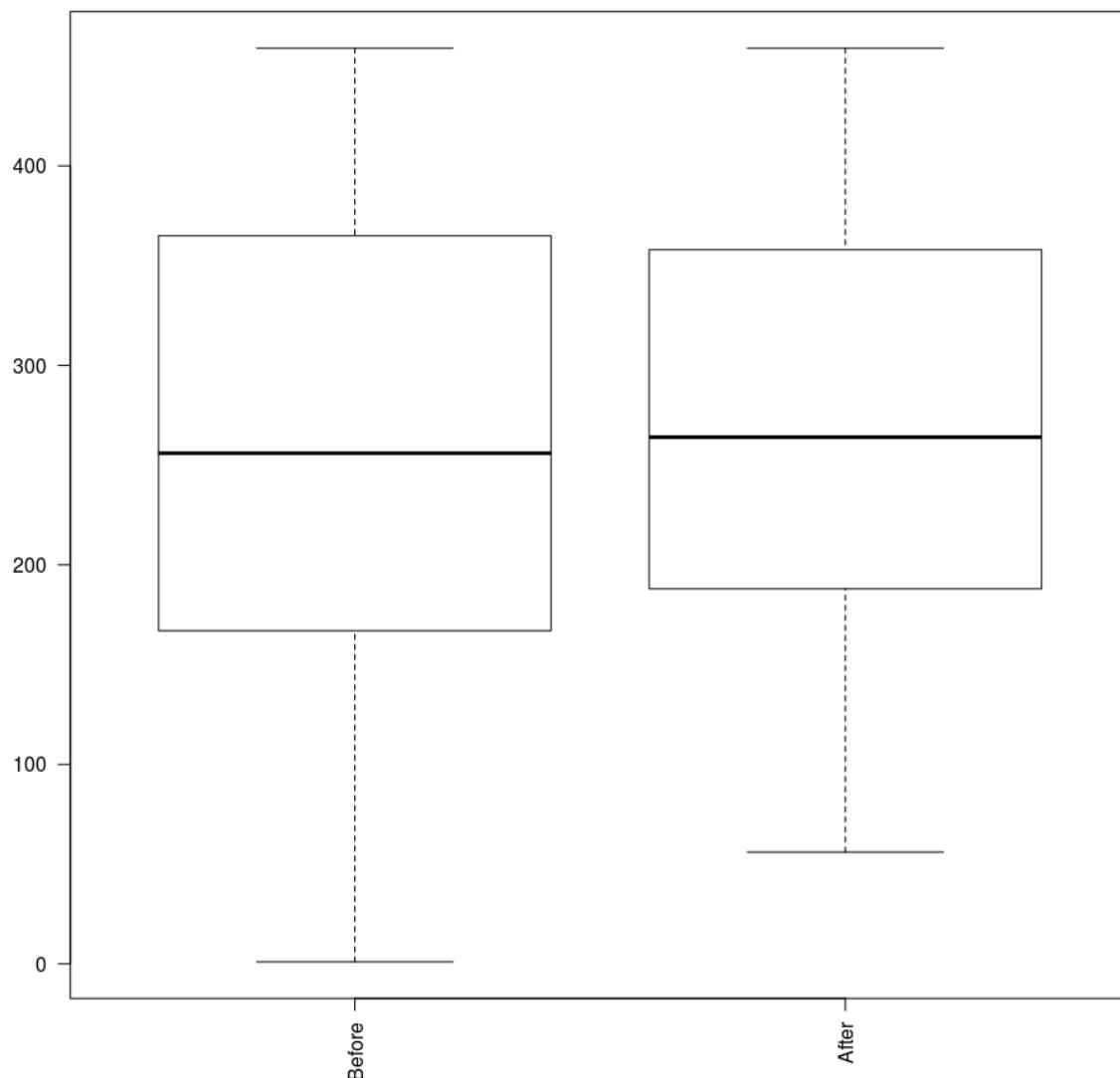
```

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

```



```
boxplot(ssd$hospitalid,ssd_incl$hospitalid,las=2,main= "Hospital IDs Before/After Inclusion/Exclusion", names = c("Before", "After"))
```

Hospital IDs Before/After Inclusion/Exclusion

```
ssd$albumin_apache[ssd$albumin_apache==(-1)] <- NA  
ssd_incl$albumin_apache[ssd_incl$albumin_apache==(-1)] <- NA
```

16 Descriptive

Describing variables before and after inclusion/exclusion

```
describe(ssd)
```

```
## Warning in w * sort(x - mean(x)): longer object length is not a multiple of  
## shorter object length
```

```

## ssd
##
## 296 Variables     2842521 Observations
## -----
## patientunitstayid
##      n    missing   distinct      Info      Mean      Gmd      .05      .10
## 2842521          0    2842521       1  1647239  1169471  142267  288023
##    .25      .50      .75      .90      .95
## 761960  1597616  2628874  3063221  3211145
##
## lowest : 1 2 3 4 5
## highest: 3353267 3353268 3353269 3353270 3353271
## -----
## exclusion_over18
##      n    missing   distinct      Info      Sum      Mean      Gmd
## 2842521          0        2     0.013    12202  0.004293  0.008548
##
## -----
## exclusion_firstadmission
##      n    missing   distinct      Info      Sum      Mean      Gmd
## 2842521          0        2     0.416    472839  0.1663  0.2773
##
## -----
## exclusion_yearfilter
##      n    missing   distinct      Info      Sum      Mean      Gmd
## 2842521          0        2     0.617    822032  0.2892  0.4111
##
## -----
## exclusion_apacheiva
##      n    missing   distinct      Info      Sum      Mean      Gmd
## 2842521          0        2     0.705   1074507  0.378   0.4702
##
## -----
## exclusion_vitalobservations
##      n    missing   distinct      Info      Sum      Mean      Gmd
## 2842521          0        2     0.276    291725  0.1026  0.1842
##
## -----
## exclusion_labobservations
##      n    missing   distinct      Info      Sum      Mean      Gmd
## 2842521          0        2     0.077    74972   0.02638  0.05136
##
## -----
## exclusion_medobservations
##      n    missing   distinct      Info      Sum      Mean      Gmd
## 2842521          0        2     0.384   428700  0.1508  0.2561
##
## -----
## hospitalid
##      n    missing   distinct      Info      Mean      Gmd      .05      .10
## 2842521          0      334       1  257.3  138.9      56      92
##    .25      .50      .75      .90      .95
## 167      256      365       420      445
##
## lowest : 1 3 4 5 6, highest: 455 456 457 458 459
## -----
## gender
##      n    missing   distinct
## 2842521          0        5
##
## Value           Female     Male   Other Unknown
## Frequency      4896 1309647 1527370      52      556
## Proportion     0.002  0.461  0.537  0.000  0.000
## -----
## age
##      n    missing   distinct      Info      Mean      Gmd      .05      .10
## 2840460          2061      91       1  62.72  19.61      28      38
##    .25      .50      .75      .90      .95
## 52      65      76       84      88
##
## lowest : 0 1 2 3 4, highest: 86 87 88 89 90
## -----
## ethnicity
##      n    missing   distinct
## 2842521          0        7
##
## (47920, 0.017), African American (304105, 0.107), Asian (45050, 0.016),
## Caucasian (2152704, 0.757), Hispanic (145350, 0.051), Native American

```

```

## (25711, 0.009), Other/Unknown (121681, 0.043)
## -----
## hospital_los
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 2842521        0       78285        1  8.941  9.314  0.9611  1.5028
##  .25      .50      .75      .90      .95
##  2.9292  5.7250 10.4799 18.6438 26.2097
##
## lowest : -6378.811 -6035.253 -4959.294 -4854.218 -4658.864
## highest: 31048.731 31504.512 36525.365 36527.378 36530.324
## -----
## hospital_size
##      n    missing   distinct
## 2842521        0         5
##
## Value          <100 100-249 250-500    >500
## Frequency  643295 141919 533513 481826 1041968
## Proportion  0.226  0.050  0.188  0.170  0.367
## -----
## hospital_teaching_status
##      n    missing   distinct
## 2842521        0         3
##
## Value          f      t
## Frequency  554798 1677818 609905
## Proportion  0.195  0.590  0.215
## -----
## hospital_region
##      n    missing   distinct
## 2842521        0         5
##
## Value          Midwest Northeast South West
## Frequency  632962  753120 165767 714254 576418
## Proportion  0.223   0.265  0.058  0.251  0.203
## -----
## hospital_discharge_disposition
##      n    missing   distinct
## 2842521        0         8
##
## Value          Death      Home NursingHome
## Frequency  39536  264032 1697524 147773
## Proportion  0.014   0.093  0.597  0.052
##
## Value          OtherExternal OtherHospital      SNF
## Frequency  136520 121664 115279 320193
## Proportion  0.048   0.043  0.041  0.113
## -----
## hospital_mortality
##      n    missing   distinct
## 2807000  35521        2
##
## Value          0      1
## Frequency  2542968 264032
## Proportion  0.906  0.094
## -----
## hospital_mortality_ultimate
##      n    missing   distinct
## 2437440  405081        2
##
## Value          0      1
## Frequency  2200750 236690
## Proportion  0.903  0.097
## -----
## hospitaladmityear
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 2842521        0        26  0.988  2012  3.238  2006  2007
##  .25      .50      .75      .90      .95
##  2010     2012     2014     2015     2015
##
## lowest : 1913 1914 1917 1927 1929, highest: 2012 2013 2014 2015 2016
## -----
## hospitaldischargeyear
##      n    missing   distinct
## 2842521        0         6
##
## Value          -2010  2011  2012  2013  2014 2015-16
## Frequency  956304 292683 341972 357883 378924 514755
## Proportion  0.336  0.103  0.120  0.126  0.133  0.181
## -----

```

```

## icu_los
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  2842521          0    46709       1  2.786    3.133   0.1139   0.3146
##  .25      .50      .75      .90      .95
##  0.8278   1.6104   3.0500   6.0618   9.4861
##
## lowest : -5.338194e+00 -1.097222e-01  0.000000e+00  6.944444e-04  1.388889e-03
## highest:  4.714410e+02  5.063722e+02  6.087215e+02  6.360187e+02  8.242104e+02
## -----
## icu_type
##      n missing distinct
##  2842521          0      18
##
## Burn-Trauma ICU (3439, 0.001), Cardiac ICU (192048, 0.068), Cardiovascular
## ICU (12612, 0.004), CCU-CTICU (227460, 0.080), CSICU (131347, 0.046),
## CTICU (78720, 0.028), Documentation Only ICU (749, 0.000), ED ICU (27874,
## 0.010), Floating (Universal) License ICU (9064, 0.003), Med-Surg ICU
## (1527054, 0.537), MICU (248339, 0.087), Mobile ICU (5317, 0.002), Neuro
## ICU (164626, 0.058), PACU ICU (356, 0.000), SICU (179514, 0.063), Trauma
## ICU (33384, 0.012), Vent ICU (528, 0.000), Virtual ICU (90, 0.000)
## -----
## icu_admit_source
##      n missing distinct
##  2842521          0      17
##
## (67402, 0.024), Acute Care/Floor (27695, 0.010), Chest Pain Center (9943,
## 0.003), Direct Admit (175631, 0.062), Emergency Department (1245659,
## 0.438), Emergency Room (149, 0.000), Floor (407519, 0.143), ICU (31038,
## 0.011), ICU to SDU (188944, 0.066), Observation (118, 0.000), Operating
## Room (367328, 0.129), Other (65, 0.000), Other Hospital (65765, 0.023),
## Other ICU (85071, 0.030), PACU (8412, 0.003), Recovery Room (109083,
## 0.038), Step-Down Unit (SDU) (52699, 0.019)
## -----
## icu_disch_location
##      n missing distinct
##  2842521          0      18
##
## (4634, 0.002), Acute Care/Floor (104668, 0.037), Death (154009, 0.054),
## Floor (1587711, 0.559), Home (250587, 0.088), ICU (7465, 0.003), Nursing
## Home (3816, 0.001), Operating Room (57, 0.000), Other (25818, 0.009),
## Other External (34327, 0.012), Other Hospital (58896, 0.021), Other ICU
## (129053, 0.045), Other ICU (CABG) (974, 0.000), Other Internal (5667,
## 0.002), Rehabilitation (10269, 0.004), Skilled Nursing Facility (20506,
## 0.007), Step-Down Unit (SDU) (291173, 0.102), Telemetry (152891, 0.054)
## -----
## icu_mortality
##      n missing distinct
##  2841877          644      2
##
## Value          0      1
## Frequency  2687868  154009
## Proportion  0.946  0.054
## -----
## admitsource
##      n missing distinct      Info      Mean      Gmd
##  2437440  405081         9  0.864    5.64    2.982
##
## Value        -1      1      2      3      4      5      6      7
## Frequency   56303  348455  104383   9730  448939  12995  63931  169146
## Proportion  0.023  0.143   0.043   0.004   0.184   0.005   0.026   0.069
##
## Value        8
## Frequency 1223558
## Proportion 0.502
## -----
## dischargelocation
##      n missing distinct      Info      Mean      Gmd
##  2437440  405081         7  0.666    5.119    1.675
##
## Value        -1      4      5      6      7      8      9
## Frequency  3755 1685490  25106  55304  208084  312857  146844
## Proportion  0.002  0.692   0.010   0.023   0.085   0.128   0.060
## -----
## bedcount
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  2437440  405081         85  0.999   26.05   15.82      10      12
##  .25      .50      .75      .90      .95
##  16      22      31      48      60
## 
```

```

## lowest : 1 2 3 4 5, highest: 142 144 168 213 252
## -----
## readmit
##      n missing distinct      Info      Sum      Mean      Gmd
## 2437440 405081          2   0.169   145671  0.05976  0.1124
##
## -----
## apacheiva
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 1831815 1010706         219      1  52.76   29.43     16      24
##    .25     .50     .75     .90     .95
##    35      49      67      88     103
##
## lowest : -1 0 1 2 3, highest: 214 215 216 218 230
## -----
## apacheadmissiondx
##      n missing distinct
## 2521180 321341         416
##
## lowest : Abdomen/extremity trauma
##          Abdomen/multiple trauma
##          Abdomen/pelvis trauma
##          highest: Vena cava filter insertion
##          effect (VSD) Repair
##          Weaning from mechanical ventilation (transfer from other unit or hospital only)
##          Whipple-surgery for pancreatic cancer
##          -----
##          dialysis
##      n missing distinct
## 2437440 405081          2
##
## Value      0      1
## Frequency 2349031  88409
## Proportion 0.964   0.036
## -----
## aids
##      n missing distinct
## 2437440 405081          2
##
## Value      0      1
## Frequency 2434536  2904
## Proportion 0.999   0.001
## -----
## hepaticfailure
##      n missing distinct
## 2437440 405081          2
##
## Value      FALSE    TRUE
## Frequency 2387412  50028
## Proportion 0.979   0.021
## -----
## cirrhosis
##      n missing distinct      Info      Sum      Mean      Gmd
## 2437440 405081          2   0.041   34067  0.01398  0.02756
##
## -----
## diabetes
##      n missing distinct
## 2437440 405081          2
##
## Value      0      1
## Frequency 1915776  521664
## Proportion 0.786   0.214
## -----
## immunsuppression
##      n missing distinct
## 2437440 405081          2
##
## Value      0      1
## Frequency 2382595  54845
## Proportion 0.977   0.023
## -----
## leukemia
##      n missing distinct
## 2437440 405081          2
##
## Value      0      1
## Frequency 2420503  16937
## Proportion 0.993   0.007

```

```

## -----
## lymphoma
##      n missing distinct
##  2437440   405081      2
##
## Value      0      1
## Frequency 2427829   9611
## Proportion 0.996   0.004
## -----
## metastaticcancer
##      n missing distinct
##  2437440   405081      2
##
## Value      0      1
## Frequency 2391741   45699
## Proportion 0.981   0.019
## -----
## thrombolytics
##      n missing distinct
##  2437440   405081      2
##
## Value      0      1
## Frequency 2396625   40815
## Proportion 0.983   0.017
## -----
## admissionheight
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  2699580   142941    2319  0.999  169.2   13.58   152.4   154.9
##      .25      .50      .75      .90      .95
##  162.5    170.0    177.8  183.0   187.0
##
## lowest :  0.00  0.09  0.10  0.12  0.18, highest: 712.20 712.70 715.20 717.50 720.00
## -----
## admissionweight
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  2509427   333094   10426   1  83.26   27.57   49.9    55.0
##      .25      .50      .75      .90      .95
##  65.8     79.4     95.8  114.7   129.4
##
## lowest :  0.00  0.04  0.09  0.10  0.11, highest: 983.50 987.30 992.50 993.70 993.80
## -----
## chartedweight
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  1347603   1494918  14441   1  83.7    27.58   49.50   55.29
##      .25      .50      .75      .90      .95
##  66.10    80.01    96.80  115.48  129.86
##
## lowest : 30.00000 30.02779 30.03000 30.04140 30.06408
## highest: 299.18928 299.37072 299.50680 299.90000 300.00000
## -----
## eyes
##      n missing distinct      Info      Mean      Gmd
##  2437440   405081      5  0.66    3.28    1.147
##
## Value      -1      1      2      3      4
## Frequency 130579  195272  102349  312300 1696940
## Proportion 0.054   0.080   0.042   0.128   0.696
## -----
## motor
##      n missing distinct      Info      Mean      Gmd
##  2437440   405081      7  0.566   5.148   1.444
##
## Value      -1      1      2      3      4      5      6
## Frequency 130579  130349  9933   15594  117089  190116 1843780
## Proportion 0.054   0.053   0.004   0.006   0.048   0.078   0.756
## -----
## verbal
##      n missing distinct      Info      Mean      Gmd
##  2437440   405081      6  0.753   3.798   1.762
##
## Value      -1      1      2      3      4      5
## Frequency 130579  396210  52559  62431  279130 1516531
## Proportion 0.054   0.163   0.022   0.026   0.115   0.622
## -----
## gcs
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  2437440   405081      14  0.807   12.23   4.297   -3       3
##      .25      .50      .75      .90      .95
##  11       15       15      15      15

```

```

## 
## Value      -3      3      4      5      6      7      8      9
## Frequency 130579 116582 11175 11828 44512 54124 48652 53429
## Proportion 0.054 0.048 0.005 0.005 0.018 0.022 0.020 0.022
##
## Value      10     11     12     13     14     15
## Frequency 72618 68388 57551 105293 257068 1405641
## Proportion 0.030 0.028 0.024 0.043 0.105 0.577
## -----
## unablegcs
##      n missing distinct      Info      Mean      Gmd
## 2437440 405081            3 0.152 -0.01734 0.104
##
## Value      -1      0      1
## Frequency 86425 2306861 44154
## Proportion 0.035 0.946 0.018
## -----
## urine
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2437440 405081 85117 0.877 965.4 1383      -1      -1
## .25      .50      .75      .90      .95
## -1       0       1519 2818 3780
##
## Value      0 200000 400000 600000 800000 1000000 3200000
## Frequency 2437411 14       6       2       2       2       1
## Proportion 1 0       0       0       0       0       0
## -----
## Value      7200000 21600000
## Frequency 1 1
## Proportion 0 0
## -----
## pao2_apache
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2437440 405081 4882 0.542 29.52 51.53      -1      -1
## .25      .50      .75      .90      .95
## -1       -1      -1 112 167
##
## lowest : -1.00 1.44 1.80 2.00 2.80, highest: 694.90 715.00 757.00 774.00 840.00
## -----
## fio2_apache
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2437440 405081 231 0.542 12.84 22.88      -1      -1
## .25      .50      .75      .90      .95
## -1       -1      -1 50 100
##
## lowest : -1.0 21.0 21.1 22.0 22.5, highest: 99.6 99.7 99.8 99.9 100.0
## -----
## pao2fio2_apache
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2437440 405081 19815 0.542 54.91 93.48      -1.0     -1.0
## .25      .50      .75      .90      .95
## -1.0     -1.0     -1.0 247.2 338.1
##
## lowest : -1.000 2.880 3.300 4.500 5.000
## highest: 2704.762 2719.048 2733.333 2804.762 2847.619
## -----
## temperature_apache
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2437440 405081 587 0.996 32.6 7.581      -1.0     -1.0
## .25      .50      .75      .90      .95
## 36.0    36.4    36.7 37.1 37.4
##
## lowest : -1.00 20.00 20.10 20.20 20.30, highest: 42.70 42.77 42.80 42.90 43.00
## -----
## respiratoryrate_apache
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2437440 405081 172 0.999 23.27 17.05      4       6
## .25      .50      .75      .90      .95
## 10       25       34 43 51
##
## lowest : -1.0 4.0 4.5 5.0 5.8, highest: 57.6 58.0 59.0 59.1 60.0
## -----
## heartrate_apache
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2437440 405081 203 1 97.11 37.35      44      52
## .25      .50      .75      .90      .95
## 70       102      119 135 145
##
## lowest : -1 20 21 22 23, highest: 216 217 218 219 220

```

```

## -----
## mbp_apache
##      n missing distinct      Info      Mean      Gmd     .05     .10
##  2437440  405081       519        1   82.31    46.77     40     43
##    .25     .50     .75     .90     .95
##    52      64      120      144     161
##
## lowest : -1.00 40.00 40.30 40.33 41.00, highest: 196.00 197.00 198.00 199.00 200.00
## -----
## albumin_apache
##      n missing distinct      Info      Mean      Gmd     .05     .10
##  944241  1898280       101      0.998   2.863   0.8002     1.7     1.9
##    .25     .50     .75     .90     .95
##    2.4     2.9     3.4      3.8     4.0
##
## lowest : 1.00 1.07 1.10 1.20 1.30, highest: 7.40 7.50 7.70 8.20 8.60
## -----
## bilirubin_apache
##      n missing distinct      Info      Mean      Gmd     .05     .10
##  2437440  405081      1175      0.725  -0.2343   1.151    -1.0    -1.0
##    .25     .50     .75     .90     .95
##   -1.0    -1.0     0.5      1.0     1.6
##
## lowest : -1.00 0.04 0.05 0.07 0.08, highest: 61.20 61.50 63.10 64.00 72.40
## -----
## bun_apache
##      n missing distinct      Info      Mean      Gmd     .05     .10
##  2437440  405081      1068      0.987   20.23   22.21     -1     -1
##    .25     .50     .75     .90     .95
##    6      15      27      48     65
##
## lowest : -1.00 1.00 1.40 1.41 1.50, highest: 251.00 252.00 253.00 254.00 255.00
## -----
## creatinine_apache
##      n missing distinct      Info      Mean      Gmd     .05     .10
##  2437440  405081      2708      0.988   0.9751   1.68    -1.00   -1.00
##    .25     .50     .75     .90     .95
##   0.45    0.82    1.35      2.50    4.04
##
## lowest : -1.00 0.10 0.11 0.12 0.13, highest: 24.91 24.94 24.95 24.97 25.00
## -----
## glucose_apache
##      n missing distinct      Info      Mean      Gmd     .05     .10
##  2437440  405081      1627      0.997   142.3   113.4     -1     -1
##    .25     .50     .75     .90     .95
##    85     118      191      271     337
##
## lowest : -1.0     1.0     1.1     1.3     1.5, highest: 2796.0 2810.0 2871.0 2890.0 2954.0
## -----
## hematocrit_apache
##      n missing distinct      Info      Mean      Gmd     .05     .10
##  2437440  405081      654      0.987   24.79   16.56    -1.0    -1.0
##    .25     .50     .75     .90     .95
##   19.6    29.9     35.9      40.2    42.6
##
## lowest : -1.0     5.0     5.1     5.2     5.3, highest: 78.0 79.8 80.0 86.0 93.0
## -----
## sodium_apache
##      n missing distinct      Info      Mean      Gmd     .05     .10
##  2437440  405081      295      0.987    107     51.2     -1     -1
##    .25     .50     .75     .90     .95
##   128     136      140      142     145
##
## lowest : -1.0     82.0    83.0    86.0    87.0, highest: 195.0 195.7 196.0 198.0 199.0
## -----
## paco2_apache
##      n missing distinct      Info      Mean      Gmd     .05     .10
##  2437440  405081     1277      0.542   8.904   15.97    -1.0    -1.0
##    .25     .50     .75     .90     .95
##   -1.0    -1.0    -1.0      41.4    48.0
##
## lowest : -1.0     2.5     3.1     3.4     3.7, highest: 148.8 149.0 149.3 149.6 150.0
## -----
## ph_apache
##      n missing distinct      Info      Mean      Gmd     .05     .10
##  2437440  405081     1067      0.542   0.918   2.962   -1.000   -1.000
##    .25     .50     .75     .90     .95
##  -1.000  -1.000  -1.000     7.386   7.434
##

```

```

## -1 (1878455, 0.771), 6.3 (1, 0.000), 6.4 (1, 0.000), 6.5 (6, 0.000), 6.6
## (38, 0.000), 6.7 (116, 0.000), 6.8 (525, 0.000), 6.9 (1644, 0.001), 7
## (4136, 0.002), 7.1 (11523, 0.005), 7.2 (39474, 0.016), 7.3 (153742,
## 0.063), 7.4 (249333, 0.102), 7.5 (87884, 0.036), 7.6 (9721, 0.004), 7.7
## (780, 0.000), 7.8 (47, 0.000), 7.9 (11, 0.000), 8 (2, 0.000), 8.6 (1,
## 0.000)
## -----
## intubated_apache
##      n missing distinct      Info      Sum      Mean      Gmd
## 2437440 405081        2     0.364   344877    0.1415    0.2429
##
## -----
## wbc_apache
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2437440 405081    6658     0.982   8.726   9.086   -1.0    -1.0
##   .25     .50     .75     .90     .95
##   -1.0     8.2    13.2    18.7    23.0
##
## lowest : -1.00 0.01 0.02 0.03 0.04, highest: 198.10 199.00 199.20 199.40 199.69
## -----
## oobintubday1_apache
##      n missing distinct      Info      Sum      Mean      Gmd
## 2437440 405081        2     0.542   576561    0.2365    0.3612
##
## -----
## oobventday1_apache
##      n missing distinct      Info      Sum      Mean      Gmd
## 2437440 405081        2     0.625   720884    0.2958    0.4166
##
## -----
## ventday1_apache
##      n missing distinct      Info      Sum      Mean      Gmd
## 2437440 405081        2     0.511   530378    0.2176    0.3405
##
## -----
## physicianspecialty
##      n missing distinct
## 2842521      0      51
##
## lowest :          allergy/immunology anesthesiology anesthesiology/CCM cardiology
## highest: surgery-transplant surgery-trauma surgery-vascular unknown urology
## -----
## acutephysiologyscore
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 1831815 1010706    202      1    41.44   26.09     11     17
##   .25     .50     .75     .90     .95
##   25      37      53      74     89
##
## lowest : -1 0 1 2 3, highest: 196 197 198 200 206
## -----
## apachescore
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 1831815 1010706    219      1    52.76   29.43     16     24
##   .25     .50     .75     .90     .95
##   35      49      67      88    103
##
## lowest : -1 0 1 2 3, highest: 214 215 216 218 230
## -----
## predictedicumortality
##      n missing distinct      Info      Mean      Gmd
## 1831815 1010706 1692781      1 -0.0002665    0.2211
##   .05     .10     .25     .50     .75     .90
## -1.000000 0.002384 0.007386  0.020175  0.058554  0.173918
##   .95
## 0.331791
##
## lowest : -1.000000e+00 2.798800e-10 5.105833e-10 5.425713e-10 5.718087e-10
## highest: 9.833071e-01 9.851197e-01 9.859533e-01 9.912570e-01 9.951461e-01
## -----
## predictediculos
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 1831815 1010706 1691249      1    3.59    2.705   -1.000    1.153
##   .25     .50     .75     .90     .95
##   2.019   3.186   5.023    7.085   8.167
##
## lowest : -1.0000000000 0.0002397692 0.0005581499 0.0010462120 0.0015511424
## highest: 16.0262378684 16.4066825345 18.7383148958 19.8923078627 19.9075117024
## -----
## predictedhospitalmortality

```

```

##      n  missing distinct      Info      Mean      Gmd      .05      .10
##  1831815  1010706  1608618  0.999 -0.01157  0.3362 -1.00000 -1.00000
##  .25      .50      .75      .90      .95
##  0.01404  0.04111  0.11272  0.27991  0.46046
##
## lowest : -1.0000000000  0.0002555227  0.0003451466  0.0003794773  0.0003825366
## highest:  0.9963869130  0.9979823377  0.9981384119  0.9993184841  0.9998248676
##
## -----
## predictedhospitallos
##      n  missing distinct      Info      Mean      Gmd      .05      .10
##  1831815  1010706  1608464  0.999  8.937   6.254  -1.000  -1.000
##  .25      .50      .75      .90      .95
##  5.815    8.822   12.041   15.587  18.469
##
## lowest : -1.000000e+00  5.815364e-05  9.883428e-04  3.367056e-03  4.531164e-03
## highest:  1.288372e+02  1.331938e+02  1.469374e+02  2.234267e+02  2.249389e+02
##
## -----
## preopmi
##      n  missing distinct      Info      Sum      Mean      Gmd
##  1831815  1010706        2     0.01    6124  0.003343  0.006664
##
## -----
## preopcardiacath
##      n  missing distinct      Info      Sum      Mean      Gmd
##  1831815  1010706        2     0.028   17018  0.00929  0.01841
##
## -----
## ptcawithin24h
##      n  missing distinct      Info      Sum      Mean      Gmd
##  1831815  1010706        2     0.177   115287  0.06294  0.118
##
## -----
## graftcount
##      n  missing distinct      Info      Mean      Gmd      .05      .10
##  2437440  405081        10    0.044    3  0.04009    3       3
##  .25      .50      .75      .90      .95
##  3       3       3       3       3
##
## Value      1       2       3       4       5       6       7       8
## Frequency  6600   11407  2400785  13860   3894    724    128    31
## Proportion 0.003  0.005  0.985  0.006  0.002  0.000  0.000  0.000
##
## Value      9       10
## Frequency  7       4
## Proportion 0.000  0.000
##
## -----
## mbp_min
##      n  missing distinct      Info      Mean      Gmd      .05      .10
##  2487252  355269        239     1  58.47   19.49    28      37
##  .25      .50      .75      .90      .95
##  48      59       70      80      86
##
## lowest :  1  2  3  4  5, highest: 330 342 345 353 360
##
## -----
## sbp_min
##      n  missing distinct      Info      Mean      Gmd      .05      .10
##  2487021  355500        223     1  60.42   19.64    30      38
##  .25      .50      .75      .90      .95
##  50      60       71      82      89
##
## lowest :  1  2  3  4  5, highest: 290 294 302 313 347
##
## -----
## temperature_min
##      n  missing distinct      Info      Mean      Gmd      .05      .10
##  215636  2626885        2261     1  40.03   12.86   25.00  31.44
##  .25      .50      .75      .90      .95
##  35.00  36.10  36.90   38.20  96.80
##
## lowest :  0.05  0.10  0.15  0.20  0.25, highest: 116.00 117.00 122.00 131.00 137.00
##
## -----
## temperature_max
##      n  missing distinct      Info      Mean      Gmd      .05      .10
##  215636  2626885        1238     0.999  43.52   11.59   36.2   36.8
##  .25      .50      .75      .90      .95
##  37.3   37.8   38.5    40.7  100.0
##
## lowest :  0.1  0.4  1.1  1.5  1.9, highest: 157.0 168.0 173.0 176.0 224.5
##
## -----
## heartrate_max

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```

##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 2533730    308791       295        1    106.9    24.84      74      80
##  .25       .50       .75       .90       .95
##  91       105       120      136      146
##
## lowest :  5   6   7   8   9, highest: 296 297 298 299 300
## -----
## respiratoryrate_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 2380824    461697       210      0.998    32.07    12.85      20      21
##  .25       .50       .75       .90       .95
##  24       28       35       46       56
##
## Value      0      500     3000    13500    19000    27000    37000    51000
## Frequency 2380814      1       1       1       1       1       1       1
## Proportion 1       0       0       0       0       0       0       0
##
## Value      57500    58500    63000
## Frequency 1       1       1
## Proportion 0       0       0
## -----
## heartrate_charted_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 2140138    702383       314        1    100.4    24.95      68      74
##  .25       .50       .75       .90       .95
##  85       98       114      130      140
##
## lowest :  1   2   3   5   6, highest: 374 379 380 383 387
## -----
## respiratoryrate_charted_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 2214083    628438       82      0.998    26.35    9.094      16      18
##  .25       .50       .75       .90       .95
##  20       25       30       37       43
##
## lowest :  1   2   3   4   5, highest: 75 76 77 78 79
## -----
## o2saturation_charted_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 1988990    853531       104     0.994    92.09    6.865      81      86
##  .25       .50       .75       .90       .95
##  91       94       96       98       99
##
## lowest :  0.5   1.0   2.0   3.0   4.0, highest:  96.0   97.0   98.0   99.0 100.0
## -----
## nibp_systolic_charted_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 2094497    748024       290        1    100.6    24.75      67      74
##  .25       .50       .75       .90       .95
##  86       99       114      129      140
##
## lowest :  1   2   3   4   5, highest: 263 264 266 269 278
## -----
## nibp_diastolic_charted_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 2095949    746572       227        1    51.67    16.42      28      34
##  .25       .50       .75       .90       .95
##  42       51       60       70       77
##
## lowest :  1   2   3   4   5, highest: 208 213 216 226 235
## -----
## nibp_mean_charted_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 2005131    837390       581        1    66.77    18.28      42      48
##  .25       .50       .75       .90       .95
##  56       66       77       88       95
##
## lowest :  0.13   0.56   0.61   0.74   0.87, highest: 215.00 219.00 223.00 232.00 242.00
## -----
## ibp_systolic_charted_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 455101    2387420       347        1    97.42    27.76      60      70
##  .25       .50       .75       .90       .95
##  82       95       111      130      142
##
## lowest :  1   2   3   4   5, highest: 346 347 348 364 390
## -----
## ibp_diastolic_charted_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10

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##   454978  2387543     297    0.999   48.81   14.45     30     34
##   .25      .50      .75     .90     .95
##   41       48       56     65      72
##
## lowest :  1.0   2.0   3.0   3.4   4.0, highest: 340.0 346.0 347.0 348.0 390.0
## -----
## ibp_mean_charted_min
##   n missing distinct   Info   Mean   Gmd   .05   .10
##  482296  2360225     440     1   65.41   18.82     40     48
##   .25      .50      .75     .90     .95
##   56       64       74     86     94
##
## lowest :  0.9   1.0   2.0   3.0   4.0, highest: 359.0 360.0 362.0 364.0 390.0
## -----
## mbp_charted_min
##   n missing distinct   Info   Mean   Gmd   .05   .10
## 2098791  743730      668     1   65.78   18.43     41     47
##   .25      .50      .75     .90     .95
##   55       65       76     87     94
##
## lowest :  0.13   0.56   0.61   0.74   0.87, highest: 293.00 318.00 325.00 347.00 359.00
## -----
## sbp_charted_min
##   n missing distinct   Info   Mean   Gmd   .05   .10
## 2139934  702587      291     1   99.09   25.16     64     73
##   .25      .50      .75     .90     .95
##   85       98      113     128    138
##
## lowest :  1   2   3   4   5, highest: 256 257 260 261 264
## -----
## temperature_charted_min
##   n missing distinct   Info   Mean   Gmd   .05   .10
## 2358568  483953      856    0.996   36.33   0.7058    35.2    35.6
##   .25      .50      .75     .90     .95
##   36.1    36.4     36.7    37.0    37.2
##
## lowest : 20.10000 20.11111 20.20000 20.22200 20.30000
## highest: 43.30000 45.00000 45.30000 46.20000 48.20000
## -----
## temperature_charted_max
##   n missing distinct   Info   Mean   Gmd   .05   .10
## 2358568  483953      781    0.997   37.25   0.7737    36.3    36.6
##   .25      .50      .75     .90     .95
##   36.8    37.1     37.6    38.2    38.7
##
## lowest : 21.00 21.70 23.70 25.10 25.60, highest: 48.88 48.90 49.00 49.05 49.30
## -----
## gcs_charted_min
##   n missing distinct   Info   Mean   Gmd   .05   .10
## 1457027  1385494      20    0.863   12.54   3.545      3      6
##   .25      .50      .75     .90     .95
##   11       15       15     15     15
##
## 3 (95412, 0.065), 4 (8918, 0.006), 4.5 (1, 0.000), 5 (8711, 0.006), 6
## (38400, 0.026), 7 (47093, 0.032), 8 (43898, 0.030), 8.5 (1, 0.000), 9
## (41618, 0.029), 9.5 (1, 0.000), 10 (64099, 0.044), 11 (51164, 0.035), 11.5
## (1, 0.000), 12 (35063, 0.024), 13 (73406, 0.050), 13.5 (1, 0.000), 14
## (204798, 0.141), 14.5 (6, 0.000), 14.6 (1, 0.000), 15 (744435, 0.511)
## -----
## bilirubin_max
##   n missing distinct   Info   Mean   Gmd   .05   .10
## 1073398  1769123     1289    0.994   1.184   1.273      0.2    0.3
##   .25      .50      .75     .90     .95
##   0.4     0.7      1.1     2.0     3.4
##
## lowest :  0.00   0.04   0.05   0.06   0.07, highest:  99.00 107.00 116.80 159.00 198.00
## -----
## creatinine_max
##   n missing distinct   Info   Mean   Gmd   .05   .10
## 2385233  457288      3017     1   1.555   1.287     0.51    0.60
##   .25      .50      .75     .90     .95
##   0.77    1.00     1.57    2.98    4.67
##
## lowest :  0.00   0.06   0.07   0.08   0.09, highest: 220.00 241.00 335.00 363.00 405.00
## -----
## lactate_min
##   n missing distinct   Info   Mean   Gmd   .05   .10
## 494007  2348514     1995    0.999   2.233   1.971      0.6    0.7
##   .25      .50      .75     .90     .95

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##      1.0      1.5      2.3      4.1      6.4
##
## lowest :  0.00  0.05  0.06  0.08  0.10, highest: 199.50 215.76 222.20 265.49 557.00
## -----
## lactate_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 494007 2348514     2418  0.999  2.987  2.824  0.700  0.800
##  .25   .50   .75   .90   .95
## 1.200 1.900  3.300  6.200  9.444
##
## lowest :  0.00  0.05  0.06  0.10  0.11, highest: 244.75 251.65 278.43 509.00 557.00
## -----
## pao2_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 927841 1914680     4444     1 102.4  57.85  45.0  54.7
##  .25   .50   .75   .90   .95
## 67.0   84.0  115.0  167.0  218.0
##
## Value      0    100    200    300    400    500    600    700    800
## Frequency 66811 738900 88379 19178 9380 4364 774 40 4
## Proportion 0.072 0.796 0.095 0.021 0.010 0.005 0.001 0.000 0.000
##
## Value      900   1000   1100   1600   2200   2500   2800   5300 11800
## Frequency 2     2     1     1     1     1     1     1     1
## Proportion 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## -----
## pao2_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 927841 1914680     5816     1 169.1 118.1 61.0 69.0
##  .25   .50   .75   .90   .95
## 86.8   126.0  214.0  348.0  424.0
##
## Value      0    500   1000   1500   2000   2500   3000   3500 4000
## Frequency 745251 182506 52     5     7     3     3     1     1
## Proportion 0.803 0.197 0.000 0.000 0.000 0.000 0.000 0.000 0.000
##
## Value      4500   5500   6000   7000  10000  12000  27500 31000
## Frequency 2     3     1     2     1     1     1     1
## Proportion 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## -----
## paco2_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 924370 1918151     1400     1 38.85 12.4 23.7 27.0
##  .25   .50   .75   .90   .95
## 31.8   37.0  43.3  53.0  61.4
##
## Value     -100     0     50    100    150    200    250    300    350
## Frequency 1     59355 849661 14957 329    32     5     5     1
## Proportion 0.000 0.064 0.919 0.016 0.000 0.000 0.000 0.000 0.000
##
## Value      400    450    500    550    750    3100   3650   3850 4550
## Frequency 4     9     4     2     1     1     1     1     1
## Proportion 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000
## -----
## paco2_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 924370 1918151     1779     1 45.91 16.07 27.6 31.0
##  .25   .50   .75   .90   .95
## 36.0   42.9  51.0  64.6  77.0
##
## lowest :  0.00  2.50  2.80  3.00  3.94
## highest: 4107.00 4560.00 6537.00 7536.00 7572.00
## -----
## platelet_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2286920 555601     1377     1 201.2 103    69    94
##  .25   .50   .75   .90   .95
## 138    189   248   317   372
##
## Value     -1e+05  0e+00  1e+03  2e+03  3e+03
## Frequency 1     2259260 27597   60     2
## Proportion 0.000 0.988 0.012 0.000 0.000
## -----
## inr_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 1005835 1836686     1602  0.993  1.609  0.8039 1.0   1.0
##  .25   .50   .75   .90   .95
## 1.1    1.3    1.6   2.5   3.4
## 
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## lowest :  0.000  0.400  0.500  0.600  0.660
## highest: 58.389  76.100  79.400  81.700 130.000
## -----
## wbc_min
##      n missing distinct      Info      Mean      Gmd     .05     .10
## 2291098 551423    6766       1   11.27   6.306    4.3    5.4
##   .25     .50     .75     .90     .95
##   7.3     9.9    13.5    18.1    22.0
##
## lowest :  0.00  0.01  0.02  0.03  0.04, highest: 774.00 776.40 778.40 788.90 813.90
## -----
## wbc_max
##      n missing distinct      Info      Mean      Gmd     .05     .10
## 2291098 551423    7404       1   12.58   7.48     4.7    5.8
##   .25     .50     .75     .90     .95
##   7.9    10.8    14.9    20.3    24.7
##
## Value      0    5000   15000  345000
## Frequency 2291094     2     1     1
## Proportion 1     0     0     0
## -----
## ptt_max
##      n missing distinct      Info      Mean      Gmd     .05     .10
## 748965 2093556   3040       1   45.34   26.29    24.0   25.7
##   .25     .50     .75     .90     .95
##   28.9    34.0    46.8    81.6   113.0
##
## Value     -200     0     50    100    150    200    250    300    350
## Frequency 1   63341 598056 59116 20435  7027   734    241     8
## Proportion 0.000  0.085 0.799  0.079  0.027  0.009  0.001  0.000  0.000
##
## Value      400     600    700   2950
## Frequency 3     1     1     1
## Proportion 0.000  0.000 0.000  0.000
## -----
## bands_max
##      n missing distinct      Info      Mean      Gmd     .05     .10
## 231838 2610683   1581   0.998  12.92   14.22     0.4    1.0
##   .25     .50     .75     .90     .95
##   3.0     8.0    18.0    32.0    43.0
##
## Value      0     50    100    200   6400
## Frequency 195803 34956 1077     1     1
## Proportion 0.845  0.151 0.005  0.000  0.000
## -----
## ph_min
##      n missing distinct      Info      Mean      Gmd     .05     .10
## 915917 1926604   1241       1   7.633   0.7309   7.118   7.190
##   .25     .50     .75     .90     .95
##   7.280   7.350   7.409   7.453   7.480
##
## Value      0   1000   7000  70000  71000
## Frequency 915892 15     7     2     1
## Proportion 1     0     0     0     0
## -----
## basedeficit_min
##      n missing distinct      Info      Mean      Gmd     .05     .10
## 144509 2698012    519   0.999   6.074   5.45     0.6    1.0
##   .25     .50     .75     .90     .95
##   2.4     4.8     8.0    13.0    17.0
##
## Value     -30    -25    -20    -15    -10    -5     0     5    10    15
## Frequency 3     8     22     43    157   379 36963 65846 24958  9350
## Proportion 0.000 0.000 0.000 0.000 0.001 0.003 0.256 0.456 0.173 0.065
##
## Value      20     25     30     35     40    100   110   405
## Frequency 4403 1893   456    24     1     1     1     1
## Proportion 0.030 0.013 0.003 0.000 0.000 0.000 0.000 0.000
## -----
## basedeficit_max
##      n missing distinct      Info      Mean      Gmd     .05     .10
## 144509 2698012    519   0.999   6.074   5.45     0.6    1.0
##   .25     .50     .75     .90     .95
##   2.4     4.8     8.0    13.0    17.0
##
## Value     -30    -25    -20    -15    -10    -5     0     5    10    15
## Frequency 3     8     22     43    157   379 36963 65846 24958  9350
## Proportion 0.000 0.000 0.000 0.000 0.001 0.003 0.256 0.456 0.173 0.065
##

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## Value      20    25    30    35    40    100   110   405
## Frequency 4403  1893  456   24     1     1     1     1
## Proportion 0.030 0.013 0.003 0.000 0.000 0.000 0.000 0.000
## -----
## ast_max
##      n missing distinct  Info   Mean   Gmd   .05   .10
## 1096980 1745541    9287     1 166.9 269.9   12    15
##   .25   .50   .75   .90   .95
##   20    32    67   182   411
##
## 0 (1090745, 0.994), 10000 (5492, 0.005), 20000 (620, 0.001), 30000 (86,
## 0.000), 40000 (21, 0.000), 50000 (4, 0.000), 60000 (2, 0.000), 110000 (1,
## 0.000), 2e+05 (1, 0.000), 210000 (1, 0.000), 260000 (1, 0.000), 440000 (1,
## 0.000), 460000 (1, 0.000), 660000 (1, 0.000), 720000 (1, 0.000), 760000
## (1, 0.000), 790000 (1, 0.000)
## -----
## alt_max
##      n missing distinct  Info   Mean   Gmd   .05   .10
## 1081566 1760955    6325     1 105.6 159.3   10    12
##   .25   .50   .75   .90   .95
##   18    29    51   122   271
##
## Value      0    5000   10000   15000   20000   25000   30000   65000
## Frequency 1074150  6686    653     62      5      1      1      1
## Proportion 0.993  0.006  0.001  0.000  0.000  0.000  0.000  0.000
##
## Value    190000  255000  275000  305000  365000  385000  475000
## Frequency 1       1       1       1       1       1       1
## Proportion 0.000  0.000  0.000  0.000  0.000  0.000  0.000
## -----
## alp_max
##      n missing distinct  Info   Mean   Gmd   .05   .10
## 1072207 1770314    1853     1 107.4 79.26   40    46
##   .25   .50   .75   .90   .95
##   59    79   111   167   230
##
## Value      0    10000   20000   720000  790000  800000  830000  860000
## Frequency 1072192  7       1       1       1       1       2       1
## Proportion 1       0       0       0       0       0       0       0
##
## Value    870000
## Frequency 1
## Proportion 0
## -----
## penicilin
##      n missing distinct  Info   Sum   Mean   Gmd
## 2370194 472327     2    0.015 12184 0.005141 0.01023
##
## -----
## penicilin_anti_staph
##      n missing distinct  Info   Sum   Mean   Gmd
## 2370194 472327     2    0.004 2800 0.001181 0.00236
##
## -----
## penicilin_anti_pseudo
##      n missing distinct  Info   Sum   Mean   Gmd
## 2370194 472327     2    0.305 272294 0.1149 0.2034
##
## -----
## augmentin_unasy
##      n missing distinct  Info   Sum   Mean   Gmd
## 2370194 472327     2    0.034 27425 0.01157 0.02287
##
## -----
## cephalosporin_1st_gen
##      n missing distinct  Info   Sum   Mean   Gmd
## 2370194 472327     2    0.108 89002 0.03755 0.07228
##
## -----
## cephalosporin_2nd_gen
##      n missing distinct  Info   Sum   Mean   Gmd
## 2370194 472327     2    0.086 69803 0.02945 0.05717
##
## -----
## cephalosporin_3rd_gen
##      n missing distinct  Info   Sum   Mean   Gmd
## 2370194 472327     2    0.199 169232 0.0714 0.1326
##
## -----

```

```

## cephalosporin_4th_5th_gen
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.082   66907  0.02823  0.05486
##
## -----
## carbapenems
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.076   61460  0.02593  0.05052
##
## -----
## monobactam
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.028   21995  0.00928  0.01839
##
## -----
## fq
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.234   201815 0.08515  0.1558
##
## -----
## vancomycin
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.402   377683 0.1593   0.2679
##
## -----
## amg
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.045   36180  0.01526  0.03006
##
## -----
## polymixins
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.002   1844   0.000778 0.001555
##
## -----
## linezolid
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.024   19052  0.008038 0.01595
##
## -----
## dapto
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.009   7331   0.003093 0.006167
##
## -----
## clinda
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.049   39628  0.01672  0.03288
##
## -----
## doxycyclin
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.021   16319  0.006885 0.01368
##
## -----
## macrolides
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.106   87141  0.03677  0.07083
##
## -----
## sulfa
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.023   18133  0.00765  0.01518
##
## -----
## metronidazole
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.122   101093 0.04265  0.08167
##
## -----
## nitrofurantoin
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.004   3376   0.001424 0.002845
##
## -----
## tigecycline
##      n missing distinct   Info     Sum     Mean     Gmd
##  2370194  472327       2    0.006   4855   0.002048 0.004088
##

```

```

## -----
## ceftriaxone
##      n missing distinct      Info      Mean      Gmd
##  2370194   472327       1       0       0       0
##
## Value      0
## Frequency 2370194
## Proportion 1
##
## -----
## cefotaxime
##      n missing distinct      Info      Mean      Gmd
##  2370194   472327       1       0       0       0
##
## Value      0
## Frequency 2370194
## Proportion 1
##
## -----
## ampicillin_sulbactam
##      n missing distinct      Info      Mean      Gmd
##  2370194   472327       1       0       0       0
##
## Value      0
## Frequency 2370194
## Proportion 1
##
## -----
## levofloxacin
##      n missing distinct      Info      Sum      Mean      Gmd
##  2370194   472327       2     0.047    37558  0.01585  0.03119
##
## -----
## moxifloxacin
##      n missing distinct      Info      Sum      Mean      Gmd
##  2370194   472327       2     0.004    3108  0.001311  0.002619
##
## -----
## piperacillin_tazobactam
##      n missing distinct      Info      Mean      Gmd
##  2370194   472327       1       0       0       0
##
## Value      0
## Frequency 2370194
## Proportion 1
##
## -----
## cefepim
##      n missing distinct      Info      Mean      Gmd
##  2370194   472327       1       0       0       0
##
## Value      0
## Frequency 2370194
## Proportion 1
##
## -----
## meropenem
##      n missing distinct      Info      Mean      Gmd
##  2370194   472327       1       0       0       0
##
## Value      0
## Frequency 2370194
## Proportion 1
##
## -----
## imipenem
##      n missing distinct      Info      Mean      Gmd
##  2370194   472327       1       0       0       0
##
## Value      0
## Frequency 2370194
## Proportion 1
##
## -----
## doripenem
##      n missing distinct      Info      Mean      Gmd
##  2370194   472327       1       0       0       0
##
## Value      0
## Frequency 2370194
## Proportion 1
##
## -----
## gentamicin
##      n missing distinct      Info      Sum      Mean      Gmd
##  2370194   472327       2       0        47  1.983e-05 3.966e-05
##

```

```

## -----
## tobramycin
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2370194    472327        2         0      349  0.0001472 0.0002944
##
## -----
## amikacin
##      n    missing   distinct     Info      Mean      Gmd
##  2370194    472327        1         0         0         0
##
## Value      0
## Frequency 2370194
## Proportion 1
## -----
## dopamine_infusion
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2842521        0        2       0.06      58203  0.02048  0.04011
##
## -----
## epinephrine_infusion
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2842521        0        2       0.024     23201  0.008162 0.01619
##
## -----
## norepinephrine_infusion
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2842521        0        2       0.172     173100  0.0609   0.1144
##
## -----
## phenylephrine_infusion
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2842521        0        2       0.06      58403  0.02055  0.04025
##
## -----
## vasopressin_infusion
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  836528  2005993        2       0.12      34844  0.04165  0.07984
##
## -----
## milrinone_infusion
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2842521        0        2       0.018     16945  0.005961 0.01185
##
## -----
## heparin_infusion
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  836528  2005993        2       0.3      94183  0.1126   0.1998
##
## -----
## dopamine_medication
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2842521        0        2       0.138     137414  0.04834  0.09201
##
## -----
## epinephrine_medication
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2842521        0        2       0.106     104423  0.03674  0.07077
##
## -----
## norepinephrine_medication
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2842521        0        2       0.233     241746  0.08505  0.1556
##
## -----
## phenylephrine_medication
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2842521        0        2       0.122     120575  0.04242  0.08124
##
## -----
## vasopressin_medication
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2370194    472327        2       0.11      90744  0.03829  0.07364
##
## -----
## milrinone_medication
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2842521        0        2       0.028     26753  0.009412 0.01865
##
## -----

```

```

## heparin_medication
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2370194    472327        2    0.525  536475  0.2263  0.3502
##
## -----
## sepsis
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2391341    451180        2    0.321  291609  0.1219  0.2141
##
## -----
## sepsis_priority
##      n    missing   distinct     Info      Mean      Gmd
##  2391341    451180        4    0.323  0.1929  0.3507
##
## Value      0      1      2      3
## Frequency 2099732 182938 47553  61118
## Proportion 0.878  0.077  0.020  0.026
##
## -----
## infection
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2391341    451180        2    0.597  655487  0.2741  0.3979
##
## -----
## infection_priority
##      n    missing   distinct     Info      Mean      Gmd
##  2391341    451180        4    0.614  0.4882  0.7754
##
## Value      0      1      2      3
## Frequency 1735854 316115 1666797 172575
## Proportion 0.726  0.132  0.070  0.072
##
## -----
## aidshiv
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2391341    451180        2    0.011  9008  0.003767 0.007505
##
## -----
## aidshiv_priority
##      n    missing   distinct     Info      Mean      Gmd
##  2391341    451180        4    0.011  0.009231  0.0184
##
## Value      0      1      2      3
## Frequency 2382333 180  4590  4238
## Proportion 0.996  0.000  0.002  0.002
##
## -----
## organfailure
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2391341    451180        2    0.719  954040  0.399  0.4796
##
## -----
## organfailure_priority
##      n    missing   distinct     Info      Mean      Gmd
##  2391341    451180        4    0.775  0.7306  1.019
##
## Value      0      1      2      3
## Frequency 1437301 418134 278763 257143
## Proportion 0.601  0.175  0.117  0.108
##
## -----
## altered_mental_status
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2391341    451180        2    0.244  213500  0.08928  0.1626
##
## -----
## altered_mental_status_priority
##      n    missing   distinct     Info      Mean      Gmd
##  2391341    451180        4    0.245  0.195  0.3614
##
## Value      0      1      2      3
## Frequency 2177841 41341  91502  80657
## Proportion 0.911  0.017  0.038  0.034
##
## -----
## infection_apache
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2437440    405081        2    0.392  377006  0.1547  0.2615
##
## -----
## organfailure_apache
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  2437440    405081        2    0.16   138153  0.05668  0.1069
##

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## -----
## prompt_inflam
##      n missing distinct      Info      Sum      Mean      Gmd
## 798808 2043713          2     0.493    165756   0.2075   0.3289
##
## -----
## prompt_severe_sepsis
##      n missing distinct      Info      Sum      Mean      Gmd
## 798808 2043713          2     0.222    64231   0.08041   0.1479
##
## -----
## prompt_sepsis
##      n missing distinct      Info      Sum      Mean      Gmd
## 798808 2043713          2     0.103    28309   0.03544   0.06837
##
## -----
## prompt_inflam_with_org_dys
##      n missing distinct      Info      Sum      Mean      Gmd
## 798808 2043713          2     0.009    2323   0.002908  0.005799
##
## -----
## prompt_clinical_response_req
##      n missing distinct      Info      Sum      Mean      Gmd
## 798808 2043713          2     0.007    796984   0.9977  0.004556
##
## -----
## sofa_respiration
##      n missing distinct      Info      Mean      Gmd
## 2842521          0      5     0.32    0.2906   0.5244
##
## Value          0      1      2      3      4
## Frequency 2498811  45660  154287  103252   40511
## Proportion  0.879  0.016  0.054  0.036   0.014
##
## -----
## sofa_coagulation
##      n missing distinct      Info      Mean      Gmd
## 2842521          0      5     0.561   0.3582   0.5818
##
## Value          0      1      2      3      4
## Frequency 2153931  431349 197458  47111   12672
## Proportion  0.758  0.152  0.069  0.017   0.004
##
## -----
## sofa_liver
##      n missing distinct      Info      Mean      Gmd
## 2842521          0      5     0.238   0.1393   0.2601
##
## Value          0      1      2      3      4
## Frequency 2595771 132730  88556  15751   9713
## Proportion  0.913  0.047  0.031  0.006   0.003
##
## -----
## sofa_cardiovascular
##      n missing distinct      Info      Mean      Gmd
## 2842521          0      3     0.824           1   0.9772
##
## Value          0      1      3
## Frequency 915581 1469117 457823
## Proportion  0.322  0.517  0.161
##
## -----
## sofa_cns
##      n missing distinct      Info      Mean      Gmd
## 2842521          0      5     0.679   0.6754   1.044
##
## Value          0      1      2      3      4
## Frequency 1941301 362361 198557 200717 139585
## Proportion  0.683  0.127  0.070  0.071   0.049
##
## -----
## sofa_renal
##      n missing distinct      Info      Mean      Gmd
## 2842521          0      5     0.731   0.7193   1.078
##
## Value          0      1      2      3      4
## Frequency 1822342 490015 204535 156907 168722
## Proportion  0.641  0.172  0.072  0.055   0.059
##
## -----
## sofa_renal_baseline
##      n missing distinct      Info      Mean      Gmd
## 2842521          0      2     0.09    0.1244   0.2411
##
## Value          0      4

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## Frequency 2754112 88409
## Proportion 0.969 0.031
## -----
## sofa_liver_baseline
##      n missing distinct      Info      Mean      Gmd
## 2842521       0        2     0.052    0.0704   0.1383
##
## Value       0        4
## Frequency 2792493 50028
## Proportion 0.982 0.018
## -----
## sofa_respiration_baseline
##      n missing distinct      Info      Mean      Gmd
## 2842521       0        2     0.483    0.403    0.6436
##
## Value       0        2
## Frequency 2269755 572766
## Proportion 0.799 0.201
## -----
## cardiovascular_baseline
##      n missing distinct
## 2842521       0        2
##
## Value       0        1
## Frequency 2290527 551994
## Proportion 0.806 0.194
## -----
## soi_alpha
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 1670335 1172186     487    0.999    2.976   0.5121    2.50    2.52
##    .25      .50      .75      .90      .95
##    2.60     2.83     3.14     3.67     4.00
##
## lowest : 2.50 2.51 2.52 2.53 2.54, highest: 7.83 7.85 7.88 7.94 8.00
## -----
## soi_minutes
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 1670335 1172186     301    0.996   196.7   316.8    -60    -60
##    .25      .50      .75      .90      .95
##    0        45     265     735     990
##
## lowest : -60 -55 -50 -45 -40, highest: 1420 1425 1430 1435 1440
## -----
## od_alpha
##      n missing distinct      Info      Mean      Gmd
## 2107497 735024       7     0.328    1.156   0.2804
##
## Value       1        2        3        4        5        6        7
## Frequency 1845543 206506 44828 9213 1289 113 5
## Proportion 0.876 0.098 0.021 0.004 0.001 0.000 0.000
## -----
## od_minutes
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2107497 735024     301    0.967   161.3   301.4    -60    -60
##    .25      .50      .75      .90      .95
##    -60     20     225     650     930
##
## lowest : -60 -55 -50 -45 -40, highest: 1420 1425 1430 1435 1440
## -----
## both_soi_alpha
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 1319513 1523008     501    0.999    3.091   0.6139    2.50    2.53
##    .25      .50      .75      .90      .95
##    2.65     2.94     3.33     3.99     4.29
##
## lowest : 2.50 2.51 2.52 2.53 2.54, highest: 7.88 7.94 7.95 8.00 9.00
## -----
## both_od_alpha
##      n missing distinct      Info      Mean      Gmd
## 1319513 1523008       7     0.656    1.426   0.6452
##
## Value       1        2        3        4        5        6        7
## Frequency 915364 278194 98368 23520 3753 307 7
## Proportion 0.694 0.211 0.075 0.018 0.003 0.000 0.000
## -----
## both_minutes
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 1319513 1523008     301    0.997   243.1   359.5    -60    -60
##    .25      .50      .75      .90      .95

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##      5     80     375     840    1075
##
## lowest : -60 -55 -50 -45 -40, highest: 1420 1425 1430 1435 1440
## -----
## soi_alteredmentalstatus
##   n missing distinct  Info   Sum   Mean   Gmd
## 1670335 1172186       2  0.136  79212  0.04742  0.09035
##
## -----
## soi_glucose
##   n missing distinct  Info   Mean   Gmd   .05   .10
## 1670335 1172186      121  0.866  0.5885  0.4758  0.0000  0.0000
##   .25     .50     .75     .90     .95
## 0.0000  0.8667  1.0000  1.0000  1.0000
##
## lowest : 0.00000000 0.01000000 0.02000000 0.03000000 0.03333333
## highest: 0.96666667 0.97000000 0.98000000 0.99000000 1.00000000
## -----
## soi_heartrate
##   n missing distinct  Info   Mean   Gmd   .05   .10
## 1670335 1172186      22  0.896  0.6656  0.4201  0.0     0.0
##   .25     .50     .75     .90     .95
## 0.3     0.9     1.0     1.0     1.0
##
## lowest : 0.000 0.050 0.100 0.150 0.200, highest: 0.850 0.900 0.925 0.950 1.000
## -----
## soi_inr
##   n missing distinct  Info   Mean   Gmd   .05   .10
## 1670335 1172186      154  0.571  0.1618  0.267   0     0
##   .25     .50     .75     .90     .95
## 0       0       0       1       1
##
## lowest : 0.00000000 0.01333333 0.01666667 0.02000000 0.03333333
## highest: 0.96666667 0.98333333 0.99666667 0.99833333 1.00000000
## -----
## soi_respiratoryrate
##   n missing distinct  Info   Mean   Gmd   .05   .10
## 1670335 1172186      64  0.96   0.6453  0.3911  0.0000  0.0000
##   .25     .50     .75     .90     .95
## 0.4167  0.7500  1.0000  1.0000  1.0000
##
## lowest : 0.00000000 0.00833333 0.027777778 0.041666667 0.083333333
## highest: 0.94444444 0.95833333 0.97222222 0.98333333 1.00000000
## -----
## soi_temperature
##   n missing distinct  Info   Mean   Gmd   .05   .10
## 1670335 1172186      309  0.689  0.152   0.244  0.0000  0.0000
##   .25     .50     .75     .90     .95
## 0.0000  0.0000  0.1765  0.6471  1.0000
##
## lowest : 0.00000000 0.001764706 0.016470588 0.028000000 0.029411765
## highest: 0.980588235 0.982235294 0.982352941 0.997160000 1.00000000
## -----
## soi_bands
##   n missing distinct  Info   Mean   Gmd   .05   .10
## 1670335 1172186      304  0.187  0.0553  0.1044  0.0000  0.0000
##   .25     .50     .75     .90     .95
## 0.0000  0.0000  0.0000  0.0000  0.6667
##
## lowest : 0.00000000 0.00500000 0.01166667 0.01666667 0.01833333
## highest: 0.97833333 0.98000000 0.98333333 0.99833333 1.00000000
## -----
## soi_wbc
##   n missing distinct  Info   Mean   Gmd   .05   .10
## 1670335 1172186      602  0.94   0.5357  0.4702  0.0000  0.0000
##   .25     .50     .75     .90     .95
## 0.0000  0.5933  1.0000  1.0000  1.0000
##
## lowest : 0.00000000 0.001666667 0.003333333 0.005000000 0.006666667
## highest: 0.99333333 0.995000000 0.996666667 0.998333333 1.00000000
## -----
## soi_lactate
##   n missing distinct  Info   Sum   Mean   Gmd
## 1670335 1172186       2  0.325  206734  0.1238  0.2169
##
## -----
## od_liver
##   n missing distinct  Info   Sum   Mean   Gmd
## 2107497 735024       2  0.307  244230  0.1159  0.2049

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## 
## -----
## od_cardiovascular
##      n   missing  distinct    Info     Sum     Mean     Gmd
##  2107497  735024       2    0.738  1186809  0.5631  0.492
##
## -----
## od_respiratory
##      n   missing  distinct    Info     Sum     Mean     Gmd
##  2107497  735024       2    0.413  347194  0.1647  0.2752
##
## -----
## od_kidney
##      n   missing  distinct    Info     Sum     Mean     Gmd
##  2107497  735024       2    0.19   142849  0.06778  0.1264
##
## -----
## od_lactate
##      n   missing  distinct    Info     Sum     Mean     Gmd
##  2107497  735024       2    0.258  199997  0.0949  0.1718
##
## -----
## od_metabolic
##      n   missing  distinct    Info     Sum     Mean     Gmd
##  2107497  735024       2    0.369  303131  0.1438  0.2463
##
## -----
## od_hematologic
##      n   missing  distinct    Info     Sum     Mean     Gmd
##  2107497  735024       2    0.018   12839  0.006092  0.01211
##
## -----
## both_soi_alteredmentalstatus
##      n   missing  distinct    Info     Sum     Mean     Gmd
##  1319513  1523008       2    0.119   54680  0.04144  0.07944
##
## -----
## both_soi_glucose
##      n   missing  distinct    Info     Mean     Gmd     .05     .10
##  1319513  1523008      121    0.865  0.5751  0.481  0.0000  0.0000
##      .25     .50     .75     .90     .95
##     0.0000  0.8333  1.0000  1.0000  1.0000
##
## lowest : 0.00000000 0.01000000 0.02000000 0.03000000 0.03333333
## highest: 0.96666667 0.97000000 0.98000000 0.99000000 1.00000000
##
## -----
## both_soi_heartrate
##      n   missing  distinct    Info     Mean     Gmd     .05     .10
##  1319513  1523008      22    0.885  0.6672  0.422  0.0     0.0
##      .25     .50     .75     .90     .95
##     0.3     0.9     1.0     1.0     1.0
##
## lowest : 0.000 0.050 0.100 0.150 0.200, highest: 0.850 0.900 0.925 0.950 1.000
##
## -----
## both_soi_inr
##      n   missing  distinct    Info     Mean     Gmd     .05     .10
##  1319513  1523008      141    0.632  0.186  0.2969  0.0000  0.0000
##      .25     .50     .75     .90     .95
##     0.0000  0.0000  0.1667  1.0000  1.0000
##
## lowest : 0.00000000 0.01666667 0.02000000 0.03333333 0.03833333
## highest: 0.95000000 0.96666667 0.98333333 0.99833333 1.00000000
##
## -----
## both_soi_respiratoryrate
##      n   missing  distinct    Info     Mean     Gmd     .05     .10
##  1319513  1523008      61    0.954  0.6495  0.3954  0.0000  0.0000
##      .25     .50     .75     .90     .95
##     0.4167  0.7500  1.0000  1.0000  1.0000
##
## lowest : 0.00000000 0.008333333 0.027777778 0.041666667 0.055555556
## highest: 0.93333333 0.944444444 0.958333333 0.972222222 1.00000000
##
## -----
## both_soi_temperature
##      n   missing  distinct    Info     Mean     Gmd     .05     .10
##  1319513  1523008      300    0.716  0.1635  0.2584  0.0     0.0
##      .25     .50     .75     .90     .95
##     0.0     0.0     0.2     0.7     1.0
##
## lowest : 0.00000000 0.001764706 0.028000000 0.029411765 0.031176471

```

```

## highest: 0.980588235 0.982235294 0.982352941 0.997160000 1.000000000
## -----
## both_soil_bands
##      n    missing   distinct     Info      Mean      Gmd     .05     .10
## 1319513 1523008       272    0.217  0.06554  0.1223      0      0
##    .25     .50     .75     .90     .95
##    0       0       0       0       1
##
## lowest : 0.000000000 0.005000000 0.008333333 0.011666667 0.016666667
## highest: 0.966666667 0.980000000 0.983333333 0.998333333 1.000000000
## -----
## both_soil_wbc
##      n    missing   distinct     Info      Mean      Gmd     .05     .10
## 1319513 1523008       602    0.932  0.5755  0.462  0.0000  0.0000
##    .25     .50     .75     .90     .95
##    0.0500  0.6833  1.0000  1.0000  1.0000
##
## lowest : 0.000000000 0.001666667 0.003333333 0.005000000 0.006666667
## highest: 0.993333333 0.995000000 0.996666667 0.998333333 1.000000000
## -----
## both_soil_lactate
##      n    missing   distinct     Info      Sum      Mean      Gmd
## 1319513 1523008       2    0.417  220210  0.1669  0.2781
##
## -----
## both_od_liver
##      n    missing   distinct     Info      Sum      Mean      Gmd
## 1319513 1523008       2    0.425  225493  0.1709  0.2834
##
## -----
## both_od_cardiovascular
##      n    missing   distinct     Info      Sum      Mean      Gmd
## 1319513 1523008       2    0.744  720954  0.5464  0.4957
##
## -----
## both_od_respiratory
##      n    missing   distinct     Info      Sum      Mean      Gmd
## 1319513 1523008       2    0.553  321698  0.2438  0.3687
##
## -----
## both_od_kidney
##      n    missing   distinct     Info      Sum      Mean      Gmd
## 1319513 1523008       2    0.201  95231  0.07217  0.1339
##
## -----
## both_od_lactate
##      n    missing   distinct     Info      Sum      Mean      Gmd
## 1319513 1523008       2    0.417  220210  0.1669  0.2781
##
## -----
## both_od_metabolic
##      n    missing   distinct     Info      Sum      Mean      Gmd
## 1319513 1523008       2    0.505  282908  0.2144  0.3369
##
## -----
## both_od_hematologic
##      n    missing   distinct     Info      Sum      Mean      Gmd
## 1319513 1523008       2    0.034  15098  0.01144  0.02262
##
## -----
## patientweight
##      n    missing   distinct     Info      Mean      Gmd     .05     .10
## 2600179 242342       17020     1    83.24  27.65  49.50  55.00
##    .25     .50     .75     .90     .95
##    65.70  79.42  96.00  114.90  129.50
##
## lowest : 0.00  0.09  0.17  0.20  0.22, highest: 956.00 967.00 969.00 992.50 993.70
## -----
## BMI
##      n    missing   distinct     Info      Mean      Gmd     .05     .10
## 2532267 310254       308878     1      Inf      NaN  18.47  20.22
##    .25     .50     .75     .90     .95
##    23.39  27.44  32.69  39.36  44.82
##
## Value      0.0e+00 1.0e+06 2.0e+06 8.0e+06 9.0e+06 1.3e+07 3.1e+07 3.4e+07
## Frequency 2530160        81        4        1        1        1        1        1
## Proportion 0.999  0.000  0.000  0.000  0.000  0.000  0.000  0.000
##
## Value      8.6e+07      Inf

```

```

## Frequency      1    2016
## Proportion   0.000   0.001
## -----
## BMI_Ranges
##   n missing distinct
## 2842521       0      5
##
## Value      (0,18.5]   (18.5,25]   (25,35]   (35,200]
## Frequency   128213     753213   1191774   453265
## Proportion   0.045     0.265     0.419     0.159
##
## Value      Other/Unknown
## Frequency   316056
## Proportion   0.111
## -----
## age_Ranges
##   n missing distinct
## 2839897       2624       8
##
## Value      (0,25]   (25,35]   (35,45]   (45,55]   (55,65]   (65,75]   (75,85]
## Frequency   105109   141150   215032   421325   585296   621393   526359
## Proportion   0.037     0.050     0.076     0.148     0.206     0.219     0.185
##
## Value      (85,100]
## Frequency   224233
## Proportion   0.079
## -----
## hospitalLOS_Ranges
##   n missing distinct
## 2839140       3381       10
##
## Value      (0,1]   (1,3]   (3,5]   (5,10]   (10,20]   (20,30]
## Frequency   150460   582206   529927   820698   507248   143837
## Proportion   0.053     0.205     0.187     0.289     0.179     0.051
##
## Value      (30,60]   (60,90]   (90,150]   (150,999]
## Frequency   85601    12058     4741     2364
## Proportion   0.030     0.004     0.002     0.001
## -----
## icuLOS_Ranges
##   n missing distinct
## 2826779       15742       8
##
## Value      (0,1]   (1,3]   (3,5]   (5,10]   (10,20]   (20,30]   (30,60]
## Frequency   928888   1168923   352746   247099   99566    20292     8379
## Proportion   0.329     0.414     0.125     0.087     0.035     0.007     0.003
##
## Value      (60,999]
## Frequency    886
## Proportion   0.000
## -----
## ethnicity2
##   n missing distinct
## 2842521       0       6
##
## Value      Caucasian African American Hispanic
## Frequency   2152704     304105   145350
## Proportion   0.757     0.107     0.051
##
## Value      Asian Native American Other/Unknown
## Frequency   45050      25711    169601
## Proportion   0.016     0.009     0.060
## -----
## gender2
##   n missing distinct
## 2842521       0       3
##
## Value      Male Female Other/Unknown
## Frequency   1527370   1309647    5504
## Proportion   0.537     0.461     0.002
## -----
## hospital_region2
##   n missing distinct
## 2842521       0       5
##
## Value      Midwest Northeast South West Unknown
## Frequency   753120    165767   714254   576418   632962
## Proportion   0.265     0.058     0.251     0.203     0.223
## -----

```

```

## sepsis_outcome
##      n missing distinct
##  2391341    451180       2
##
## Value      FALSE     TRUE
## Frequency  1906183  485158
## Proportion  0.797   0.203
## -----
## group
##      n missing distinct
##  2833373    9148       12
##
## Cardiovascular (839352, 0.296), Gastrointestinal (266781, 0.094),
## Gynaecological (6754, 0.002), Hematological (18705, 0.007), Metabolic
## (193873, 0.068), Muscoskeletal/Skin disease (35740, 0.013), Neurological
## (323997, 0.114), Renal/Genitourinary (61926, 0.022), Respiratory (381474,
## 0.135), Sepsis (571651, 0.202), Trauma (111731, 0.039), Undefined (21389,
## 0.008)
## -----
## post_operative
##      n missing distinct      Info      Sum      Mean      Gmd
##  2833373    9148       2     0.423    480702   0.1697   0.2817
##
## -----
## code
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  2833373    9148       379    0.998    527.3   454.5    104     106
##  .25      .50      .75     .90     .95
##  206      410       702    1208    1408
##
## lowest :  0.01  0.02  0.03  0.04  0.05
## highest: 2201.01 2201.02 2201.03 2201.04 2201.05
## -----
## dx
##      n missing distinct
##  2833373    9148       379
##
## lowest : Abdomen/extremity trauma
##          Abdomen/multiple trauma
##          Abdomen/pelvis trauma
##          highest: Vena cava clipping
##                      Ventrileostomy
##          Weaning from mechanical ventilation (transfer from other unit or hospital only)
##          Whipple surgery for pancreatic cancer
##          Vena cava filer insertion
##          Abdomen only trauma
## -----
## number
##      n missing distinct      Info      Mean      Gmd
##  2833373    9148       6     0.155    1.134   0.2576
##
## Value      1      2      3      4      5      6
## Frequency  2679142  48853  30056  41793  22294  11235
## Proportion  0.946   0.017  0.011  0.015  0.008  0.004
## -----
## admitdiagnosis
##      n missing distinct
##  2833373    9148       402
##
## lowest : ACIDBASE  ACUHEPFAIL ADDISON    ADRENNEO    AIROBSTRX
## highest: UNSTANGINA VARICBLEED VASCULITIS VIRALMYOSI WEANVENT
## -----
## admitedxpath
##      n missing distinct
##  2833373    9148       402
##
## lowest :
## admission diagnosis|All Diagnosis|Non-operative|Diagnosis|Cardiovascular|Anaphylaxis
## admission diagnosis|All Diagnosis|Non-operative|Diagnosis|Cardiovascular|Aneurysm, dissecting aortic
## admission diagnosis|All Diagnosis|Non-operative|Diagnosis|Cardiovascular|Aneurysm/pseudoaneurysm, other
## admission diagnosis|All Diagnosis|Non-operative|Diagnosis|Cardiovascular|Angina, stable (asymp or stable pattern of symptoms w/meds)
## highest: admission diagnosis|All Diagnosis|Operative|Diagnosis|Trauma|Extremity/multiple trauma, surgery for
## admission diagnosis|All Diagnosis|Operative|Diagnosis|Trauma|Extremity only trauma, surgery for
## admission diagnosis|All Diagnosis|Operative|Diagnosis|Trauma|Face/multiple trauma, surgery for
## admission diagnosis|All Diagnosis|Operative|Diagnosis|Trauma|Face only trauma, surgery for
## admission diagnosis|All Diagnosis|Operative|Diagnosis|Trauma|Trauma surgery, other
## -----
## numobs
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  2512032    330489    235      1     2519    2558      43     129

```

```

##      .25      .50      .75      .90      .95
##      484     1819    4354    6262    6790
##
## lowest :   0    1    2    3    4, highest: 5003 5989 6262 6790 8375
## -----
## possible.group
##      n missing distinct      Info      Mean      Gmd
## 20200 2822321          8    0.887    975.9    602.3
##
## Value      312.00 408.02 602.09 802.00 1208.00 1504.00 1701.00 1705.03
## Frequency  6838    1331      66    1188    1258    8471      446      602
## Proportion 0.339    0.066    0.003    0.059    0.062    0.419    0.022    0.030
## -----
## X
##      n missing distinct
## 2833373    9148      13
##
## lowest :
## addition
## gories won't map well, but collapsing to hierarchy (1206) should work ANZICS addition - we have invented this dia
## gnosis code
## assumes admitted in eICU due to rejection
## highest: Chest pain, unknown origin
##               fuzzy
## match
## presumably ANZICS only allows the surgical version of this code
##               multiple matches
## ries for this in eICU
##               there are 6 catego
## -----
## c_temp_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2522673 319848    1765    0.996    36.42    0.9129    35.2    35.6
##      .25      .50      .75      .90      .95
##      36.1     36.4     36.7     37.0     37.2
##
## lowest :   0.10    0.20    0.50    0.60    0.75, highest: 103.00 103.20 103.30 103.50 108.30
## -----
## c_temp_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2522673 319848    1226    0.997    37.31    0.9948    36.2    36.5
##      .25      .50      .75      .90      .95
##      36.8     37.1     37.6     38.2     38.7
##
## lowest :   0.10    2.00    4.70   11.00   11.85, highest: 110.00 110.40 111.20 112.05 112.60
## -----
## c_HR_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2730479 112042    314      1    101.4    25.05      68      74
##      .25      .50      .75      .90      .95
##      86       99     115     131     141
##
## lowest :   1    2    3    5    6, highest: 374 379 380 383 387
## -----
## c_resp_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2707796 134725    201    0.998    26.98    9.668      16      18
##      .25      .50      .75      .90      .95
##      21       25      30      38      44
##
## lowest :   1    2    3    4    5, highest: 194 196 197 199 200
## -----
## c_sbp_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2643599 198922    299      1    92.01    29.63      48      58
##      .25      .50      .75      .90      .95
##      75       92     109     125     136
##
## lowest :   1    2    3    4    5, highest: 290 294 302 313 347
## -----
## c_mbp_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2592405 250116    680      1    70.12    24.33      42      47
##      .25      .50      .75      .90      .95
##      56       66      78      97     120
##
## lowest :   0.13    0.56    0.61    0.74    0.87, highest: 293.00 318.00 325.00 347.00 359.00
## -----
## icu_admit_source2
##      n missing distinct
## 2842521      0       6
##
## Value           Floor           OR/Proc Area           Direct Admit

```

```

## Frequency          435214          494766          241396
## Proportion        0.153           0.174          0.085
##
## Value      Emergency Department          Other          Step-Down Unit
## Frequency       1245659          183843          241643
## Proportion      0.438           0.065          0.085
## -----
## icu_type2
##      n missing distinct
## 2842521      0      8
##
## Trauma ICU (36823, 0.013), Cardiac Care ICU (192048, 0.068),
## Cardiac/Surgical Care ICU (437527, 0.154), Medical/Surgical ICU (1527054,
## 0.537), Medical ICU (248339, 0.087), Other ICU (56590, 0.020), Neuro ICU
## (164626, 0.058), Surgical ICU (179514, 0.063)
## -----
## icu_disch_location2
##      n missing distinct
## 2842521      0      7
##
## Value      Floor          Death          Home          SNF/Rehab
## Frequency    1850937        154009        250587        34591
## Proportion   0.651         0.054         0.088         0.012
##
## Value      Other Hospital Step-Down Unit
## Frequency    202328         58896         291173
## Proportion   0.071         0.021         0.102
## -----
## physicianSpeciality2
##      n missing distinct
## 2842521      0      2
##
## Value      Critical Care Speciality-Other
## Frequency     473200        2369321
## Proportion   0.166         0.834
## -----
## sofa_respiration_baseline2
##      n missing distinct
## 2842521      0      2
##
## Value      FALSE      TRUE
## Frequency   2269755      572766
## Proportion   0.799         0.201
## -----
## sofa_renal_baseline2
##      n missing distinct
## 2842521      0      2
##
## Value      FALSE      TRUE
## Frequency   2754112      88409
## Proportion   0.969         0.031
## -----
## sofa_liver_baseline2
##      n missing distinct
## 2842521      0      2
##
## Value      FALSE      TRUE
## Frequency   2792493      50028
## Proportion   0.982         0.018
## -----
## SOFA_Change
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2842521      0      24      0.976      2.975      2.964      0      0
##    .25      .50      .75      .90      .95
##    1       2       4       7       9
##
## lowest : 0 1 2 3 4, highest: 19 20 21 22 23
## -----
## SOFA_Positive
##      n missing distinct
## 2842521      0      2
##
## Value      FALSE      TRUE
## Frequency  1141836  1700685
## Proportion  0.402      0.598
## -----
## SOFA_Score
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 2842521      0      24      0.979      3.183      3.164      0      0

```

```

##      .25      .50      .75      .90      .95
##      1         2         5         7         9
##
## lowest :  0  1  2  3  4, highest: 19 20 21 22 23
## -----
## SOFA_Positive2
##      n missing distinct
## 2842521          0         2
##
## Value      FALSE      TRUE
## Frequency 1092979 1749542
## Proportion 0.385   0.615
## -----
## GCS_qSOFA
##      n missing distinct
## 2437440 405081          2
##
## Value      FALSE      TRUE
## Frequency 1536220 901220
## Proportion 0.63    0.37
## -----
## BP_qSOFA
##      n missing distinct
## 2643599 198922          2
##
## Value      FALSE      TRUE
## Frequency 961957 1681642
## Proportion 0.364   0.636
## -----
## Resp_qSOFA
##      n missing distinct
## 2707796 134725          2
##
## Value      FALSE      TRUE
## Frequency 760333 1947463
## Proportion 0.281   0.719
## -----
## qSOFA_total
##      n missing distinct      Info      Mean      Gmd
## 2842521          0         4     0.905     1.594     1.016
##
## Value      0         1         2         3
## Frequency 401017 835190 1123807 482507
## Proportion 0.141   0.294   0.395   0.170
## -----
## qSOFA_Positive
##      n missing distinct
## 2842521          0         2
##
## Value      FALSE      TRUE
## Frequency 1236207 1606314
## Proportion 0.435   0.565
## -----
## temp_SIRS
##      n missing distinct
## 2522673 319848          2
##
## Value      FALSE      TRUE
## Frequency 1798187 724486
## Proportion 0.713   0.287
## -----
## wbc_SIRS
##      n missing distinct
## 2291983 550538          2
##
## Value      FALSE      TRUE
## Frequency 1240013 1051970
## Proportion 0.541   0.459
## -----
## resp_SIRS
##      n missing distinct
## 2723605 118916          2
##
## Value      FALSE      TRUE
## Frequency 591013 2132592
## Proportion 0.217   0.783
## -----
## HR_SIRS
##      n missing distinct

```

```

## 2730479 112042      2
##
## Value      FALSE     TRUE
## Frequency 925082 1805397
## Proportion 0.339   0.661
## -----
## SIRS_total
##      n missing distinct    Info    Mean     Gmd
## 2842521      0      5    0.934    2.01   1.247
##
## Value      0      1      2      3      4
## Frequency 310612 593666 954052 724089 260102
## Proportion 0.109  0.209  0.336  0.255  0.092
## -----
## SIRS_Positive
##      n missing distinct
## 2842521      0      2
##
## Value      FALSE     TRUE
## Frequency 904278 1938243
## Proportion 0.318   0.682
## -----
## StickyMinutes
##      n missing distinct    Info    Mean     Gmd   .05   .10
## 1422699 1419822      301    0.998   270.4   382.6   -60   -60
##   .25     .50     .75     .90     .95
##   5      100     440     890    1110
##
## lowest : -60 -55 -50 -45 -40, highest: 1420 1425 1430 1435 1440
## -----
## FuzzyTotal1
##      n missing distinct    Info    Mean     Gmd
## 2842521      0      3    0.834    1.329   0.7841
##
## Value      0      1      2
## Frequency 487388 932434 1422699
## Proportion 0.171  0.328  0.501
## -----
## SimultaneousMinutes
##      n missing distinct
## 2842521      0      2
##
## Value      FALSE     TRUE
## Frequency 1523008 1319513
## Proportion 0.536   0.464
## -----
## SepsisFuzzyLogicPositive
##      n missing distinct
## 2842521      0      2
##
## Value      FALSE     TRUE
## Frequency 1523008 1319513
## Proportion 0.536   0.464
## -----
## SepsisFuzzyLogicPositive2
##      n missing distinct
## 2842521      0      2
##
## Value      FALSE     TRUE
## Frequency 1523008 1319513
## Proportion 0.536   0.464
## -----
## hasDiagnosisCodes
##      n missing distinct
## 2842521      0      2
##
## Value      FALSE     TRUE
## Frequency 451180 2391341
## Proportion 0.159   0.841
## -----
## inclusiongroup
##      n missing distinct    Info    Sum     Mean     Gmd
## 2842521      0      2    0.654   912514   0.321   0.4359
##
## -----
## 
## Variables with all observations missing:

```

```
##  
## [1] hospital_type icu_size  
  
describe(ssd_incl)  
  
## Warning in w * sort(x - mean(x)): longer object length is not a multiple of  
## shorter object length
```

```

## ssd_incl
##
## 295 Variables     912509 Observations
## -----
## patientunitstayid
##   n missing distinct      Info      Mean      Gmd      .05      .10
## 912509          0  912509          1  1758473  1107580  244862  371830
##   .25      .50      .75      .90      .95
## 1014642  1702955  2585746  3107552  3214507
##
## lowest : 141136 141137 141139 141141 141142
## highest: 3353265 3353266 3353268 3353269 3353271
## -----
## exclusion_over18
##   n missing distinct      Info      Mean      Gmd
## 912509          0          1          0          0          0
##
## Value      0
## Frequency 912509
## Proportion 1
## -----
## exclusion_firstadmission
##   n missing distinct      Info      Mean      Gmd
## 912509          0          1          0          0          0
##
## Value      0
## Frequency 912509
## Proportion 1
## -----
## exclusion_yearfilter
##   n missing distinct      Info      Mean      Gmd
## 912509          0          1          0          0          0
##
## Value      0
## Frequency 912509
## Proportion 1
## -----
## exclusion_apacheiva
##   n missing distinct      Info      Mean      Gmd
## 912509          0          1          0          0          0
##
## Value      0
## Frequency 912509
## Proportion 1
## -----
## exclusion_vitalobservations
##   n missing distinct      Info      Mean      Gmd
## 912509          0          1          0          0          0
##
## Value      0
## Frequency 912509
## Proportion 1
## -----
## exclusion_labobservations
##   n missing distinct      Info      Mean      Gmd
## 912509          0          1          0          0          0
##
## Value      0
## Frequency 912509
## Proportion 1
## -----
## exclusion_medobservations
##   n missing distinct      Info      Mean      Gmd
## 912509          0          1          0          0          0
##
## Value      0
## Frequency 912509
## Proportion 1
## -----
## hospitalid
##   n missing distinct      Info      Mean      Gmd      .05      .10
## 912509          0         183          1    271.7   127.2      79      122
##   .25      .50      .75      .90      .95
## 188        264        358        421        449
##
## lowest : 56 58 59 60 61, highest: 447 449 452 458 459
## -----
## gender

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##      n missing distinct
##  912509       0      5
##
## Value          Female    Male   Other Unknown
## Frequency     53  421748  490533     26    149
## Proportion   0.000  0.462  0.538  0.000  0.000
## -----
## age
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  912509       0      73        1    62.94    19.34      29      38
##  .25       .50      .75      .90      .95
##  52       65      76      84      88
##
## lowest : 18 19 20 21 22, highest: 86 87 88 89 90
## -----
## ethnicity
##      n missing distinct
##  912509       0      7
##
## (11604, 0.013), African American (105292, 0.115), Asian (11695, 0.013),
## Caucasian (695367, 0.762), Hispanic (41393, 0.045), Native American (6765,
## 0.007), Other/Unknown (40393, 0.044)
## -----
## hospital_los
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  912509       0    57044        1    7.716    7.273    1.035    1.574
##  .25       .50      .75      .90      .95
##  2.877    5.299    9.396   15.976   21.925
##
## lowest : 3.194444e-02 3.958333e-02 5.208333e-02 8.333333e-02 9.027778e-02
## highest: 9.192007e+02 9.810410e+02 1.099160e+03 1.190723e+03 1.224962e+03
## -----
## hospital_size
##      n missing distinct
##  912509       0      5
##
## Value          <100  100-249  250-500    >500
## Frequency    72678  36772  207117  167113  428829
## Proportion   0.080  0.040  0.227  0.183  0.470
## -----
## hospital_teaching_status
##      n missing distinct
##  912509       0      3
##
## Value          f      t
## Frequency   37915  598042  276552
## Proportion  0.042  0.655  0.303
## -----
## hospital_region
##      n missing distinct
##  912509       0      5
##
## Value          Midwest Northeast     South      West
## Frequency    55141  383075  73523  283987  116783
## Proportion  0.060  0.420   0.081  0.311   0.128
## -----
## hospital_dischargeDisposition
##      n missing distinct
##  912509       0      7
##
## Value          Death      Home NursingHome      Other
## Frequency    86219  560422  49569  25746
## Proportion  0.094  0.614   0.054  0.028
## 
## Value          OtherExternal OtherHospital      SNF
## Frequency    41679   37692  111182
## Proportion  0.046  0.041   0.122
## -----
## hospital_mortality
##      n missing distinct
##  912509       0      2
##
## Value          0      1
## Frequency   826290  86219
## Proportion  0.906  0.094
## -----
## hospital_mortality_ultimate
##      n missing distinct
##  912509       0      2

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## 
## Value      0      1
## Frequency 826290 86219
## Proportion 0.906 0.094
## -----
## hospitaladmityear
##       n missing distinct   Info    Mean     Gmd
##  912509      0        7    0.97    2013  1.888
## 
## Value      2009  2010  2011  2012  2013  2014  2015
## Frequency 1331 112863 122110 149856 167202 178896 180251
## Proportion 0.001 0.124 0.134 0.164 0.183 0.196 0.198
## -----
## hospitaldischargeyear
##       n missing distinct
##  912509      0        6
## 
## Value      -2010  2011  2012  2013  2014 2015-16
## Frequency 111530 122036 149169 167298 178187 184289
## Proportion 0.122 0.134 0.163 0.183 0.195 0.202
## -----
## icu_los
##       n missing distinct   Info    Mean     Gmd    .05    .10
##  912509      0    34183      1  3.078  3.151  0.5257  0.7000
##    .25    .50    .75    .90    .95
##  1.0118  1.8444  3.3646  6.6014 10.0431
## 
## lowest :  0.1666667  0.1673611  0.1680556  0.1687500  0.1694444
## highest: 158.5472222 165.7777778 192.9875000 246.9041667 298.9916667
## -----
## icu_type
##       n missing distinct
##  912509      0        11
## 
## Cardiac ICU (65472, 0.072), CCU-CTICU (86619, 0.095), CSICU (25733,
## 0.028), CTICU (28922, 0.032), Floating (Universal) License ICU (2596,
## 0.003), Med-Surg ICU (468867, 0.514), MICU (86772, 0.095), Neuro ICU
## (71250, 0.078), SICU (65312, 0.072), Trauma ICU (10946, 0.012), Vent ICU
## (20, 0.000)
## -----
## icu_admit_source
##       n missing distinct
##  912509      0        16
## 
## (1301, 0.001), Acute Care/Floor (11475, 0.013), Chest Pain Center (3394,
## 0.004), Direct Admit (75096, 0.082), Emergency Department (456475, 0.500),
## Floor (143161, 0.157), ICU (286, 0.000), ICU to SDU (577, 0.001),
## Observation (26, 0.000), Operating Room (124573, 0.137), Other (21,
## 0.000), Other Hospital (22942, 0.025), Other ICU (6129, 0.007), PACU
## (3881, 0.004), Recovery Room (44595, 0.049), Step-Down Unit (SDU) (18577,
## 0.020)
## -----
## icu_disch_location
##       n missing distinct
##  912509      0        18
## 
## (350, 0.000), Acute Care/Floor (44010, 0.048), Death (61357, 0.067), Floor
## (559247, 0.613), Home (88591, 0.097), ICU (42, 0.000), Nursing Home (1118,
## 0.001), Operating Room (7, 0.000), Other (6359, 0.007), Other External
## (16427, 0.018), Other Hospital (20636, 0.023), Other ICU (6129, 0.007),
## Other ICU (CABG) (1, 0.000), Other Internal (1576, 0.002), Rehabilitation
## (4052, 0.004), Skilled Nursing Facility (8946, 0.010), Step-Down Unit
## (SDU) (33478, 0.037), Telemetry (60183, 0.066)
## -----
## icu_mortality
##       n missing distinct
##  912456      53      2
## 
## Value      0      1
## Frequency 851099 61357
## Proportion 0.933 0.067
## -----
## admitsource
##       n missing distinct   Info    Mean     Gmd
##  912509      0        9    0.852  5.857    2.77
## 
## Value      -1      1      2      3      4      5      6      7      8
## Frequency 1364 124576 44595 3394 162679 5098 22945 75102 472756
## Proportion 0.001 0.137 0.049 0.004 0.178 0.006 0.025 0.082 0.518

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## -----
## dischargelocation
##      n   missing  distinct    Info     Mean     Gmd
##  912509       0        7     0.72    5.303   1.818
##
## Value      -1      4      5      6      7      8      9
## Frequency  350 593099  5756 20636  88591 142720  61357
## Proportion 0.000 0.650  0.006 0.023  0.097 0.156  0.067
##
## -----
## bedcount
##      n   missing  distinct    Info     Mean     Gmd   .05   .10
##  912509       0        52    0.998   26.08   15.32   10    12
##   .25      .50      .75      .90      .95
##   16       22       32       45       62
##
## lowest : 2 3 4 5 6, highest: 60 62 68 71 84
##
## -----
## readmit
##      n   missing  distinct    Info     Sum     Mean     Gmd
##  912509       0        2     0.145   46464   0.05092  0.09665
##
## -----
## apacheiva
##      n   missing  distinct    Info     Mean     Gmd   .05   .10
##  912509       0        212      1    55.54   27.83   23    28
##   .25      .50      .75      .90      .95
##   37       51       68       90      106
##
## lowest : 1 2 3 4 5, highest: 208 209 211 214 230
##
## -----
## apacheadmissiondx
##      n   missing  distinct
##  911985       524      400
##
## lowest : Abdomen/extremity trauma          Abdomen/face trauma
## Abdomen/multiple trauma                   Abdomen only trauma
## Abdomen/pelvis trauma
## highest: Vena cava filter insertion      Ventricular Septal De
## ffect (VSD) Repair                      Ventriculostomy
## Weaning from mechanical ventilation (transfer from other unit or hospital only) Whipple-surgery for pancreatic ca
## ncer
##
## -----
## dialysis
##      n   missing  distinct
##  912509       0        2
##
## Value      0      1
## Frequency  881875  30634
## Proportion 0.966  0.034
##
## -----
## aids
##      n   missing  distinct
##  912509       0        2
##
## Value      0      1
## Frequency  911619  890
## Proportion 0.999  0.001
##
## -----
## hepaticfailure
##      n   missing  distinct
##  912509       0        2
##
## Value     FALSE    TRUE
## Frequency 893444  19065
## Proportion 0.979  0.021
##
## -----
## cirrhosis
##      n   missing  distinct    Info     Sum     Mean     Gmd
##  912509       0        2     0.043   13319   0.0146  0.02877
##
## -----
## diabetes
##      n   missing  distinct
##  912509       0        2
##
## Value      0      1
## Frequency  712693 199816
## Proportion 0.781  0.219
## -----

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## immunosuppression
##      n missing distinct
##  912509          0         2
##
## Value      0      1
## Frequency 891128 21381
## Proportion 0.977  0.023
## -----
## leukemia
##      n missing distinct
##  912509          0         2
##
## Value      0      1
## Frequency 905925 6584
## Proportion 0.993  0.007
## -----
## lymphoma
##      n missing distinct
##  912509          0         2
##
## Value      0      1
## Frequency 908895 3614
## Proportion 0.996  0.004
## -----
## metastaticcancer
##      n missing distinct
##  912509          0         2
##
## Value      0      1
## Frequency 895002 17507
## Proportion 0.981  0.019
## -----
## thrombolytics
##      n missing distinct
##  912509          0         2
##
## Value      0      1
## Frequency 895774 16735
## Proportion 0.982  0.018
## -----
## admissionheight
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  889741   22768    1512  0.999  169.5   13.63  152.4   155.0
##  .25      .50     .75   .90     .95
##  162.5   170.0   177.8  183.0   187.9
##
## lowest :  0.00  0.66  0.88  0.90  0.91, highest: 670.00 700.00 701.00 702.90 712.20
## -----
## admissionweight
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  869001   43508    8190    1  83.83   27.63   50.0   55.7
##  .25      .50     .75   .90     .95
##  66.1    80.0    96.6  115.5   130.0
##
## lowest :  0.00  0.04  0.09  0.10  0.11, highest: 969.00 970.50 982.00 983.50 987.30
## -----
## chartedweight
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  548040   364469   11291    1  84.12   27.81   49.80   55.54
##  .25      .50     .75   .90     .95
##  66.40   80.50   97.40  116.30   130.60
##
## lowest : 30.00000 30.02779 30.03000 30.07000 30.07315
## highest: 297.00000 298.00000 298.46354 299.37072 299.90000
## -----
## eyes
##      n missing distinct      Info      Mean      Gmd
##  912509          0         5  0.65   3.428  0.9003
##
## Value      -1      1      2      3      4
## Frequency 9882  83374  43799 135140 640314
## Proportion 0.011 0.091 0.048 0.148 0.702
## -----
## motor
##      n missing distinct      Info      Mean      Gmd
##  912509          0         7  0.524   5.393  1.045
##
## Value      -1      1      2      3      4      5      6
## Frequency 9882  55220  3985   6251  49127  75881  712163

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## Proportion 0.011 0.061 0.004 0.007 0.054 0.083 0.780
## -----
## verbal
##      n    missing   distinct     Info      Mean      Gmd
##  912509       0          6     0.745     3.944    1.538
##
## Value      -1       1       2       3       4       5
## Frequency  9882 167720 20933 28514 113272 572188
## Proportion 0.011 0.184 0.023 0.031 0.124 0.627
## -----
## gcs
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0          14    0.809    12.76    3.415      3        7
##  .25       .50       .75       .90       .95
##  12       15       15       15       15
##
## Value      -3       3       4       5       6       7       8       9       10
## Frequency  9882 49468 4676 5010 18944 23458 20484 21959 30397
## Proportion 0.011 0.054 0.005 0.005 0.021 0.026 0.022 0.024 0.033
##
## Value      11      12      13      14      15
## Frequency 28152 23840 44576 108048 523615
## Proportion 0.031 0.026 0.049 0.118 0.574
## -----
## unablegcs
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  912509       0          2    0.032    9882 0.01083 0.02142
##
## -----
## urine
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0       68282    0.896    998.4    1383    -1.0    -1.0
##  .25       .50       .75       .90       .95
##  -1.0      175.7    1609.5   2881.8   3829.8
##
## lowest : -1.0000 0.0000 0.6912 0.7776 0.8640
## highest: 84324.2400 85489.7760 98655.2352 155900.0736 501725.8368
## -----
## pao2_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0       3996    0.565    31.19    53.79    -1       -1
##  .25       .50       .75       .90       .95
##  -1       -1       -1       116      173
##
## lowest : -1.0 2.0 4.0 4.5 9.0, highest: 663.8 664.0 677.0 685.4 686.0
## -----
## fio2_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0       197    0.565    13.76    24.1    -1       -1
##  .25       .50       .75       .90       .95
##  -1       -1       -1       60       100
##
## lowest : -1.0 21.0 22.0 23.0 23.5, highest: 99.6 99.7 99.8 99.9 100.0
## -----
## pao2fio2_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0      14034    0.565    57.48    96.84    -1.0    -1.0
##  .25       .50       .75       .90       .95
##  -1.0     -1.0     -1.0     252.4    342.5
##
## lowest : -1.00000 9.52381 10.00000 11.00000 12.00000
## highest: 2365.21739 2500.00000 2704.76190 2719.04762 2804.76190
## -----
## temperature_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0       536    0.997    35.15    3.215    33.90    35.50
##  .25       .50       .75       .90       .95
##  36.10     36.40    36.70    37.05    37.33
##
## lowest : -1.00 20.00 20.10 20.20 20.30, highest: 42.66 42.70 42.80 42.90 43.00
## -----
## respiratoryrate_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0       134    0.999    24.88    17.09      5        7
##  .25       .50       .75       .90       .95
##  10       27       35       45       52
##
## lowest : 4.0 5.0 6.0 6.6 6.7, highest: 57.0 58.0 59.0 59.1 60.0
## -----

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## heartrate_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        201        1  100.1    34.69      48      53
##  .25       .50       .75     .90     .95
##  87       104       120     136     146
##
## lowest :  20  21  22  23  24, highest: 216 217 218 219 220
## -----
## mbp_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        161        1  85.71    45.43      42      45
##  .25       .50       .75     .90     .95
##  53       64       123     146     163
##
## lowest :  40  41  42  43  44, highest: 196 197 198 199 200
## -----
## albumin_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 363837  548672       63  0.998    2.92  0.7948      1.7      2.0
##  .25       .50       .75     .90     .95
##  2.4      2.9       3.4     3.8     4.0
##
## lowest : 1.0 1.1 1.2 1.3 1.4, highest: 6.3 6.7 6.9 7.0 8.2
## -----
## bilirubin_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        966    0.745 -0.1945    1.194     -1.0     -1.0
##  .25       .50       .75     .90     .95
##  -1.0     -1.0       0.5     1.0     1.7
##
## lowest : -1.00  0.05  0.09  0.10  0.11, highest: 60.30 61.50 63.10 64.00 72.40
## -----
## bun_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        944    0.992    21.28    22.29      -1      -1
##  .25       .50       .75     .90     .95
##  8        16       28      49      66
##
## lowest : -1.0   1.0   2.0   2.3   2.5, highest: 251.0 252.0 253.0 254.0 255.0
## -----
## creatinine_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        2398   0.993    1.05    1.628     -1.00     -1.00
##  .25       .50       .75     .90     .95
##  0.53     0.84     1.38     2.57     4.08
##
## lowest : -1.00  0.10  0.11  0.12  0.13, highest: 24.89 24.91 24.94 24.95 25.00
## -----
## glucose_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        1384   0.999    148.1    110.2      -1      -1
##  .25       .50       .75     .90     .95
##  89       121       194     275     342
##
## lowest : -1.0   1.0   1.1   1.3   1.5, highest: 2356.0 2357.0 2796.0 2810.0 2954.0
## -----
## hematocrit_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        612    0.992    25.91    15.7     -1.0     -1.0
##  .25       .50       .75     .90     .95
##  22.3     30.3     36.1     40.4     42.8
##
## lowest : -1.0   5.0   5.1   5.9   6.0, highest: 70.2 70.8 71.0 72.7 78.0
## -----
## sodium_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        253    0.991    112.2    45.42      -1      -1
##  .25       .50       .75     .90     .95
##  131      137       140     142     145
##
## lowest : -1  88  90  91  95, highest: 190 192 194 196 198
## -----
## paco2_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        1164   0.565    9.506   16.71      -1      -1
##  .25       .50       .75     .90     .95
##  -1       -1       -1      42      49
##
## lowest : -1.0   3.1   6.9   7.0   7.3, highest: 147.7 147.8 148.0 148.8 150.0

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## -----
## ph_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        967     0.565     1.025     3.076   -1.000   -1.000
##  .25       .50       .75     .90      .95
##  -1.000   -1.000   -1.000     7.390     7.435
##
##  -1 (691448, 0.758), 6.3 (1, 0.000), 6.5 (5, 0.000), 6.6 (11, 0.000), 6.7
##  (46, 0.000), 6.8 (217, 0.000), 6.9 (690, 0.001), 7 (1738, 0.002), 7.1
##  (4958, 0.005), 7.2 (16712, 0.018), 7.3 (62997, 0.069), 7.4 (96463, 0.106),
##  7.5 (33188, 0.036), 7.6 (3721, 0.004), 7.7 (291, 0.000), 7.8 (19, 0.000),
##  7.9 (2, 0.000), 8 (1, 0.000), 8.6 (1, 0.000)
##
## -----
## intubated_apache
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  912509       0        2     0.393    141662    0.1552    0.2623
##
## -----
## wbc_apache
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        5611    0.988     9.145     8.983   -1.00     -1.00
##  .25       .50       .75     .90      .95
##  3.60      8.50     13.40    18.90    23.28
##
## lowest : -1.00  0.01  0.02  0.03  0.04, highest: 196.80 197.00 197.70 199.00 199.20
##
## -----
## oobintubday1_apache
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  912509       0        2     0.574    235413    0.258    0.3829
##
## -----
## oobventday1_apache
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  912509       0        2     0.657    295615    0.324    0.438
##
## -----
## ventday1_apache
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  912509       0        2     0.547    218677    0.2396   0.3644
##
## -----
## physicianspeciality
##      n    missing   distinct
##  912509       0        49
##
## lowest : allergy/immunology          anesthesiology          anesthesiology/CCM          cardiology
## critical care medicine (CCM)
## highest: surgery-transplant         surgery-trauma          surgery-vascular          unknown
## urology
##
## -----
## acutephysiologyscore
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        198      1     43.81     25.13      16      20
##  .25       .50       .75     .90      .95
##  27       38       54      76      92
##
## lowest : 0  1  2  3  4, highest: 194 195 198 200 206
##
## -----
## apachescore
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0        212      1     55.54     27.83      23      28
##  .25       .50       .75     .90      .95
##  37       51       68      90     106
##
## lowest : 1  2  3  4  5, highest: 208 209 211 214 230
##
## -----
## predictedicumortality
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0    889923      1     0.05459    0.1406  0.002357  0.004004
##  .25       .50       .75     .90      .95
##  0.009022  0.022689  0.064605  0.194698  0.368231
##
## lowest : -1.000000e+00  7.088864e-10  7.633918e-10  7.749529e-10  7.966238e-10
## highest: 9.831448e-01  9.833071e-01  9.851197e-01  9.859533e-01  9.951461e-01
##
## -----
## predictedicullos
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0    889227      1     3.851     2.513     1.135    1.555
##  .25       .50       .75     .90      .95

```

```

##      2.184    3.319    5.192    7.244    8.309
##
## lowest : -1.0000000000  0.0005581499  0.0010462120  0.0033882155  0.0036456098
## highest: 15.2146312944 15.3433721860 15.3576234639 16.0262378684 19.9075117024
## -----
## predictedhospitalmortality
##      n missing distinct      Info      Mean      Gmd      .05
##  912509       0     846588       1  0.04401   0.2669 -1.000000
##  .10       .25       .50       .75       .90       .95
##  0.005689  0.017526  0.046130  0.122479  0.304494  0.494634
##
## lowest : -1.0000000000  0.0003451466  0.0003794773  0.0003825366  0.0004188721
## highest: 0.9930928093  0.9930994412  0.9932010502  0.9979823377  0.9981384119
## -----
## predictedhospitallos
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  912509       0     846540       1  9.384   5.737 -1.000   3.711
##  .25       .50       .75       .90       .95
##  6.308    9.053   12.161   15.609   18.401
##
## lowest : -1.000000e+00  9.883428e-04  3.367056e-03  9.694190e-03  1.226688e-02
## highest: 9.934482e+01  1.021803e+02  1.039875e+02  1.066029e+02  1.469374e+02
## -----
## preopmi
##      n missing distinct      Info      Sum      Mean      Gmd
##  912509       0       2     0.009   2663  0.002918  0.00582
##
## -----
## preopcardiaccath
##      n missing distinct      Info      Sum      Mean      Gmd
##  912509       0       2     0.023   6932  0.007597  0.01508
##
## -----
## ptcawithin24h
##      n missing distinct      Info      Sum      Mean      Gmd
##  912509       0       2     0.188   61222  0.06709  0.1252
##
## -----
## graftcount
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  912509       0       10     0.04   2.999  0.03646       3       3
##  .25       .50       .75       .90       .95
##  3        3       3       3       3
##
## Value      1      2      3      4      5      6      7      8      9
## Frequency  2419  3927 900090  4513  1288  227   34    9    1
## Proportion 0.003 0.004 0.986  0.005 0.001 0.000  0.000 0.000 0.000
##
## Value      10
## Frequency  1
## Proportion 0.000
##
## -----
## mbp_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  911199     1310     152       1  57.02   18.97     26     35
##  .25       .50       .75       .90       .95
##  47       58       68       78       84
##
## lowest :  1   2   3   4   5, highest: 157 162 165 292 296
##
## -----
## sbp_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  911192     1317     172       1  58.88   18.98     29     37
##  .25       .50       .75       .90       .95
##  49       59       70       80       86
##
## lowest :  1   2   3   4   5, highest: 174 175 176 177 179
##
## -----
## temperature_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  74236    838273    1881       1  40.71   14.61    23.9    30.7
##  .25       .50       .75       .90       .95
##  34.8    36.1    36.9     80.3    97.0
##
## lowest :  0.05  0.10  0.20  0.25  0.30, highest: 105.20 105.60 106.00 108.40 109.70
##
## -----
## temperature_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  74236    838273     901    0.999  44.57   13.26    36.10   36.72

```

```

##      .25      .50      .75      .90      .95
##  37.30   37.80   38.60   97.80  100.10
##
## lowest :  0.10  0.40  3.20  4.35  4.40, highest: 112.15 112.50 112.70 112.90 151.00
## -----
## heartrate_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  911360    1149     263        1    107.9    24.68      76      81
##      .25      .50      .75      .90      .95
##     92     106     121      137      147
##
## lowest :  29  30  31  32  33, highest: 296 297 298 299 300
## -----
## respiratoryrate_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  864221    48288     208    0.998    33.09    13.66      20      22
##      .25      .50      .75      .90      .95
##     24      29      36      47      57
##
## Value      0      500    13500   19000   27000   37000   51000   57500   58500
## Frequency  864212      1       1       1       1       1       1       1       1
## Proportion  1       0       0       0       0       0       0       0       0
##
## Value      63000
## Frequency  1
## Proportion 0
##
## heartrate_charted_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  829506    83003     272        1    102.4    24.91      70      76
##      .25      .50      .75      .90      .95
##     87     100     116      132      142
##
## lowest :  5  7  14  15  18, highest: 320 347 360 361 379
## -----
## respiratoryrate_charted_max
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  834367    78142     79    0.998    27.72    9.502      17      19
##      .25      .50      .75      .90      .95
##     22      26      31      39      46
##
## lowest :  1  2  3  4  5, highest: 75 76 77 78 79
## -----
## o2saturation_charted_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  792701   119808     101    0.995    91.37    7.124      79      85
##      .25      .50      .75      .90      .95
##     90      93      96      98      99
##
## lowest :  1  2  3  4  5, highest:  96  97  98  99  100
## -----
## nibp_systolic_charted_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  808844   103665     268        1    97.44    23.54      65      72
##      .25      .50      .75      .90      .95
##     84      96     110      124      134
##
## lowest :  1  2  3  4  5, highest: 246 248 256 261 269
## -----
## nibp_diastolic_charted_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  809166   103343     195    0.999    49.74    15.58      27      33
##      .25      .50      .75      .90      .95
##     41      49      58      67      74
##
## lowest :  1  2  3  4  5, highest: 185 187 188 190 226
## -----
## nibp_mean_charted_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  767729   144780     195        1    64.52    17.6       40      46
##      .25      .50      .75      .90      .95
##     54      63      74      85      92
##
## lowest :  0.13  0.61  0.74  0.87  1.00, highest: 194.00 195.00 196.00 200.00 232.00
## -----
## ibp_systolic_charted_min
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  197536   714973     294        1    95.91    27.39      58      69
##      .25      .50      .75      .90      .95

```

```

##      82      94     110     128     139
##
## lowest :  1  2  3  4  5, highest: 319 334 338 348 390
## -----
## ibp_diastolic_charted_min
##   n missing distinct  Info  Mean  Gmd  .05  .10
## 197464  715045     215  0.999  48.2 14.36  29   34
##   .25    .50     .75  .90   .95
##   40     47     55   64   70
##
## lowest :  1  2  3  4  5, highest: 316 333 334 348 390
## -----
## ibp_mean_charted_min
##   n missing distinct  Info  Mean  Gmd  .05  .10
## 214633  697876     388  0.999  64.33 18.53  38   47
##   .25    .50     .75  .90   .95
##   55     63     73   84   92
##
## lowest :  1  2  3  4  5, highest: 357 359 360 364 390
## -----
## mbp_charted_min
##   n missing distinct  Info  Mean  Gmd  .05  .10
## 814231  98278    265     1  63.45 17.71  39   45
##   .25    .50     .75  .90   .95
##   54     63     73   84   91
##
## lowest :  0.13   0.61   0.74   0.87   1.00, highest: 194.00 196.00 200.00 232.00 287.00
## -----
## sbp_charted_min
##   n missing distinct  Info  Mean  Gmd  .05  .10
## 822995  89514     271     1  95.7  23.86  62   71
##   .25    .50     .75  .90   .95
##   82     95    109   123   132
##
## lowest :  1  2  3  4  5, highest: 240 244 246 248 256
## -----
## temperature_charted_min
##   n missing distinct  Info  Mean  Gmd  .05  .10
## 893018  19491     684  0.996  36.27 0.7088  35.1  35.6
##   .25    .50     .75  .90   .95
##   36.1   36.4    36.7   36.9   37.1
##
## lowest : 20.10 20.20 20.22 20.30 20.40, highest: 42.10 42.70 45.30 46.20 48.20
## -----
## temperature_charted_max
##   n missing distinct  Info  Mean  Gmd  .05  .10
## 893018  19491     577  0.997  37.29 0.7655  36.40  36.60
##   .25    .50     .75  .90   .95
##   36.90  37.16   37.60   38.20   38.70
##
## lowest : 21.70 27.90 28.10 28.80 28.88, highest: 48.33 48.60 48.70 48.80 48.90
## -----
## gcs_charted_min
##   n missing distinct  Info  Mean  Gmd  .05  .10
## 619639  292870     14  0.878  12.4  3.671     3     6
##   .25    .50     .75  .90   .95
##   10     14     15   15    15
##
## Value      3.0     4.0     5.0     6.0     7.0     8.0     9.0    10.0    11.0
## Frequency  43551   4164   3990  17521  21691  19150  18104  27352  21557
## Proportion 0.070  0.007  0.006  0.028  0.035  0.031  0.029  0.044  0.035
##
## Value      12.0    13.0    14.0    14.5    15.0
## Frequency 15589  33320  89442     1 304207
## Proportion 0.025  0.054  0.144  0.000  0.491
##
## -----
## bilirubin_max
##   n missing distinct  Info  Mean  Gmd  .05  .10
## 377882  534627    1016  0.994  1.195  1.291     0.2   0.3
##   .25    .50     .75  .90   .95
##   0.4     0.7     1.1    2.1    3.5
##
## lowest :  0.00   0.05   0.09   0.10   0.11, highest: 61.50 63.10 64.00 67.90 72.40
## -----
## creatinine_max
##   n missing distinct  Info  Mean  Gmd  .05  .10
## 823925  88584    2539     1  1.547  1.279     0.51   0.60
##   .25    .50     .75  .90   .95
##   0.76   1.00    1.57   2.95   4.60

```

```

## 
## lowest :  0.00  0.06  0.07  0.10  0.11, highest: 48.59 50.70 51.70 56.00 107.00
## -----
## lactate_min
##      n missing distinct    Info   Mean    Gmd   .05   .10
##  214669 697840     1105  0.999  2.107  1.778  0.6   0.7
##    .25    .50    .75    .90   .95
##    1.0    1.5    2.3    3.8   5.9
##
## lowest :  0.00  0.10  0.11  0.20  0.24, highest: 36.90 38.50 38.90 39.73 40.90
## -----
## lactate_max
##      n missing distinct    Info   Mean    Gmd   .05   .10
##  214669 697840     1550  0.999  2.909  2.698  0.7   0.8
##    .25    .50    .75    .90   .95
##    1.2    1.8    3.2    6.1   9.2
##
## Value      0      5     10    15    20    25    30    35    40
## Frequency 141487 57611 9968 3630 1381 419 128 31 8
## Proportion 0.659 0.268 0.046 0.017 0.006 0.002 0.001 0.000 0.000
##
## Value      45     510
## Frequency 5      1
## Proportion 0.000 0.000
## -----
## pao2_min
##      n missing distinct    Info   Mean    Gmd   .05   .10
##  346221 566288     3508    1 101.6  57.56  44 54
##    .25    .50    .75    .90   .95
##    66     83    115    166   216
##
## Value      0     100    200    300    400    500    600    700   1000
## Frequency 27177 273711 33100 7093 3447 1448 233 7 2
## Proportion 0.078 0.791 0.096 0.020 0.010 0.004 0.001 0.000 0.000
##
## Value      1100  2800 11800
## Frequency 1      1      1
## Proportion 0.000 0.000 0.000
## -----
## pao2_max
##      n missing distinct    Info   Mean    Gmd   .05   .10
##  346221 566288     4902    1 165.3  113 61.9 69.2
##    .25    .50    .75    .90   .95
##    87.0   125.0 206.0 335.0 413.0
##
## 0 (5543, 0.016), 100 (202735, 0.586), 200 (75124, 0.217), 300 (31943,
## 0.092), 400 (19609, 0.057), 500 (9384, 0.027), 600 (1778, 0.005), 700 (85,
## 0.000), 800 (8, 0.000), 900 (1, 0.000), 1000 (2, 0.000), 1100 (2, 0.000),
## 1200 (1, 0.000), 1700 (1, 0.000), 2100 (1, 0.000), 2800 (1, 0.000), 3600
## (1, 0.000), 5400 (1, 0.000), 11800 (1, 0.000)
## -----
## paco2_min
##      n missing distinct    Info   Mean    Gmd   .05   .10
##  346097 566412     1146    1 38.87  12.46  23.3 26.7
##    .25    .50    .75    .90   .95
##    31.7   37.0   43.7  53.0  61.2
##
## Value     -100      0     50    100    150    200    250    300    400
## Frequency 1 23031 317541 5413 90 9 2 1 2
## Proportion 0.000 0.067 0.917 0.016 0.000 0.000 0.000 0.000 0.000
##
## Value      450    3650 4550
## Frequency 5      1      1
## Proportion 0.000 0.000 0.000
## -----
## paco2_max
##      n missing distinct    Info   Mean    Gmd   .05   .10
##  346097 566412     1487    1 46.07  16.28  27.4 31.0
##    .25    .50    .75    .90   .95
##    36.0   43.0   51.0  65.0  78.0
##
## Value      0     100    200    300    400    500    600    700   3600
## Frequency 253905 91948 216 7 10 5 2 1 1
## Proportion 0.734 0.266 0.001 0.000 0.000 0.000 0.000 0.000 0.000
##
## Value      4600  7500
## Frequency 1      1
## Proportion 0.000 0.000
## -----

```

```

## platelet_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 791142    121367      1099       1  197.2  99.31      68      94
##  .25      .50      .75      .90      .95
##  137      186      243      308      361
##
## lowest :  0.00  1.00  1.05  2.00  3.00
## highest: 2113.00 2221.00 2353.00 2371.00 2449.00
## -----
## inr_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 364715    547794      1085     0.993  1.614  0.815      1.00      1.00
##  .25      .50      .75      .90      .95
##  1.10     1.30     1.60      2.50      3.45
##
## lowest :  0.00  0.50  0.60  0.66  0.70, highest:  24.50  27.20  32.10  38.10 130.00
## -----
## wbc_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 794580    117929      5349       1 11.29  6.364      4.3      5.4
##  .25      .50      .75      .90      .95
##  7.3      9.9     13.5      18.1      22.1
##
## lowest :  0.00  0.01  0.02  0.03  0.04, highest: 613.40 774.00 776.40 778.40 813.90
## -----
## wbc_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 794580    117929      5938       1 12.52  7.252      4.7      5.8
##  .25      .50      .75      .90      .95
##  7.9     10.9     15.0      20.5      25.0
##
## lowest :  0.00  0.01  0.02  0.03  0.04, highest: 657.46 774.00 776.40 778.40 813.90
## -----
## ptt_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 266885    645624      2321       1 44.02  24.64      24.0      25.4
##  .25      .50      .75      .90      .95
## 28.5     33.9     45.1      77.1      107.0
##
## lowest : 12.2  14.2  14.5  15.0  15.1, highest: 296.3 296.9 298.5 300.0 380.0
## -----
## bands_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 76228    836281      737      0.997 12.54  13.61      1         1
##  .25      .50      .75      .90      .95
##  3        8       17      31        40
##
## Value      0     50     100    6400
## Frequency 65175 10762     290      1
## Proportion 0.855 0.141 0.004 0.000
## -----
## ph_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 335524    576985      1028       1  7.375  0.2206    7.110    7.180
##  .25      .50      .75      .90      .95
## 7.271    7.341     7.401     7.450     7.480
##
## Value      0     100    700    7200    7300
## Frequency 335518      2       2       1       1
## Proportion 1        0       0       0       0
## -----
## basedeficit_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 59048     853461      429      0.999  6.095  5.381      0.7      1.0
##  .25      .50      .75      .90      .95
##  2.5      4.9      8.0      13.0      17.0
##
## lowest : -30.0 -24.4 -23.9 -21.0 -18.2, highest:  34.3  34.4  34.7  35.0  36.6
## -----
## basedeficit_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 59048     853461      429      0.999  6.095  5.381      0.7      1.0
##  .25      .50      .75      .90      .95
##  2.5      4.9      8.0      13.0      17.0
##
## lowest : -30.0 -24.4 -23.9 -21.0 -18.2, highest:  34.3  34.4  34.7  35.0  36.6
## -----
## ast_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10

```

```

##   383902   528607    6246      1   178.8    291.4     12     15
##   .25      .50      .75      .90      .95
##   20       32       69      198     467
##
## lowest :   0     1     2     3     4, highest:  43957  46817  54043  56238  200111
## -----
## alt_max
##   n missing distinct   Info   Mean   Gmd   .05   .10
## 378856  533653    4501      1   109   166.2     10     12
##   .25      .50      .75      .90      .95
##   17       28       51      128     299
##
## lowest :   0     1     2     3     4, highest: 16185 16738 17091 18200 18978
## -----
## alp_max
##   n missing distinct   Info   Mean   Gmd   .05   .10
## 371564  540945    1430      1   101.2   68.55     39     46
##   .25      .50      .75      .90      .95
##   59       78       110     165     228
##
## lowest : -154.0     1.0     2.0     3.0     3.7
## highest: 4254.0 4956.0 7443.0 8146.0 10001.0
## -----
## penicilin
##   n missing distinct   Info   Sum   Mean   Gmd
## 903501  9008       2   0.016   4748 0.005255 0.01046
##
## -----
## penicilin_anti_staph
##   n missing distinct   Info   Sum   Mean   Gmd
## 903501  9008       2   0.003   1015 0.001123 0.002244
##
## -----
## penicilin_anti_pseudo
##   n missing distinct   Info   Sum   Mean   Gmd
## 903501  9008       2   0.352  122743 0.1359 0.2348
##
## -----
## augmentin_unasyn
##   n missing distinct   Info   Sum   Mean   Gmd
## 903501  9008       2   0.036   10897 0.01206 0.02383
##
## -----
## cephalosporin_1st_gen
##   n missing distinct   Info   Sum   Mean   Gmd
## 903501  9008       2   0.132   41557 0.046 0.08776
##
## -----
## cephalosporin_2nd_gen
##   n missing distinct   Info   Sum   Mean   Gmd
## 903501  9008       2   0.077   23685 0.02621 0.05106
##
## -----
## cephalosporin_3rd_gen
##   n missing distinct   Info   Sum   Mean   Gmd
## 903501  9008       2   0.209   68100 0.07537 0.1394
##
## -----
## cephalosporin_4th_5th_gen
##   n missing distinct   Info   Sum   Mean   Gmd
## 903501  9008       2   0.094   29182 0.0323 0.06251
##
## -----
## carbapenems
##   n missing distinct   Info   Sum   Mean   Gmd
## 903501  9008       2   0.086   26826 0.02969 0.05762
##
## -----
## monobactam
##   n missing distinct   Info   Sum   Mean   Gmd
## 903501  9008       2   0.034   10318 0.01142 0.02258
##
## -----
## fq
##   n missing distinct   Info   Sum   Mean   Gmd
## 903501  9008       2   0.253   84164 0.09315 0.169
##
## -----
## vancomycin

```

```

##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.464    173027   0.1915   0.3097
##
## -----
## amg
##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.044    13504    0.01495   0.02945
##
## -----
## polymixins
##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.003    769     0.0008511   0.001701
##
## -----
## linezolid
##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.024    7163    0.007928   0.01573
##
## -----
## dapto
##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.01     3080    0.003409   0.006795
##
## -----
## clinda
##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.051    15696   0.01737   0.03414
##
## -----
## doxycyclin
##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.023    7049    0.007802   0.01548
##
## -----
## macrolides
##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.115    36029   0.03988   0.07657
##
## -----
## sulfa
##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.025    7480    0.008279   0.01642
##
## -----
## metronidazole
##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.132    41517   0.04595   0.08768
##
## -----
## nitrofurantoin
##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.004    1250    0.001384   0.002763
##
## -----
## tigecycline
##      n missing distinct      Info      Sum      Mean      Gmd
## 903501    9008       2     0.007    2127    0.002354   0.004697
##
## -----
## ceftriaxone
##      n missing distinct      Info      Mean      Gmd
## 903501    9008       1       0       0       0
##
## Value      0
## Frequency 903501
## Proportion 1
##
## -----
## cefotaxime
##      n missing distinct      Info      Mean      Gmd
## 903501    9008       1       0       0       0
##
## Value      0
## Frequency 903501
## Proportion 1
##
## -----
## ampicillin_sulbactam
##      n missing distinct      Info      Mean      Gmd
## 903501    9008       1       0       0       0
##

```

```

## Value          0
## Frequency   903501
## Proportion    1
##
## -----
## levofloxacin
##      n missing distinct     Info      Sum      Mean      Gmd
##  903501     9008         2     0.033     9936    0.011    0.02175
##
## -----
## moxifloxacin
##      n missing distinct     Info      Sum      Mean      Gmd
##  903501     9008         2     0.004     1097  0.001214  0.002425
##
## -----
## piperacillin_tazobactam
##      n missing distinct     Info      Mean      Gmd
##  903501     9008         1       0        0        0
##
## Value          0
## Frequency   903501
## Proportion    1
##
## -----
## cefepim
##      n missing distinct     Info      Mean      Gmd
##  903501     9008         1       0        0        0
##
## Value          0
## Frequency   903501
## Proportion    1
##
## -----
## meropenem
##      n missing distinct     Info      Mean      Gmd
##  903501     9008         1       0        0        0
##
## Value          0
## Frequency   903501
## Proportion    1
##
## -----
## imipenem
##      n missing distinct     Info      Mean      Gmd
##  903501     9008         1       0        0        0
##
## Value          0
## Frequency   903501
## Proportion    1
##
## -----
## doripenem
##      n missing distinct     Info      Mean      Gmd
##  903501     9008         1       0        0        0
##
## Value          0
## Frequency   903501
## Proportion    1
##
## -----
## gentamicin
##      n missing distinct     Info      Sum      Mean      Gmd
##  903501     9008         2       0        22  2.435e-05  4.87e-05
##
## -----
## tobramycin
##      n missing distinct     Info      Sum      Mean      Gmd
##  903501     9008         2     0.001     172  0.0001904  0.0003807
##
## -----
## amikacin
##      n missing distinct     Info      Mean      Gmd
##  903501     9008         1       0        0        0
##
## Value          0
## Frequency   903501
## Proportion    1
##
## -----
## dopamine_infusion
##      n missing distinct     Info      Sum      Mean      Gmd
##  912509       0         2     0.076    23820    0.0261   0.05084
##
## -----
## epinephrine_infusion
##      n missing distinct     Info      Sum      Mean      Gmd
##  912509       0         2     0.076    23820    0.0261   0.05084

```

```

## 912509      0      2    0.032    9938  0.01089  0.02154
##
## -----
## norepinephrine_infusion
##   n missing distinct      Info      Sum      Mean      Gmd
## 912509      0      2    0.234    77890  0.08536  0.1561
##
## -----
## phenylephrine_infusion
##   n missing distinct      Info      Sum      Mean      Gmd
## 912509      0      2    0.083    26080  0.02858  0.05553
##
## -----
## vasopressin_infusion
##   n missing distinct      Info      Sum      Mean      Gmd
## 347509  565000      2    0.132    16059  0.04621  0.08815
##
## -----
## milrinone_infusion
##   n missing distinct      Info      Sum      Mean      Gmd
## 912509      0      2    0.019    5782  0.006336  0.01259
##
## -----
## heparin_infusion
##   n missing distinct      Info      Sum      Mean      Gmd
## 347509  565000      2    0.303    39684  0.1142   0.2023
##
## -----
## dopamine_medication
##   n missing distinct      Info      Sum      Mean      Gmd
## 912509      0      2    0.142    45389  0.04974  0.09453
##
## -----
## epinephrine_medication
##   n missing distinct      Info      Sum      Mean      Gmd
## 912509      0      2    0.101    31830  0.03488  0.06733
##
## -----
## norepinephrine_medication
##   n missing distinct      Info      Sum      Mean      Gmd
## 912509      0      2    0.314    108457  0.1189   0.2095
##
## -----
## phenylephrine_medication
##   n missing distinct      Info      Sum      Mean      Gmd
## 912509      0      2    0.165    53473  0.0586   0.1103
##
## -----
## vasopressin_medication
##   n missing distinct      Info      Sum      Mean      Gmd
## 903501  9008      2    0.097    30270  0.0335   0.06476
##
## -----
## milrinone_medication
##   n missing distinct      Info      Sum      Mean      Gmd
## 912509      0      2    0.03     9190  0.01007  0.01994
##
## -----
## heparin_medication
##   n missing distinct      Info      Sum      Mean      Gmd
## 903501  9008      2    0.581    237112  0.2624   0.3871
##
## -----
## sepsis
##   n missing distinct      Info      Sum      Mean      Gmd
## 912509      0      2    0.318    109798  0.1203   0.2117
##
## -----
## sepsis_priority
##   n missing distinct      Info      Mean      Gmd
## 912509      0      4    0.319    0.1965   0.3579
##
## Value      0      1      2      3
## Frequency 802711  66404  17251  26143
## Proportion 0.880  0.073  0.019  0.029
##
## -----
## infection
##   n missing distinct      Info      Sum      Mean      Gmd
## 912509      0      2    0.597    250420  0.2744   0.3982

```

```

## -----
## infection_priority
##      n missing distinct      Info      Mean      Gmd
##  912509       0        4     0.615     0.495     0.7861
##
## Value       0       1       2       3
## Frequency 662089 118863 61871 69686
## Proportion 0.726 0.130 0.068 0.076
## -----
## aidshiv
##      n missing distinct      Info      Sum      Mean      Gmd
##  912509       0        2      0.01    2961 0.003245 0.006469
##
## -----
## aidshiv_priority
##      n missing distinct      Info      Mean      Gmd
##  912509       0        4      0.01 0.007939 0.01583
##
## Value       0       1       2       3
## Frequency 909548   48   1543 1370
## Proportion 0.997 0.000 0.002 0.002
## -----
## organfailure
##      n missing distinct      Info      Sum      Mean      Gmd
##  912509       0        2      0.725 372946 0.4087 0.4833
##
## -----
## organfailure_priority
##      n missing distinct      Info      Mean      Gmd
##  912509       0        4      0.785 0.7615 1.051
##
## Value       0       1       2       3
## Frequency 539563 159065 105867 108014
## Proportion 0.591 0.174 0.116 0.118
## -----
## altered_mental_status
##      n missing distinct      Info      Sum      Mean      Gmd
##  912509       0        2      0.261 87685 0.09609 0.1737
##
## -----
## altered_mental_status_priority
##      n missing distinct      Info      Mean      Gmd
##  912509       0        4      0.261 0.2117 0.3901
##
## Value       0       1       2       3
## Frequency 824824 16981 35888 34816
## Proportion 0.904 0.019 0.039 0.038
## -----
## infection_apache
##      n missing distinct      Info      Sum      Mean      Gmd
##  912509       0        2      0.416 151832 0.1664 0.2774
##
## -----
## organfailure_apache
##      n missing distinct      Info      Sum      Mean      Gmd
##  912509       0        2      0.176 57210 0.0627 0.1175
##
## -----
## prompt_inflam
##      n missing distinct      Info      Sum      Mean      Gmd
## 380100 532409       2      0.568 96341 0.2535 0.3784
##
## -----
## prompt_severe_sepsis
##      n missing distinct      Info      Sum      Mean      Gmd
## 380100 532409       2      0.254 35505 0.09341 0.1694
##
## -----
## prompt_sepsis
##      n missing distinct      Info      Sum      Mean      Gmd
## 380100 532409       2      0.12 15907 0.04185 0.0802
##
## -----
## prompt_inflam_with_org_dys
##      n missing distinct      Info      Sum      Mean      Gmd
## 380100 532409       2          0          4 1.052e-05 2.105e-05
##
## -----

```

```

## prompt_clinical_responce_req
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  380100    532409        2    0.004   379551  0.9986  0.002885
##
## -----
## sofa_respiration
##      n    missing   distinct     Info      Mean      Gmd
##  912509        0        5    0.386    0.3666  0.6443
##
## Value      0      1      2      3      4
## Frequency 775552 17318 59473 42413 17753
## Proportion 0.850 0.019 0.065 0.046 0.019
##
## -----
## sofa_coagulation
##      n    missing   distinct     Info      Mean      Gmd
##  912509        0        5    0.603    0.3963  0.6278
##
## Value      0      1      2      3      4
## Frequency 667848 153552 69848 16638 4623
## Proportion 0.732 0.168 0.077 0.018 0.005
##
## -----
## sofa_liver
##      n    missing   distinct     Info      Mean      Gmd
##  912509        0        5    0.261    0.155  0.2872
##
## Value      0      1      2      3      4
## Frequency 824760 46708 31852 5737 3452
## Proportion 0.904 0.051 0.035 0.006 0.004
##
## -----
## sofa_cardiovascular
##      n    missing   distinct     Info      Mean      Gmd
##  912509        0        3    0.778    1.185  0.97
##
## Value      0      1      3
## Frequency 193336 538176 180997
## Proportion 0.212 0.590 0.198
##
## -----
## sofa_cns
##      n    missing   distinct     Info      Mean      Gmd
##  912509        0        5    0.794    0.8861  1.246
##
## Value      0      1      2      3      4
## Frequency 533497 152624 82389 84845 59154
## Proportion 0.585 0.167 0.090 0.093 0.065
##
## -----
## sofa_renal
##      n    missing   distinct     Info      Mean      Gmd
##  912509        0        5    0.759    0.7813  1.143
##
## Value      0      1      2      3      4
## Frequency 562276 163728 70095 56639 59771
## Proportion 0.616 0.179 0.077 0.062 0.066
##
## -----
## sofa_renal_baseline
##      n    missing   distinct     Info      Mean      Gmd
##  912509        0        2    0.097    0.1343  0.2596
##
## Value      0      4
## Frequency 881875 30634
## Proportion 0.966 0.034
##
## -----
## sofa_liver_baseline
##      n    missing   distinct     Info      Mean      Gmd
##  912509        0        2    0.061    0.08357  0.1637
##
## Value      0      4
## Frequency 893444 19065
## Proportion 0.979 0.021
##
## -----
## sofa_respiration_baseline
##      n    missing   distinct     Info      Mean      Gmd
##  912509        0        2    0.549    0.4819  0.7315
##
## Value      0      2
## Frequency 692652 219857
## Proportion 0.759 0.241
##
## -----
## cardiovascular_baseline
##      n    missing   distinct

```

```

##    912509      0      2
##
## Value      0      1
## Frequency 705303 207206
## Proportion 0.773 0.227
## -----
## soi_alpha
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 614401 298108      468  0.999  2.997  0.536   2.50   2.52
##  .25     .50     .75     .90     .95
##  2.60    2.83    3.17   3.74   4.03
##
## lowest : 2.50 2.51 2.52 2.53 2.54, highest: 7.60 7.61 7.88 7.94 8.00
## -----
## soi_minutes
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 614401 298108      301  0.994 176.2 300.6   -60   -60
##  .25     .50     .75     .90     .95
##  -5      30     215    695   965
##
## lowest : -60  -55  -50  -45  -40, highest: 1420 1425 1430 1435 1440
## -----
## od_alpha
##      n missing distinct      Info      Mean      Gmd
## 760467 152042      7   0.352  1.173  0.3065
##
## Value      1      2      3      4      5      6      7
## Frequency 657571 79763 18657 3839  572   63     2
## Proportion 0.865 0.105 0.025 0.005 0.001 0.000 0.000
## -----
## od_minutes
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 760467 152042      301  0.961 149.8 291.5   -60   -60
##  .25     .50     .75     .90     .95
##  -60     15     200    625   910
##
## lowest : -60  -55  -50  -45  -40, highest: 1420 1425 1430 1435 1440
## -----
## both_soi_alpha
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 502508 410001      482  0.999  3.111  0.636   2.50   2.53
##  .25     .50     .75     .90     .95
##  2.65    2.95    3.35   4.00   4.37
##
## lowest : 2.50 2.51 2.52 2.53 2.54, highest: 7.83 7.88 7.94 8.00 9.00
## -----
## both_od_alpha
##      n missing distinct      Info      Mean      Gmd
## 502508 410001      7   0.675  1.45   0.672
##
## Value      1      2      3      4      5      6      7
## Frequency 341634 109399 39914 9748  1662   147    4
## Proportion 0.680 0.218 0.079 0.019 0.003 0.000 0.000
## -----
## both_minutes
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 502508 410001      301  0.996 225.9 347.6   -60   -60
##  .25     .50     .75     .90     .95
##  0       65     330    815   1055
##
## lowest : -60  -55  -50  -45  -40, highest: 1420 1425 1430 1435 1440
## -----
## soi_alteredmentalstatus
##      n missing distinct      Info      Sum      Mean      Gmd
## 614401 298108      2   0.148 32028  0.05213  0.09882
##
## -----
## soi_glucose
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 614401 298108      121  0.873  0.5743  0.4798   0.0     0.0
##  .25     .50     .75     .90     .95
##  0.0     0.8     1.0     1.0     1.0
##
## lowest : 0.0000000 0.0100000 0.0200000 0.0300000 0.03333333
## highest: 0.96666667 0.97000000 0.98000000 0.99000000 1.00000000
## -----
## soi_heartrate
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 614401 298108      21   0.896  0.6629  0.4226   0.0     0.0

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##      .25      .50      .75      .90      .95
##      0.3       0.9      1.0      1.0      1.0
##
## lowest : 0.00 0.05 0.10 0.15 0.20, highest: 0.80 0.85 0.90 0.95 1.00
## -----
## soi_inr
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 614401 298108        61      0.57    0.1606    0.2655      0       0
##      .25      .50      .75      .90      .95
##      0       0       0       1       1
##
## lowest : 0.00000000 0.01666667 0.03333333 0.05000000 0.06666667
## highest: 0.93333333 0.95000000 0.96666667 0.98333333 1.00000000
## -----
## soi_respiratoryrate
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 614401 298108        53      0.956    0.661    0.3808    0.0000    0.0000
##      .25      .50      .75      .90      .95
##      0.4167   0.7500   1.0000   1.0000   1.0000
##
## lowest : 0.00000000 0.008333333 0.027777778 0.041666667 0.083333333
## highest: 0.94444444 0.958333333 0.972222222 0.983333333 1.00000000
## -----
## soi_temperature
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 614401 298108        257     0.724    0.1621    0.2557      0.0       0.0
##      .25      .50      .75      .90      .95
##      0.0       0.0       0.2       0.7       1.0
##
## lowest : 0.00000000 0.001764706 0.016470588 0.029411765 0.032679739
## highest: 0.980588235 0.982235294 0.982352941 0.997160000 1.000000000
## -----
## soi_bands
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 614401 298108        188     0.168    0.04862   0.09242      0.0       0.0
##      .25      .50      .75      .90      .95
##      0.0       0.0       0.0       0.0       0.5
##
## lowest : 0.00000000 0.00500000 0.01666667 0.01833333 0.02833333
## highest: 0.95166667 0.96000000 0.96666667 0.98333333 1.00000000
## -----
## soi_wbc
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 614401 298108        601     0.943    0.5307    0.4695    0.0000    0.0000
##      .25      .50      .75      .90      .95
##      0.0000   0.5667   1.0000   1.0000   1.0000
##
## lowest : 0.00000000 0.001666667 0.003333333 0.005000000 0.006666667
## highest: 0.993333333 0.995000000 0.996666667 0.998333333 1.000000000
## -----
## soi_lactate
##      n missing distinct      Info      Sum      Mean      Gmd
## 614401 298108        2      0.371    88766    0.1445    0.2472
##
## -----
## od_liver
##      n missing distinct      Info      Sum      Mean      Gmd
## 760467 152042        2      0.294    83849    0.1103    0.1962
##
## -----
## od_cardiovascular
##      n missing distinct      Info      Sum      Mean      Gmd
## 760467 152042        2      0.74    423395    0.5568    0.4936
##
## -----
## od_respiratory
##      n missing distinct      Info      Sum      Mean      Gmd
## 760467 152042        2      0.416    126479    0.1663    0.2773
##
## -----
## od_kidney
##      n missing distinct      Info      Sum      Mean      Gmd
## 760467 152042        2      0.214    58932    0.07749    0.143
##
## -----
## od_lactate
##      n missing distinct      Info      Sum      Mean      Gmd
## 760467 152042        2      0.296    84365    0.1109    0.1973
##

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```

## -----
## od_metabolic
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  760467    152042        2    0.371   110108   0.1448   0.2477
##
## -----
## od_hematologic
##      n    missing   distinct     Info      Sum      Mean      Gmd
##  760467    152042        2    0.018    4548  0.005981   0.01189
##
## -----
## both_soi_alteredmentalstatus
##      n    missing   distinct     Info      Sum      Mean      Gmd
## 502508    410001        2    0.131   22935  0.04564   0.08712
##
## -----
## both_soi_glucose
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 502508    410001       121    0.87   0.5656   0.4832      0.0      0.0
##   .25      .50      .75      .90      .95
##   0.0      0.8      1.0      1.0      1.0
##
## lowest : 0.00000000 0.01000000 0.02000000 0.03000000 0.03333333
## highest: 0.96666667 0.97000000 0.98000000 0.99000000 1.00000000
##
## -----
## both_soi_heartrate
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 502508    410001       21    0.884   0.6666   0.4229      0.0      0.0
##   .25      .50      .75      .90      .95
##   0.3      0.9      1.0      1.0      1.0
##
## lowest : 0.00 0.05 0.10 0.15 0.20, highest: 0.80 0.85 0.90 0.95 1.00
##
## -----
## both_soi_inr
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 502508    410001       61    0.624   0.1812   0.2912      0.0000  0.0000
##   .25      .50      .75      .90      .95
##   0.0000  0.0000  0.1667   1.0000  1.0000
##
## lowest : 0.00000000 0.01666667 0.03333333 0.05000000 0.06666667
## highest: 0.93333333 0.95000000 0.96666667 0.98333333 1.00000000
##
## -----
## both_soi_respiratoryrate
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 502508    410001       51    0.949   0.6678   0.3831      0.0000  0.0000
##   .25      .50      .75      .90      .95
##   0.4167  0.7500   1.0000   1.0000  1.0000
##
## lowest : 0.00000000 0.008333333 0.027777778 0.041666667 0.055555556
## highest: 0.93333333 0.944444444 0.958333333 0.972222222 1.00000000
##
## -----
## both_soi_temperature
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 502508    410001      258    0.744   0.172   0.2677      0.0      0.0
##   .25      .50      .75      .90      .95
##   0.0      0.0      0.2      0.7      1.0
##
## lowest : 0.00000000 0.001764706 0.029411765 0.032679739 0.032941176
## highest: 0.980588235 0.982235294 0.982352941 0.997160000 1.00000000
##
## -----
## both_soi_bands
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 502508    410001      168    0.194   0.05737   0.108      0.0000  0.0000
##   .25      .50      .75      .90      .95
##   0.0000  0.0000  0.0000   0.0000  0.8333
##
## lowest : 0.00000000 0.008333333 0.016666667 0.018333333 0.028333333
## highest: 0.953333333 0.960000000 0.966666667 0.983333333 1.00000000
##
## -----
## both_soi_wbc
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
## 502508    410001      601    0.936   0.5657   0.464      0.0000  0.0000
##   .25      .50      .75      .90      .95
##   0.02333 0.65833   1.00000  1.00000 1.00000
##
## lowest : 0.00000000 0.001666667 0.003333333 0.005000000 0.006666667
## highest: 0.993333333 0.995000000 0.996666667 0.998333333 1.00000000
##
## -----
## both_soi_lactate

```

```

##      n missing distinct      Info      Sum      Mean      Gmd
## 502508 410001       2     0.459    94798   0.1886   0.3061
##
## -----
## both_od_liver
##      n missing distinct      Info      Sum      Mean      Gmd
## 502508 410001       2     0.41     81993   0.1632   0.2731
##
## -----
## both_od_cardiovascular
##      n missing distinct      Info      Sum      Mean      Gmd
## 502508 410001       2     0.745    271953   0.5412   0.4966
##
## -----
## both_od_respiratory
##      n missing distinct      Info      Sum      Mean      Gmd
## 502508 410001       2     0.556    123498   0.2458   0.3707
##
## -----
## both_od_kidney
##      n missing distinct      Info      Sum      Mean      Gmd
## 502508 410001       2     0.234    42853   0.08528   0.156
##
## -----
## both_od_lactate
##      n missing distinct      Info      Sum      Mean      Gmd
## 502508 410001       2     0.459    94798   0.1886   0.3061
##
## -----
## both_od_metabolic
##      n missing distinct      Info      Sum      Mean      Gmd
## 502508 410001       2     0.506    107853   0.2146   0.3371
##
## -----
## both_od_hematologic
##      n missing distinct      Info      Sum      Mean      Gmd
## 502508 410001       2     0.032     5438   0.01082   0.02141
##
## -----
## patientweight
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 898761 13748   13119       1     83.7    27.75   49.80   55.30
##   .25     .50     .75     .90     .95
## 66.00   80.00   96.71   115.67   130.00
##
## lowest :  0.00   0.09   0.27   0.40   0.50, highest: 909.90 949.00 953.00 956.00 969.00
##
## -----
## BMI
##      n missing distinct      Info      Mean      Gmd      .05      .10
## 882077 30432 184910       1     Inf     NaN   18.50   20.29
##   .25     .50     .75     .90     .95
## 23.47   27.55   32.87   39.52   44.84
##
## lowest : 0.000000e+00 1.020408e-02 1.937504e-02 2.547485e-02 1.132216e-01
## highest: 1.352158e+06 1.504164e+06 1.598657e+06 1.999887e+06           Inf
##
## -----
## BMI_Ranges
##      n missing distinct
## 912509       0       5
##
## Value      (0,18.5]    (18.5,25]    (25,35]    (35,200]
## Frequency  44009     257638     416522     162054
## Proportion 0.048      0.282      0.456      0.178
##
## Value      Other/Unknown
## Frequency  32286
## Proportion 0.035
##
## -----
## age_Ranges
##      n missing distinct
## 912509       0       8
##
## Value      (0,25]    (25,35]    (35,45]    (45,55]    (55,65]    (65,75]    (75,85]
## Frequency  30083     45906     67771     136077     191660     200706     165443
## Proportion 0.033     0.050     0.074     0.149      0.210     0.220      0.181
##
## Value      (85,100]
## Frequency  74863
## Proportion 0.082

```

```

## -----
## hospitalLOS_Ranges
##   n missing distinct
##   912506      3      10
##
## Value      (0,1]    (1,3]    (3,5]    (5,10]   (10,20]   (20,30]
## Frequency  42243    201490   185718   274367   152013    36187
## Proportion 0.046     0.221    0.204    0.301    0.167    0.040
##
## Value      (30,60]  (60,90]  (90,150] (150,999]
## Frequency  17656    1914     710      208
## Proportion 0.019     0.002    0.001    0.000
## -----
## icuLOS_Ranges
##   n missing distinct
##   912509      0      8
##
## Value      (0,1]    (1,3]    (3,5]    (5,10]   (10,20]   (20,30]   (30,60]
## Frequency  222500   426937   128031   89011    36285    7092     2475
## Proportion 0.244     0.468    0.140    0.098    0.040    0.008    0.003
##
## Value      (60,999]
## Frequency  178
## Proportion 0.000
## -----
## ethnicity2
##   n missing distinct
##   912509      0      6
##
## Value      Caucasian African American Hispanic
## Frequency  695367      105292      41393
## Proportion 0.762       0.115       0.045
##
## Value      Asian Native American Other/Unknown
## Frequency  11695       6765       51997
## Proportion 0.013       0.007       0.057
## -----
## gender2
##   n missing distinct
##   912509      0      3
##
## Value      Male Female Other/Unknown
## Frequency  490533     421748      228
## Proportion 0.538       0.462       0.000
## -----
## hospital_region2
##   n missing distinct
##   912509      0      5
##
## Value      Midwest Northeast South West Unknown
## Frequency  383075     73523     283987   116783    55141
## Proportion 0.420       0.081       0.311     0.128     0.060
## -----
## sepsis_outcome
##   n missing distinct
##   912509      0      2
##
## Value      FALSE  TRUE
## Frequency  725639  186870
## Proportion 0.795   0.205
## -----
## group
##   n missing distinct
##   912509      0      12
##
## Cardiovascular (295348, 0.324), Gastrointestinal (94673, 0.104),
## Gynaecological (2410, 0.003), Hematological (6819, 0.007), Metabolic
## (74865, 0.082), Musculoskeletal/Skin disease (11455, 0.013), Neurological
## (122910, 0.135), Renal/Genitourinary (22125, 0.024), Respiratory (136055,
## 0.149), Sepsis (97598, 0.107), Trauma (40495, 0.044), Undefined (7756,
## 0.008)
## -----
## post.operative
##   n missing distinct Info Sum Mean Gmd
##   912509      0      2  0.459  172015  0.1885  0.3059
##
## -----
## code
##   n missing distinct Info Mean Gmd .05 .10

```

```

##   912509      0    378    0.999    531    482.9    104    106
##   .25      .50    .75    .90    .95
##   201     403    703   1212   1413
##
## lowest :   0.01   0.02   0.03   0.04   0.05
## highest: 2201.01 2201.02 2201.03 2201.04 2201.05
## -----
## dx
##   n missing distinct
##   912509      0    378
##
## lowest : Abdomen/extremity trauma          Abdomen/face trauma
Abdomen/multiple trauma                      Abdomen only trauma
Abdomen/pelvis trauma
## highest: Vena cava clipping                Vena cava filer inser
tion                                         Ventriculostomy
Weaning from mechanical ventilation (transfer from other unit or hospital only) Whipple surgery for pancreatic ca
ncer
## -----
## number
##   n missing distinct      Info      Mean      Gmd
##   912509      0       6    0.165    1.147    0.2811
##
## Value      1      2      3      4      5      6
## Frequency 859197 16144 11817 11814 9081 4456
## Proportion 0.942 0.018 0.013 0.013 0.010 0.005
## -----
## admitdiagnosis
##   n missing distinct
##   912509      0    401
##
## lowest : ACIDBASE ACUHEPFAIL ADDISON ADRENNEO AIROBSTRX
## highest: UNSTANGINA VARICBLEED VASCULITIS VIRALMYOSI WEANVENT
## -----
## admitdxpath
##   n missing distinct
##   912509      0    401
##
## lowest :
admission diagnosis|All Diagnosis|Non-operative|Diagnosis|Cardiovascular|Anaphylaxis
admission diagnosis|All Diagnosis|Non-operative|Diagnosis|Cardiovascular|Aneurysm, dissecting aortic
admission diagnosis|All Diagnosis|Non-operative|Diagnosis|Cardiovascular|Aneurysm/pseudoaneurysm, other
admission diagnosis|All Diagnosis|Non-operative|Diagnosis|Cardiovascular|Angina, stable (asymp or stable pattern
of symptoms w/meds)
## highest: admission diagnosis|All Diagnosis|Operative|Diagnosis|Trauma|Extremity/multiple trauma, surgery for
admission diagnosis|All Diagnosis|Operative|Diagnosis|Trauma|Extremity only trauma, surgery for
admission diagnosis|All Diagnosis|Operative|Diagnosis|Trauma|Face/multiple trauma, surgery for
admission diagnosis|All Diagnosis|Operative|Diagnosis|Trauma|Face only trauma, surgery for
admission diagnosis|All Diagnosis|Operative|Diagnosis|Trauma|Trauma surgery, other
## -----
## numobs
##   n missing distinct      Info      Mean      Gmd      .05      .10
##   911985      524    235        1    2610    2596      54     138
##   .25      .50    .75    .90    .95
##   548     2110    4389    6262    6790
##
## lowest :   0      1      2      3      4, highest: 5003 5989 6262 6790 8375
## -----
## possible.group
##   n missing distinct      Info      Mean      Gmd
##   7451    905055        8    0.868    1030    589.9
##
## Value      312.00  408.02  602.09  802.00 1208.00 1504.00 1701.00 1705.03
## Frequency  2110     678      12     345     348     3551     178     232
## Proportion 0.283    0.091    0.002    0.046    0.047    0.476    0.024    0.031
## -----
## X
##   n missing distinct
##   912509      0     13
##
## lowest :
addition                                     ANZICS
gories won't map well, but collapsing to hierarchy (1206) should work ANZICS addition -- we have invented this dia
gnosis code                                     ANZICS Addition. Sub-cate
assumes admitted in eICU due to rejection
## highest: Chest pain, unknown origin           fuzzy
match                                         multiple matches
presumably ANZICS only allows the surgical version of this code
ries for this in eICU                         there are 6 catego
## -----

```

```

## c_temp_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  895122     17387     1044  0.996   36.29  0.7768   35.1    35.6
##    .25      .50      .75    .90    .95
##    36.1     36.4     36.7   36.9    37.1
##
## lowest :  0.1  0.2  0.5  0.6  0.8, highest: 100.3 100.7 100.8 100.9 101.0
## -----
## c_temp_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  895122     17387     757  0.997   37.32  0.8268   36.40   36.60
##    .25      .50      .75    .90    .95
##   36.90    37.17    37.60   38.20   38.70
##
## lowest :  0.10 19.90 21.70 24.40 27.40, highest: 104.50 105.55 105.80 107.20 111.20
## -----
## c_HR_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0    274    1  102.9   24.95    70     76
##    .25      .50      .75    .90    .95
##    87      101     116   132    143
##
## lowest :  5  7  14  15  18, highest: 320 347 360 361 379
## -----
## c_resp_max
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0    181  0.998   28.01   9.715    18     19
##    .25      .50      .75    .90    .95
##    22      26      31    39     46
##
## lowest :  1  2  3  4  5, highest: 187 194 196 197 199
## -----
## c_sbp_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912325     184     271    1  92.14   26.45    52     62
##    .25      .50      .75    .90    .95
##    78      92     107   121    131
##
## lowest :  1  2  3  4  5, highest: 240 244 246 248 256
## -----
## c_mbp_min
##      n    missing   distinct     Info      Mean      Gmd      .05      .10
##  912509       0    282    1  66.76   21.4     41     46
##    .25      .50      .75    .90    .95
##    54      64      75    89    104
##
## lowest :  0.13  0.61  0.74  0.87  1.00, highest: 198.00 199.00 200.00 232.00 287.00
## -----
## icu_admit_source2
##      n    missing   distinct
##  912509       0      6
##
## Value          Floor        OR/Proc Area      Direct Admit
## Frequency      154636      176443           98038
## Proportion     0.169       0.193            0.107
##
## Value          Emergency Department      Other      Step-Down Unit
## Frequency      456475       7763            19154
## Proportion     0.500        0.009           0.021
##
## icu_type2
##      n    missing   distinct
##  912509       0      8
##
## Trauma ICU (10946, 0.012), Cardiac Care ICU (65472, 0.072),
## Cardiac/Surgical Care ICU (141274, 0.155), Medical/Surgical ICU (468867,
## 0.514), Medical ICU (86772, 0.095), Other ICU (2616, 0.003), Neuro ICU
## (71250, 0.078), Surgical ICU (65312, 0.072)
## -----
## icu_disch_location2
##      n    missing   distinct
##  912509       0      7
##
## Value          Floor        Death      Home      SNF/Rehab
## Frequency      665016      61357      88591      14116
## Proportion     0.729       0.067      0.097      0.015
##
## Value          Other Other Hospital Step-Down Unit
## Frequency      29315       20636      33478

```

```

## Proportion      0.032      0.023      0.037
##
## physicianSpeciality2
##   n missing distinct
##  912509      0      2
##
## Value      Critical Care Speciality-Other
## Frequency      267236      645273
## Proportion      0.293      0.707
##
## sofa_respiration_baseline2
##   n missing distinct
##  912509      0      2
##
## Value      FALSE  TRUE
## Frequency    692652  219857
## Proportion    0.759  0.241
##
## sofa_renal_baseline2
##   n missing distinct
##  912509      0      2
##
## Value      FALSE  TRUE
## Frequency    881875  30634
## Proportion    0.966  0.034
##
## sofa_liver_baseline2
##   n missing distinct
##  912509      0      2
##
## Value      FALSE  TRUE
## Frequency    893444  19065
## Proportion    0.979  0.021
##
## SOFA_Change
##   n missing distinct      Info      Mean      Gmd      .05      .10
##  912509      0      24     0.98     3.519     3.134      0       1
##  .25      .50      .75     .90      .95
##  1       3       5      8       9
##
## lowest :  0  1  2  3  4, highest: 19  20  21  22  23
##
## SOFA_Positive
##   n missing distinct
##  912509      0      2
##
## Value      FALSE  TRUE
## Frequency    284293  628216
## Proportion    0.312  0.688
##
## SOFA_Score
##   n missing distinct      Info      Mean      Gmd      .05      .10
##  912509      0      24     0.983     3.77     3.341      0       1
##  .25      .50      .75     .90      .95
##  1       3       5      8      10
##
## lowest :  0  1  2  3  4, highest: 19  20  21  22  23
##
## SOFA_Positive2
##   n missing distinct
##  912509      0      2
##
## Value      FALSE  TRUE
## Frequency    267445  645064
## Proportion    0.293  0.707
##
## GCS_qSOFA
##   n missing distinct
##  912509      0      2
##
## Value      FALSE  TRUE
## Frequency    533497  379012
## Proportion    0.585  0.415
##
## BP_qSOFA
##   n missing distinct
##  912325     184      2
##
## Value      FALSE  TRUE

```

```

## Frequency 314799 597526
## Proportion 0.345 0.655
##
## -----
## Resp_qSOFA
##      n missing distinct
##  912509      0      2
##
## Value FALSE TRUE
## Frequency 208008 704501
## Proportion 0.228 0.772
##
## -----
## qSOFA_total
##      n missing distinct      Info      Mean      Gmd
##  912509      0      4    0.889    1.842    0.9391
##
## Value      0      1      2      3
## Frequency 64765 234728 392737 220279
## Proportion 0.071 0.257 0.430 0.241
##
## -----
## qSOFA_Positive
##      n missing distinct
##  912509      0      2
##
## Value FALSE TRUE
## Frequency 299493 613016
## Proportion 0.328 0.672
##
## -----
## temp_SIRS
##      n missing distinct
##  895122    17387      2
##
## Value FALSE TRUE
## Frequency 618206 276916
## Proportion 0.691 0.309
##
## -----
## wbc_SIRS
##      n missing distinct
##  794753   117756      2
##
## Value FALSE TRUE
## Frequency 424426 370327
## Proportion 0.534 0.466
##
## -----
## resp_SIRS
##      n missing distinct
##  912509      0      2
##
## Value FALSE TRUE
## Frequency 149689 762820
## Proportion 0.164 0.836
##
## -----
## HR_SIRS
##      n missing distinct
##  912509      0      2
##
## Value FALSE TRUE
## Frequency 284634 627875
## Proportion 0.312 0.688
##
## -----
## SIRS_total
##      n missing distinct      Info      Mean      Gmd
##  912509      0      5    0.924    2.233    1.157
##
## Value      0      1      2      3      4
## Frequency 49299 169356 319467 267900 106487
## Proportion 0.054 0.186 0.350 0.294 0.117
##
## -----
## SIRS_Positive
##      n missing distinct
##  912509      0      2
##
## Value FALSE TRUE
## Frequency 218655 693854
## Proportion 0.24 0.76
##
## -----
## StickyMinutes
##      n missing distinct      Info      Mean      Gmd      .05      .10
##  540443 372066    301    0.997    252.6   371.6    -60     -60
##      .25      .50      .75      .90      .95

```

```

##      5     80     400     865    1095
##
## lowest : -60 -55 -50 -45 -40, highest: 1420 1425 1430 1435 1440
## -----
## FuzzyTotal1
##      n missing distinct   Info   Mean   Gmd
## 912509      0        3  0.758  1.507  0.6395
##
## Value      0     1     2
## Frequency 78084 293982 540443
## Proportion 0.086 0.322 0.592
## -----
## SimultaneousMinutes
##      n missing distinct
## 912509      0        2
##
## Value      FALSE  TRUE
## Frequency 410001 502508
## Proportion 0.449 0.551
## -----
## SepsisFuzzyLogicPositive
##      n missing distinct
## 912509      0        2
##
## Value      FALSE  TRUE
## Frequency 410001 502508
## Proportion 0.449 0.551
## -----
## SepsisFuzzyLogicPositive2
##      n missing distinct
## 912509      0        2
##
## Value      FALSE  TRUE
## Frequency 410001 502508
## Proportion 0.449 0.551
## -----
## hasDiagnosisCodes
##      n missing distinct   value
## 912509      0        1     TRUE
##
## Value      TRUE
## Frequency 912509
## Proportion 1
## -----
## 
## Variables with all observations missing:
## 
## [1] hospital_type icu_size

```

17 Seeding/Splitting

Setting the seed and splitting into datasets for training and testing the model

```

#install.packages("caret")
library(caret); library(Hmisc)

## 
## Attaching package: 'caret'

## The following object is masked from 'package:purrr':
## 
##     lift

## The following object is masked from 'package:survival':
## 
##     cluster

set.seed(999)

ssd_incl <- ssd_incl %>% mutate(SOFA_Change=cut2(SOFA_Change, seq(0,18)))

datasplit <- createDataPartition(ssd_incl$hospital_mortality_ultimate==1,times=1,p=0.7)
ssd_incl_tr <- ssd_incl[datasplit[[1]],]
nrow(ssd_incl_tr)

```

```
## [1] 638757

ssd_incl_tr$hospital_mortality_ultimate<-as.factor (ssd_incl_tr$hospital_mortality_ultimate)
ssd_incl_tr$sepsis_outcome<-as.factor (ssd_incl_tr$sepsis_outcome)
```

18 Baseline Mortality

GLM and Train on training set and predictions/performance (ROC, SENS, SPEC, PPV, NPV, accuracy) on test set

```
library(sjPlot); library(ROCR); library(Hmisc); library(pROC); library(randomForest)
```

```
## Loading required package: gplots
```

```
##
## Attaching package: 'gplots'
```

```
## The following object is masked from 'package:stats':
##
##     lowess
```

```
## Type 'citation("pROC")' for a citation.
```

```
##
## Attaching package: 'pROC'
```

```
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
```

```
## randomForest 4.6-12
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
##
## Attaching package: 'randomForest'
```

```
## The following object is masked from 'package:ggplot2':
##
##     margin
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
Baseline_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_adm
it_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischargeyear + dialysis +
aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer + thrombolytics + s
ofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.action = na.omit)
```

```
#sjp.glm(Baseline_Hosp_Mort_tr)
#sjt.glm(Baseline_Hosp_Mort_tr)
```

```
#drop1(Baseline_Hosp_Mort_tr,test="Chisq")
```

```
summary(Baseline_Hosp_Mort_tr)
```

```

## 
## Call:
## glm(formula = hospital_mortality_ultimate ~ age_Ranges + gender2 +
##     ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status +
##     hospital_size + physicianSpeciality2 + hospitaldischargeyear +
##     dialysis + aids + hepaticfailure + diabetes + immunosuppression +
##     leukemia + lymphoma + metastaticcancer + thrombolytics +
##     sofa_respiration_baseline2 + cardiovascular_baseline, family = "binomial",
##     data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.6276   -0.4936   -0.3733   -0.2677   3.1470
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -2.250932  0.050527 -44.549
## age_Ranges(25,35]            0.229442  0.049062  4.677
## age_Ranges(35,45]            0.418396  0.045277  9.241
## age_Ranges(45,55]            0.757457  0.041906 18.075
## age_Ranges(55,65]            1.026053  0.041085 24.974
## age_Ranges(65,75]            1.282694  0.040902 31.360
## age_Ranges(75,85]            1.578865  0.040839 38.661
## age_Ranges(85,100]           1.824671  0.041638 43.822
## gender2Female               -0.067416  0.008936 -7.544
## gender2Other/Unknown         1.840225  0.177099 10.391
## ethnicity2African American -0.006201  0.014720 -0.421
## ethnicity2Hispanic           0.075543  0.021220  3.560
## ethnicity2Asian              0.140192  0.037547  3.734
## ethnicity2Native American   0.413400  0.048960  8.444
## ethnicity2Other/Unknown     0.196662  0.018991 10.355
## BMI_Ranges(18.5,25]          -0.328096  0.018575 -17.663
## BMI_Ranges(25,35]            -0.504116  0.018321 -27.516
## BMI_Ranges(35,200]           -0.375889  0.020472 -18.361
## BMI_RangesOther/Unknown     -0.051990  0.026790 -1.941
## icu_admit_source2OR/Proc Area -1.475248  0.017523 -84.191
## icu_admit_source2Direct Admit -0.393215  0.015587 -25.227
## icu_admit_source2Emergency Department -0.489498  0.010756 -45.509
## icu_admit_source2Other       -0.093568  0.040517 -2.309
## icu_admit_source2Step-Down Unit 0.167136  0.024843  6.728
## hospital_teaching_statusf   -0.053537  0.032153 -1.665
## hospital_teaching_statust   -0.144347  0.032493 -4.442
## hospital_size<100           -0.560120  0.036404 -15.386
## hospital_size100-249         -0.057453  0.025300 -2.271
## hospital_size250-500         0.085279  0.025555  3.337
## hospital_size>500            0.229786  0.023791  9.659
## physicianSpeciality2Speciality-Other -0.431226  0.009850 -43.778
## hospitaldischargeyear2011   -0.024672  0.016825 -1.466
## hospitaldischargeyear2012   -0.070520  0.016231 -4.345
## hospitaldischargeyear2013   -0.121428  0.015964 -7.607
## hospitaldischargeyear2014   -0.172203  0.015908 -10.825
## hospitaldischargeyear2015-16 -0.139292  0.015732 -8.854
## dialysis1                   0.330458  0.022266 14.841
## aids1                        0.556828  0.117003  4.759
## hepaticfailureTRUE           0.760290  0.024386 31.178
## diabetes1                   -0.279194  0.011551 -24.170
## immunosuppression1           0.379349  0.025108 15.108
## leukemial                    0.511737  0.039519 12.949
## lymphomal                    0.287931  0.056424  5.103
## metastaticcancer1            0.681493  0.026194 26.017
## thrombolytics1               -0.034820  0.034356 -1.014
## sofa_respiration_baseline2TRUE 0.086748  0.010077  8.608
## cardiovascular_baseline1    0.110204  0.010275 10.726
##
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## age_Ranges(25,35] 2.92e-06 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female 4.55e-14 ***
## gender2Other/Unknown < 2e-16 ***
## ethnicity2African American 0.673568
## ethnicity2Hispanic 0.000371 ***
## ethnicity2Asian 0.000189 ***
## ethnicity2Native American < 2e-16 ***

```

```

## ethnicity2Other/Unknown < 2e-16 ***
## BMI_Ranges(18.5,25] < 2e-16 ***
## BMI_Ranges(25,35] < 2e-16 ***
## BMI_Ranges(35,200] < 2e-16 ***
## BMI_RangesOther/Unknown 0.052304 .
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other 0.020926 *
## icu_admit_source2Step-Down Unit 1.72e-11 ***
## hospital_teaching_statusf 0.095900 .
## hospital_teaching_statust 8.90e-06 ***
## hospital_size<100 < 2e-16 ***
## hospital_size100-249 0.023158 *
## hospital_size250-500 0.000847 ***
## hospital_size>500 < 2e-16 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 0.142539
## hospitaldischargeyear2012 1.40e-05 ***
## hospitaldischargeyear2013 2.81e-14 ***
## hospitaldischargeyear2014 < 2e-16 ***
## hospitaldischargeyear2015-16 < 2e-16 ***
## dialysis1 < 2e-16 ***
## aids1 1.94e-06 ***
## hepaticfailureTRUE < 2e-16 ***
## diabetes1 < 2e-16 ***
## immunosuppression1 < 2e-16 ***
## leukemial < 2e-16 ***
## lymphomal 3.34e-07 ***
## metastaticcancer1 < 2e-16 ***
## thrombolytics1 0.310814
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603 on 638756 degrees of freedom
## Residual deviance: 370829 on 638710 degrees of freedom
## AIC: 370923
##
## Number of Fisher Scoring iterations: 6

```

```

ssd_incl_te <- ssd_incl[-datasplit[[1]],]
nrow(ssd_incl_te)

```

```

## [1] 273752

```

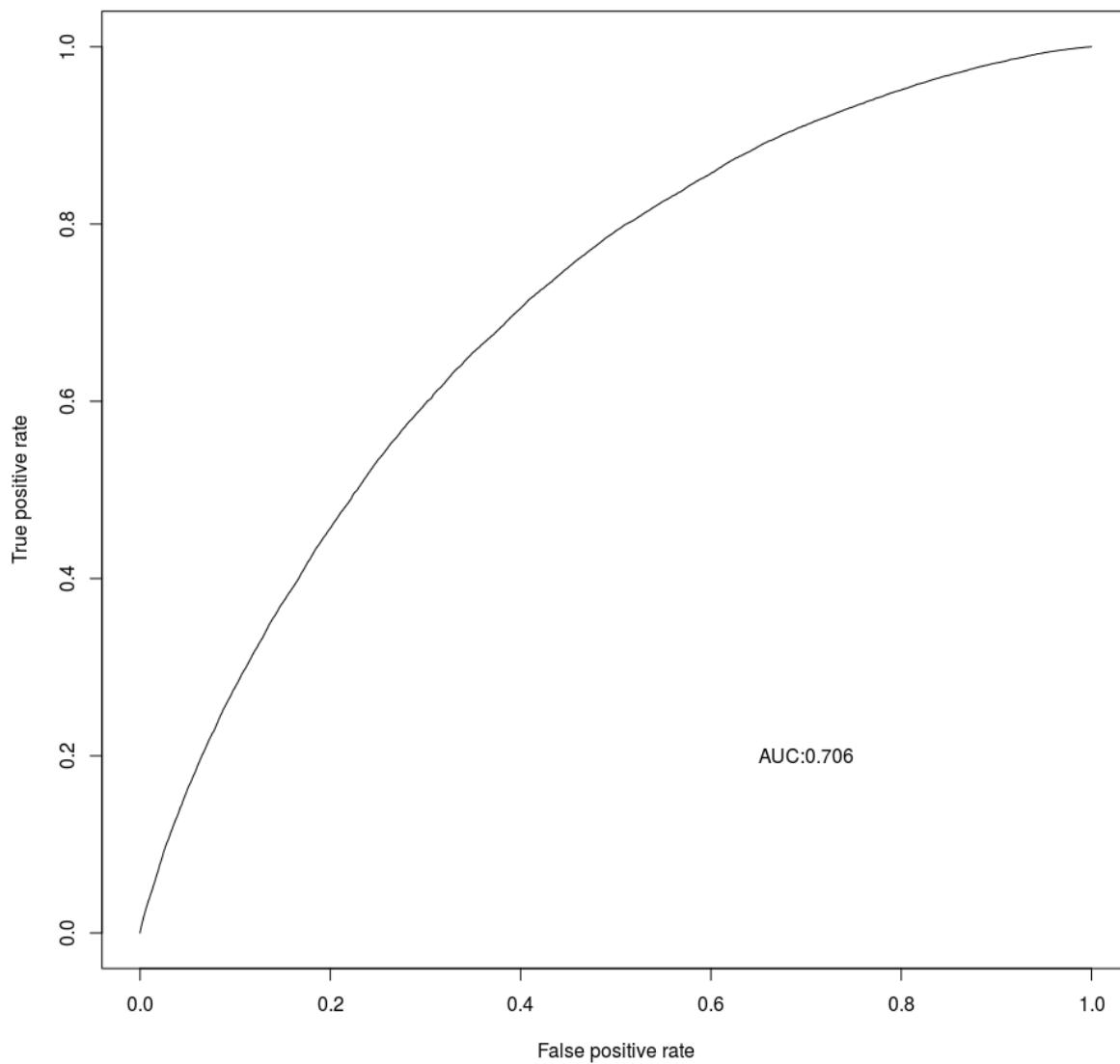
```

ssd_incl_te$BaselineHospMortPred <- predict(Baseline_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
ssd_incl_te$BaselineDec <- cut2(ssd_incl_te$BaselineHospMortPred, g=10)

BaselineMort.Pred <- prediction(ssd_incl_te$BaselineHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
BaselineMort.Perf <- performance(BaselineMort.Pred, "tpr", "fpr")
plot(BaselineMort.Perf, main = "Baseline Mortality
Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(BaselineMort.Pred,"auc")@y.values[[1]],3)))

```

Baseline Mortality Prediction Test Model



```
performance(BaselineMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7063341
##
## Slot "alpha.values":
## list()
```

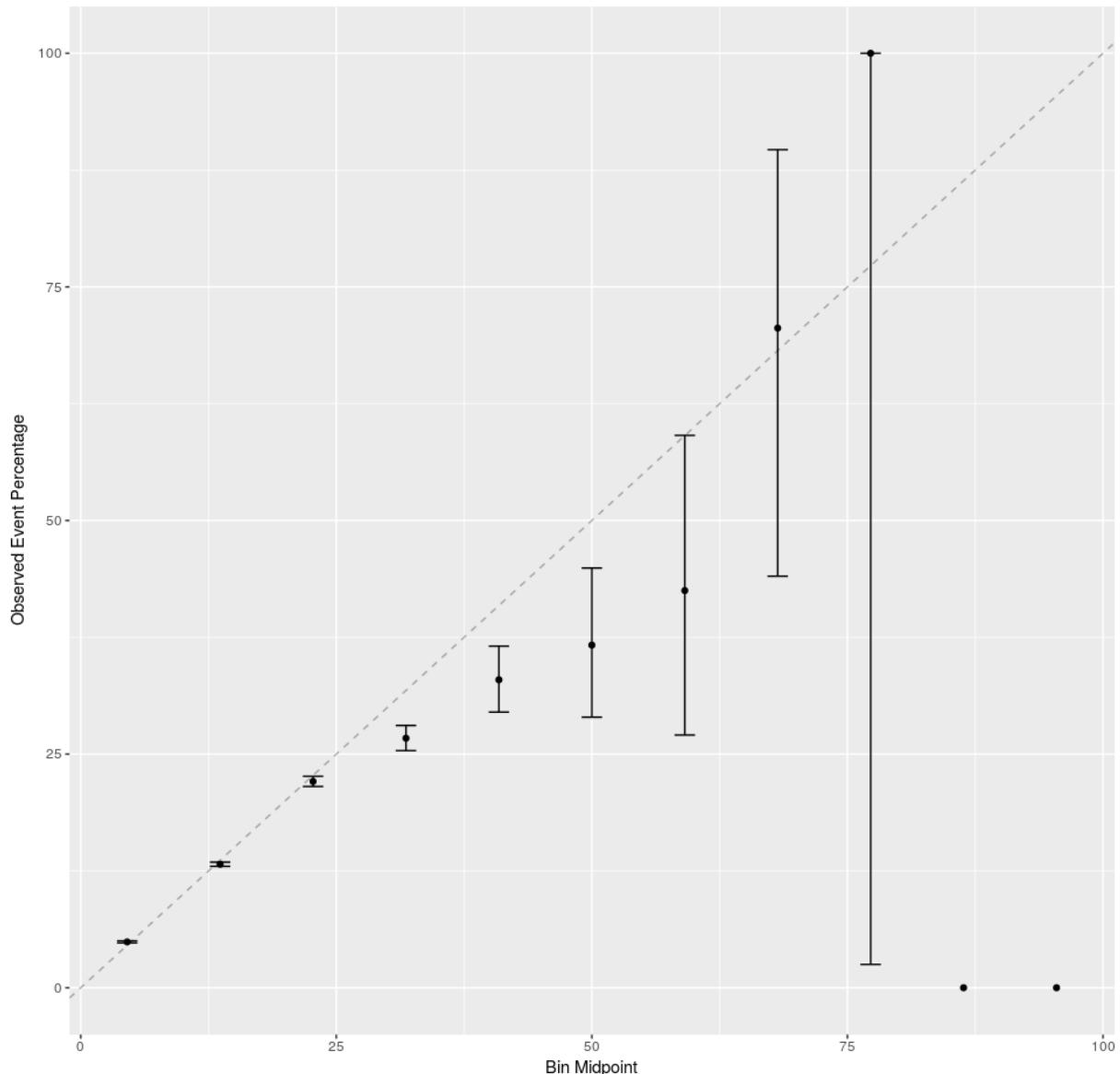
```
BaselineMort.Pred.roc <- roc(hospital_mortality_ultimate~BaselineHospMortPred,data=ssd_incl_te,algorithm=3,ci=TRUE)
try(ci(BaselineMort.Pred.roc, conf.level=0.99))
```

```
## 99% CI: 0.7021-0.7105 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~BaselineHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of Baseline Mortality Prediction")
```

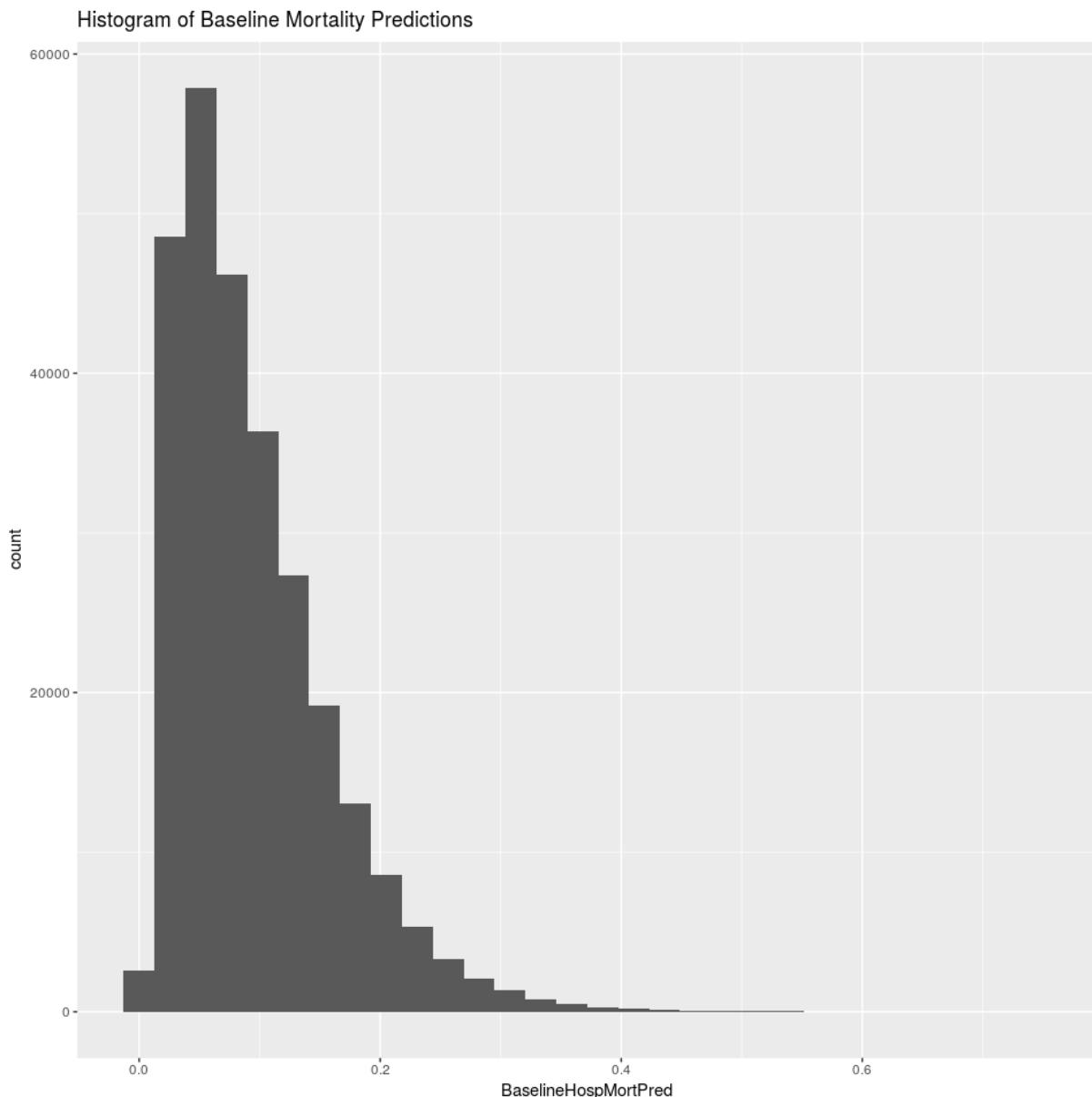
```
## Warning: Removed 2 rows containing missing values (geom_errorbar).
```

Calibration of Baseline Mortality Prediction



```
qplot(BaselineHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of Baseline Mortality Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



19 Cross validation

partitions the data into 5 groups and then uses the 4 groups to predict the 5th group. It does this 5 times and then takes the average, ROC curves,

Train/glm completed on the train dataset; prediction and performance completed on the test dataset.

```
SIRS1_ADJ_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(SIRS_total) + age_Ranges + gender2 + ethnicit
y2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitald
ischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastati
ccancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomia
l",na.action = na.omit)

#sjp.glm(SIRS1_ADJ_Hosp_Mort_tr)
#sjt.glm(SIRS1_ADJ_Hosp_Mort_tr)

#drop1(SIRS1_ADJ_Hosp_Mort_tr,test="Chisq")

summary(SIRS1_ADJ_Hosp_Mort_tr)
```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(SIRS_total) +
##     age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 +
##     hospital_teaching_status + hospital_size + physicianSpeciality2 +
##     hospitaldischargeyear + dialysis + aids + hepaticfailure +
##     diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer +
##     thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline,
##     family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q  Median      3Q     Max
## -1.9172 -0.4682 -0.3119 -0.1981  3.5016
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -4.4033273  0.0669083 -65.811
## as.factor(SIRS_total)1        0.5500217  0.0456838  12.040
## as.factor(SIRS_total)2        1.3688529  0.0433032  31.611
## as.factor(SIRS_total)3        2.1573331  0.0430423  50.121
## as.factor(SIRS_total)4        2.9515996  0.0434567  67.920
## age_Ranges(25,35]            0.2570893  0.0496437  5.179
## age_Ranges(35,45]            0.4780080  0.0458350 10.429
## age_Ranges(45,55]            0.8663145  0.0424222 20.421
## age_Ranges(55,65]            1.1531623  0.0415890 27.728
## age_Ranges(65,75]            1.4393826  0.0414225 34.749
## age_Ranges(75,85]            1.7665530  0.0413879 42.683
## age_Ranges(85,100]           2.0380748  0.0422738 48.211
## gender2Female                -0.0819955  0.0092092 -8.904
## gender2Other/Unknown          1.6827393  0.1915034  8.787
## ethnicity2African American    0.0242863  0.0151634  1.602
## ethnicity2Hispanic             0.0695744  0.0219392  3.171
## ethnicity2Asian                0.1390930  0.0388335  3.582
## ethnicity2Native American      0.3755676  0.0506218  7.419
## ethnicity2Other/Unknown         0.2039346  0.0196154 10.397
## BMI_Ranges(18.5,25]           -0.2889067  0.0192326 -15.022
## BMI_Ranges(25,35]              -0.4412794  0.0189637 -23.270
## BMI_Ranges(35,200]             -0.3240074  0.0211512 -15.319
## BMI_RangesOther/Unknown        0.1534701  0.0278737  5.506
## icu_admit_source2OR/Proc Area -1.5161274  0.0178884 -84.755
## icu_admit_source2Direct Admit -0.2696384  0.0161692 -16.676
## icu_admit_source2Emergency Department -0.3857470  0.0111422 -34.620
## icu_admit_source2Other         -0.1105148  0.0419398 -2.635
## icu_admit_source2Step-Down Unit 0.1265906  0.0257888  4.909
## hospital_teaching_statusf     -0.0858692  0.0331260 -2.592
## hospital_teaching_statust     -0.2064886  0.0336210 -6.142
## hospital_size<100             -0.4533840  0.0372893 -12.159
## hospital_size100-249           0.0006072  0.0260174  0.023
## hospital_size250-500           0.0593403  0.0262684  2.259
## hospital_size>500              0.2299083  0.0245490  9.365
## physicianSpeciality2Speciality-Other -0.2499178  0.0101859 -24.536
## hospitaldischargeyear2011      -0.0510514  0.0174171 -2.931
## hospitaldischargeyear2012      -0.0858751  0.0167892 -5.115
## hospitaldischargeyear2013      -0.1243127  0.0165072 -7.531
## hospitaldischargeyear2014      -0.1521628  0.0164394 -9.256
## hospitaldischargeyear2015-16   -0.1431594  0.0162584 -8.805
## dialysis1                      0.3714920  0.0230898 16.089
## aids1                           0.4083058  0.1206597  3.384
## hepaticfailureTRUE               0.7758289  0.0253976 30.547
## diabetes1                       -0.2798912  0.0118792 -23.561
## immunosuppression1              0.2714149  0.0259178 10.472
## leukemial                        0.2929703  0.0409368  7.157
## lymphomal                         0.1928275  0.0583328  3.306
## metastaticcancer1                0.6544569  0.0271533 24.102
## thrombolytics1                   0.1077904  0.0355692  3.030
## sofa_respiration_baseline2TRUE   0.0299530  0.0103894  2.883
## cardiovascular_baseline1         0.1949686  0.0106352 18.332
##
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## as.factor(SIRS_total)1 < 2e-16 ***
## as.factor(SIRS_total)2 < 2e-16 ***
## as.factor(SIRS_total)3 < 2e-16 ***
## as.factor(SIRS_total)4 < 2e-16 ***
## age_Ranges(25,35] 2.23e-07 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***

```

```

## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female < 2e-16 ***
## gender2Other/Unknown < 2e-16 ***
## ethnicity2African American 0.109234
## ethnicity2Hispanic 0.001518 **
## ethnicity2Asian 0.000341 ***
## ethnicity2Native American 1.18e-13 ***
## ethnicity2Other/Unknown < 2e-16 ***
## BMI_Ranges(18.5,25] < 2e-16 ***
## BMI_Ranges(25,35] < 2e-16 ***
## BMI_Ranges(35,200] < 2e-16 ***
## BMI_RangesOther/Unknown 3.67e-08 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other 0.008412 **
## icu_admit_source2Step-Down Unit 9.17e-07 ***
## hospital_teaching_statusf 0.009536 **
## hospital_teaching_statust 8.17e-10 ***
## hospital_size<100 < 2e-16 ***
## hospital_size100-249 0.981380
## hospital_size250-500 0.023883 *
## hospital_size>500 < 2e-16 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 0.003378 **
## hospitaldischargeyear2012 3.14e-07 ***
## hospitaldischargeyear2013 5.04e-14 ***
## hospitaldischargeyear2014 < 2e-16 ***
## hospitaldischargeyear2015-16 < 2e-16 ***
## dialysis1 < 2e-16 ***
## aids1 0.000715 ***
## hepaticfailureTRUE < 2e-16 ***
## diabetes1 < 2e-16 ***
## immunosuppression1 < 2e-16 ***
## leukemial 8.27e-13 ***
## lymphomal 0.000948 ***
## metastaticcancer1 < 2e-16 ***
## thrombolytics1 0.002442 **
## sofa_respiration_baseline2TRUE 0.003939 **
## cardiovascular_baseline1 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603 on 638756 degrees of freedom
## Residual deviance: 342338 on 638706 degrees of freedom
## AIC: 342440
##
## Number of Fisher Scoring iterations: 6

```

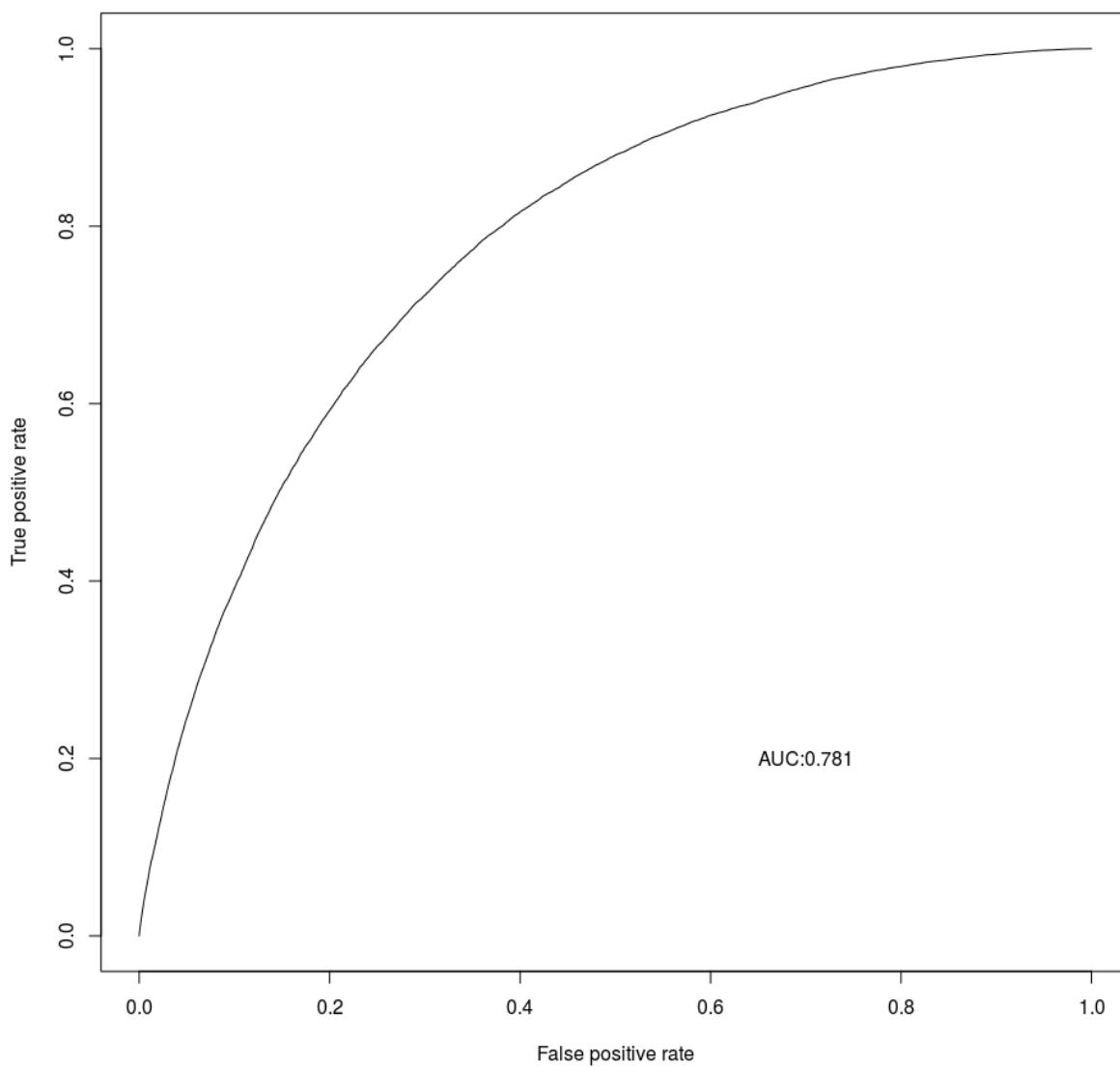
```

ssd_incl_te$SIRS1ADJHospMortPred <- predict(SIRS1_ADJ_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")

SIRS1ADJMort.Pred <- prediction(ssd_incl_te$SIRS1ADJHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
SIRS1ADJMort.Perf <- performance(SIRS1ADJMort.Pred, "tpr", "fpr")
plot(SIRS1ADJMort.Perf, main = "SIRS Continuous Adjusted Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SIRS1ADJMort.Pred,"auc")@y.values[[1]],3)))

```

**SIRS Continuous Adjusted
Mortality Prediction Test Model**



```
performance(SIRS1ADJMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.781489
##
## Slot "alpha.values":
## list()
```

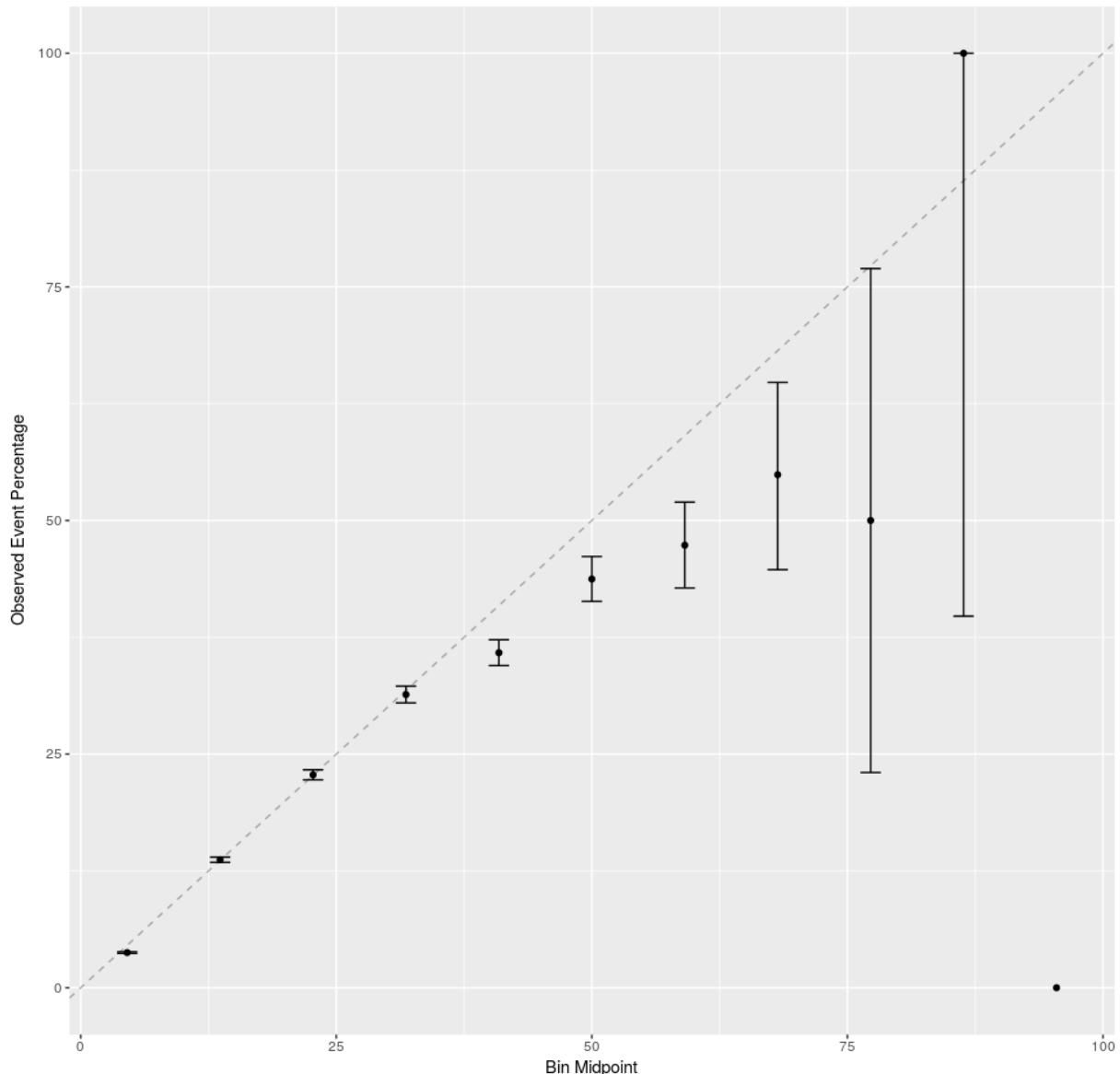
```
SIRS1ADJMort.Pred.roc <- roc(hospital_mortality_ultimate~ SIRS1ADJHospMortPred,data=ssd_incl_te)
ci(SIRS1ADJMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7779-0.7851 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~SIRS1ADJHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of ADJ Mortality SIRS Total Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

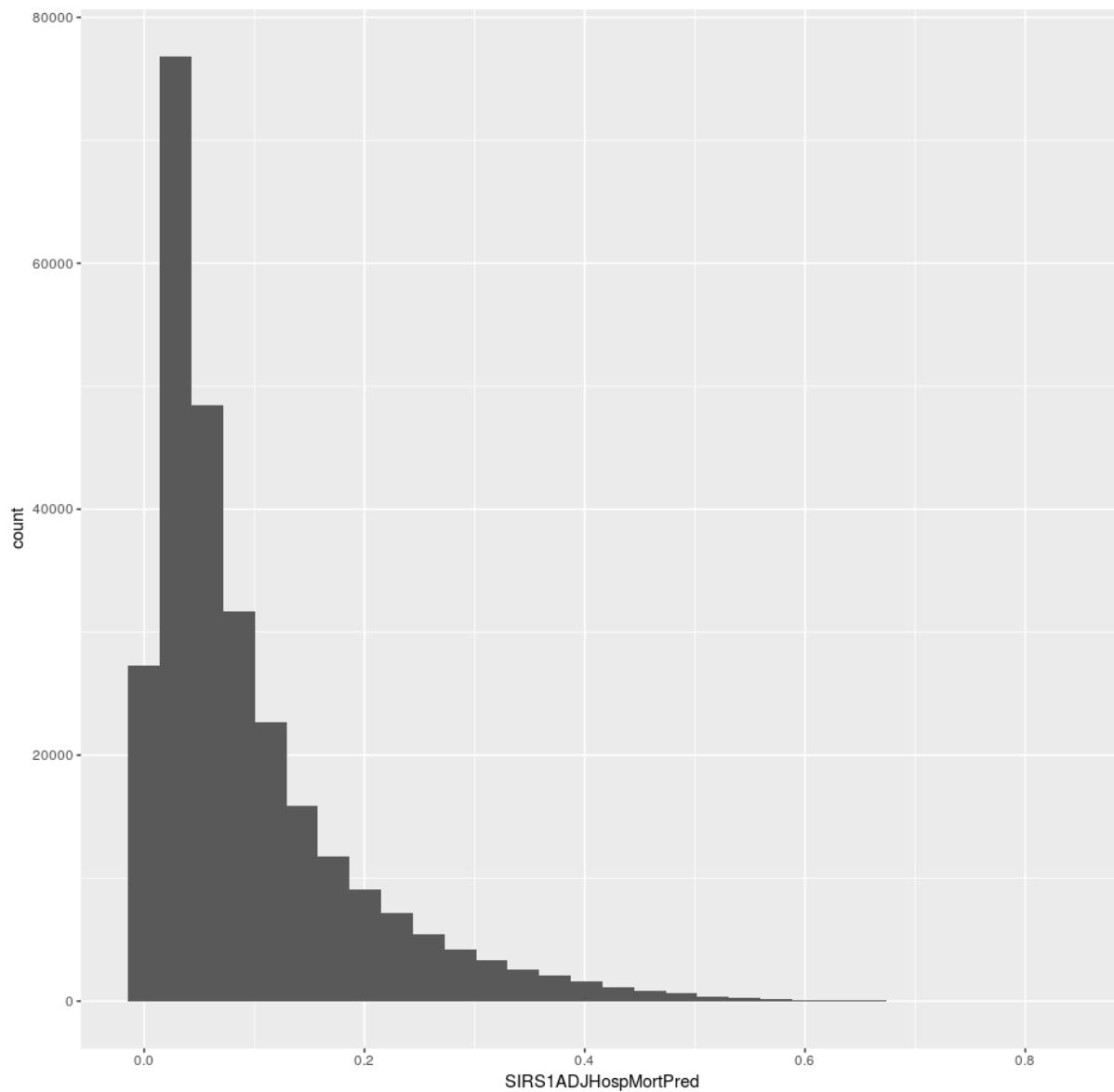
Calibration of ADJ Mortality SIRS Total Prediction



```
qplot(SIRS1ADJHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of ADJ Mortality SIRS Total Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of ADJ Mortality SIRS Total Predictions



```
SIRS2_ADJ_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(SIRS_Positive) + age_Ranges + gender2 + ethni
city2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospit
aldischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metast
aticcancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binom
ial",na.action = na.omit)

#sjp.glm(SIRS2_ADJ_Hosp_Mort_tr)
#sjt.glm(SIRS2_ADJ_Hosp_Mort_tr)

#drop1(SIRS2_ADJ_Hosp_Mort_tr,test="Chisq")

summary(SIRS2_ADJ_Hosp_Mort_tr)
```

```

## 
## Call:
## glm(formula = hospital_mortality_ultimate ~ as.factor(SIRS_Positive) +
##     age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 +
##     hospital_teaching_status + hospital_size + physicianSpeciality2 +
##     hospitaldischargeyear + dialysis + aids + hepaticfailure +
##     diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer +
##     thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline,
##     family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.7460 -0.5041 -0.3420 -0.2201  3.5149
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -3.7353712  0.0533820 -69.974
## as.factor(SIRS_Positive)TRUE 1.5501007  0.0166049  93.352
## age_Ranges(25,35]            0.2341878  0.0491700   4.763
## age_Ranges(35,45]            0.4422036  0.0453825   9.744
## age_Ranges(45,55]            0.8133442  0.0420051  19.363
## age_Ranges(55,65]            1.1012734  0.0411813  26.742
## age_Ranges(65,75]            1.3673261  0.0410022  33.348
## age_Ranges(75,85]            1.6711568  0.0409490  40.811
## age_Ranges(85,100]           1.9118926  0.0417794  45.762
## gender2Female               -0.0827101  0.0090284 -9.161
## gender2Other/Unknown         1.8353850  0.1840623   9.972
## ethnicity2African American -0.0001864  0.0148589 -0.013
## ethnicity2Hispanic           0.0817242  0.0214713   3.806
## ethnicity2Asian              0.1443329  0.0380038   3.798
## ethnicity2Native American   0.4002222  0.0495443   8.078
## ethnicity2Other/Unknown     0.2080260  0.0192215  10.823
## BMI_Ranges(18.5,25]          -0.2970890  0.0187827 -15.817
## BMI_Ranges(25,35]            -0.4496792  0.0185246 -24.275
## BMI_Ranges(35,200]           -0.3290523  0.0206832 -15.909
## BMI_RangesOther/Unknown     0.0630207  0.0272240   2.315
## icu_admit_source2OR/Proc Area -1.4644246  0.0176261 -83.083
## icu_admit_source2Direct Admit -0.3052330  0.0158092 -19.307
## icu_admit_source2Emergency Department -0.4319494  0.0108865 -39.677
## icu_admit_source2Other       -0.0931470  0.0409624 -2.274
## icu_admit_source2Step-Down Unit 0.1531999  0.0251306   6.096
## hospital_teaching_statusf   -0.1022073  0.0324836 -3.146
## hospital_teaching_statust   -0.2091128  0.0328309 -6.369
## hospital_size<100           -0.4951941  0.0367083 -13.490
## hospital_size100-249        -0.0014247  0.0255296 -0.056
## hospital_size250-500        0.1068927  0.0257786   4.147
## hospital_size>500           0.2642215  0.0240025  11.008
## physicianSpeciality2Speciality-Other -0.3415485  0.0099516 -34.321
## hospitaldischargeyear2011   -0.0458901  0.0170360 -2.694
## hospitaldischargeyear2012   -0.0964850  0.0164294 -5.873
## hospitaldischargeyear2013   -0.1540092  0.0161579 -9.531
## hospitaldischargeyear2014   -0.1953215  0.0160985 -12.133
## hospitaldischargeyear2015-16 -0.1779590  0.0159188 -11.179
## dialysis1                   0.3472659  0.0225635  15.391
## aids1                        0.5049126  0.1177279   4.289
## hepaticfailureTRUE           0.7541447  0.0247125  30.517
## diabetes1                   -0.2783472  0.0116522 -23.888
## immunosuppression1           0.3302446  0.0252849  13.061
## leukemial                    0.4274687  0.0398403  10.730
## lymphomai                     0.2517849  0.0569702   4.420
## metastaticcancer1            0.6437225  0.0264597  24.328
## thrombolytics1               0.0868257  0.0348889   2.489
## sofa_respiration_baseline2TRUE 0.0241130  0.0101831   2.368
## cardiovascular_baseline1    0.1469103  0.0104055  14.119
## 
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## as.factor(SIRS_Positive)TRUE < 2e-16 ***
## age_Ranges(25,35] 1.91e-06 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female < 2e-16 ***
## gender2Other/Unknown < 2e-16 ***
## ethnicity2African American 0.989992
## ethnicity2Hispanic 0.000141 ***

```

```

## ethnicity2Asian          0.000146 ***
## ethnicity2Native American 6.58e-16 ***
## ethnicity2Other/Unknown   < 2e-16 ***
## BMI_Ranges(18.5,25]      < 2e-16 ***
## BMI_Ranges(25,35]        < 2e-16 ***
## BMI_Ranges(35,200]       < 2e-16 ***
## BMI_RangesOther/Unknown  0.020619 *
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other     0.022968 *
## icu_admit_source2Step-Down Unit 1.09e-09 ***
## hospital_teaching_statusf 0.001653 **
## hospital_teaching_statust 1.90e-10 ***
## hospital_size<100         < 2e-16 ***
## hospital_size100-249      0.955496
## hospital_size250-500      3.37e-05 ***
## hospital_size>500         < 2e-16 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 0.007066 **
## hospitaldischargeyear2012 4.29e-09 ***
## hospitaldischargeyear2013 < 2e-16 ***
## hospitaldischargeyear2014 < 2e-16 ***
## hospitaldischargeyear2015-16 < 2e-16 ***
## dialysis1                 < 2e-16 ***
## aids1                      1.80e-05 ***
## hepaticfailureTRUE         < 2e-16 ***
## diabetes1                 < 2e-16 ***
## immunosuppression1        < 2e-16 ***
## leukemial                  < 2e-16 ***
## lymphoma1                  9.89e-06 ***
## metastaticcancer1         < 2e-16 ***
## thrombolytics1             0.012824 *
## sofa_respiration_baseline2TRUE 0.017888 *
## cardiovascular_baseline1  < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603 on 638756 degrees of freedom
## Residual deviance: 358142 on 638709 degrees of freedom
## AIC: 358238
##
## Number of Fisher Scoring iterations: 6

```

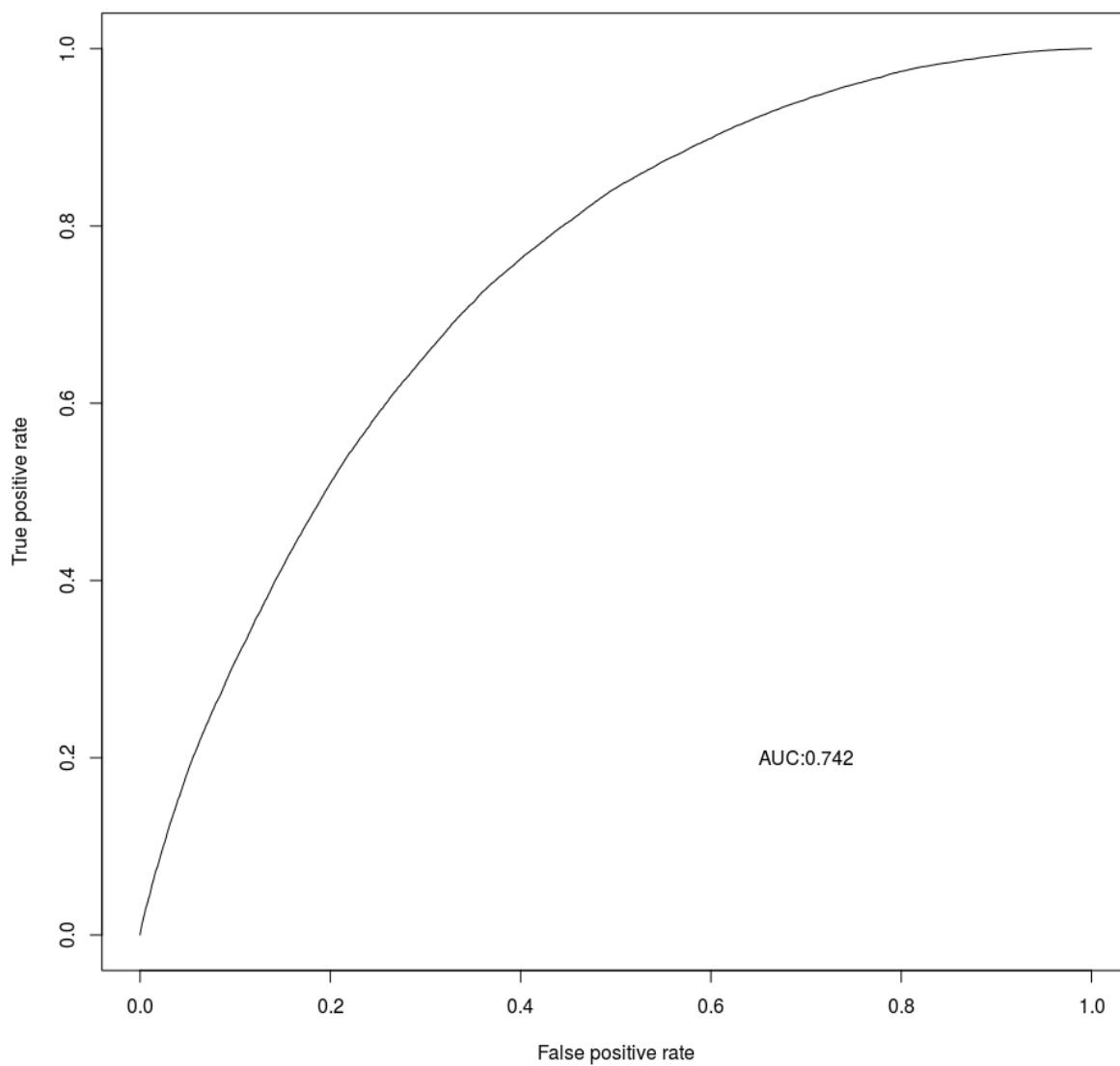
```

ssd_incl_te$SIRS2ADJHospMortPred <- predict (SIRS2_ADJ_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type="r
esponse")

SIRS2ADJMort.Pred <- prediction(ssd_incl_te$SIRS2ADJHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
SIRS2ADJMort.Perf <- performance(SIRS2ADJMort.Pred, "tpr", "fpr")
plot(SIRS2ADJMort.Perf, main = "SIRS Positive Adjusted
Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SIRS2ADJMort.Pred,"auc")@y.values[[1]],3)))

```

**SIRS Positive Adjusted
Mortality Prediction Test Model**



```
performance(SIRS2ADJMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7423965
##
## Slot "alpha.values":
## list()
```

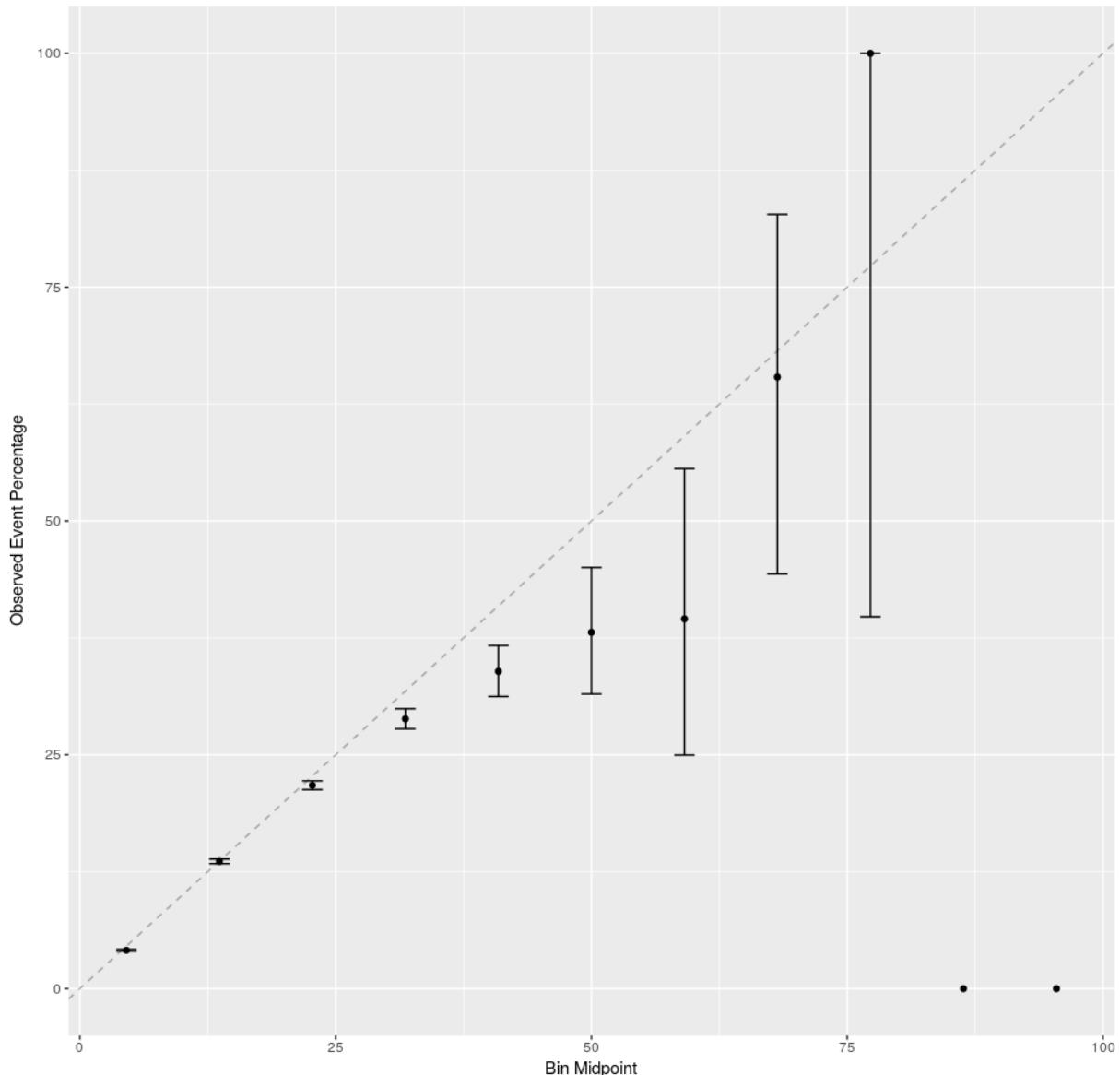
```
SIRS2ADJMort.Pred.roc <- roc(hospital_mortality_ultimate~ SIRS2ADJHospMortPred,data=ssd_incl_te)
ci(SIRS2ADJMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7386-0.7462 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~SIRS2ADJHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of ADJ Mortality SIRS Positive Prediction")
```

```
## Warning: Removed 2 rows containing missing values (geom_errorbar).
```

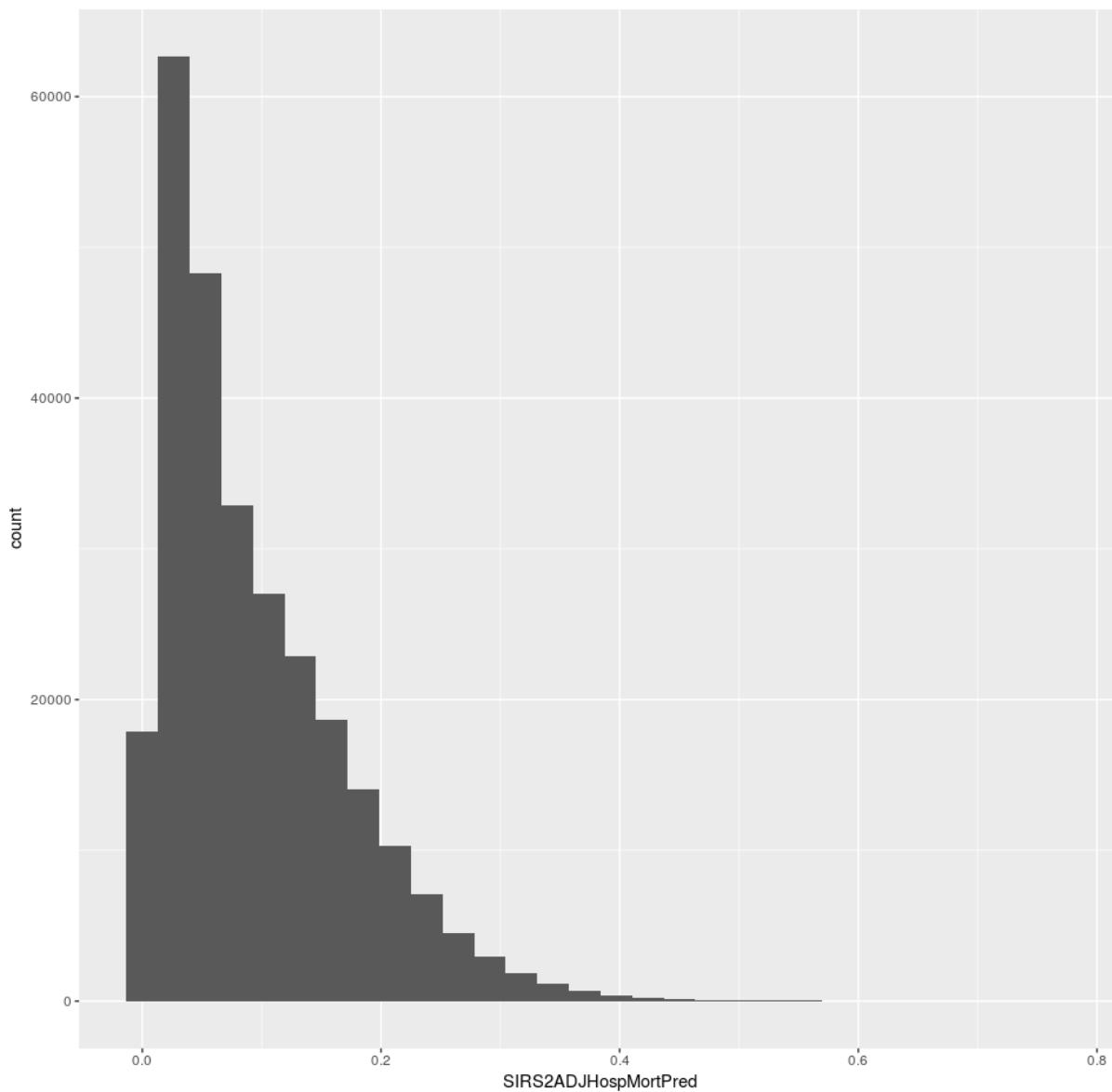
Calibration of ADJ Mortality SIRS Positive Prediction



```
qplot(SIRS2ADJHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of ADJ Mortality SIRS Positive Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of ADJ Mortality SIRS Positive Predictions



```
SOFA1_ADJ_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(SOFA_Change) + age_Ranges + gender2 + ethnici
ty2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospital
dischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastat
iccancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial"
1",na.action = na.omit)

#sjp.glm(SOFA1_ADJ_Hosp_Mort_tr)
#sjt.glm(SOFA1_ADJ_Hosp_Mort_tr)

#drop1(SOFA1_ADJ_Hosp_Mort_tr,test="Chisq")

summary(SOFA1_ADJ_Hosp_Mort_tr)
```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(SOFA_Change) +
##     age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 +
##     hospital_teaching_status + hospital_size + physicianSpeciality2 +
##     hospitaldischargeyear + dialysis + aids + hepaticfailure +
##     diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer +
##     thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline,
##     family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.4428 -0.4058 -0.2414 -0.1429  3.5627
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -4.77549  0.07031 -67.926 < 2e-16
## as.factor(SOFA_Change) 1       0.51755  0.04790  10.806 < 2e-16
## as.factor(SOFA_Change) 2       0.94833  0.04766  19.897 < 2e-16
## as.factor(SOFA_Change) 3       1.50675  0.04653  32.381 < 2e-16
## as.factor(SOFA_Change) 4       1.93885  0.04604  42.111 < 2e-16
## as.factor(SOFA_Change) 5       2.36041  0.04592  51.399 < 2e-16
## as.factor(SOFA_Change) 6       2.59633  0.04636  56.005 < 2e-16
## as.factor(SOFA_Change) 7       3.12266  0.04626  67.496 < 2e-16
## as.factor(SOFA_Change) 8       3.39608  0.04699  72.268 < 2e-16
## as.factor(SOFA_Change) 9       3.72733  0.04787  77.864 < 2e-16
## as.factor(SOFA_Change)10      4.02493  0.04912  81.938 < 2e-16
## as.factor(SOFA_Change)11      4.45056  0.05076  87.686 < 2e-16
## as.factor(SOFA_Change)12      4.70142  0.05401  87.053 < 2e-16
## as.factor(SOFA_Change)13      5.02838  0.05860  85.804 < 2e-16
## as.factor(SOFA_Change)14      5.30110  0.06647  79.756 < 2e-16
## as.factor(SOFA_Change)15      5.59238  0.07855  71.199 < 2e-16
## as.factor(SOFA_Change)16      6.00864  0.09983  60.186 < 2e-16
## as.factor(SOFA_Change)17      6.35174  0.14533  43.706 < 2e-16
## as.factor(SOFA_Change)[18,23]  6.72698  0.15509  43.375 < 2e-16
## age_Ranges[25,35]             0.15128  0.05287  2.861 0.004220
## age_Ranges[35,45]              0.25870  0.04883  5.298 1.17e-07
## age_Ranges[45,55]              0.52916  0.04508  11.738 < 2e-16
## age_Ranges[55,65]              0.75028  0.04416  16.991 < 2e-16
## age_Ranges[65,75]              1.02159  0.04396  23.241 < 2e-16
## age_Ranges[75,85]              1.32943  0.04389  30.289 < 2e-16
## age_Ranges[85,100]             1.60371  0.04479  35.805 < 2e-16
## gender2Female                 0.07669  0.00984  7.794 6.49e-15
## gender2Other/Unknown          2.04771  0.20408  10.034 < 2e-16
## ethnicity2African American   -0.16619  0.01631 -10.191 < 2e-16
## ethnicity2Hispanic            -0.08934  0.02351 -3.800 0.000145
## ethnicity2Asian               -0.03644  0.04193 -0.869 0.384822
## ethnicity2Native American    -0.06771  0.05532 -1.224 0.220960
## ethnicity2Other/Unknown       0.05483  0.02113  2.595 0.009461
## BMI_Ranges[18.5,25]           -0.30707  0.02044 -15.020 < 2e-16
## BMI_Ranges[25,35]              -0.54280  0.02019 -26.879 < 2e-16
## BMI_Ranges[35,200]             -0.55380  0.02260 -24.501 < 2e-16
## BMI_RangesOther/Unknown       0.08910  0.02987  2.983 0.002858
## icu_admit_source2OR/Proc Area -1.48921  0.01886 -78.945 < 2e-16
## icu_admit_source2Direct Admit -0.31881  0.01750 -18.221 < 2e-16
## icu_admit_source2Emergency Department -0.32144  0.01195 -26.897 < 2e-16
## icu_admit_source2Other        -0.10907  0.04515 -2.416 0.015704
## icu_admit_source2Step-Down Unit 0.18099  0.02766  6.544 5.98e-11
## hospital_teaching_statusf    0.17821  0.03549  5.021 5.14e-07
## hospital_teaching_statust    0.05926  0.03605  1.644 0.100152
## hospital_size<100            -0.34572  0.03910 -8.842 < 2e-16
## hospital_size100-249          -0.04716  0.02768 -1.704 0.088453
## hospital_size250-500          -0.04072  0.02799 -1.455 0.145687
## hospital_size>500             0.13895  0.02617  5.310 1.10e-07
## physicianSpeciality2Speciality-Other -0.06818  0.01100 -6.198 5.73e-10
## hospitaldischargeyear2011     -0.04850  0.01857 -2.611 0.009015
## hospitaldischargeyear2012     -0.05542  0.01792 -3.093 0.001982
## hospitaldischargeyear2013     -0.05490  0.01758 -3.123 0.001791
## hospitaldischargeyear2014     -0.11714  0.01753 -6.684 2.33e-11
## hospitaldischargeyear2015-16   -0.16845  0.01737 -9.700 < 2e-16
## dialysis1                      0.72138  0.02434  29.635 < 2e-16
## aids1                          0.39881  0.13002  3.067 0.002160
## hepaticfailureTRUE              0.38666  0.02700 14.322 < 2e-16
## diabetes1                      -0.25365  0.01263 -20.077 < 2e-16
## immunosuppression1              0.32414  0.02816 11.509 < 2e-16
## leukemia1                      0.13061  0.04464  2.926 0.003435
## lymphomai                        0.12959  0.06356  2.039 0.041448
## metastaticcancer1               0.79487  0.02945 26.992 < 2e-16

```

```

## thrombolytics1          0.23682   0.03927   6.030 1.64e-09
## sofa_respiration_baseline2TRUE 0.41765   0.01111   37.599 < 2e-16
## cardiovascular_baseline1    0.02912   0.01128   2.582  0.009813

##
## (Intercept)               ***
## as.factor(SOFA_Change) 1   ***
## as.factor(SOFA_Change) 2   ***
## as.factor(SOFA_Change) 3   ***
## as.factor(SOFA_Change) 4   ***
## as.factor(SOFA_Change) 5   ***
## as.factor(SOFA_Change) 6   ***
## as.factor(SOFA_Change) 7   ***
## as.factor(SOFA_Change) 8   ***
## as.factor(SOFA_Change) 9   ***
## as.factor(SOFA_Change)10  ***
## as.factor(SOFA_Change)11  ***
## as.factor(SOFA_Change)12  ***
## as.factor(SOFA_Change)13  ***
## as.factor(SOFA_Change)14  ***
## as.factor(SOFA_Change)15  ***
## as.factor(SOFA_Change)16  ***
## as.factor(SOFA_Change)17  ***
## as.factor(SOFA_Change)[18,23] ***
## age_Ranges(25,35]          **
## age_Ranges(35,45]          ***
## age_Ranges(45,55]          ***
## age_Ranges(55,65]          ***
## age_Ranges(65,75]          ***
## age_Ranges(75,85]          ***
## age_Ranges(85,100]          ***
## gender2Female              ***
## gender2Other/Unknown       ***
## ethnicity2African American ***
## ethnicity2Hispanic         ***
## ethnicity2Asian             ***
## ethnicity2Native American  ***
## ethnicity2Other/Unknown    **
## BMI_Ranges(18.5,25]        ***
## BMI_Ranges(25,35]          ***
## BMI_Ranges(35,200]         ***
## BMI_Rangesother/Unknown    **
## icu_admit_source2OR/Proc Area ***
## icu_admit_source2Direct Admit ***
## icu_admit_source2Emergency Department ***
## icu_admit_source2Other      *
## icu_admit_source2Step-Down Unit ***
## hospital_teaching_statusf ***
## hospital_teaching_statust  ***
## hospital_size<100          ***
## hospital_size100-249        .
## hospital_size250-500        ***
## hospital_size>500          ***
## physicianSpeciality2Speciality-Other ***
## hospitaldischargeyear2011   **
## hospitaldischargeyear2012   **
## hospitaldischargeyear2013   **
## hospitaldischargeyear2014   ***
## hospitaldischargeyear2015-16 ***
## dialysis1                  ***
## aids1                      **
## hepaticfailureTRUE          ***
## diabetes1                  ***
## immunosuppression1          ***
## leukemial                   **
## lymphomal                   *
## metastaticcancer1          ***
## thrombolytics1              ***
## sofa_respiration_baseline2TRUE ***
## cardiovascular_baseline1    **

##
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## (Dispersion parameter for binomial family taken to be 1)

##
## Null deviance: 399603  on 638756  degrees of freedom
## Residual deviance: 298942  on 638692  degrees of freedom
## AIC: 299072

```

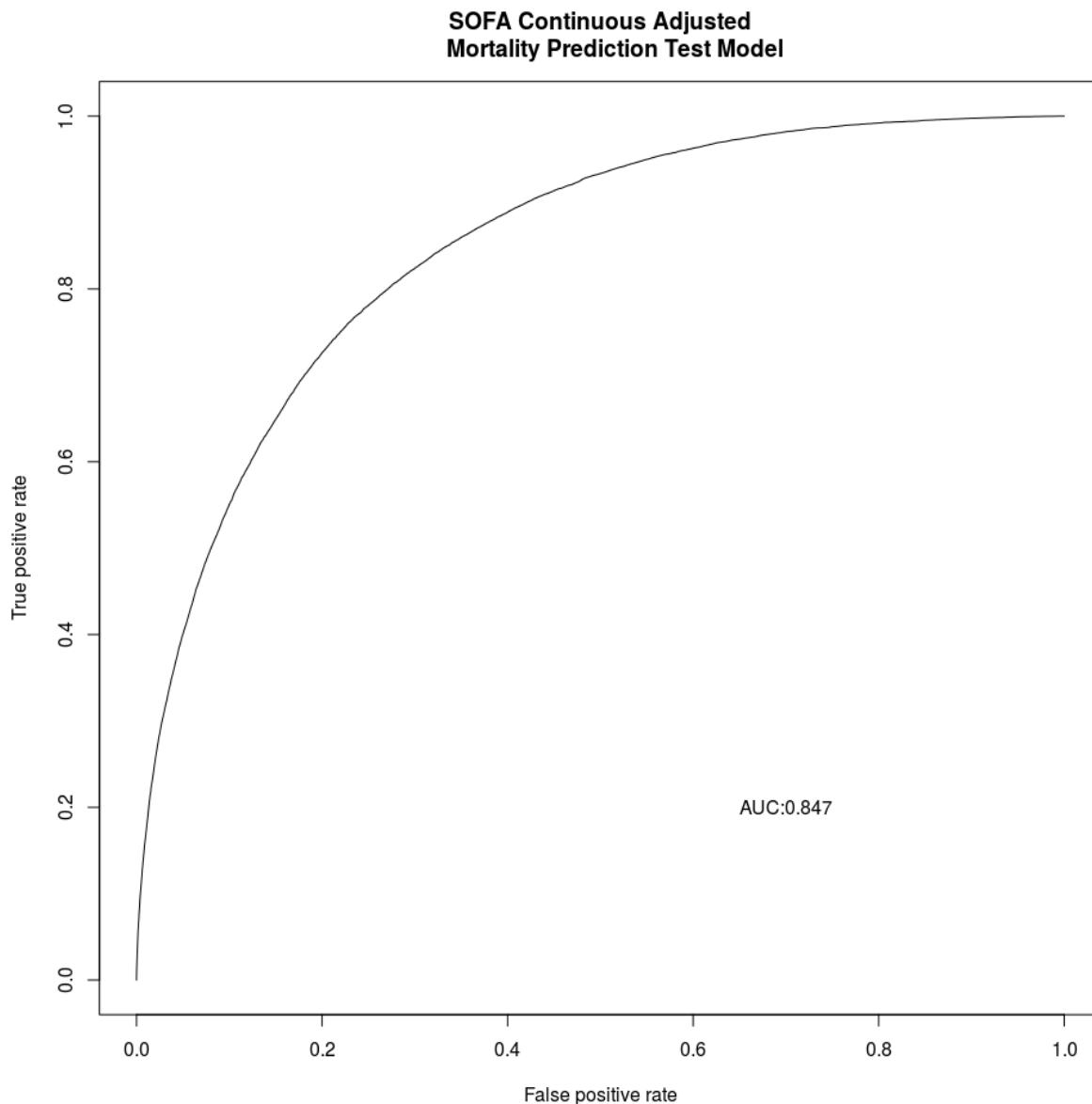
```

## 
## Number of Fisher Scoring iterations: 7

ssd_incl_te$SOFA1ADJHospMortPred <- predict (SOFA1_ADJ_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type="r
esponse")

SOFA1ADJMort.Pred <- prediction(ssd_incl_te$SOFA1ADJHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
SOFA1ADJMort.Perf <- performance(SOFA1ADJMort.Pred, "tpr", "fpr")
plot(SOFA1ADJMort.Perf, main = "SOFA Continuous Adjusted
Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA1ADJMort.Pred,"auc")@y.values[[1]],3)))

```



```
performance(SOFA1ADJMort.Pred, "auc")
```

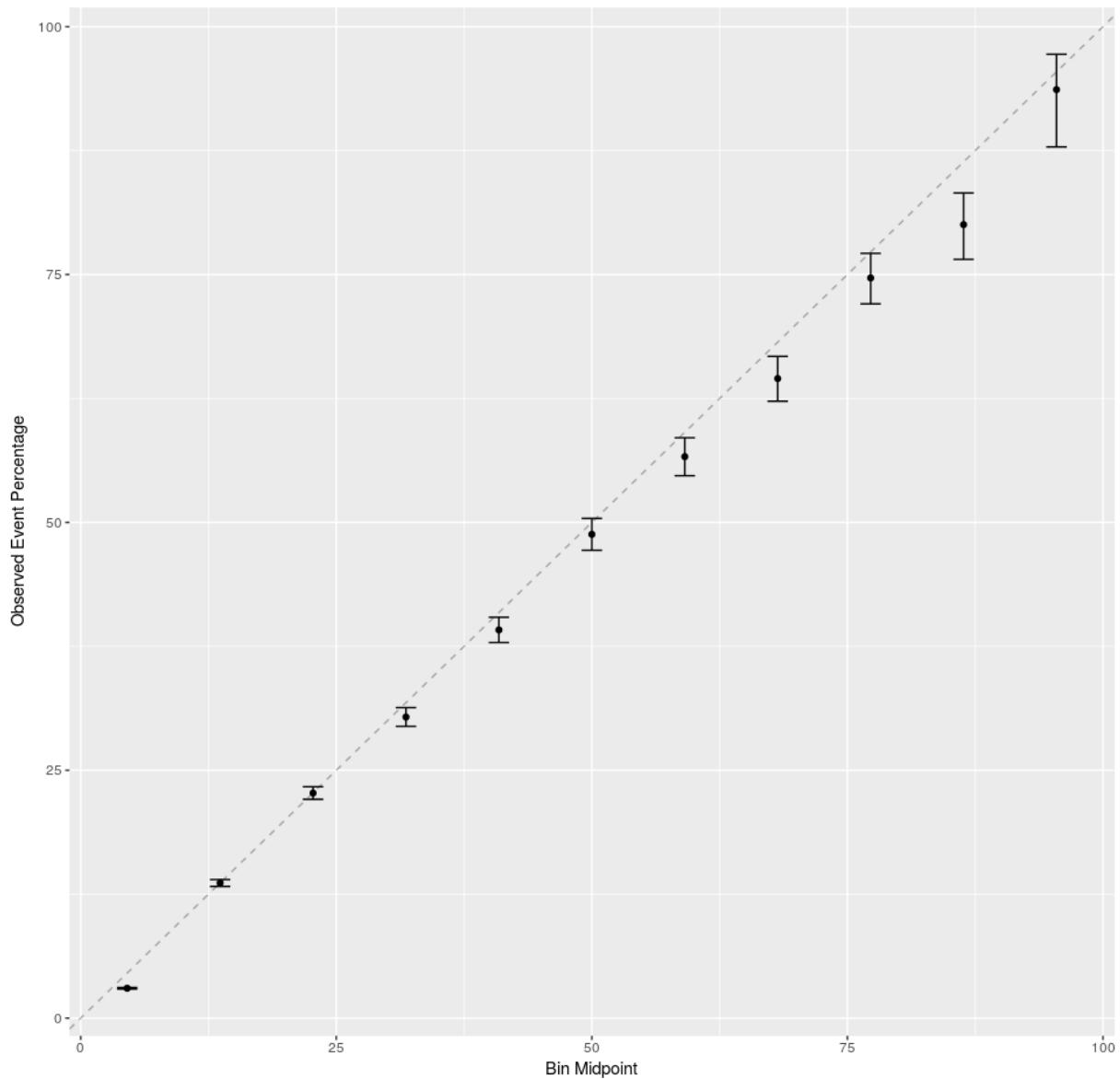
```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.8472926
##
##
## Slot "alpha.values":
## list()
```

```
SOFA1ADJMort.Pred.roc <- roc(hospital_mortality_ultimate~ SOFA1ADJHospMortPred, data=ssd_incl_te)
ci(SOFA1ADJMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.8442-0.8504 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~SOFA1ADJHospMortPred, data = ssd_incl_te))+ggtitle
("Calibration of ADJ Mortality SOFA Total Prediction")
```

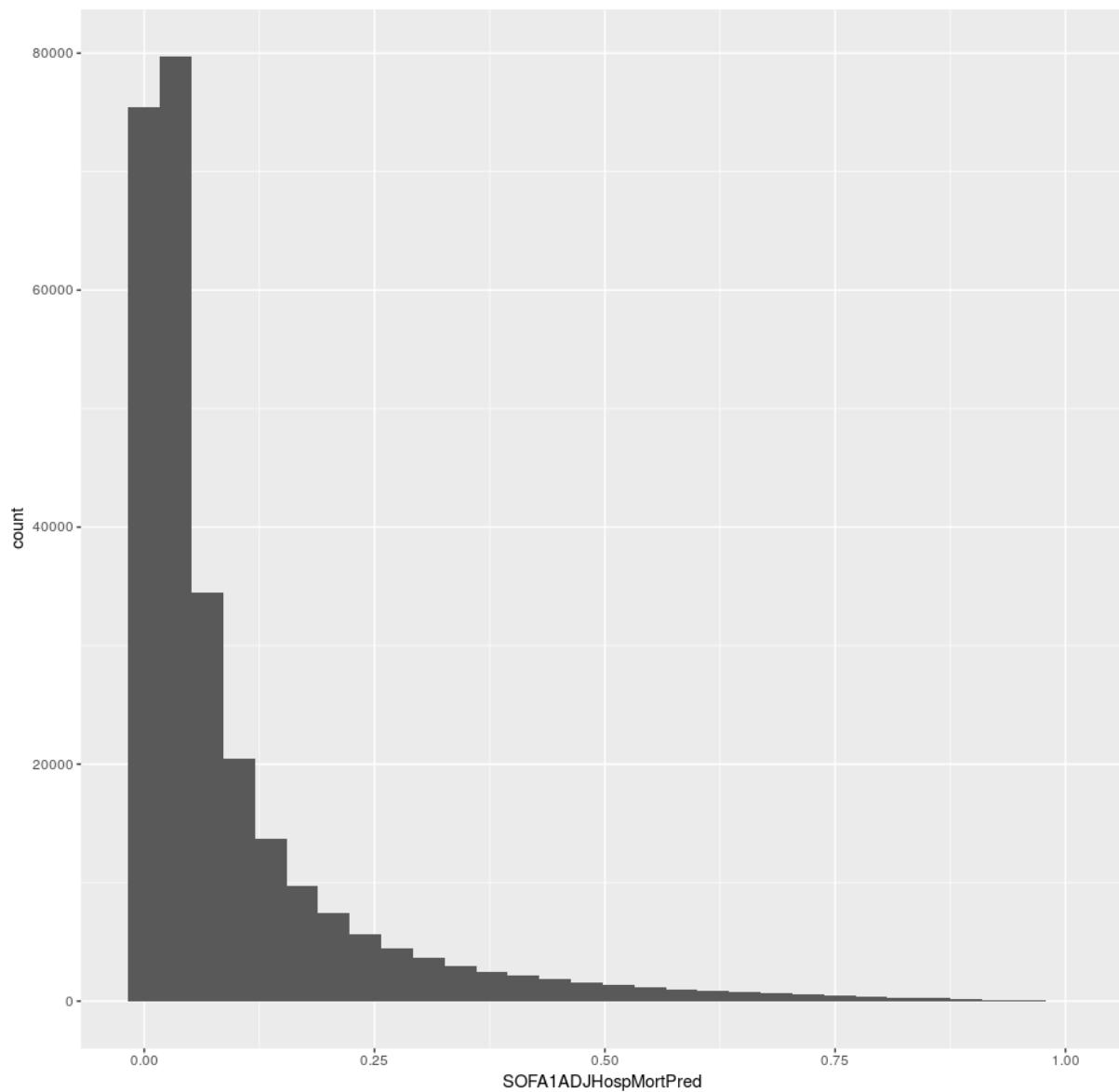
Calibration of ADJ Mortality SOFA Total Prediction



```
qplot(SOFA1ADJHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of ADJ Mortality SOFA Total Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of ADJ Mortality SOFA Total Predictions



```
SOFA2_ADJ_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(SOFA_Positive) + age_Ranges + gender2 + ethni
city2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospit
aldischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metast
aticcancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binom
ial",na.action = na.omit)

#sjp.glm(SOFA2_ADJ_Hosp_Mort_tr)
#sjt.glm(SOFA2_ADJ_Hosp_Mort_tr)

#drop1(SOFA2_ADJ_Hosp_Mort_tr,test="Chisq")

summary(SOFA2_ADJ_Hosp_Mort_tr)
```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(SOFA_Positive) +
##     age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 +
##     hospital_teaching_status + hospital_size + physicianSpeciality2 +
##     hospitaldischargeyear + dialysis + aids + hepaticfailure +
##     diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer +
##     thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline,
##     family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.8380 -0.5240 -0.3328 -0.1673  3.4801
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -3.978119  0.053948 -73.740
## as.factor(SOFA_Positive)TRUE 2.020614  0.018376 109.959
## age_Ranges(25,35]            0.215132  0.049528  4.344
## age_Ranges(35,45]            0.395554  0.045716  8.652
## age_Ranges(45,55]            0.689357  0.042315 16.291
## age_Ranges(55,65]            0.916742  0.041492 22.095
## age_Ranges(65,75]            1.130514  0.041313 27.365
## age_Ranges(75,85]            1.369151  0.041246 33.195
## age_Ranges(85,100]           1.562525  0.042060 37.150
## gender2Female               -0.019092  0.009065 -2.106
## gender2Other/Unknown         1.934512  0.186694 10.362
## ethnicity2African American  -0.033650  0.014909 -2.257
## ethnicity2Hispanic           0.047706  0.021550  2.214
## ethnicity2Asian              0.094731  0.038058  2.489
## ethnicity2Native American    0.294545  0.049580  5.941
## ethnicity2Other/Unknown       0.174577  0.019311  9.040
## BMI_Ranges(18.5,25]          -0.313238  0.018909 -16.566
## BMI_Ranges(25,35]            -0.477467  0.018647 -25.605
## BMI_Ranges(35,200]           -0.389262  0.020822 -18.695
## BMI_RangesOther/Unknown      0.031327  0.027394  1.144
## icu_admit_source2OR/Proc Area -1.449279  0.017681 -81.968
## icu_admit_source2Direct Admit -0.311429  0.015879 -19.613
## icu_admit_source2Emergency Department -0.424613  0.010937 -38.825
## icu_admit_source2Other        -0.085987  0.041144 -2.090
## icu_admit_source2Step-Down Unit 0.146360  0.025244  5.798
## hospital_teaching_statusf    -0.037912  0.032651 -1.161
## hospital_teaching_statust   -0.152785  0.033018 -4.627
## hospital_size<100           -0.492326  0.036909 -13.339
## hospital_size100-249         -0.032021  0.025680 -1.247
## hospital_size250-500         0.069264  0.025923  2.672
## hospital_size>500            0.215502  0.024158  8.920
## physicianSpeciality2Speciality-Other -0.302475  0.010021 -30.183
## hospitaldischargeyear2011    -0.034288  0.017083 -2.007
## hospitaldischargeyear2012    -0.063331  0.016481 -3.843
## hospitaldischargeyear2013    -0.091968  0.016212 -5.673
## hospitaldischargeyear2014    -0.136227  0.016154 -8.433
## hospitaldischargeyear2015-16 -0.122819  0.015973 -7.689
## dialysis1                     0.417044  0.022762 18.322
## aids1                         0.475890  0.118844  4.004
## hepaticfailureTRUE            0.558113  0.024573 22.713
## diabetes1                     -0.308962  0.011711 -26.381
## immunosuppression1            0.344634  0.025615 13.454
## leukemial                      0.393989  0.040016  9.846
## lymphomai                      0.247094  0.057337  4.310
## metastaticcancer1             0.684668  0.026839 25.510
## thrombolytics1                 0.243885  0.035466  6.877
## sofa_respiration_baseline2TRUE 0.115258  0.010233 11.263
## cardiovascular_baseline1      0.057819  0.010430  5.544
## 
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## as.factor(SOFA_Positive)TRUE < 2e-16 ***
## age_Ranges(25,35] 1.40e-05 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female 0.035194 *
## gender2Other/Unknown < 2e-16 ***
## ethnicity2African American 0.024005 *
## ethnicity2Hispanic 0.026843 *

```

```

## ethnicity2Asian          0.012805 *
## ethnicity2Native American 2.84e-09 ***
## ethnicity2Other/Unknown   < 2e-16 ***
## BMI_Ranges(18.5,25]      < 2e-16 ***
## BMI_Ranges(25,35]        < 2e-16 ***
## BMI_Ranges(35,200]       < 2e-16 ***
## BMI_RangesOther/Unknown  0.252815
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other      0.036629 *
## icu_admit_source2Step-Down Unit 6.72e-09 ***
## hospital_teaching_statusf 0.245594
## hospital_teaching_statust 3.70e-06 ***
## hospital_size<100         < 2e-16 ***
## hospital_size100-249       0.212422
## hospital_size250-500       0.007543 **
## hospital_size>500         < 2e-16 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 0.044739 *
## hospitaldischargeyear2012 0.000122 ***
## hospitaldischargeyear2013 1.41e-08 ***
## hospitaldischargeyear2014 < 2e-16 ***
## hospitaldischargeyear2015-16 1.48e-14 ***
## dialysis1                  < 2e-16 ***
## aids1                      6.22e-05 ***
## hepaticfailureTRUE         < 2e-16 ***
## diabetes1                 < 2e-16 ***
## immunosuppression1        < 2e-16 ***
## leukemial                  < 2e-16 ***
## lymphoma1                  1.64e-05 ***
## metastaticcancer1         < 2e-16 ***
## thrombolytics1             6.13e-12 ***
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1  2.96e-08 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603 on 638756 degrees of freedom
## Residual deviance: 350403 on 638709 degrees of freedom
## AIC: 350499
##
## Number of Fisher Scoring iterations: 6

```

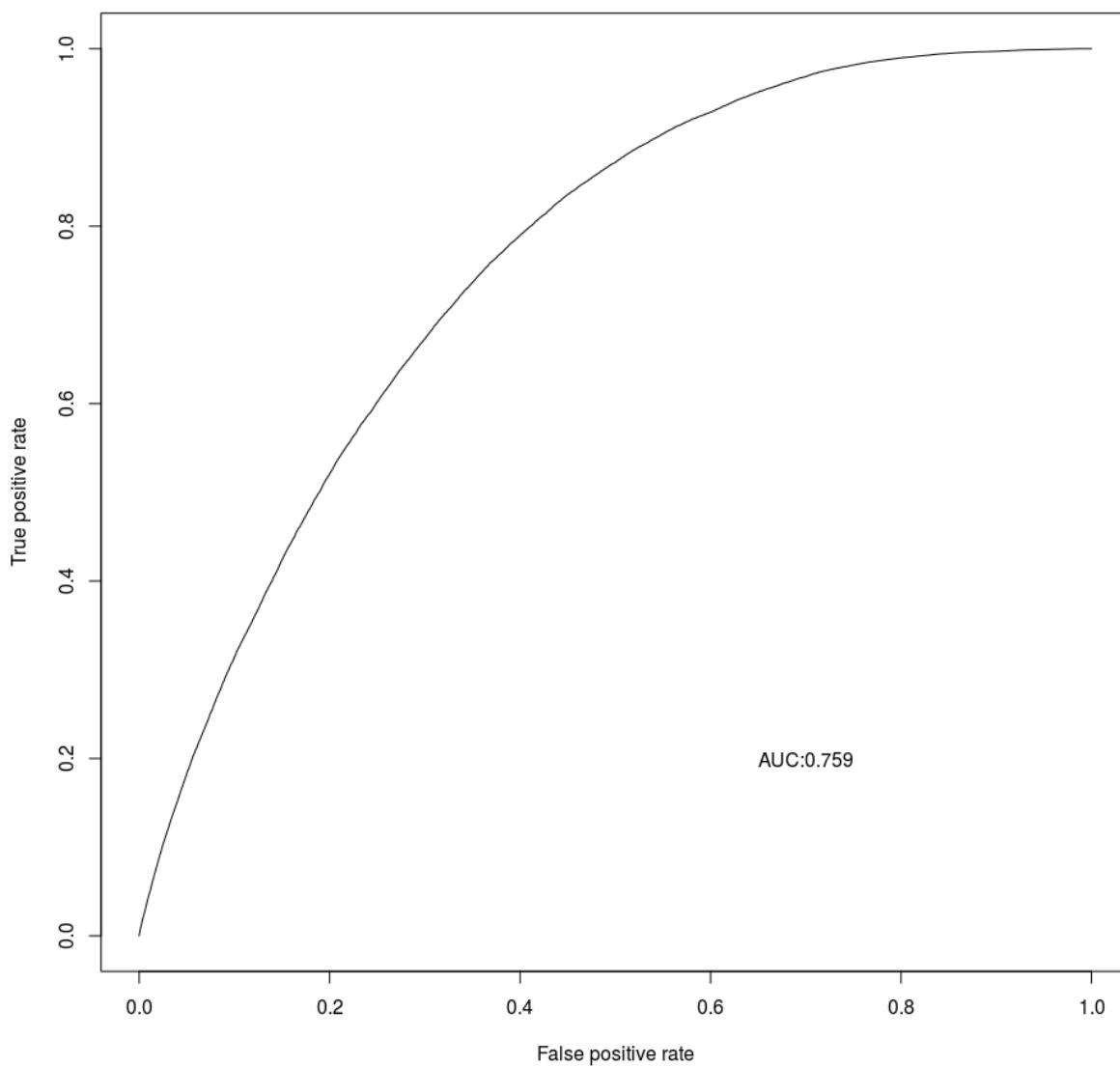
```

ssd_incl_te$SOFA2ADJHospMortPred <- predict(SOFA2_ADJ_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")

SOFA2ADJMort.Pred <- prediction(ssd_incl_te$SOFA2ADJHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
SOFA2ADJMort.Perf <- performance(SOFA2ADJMort.Pred, "tpr", "fpr")
plot(SOFA2ADJMort.Perf, main = "SOFA Positive Adjusted
Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA2ADJMort.Pred,"auc")@y.values[[1]],3)))

```

**SOFA Positive Adjusted
Mortality Prediction Test Model**



```
performance(SOFA2ADJMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7592311
##
## Slot "alpha.values":
## list()
```

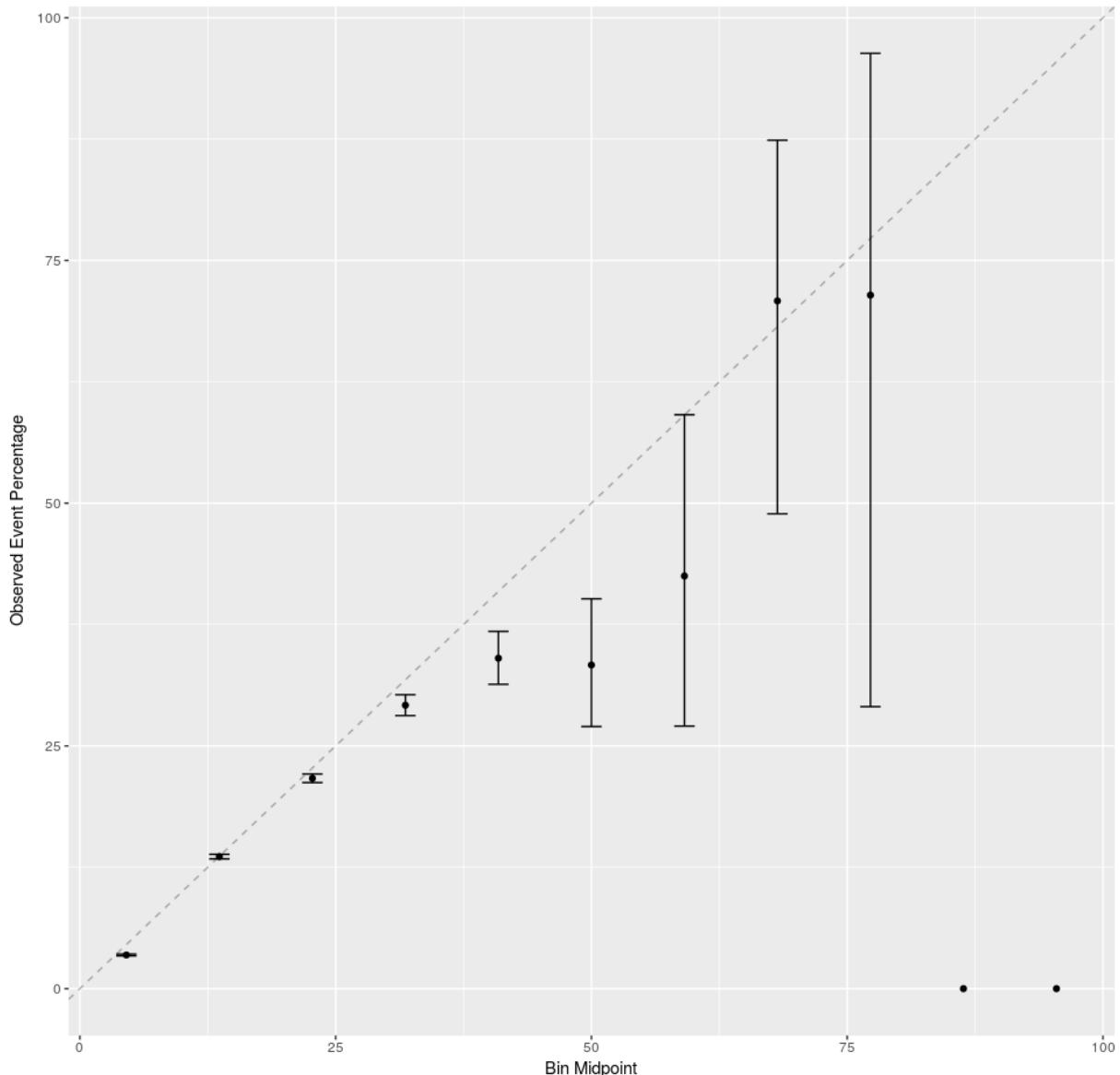
```
SOFA2ADJMort.Pred.roc <- roc(hospital_mortality_ultimate~ SOFA2ADJHospMortPred,data=ssd_incl_te)
ci(SOFA2ADJMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7557-0.7627 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~SOFA2ADJHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of ADJ Mortality SOFA Positive Prediction")
```

```
## Warning: Removed 2 rows containing missing values (geom_errorbar).
```

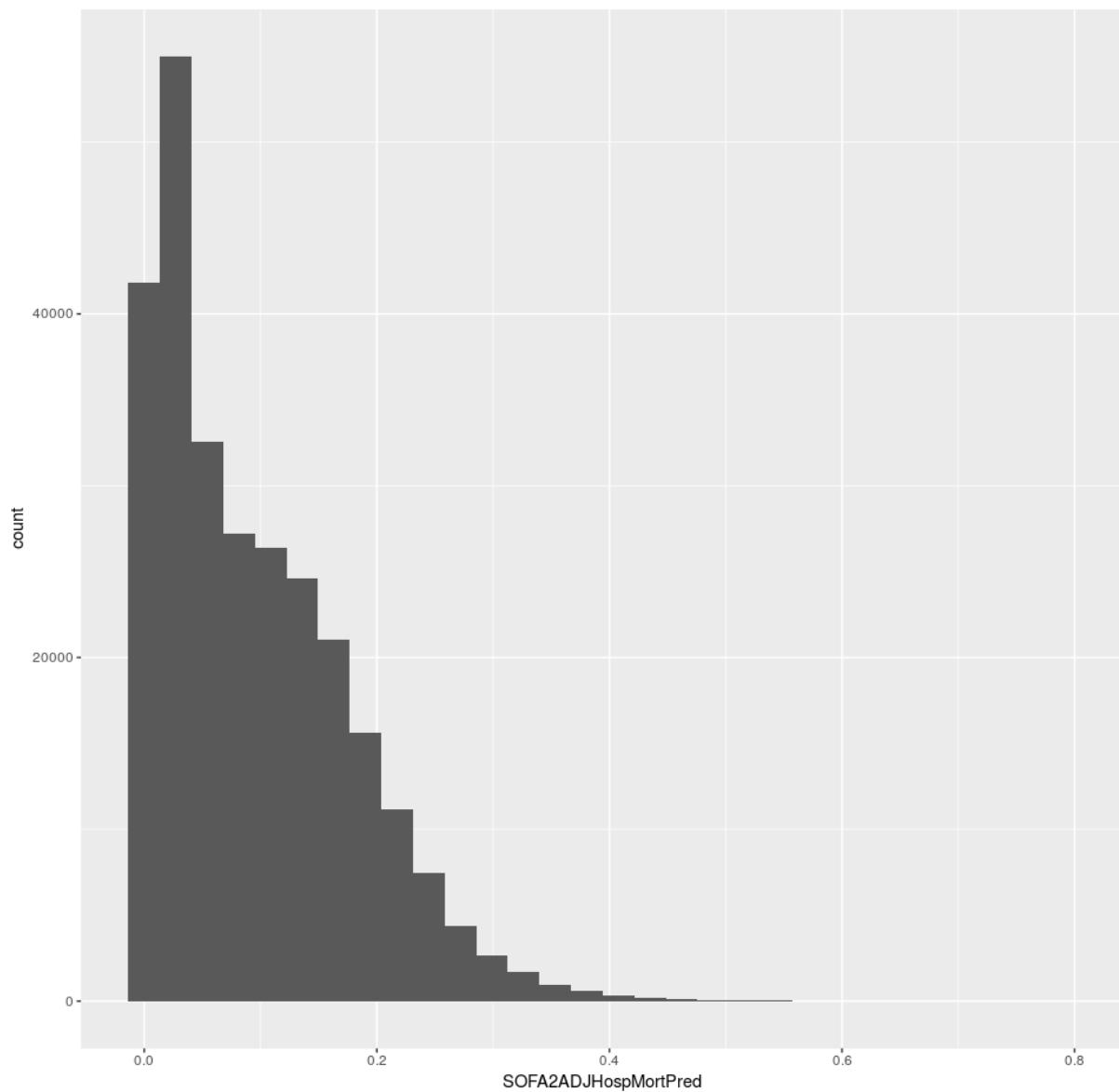
Calibration of ADJ Mortality SOFA Positive Prediction



```
qplot(SOFA2ADJHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of ADJ Mortality SOFA Positive Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of ADJ Mortality SOFA Positive Predictions



SOFA score positive without baseline SOFA

```

SOFA3_ADJ_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(SOFA_Positive2) + age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SOFA3_ADJ_Hosp_Mort_tr)
#sjt.glm(SOFA3_ADJ_Hosp_Mort_tr)

#drop1(SOFA3_ADJ_Hosp_Mort_tr,test="Chisq")

summary(SOFA3_ADJ_Hosp_Mort_tr)

```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(SOFA_Positive2) +
##     age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 +
##     hospital_teaching_status + hospital_size + physicianSpeciality2 +
##     hospitaldischargeyear + dialysis + aids + hepaticfailure +
##     diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer +
##     thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline,
##     family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.8265 -0.5241 -0.3413 -0.1648  3.4979
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -4.022666  0.054342 -74.025
## as.factor(SOFA_Positive2)TRUE 2.070136  0.019691 105.128
## age_Ranges(25,35]            0.206791  0.049510  4.177
## age_Ranges(35,45]            0.386802  0.045701  8.464
## age_Ranges(45,55]            0.685480  0.042302 16.205
## age_Ranges(55,65]            0.915737  0.041479 22.077
## age_Ranges(65,75]            1.133289  0.041300 27.440
## age_Ranges(75,85]            1.375282  0.041235 33.352
## age_Ranges(85,100]           1.571159  0.042050 37.364
## gender2Female               -0.022891  0.009053 -2.529
## gender2Other/Unknown         1.909668  0.186607 10.234
## ethnicity2African American -0.037713  0.014880 -2.535
## ethnicity2Hispanic          0.039776  0.021506  1.850
## ethnicity2Asian              0.096467  0.037981  2.540
## ethnicity2Native American   0.307064  0.049439  6.211
## ethnicity2Other/Unknown     0.173564  0.019283  9.001
## BMI_Ranges(18.5,25]          -0.314244  0.018874 -16.650
## BMI_Ranges(25,35]            -0.477045  0.018613 -25.629
## BMI_Ranges(35,200]           -0.390237  0.020781 -18.778
## BMI_RangesOther/Unknown     0.028400  0.027349  1.038
## icu_admit_source2OR/Proc Area -1.445876  0.017671 -81.821
## icu_admit_source2Direct Admit -0.311644  0.015853 -19.658
## icu_admit_source2Emergency Department -0.425477  0.010916 -38.977
## icu_admit_source2Other       -0.076304  0.041097 -1.857
## icu_admit_source2Step-Down Unit 0.150637  0.025189  5.980
## hospital_teaching_statusf   -0.039567  0.032606 -1.213
## hospital_teaching_statust   -0.151906  0.032980 -4.606
## hospital_size<100          -0.498093  0.036872 -13.509
## hospital_size100-249        -0.035545  0.025642 -1.386
## hospital_size250-500        0.071683  0.025888  2.769
## hospital_size>500           0.214426  0.024128  8.887
## physicianSpeciality2Speciality-Other -0.301722  0.010010 -30.142
## hospitaldischargeyear2011   -0.034558  0.017062 -2.025
## hospitaldischargeyear2012   -0.064082  0.016461 -3.893
## hospitaldischargeyear2013   -0.096544  0.016190 -5.963
## hospitaldischargeyear2014   -0.139689  0.016131 -8.660
## hospitaldischargeyear2015-16 -0.126314  0.015951 -7.919
## dialysis1                   0.094191  0.022225  4.238
## aids1                        0.495812  0.118478  4.185
## hepaticfailureTRUE          0.553304  0.024479 22.603
## diabetes1                  -0.305693  0.011685 -26.162
## immunosuppression1          0.340377  0.025563 13.315
## leukemial                    0.405643  0.039939 10.156
## lymphomai                    0.252952  0.057272  4.417
## metastaticcancer1           0.684713  0.026800 25.549
## thrombolytics1              0.250331  0.035468  7.058
## sofa_respiration_baseline2TRUE 0.075186  0.010211  7.363
## cardiovascular_baseline1    0.058011  0.010409  5.573
## 
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## as.factor(SOFA_Positive2)TRUE 2.96e-05 ***
## age_Ranges(25,35] < 2e-16 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female 0.01145 *
## gender2Other/Unknown < 2e-16 ***
## ethnicity2African American 0.01126 *
## ethnicity2Hispanic 0.06438 .

```

```

## ethnicity2Asian          0.01109 *
## ethnicity2Native American 5.27e-10 ***
## ethnicity2Other/Unknown   < 2e-16 ***
## BMI_Ranges(18.5,25]      < 2e-16 ***
## BMI_Ranges(25,35]        < 2e-16 ***
## BMI_Ranges(35,200]       < 2e-16 ***
## BMI_RangesOther/Unknown  0.29908
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other      0.06336 .
## icu_admit_source2Step-Down Unit 2.23e-09 ***
## hospital_teaching_statusf 0.22494
## hospital_teaching_statust 4.10e-06 ***
## hospital_size<100         < 2e-16 ***
## hospital_size100-249      0.16568
## hospital_size250-500      0.00562 **
## hospital_size>500         < 2e-16 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 0.04282 *
## hospitaldischargeyear2012 9.90e-05 ***
## hospitaldischargeyear2013 2.47e-09 ***
## hospitaldischargeyear2014 < 2e-16 ***
## hospitaldischargeyear2015-16 2.39e-15 ***
## dialysis1                  2.25e-05 ***
## aids1                      2.85e-05 ***
## hepaticfailureTRUE         < 2e-16 ***
## diabetes1                 < 2e-16 ***
## immunosuppression1        < 2e-16 ***
## leukemial                  < 2e-16 ***
## lymphoma1                  1.00e-05 ***
## metastaticcancer1         < 2e-16 ***
## thrombolytics1             1.69e-12 ***
## sofa_respiration_baseline2TRUE 1.80e-13 ***
## cardiovascular_baseline1   2.50e-08 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603 on 638756 degrees of freedom
## Residual deviance: 351548 on 638709 degrees of freedom
## AIC: 351644
##
## Number of Fisher Scoring iterations: 7

```

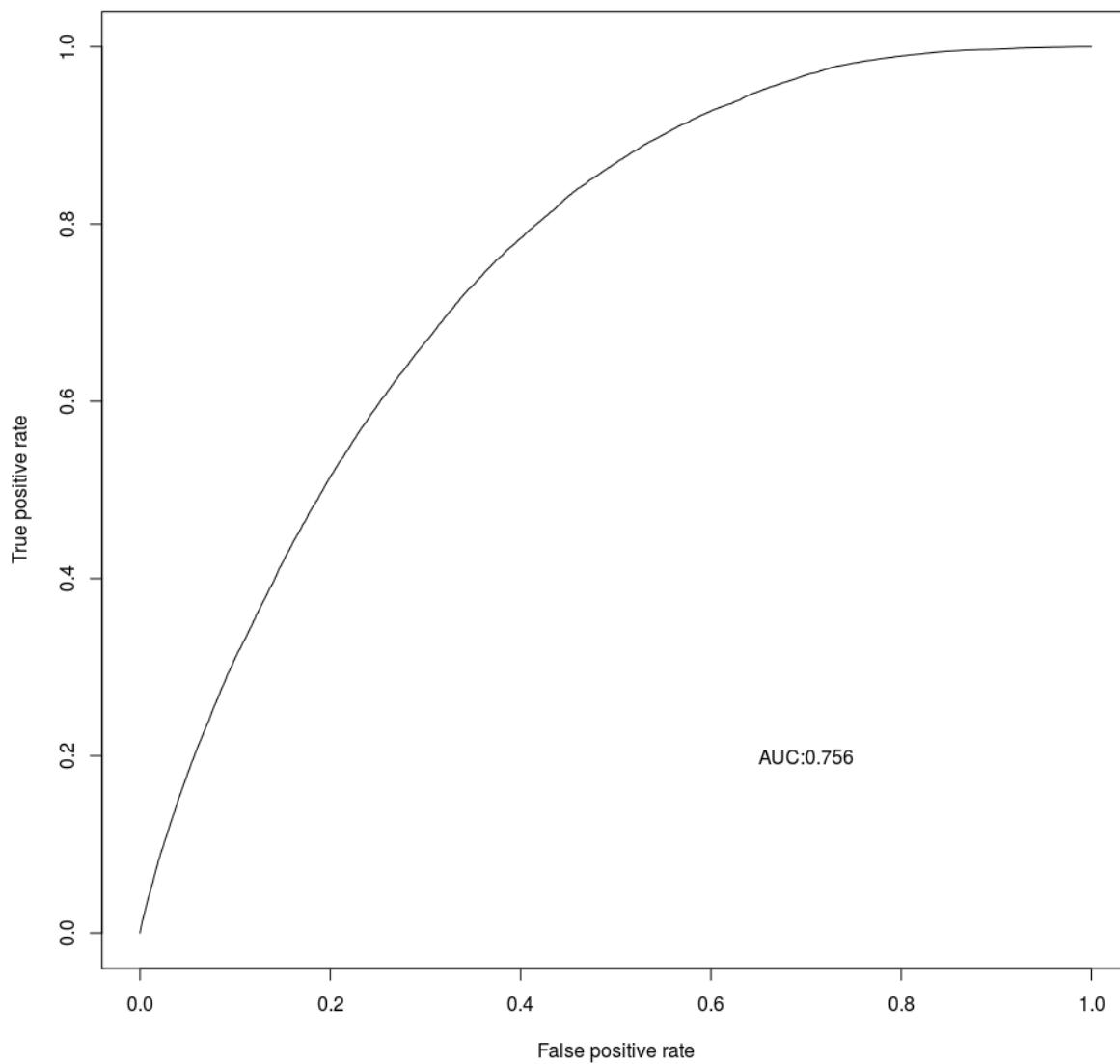
```

ssd_incl_te$SOFA3ADJHospMortPred <- predict(SOFA3_ADJ_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")

SOFA3ADJMort.Pred <- prediction(ssd_incl_te$SOFA3ADJHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
SOFA3ADJMort.Perf <- performance(SOFA3ADJMort.Pred, "tpr", "fpr")
plot(SOFA3ADJMort.Perf, main = "SOFA Positive w/o Baseline Adjusted
Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA3ADJMort.Pred,"auc")@y.values[[1]],3)))

```

**SOFA Positive w/o Baseline Adjusted
Mortality Prediction Test Model**



```
performance(SOFA3ADJMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7562943
##
## Slot "alpha.values":
## list()
```

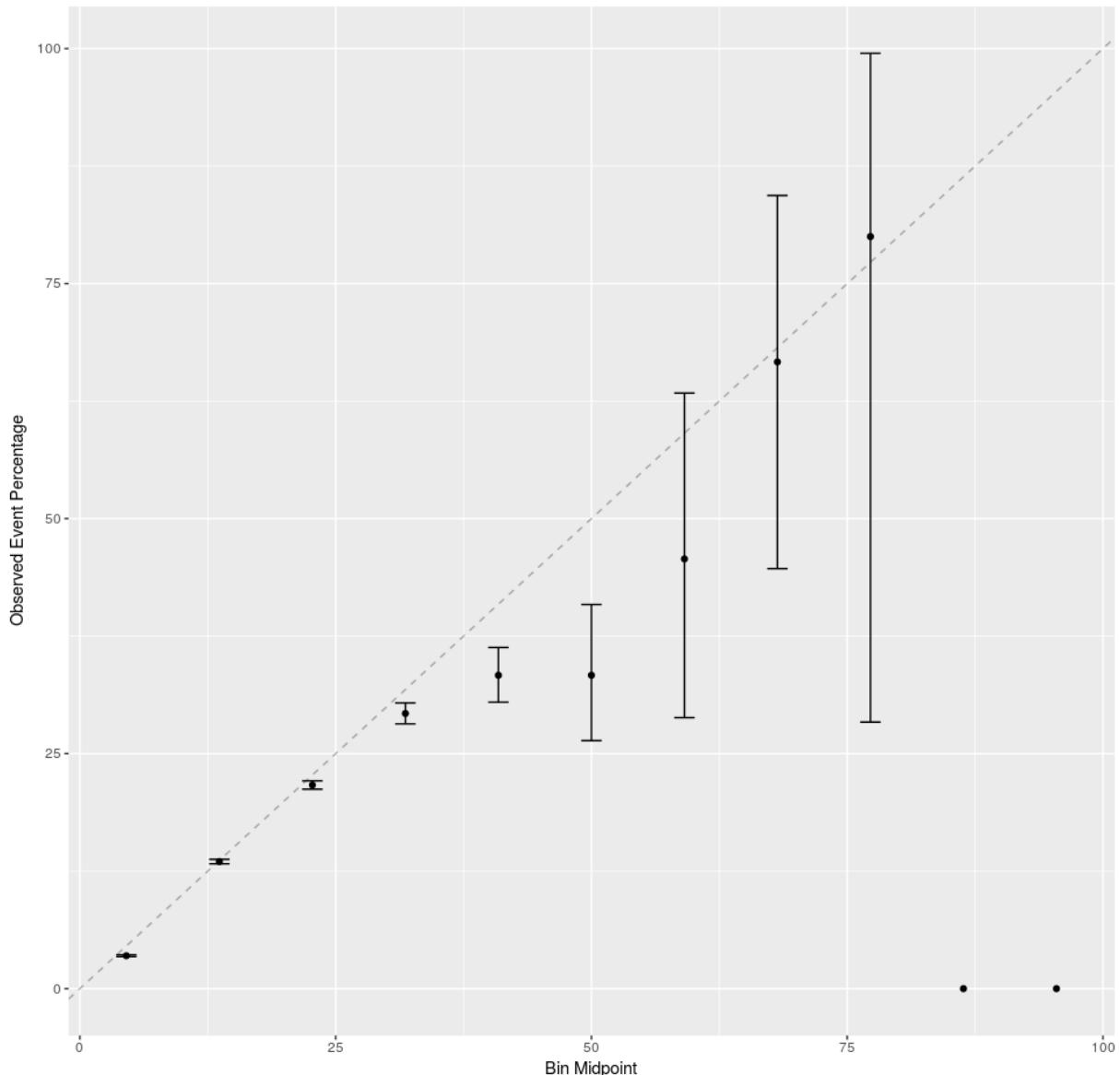
```
SOFA3ADJMort.Pred.roc <- roc(hospital_mortality_ultimate~ SOFA3ADJHospMortPred,data=ssd_incl_te)
ci(SOFA3ADJMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7528-0.7598 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~SOFA3ADJHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of ADJ Mortality SOFA Positive w/o Baseline Prediction")
```

```
## Warning: Removed 2 rows containing missing values (geom_errorbar).
```

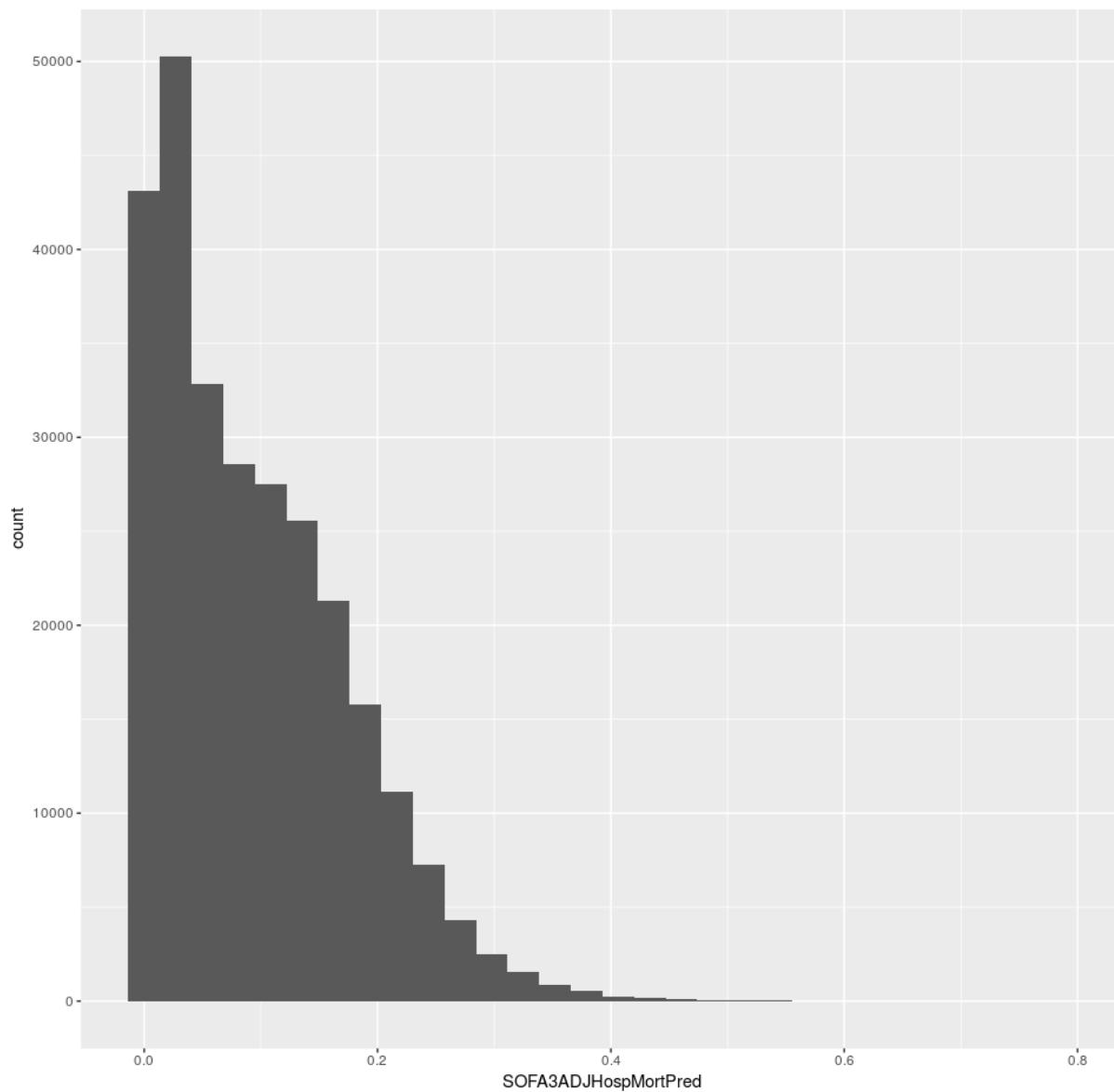
Calibration of ADJ Mortality SOFA Positive w/o Baseline Prediction



```
qplot(SOFA3ADJHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of ADJ Mortality SOFA Positive w/o Baseline Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of ADJ Mortality SOFA Positive w/o Baseline Predictions



```
qSOFA1_ADJ_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(qSOFA_total) + age_Ranges + gender2 + ethnic
ity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospita
ldischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastas
ticcancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomi
al",na.action = na.omit)

#sjp.glm(qSOFA1_ADJ_Hosp_Mort_tr)
#sjt.glm(qSOFA1_ADJ_Hosp_Mort_tr)

#drop1(qSOFA1_ADJ_Hosp_Mort_tr,test="Chisq")

summary(qSOFA1_ADJ_Hosp_Mort_tr)
```

```

## Call:
## glm(formula = hospital_mortality_ultimate ~ as.factor(qSOFA_total) +
##       age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 +
##       hospital_teaching_status + hospital_size + physicianSpeciality2 +
##       hospitaldischargeyear + dialysis + aids + hepaticfailure +
##       diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer +
##       thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline,
##       family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.0781 -0.4725 -0.3128 -0.1937  3.5246
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -4.48635  0.06848 -65.509 < 2e-16
## as.factor(qSOFA_total)1     1.00808  0.04734  21.293 < 2e-16
## as.factor(qSOFA_total)2     1.94445  0.04577  42.483 < 2e-16
## as.factor(qSOFA_total)3     2.95871  0.04575  64.676 < 2e-16
## age_Ranges(25,35]           0.24743  0.04965  4.984 6.24e-07
## age_Ranges(35,45]           0.42222  0.04584  9.210 < 2e-16
## age_Ranges(45,55]           0.73252  0.04242 17.267 < 2e-16
## age_Ranges(55,65]           0.98791  0.04159 23.752 < 2e-16
## age_Ranges(65,75]           1.22975  0.04141 29.698 < 2e-16
## age_Ranges(75,85]           1.49355  0.04134 36.125 < 2e-16
## age_Ranges(85,100]          1.66198  0.04219 39.393 < 2e-16
## gender2Female               -0.09968  0.00918 -10.858 < 2e-16
## gender2Other/Unknown        1.85305  0.18824  9.844 < 2e-16
## ethnicity2African American  0.03574  0.01514  2.360 0.018255
## ethnicity2Hispanic          0.11388  0.02188  5.205 1.94e-07
## ethnicity2Asian              0.14790  0.03872  3.820 0.000134
## ethnicity2Native American   0.31628  0.05041  6.274 3.51e-10
## ethnicity2Other/Unknown     0.23091  0.01960 11.781 < 2e-16
## BMI_Ranges(18.5,25]         -0.25980  0.01918 -13.548 < 2e-16
## BMI_Ranges(25,35]           -0.37658  0.01892 -19.909 < 2e-16
## BMI_Ranges(35,200]          -0.26780  0.02112 -12.680 < 2e-16
## BMI_RangesOther/Unknown    0.11647  0.02776  4.196 2.72e-05
## icu_admit_source2OR/Proc Area -1.36067  0.01785 -76.233 < 2e-16
## icu_admit_source2Direct Admit -0.24365  0.01612 -15.119 < 2e-16
## icu_admit_source2Emergency Department -0.39992  0.01111 -35.980 < 2e-16
## icu_admit_source2Other      -0.10582  0.04178 -2.533 0.011308
## icu_admit_source2Step-Down Unit 0.14124  0.02571  5.493 3.94e-08
## hospital_teaching_statusf   -0.22706  0.03302 -6.878 6.09e-12
## hospital_teaching_statust   -0.35201  0.03319 -10.606 < 2e-16
## hospital_size<100          -0.25685  0.03725 -6.896 5.35e-12
## hospital_size100-249        0.18021  0.02594  6.948 3.70e-12
## hospital_size250-500        0.25599  0.02618  9.778 < 2e-16
## hospital_size>500           0.38362  0.02426 15.814 < 2e-16
## physicianSpeciality2Speciality-Other -0.25256  0.01014 -24.904 < 2e-16
## hospitaldischargeyear2011   -0.08942  0.01737 -5.147 2.65e-07
## hospitaldischargeyear2012   -0.16375  0.01675 -9.777 < 2e-16
## hospitaldischargeyear2013   -0.20339  0.01646 -12.355 < 2e-16
## hospitaldischargeyear2014   -0.23849  0.01640 -14.542 < 2e-16
## hospitaldischargeyear2015-16 -0.24052  0.01622 -14.824 < 2e-16
## dialysis1                   0.30372  0.02307 13.166 < 2e-16
## aids1                        0.47169  0.12083  3.904 9.47e-05
## hepaticfailureTRUE           0.66597  0.02526 26.366 < 2e-16
## diabetes1                   -0.26099  0.01188 -21.968 < 2e-16
## immunosuppression1           0.42742  0.02603 16.422 < 2e-16
## leukemial                    0.51659  0.04108 12.575 < 2e-16
## lymphomai                     0.29826  0.05838  5.109 3.24e-07
## metastaticcancer1            0.70288  0.02718 25.858 < 2e-16
## thrombolytics1                0.15957  0.03535  4.514 6.35e-06
## sofa_respiration_baseline2TRUE 0.02806  0.01036  2.708 0.006764
## cardiovascular_baseline1     0.11607  0.01059 10.961 < 2e-16
##
## (Intercept)                 ***
## as.factor(qSOFA_total)1      ***
## as.factor(qSOFA_total)2      ***
## as.factor(qSOFA_total)3      ***
## age_Ranges(25,35]            ***
## age_Ranges(35,45]            ***
## age_Ranges(45,55]            ***
## age_Ranges(55,65]            ***
## age_Ranges(65,75]            ***
## age_Ranges(75,85]            ***
## age_Ranges(85,100]           ***

```

```

## gender2Female      ***
## gender2Other/Unknown ***
## ethnicity2African American *
## ethnicity2Hispanic   ***
## ethnicity2Asian     ***
## ethnicity2Native American ***
## ethnicity2Other/Unknown ***
## BMI_Ranges(18.5,25] ***
## BMI_Ranges(25,35]   ***
## BMI_Ranges(35,200]  ***
## BMI_RangesOther/Unknown ***
## icu_admit_source2OR/Proc Area ***
## icu_admit_source2Direct Admit ***
## icu_admit_source2Emergency Department ***
## icu_admit_source2Other    *
## icu_admit_source2Step-Down Unit ***
## hospital_teaching_statusf ***
## hospital_teaching_statust ***
## hospital_size<100    ***
## hospital_size100-249  ***
## hospital_size250-500  ***
## hospital_size>500    ***
## physicianSpeciality2Speciality-Other ***
## hospitaldischargeyear2011 ***
## hospitaldischargeyear2012 ***
## hospitaldischargeyear2013 ***
## hospitaldischargeyear2014 ***
## hospitaldischargeyear2015-16 ***
## dialysis1      ***
## aids1        ***
## hepaticfailureTRUE ***
## diabetes1    ***
## immunosuppression1 ***
## leukemia1    ***
## lymphoma1    ***
## metastaticcancer1 ***
## thrombolytics1 ***
## sofa_respiration_baseline2TRUE **
## cardiovascular_baseline1 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603 on 638756 degrees of freedom
## Residual deviance: 343488 on 638707 degrees of freedom
## AIC: 343588
##
## Number of Fisher Scoring iterations: 7

```

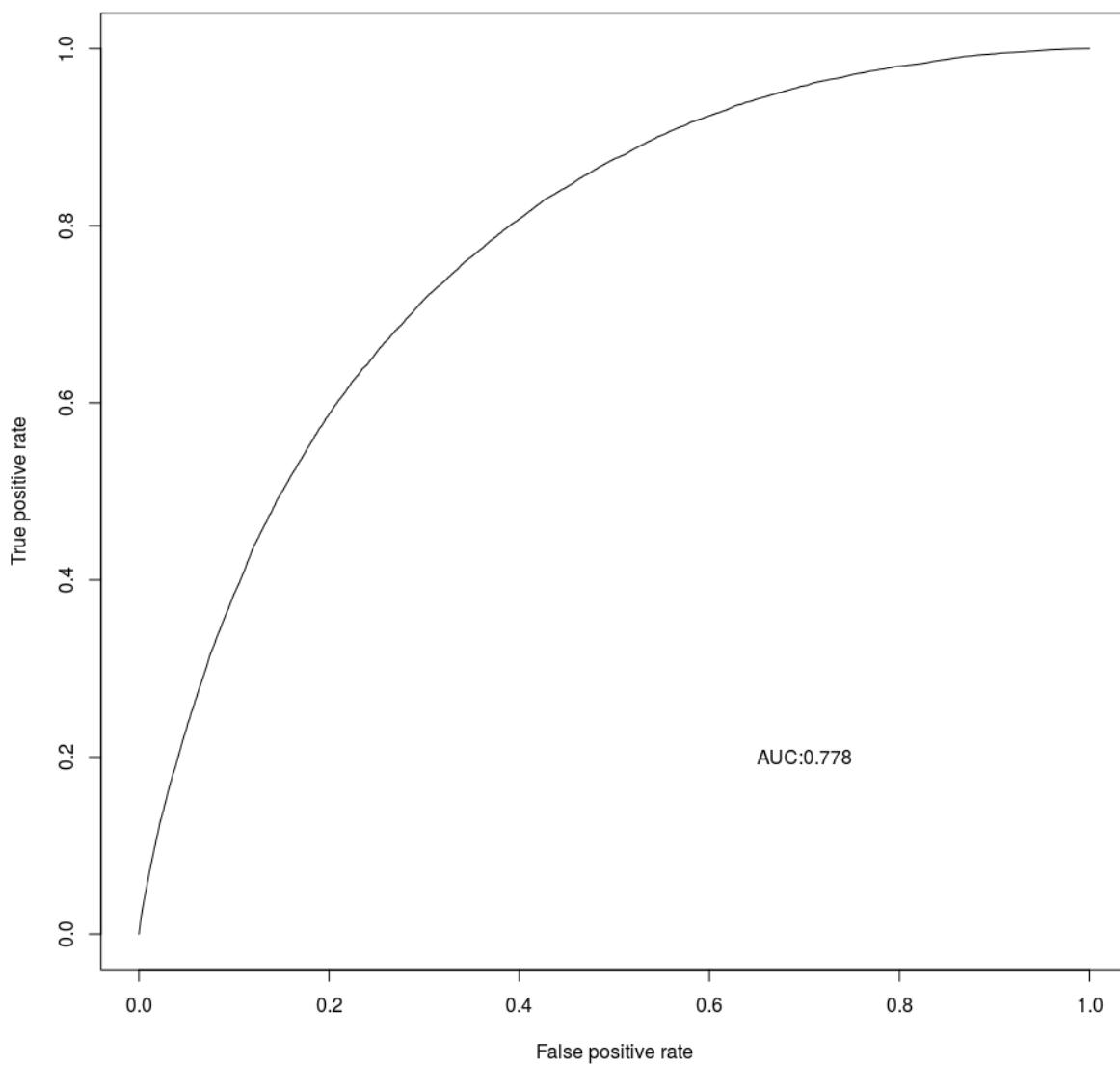
```

ssd_incl_te$qSOFA1ADJHospMortPred <- predict(qSOFA1_ADJ_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

qSOFA1ADJMort.Pred <- prediction(ssd_incl_te$qSOFA1ADJHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
qSOFA1ADJMort.Perf <- performance(qSOFA1ADJMort.Pred, "tpr", "fpr")
plot(qSOFA1ADJMort.Perf, main = "qSOFA1 Continuous Adjusted Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(qSOFA1ADJMort.Pred,"auc")@y.values[[1]],3)))

```

**qSOFA1 Continuous Adjusted
Mortality Prediction Test Model**



```
performance(qSOFA1ADJMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7777231
##
## Slot "alpha.values":
## list()
```

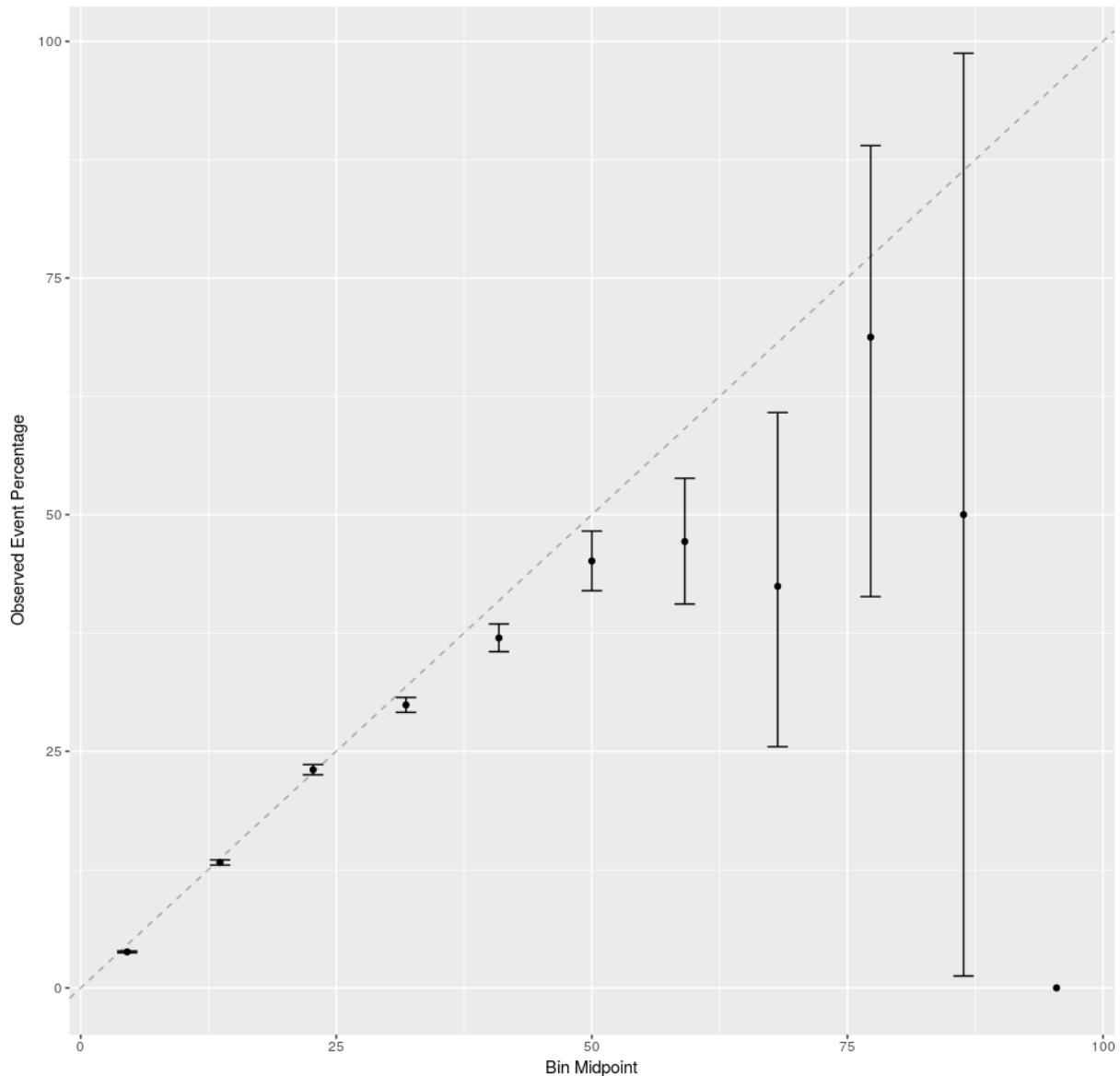
```
qSOFA1ADJMort.Pred.roc <- roc(hospital_mortality_ultimate~ qSOFA1ADJHospMortPred,data=ssd_incl_te)
ci(qSOFA1ADJMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7741-0.7814 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~qSOFA1ADJHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of ADJ Mortality qSOFA Total Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

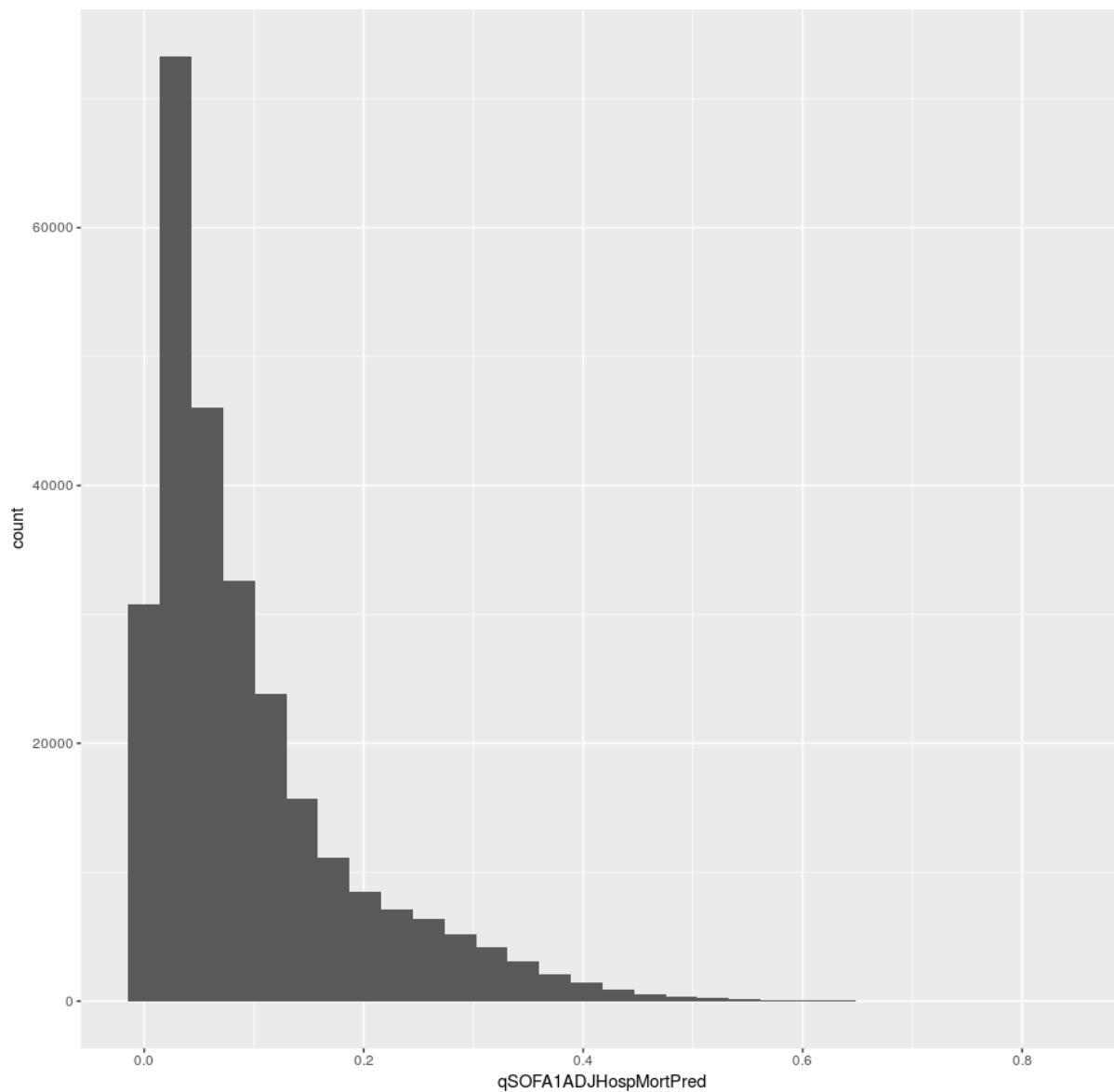
Calibration of ADJ Mortality qSOFA Total Prediction



```
qplot(qSOFA1ADJHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of ADJ Mortality qSOFA Total Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of ADJ Mortality qSOFA Total Predictions



```
qSOFA2_ADJ_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(qSOFA_Positive) + age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(qSOFA2_ADJ_Hosp_Mort_tr)
#sjt.glm(qSOFA2_ADJ_Hosp_Mort_tr)

#drop1(qSOFA2_ADJ_Hosp_Mort_tr,test="Chisq")

summary(qSOFA2_ADJ_Hosp_Mort_tr)
```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(qSOFA_Positive) +
##     age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 +
##     hospital_teaching_status + hospital_size + physicianSpeciality2 +
##     hospitaldischargeyear + dialysis + aids + hepaticfailure +
##     diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer +
##     thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline,
##     family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.8052 -0.5088 -0.3339 -0.2045  3.4565
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -3.508901  0.052607 -66.701
## as.factor(qSOFA_Positive)TRUE 1.525327  0.014401 105.917
## age_Ranges(25,35]            0.241662  0.049333  4.899
## age_Ranges(35,45]            0.420857  0.045539  9.242
## age_Ranges(45,55]            0.737753  0.042141 17.507
## age_Ranges(55,65]            1.000275  0.041316 24.211
## age_Ranges(65,75]            1.244254  0.041131 30.251
## age_Ranges(75,85]            1.521611  0.041065 37.054
## age_Ranges(85,100]           1.730355  0.041881 41.316
## gender2Female               -0.093649  0.009044 -10.354
## gender2Other/Unknown         1.843265  0.184148 10.010
## ethnicity2African American  0.038999  0.014918  2.614
## ethnicity2Hispanic           0.106499  0.021534  4.946
## ethnicity2Asian              0.137830  0.038050  3.622
## ethnicity2Native American    0.367605  0.049623  7.408
## ethnicity2Other/Unknown       0.230829  0.019291 11.966
## BMI_Ranges(18.5,25]          -0.291869  0.018827 -15.502
## BMI_Ranges(25,35]             -0.432094  0.018573 -23.265
## BMI_Ranges(35,200]            -0.312671  0.020749 -15.069
## BMI_RangesOther/Unknown       0.048488  0.027255  1.779
## icu_admit_source2OR/Proc Area -1.412684  0.017669 -79.954
## icu_admit_source2Direct Admit -0.302155  0.015838 -19.078
## icu_admit_source2Emergency Department -0.435392  0.010916 -39.887
## icu_admit_source2Other         -0.093011  0.041049 -2.266
## icu_admit_source2Step-Down Unit 0.148979  0.025197  5.913
## hospital_teaching_statusf    -0.211453  0.032528 -6.501
## hospital_teaching_statust    -0.325831  0.032722 -9.957
## hospital_size<100            -0.347279  0.036784 -9.441
## hospital_size100-249          0.120466  0.025548  4.715
## hospital_size250-500          0.237521  0.025803  9.205
## hospital_size>500             0.364198  0.023914 15.229
## physicianSpeciality2Speciality-Other -0.330597  0.009956 -33.206
## hospitaldischargeyear2011     -0.072053  0.017091 -4.216
## hospitaldischargeyear2012     -0.140386  0.016480 -8.519
## hospitaldischargeyear2013     -0.195734  0.016207 -12.077
## hospitaldischargeyear2014     -0.230626  0.016150 -14.281
## hospitaldischargeyear2015-16   -0.210284  0.015972 -13.166
## dialysis1                      0.324834  0.022633 14.352
## aids1                          0.479190  0.118795  4.034
## hepaticfailureTRUE              0.705191  0.024767 28.473
## diabetes1                      -0.262420  0.011702 -22.426
## immunosuppression1              0.381358  0.025520 14.943
## leukemial                       0.491629  0.040230 12.220
## lymphomai                        0.275756  0.057416  4.803
## metastaticcancer1               0.680467  0.026658 25.526
## thrombolytics1                  0.054774  0.034907  1.569
## sofa_respiration_baseline2TRUE  0.049611  0.010198  4.865
## cardiovascular_baseline1        0.098528  0.010413  9.462
## 
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## as.factor(qSOFA_Positive)TRUE < 2e-16 ***
## age_Ranges(25,35] 9.65e-07 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female < 2e-16 ***
## gender2Other/Unknown < 2e-16 ***
## ethnicity2African American 0.008944 **
## ethnicity2Hispanic 7.59e-07 ***

```

```

## ethnicity2Asian          0.000292 ***
## ethnicity2Native American 1.28e-13 ***
## ethnicity2Other/Unknown   < 2e-16 ***
## BMI_Ranges(18.5,25]      < 2e-16 ***
## BMI_Ranges(25,35]        < 2e-16 ***
## BMI_Ranges(35,200]       < 2e-16 ***
## BMI_RangesOther/Unknown  0.075230 .
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other     0.023460 *
## icu_admit_source2Step-Down Unit 3.37e-09 ***
## hospital_teaching_statusf 8.00e-11 ***
## hospital_teaching_statust  < 2e-16 ***
## hospital_size<100         < 2e-16 ***
## hospital_size100-249       2.41e-06 ***
## hospital_size250-500       < 2e-16 ***
## hospital_size>500         < 2e-16 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 2.49e-05 ***
## hospitaldischargeyear2012  < 2e-16 ***
## hospitaldischargeyear2013  < 2e-16 ***
## hospitaldischargeyear2014  < 2e-16 ***
## hospitaldischargeyear2015-16 < 2e-16 ***
## dialysis1                  < 2e-16 ***
## aids1                      5.49e-05 ***
## hepaticfailureTRUE         < 2e-16 ***
## diabetes1                 < 2e-16 ***
## immunosuppression1        < 2e-16 ***
## leukemial                  < 2e-16 ***
## lymphoma1                  1.57e-06 ***
## metastaticcancer1         < 2e-16 ***
## thrombolytics1             0.116617
## sofa_respiration_baseline2TRUE 1.15e-06 ***
## cardiovascular_baseline1   < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603 on 638756 degrees of freedom
## Residual deviance: 355239 on 638709 degrees of freedom
## AIC: 355335
##
## Number of Fisher Scoring iterations: 6

```

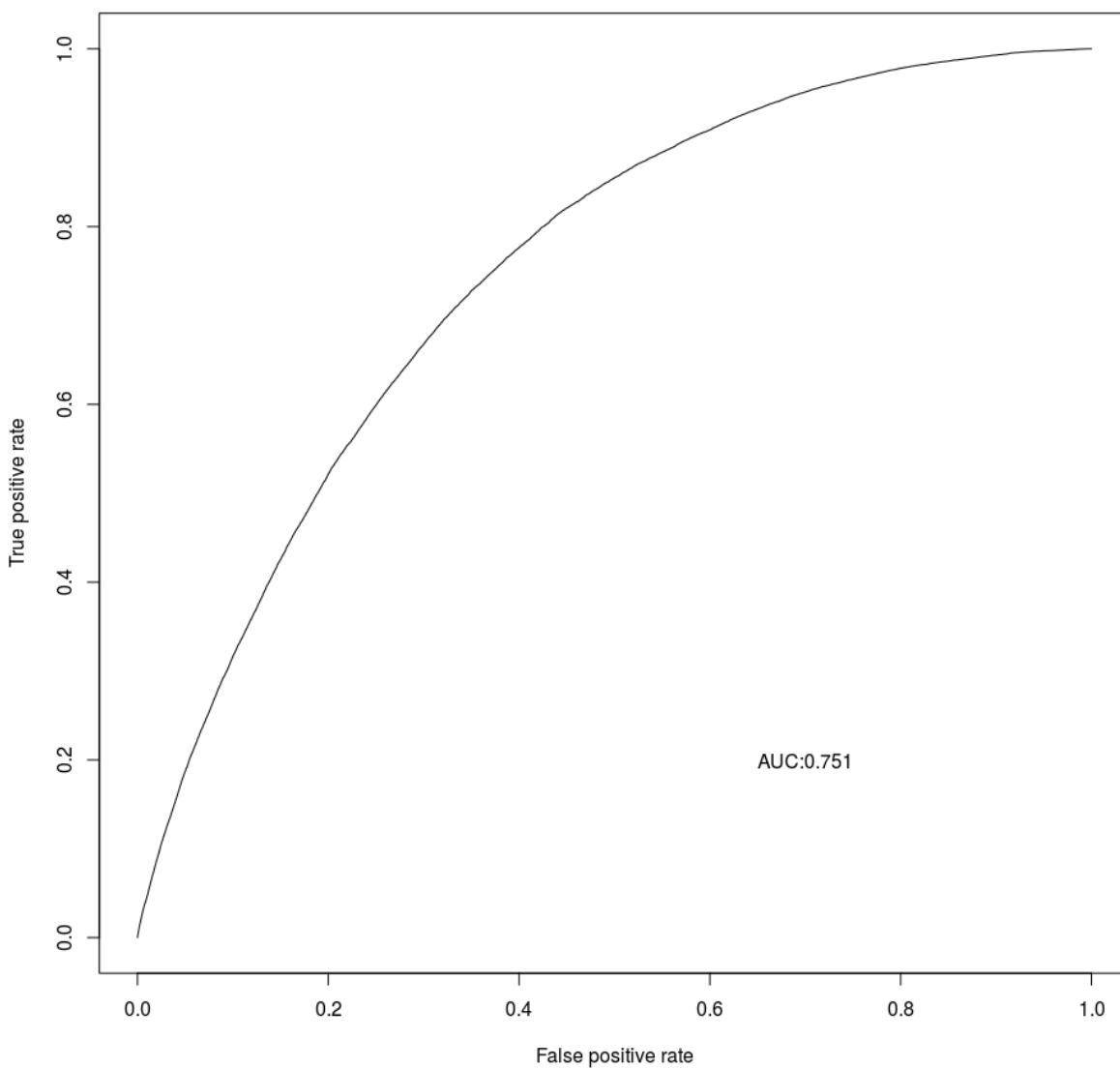
```

ssd_incl_te$qSOFA2ADJHospMortPred <- predict(qSOFA2_ADJ_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type
      ="response")
library(sjPlot)
library(ROCR)

qSOFA2ADJMort.Pred <- prediction(ssd_incl_te$qSOFA2ADJHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
qSOFA2ADJMort.Perf <- performance(qSOFA2ADJMort.Pred, "tpr", "fpr")
plot(qSOFA2ADJMort.Perf, main = "qSOFA Positive Adjusted
                           Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(qSOFA2ADJMort.Pred,"auc")@y.values[[1]],3)))

```

**qSOFA Positive Adjusted
Mortality Prediction Test Model**



```
performance(qSOFA2ADJMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7505584
##
## Slot "alpha.values":
## list()
```

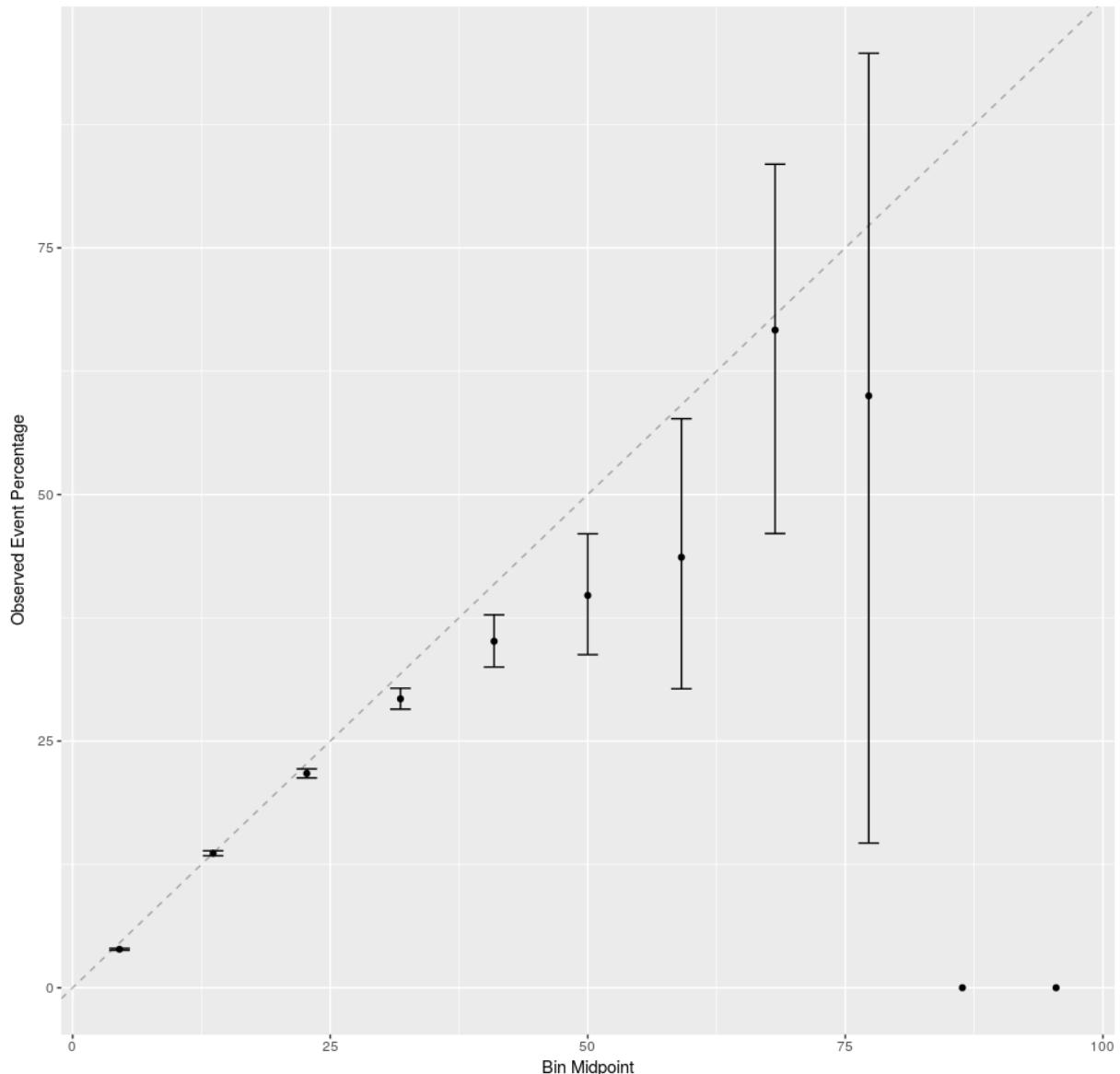
```
qSOFA2ADJMort.Pred.roc <- roc(hospital_mortality_ultimate~ qSOFA2ADJHospMortPred,data=ssd_incl_te)
ci(qSOFA2ADJMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7468-0.7543 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~qSOFA2ADJHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of ADJ Mortality qSOFA Positive Prediction")
```

```
## Warning: Removed 2 rows containing missing values (geom_errorbar).
```

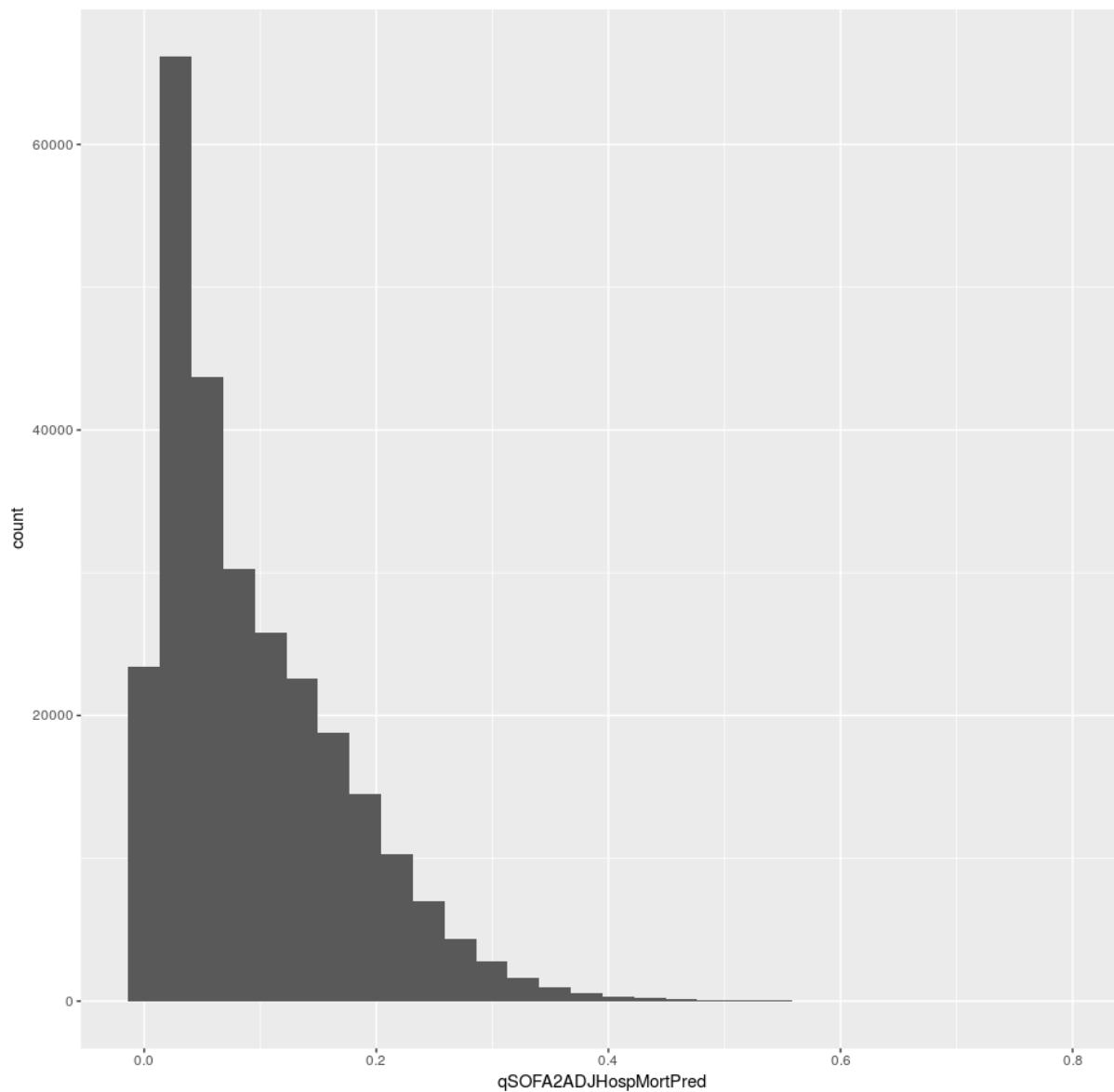
Calibration of ADJ Mortality qSOFA Positive Prediction



```
qplot(qSOFA2ADJHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of ADJ Mortality qSOFA Positive Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of ADJ Mortality qSOFA Positive Predictions



```
FuzzyLogic_ADJ_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(SepsisFuzzyLogicPositive) + age_Ranges +
  gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeci-
  ality2 + hospitaldischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + ly-
  mphoma + metastaticcancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_t
  r,family="binomial",na.action = na.omit)

#sjp.glm(FuzzyLogic_ADJ_Hosp_Mort_tr)
#sjt.glm(FuzzyLogic_ADJ_Hosp_Mort_tr)

#drop1(FuzzyLogic_ADJ_Hosp_Mort_tr,test="Chisq")

summary(FuzzyLogic_ADJ_Hosp_Mort_tr)
```

```

## 
## Call:
## glm(formula = hospital_mortality_ultimate ~ as.factor(SepsisFuzzyLogicPositive) +
##     age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 +
##     hospital_teaching_status + hospital_size + physicianSpeciality2 +
##     hospitaldischargeyear + dialysis + aids + hepaticfailure +
##     diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer +
##     thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline,
##     family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.8613 -0.5004 -0.2999 -0.1855  3.4055
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -3.703509  0.052600 -70.409
## as.factor(SepsisFuzzyLogicPositive)TRUE 1.759015  0.012570 139.935
## age_Ranges(25,35]            0.263667  0.049480  5.329
## age_Ranges(35,45]            0.477884  0.045685 10.460
## age_Ranges(45,55]            0.800031  0.042270 18.927
## age_Ranges(55,65]            1.054713  0.041430 25.458
## age_Ranges(65,75]            1.297053  0.041250 31.444
## age_Ranges(75,85]            1.595510  0.041199 38.727
## age_Ranges(85,100]           1.846771  0.042060 43.907
## gender2Female               -0.088610  0.009142 -9.692
## gender2Other/Unknown         1.881151  0.189779  9.912
## ethnicity2African American  0.063468  0.015096  4.204
## ethnicity2Hispanic           0.042223  0.021731  1.943
## ethnicity2Asian              0.168140  0.038579  4.358
## ethnicity2Native American   0.336567  0.050201  6.704
## ethnicity2Other/Unknown      0.169244  0.019481  8.688
## BMI_Ranges(18.5,25]          -0.294102  0.019073 -15.420
## BMI_Ranges(25,35]            -0.456729  0.018798 -24.297
## BMI_Ranges(35,200]           -0.375163  0.020956 -17.903
## BMI_RangesOther/Unknown      0.130032  0.027747  4.686
## icu_admit_source2OR/Proc Area -1.469098  0.017785 -82.603
## icu_admit_source2Direct Admit -0.183843  0.016137 -11.392
## icu_admit_source2Emergency Department -0.440011  0.011052 -39.815
## icu_admit_source2Other        0.009575  0.041861  0.229
## icu_admit_source2Step-Down Unit 0.203620  0.025668  7.933
## hospital_teaching_statusf    -0.074412  0.032934 -2.259
## hospital_teaching_statust   -0.196285  0.033411 -5.875
## hospital_size<100           -0.541007  0.037110 -14.578
## hospital_size100-249         -0.035444  0.025884 -1.369
## hospital_size250-500         0.068296  0.026132  2.614
## hospital_size>500            0.220763  0.024403  9.047
## physicianSpeciality2Speciality-Other -0.254490  0.010172 -25.019
## hospitaldischargeyear2011    -0.040090  0.017261 -2.323
## hospitaldischargeyear2012    -0.067581  0.016650 -4.059
## hospitaldischargeyear2013    -0.111525  0.016367 -6.814
## hospitaldischargeyear2014    -0.143785  0.016309 -8.816
## hospitaldischargeyear2015-16 -0.129634  0.016130 -8.037
## dialysis1                     0.338289  0.022950 14.740
## aids1                         0.466865  0.119626  3.903
## hepaticfailureTRUE            0.574390  0.024879 23.087
## diabetes1                     -0.144764  0.011815 -12.253
## immunosuppression1            0.295457  0.025719 11.488
## leukemial                      0.398376  0.040567  9.820
## lymphomai                      0.220802  0.057899  3.814
## metastaticcancer1             0.640238  0.026978 23.732
## thrombolytics1                 0.191425  0.035568  5.382
## sofa_respiration_baseline2TRUE -0.027827  0.010317 -2.697
## cardiovascular_baseline1       0.113244  0.010540 10.744
## 
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## as.factor(SepsisFuzzyLogicPositive)TRUE < 2e-16 ***
## age_Ranges(25,35] 9.89e-08 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female < 2e-16 ***
## gender2Other/Unknown < 2e-16 ***
## ethnicity2African American 2.62e-05 ***
## ethnicity2Hispanic 0.052014 .

```

```

## ethnicity2Asian          1.31e-05 ***
## ethnicity2Native American 2.02e-11 ***
## ethnicity2Other/Unknown   < 2e-16 ***
## BMI_Ranges(18.5,25]      < 2e-16 ***
## BMI_Ranges(25,35]        < 2e-16 ***
## BMI_Ranges(35,200]       < 2e-16 ***
## BMI_RangesOther/Unknown  2.78e-06 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other      0.819081
## icu_admit_source2Step-Down Unit 2.14e-15 ***
## hospital_teaching_statusf 0.023857 *
## hospital_teaching_statust 4.23e-09 ***
## hospital_size<100         < 2e-16 ***
## hospital_size100-249       0.170899
## hospital_size250-500       0.008961 **
## hospital_size>500         < 2e-16 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 0.020203 *
## hospitaldischargeyear2012 4.93e-05 ***
## hospitaldischargeyear2013 9.49e-12 ***
## hospitaldischargeyear2014 < 2e-16 ***
## hospitaldischargeyear2015-16 9.23e-16 ***
## dialysis1                  < 2e-16 ***
## aids1                      9.51e-05 ***
## hepaticfailureTRUE         < 2e-16 ***
## diabetes1                 < 2e-16 ***
## immunosuppression1        < 2e-16 ***
## leukemial                  < 2e-16 ***
## lymphoma1                  0.000137 ***
## metastaticcancer1         < 2e-16 ***
## thrombolytics1             7.37e-08 ***
## sofa_respiration_baseline2TRUE 0.006994 **
## cardiovascular_baseline1   < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603 on 638756 degrees of freedom
## Residual deviance: 344313 on 638709 degrees of freedom
## AIC: 344409
##
## Number of Fisher Scoring iterations: 6

```

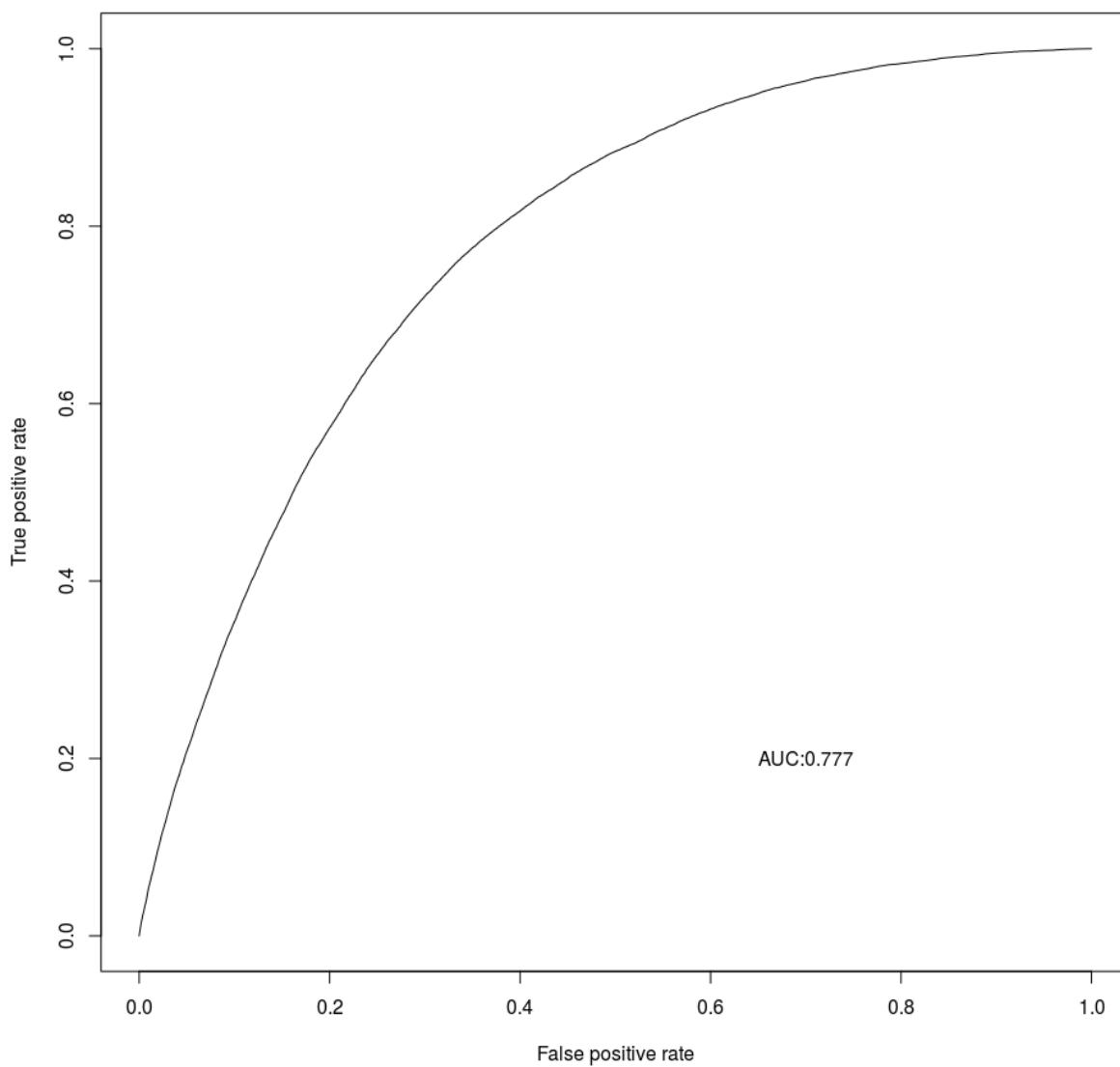
```

ssd_incl_te$FuzzyLogicADJHospMortPred <- predict(FuzzyLogic_ADJ_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

FuzzyLogicADJMort.Pred <- prediction(ssd_incl_te$FuzzyLogicADJHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
FuzzyLogicADJMort.Perf <- performance(FuzzyLogicADJMort.Pred, "tpr", "fpr")
plot(FuzzyLogicADJMort.Perf, main = "FuzzyLogic Positive Adjusted Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(FuzzyLogicADJMort.Pred,"auc")@y.values[[1]],3)))

```

**FuzzyLogic Positive Adjusted
Mortality Prediction Test Model**



```
performance(FuzzyLogicADJMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7767738
##
## Slot "alpha.values":
## list()
```

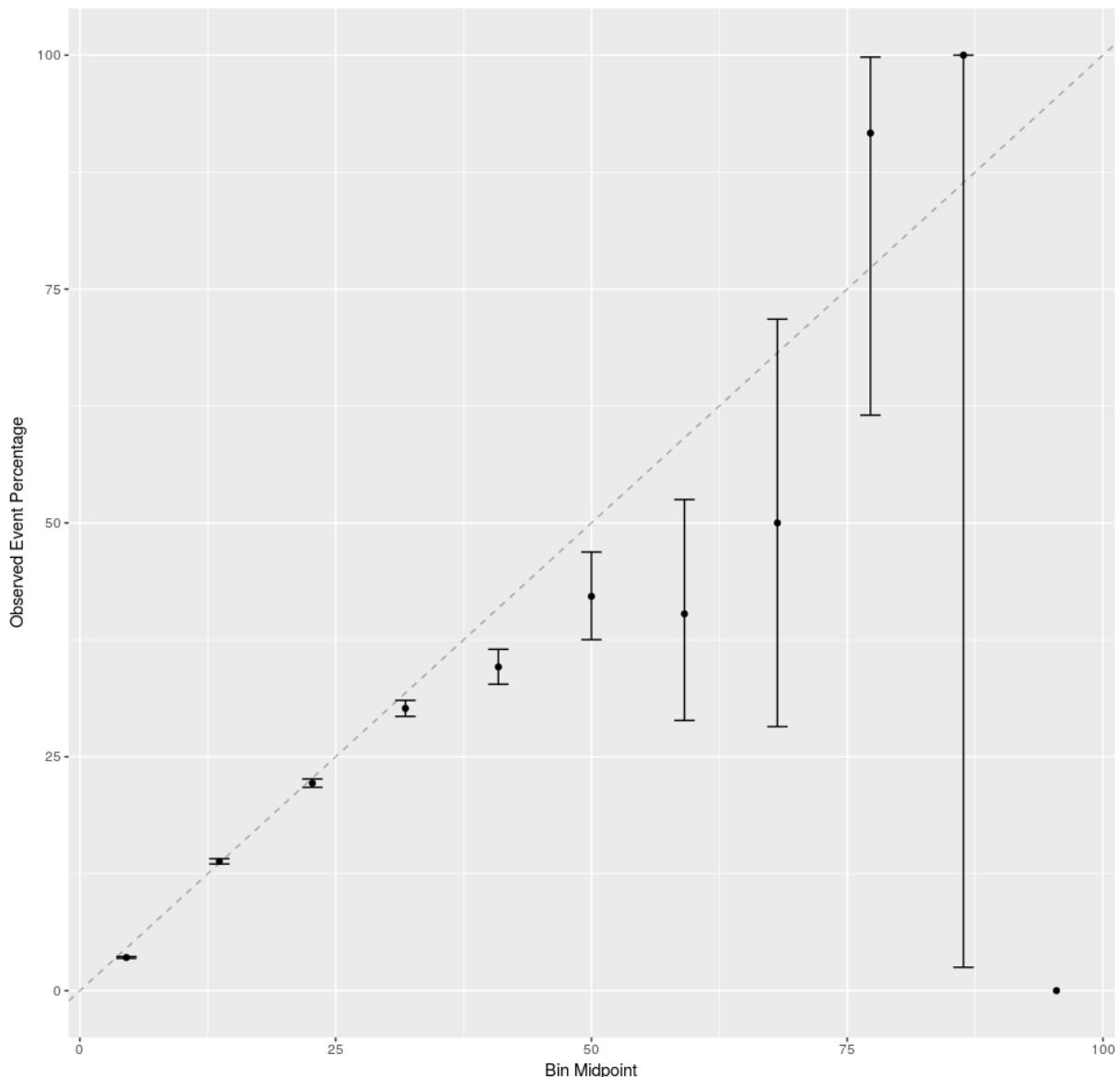
```
FuzzyLogicADJMort.Pred.roc <- roc(hospital_mortality_ultimate~ FuzzyLogicADJHospMortPred,data=ssd_incl_te)
ci(FuzzyLogicADJMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7733-0.7803 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~FuzzyLogicADJHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of ADJ Mortality FuzzyLogic Positive Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

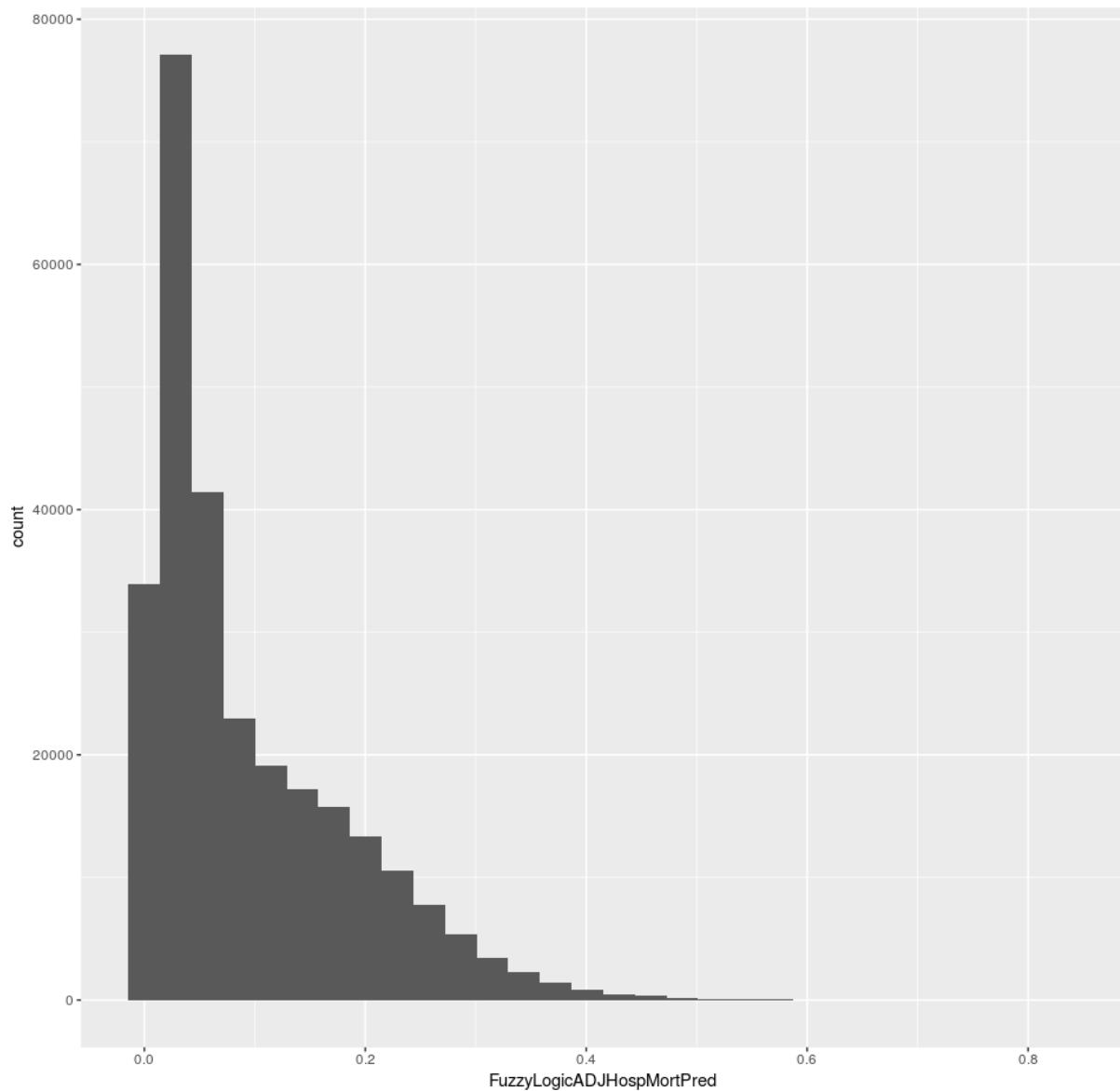
Calibration of ADJ Mortality FuzzyLogic Positive Prediction



```
qplot(FuzzyLogicADJHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of ADJ Mortality FuzzyLogic Positive Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of ADJ Mortality FuzzyLogic Positive Predictions



```
SIRS1_Crude_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(SIRS_total), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SIRS1_Crude_Hosp_Mort_tr)
#sjt.glm(SIRS1_Crude_Hosp_Mort_tr)

#drop1(SIRS1_Crude_Hosp_Mort_tr,test="Chisq")

summary(SIRS1_Crude_Hosp_Mort_tr)
```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(SIRS_total),
##       family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q  Median      3Q     Max
## -0.7314 -0.5259 -0.3661 -0.2475  2.8642
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -4.08504   0.04215 -96.91 <2e-16 ***
## as.factor(SIRS_total)1  0.61417   0.04544  13.52 <2e-16 ***
## as.factor(SIRS_total)2  1.41584   0.04302  32.91 <2e-16 ***
## as.factor(SIRS_total)3  2.17657   0.04271  50.96 <2e-16 ***
## as.factor(SIRS_total)4  2.90312   0.04303  67.47 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603  on 638756  degrees of freedom
## Residual deviance: 370766  on 638752  degrees of freedom
## AIC: 370776
##
## Number of Fisher Scoring iterations: 6

```

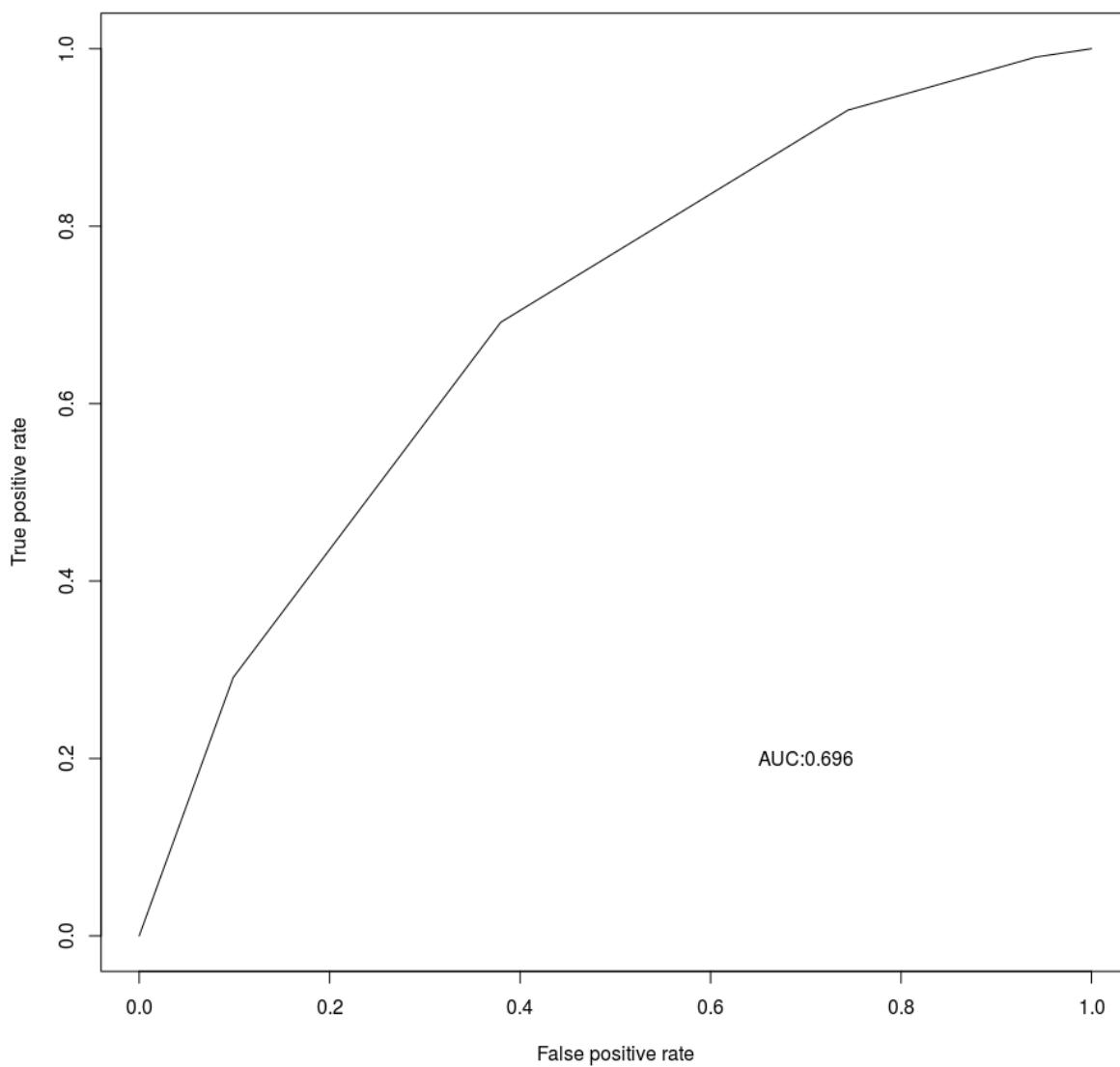
```

ssd_incl_te$SIRS1CrudeHospMortPred <- predict(SIRS1_Crude_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type
="response")

SIRS1CrudeMort.Pred <- prediction(ssd_incl_te$SIRS1CrudeHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
SIRS1CrudeMort.Perf <- performance(SIRS1CrudeMort.Pred, "tpr", "fpr")
plot(SIRS1CrudeMort.Perf, main = "SIRS Continuous Crude
Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SIRS1CrudeMort.Pred,"auc")@y.values[[1]],3)))

```

**SIRS Continuous Crude
Mortality Prediction Test Model**



```
performance(SIRS1CrudeMort.Pred, "auc")
```

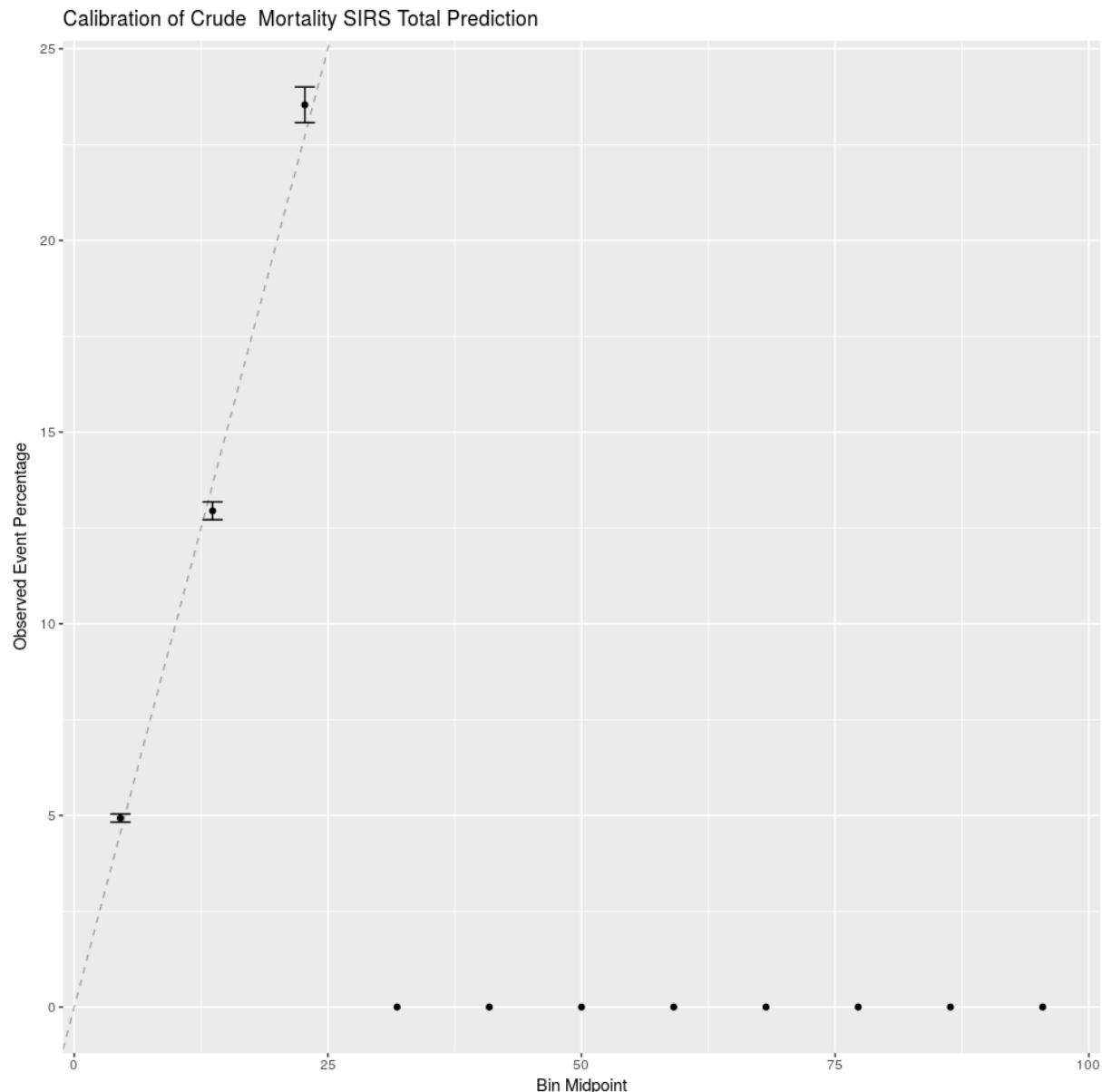
```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.6959156
##
## Slot "alpha.values":
## list()
```

```
SIRS1CrudeMort.Pred.roc <- roc(hospital_mortality_ultimate~ SIRS1CrudeHospMortPred,data=ssd_incl_te)
ci(SIRS1CrudeMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.6918-0.7 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~SIRS1CrudeHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of Crude Mortality SIRS Total Prediction")
```

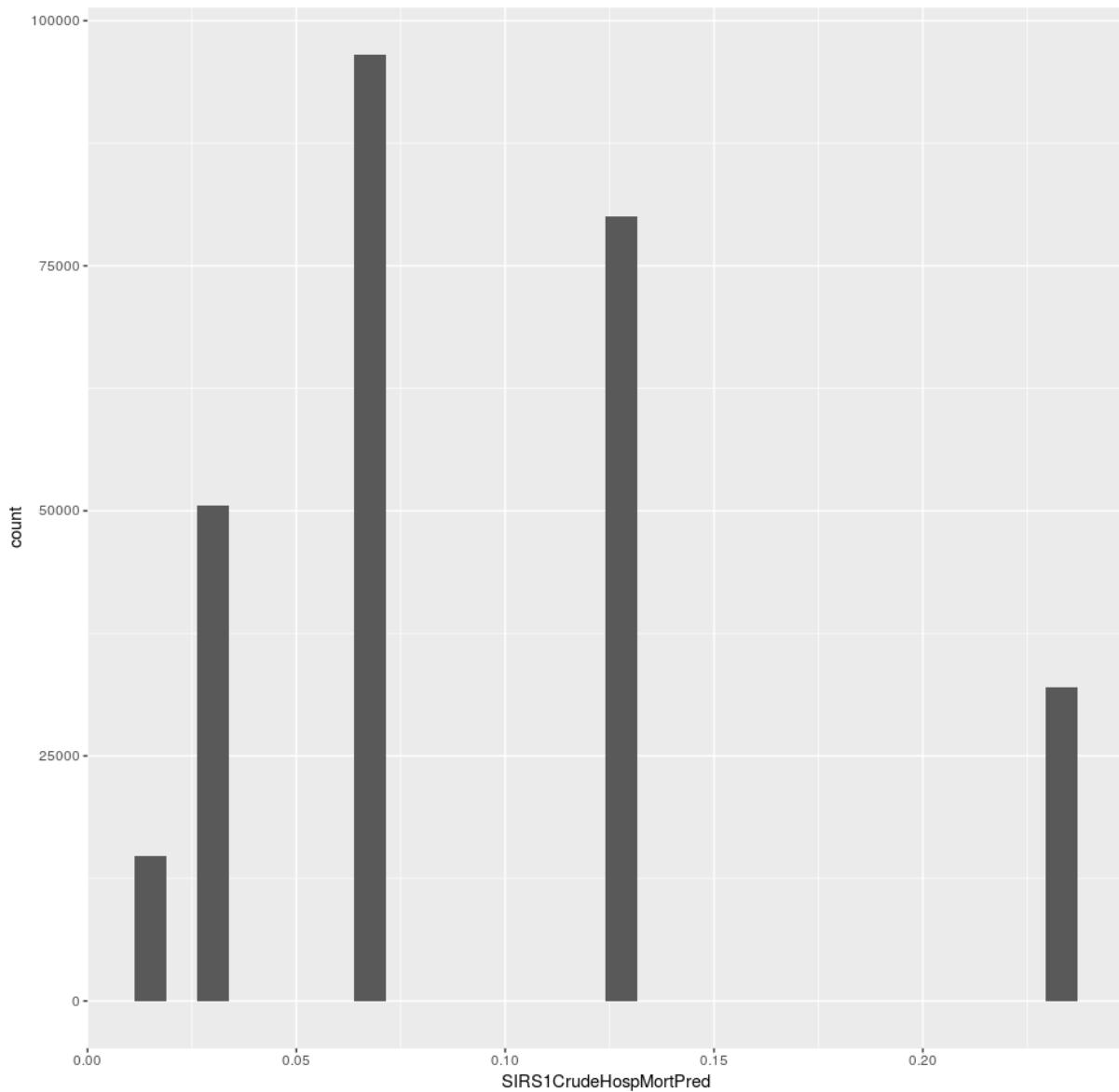
```
## Warning: Removed 8 rows containing missing values (geom_errorbar).
```



```
qplot(SIRS1CrudeHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of Crude Mortality SIRS Total Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of Crude Mortality SIRS Total Predictions



```
SIRS2_Crude_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(SIRS_Positive), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SIRS2_Crude_Hosp_Mort_tr)
#sjt.glm(SIRS2_Crude_Hosp_Mort_tr)

#drop1(SIRS2_Crude_Hosp_Mort_tr,test="Chisq")

summary(SIRS2_Crude_Hosp_Mort_tr)
```

```

## Call:
## glm(formula = hospital_mortality_ultimate ~ as.factor(SIRS_Positive),
##      family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q   Median      3Q     Max
## -0.4961 -0.4961 -0.4961 -0.2344  2.6865
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -3.58127   0.01573 -227.73 <2e-16 ***
## as.factor(SIRS_Positive)TRUE  1.54841   0.01635   94.68 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603  on 638756  degrees of freedom
## Residual deviance: 386134  on 638755  degrees of freedom
## AIC: 386138
##
## Number of Fisher Scoring iterations: 6

```

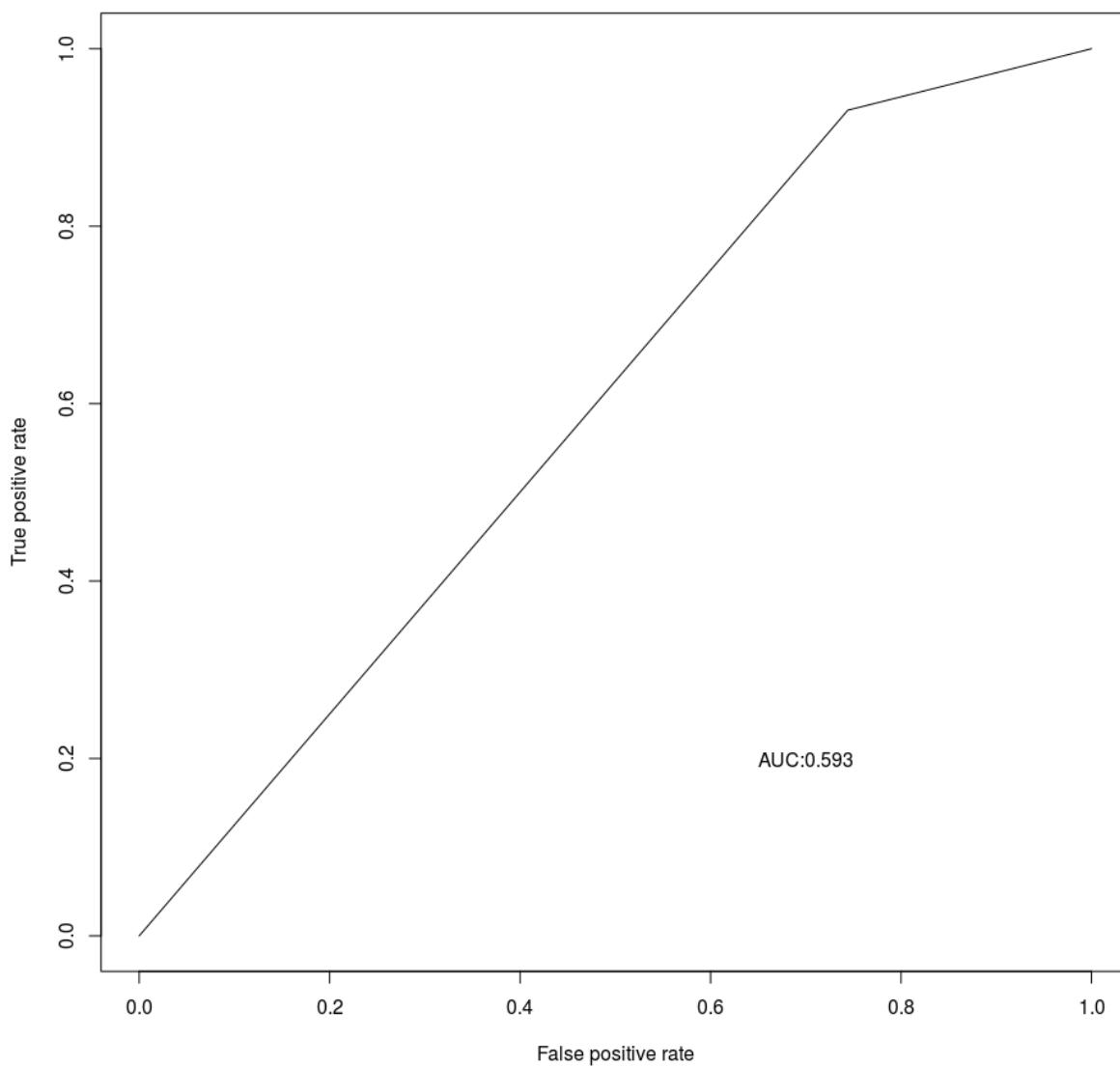
```

ssd_incl_te$SIRS2CrudeHospMortPred <- predict(SIRS2_Crude_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type
="response")

SIRS2CrudeMort.Pred <- prediction(ssd_incl_te$SIRS2CrudeHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
SIRS2CrudeMort.Perf <- performance(SIRS2CrudeMort.Pred, "tpr", "fpr")
plot(SIRS2CrudeMort.Perf, main = "SIRS Positive Crude
Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SIRS2CrudeMort.Pred, "auc")@y.values[[1]],3)))

```

**SIRS Positive Crude
Mortality Prediction Test Model**



```
performance(SIRS2CrudeMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.5932939
##
## Slot "alpha.values":
## list()
```

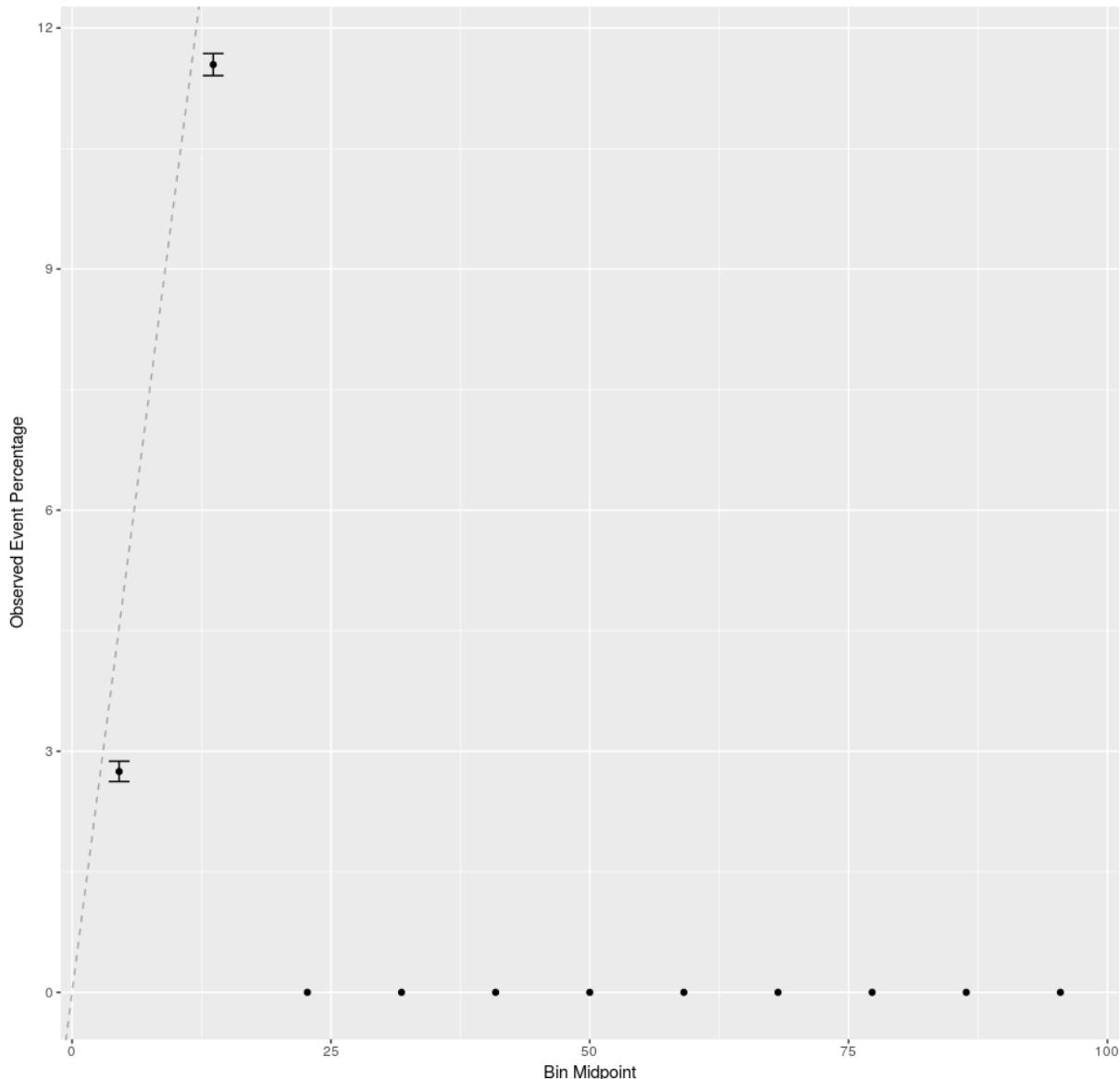
```
SIRS2CrudeMort.Pred.roc <- roc(hospital_mortality_ultimate~ SIRS2CrudeHospMortPred,data=ssd_incl_te)
ci(SIRS2CrudeMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.591–0.5956 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~SIRS2CrudeHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of Crude Mortality SIRS Positive Prediction")
```

```
## Warning: Removed 9 rows containing missing values (geom_errorbar).
```

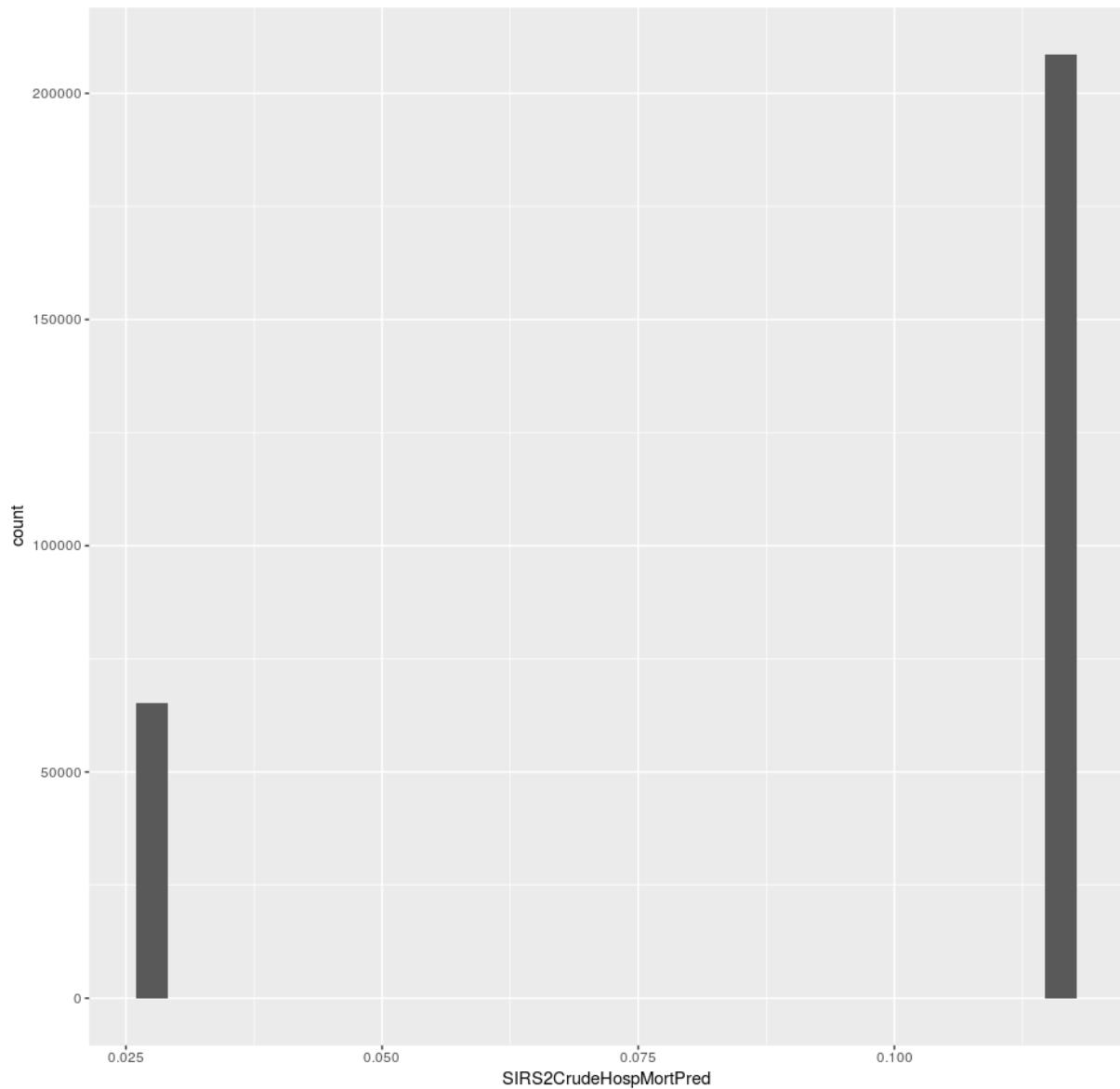
Calibration of Crude Mortality SIRS Positive Prediction



```
qplot(SIRS2CrudeHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of Crude Mortality SIRS Positive Prediction s")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of Crude Mortality SIRS Positive Predictions



```
SOFA1_Crude_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(SOFA_Change), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SOFA1_Crude_Hosp_Mort_tr)
#sjt.glm(SOFA1_Crude_Hosp_Mort_tr)

#drop1(SOFA1_Crude_Hosp_Mort_tr,test="Chisq")

summary(SOFA1_Crude_Hosp_Mort_tr)
```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(SOFA_Change),
##       family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q  Median      3Q     Max
## -1.9792 -0.4160 -0.2553 -0.1955  3.0374
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -4.60300  0.04361 -105.54 <2e-16 ***
## as.factor(SOFA_Change) 1    0.65495  0.04767   13.74 <2e-16 ***
## as.factor(SOFA_Change) 2    1.19523  0.04735   25.24 <2e-16 ***
## as.factor(SOFA_Change) 3    1.77503  0.04620   38.42 <2e-16 ***
## as.factor(SOFA_Change) 4    2.19953  0.04568   48.15 <2e-16 ***
## as.factor(SOFA_Change) 5    2.59747  0.04553   57.05 <2e-16 ***
## as.factor(SOFA_Change) 6    2.82348  0.04590   61.52 <2e-16 ***
## as.factor(SOFA_Change) 7    3.28928  0.04577   71.87 <2e-16 ***
## as.factor(SOFA_Change) 8    3.52648  0.04639   76.02 <2e-16 ***
## as.factor(SOFA_Change) 9    3.81251  0.04714   80.88 <2e-16 ***
## as.factor(SOFA_Change)10  4.07496  0.04821   84.52 <2e-16 ***
## as.factor(SOFA_Change)11  4.46872  0.04968   89.95 <2e-16 ***
## as.factor(SOFA_Change)12  4.66489  0.05261   88.66 <2e-16 ***
## as.factor(SOFA_Change)13  4.97242  0.05686   87.46 <2e-16 ***
## as.factor(SOFA_Change)14  5.19252  0.06406   81.05 <2e-16 ***
## as.factor(SOFA_Change)15  5.49670  0.07577   72.54 <2e-16 ***
## as.factor(SOFA_Change)16  5.81940  0.09627   60.45 <2e-16 ***
## as.factor(SOFA_Change)17  6.17905  0.14112   43.79 <2e-16 ***
## as.factor(SOFA_Change)[18,23] 6.40953  0.15064   42.55 <2e-16 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603  on 638756  degrees of freedom
## Residual deviance: 322950  on 638738  degrees of freedom
## AIC: 322988
##
## Number of Fisher Scoring iterations: 7

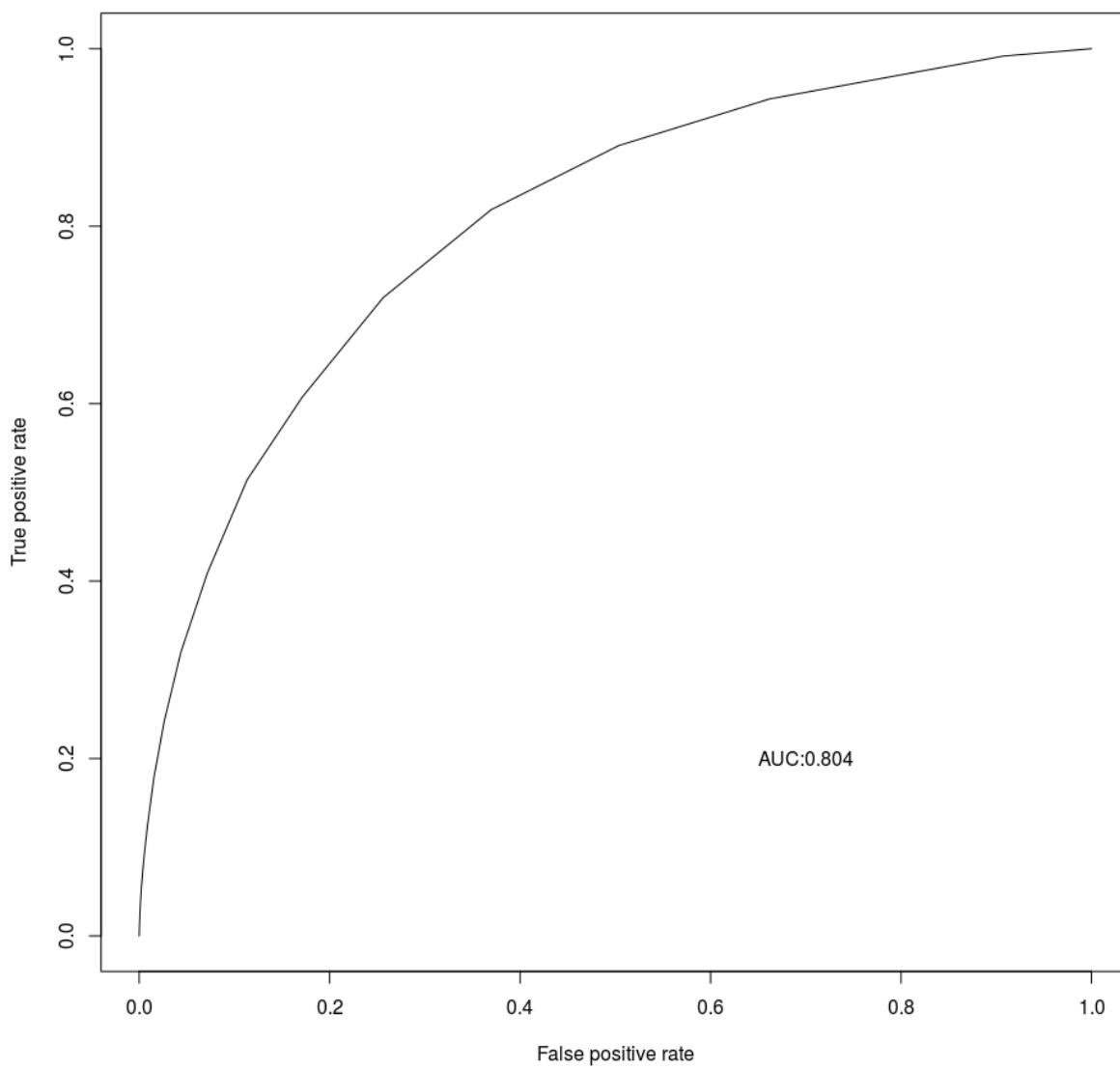
```

```

ssd_incl_te$SOFA1CrudeHospMortPred <- predict(SOFA1_Crude_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type
="response")

SOFA1CrudeMort.Pred <- prediction(ssd_incl_te$SOFA1CrudeHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
SOFA1CrudeMort.Perf <- performance(SOFA1CrudeMort.Pred, "tpr", "fpr")
plot(SOFA1CrudeMort.Perf, main = "SOFA Continuous Crude Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA1CrudeMort.Pred,"auc")@y.values[[1]],3)))

```

SOFA Continuous Crude Mortality Prediction Test Model

```
performance(SOFA1CrudeMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.8037549
##
## Slot "alpha.values":
## list()
```

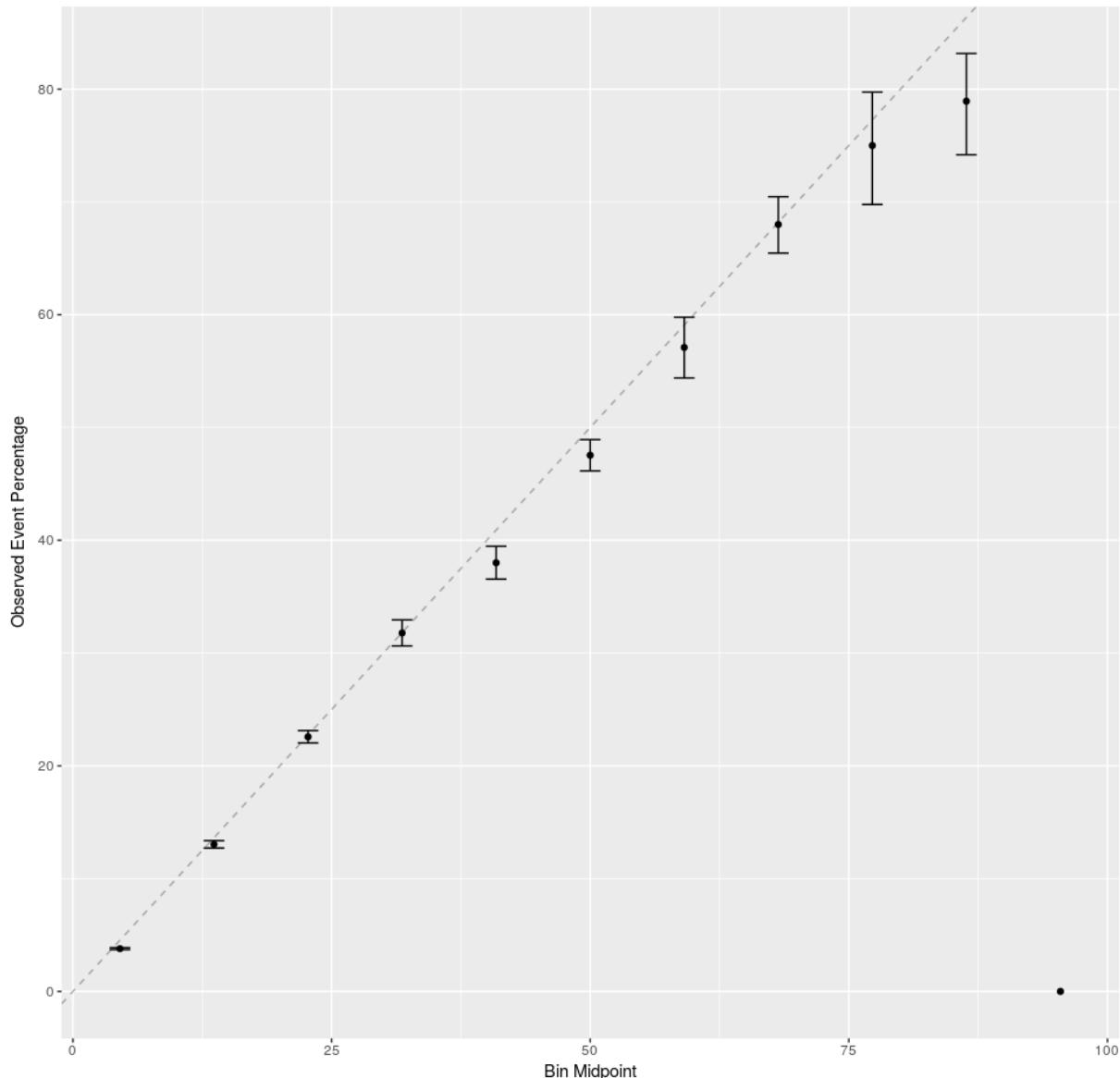
```
SOFA1CrudeMort.Pred.roc <- roc(hospital_mortality_ultimate~ SOFA1CrudeHospMortPred,data=ssd_incl_te)
ci(SOFA1CrudeMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.8001-0.8074 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~SOFA1CrudeHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of Crude Mortality SOFA Total Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

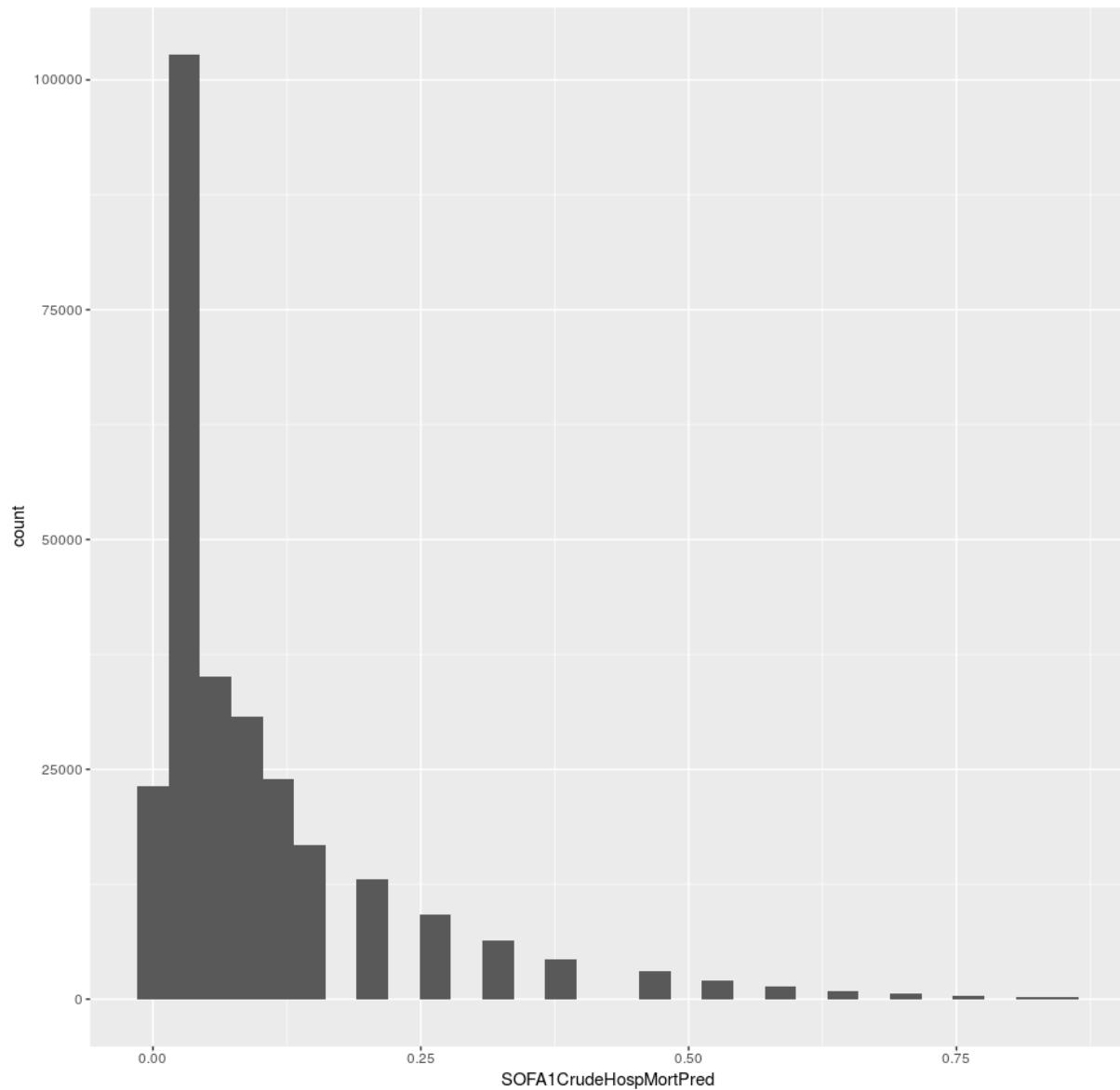
Calibration of Crude Mortality SOFA Total Prediction



```
qplot(SOFA1CrudeHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of Crude Mortality SOFA Total Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of Crude Mortality SOFA Total Predictions



```
SOFA2_Crude_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(SOFA_Positive), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SOFA2_Crude_Hosp_Mort_tr)
#sjt.glm(SOFA2_Crude_Hosp_Mort_tr)

#drop1(SOFA2_Crude_Hosp_Mort_tr,test="Chisq")

summary(SOFA2_Crude_Hosp_Mort_tr)
```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(SOFA_Positive),
##       family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q     Median      3Q      Max
## -0.5273 -0.5273 -0.5273 -0.1825  2.8650
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -4.08741   0.01759 -232.4 <2e-16 ***
## as.factor(SOFA_Positive)TRUE 2.18450   0.01815  120.3 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603  on 638756  degrees of freedom
## Residual deviance: 372927  on 638755  degrees of freedom
## AIC: 372931
##
## Number of Fisher Scoring iterations: 6

```

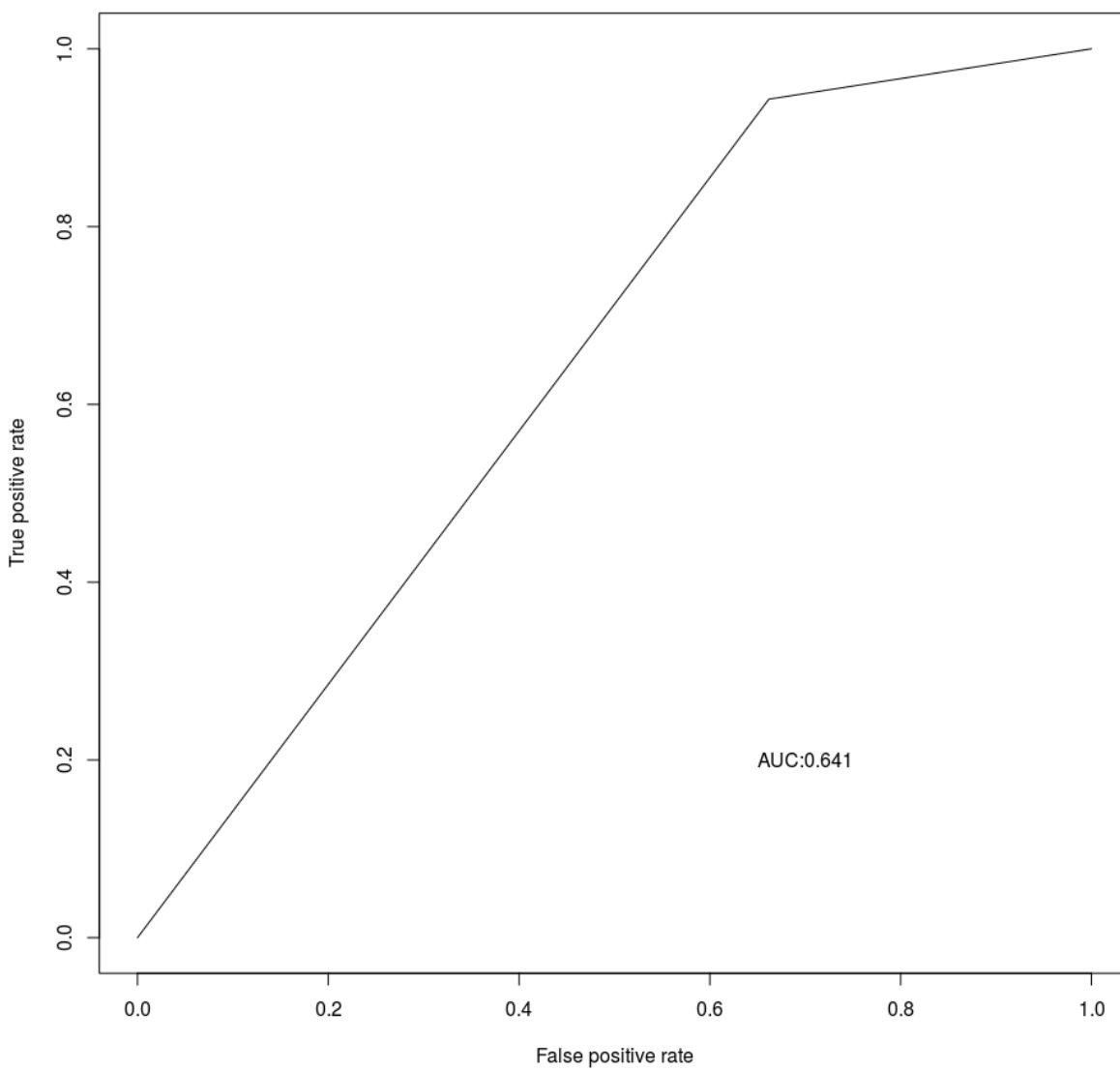
```

ssd_incl_te$SOFA2CrudeHospMortPred <- predict(SOFA2_Crude_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type
="response")

SOFA2CrudeMort.Pred <- prediction(ssd_incl_te$SOFA2CrudeHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
SOFA2CrudeMort.Perf <- performance(SOFA2CrudeMort.Pred, "tpr", "fpr")
plot(SOFA2CrudeMort.Perf, main = "SOFA Positive Crude
Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA2CrudeMort.Pred, "auc")@y.values[[1]],3)))

```

**SOFA Positive Crude
Mortality Prediction Test Model**



```
performance(SOFA2CrudeMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.640742
##
## Slot "alpha.values":
## list()
```

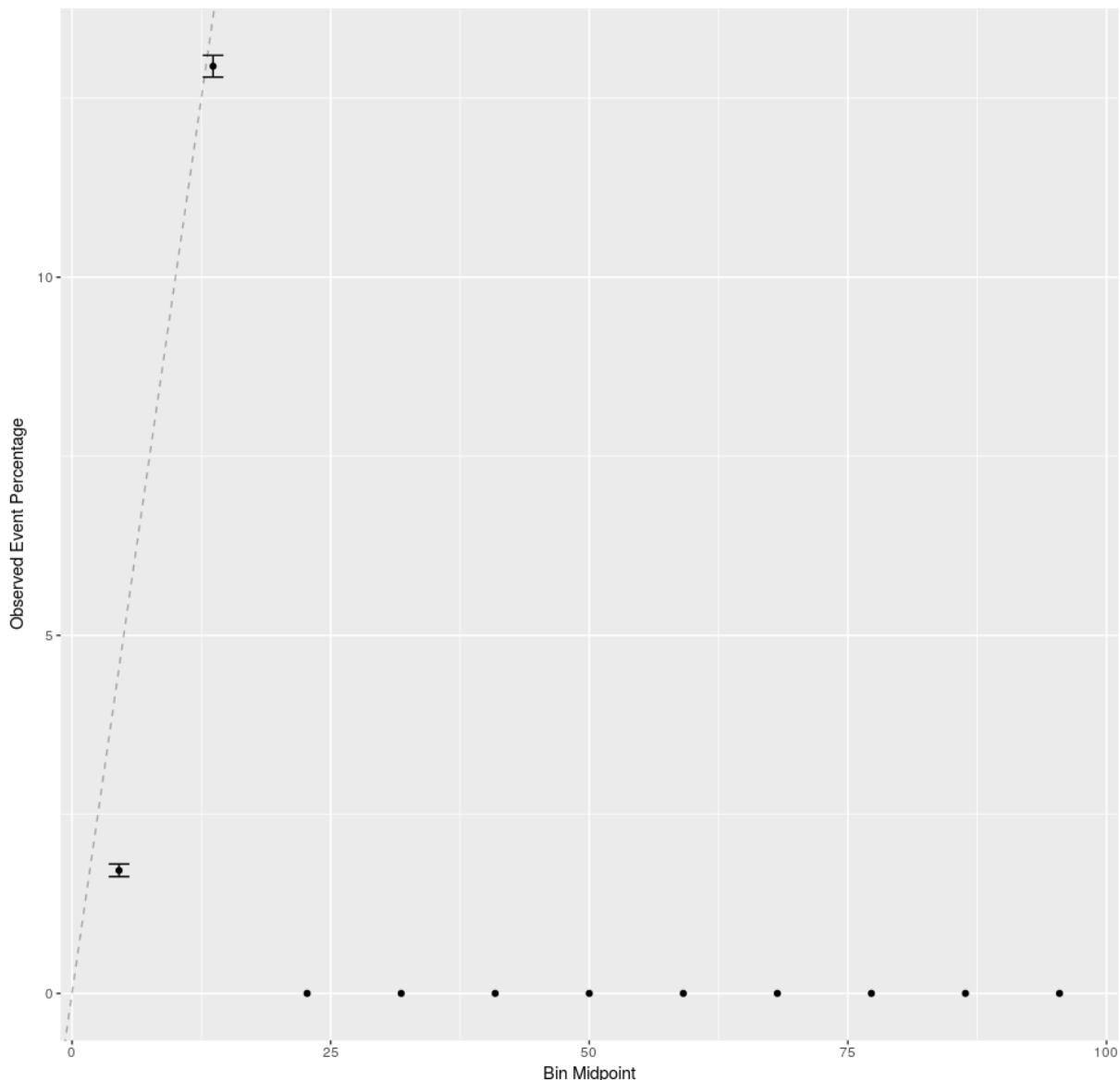
```
SOFA2CrudeMort.Pred.roc <- roc(hospital_mortality_ultimate~ SOFA2CrudeHospMortPred,data=ssd_incl_te)
ci(SOFA2CrudeMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.6385-0.643 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~SOFA2CrudeHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of Crude Mortality SOFA Positive Prediction")
```

```
## Warning: Removed 9 rows containing missing values (geom_errorbar).
```

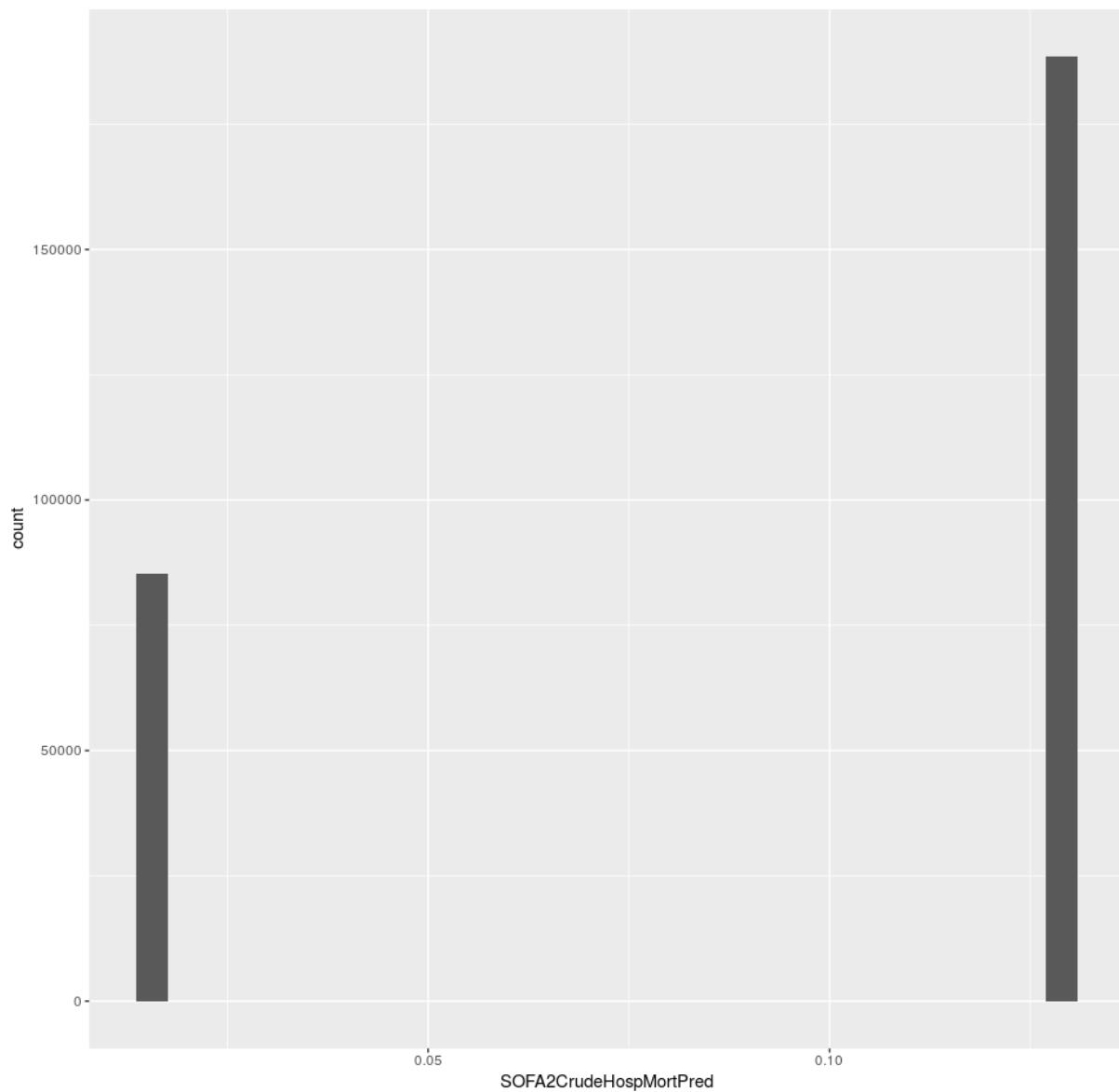
Calibration of Crude Mortality SOFA Positive Prediction



```
qplot(SOFA2CrudeHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of Crude Mortality SOFA Positive Prediction s")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of Crude Mortality SOFA Positive Predictions



```
SOFA3_Crude_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(SOFA_Positive2), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SOFA3_Crude_Hosp_Mort_tr)
#sjt.glm(SOFA3_Crude_Hosp_Mort_tr)

#drop1(SOFA3_Crude_Hosp_Mort_tr,test="Chisq")

summary(SOFA3_Crude_Hosp_Mort_tr)
```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(SOFA_Positive2),
##       family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q     Median      3Q      Max
## -0.5221 -0.5221 -0.5221 -0.1746  2.8952
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -4.17576   0.01892 -220.7   <2e-16 ***
## as.factor(SOFA_Positive2)TRUE  2.25170   0.01944   115.8   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603  on 638756  degrees of freedom
## Residual deviance: 373781  on 638755  degrees of freedom
## AIC: 373785
##
## Number of Fisher Scoring iterations: 6

```

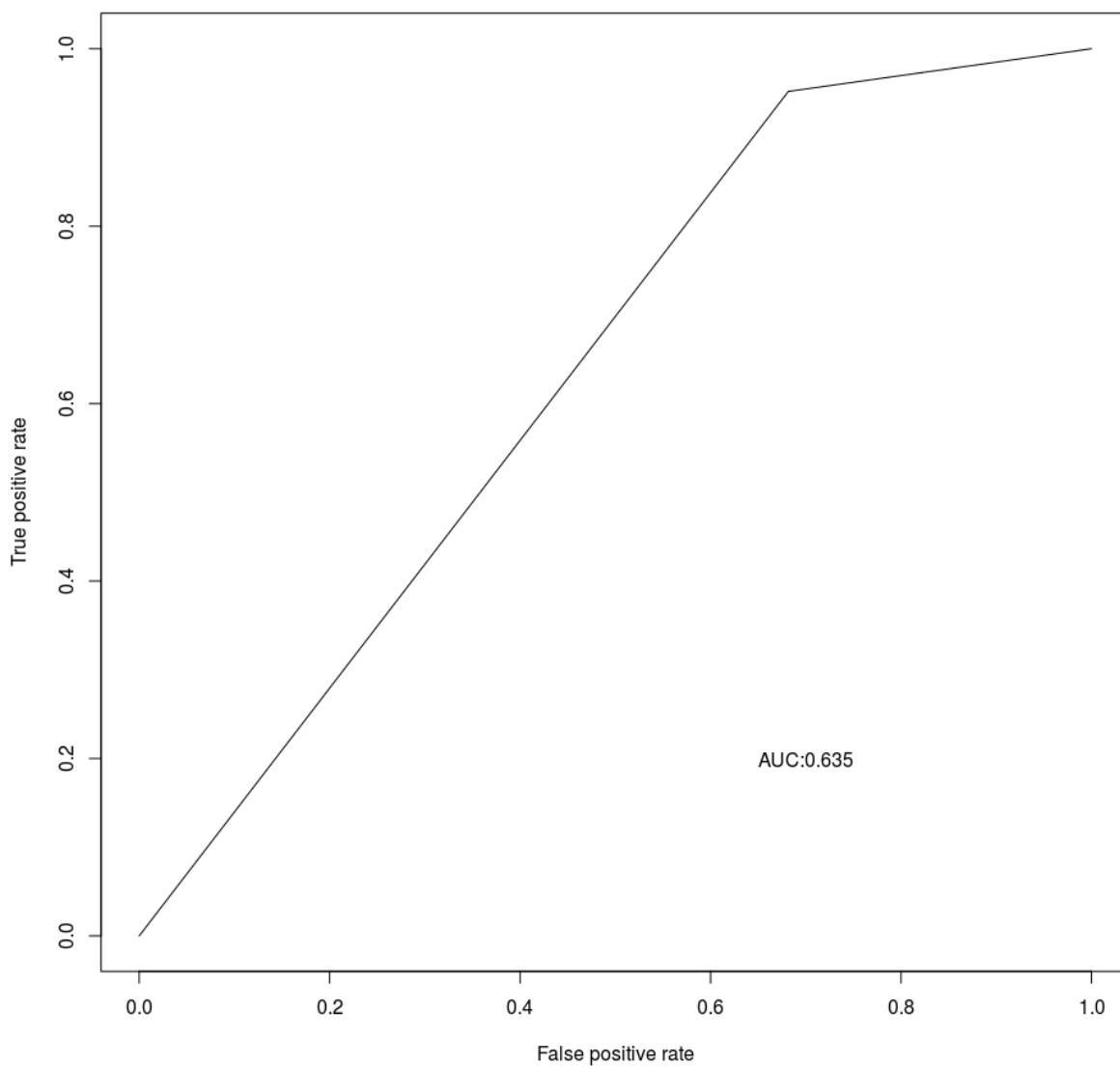
```

ssd_incl_te$SOFA3CrudeHospMortPred <- predict(SOFA3_Crude_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type
="response")

SOFA3CrudeMort.Pred <- prediction(ssd_incl_te$SOFA3CrudeHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
SOFA3CrudeMort.Perf <- performance(SOFA3CrudeMort.Pred, "tpr", "fpr")
plot(SOFA3CrudeMort.Perf, main = "SOFA Positive w/o Baseline Crude
Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA3CrudeMort.Pred, "auc")@y.values[[1]],3)))

```

SOFA Positive w/o Baseline Crude Mortality Prediction Test Model



```
performance(SOFA3CrudeMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.6351032
##
## Slot "alpha.values":
## list()
```

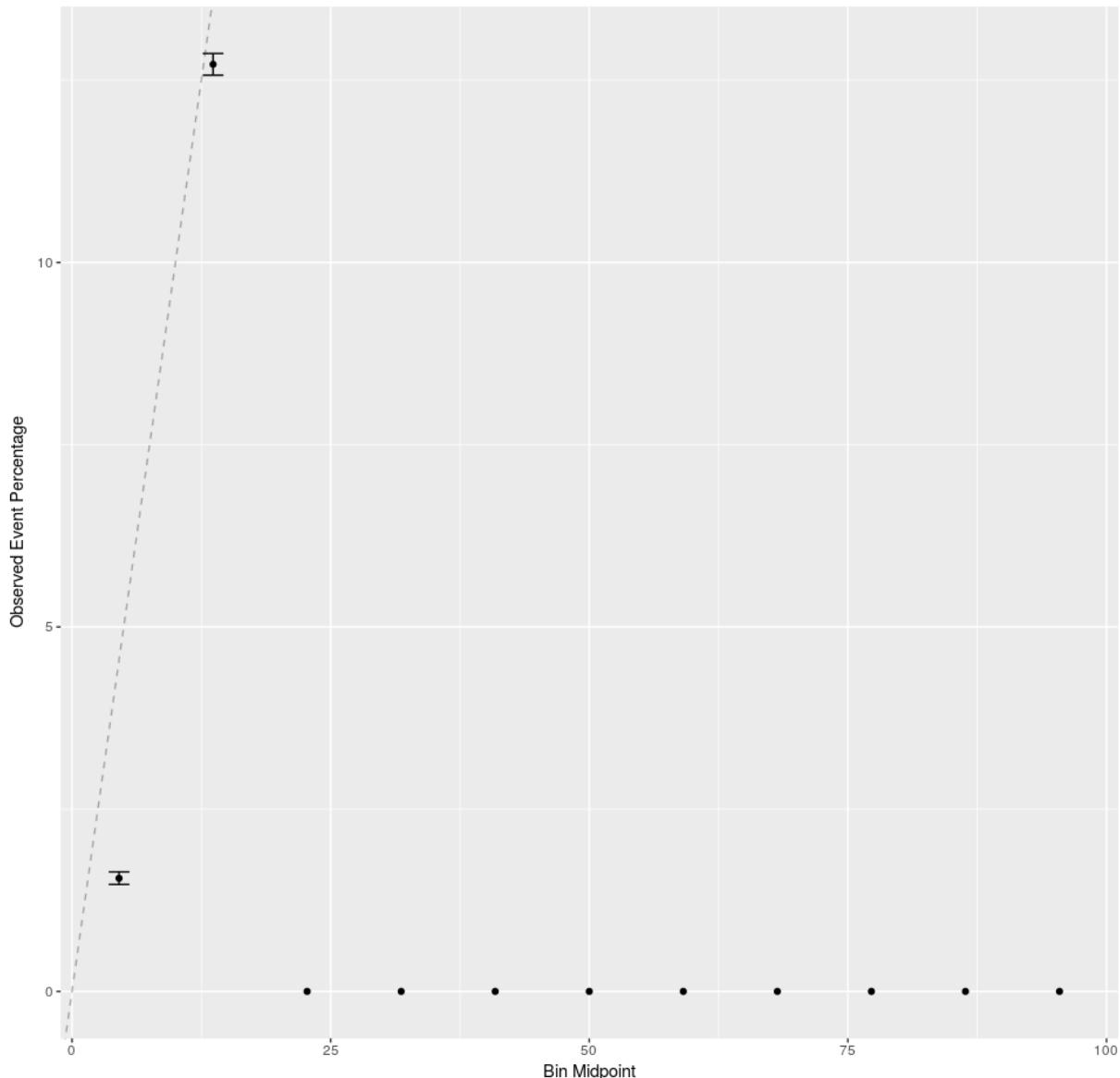
```
SOFA3CrudeMort.Pred.roc <- roc(hospital_mortality_ultimate~ SOFA3CrudeHospMortPred,data=ssd_incl_te)
ci(SOFA3CrudeMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.633–0.6372 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~SOFA3CrudeHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of Crude Mortality SOFA Positive w/o Baseline Prediction")
```

```
## Warning: Removed 9 rows containing missing values (geom_errorbar).
```

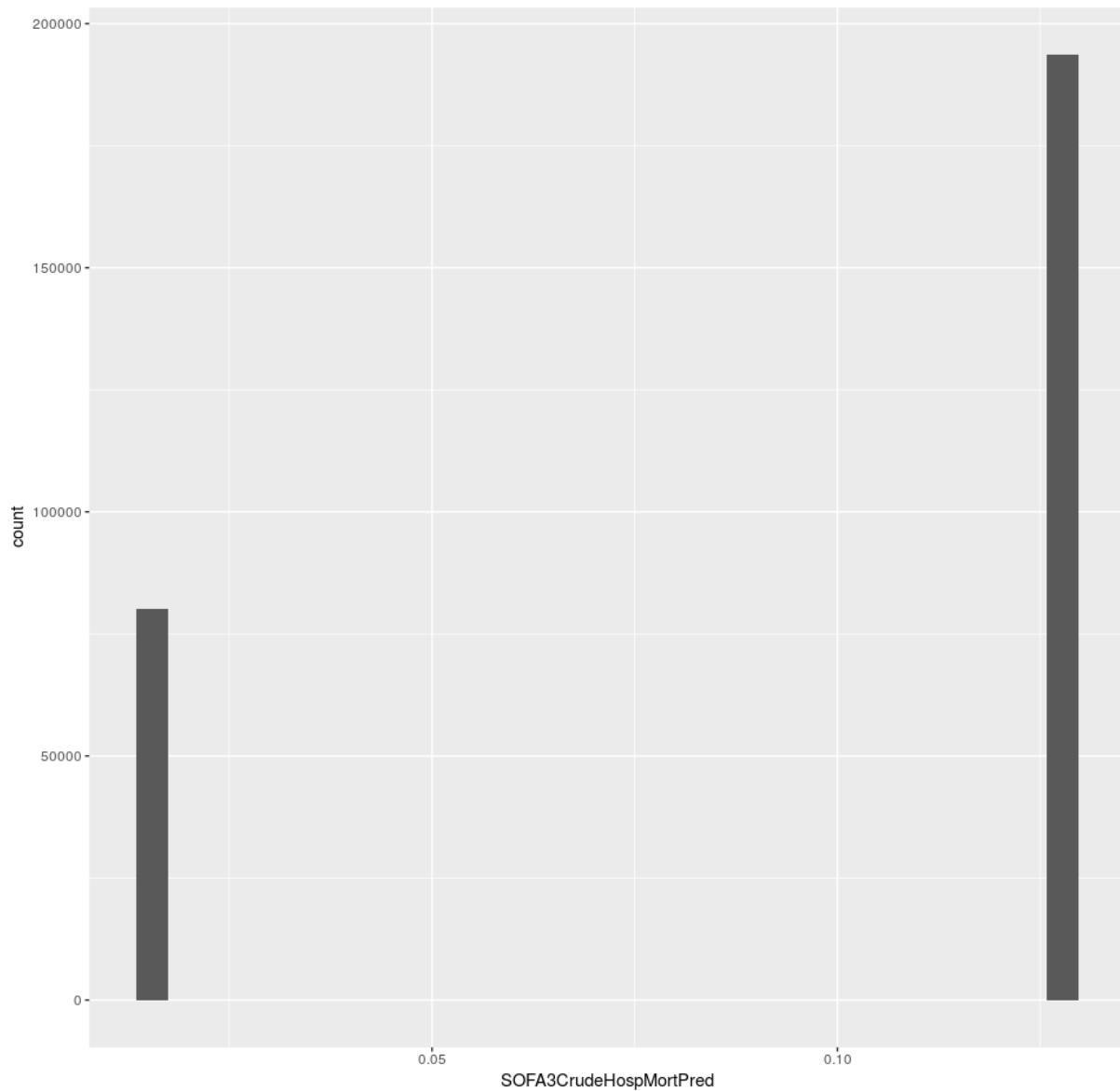
Calibration of Crude Mortality SOFA Positive w/o Baseline Prediction



```
qplot(SOFA3CrudeHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of Crude Mortality SOFA Positive w/o Baseline Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of Crude Mortality SOFA Positive w/o Baseline Predictions



```
qSOFA1_Crude_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(qSOFA_total), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(qSOFA1_Crude_Hosp_Mort_tr)
#sjt.glm(qSOFA1_Crude_Hosp_Mort_tr)

#drop1(qSOFA1_Crude_Hosp_Mort_tr,test="Chisq")

summary(qSOFA1_Crude_Hosp_Mort_tr)
```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(qSOFA_total),
##       family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q  Median      3Q     Max
## -0.6843 -0.4132 -0.4132 -0.2540  3.0033
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -4.49890   0.04501 -99.94 <2e-16 ***
## as.factor(qSOFA_total)1 1.08072   0.04716  22.91 <2e-16 ***
## as.factor(qSOFA_total)2 2.08091   0.04555  45.69 <2e-16 ***
## as.factor(qSOFA_total)3 3.16630   0.04545  69.67 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603  on 638756  degrees of freedom
## Residual deviance: 365260  on 638753  degrees of freedom
## AIC: 365268
##
## Number of Fisher Scoring iterations: 7

```

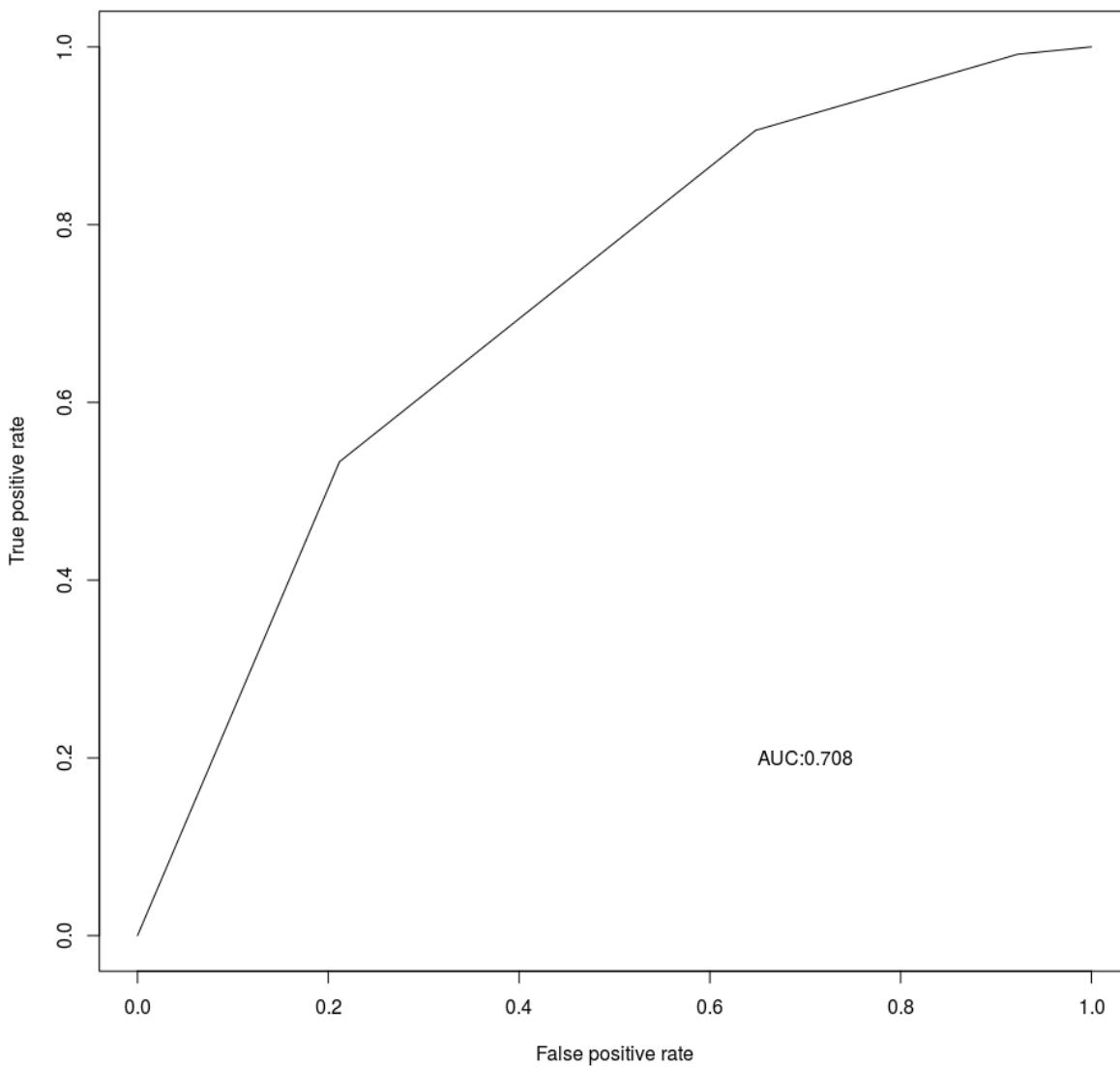
```

ssd_incl_te$qSOFA1CrudeHospMortPred <- predict(qSOFA1_Crude_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

qSOFA1CrudeMort.Pred <- prediction(ssd_incl_te$qSOFA1CrudeHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
qSOFA1CrudeMort.Perf <- performance(qSOFA1CrudeMort.Pred, "tpr", "fpr")
plot(qSOFA1CrudeMort.Perf, main = "qSOFA1 Continuous Crude Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(qSOFA1CrudeMort.Pred,"auc")@y.values[[1]],3)))

```

**qSOFA1 Continuous Crude
Mortality Prediction Test Model**



```
performance(qSOFA1CrudeMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.708034
##
## Slot "alpha.values":
## list()
```

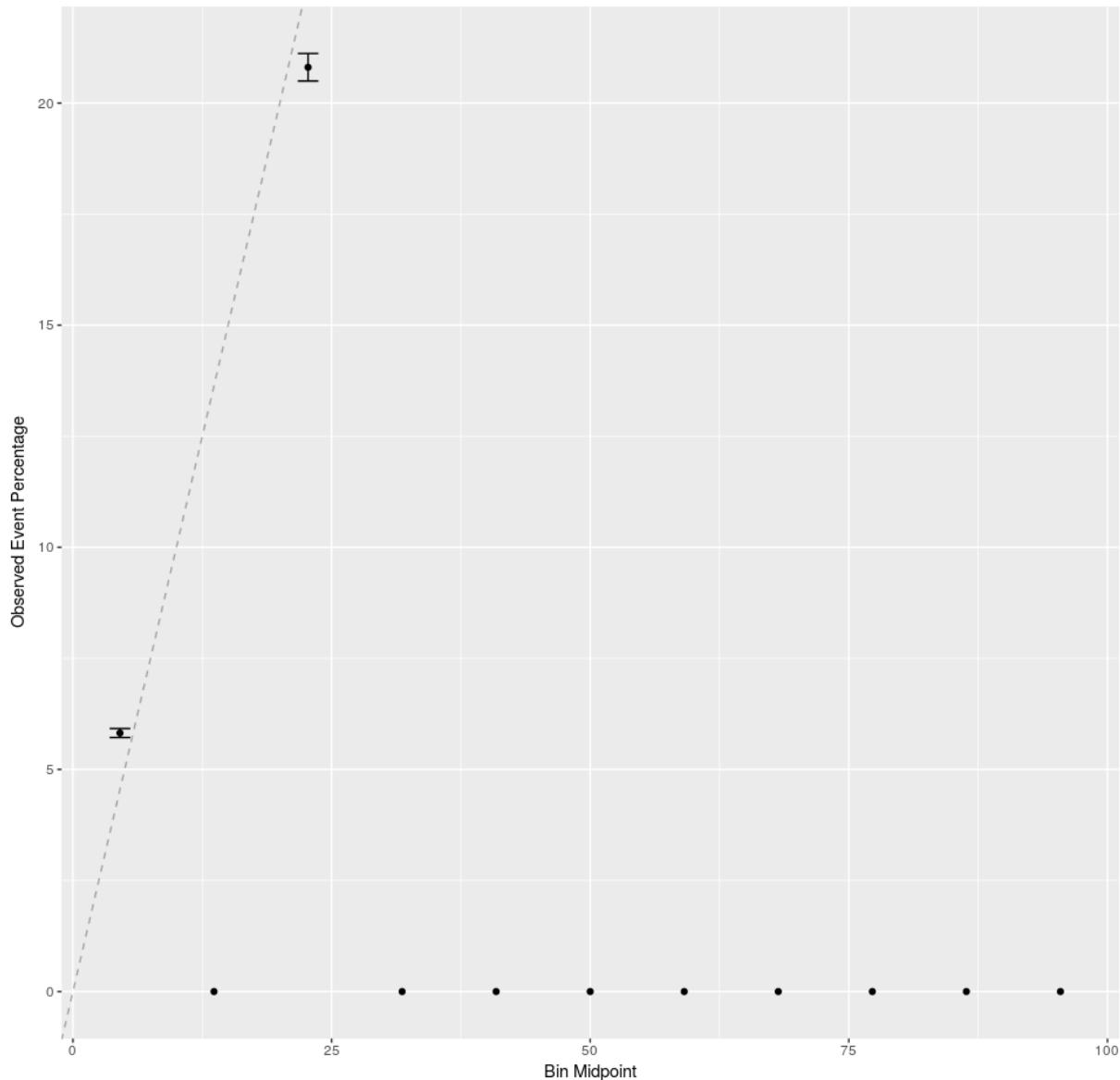
```
qSOFA1CrudeMort.Pred.roc <- roc(hospital_mortality_ultimate~ qSOFA1CrudeHospMortPred,data=ssd_incl_te)
ci(qSOFA1CrudeMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7042-0.7118 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~qSOFA1CrudeHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of Crude Mortality qSOFA Total Prediction")
```

```
## Warning: Removed 9 rows containing missing values (geom_errorbar).
```

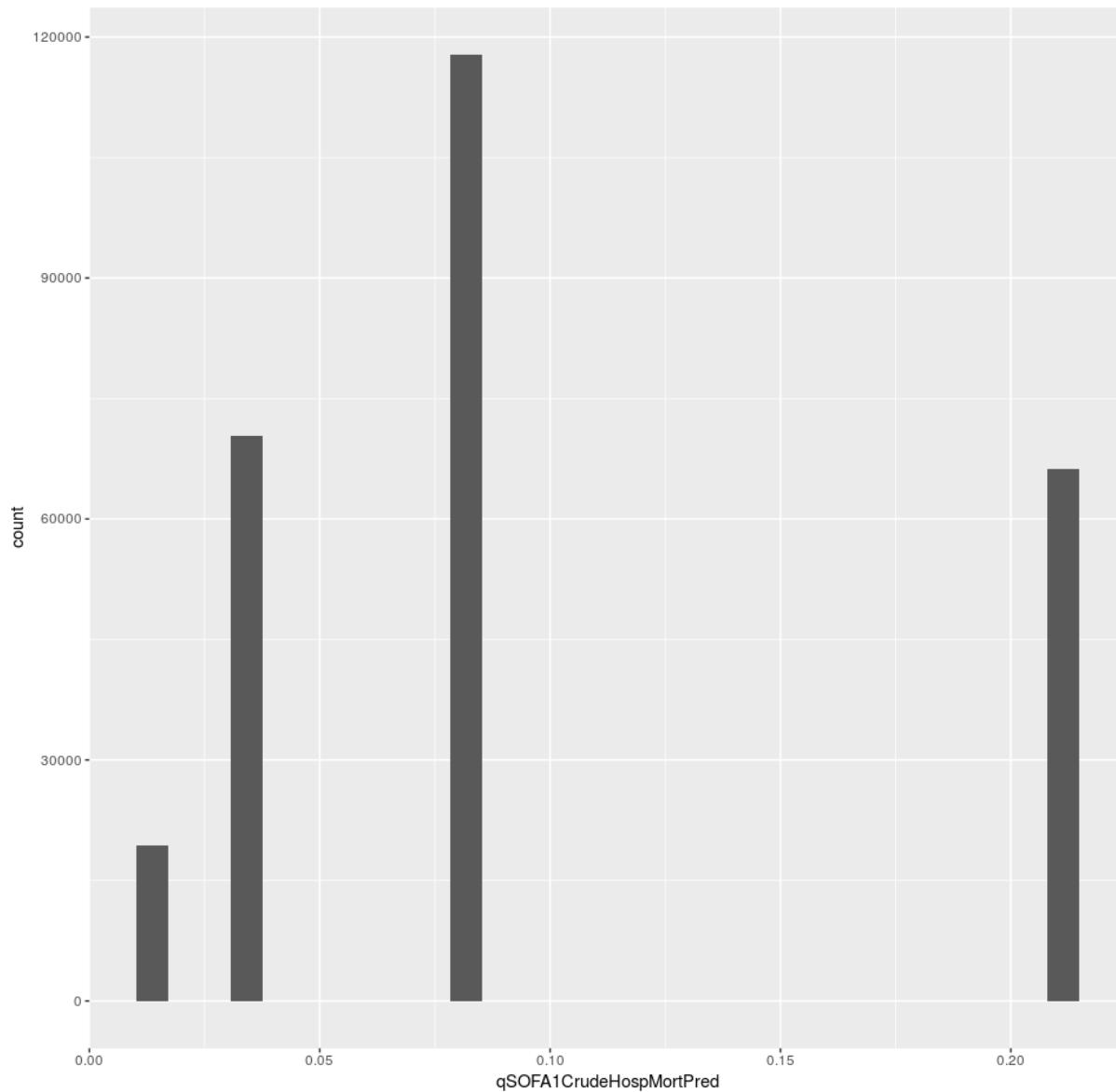
Calibration of Crude Mortality qSOFA Total Prediction



```
qplot(qSOFA1CrudeHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of Crude Mortality qSOFA Total Prediction s")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of Crude Mortality qSOFA Total Predictions



```
qSOFA2_Crude_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor(qSOFA_Positive), data=ssd_incl_tr,family = "binomial",na.action = na.omit)

#sjp.glm(qSOFA2_Crude_Hosp_Mort_tr)
#sjt.glm(qSOFA2_Crude_Hosp_Mort_tr)

#drop1(qSOFA2_Crude_Hosp_Mort_tr,test="Chisq")

summary(qSOFA2_Crude_Hosp_Mort_tr)
```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(qSOFA_Positive),
##       family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q     Median      3Q      Max
## -0.5220 -0.5220 -0.5220 -0.2351  2.6843
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -3.57512   0.01341 -266.6 <2e-16 ***
## as.factor(qSOFA_Positive)TRUE 1.65074   0.01417   116.5 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603  on 638756  degrees of freedom
## Residual deviance: 379643  on 638755  degrees of freedom
## AIC: 379647
##
## Number of Fisher Scoring iterations: 6

```

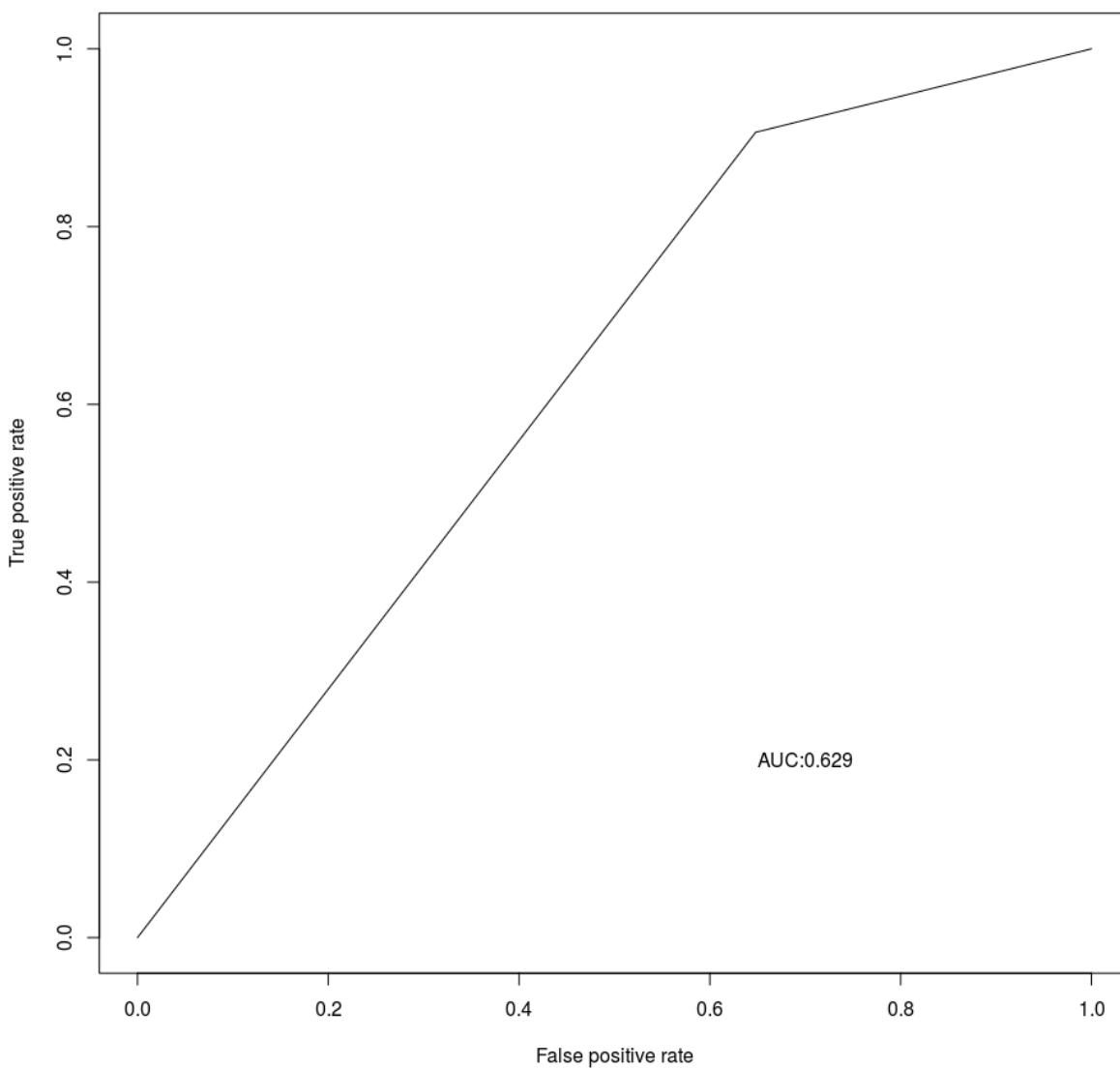
```

ssd_incl_te$qSOFA2CrudeHospMortPred <- predict(qSOFA2_Crude_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

qSOFA2CrudeMort.Pred <- prediction(ssd_incl_te$qSOFA2CrudeHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
qSOFA2CrudeMort.Perf <- performance(qSOFA2CrudeMort.Pred, "tpr", "fpr")
plot(qSOFA2CrudeMort.Perf, main = "qSOFA Positive Crude
    Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(qSOFA2CrudeMort.Pred,"auc")@y.values[[1]],3)))

```

**qSOFA Positive Crude
Mortality Prediction Test Model**



```
performance(qSOFA2CrudeMort.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.6290462
##
## Slot "alpha.values":
## list()
```

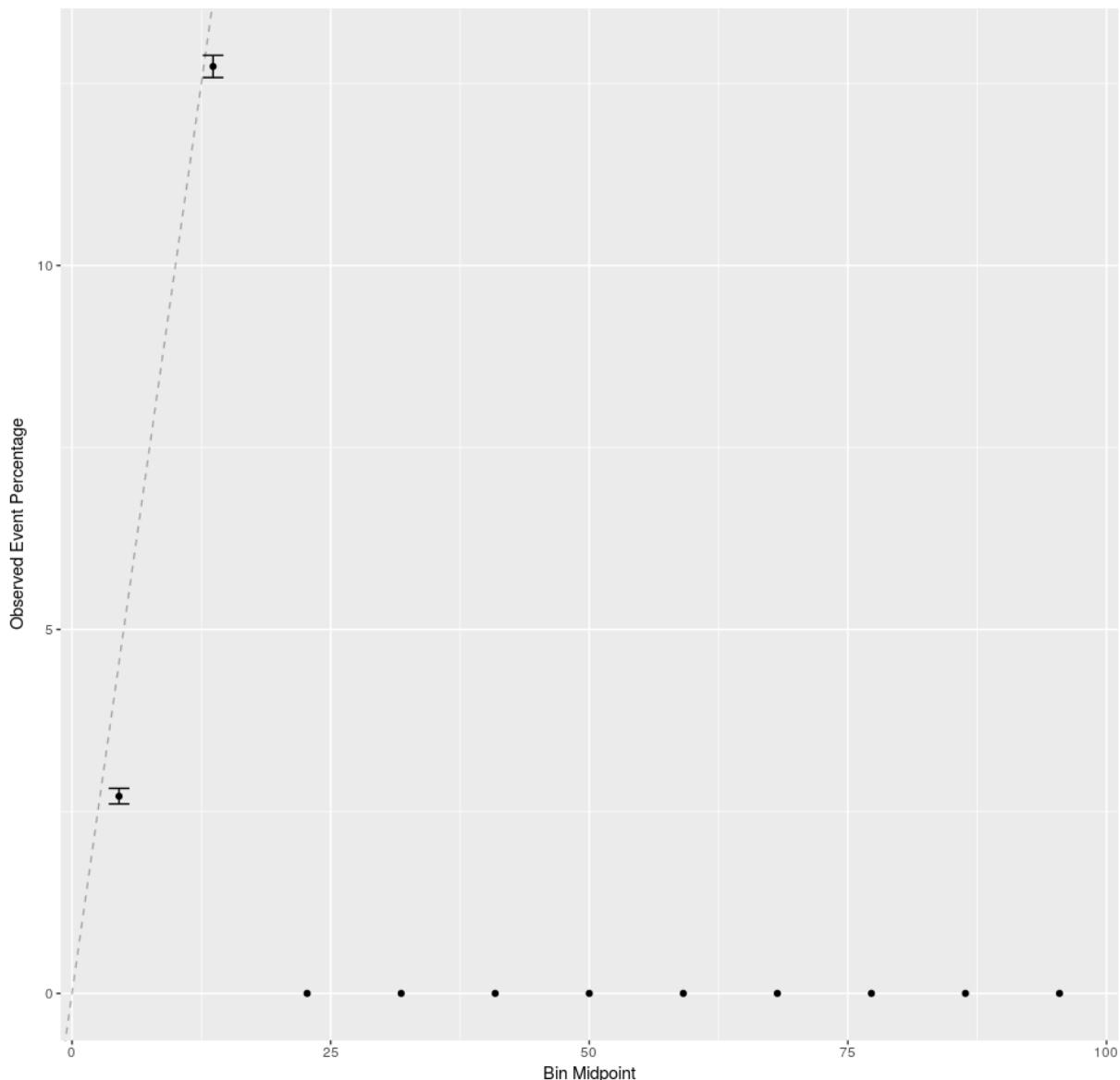
```
qSOFA2CrudeMort.Pred.roc <- roc(hospital_mortality_ultimate~ qSOFA2CrudeHospMortPred,data=ssd_incl_te)
ci(qSOFA2CrudeMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.6264-0.6317 (DeLong)
```

```
ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~qSOFA2CrudeHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of Crude Mortality qSOFA Positive Prediction")
```

```
## Warning: Removed 9 rows containing missing values (geom_errorbar).
```

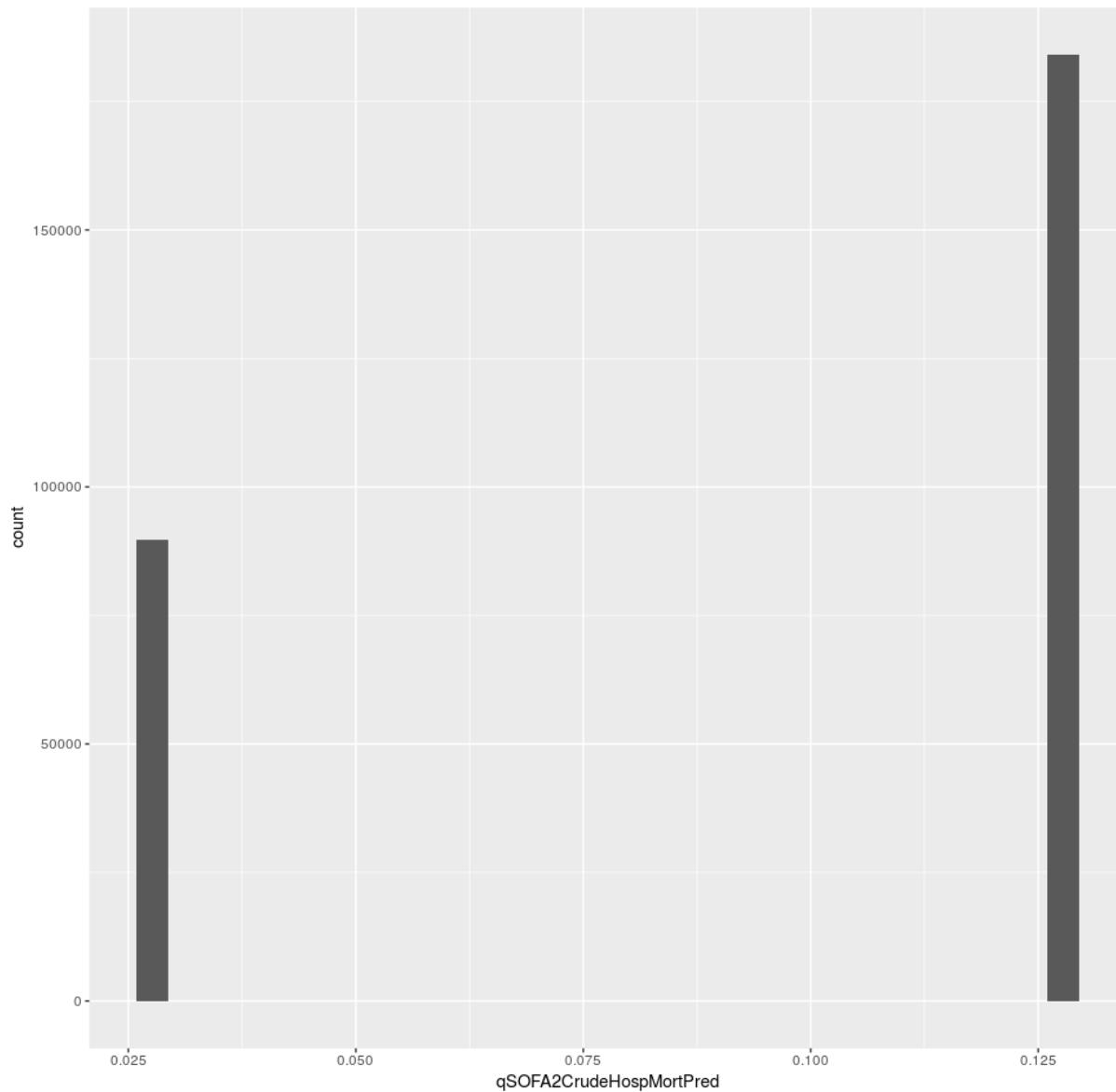
Calibration of Crude Mortality qSOFA Positive Prediction



```
qplot(qSOFA2CrudeHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of Crude Mortality qSOFA Positive Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of Crude Mortality qSOFA Positive Predictions



```
FuzzyLogic_Crude_Hosp_Mort_tr<-glm(hospital_mortality_ultimate ~ as.factor (SepsisFuzzyLogicPositive), data=ssd_i
ncl_tr,family="binomial",na.action = na.omit)

#sjp.glm(FuzzyLogic_Crude_Hosp_Mort_tr)
#sjt.glm(FuzzyLogic_Crude_Hosp_Mort_tr)

#drop1(FuzzyLogic_Crude_Hosp_Mort_tr,test="Chisq")

summary(FuzzyLogic_Crude_Hosp_Mort_tr)
```

```

## 
## Call:
##   glm(formula = hospital_mortality_ultimate ~ as.factor(SepsisFuzzyLogicPositive),
##       family = "binomial", data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q     Median      3Q      Max
## -0.5675 -0.5675 -0.2384 -0.2384  2.6739
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)             -3.54651   0.01131 -313.6
## as.factor(SepsisFuzzyLogicPositive)TRUE 1.80202   0.01226  147.0
##                               Pr(>|z|)
## (Intercept) <2e-16 ***
## as.factor(SepsisFuzzyLogicPositive)TRUE <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 399603  on 638756  degrees of freedom
## Residual deviance: 369149  on 638755  degrees of freedom
## AIC: 369153
##
## Number of Fisher Scoring iterations: 6

```

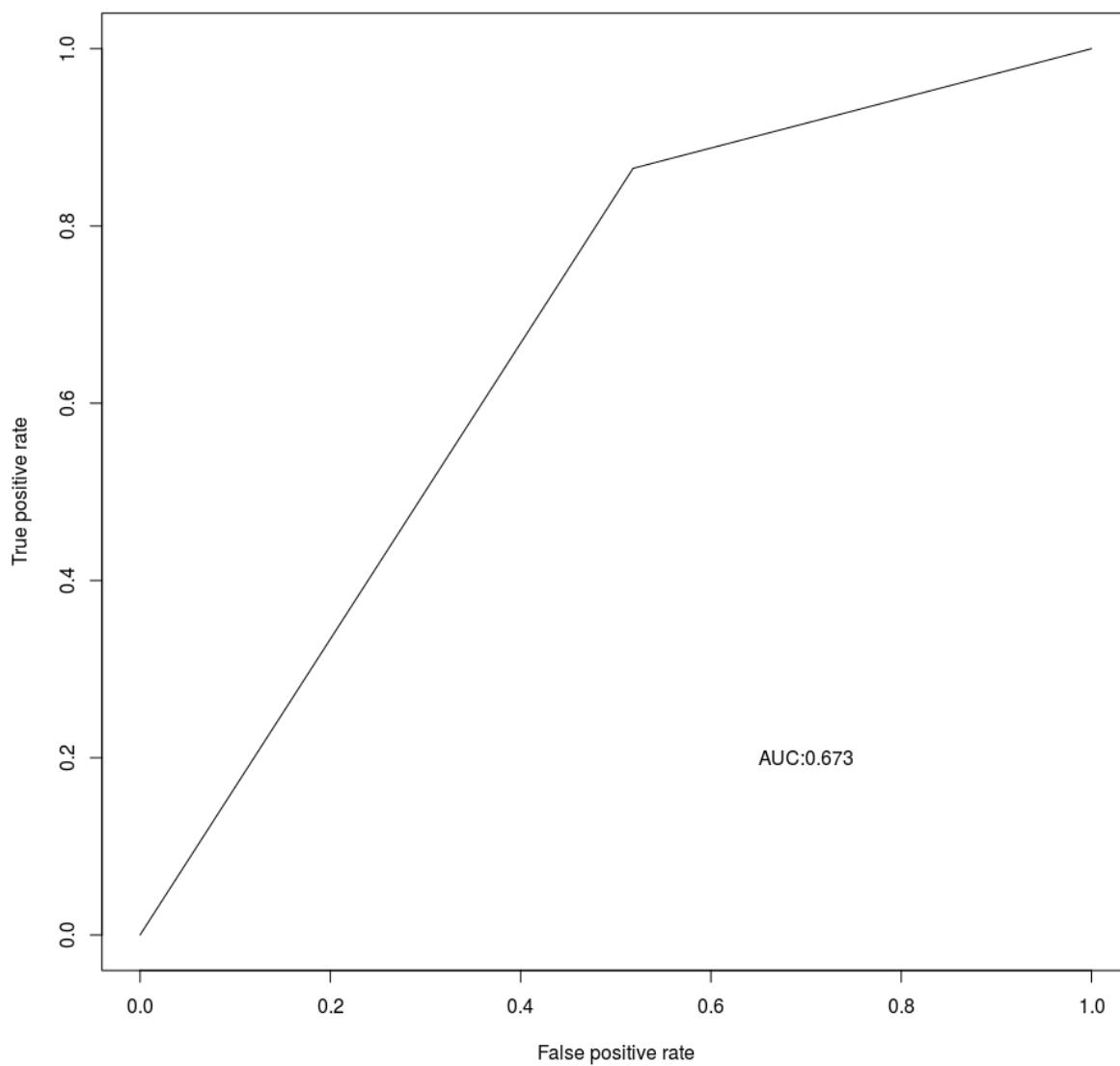
```

ssd_incl_te$FuzzyLogicCrudeHospMortPred <- predict(FuzzyLogic_Crude_Hosp_Mort_tr,newdata=ssd_incl_te,na.action=a.pass,type="response")
library(sjPlot)
library(ROCR)

FuzzyLogicCrudeMort.Pred <- prediction(ssd_incl_te$FuzzyLogicCrudeHospMortPred, ssd_incl_te$hospital_mortality_ultimate)
FuzzyLogicCrudeMort.Perf <- performance(FuzzyLogicCrudeMort.Pred, "tpr", "fpr")
plot(FuzzyLogicCrudeMort.Perf, main = "FuzzyLogic Positive Crude Mortality Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(FuzzyLogicCrudeMort.Pred,"auc")@y.values[[1]],3)))

```

FuzzyLogic Positive Crude Mortality Prediction Test Model



```
performance(FuzzyLogicCrudeMort.Pred, "auc")
```

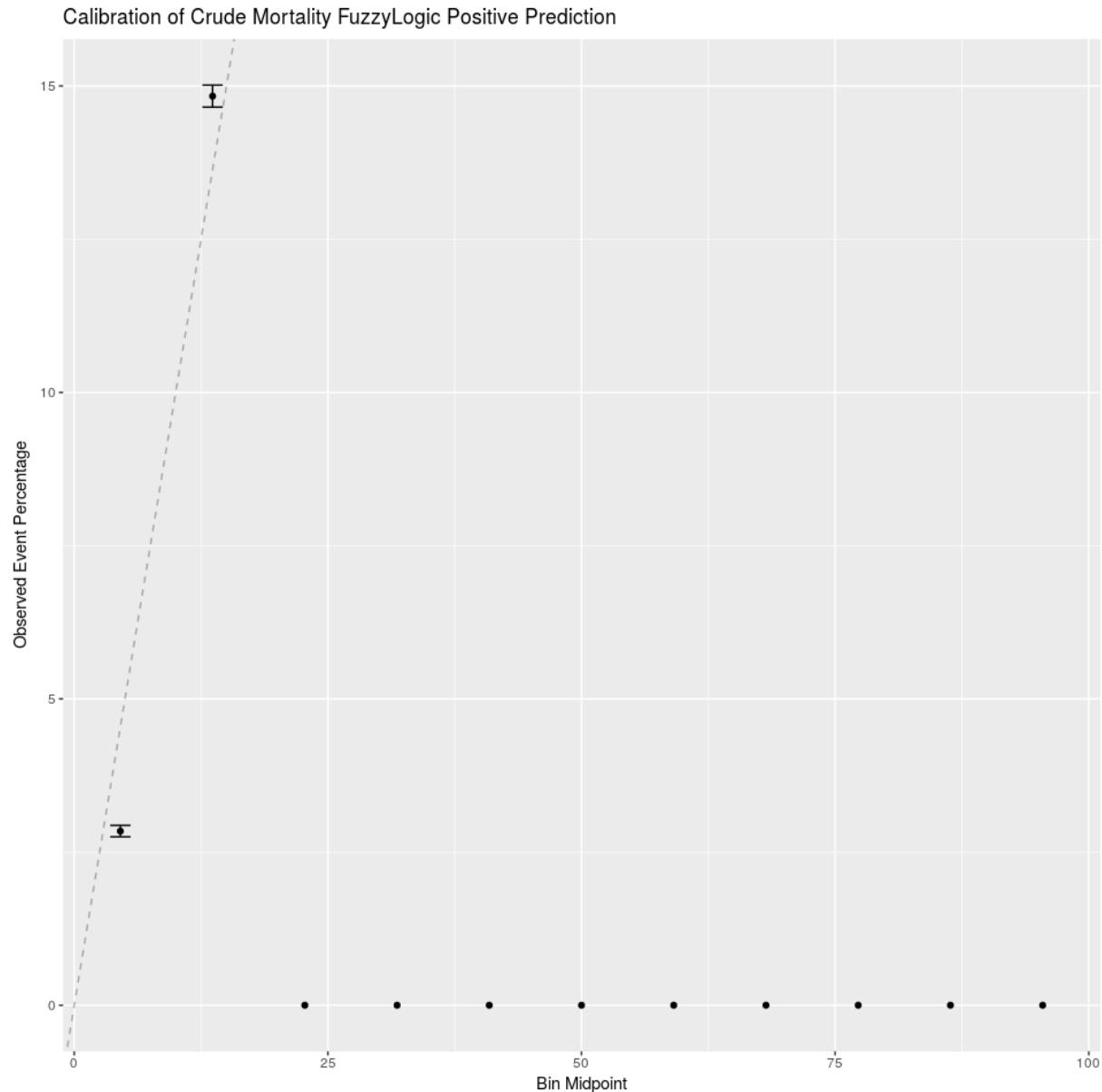
```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.6734078
##
## Slot "alpha.values":
## list()
```

```
FuzzyLogicCrudeMort.Pred.roc <- roc(hospital_mortality_ultimate~ FuzzyLogicCrudeHospMortPred,data=ssd_incl_te)
ci(FuzzyLogicCrudeMort.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.6704-0.6764 (DeLong)

ggplot(calibration(as.factor(hospital_mortality_ultimate==0)~FuzzyLogicCrudeHospMortPred, data = ssd_incl_te))+ggtitle("Calibration of Crude Mortality FuzzyLogic Positive Prediction")

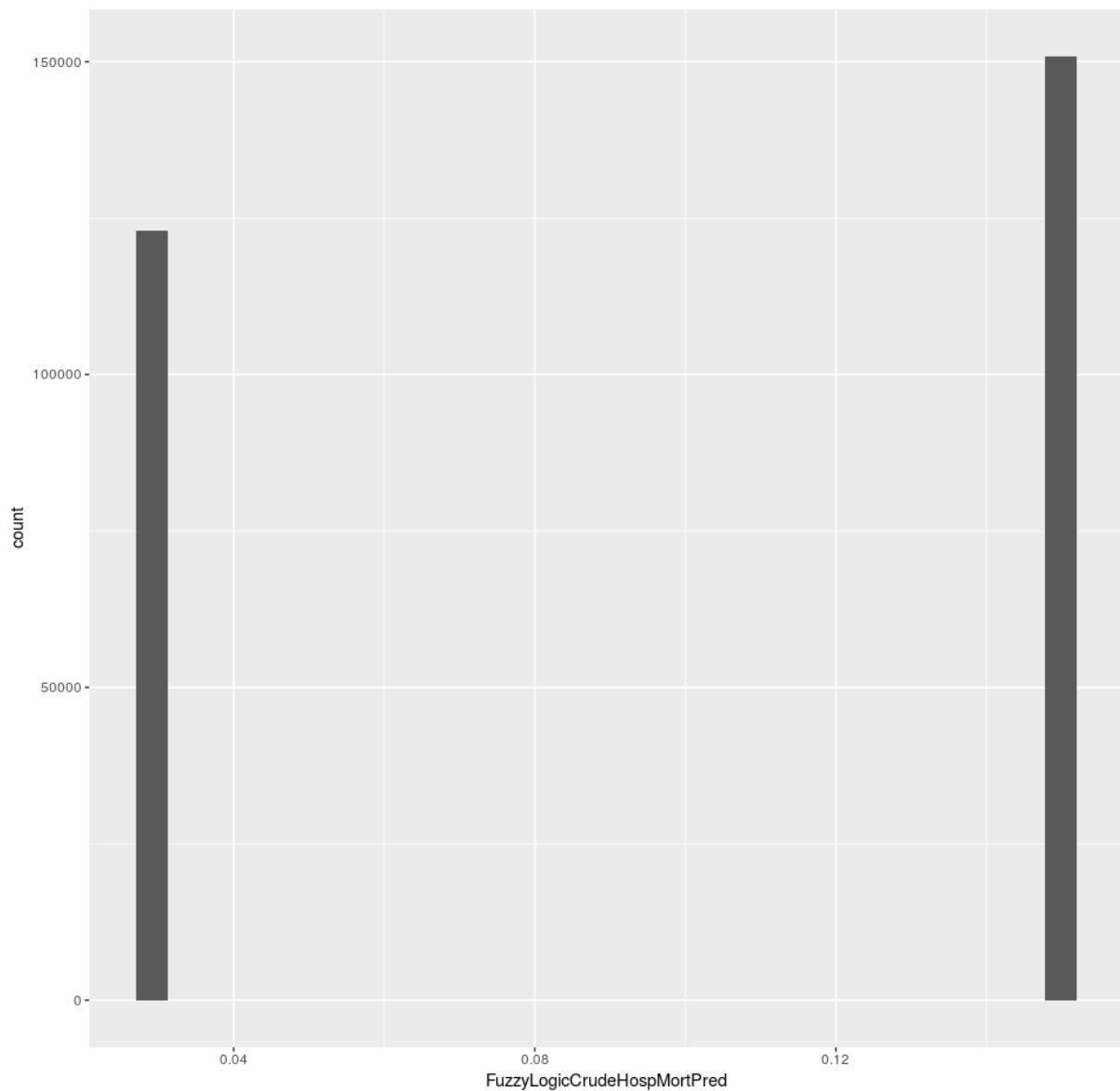
## Warning: Removed 9 rows containing missing values (geom_errorbar).
```



```
qplot(FuzzyLogicCrudeHospMortPred, data = ssd_incl_te)+ggtitle("Histogram of Crude Mortality FuzzyLogic Positive Predictions")

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of Crude Mortality FuzzyLogic Positive Predictions



20 Setting up variables to analyze interactions

```
ssd_incl_te <- ssd_incl_te %>% mutate(hospital_mortality_ultimate2=hospital_mortality_ultimate)
ssd_incl_te <- ssd_incl_te %>% mutate(hospital_mortality_ultimate=as.logical(hospital_mortality_ultimate==1))
ssd_incl_te <- ssd_incl_te %>% mutate(SOFA2TruthMort=interaction(SOFA_Positive,hospital_mortality_ultimate))
ssd_incl_te <- ssd_incl_te %>% mutate(FuzzyLogicTruthMort=interaction(SepsisFuzzyLogicPositive, hospital_mortality_ultimate))
ssd_incl_te <- ssd_incl_te %>% mutate(qSOFA2TruthMort=interaction(qSOFA_Positive,hospital_mortality_ultimate))
ssd_incl_te <- ssd_incl_te %>% mutate(SIRS2TruthMort=interaction(SIRS_Positive,hospital_mortality_ultimate))
```

```

vars5 <- c("age_Ranges", "gender2", "ethnicity2", "BMI_Ranges", "physicianSpeciality2", "icu_admit_source2", "icu_disch_location2", "hospitaldischargeyear", "dischargelocation", "dialysis", "aids", "hepaticfailure", "diabetes", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baseline2", "sofa_liver_baseline2", "sofa_renal_baseline2", "cardiovascular_baseline", "group")

library(dplyr); library(Hmisc); library(ggplot2); library(sjPlot)

if(!(tableone %in% rownames(installed.packages())))
  install.packages("tableone")
}

library(tableone)

CreateTableOne(data=ssd_incl_te ,vars=vars5,strata="SIRS2TruthMort",test=FALSE, includeNA=TRUE
) %>% print(nonnormals= c("sofa_respiration_baseline2", "sofa_liver_baseline2", "sofa_renal_baseline2"),minMax=TRUE
E,
  printToggle      = FALSE,
  showAllLevels   = TRUE,
  cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names          = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="SIRS Positive Hospital Mortality TRUE/FALSE")

```

SIRS Positive Hospital Mortality TRUE/FALSE

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
n		63427	184460	1792	24073
age_Ranges (%)	(0,25]	1546 (2.4)	7255 (3.9)	1 (0.1)	249 (1.0)
	(25,35]	2623 (4.1)	10909 (5.9)	14 (0.8)	514 (2.1)
	(35,45]	4182 (6.6)	15147 (8.2)	22 (1.2)	977 (4.1)
	(45,55]	9477 (14.9)	28450 (15.4)	136 (7.6)	2466 (10.2)
	(55,65]	13742 (21.7)	38541 (20.9)	263 (14.7)	4558 (18.9)
	(65,75]	14753 (23.3)	39638 (21.5)	426 (23.8)	5789 (24.0)
	(75,85]	12022 (19.0)	30967 (16.8)	584 (32.6)	6049 (25.1)
	(85,100]	5082 (8.0)	13553 (7.3)	346 (19.3)	3471 (14.4)
gender2 (%)	Male	35515 (56.0)	97773 (53.0)	946 (52.8)	12668 (52.6)
	Female	27900 (44.0)	86658 (47.0)	844 (47.1)	11368 (47.2)
	Other/Unknown	12 (0.0)	29 (0.0)	2 (0.1)	37 (0.2)
ethnicity2 (%)	Caucasian	48120 (75.9)	140669 (76.3)	1397 (78.0)	18502 (76.9)
	African American	7152 (11.3)	21798 (11.8)	175 (9.8)	2604 (10.8)
	Hispanic	2982 (4.7)	8115 (4.4)	96 (5.4)	1092 (4.5)
	Asian	822 (1.3)	2349 (1.3)	23 (1.3)	339 (1.4)
	Native American	452 (0.7)	1382 (0.7)	8 (0.4)	170 (0.7)
	Other/Unknown	3899 (6.1)	10147 (5.5)	93 (5.2)	1366 (5.7)
BMI_Ranges (%)	(0,18.5]	2426 (3.8)	9110 (4.9)	109 (6.1)	1803 (7.5)
	(18.5,25]	16805 (26.5)	51771 (28.1)	519 (29.0)	7780 (32.3)
	(25,35]	30888 (48.7)	83875 (45.5)	741 (41.4)	9708 (40.3)
	(35,200]	10559 (16.6)	33940 (18.4)	308 (17.2)	3650 (15.2)
	Other/Unknown	2749 (4.3)	5764 (3.1)	115 (6.4)	1132 (4.7)
physicianSpeciality2 (%)	Critical Care	12577 (19.8)	57963 (31.4)	566 (31.6)	9189 (38.2)
	Speciality-Other	50850 (80.2)	126497 (68.6)	1226 (68.4)	14884 (61.8)
icu_admit_source2 (%)	Floor	8750 (13.8)	30563 (16.6)	479 (26.7)	6642 (27.6)
	OR/Proc Area	11420 (18.0)	39542 (21.4)	139 (7.8)	1830 (7.6)
	Direct Admit	7814 (12.3)	18602 (10.1)	204 (11.4)	2851 (11.8)

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	Emergency Department	34138 (53.8)	90266 (48.9)	896 (50.0)	11374 (47.2)
	Other	397 (0.6)	1598 (0.9)	19 (1.1)	346 (1.4)
	Step-Down Unit	908 (1.4)	3889 (2.1)	55 (3.1)	1030 (4.3)
icu_disch_location2 (%)	Floor	46120 (72.7)	146188 (79.3)	667 (37.2)	6444 (26.8)
	Death	0 (0.0)	0 (0.0)	1084 (60.5)	17271 (71.7)
	Home	11549 (18.2)	15112 (8.2)	2 (0.1)	20 (0.1)
	SNF/Rehab	848 (1.3)	3408 (1.8)	0 (0.0)	2 (0.0)
	Other	1727 (2.7)	6959 (3.8)	15 (0.8)	104 (0.4)
	Other Hospital	1363 (2.1)	4775 (2.6)	4 (0.2)	14 (0.1)
	Step-Down Unit	1820 (2.9)	8018 (4.3)	20 (1.1)	218 (0.9)
hospitaldischargeyear (%)	-2010	8716 (13.7)	21266 (11.5)	263 (14.7)	3103 (12.9)
	2011	8885 (14.0)	24249 (13.1)	301 (16.8)	3379 (14.0)
	2012	10336 (16.3)	30215 (16.4)	273 (15.2)	3986 (16.6)
	2013	11374 (17.9)	34135 (18.5)	312 (17.4)	4441 (18.4)
	2014	12378 (19.5)	36465 (19.8)	312 (17.4)	4396 (18.3)
	2015-16	11738 (18.5)	38130 (20.7)	331 (18.5)	4768 (19.8)
dischargelocation (mean (sd))		5.15 (1.63)	5.02 (1.64)	7.17 (2.38)	7.69 (2.18)
dialysis (%)	0	61202 (96.5)	178604 (96.8)	1691 (94.4)	22997 (95.5)
	1	2225 (3.5)	5856 (3.2)	101 (5.6)	1076 (4.5)
aids (%)	0	63396 (100.0)	184261 (99.9)	1790 (99.9)	24042 (99.9)
	1	31 (0.0)	199 (0.1)	2 (0.1)	31 (0.1)
hepaticfailure (%)	FALSE	62336 (98.3)	180827 (98.0)	1719 (95.9)	23189 (96.3)
	TRUE	1091 (1.7)	3633 (2.0)	73 (4.1)	884 (3.7)
diabetes (%)	0	49225 (77.6)	143639 (77.9)	1403 (78.3)	19653 (81.6)
	1	14202 (22.4)	40821 (22.1)	389 (21.7)	4420 (18.4)
immunosuppression (%)	0	62554 (98.6)	180037 (97.6)	1752 (97.8)	23043 (95.7)
	1	873 (1.4)	4423 (2.4)	40 (2.2)	1030 (4.3)
leukemia (%)	0	63177 (99.6)	183156 (99.3)	1787 (99.7)	23694 (98.4)
	1	250 (0.4)	1304 (0.7)	5 (0.3)	379 (1.6)
lymphoma (%)	0	63262 (99.7)	183762 (99.6)	1783 (99.5)	23915 (99.3)
	1	165 (0.3)	698 (0.4)	9 (0.5)	158 (0.7)
metastaticcancer (%)	0	62573 (98.7)	180962 (98.1)	1748 (97.5)	23163 (96.2)
	1	854 (1.3)	3498 (1.9)	44 (2.5)	910 (3.8)
thrombolytics (%)	0	61472 (96.9)	181851 (98.6)	1764 (98.4)	23697 (98.4)
	1	1955 (3.1)	2609 (1.4)	28 (1.6)	376 (1.6)
sofa_respiration_baseline2 (%)	FALSE	51153 (80.6)	138294 (75.0)	1296 (72.3)	17265 (71.7)
	TRUE	12274 (19.4)	46166 (25.0)	496 (27.7)	6808 (28.3)
sofa_liver_baseline2 (%)	FALSE	62336 (98.3)	180827 (98.0)	1719 (95.9)	23189 (96.3)
	TRUE	1091 (1.7)	3633 (2.0)	73 (4.1)	884 (3.7)
sofa_renal_baseline2 (%)	FALSE	61202 (96.5)	178604 (96.8)	1691 (94.4)	22997 (95.5)
	TRUE	2225 (3.5)	5856 (3.2)	101 (5.6)	1076 (4.5)
cardiovascular_baseline (%)	0	47719 (75.2)	145389 (78.8)	1135 (63.3)	17618 (73.2)
	1	15708 (24.8)	39071 (21.2)	657 (36.7)	6455 (26.8)
group (%)	Cardiovascular	27116 (42.8)	53849 (29.2)	534 (29.8)	6864 (28.5)
	Gastrointestinal	5746 (9.1)	20519 (11.1)	160 (8.9)	2119 (8.8)
	Gynaecological	105 (0.2)	601 (0.3)	0 (0.0)	9 (0.0)

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	Hematological	418 (0.7)	1497 (0.8)	11 (0.6)	160 (0.7)
	Metabolic	5782 (9.1)	16247 (8.8)	41 (2.3)	391 (1.6)
	Muscoskeletal/Skin disease	718 (1.1)	2614 (1.4)	8 (0.4)	118 (0.5)
	Neurological	10296 (16.2)	23204 (12.6)	364 (20.3)	2973 (12.3)
	Renal/Genitourinary	1532 (2.4)	4569 (2.5)	39 (2.2)	436 (1.8)
	Respiratory	5980 (9.4)	29736 (16.1)	364 (20.3)	4778 (19.8)
	Sepsis	2424 (3.8)	21609 (11.7)	185 (10.3)	5119 (21.3)
	Trauma	2837 (4.5)	8359 (4.5)	74 (4.1)	855 (3.6)
	Undefined	473 (0.7)	1656 (0.9)	12 (0.7)	251 (1.0)

```

vars5 <- c("age_Ranges", "gender2", "ethnicity2", "BMI_Ranges", "physicianSpeciality2", "icu_admit_source2", "icu
_disch_location2", "hospitaldischargeyear", "dischargelocation", "dialysis", "aids", "hepaticfailure", "diabete
s", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baselin
e2", "sofa_liver_baseline2", "sofa_renal_baseline2", "cardiovascular_baseline", "group")

if(!(tableone %in% rownames(installed.packages())))) {
  install.packages("tableone")
}
library(dplyr); library(Hmisc); library(ggplot2); #library(sjPlot)
library(tableone)

CreateTableOne(data=ssd_incl_te ,vars=vars5,strata="qSOFA2TruthMort",test=FALSE, includeNA=TRUE
) %>% print(nonnormals= c("sofa_respiration_baseline2", "sofa_liver_baseline2", "sofa_renal_baseline2"),minMax=TRU
E,
  printToggle      = FALSE,
  showAllLevels   = TRUE,
  cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE), ,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="qSOFA Positive Hospital Mortality TRUE/FALSE")

```

qSOFA Positive Hospital Mortality TRUE/FALSE

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
n		87257	160630	2429	23436
age_Ranges (%)	(0,25]	3389 (3.9)	5412 (3.4)	14 (0.6)	236 (1.0)
	(25,35]	5308 (6.1)	8224 (5.1)	38 (1.6)	490 (2.1)
	(35,45]	7662 (8.8)	11667 (7.3)	92 (3.8)	907 (3.9)
	(45,55]	14184 (16.3)	23743 (14.8)	208 (8.6)	2394 (10.2)
	(55,65]	18886 (21.6)	33397 (20.8)	451 (18.6)	4370 (18.6)
	(65,75]	18746 (21.5)	35645 (22.2)	642 (26.4)	5573 (23.8)
	(75,85]	13930 (16.0)	29059 (18.1)	689 (28.4)	5944 (25.4)
	(85,100]	5152 (5.9)	13483 (8.4)	295 (12.1)	3522 (15.0)
gender2 (%)	Male	49579 (56.8)	83709 (52.1)	1318 (54.3)	12296 (52.5)
	Female	37660 (43.2)	76898 (47.9)	1106 (45.5)	11106 (47.4)
	Other/Unknown	18 (0.0)	23 (0.0)	5 (0.2)	34 (0.1)
ethnicity2 (%)	Caucasian	64139 (73.5)	124650 (77.6)	1885 (77.6)	18014 (76.9)
	African American	11434 (13.1)	17516 (10.9)	252 (10.4)	2527 (10.8)
	Hispanic	4310 (4.9)	6787 (4.2)	117 (4.8)	1071 (4.6)
	Asian	1074 (1.2)	2097 (1.3)	23 (0.9)	339 (1.4)
	Native American	620 (0.7)	1214 (0.8)	15 (0.6)	163 (0.7)
	Other/Unknown	5680 (6.5)	8366 (5.2)	137 (5.6)	1322 (5.6)

Combined Code Near Final

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
BMI_Ranges (%)	(0,18.5]	3337 (3.8)	8199 (5.1)	166 (6.8)	1746 (7.5)
	(18.5,25]	22470 (25.8)	46106 (28.7)	779 (32.1)	7520 (32.1)
	(25,35]	42118 (48.3)	72645 (45.2)	981 (40.4)	9468 (40.4)
	(35,200]	15898 (18.2)	28601 (17.8)	377 (15.5)	3581 (15.3)
	Other/Unknown	3434 (3.9)	5079 (3.2)	126 (5.2)	1121 (4.8)
physicianSpeciality2 (%)	Critical Care	18845 (21.6)	51695 (32.2)	778 (32.0)	8977 (38.3)
	Speciality-Other	68412 (78.4)	108935 (67.8)	1651 (68.0)	14459 (61.7)
icu_admit_source2 (%)	Floor	12015 (13.8)	27298 (17.0)	632 (26.0)	6489 (27.7)
	OR/Proc Area	18237 (20.9)	32725 (20.4)	242 (10.0)	1727 (7.4)
	Direct Admit	9788 (11.2)	16628 (10.4)	300 (12.4)	2755 (11.8)
	Emergency Department	45347 (52.0)	79057 (49.2)	1133 (46.6)	11137 (47.5)
	Other	580 (0.7)	1415 (0.9)	29 (1.2)	336 (1.4)
	Step-Down Unit	1290 (1.5)	3507 (2.2)	93 (3.8)	992 (4.2)
icu_disch_location2 (%)	Floor	65372 (74.9)	126936 (79.0)	816 (33.6)	6295 (26.9)
	Death	0 (0.0)	0 (0.0)	1552 (63.9)	16803 (71.7)
	Home	13771 (15.8)	12890 (8.0)	4 (0.2)	18 (0.1)
	SNF/Rehab	952 (1.1)	3304 (2.1)	0 (0.0)	2 (0.0)
	Other	2252 (2.6)	6434 (4.0)	19 (0.8)	100 (0.4)
	Other Hospital	1733 (2.0)	4405 (2.7)	2 (0.1)	16 (0.1)
	Step-Down Unit	3177 (3.6)	6661 (4.1)	36 (1.5)	202 (0.9)
hospitaldischargeyear (%)	-2010	12131 (13.9)	17851 (11.1)	455 (18.7)	2911 (12.4)
	2011	12029 (13.8)	21105 (13.1)	393 (16.2)	3287 (14.0)
	2012	13867 (15.9)	26684 (16.6)	364 (15.0)	3895 (16.6)
	2013	15366 (17.6)	30143 (18.8)	412 (17.0)	4341 (18.5)
	2014	17035 (19.5)	31808 (19.8)	393 (16.2)	4315 (18.4)
	2015-16	16829 (19.3)	33039 (20.6)	412 (17.0)	4687 (20.0)
dischargelocation (mean (sd))		5.06 (1.60)	5.05 (1.66)	7.33 (2.34)	7.68 (2.18)
dialysis (%)	0	84312 (96.6)	155494 (96.8)	2327 (95.8)	22361 (95.4)
	1	2945 (3.4)	5136 (3.2)	102 (4.2)	1075 (4.6)
aids (%)	0	87187 (99.9)	160470 (99.9)	2427 (99.9)	23405 (99.9)
	1	70 (0.1)	160 (0.1)	2 (0.1)	31 (0.1)
hepaticfailure (%)	FALSE	85884 (98.4)	157279 (97.9)	2365 (97.4)	22543 (96.2)
	TRUE	1373 (1.6)	3351 (2.1)	64 (2.6)	893 (3.8)
diabetes (%)	0	67023 (76.8)	125841 (78.3)	1952 (80.4)	19104 (81.5)
	1	20234 (23.2)	34789 (21.7)	477 (19.6)	4332 (18.5)
immunosuppression (%)	0	85620 (98.1)	156971 (97.7)	2308 (95.0)	22487 (96.0)
	1	1637 (1.9)	3659 (2.3)	121 (5.0)	949 (4.0)
leukemia (%)	0	86780 (99.5)	159553 (99.3)	2397 (98.7)	23084 (98.5)
	1	477 (0.5)	1077 (0.7)	32 (1.3)	352 (1.5)
lymphoma (%)	0	87015 (99.7)	160009 (99.6)	2413 (99.3)	23285 (99.4)
	1	242 (0.3)	621 (0.4)	16 (0.7)	151 (0.6)
metastaticcancer (%)	0	85825 (98.4)	157710 (98.2)	2335 (96.1)	22576 (96.3)
	1	1432 (1.6)	2920 (1.8)	94 (3.9)	860 (3.7)
thrombolytics (%)	0	85090 (97.5)	158233 (98.5)	2391 (98.4)	23070 (98.4)
	1	2167 (2.5)	2397 (1.5)	38 (1.6)	366 (1.6)
sofa_respiration_baseline2 (%)	FALSE	69286 (79.4)	120161 (74.8)	1672 (68.8)	16889 (72.1)

Combined Code Near Final

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	TRUE	17971 (20.6)	40469 (25.2)	757 (31.2)	6547 (27.9)
sofa_liver_baseline2 (%)	FALSE	85884 (98.4)	157279 (97.9)	2365 (97.4)	22543 (96.2)
	TRUE	1373 (1.6)	3351 (2.1)	64 (2.6)	893 (3.8)
sofa_renal_baseline2 (%)	FALSE	84312 (96.6)	155494 (96.8)	2327 (95.8)	22361 (95.4)
	TRUE	2945 (3.4)	5136 (3.2)	102 (4.2)	1075 (4.6)
cardiovascular_baseline (%)	0	69275 (79.4)	123833 (77.1)	1744 (71.8)	17009 (72.6)
	1	17982 (20.6)	36797 (22.9)	685 (28.2)	6427 (27.4)
group (%)	Cardiovascular	33024 (37.8)	47941 (29.8)	690 (28.4)	6708 (28.6)
	Gastrointestinal	9742 (11.2)	16523 (10.3)	211 (8.7)	2068 (8.8)
	Gynaecological	276 (0.3)	430 (0.3)	0 (0.0)	9 (0.0)
	Hematological	795 (0.9)	1120 (0.7)	18 (0.7)	153 (0.7)
	Metabolic	8223 (9.4)	13806 (8.6)	38 (1.6)	394 (1.7)
	Muscoskeletal/Skin disease	1196 (1.4)	2136 (1.3)	11 (0.5)	115 (0.5)
	Neurological	11591 (13.3)	21909 (13.6)	429 (17.7)	2908 (12.4)
	Renal/Genitourinary	2151 (2.5)	3950 (2.5)	45 (1.9)	430 (1.8)
	Respiratory	10416 (11.9)	25300 (15.8)	542 (22.3)	4600 (19.6)
	Sepsis	4434 (5.1)	19599 (12.2)	303 (12.5)	5001 (21.3)
	Trauma	4534 (5.2)	6662 (4.1)	108 (4.4)	821 (3.5)
	Undefined	875 (1.0)	1254 (0.8)	34 (1.4)	229 (1.0)

```

vars5 <- c("age_Ranges", "gender2", "ethnicity2", "BMI_Ranges", "physicianSpeciality2", "icu_admit_source2", "icu_disch_location2", "hospitaldischargeyear", "dischargelocation", "dialysis", "aids", "hepaticfailure", "diabetes", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baseline2", "sofa_liver_baseline2", "sofa_renal_baseline2", "cardiovascular_baseline", "group")

if(!(tableone %in% rownames(installed.packages()))) {
  install.packages("tableone")
}

library(tableone)

CreateTableOne(data=ssd_incl_te ,vars=vars5,strata="SOFA2TruthMort",test=FALSE, includeNA=TRUE
) %>% print(nonnormal= c("sofa_respiration_baseline2", "sofa_liver_baseline2", "sofa_renal_baseline2"),minMax=TRUE,
E,
  printToggle      = FALSE,
  showAllLevels   = TRUE,
  cramVars        = "kon"
) %>%
{data.frame(
  variable_name    = gsub(" ", " ", rownames(.), fixed = TRUE),
  row.names        = NULL,
  check.names     = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="SOFA Positive Hospital Mortality TRUE/FALSE")

```

SOFA Positive Hospital Mortality TRUE/FALSE

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
n		83807	164080	1464	24401
age_Ranges (%)	(0,25]	4029 (4.8)	4772 (2.9)	5 (0.3)	245 (1.0)
	(25,35]	5833 (7.0)	7699 (4.7)	14 (1.0)	514 (2.1)
	(35,45]	8346 (10.0)	10983 (6.7)	35 (2.4)	964 (4.0)
	(45,55]	15061 (18.0)	22866 (13.9)	120 (8.2)	2482 (10.2)
	(55,65]	18448 (22.0)	33835 (20.6)	296 (20.2)	4525 (18.5)
	(65,75]	16686 (19.9)	37705 (23.0)	402 (27.5)	5813 (23.8)
	(75,85]	11248 (13.4)	31741 (19.3)	405 (27.7)	6228 (25.5)

Combined Code Near Final

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	(85,100]	4156 (5.0)	14479 (8.8)	187 (12.8)	3630 (14.9)
gender2 (%)	Male	43050 (51.4)	90238 (55.0)	692 (47.3)	12922 (53.0)
	Female	40746 (48.6)	73812 (45.0)	770 (52.6)	11442 (46.9)
	Other/Unknown	11 (0.0)	30 (0.0)	2 (0.1)	37 (0.2)
ethnicity2 (%)	Caucasian	63802 (76.1)	124987 (76.2)	1207 (82.4)	18692 (76.6)
	African American	9866 (11.8)	19084 (11.6)	111 (7.6)	2668 (10.9)
	Hispanic	3658 (4.4)	7439 (4.5)	52 (3.6)	1136 (4.7)
	Asian	1019 (1.2)	2152 (1.3)	20 (1.4)	342 (1.4)
	Native American	553 (0.7)	1281 (0.8)	1 (0.1)	177 (0.7)
	Other/Unknown	4909 (5.9)	9137 (5.6)	73 (5.0)	1386 (5.7)
BMI_Ranges (%)	(0,18.5]	3586 (4.3)	7950 (4.8)	155 (10.6)	1757 (7.2)
	(18.5,25]	22640 (27.0)	45936 (28.0)	519 (35.5)	7780 (31.9)
	(25,35]	39257 (46.8)	75506 (46.0)	569 (38.9)	9880 (40.5)
	(35,200]	14808 (17.7)	29691 (18.1)	166 (11.3)	3792 (15.5)
	Other/Unknown	3516 (4.2)	4997 (3.0)	55 (3.8)	1192 (4.9)
physicianSpeciality2 (%)	Critical Care	16917 (20.2)	53623 (32.7)	471 (32.2)	9284 (38.0)
	Speciality-Other	66890 (79.8)	110457 (67.3)	993 (67.8)	15117 (62.0)
icu_admit_source2 (%)	Floor	11167 (13.3)	28146 (17.2)	488 (33.3)	6633 (27.2)
	OR/Proc Area	15787 (18.8)	35175 (21.4)	87 (5.9)	1882 (7.7)
	Direct Admit	9574 (11.4)	16842 (10.3)	154 (10.5)	2901 (11.9)
	Emergency Department	45511 (54.3)	78893 (48.1)	654 (44.7)	11616 (47.6)
	Other	551 (0.7)	1444 (0.9)	19 (1.3)	346 (1.4)
	Step-Down Unit	1217 (1.5)	3580 (2.2)	62 (4.2)	1023 (4.2)
icu_disch_location2 (%)	Floor	62101 (74.1)	130207 (79.4)	593 (40.5)	6518 (26.7)
	Death	0 (0.0)	0 (0.0)	830 (56.7)	17525 (71.8)
	Home	14699 (17.5)	11962 (7.3)	2 (0.1)	20 (0.1)
	SNF/Rehab	683 (0.8)	3573 (2.2)	0 (0.0)	2 (0.0)
	Other	2198 (2.6)	6488 (4.0)	5 (0.3)	114 (0.5)
	Other Hospital	1623 (1.9)	4515 (2.8)	6 (0.4)	12 (0.0)
	Step-Down Unit	2503 (3.0)	7335 (4.5)	28 (1.9)	210 (0.9)
hospitaldischargeyear (%)	-2010	9788 (11.7)	20194 (12.3)	193 (13.2)	3173 (13.0)
	2011	10699 (12.8)	22435 (13.7)	200 (13.7)	3480 (14.3)
	2012	13477 (16.1)	27074 (16.5)	234 (16.0)	4025 (16.5)
	2013	15974 (19.1)	29535 (18.0)	287 (19.6)	4466 (18.3)
	2014	17191 (20.5)	31652 (19.3)	263 (18.0)	4445 (18.2)
	2015-16	16678 (19.9)	33190 (20.2)	287 (19.6)	4812 (19.7)
dischargelocation (mean (sd))		5.16 (1.65)	5.00 (1.63)	7.01 (2.41)	7.69 (2.18)
dialysis (%)	0	80629 (96.2)	159177 (97.0)	1390 (94.9)	23298 (95.5)
	1	3178 (3.8)	4903 (3.0)	74 (5.1)	1103 (4.5)
aids (%)	0	83751 (99.9)	163906 (99.9)	1462 (99.9)	24370 (99.9)
	1	56 (0.1)	174 (0.1)	2 (0.1)	31 (0.1)
hepaticfailure (%)	FALSE	83104 (99.2)	160059 (97.5)	1438 (98.2)	23470 (96.2)
	TRUE	703 (0.8)	4021 (2.5)	26 (1.8)	931 (3.8)
diabetes (%)	0	66157 (78.9)	126707 (77.2)	1217 (83.1)	19839 (81.3)
	1	17650 (21.1)	37373 (22.8)	247 (16.9)	4562 (18.7)
immunosuppression (%)	0	82356 (98.3)	160235 (97.7)	1372 (93.7)	23423 (96.0)

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	1	1451 (1.7)	3845 (2.3)	92 (6.3)	978 (4.0)
leukemia (%)	0	83514 (99.7)	162819 (99.2)	1454 (99.3)	24027 (98.5)
	1	293 (0.3)	1261 (0.8)	10 (0.7)	374 (1.5)
lymphoma (%)	0	83612 (99.8)	163412 (99.6)	1459 (99.7)	24239 (99.3)
	1	195 (0.2)	668 (0.4)	5 (0.3)	162 (0.7)
metastaticcancer (%)	0	82448 (98.4)	161087 (98.2)	1372 (93.7)	23539 (96.5)
	1	1359 (1.6)	2993 (1.8)	92 (6.3)	862 (3.5)
thrombolytics (%)	0	81143 (96.8)	162180 (98.8)	1439 (98.3)	24022 (98.4)
	1	2664 (3.2)	1900 (1.2)	25 (1.7)	379 (1.6)
sofa_respiration_baseline2 (%)	FALSE	64372 (76.8)	125075 (76.2)	788 (53.8)	17773 (72.8)
	TRUE	19435 (23.2)	39005 (23.8)	676 (46.2)	6628 (27.2)
sofa_liver_baseline2 (%)	FALSE	83104 (99.2)	160059 (97.5)	1438 (98.2)	23470 (96.2)
	TRUE	703 (0.8)	4021 (2.5)	26 (1.8)	931 (3.8)
sofa_renal_baseline2 (%)	FALSE	80629 (96.2)	159177 (97.0)	1390 (94.9)	23298 (95.5)
	TRUE	3178 (3.8)	4903 (3.0)	74 (5.1)	1103 (4.5)
cardiovascular_baseline (%)	0	68828 (82.1)	124280 (75.7)	1060 (72.4)	17693 (72.5)
	1	14979 (17.9)	39800 (24.3)	404 (27.6)	6708 (27.5)
group (%)	Cardiovascular	30780 (36.7)	50185 (30.6)	343 (23.4)	7055 (28.9)
	Gastrointestinal	8099 (9.7)	18166 (11.1)	109 (7.4)	2170 (8.9)
	Gynaecological	263 (0.3)	443 (0.3)	3 (0.2)	6 (0.0)
	Hematological	483 (0.6)	1432 (0.9)	5 (0.3)	166 (0.7)
	Metabolic	8569 (10.2)	13460 (8.2)	15 (1.0)	417 (1.7)
	Muscoskeletal/Skin disease	1209 (1.4)	2123 (1.3)	4 (0.3)	122 (0.5)
	Neurological	12651 (15.1)	20849 (12.7)	159 (10.9)	3178 (13.0)
	Renal/Genitourinary	980 (1.2)	5121 (3.1)	15 (1.0)	460 (1.9)
	Respiratory	12189 (14.5)	23527 (14.3)	576 (39.3)	4566 (18.7)
	Sepsis	3416 (4.1)	20617 (12.6)	154 (10.5)	5150 (21.1)
	Trauma	4140 (4.9)	7056 (4.3)	36 (2.5)	893 (3.7)
	Undefined	1028 (1.2)	1101 (0.7)	45 (3.1)	218 (0.9)

```

vars5 <- c("age_Ranges", "gender2", "ethnicity2", "BMI_Ranges", "physicianSpeciality2", "icu_admit_source2", "icu
 _disch_location2", "hospitaldischargeyear", "dischargelocation", "dialysis", "aids", "hepaticefailure", "diabete
 s", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baselin
 e2", "sofa_liver_baseline2", "sofa_renal_baseline2", "cardiovascular_baseline", "group")

library(dplyr); library(Hmisc); library(ggplot2); #library(sjPlot)

if(!(tableone" %in% rownames(installed.packages()))){
  install.packages("tableone")
}
library(dplyr); library(Hmisc); library(ggplot2); #library(sjPlot)
library(tableone)

CreateTableOne(data=ssd_incl_te ,vars=vars5,strata="FuzzyLogicTruthMort",test=FALSE, includeNA=TRUE
 ) %>% print(nonnorma= c("sofa_respiration_baseline2", "sofa_liver_baseline2", "sofa_renal_baseline2"),minMax=TRU
 E,
 printToggle      = FALSE,
 showAllLevels   = TRUE,
 cramVars        = "kon"
 ) %>%
{data.frame(
  variable_name      = gsub(" ", "&nbsp;", rownames(.), fixed = TRUE), ,
  row.names          = NULL,
  check.names        = FALSE,
  stringsAsFactors  = FALSE)} %>%
knitr::kable(caption="FuzzyLogic Positive Hospital Mortality TRUE/FALSE")

```

FuzzyLogic Positive Hospital Mortality TRUE/FALSE

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
n		119438	128449	3492	22373
age_Ranges (%)	(0,25]	4013 (3.4)	4788 (3.7)	10 (0.3)	240 (1.1)
	(25,35]	6627 (5.5)	6905 (5.4)	38 (1.1)	490 (2.2)
	(35,45]	9846 (8.2)	9483 (7.4)	93 (2.7)	906 (4.0)
	(45,55]	18948 (15.9)	18979 (14.8)	266 (7.6)	2336 (10.4)
	(55,65]	25293 (21.2)	26990 (21.0)	560 (16.0)	4261 (19.0)
	(65,75]	25677 (21.5)	28714 (22.4)	836 (23.9)	5379 (24.0)
	(75,85]	20248 (17.0)	22741 (17.7)	1042 (29.8)	5591 (25.0)
	(85,100]	8786 (7.4)	9849 (7.7)	647 (18.5)	3170 (14.2)
gender2 (%)	Male	65930 (55.2)	67358 (52.4)	1846 (52.9)	11768 (52.6)
	Female	53490 (44.8)	61068 (47.5)	1638 (46.9)	10574 (47.3)
	Other/Unknown	18 (0.0)	23 (0.0)	8 (0.2)	31 (0.1)
ethnicity2 (%)	Caucasian	89699 (75.1)	99090 (77.1)	2680 (76.7)	17219 (77.0)
	African American	15185 (12.7)	13765 (10.7)	393 (11.3)	2386 (10.7)
	Hispanic	5262 (4.4)	5835 (4.5)	137 (3.9)	1051 (4.7)
	Asian	1590 (1.3)	1581 (1.2)	53 (1.5)	309 (1.4)
	Native American	865 (0.7)	969 (0.8)	19 (0.5)	159 (0.7)
	Other/Unknown	6837 (5.7)	7209 (5.6)	210 (6.0)	1249 (5.6)
BMI_Ranges (%)	(0,18.5]	4891 (4.1)	6645 (5.2)	244 (7.0)	1668 (7.5)
	(18.5,25]	32335 (27.1)	36241 (28.2)	1131 (32.4)	7168 (32.0)
	(25,35]	56696 (47.5)	58067 (45.2)	1420 (40.7)	9029 (40.4)
	(35,200]	20582 (17.2)	23917 (18.6)	506 (14.5)	3452 (15.4)
	Other/Unknown	4934 (4.1)	3579 (2.8)	191 (5.5)	1056 (4.7)
physicianSpeciality2 (%)	Critical Care	26125 (21.9)	44415 (34.6)	1099 (31.5)	8656 (38.7)
	Speciality-Other	93313 (78.1)	84034 (65.4)	2393 (68.5)	13717 (61.3)
icu_admit_source2 (%)	Floor	17596 (14.7)	21717 (16.9)	962 (27.5)	6159 (27.5)
	OR/Proc Area	22718 (19.0)	28244 (22.0)	261 (7.5)	1708 (7.6)
	Direct Admit	15459 (12.9)	10957 (8.5)	518 (14.8)	2537 (11.3)
	Emergency Department	60592 (50.7)	63812 (49.7)	1542 (44.2)	10728 (48.0)
	Other	955 (0.8)	1040 (0.8)	63 (1.8)	302 (1.3)
	Step-Down Unit	2118 (1.8)	2679 (2.1)	146 (4.2)	939 (4.2)
icu_disch_location2 (%)	Floor	88826 (74.4)	103482 (80.6)	1415 (40.5)	5696 (25.5)
	Death	0 (0.0)	0 (0.0)	1983 (56.8)	16372 (73.2)
	Home	19229 (16.1)	7432 (5.8)	3 (0.1)	19 (0.1)
	SNF/Rehab	1476 (1.2)	2780 (2.2)	0 (0.0)	2 (0.0)
	Other	3571 (3.0)	5115 (4.0)	23 (0.7)	96 (0.4)
	Other Hospital	2457 (2.1)	3681 (2.9)	9 (0.3)	9 (0.0)
	Step-Down Unit	3879 (3.2)	5959 (4.6)	59 (1.7)	179 (0.8)
hospitaldischargeyear (%)	-2010	14311 (12.0)	15671 (12.2)	480 (13.7)	2886 (12.9)
	2011	15532 (13.0)	17602 (13.7)	467 (13.4)	3213 (14.4)
	2012	19360 (16.2)	21191 (16.5)	571 (16.4)	3688 (16.5)
	2013	22159 (18.6)	23350 (18.2)	683 (19.6)	4070 (18.2)
	2014	24018 (20.1)	24825 (19.3)	630 (18.0)	4078 (18.2)
	2015-16	24058 (20.1)	25810 (20.1)	661 (18.9)	4438 (19.8)
dischargelocation (mean (sd))		5.15 (1.65)	4.97 (1.62)	7.00 (2.42)	7.75 (2.15)

Combined Code Near Final

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
dialysis (%)	0	115245 (96.5)	124561 (97.0)	3281 (94.0)	21407 (95.7)
	1	4193 (3.5)	3888 (3.0)	211 (6.0)	966 (4.3)
aids (%)	0	119343 (99.9)	128314 (99.9)	3486 (99.8)	22346 (99.9)
	1	95 (0.1)	135 (0.1)	6 (0.2)	27 (0.1)
hepaticfailure (%)	FALSE	117974 (98.8)	125189 (97.5)	3435 (98.4)	21473 (96.0)
	TRUE	1464 (1.2)	3260 (2.5)	57 (1.6)	900 (4.0)
diabetes (%)	0	89700 (75.1)	103164 (80.3)	2498 (71.5)	18558 (82.9)
	1	29738 (24.9)	25285 (19.7)	994 (28.5)	3815 (17.1)
immunosuppression (%)	0	117440 (98.3)	125151 (97.4)	3364 (96.3)	21431 (95.8)
	1	1998 (1.7)	3298 (2.6)	128 (3.7)	942 (4.2)
leukemia (%)	0	118868 (99.5)	127465 (99.2)	3450 (98.8)	22031 (98.5)
	1	570 (0.5)	984 (0.8)	42 (1.2)	342 (1.5)
lymphoma (%)	0	119099 (99.7)	127925 (99.6)	3468 (99.3)	22230 (99.4)
	1	339 (0.3)	524 (0.4)	24 (0.7)	143 (0.6)
metastaticcancer (%)	0	117589 (98.5)	125946 (98.1)	3389 (97.1)	21522 (96.2)
	1	1849 (1.5)	2503 (1.9)	103 (2.9)	851 (3.8)
thrombolytics (%)	0	116194 (97.3)	127129 (99.0)	3444 (98.6)	22017 (98.4)
	1	3244 (2.7)	1320 (1.0)	48 (1.4)	356 (1.6)
sofa_respiration_baseline2 (%)	FALSE	95583 (80.0)	93864 (73.1)	2514 (72.0)	16047 (71.7)
	TRUE	23855 (20.0)	34585 (26.9)	978 (28.0)	6326 (28.3)
sofa_liver_baseline2 (%)	FALSE	117974 (98.8)	125189 (97.5)	3435 (98.4)	21473 (96.0)
	TRUE	1464 (1.2)	3260 (2.5)	57 (1.6)	900 (4.0)
sofa_renal_baseline2 (%)	FALSE	115245 (96.5)	124561 (97.0)	3281 (94.0)	21407 (95.7)
	TRUE	4193 (3.5)	3888 (3.0)	211 (6.0)	966 (4.3)
cardiovascular_baseline (%)	0	93442 (78.2)	99666 (77.6)	2390 (68.4)	16363 (73.1)
	1	25996 (21.8)	28783 (22.4)	1102 (31.6)	6010 (26.9)
group (%)	Cardiovascular	46150 (38.6)	34815 (27.1)	883 (25.3)	6515 (29.1)
	Gastrointestinal	10652 (8.9)	15613 (12.2)	193 (5.5)	2086 (9.3)
	Gynaecological	247 (0.2)	459 (0.4)	1 (0.0)	8 (0.0)
	Hematological	852 (0.7)	1063 (0.8)	22 (0.6)	149 (0.7)
	Metabolic	11088 (9.3)	10941 (8.5)	58 (1.7)	374 (1.7)
	Muscoskeletal/Skin disease	1538 (1.3)	1794 (1.4)	16 (0.5)	110 (0.5)
	Neurological	21786 (18.2)	11714 (9.1)	1048 (30.0)	2289 (10.2)
	Renal/Genitourinary	2731 (2.3)	3370 (2.6)	60 (1.7)	415 (1.9)
	Respiratory	13352 (11.2)	22364 (17.4)	784 (22.5)	4358 (19.5)
	Sepsis	4077 (3.4)	19956 (15.5)	242 (6.9)	5062 (22.6)
Trauma		5785 (4.8)	5411 (4.2)	140 (4.0)	789 (3.5)
	Undefined	1180 (1.0)	949 (0.7)	45 (1.3)	218 (1.0)

```
library(tidyr)
ssd_incl_te %>% group_by(gender2=="Male", FuzzyLogicTruthMort) %>% summarise(n=n()) %>% spread(FuzzyLogicTruthMort, n) %>%
  mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

gender2 == "Male"	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
FALSE	53508	61091	1646	10605	0.8656436	0.4669151
TRUE	65930	67358	1846	11768	0.8644043	0.4946432

```
ssd_incl_te %>% group_by(ethnicity2,FuzzyLogicTruthMort) %>%summarise(n=n())%>%spread(FuzzyLogicTruthMort,n)%>%mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE),SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE))%>%knitr::kable()
```

ethnicity2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Caucasian	89699	99090	2680	17219	0.8653199	0.4751283
African American	15185	13765	393	2386	0.8585822	0.5245250
Hispanic	5262	5835	137	1051	0.8846801	0.4741822
Asian	1590	1581	53	309	0.8535912	0.5014191
Native American	865	969	19	159	0.8932584	0.4716467
Other/Unknown	6837	7209	210	1249	0.8560658	0.4867578

```
ssd_incl_te %>% group_by(icu_admit_source2,FuzzyLogicTruthMort) %>%summarise(n=n())%>%spread(FuzzyLogicTruthMort,n)%>%mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE),SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE))%>%knitr::kable()
```

icu_admit_source2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Floor	17596	21717	962	6159	0.8649066	0.4475873
OR/Proc Area	22718	28244	261	1708	0.8674454	0.4457831
Direct Admit	15459	10957	518	2537	0.8304419	0.5852135
Emergency Department	60592	63812	1542	10728	0.8743276	0.4870583
Other	955	1040	63	302	0.8273973	0.4786967
Step-Down Unit	2118	2679	146	939	0.8654378	0.4415260

21 Baseline Sepsis Test/Train

```
Baseline_Sepsis_tr<-glm(sepsis_outcome ~ age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer + thrombolytics + sofa_respiratory_n_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(Baseline_Sepsis_tr)
#sjt.glm(Baseline_Sepsis_tr)

#drop1(Baseline_Sepsis_tr,test="Chisq")

summary(Baseline_Sepsis_tr)
```

```

## 
## Call:
## glm(formula = sepsis_outcome ~ age_Ranges + gender2 + ethnicity2 +
##      BMI_Ranges + icu_admit_source2 + hospital_teaching_status +
##      hospital_size + physicianSpeciality2 + hospitaldischargeyear +
##      dialysis + aids + hepaticfailure + diabetes + immunosuppression +
##      leukemia + lymphoma + metastaticcancer + thrombolytics +
##      sofa_respiration_baseline2 + cardiovascular_baseline, family = "binomial",
##      data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.0071 -0.7316 -0.5589 -0.2665  3.3612
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                 -0.948952  0.032059 -29.600
## age_Ranges(25,35]            0.157222  0.026835  5.859
## age_Ranges(35,45]            0.305391  0.024934 12.248
## age_Ranges(45,55]            0.480932  0.023066 20.851
## age_Ranges(55,65]            0.664639  0.022559 29.463
## age_Ranges(65,75]            0.718137  0.022549 31.849
## age_Ranges(75,85]            0.801259  0.022662 35.357
## age_Ranges(85,100]           0.934297  0.023815 39.232
## gender2Female                0.055373  0.006581  8.414
## gender2Other/Unknown         -0.933627  0.263338 -3.545
## ethnicity2African American   -0.095562  0.010658 -8.966
## ethnicity2Hispanic            0.395323  0.014683 26.923
## ethnicity2Asian               0.083708  0.028682  2.918
## ethnicity2Native American     0.322652  0.036496  8.841
## ethnicity2Other/Unknown       0.073306  0.014404  5.089
## BMI_Ranges(18.5,25]          -0.259430  0.014657 -17.700
## BMI_Ranges(25,35]             -0.346922  0.014359 -24.160
## BMI_Ranges(35,200]            -0.142435  0.015579 -9.143
## BMI_RangesOther/Unknown       -0.604858  0.022942 -26.364
## icu_admit_source2OR/Proc Area -1.957638  0.014310 -136.805
## icu_admit_source2Direct Admit -0.619162  0.012410 -49.891
## icu_admit_source2Emergency Department -0.320082  0.008116 -39.439
## icu_admit_source2Other        -0.188787  0.032393 -5.828
## icu_admit_source2Step-Down Unit 0.033255  0.020519  1.621
## hospital_teaching_statusf    -0.211799  0.023996 -8.827
## hospital_teaching_statust    -0.161197  0.024168 -6.670
## hospital_size<100            0.537067  0.022878 23.476
## hospital_size100-249          0.273145  0.018688 14.616
## hospital_size250-500          0.262396  0.019027 13.791
## hospital_size>500             0.124338  0.017769  6.997
## physicianSpeciality2Speciality-Other -0.640748  0.007362 -87.036
## hospitaldischargeyear2011     0.100206  0.012669  7.910
## hospitaldischargeyear2012     -0.043243  0.012306 -3.514
## hospitaldischargeyear2013     -0.050617  0.012027 -4.208
## hospitaldischargeyear2014     -0.090001  0.011937 -7.540
## hospitaldischargeyear2015-16   -0.036695  0.011814 -3.106
## dialysis1                     0.246276  0.017038 14.455
## aids1                          1.344545  0.084849 15.846
## hepaticfailureTRUE              0.183669  0.020985  8.752
## diabetes1                      -0.074419  0.008111 -9.175
## immunosuppression1              0.590598  0.019733 29.929
## leukemia1                      0.508674  0.032829 15.494
## lymphoma1                       0.411006  0.044722  9.190
## metastaticcancer1              0.096858  0.023419  4.136
## thrombolytics1                  -2.219547  0.060013 -36.985
## sofa_respiration_baseline2TRUE  0.477844  0.007251 65.897
## cardiovascular_baseline1       -0.069130  0.007952 -8.694
##
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## age_Ranges(25,35] 4.66e-09 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female < 2e-16 ***
## gender2Other/Unknown 0.000392 ***
## ethnicity2African American < 2e-16 ***
## ethnicity2Hispanic < 2e-16 ***
## ethnicity2Asian 0.003518 **
## ethnicity2Native American < 2e-16 ***

```

```

## ethnicity2Other/Unknown          3.59e-07 ***
## BMI_Ranges(18.5,25]            < 2e-16 ***
## BMI_Ranges(25,35]              < 2e-16 ***
## BMI_Ranges(35,200]             < 2e-16 ***
## BMI_RangesOther/Unknown        < 2e-16 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other         5.61e-09 ***
## icu_admit_source2Step-Down Unit 0.105083
## hospital_teaching_statusf    < 2e-16 ***
## hospital_teaching_statust    2.56e-11 ***
## hospital_size<100             < 2e-16 ***
## hospital_size100-249          < 2e-16 ***
## hospital_size250-500          < 2e-16 ***
## hospital_size>500             2.61e-12 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011     2.58e-15 ***
## hospitaldischargeyear2012     0.000442 ***
## hospitaldischargeyear2013     2.57e-05 ***
## hospitaldischargeyear2014     4.72e-14 ***
## hospitaldischargeyear2015-16   0.001895 **
## dialysis1                      < 2e-16 ***
## aids1                          < 2e-16 ***
## hepaticfailureTRUE             < 2e-16 ***
## diabetes1                     < 2e-16 ***
## immunosuppression1            < 2e-16 ***
## leukemial                      < 2e-16 ***
## lymphomal                       < 2e-16 ***
## metastaticcancer1             3.54e-05 ***
## thrombolytics1                 < 2e-16 ***
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1      < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128  on 638756  degrees of freedom
## Residual deviance: 590208  on 638710  degrees of freedom
## AIC: 590302
##
## Number of Fisher Scoring iterations: 6

```

```
nrow(ssd_incl_te)
```

```
## [1] 273752
```

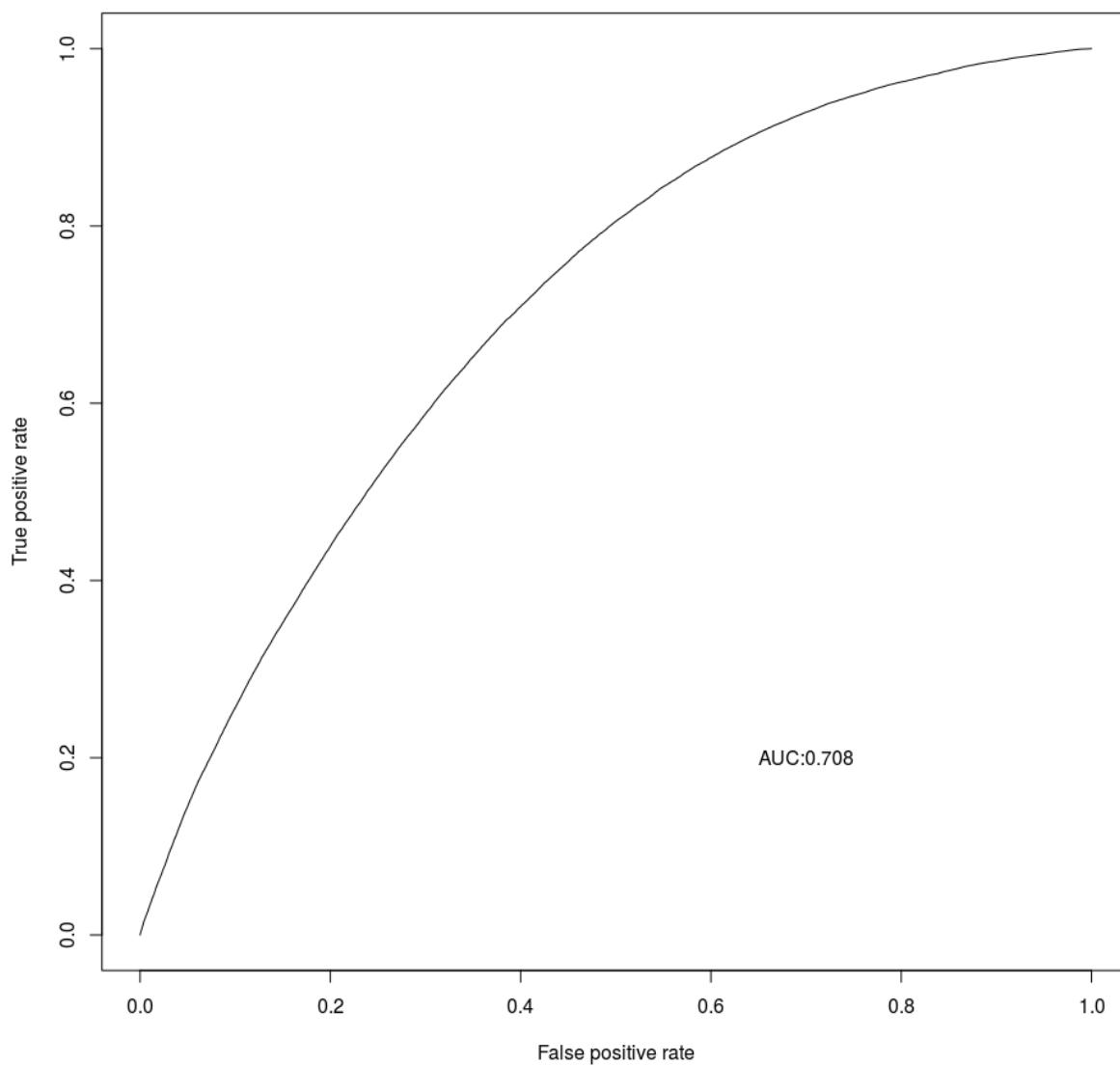
```

ssd_incl_te$BaselineSepsisPred <- predict(Baseline_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

BaselineSepsis.Pred <- prediction(ssd_incl_te$BaselineSepsisPred, ssd_incl_te$sepsis_outcome)
BaselineSepsis.Perf <- performance(BaselineSepsis.Pred, "tpr", "fpr")
plot(BaselineSepsis.Perf, main = "Baseline Sepsis
Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(BaselineSepsis.Pred,"auc")@y.values[[1]],3)))

```

**Baseline Sepsis
Prediction Test Model**



```
performance(BaselineSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7078539
##
## Slot "alpha.values":
## list()
```

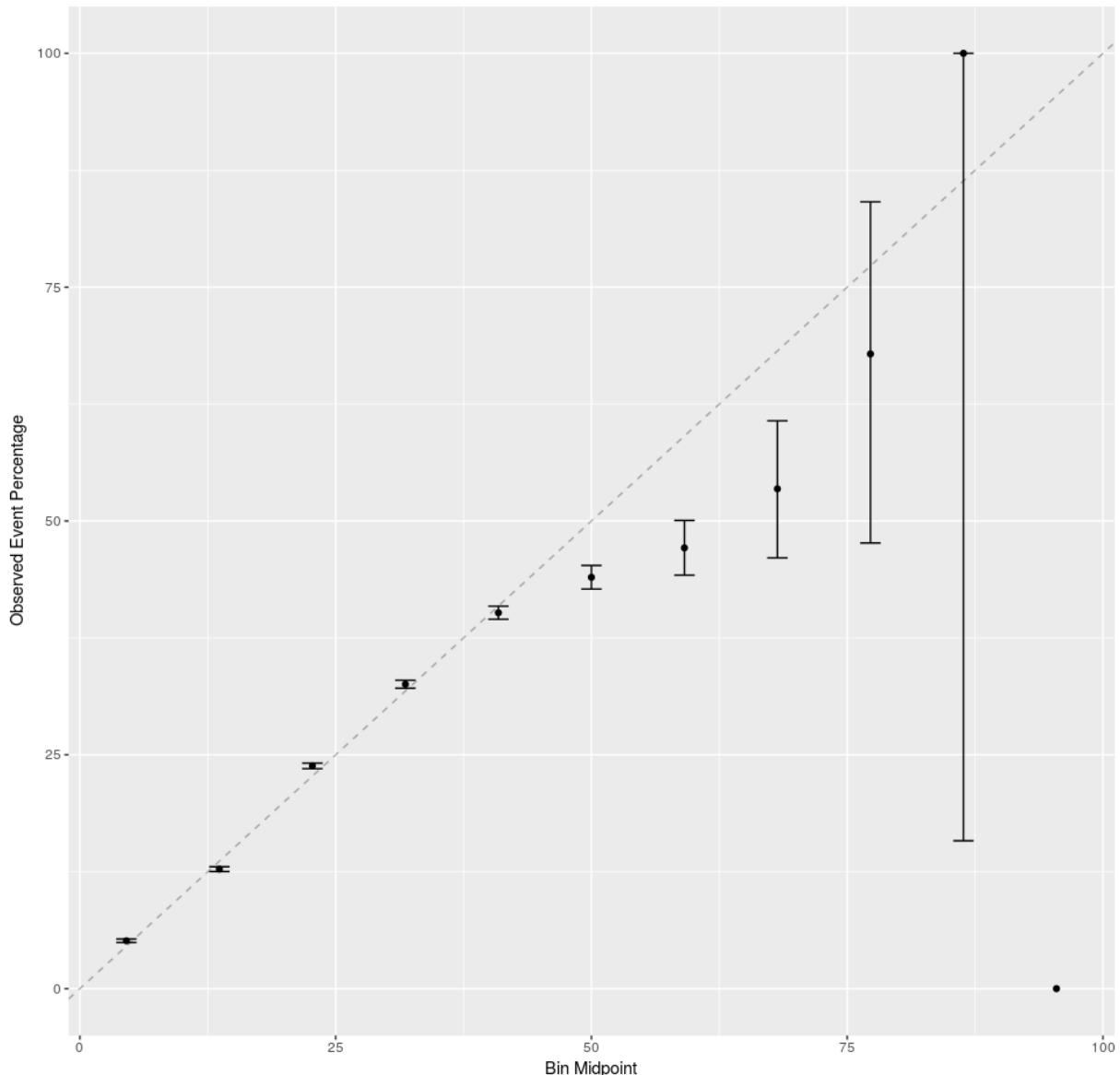
```
BaselineSepsis.Pred.roc <- roc(sepsis_outcome~BaselineSepsisPred,data=ssd_incl_te)
try({ci(BaselineSepsis.Pred.roc, conf.level=0.99)},silent=TRUE)
```

```
## 99% CI: 0.7049-0.7108 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~BaselineSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of Baseline Sepsis Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

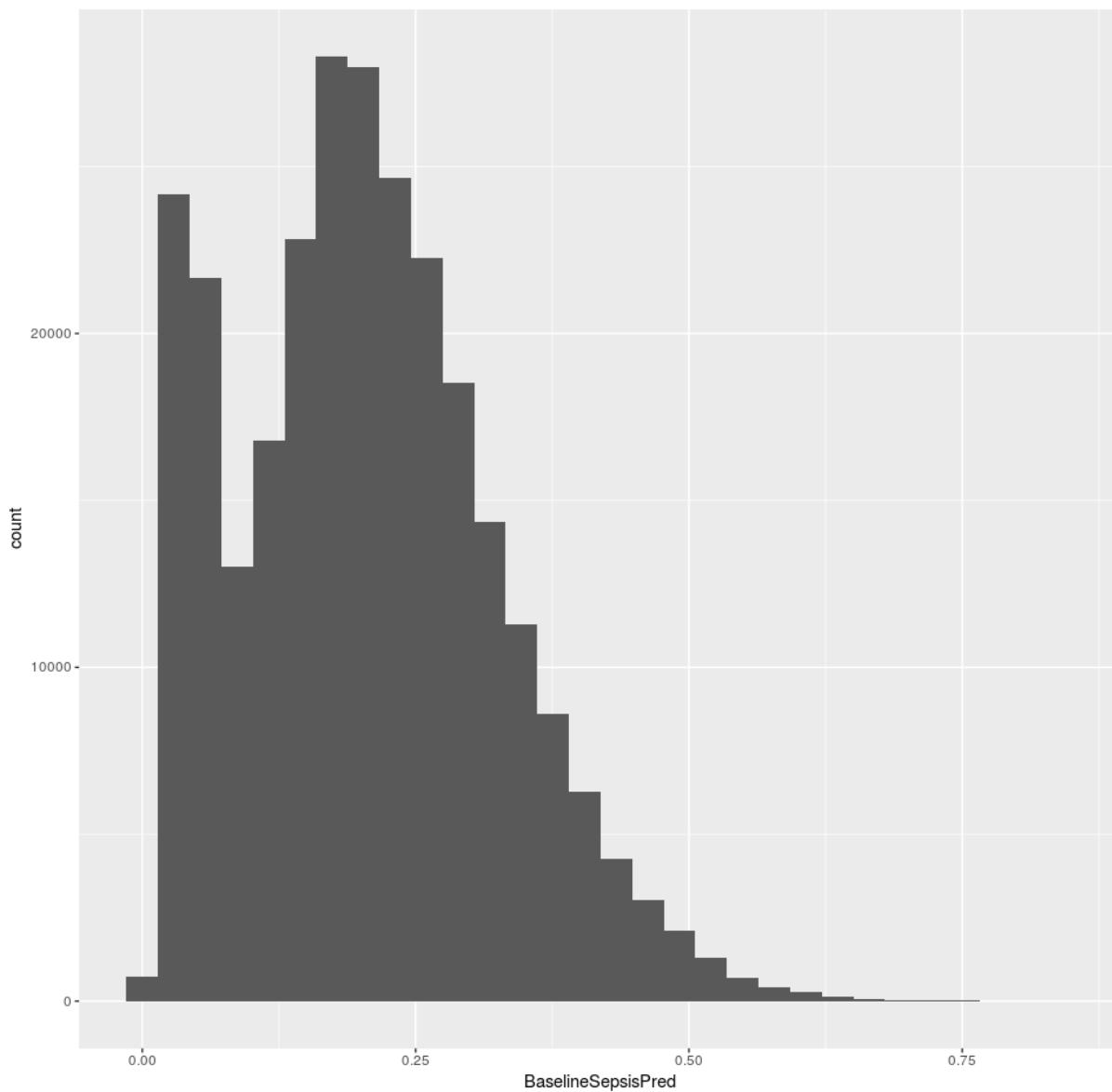
Calibration of Baseline Sepsis Prediction



```
qplot(BaselineSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of Baseline Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of Baseline Sepsis Predictions



22 Cross validation

partitions the data into 5 groups and then uses the 4 groups to predict the 5th group. It does this 5 times and then takes the average, ROC curves,

```
SIRS1_ADJ_Sepsis_tr<-glm(sepsis_outcome ~ as.factor(SIRS_total) + age_Ranges + gender2 + ethnicity2 + BMI_Ranges
+ icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischargeyear + d
ialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer + thromb
olytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.action = n
a.omit)

#sjp.glm(SIRS1_ADJ_Sepsis_tr)
#sjt.glm(SIRS1_ADJ_Sepsis_tr)

#drop1(SIRS1_ADJ_Sepsis_tr,test="Chisq")

summary(SIRS1_ADJ_Sepsis_tr)
```

```

## 
## Call:
##   glm(formula = sepsis_outcome ~ as.factor(SIRS_total) + age_Ranges +
##     gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status +
##     hospital_size + physicianSpeciality2 + hospitaldischargeyear +
##     dialysis + aids + hepaticfailure + diabetes + immunosuppression +
##     leukemia + lymphoma + metastaticcancer + thrombolytics +
##     sofa_respiration_baseline2 + cardiovascular_baseline, family = "binomial",
##     data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.1495 -0.7000 -0.4704 -0.2145  3.5849
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                 -2.429719  0.039665 -61.257
## as.factor(SIRS_total)1       0.436152  0.023983 18.186
## as.factor(SIRS_total)2       0.940994  0.022745 41.372
## as.factor(SIRS_total)3       1.609766  0.022686 70.960
## as.factor(SIRS_total)4       2.123455  0.023522 90.276
## age_Ranges(25,35]            0.172778  0.027345  6.318
## age_Ranges(35,45]            0.349355  0.025416 13.745
## age_Ranges(45,55]            0.561817  0.023515 23.892
## age_Ranges(55,65]            0.758603  0.023001 32.981
## age_Ranges(65,75]            0.825533  0.022998 35.895
## age_Ranges(75,85]            0.918961  0.023125 39.738
## age_Ranges(85,100]           1.060331  0.024332 43.578
## gender2Female                0.047199  0.006766  6.976
## gender2Other/Unknown          -1.227754  0.268623 -4.571
## ethnicity2African American   -0.075559  0.010939 -6.907
## ethnicity2Hispanic            0.423319  0.015132 27.976
## ethnicity2Asian               0.077548  0.029551  2.624
## ethnicity2Native American     0.299836  0.037605  7.973
## ethnicity2Other/Unknown        0.074933  0.014816  5.058
## BMI_Ranges(18.5,25]           -0.223233  0.015089 -14.795
## BMI_Ranges(25,35]              -0.287623  0.014782 -19.457
## BMI_Ranges(35,200]             -0.087281  0.016028 -5.445
## BMI_RangesOther/Unknown        -0.474443  0.023598 -20.106
## icu_admit_source2OR/Proc Area -2.013520  0.014539 -138.490
## icu_admit_source2Direct Admit -0.545531  0.012789 -42.657
## icu_admit_source2Emergency Department -0.231184  0.008369 -27.623
## icu_admit_source2Other         -0.210439  0.033315 -6.317
## icu_admit_source2Step-Down Unit -0.007810  0.021107 -0.370
## hospital_teaching_statusf     -0.244631  0.024645 -9.926
## hospital_teaching_statust     -0.207217  0.024870 -8.332
## hospital_size<100             0.667845  0.023520 28.395
## hospital_size100-249           0.333243  0.019163 17.390
## hospital_size250-500            0.254919  0.019497 13.075
## hospital_size>500              0.119283  0.018237  6.541
## physicianSpeciality2Speciality-Other -0.517197  0.007584 -68.200
## hospitaldischargeyear2011      0.086893  0.013067  6.650
## hospitaldischargeyear2012      -0.057270  0.012681 -4.516
## hospitaldischargeyear2013      -0.056253  0.012392 -4.539
## hospitaldischargeyear2014      -0.078709  0.012296 -6.401
## hospitaldischargeyear2015-16   -0.040295  0.012168 -3.311
## dialysis1                      0.280215  0.017545 15.972
## aids1                           1.262548  0.087496 14.430
## hepaticfailureTRUE              0.166797  0.021570  7.733
## diabetes1                       -0.064800  0.008329 -7.780
## immunosuppression1              0.512198  0.020312 25.217
## leukemial                        0.332608  0.033869  9.821
## lymphomal                         0.335520  0.046166  7.268
## metastaticcancer1                0.035127  0.024025  1.462
## thrombolytics1                  -2.191144  0.060462 -36.240
## sofa_respiration_baseline2TRUE   0.447371  0.007468 59.904
## cardiovascular_baseline1        -0.012943  0.008184 -1.581
##
## Pr(>|z| )
## (Intercept) < 2e-16 ***
## as.factor(SIRS_total)1 < 2e-16 ***
## as.factor(SIRS_total)2 < 2e-16 ***
## as.factor(SIRS_total)3 < 2e-16 ***
## as.factor(SIRS_total)4 < 2e-16 ***
## age_Ranges(25,35] 2.64e-10 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***

```

```

## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female 3.03e-12 ***
## gender2Other/Unknown 4.86e-06 ***
## ethnicity2African American 4.95e-12 ***
## ethnicity2Hispanic < 2e-16 ***
## ethnicity2Asian 0.008685 **
## ethnicity2Native American 1.54e-15 ***
## ethnicity2Other/Unknown 4.24e-07 ***
## BMI_Ranges(18.5,25] < 2e-16 ***
## BMI_Ranges(25,35] < 2e-16 ***
## BMI_Ranges(35,200] 5.17e-08 ***
## BMI_RangesOther/Unknown < 2e-16 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other 2.67e-10 ***
## icu_admit_source2Step-Down Unit 0.711369
## hospital_teaching_statusf < 2e-16 ***
## hospital_teaching_statust < 2e-16 ***
## hospital_size<100 < 2e-16 ***
## hospital_size100-249 < 2e-16 ***
## hospital_size250-500 < 2e-16 ***
## hospital_size>500 6.12e-11 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 2.94e-11 ***
## hospitaldischargeyear2012 6.29e-06 ***
## hospitaldischargeyear2013 5.64e-06 ***
## hospitaldischargeyear2014 1.54e-10 ***
## hospitaldischargeyear2015-16 0.000928 ***
## dialysis1 < 2e-16 ***
## aids1 < 2e-16 ***
## hepaticfailureTRUE 1.05e-14 ***
## diabetes1 7.28e-15 ***
## immunosuppression1 < 2e-16 ***
## leukemial < 2e-16 ***
## lymphomal 3.66e-13 ***
## metastaticcancer1 0.143703
## thrombolytics1 < 2e-16 ***
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1 0.113769
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128 on 638756 degrees of freedom
## Residual deviance: 560649 on 638706 degrees of freedom
## AIC: 560751
##
## Number of Fisher Scoring iterations: 6

```

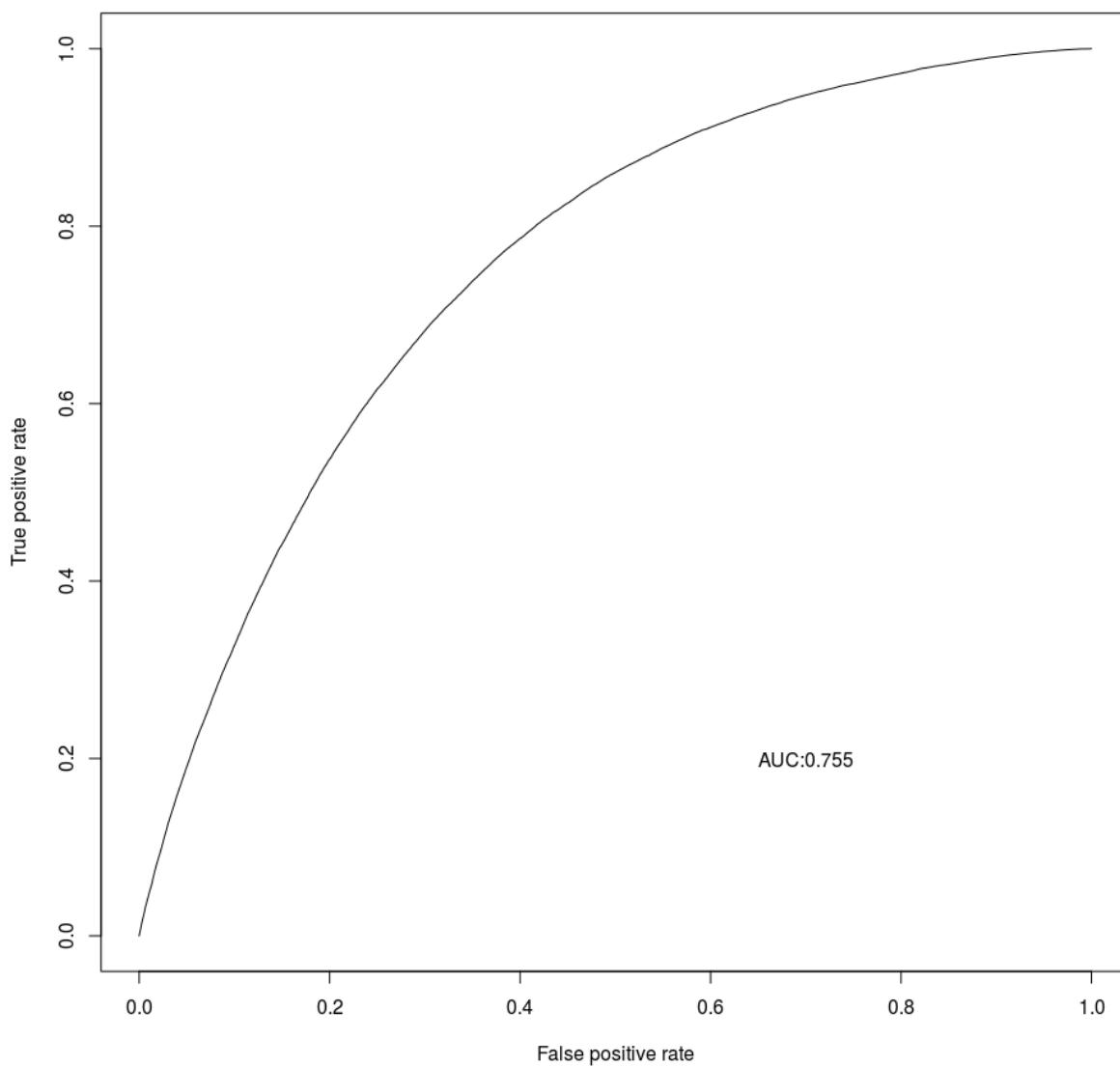
```

ssd_incl_te$SIRS1ADJSepsisPred <- predict(SIRS1_ADJ_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

SIRS1ADJSepsis.Pred <- prediction(ssd_incl_te$SIRS1ADJSepsisPred, ssd_incl_te$sepsis_outcome)
SIRS1ADJSepsis.Perf <- performance(SIRS1ADJSepsis.Pred, "tpr", "fpr")
plot(SIRS1ADJSepsis.Perf, main = "SIRS Total Adjusted Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SIRS1ADJSepsis.Pred,"auc")@y.values[[1]],3)))

```

**SIRS Total Adjusted
Sepsis Prediction Test Model**



```
performance(SIRS1ADJSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7553989
##
## Slot "alpha.values":
## list()
```

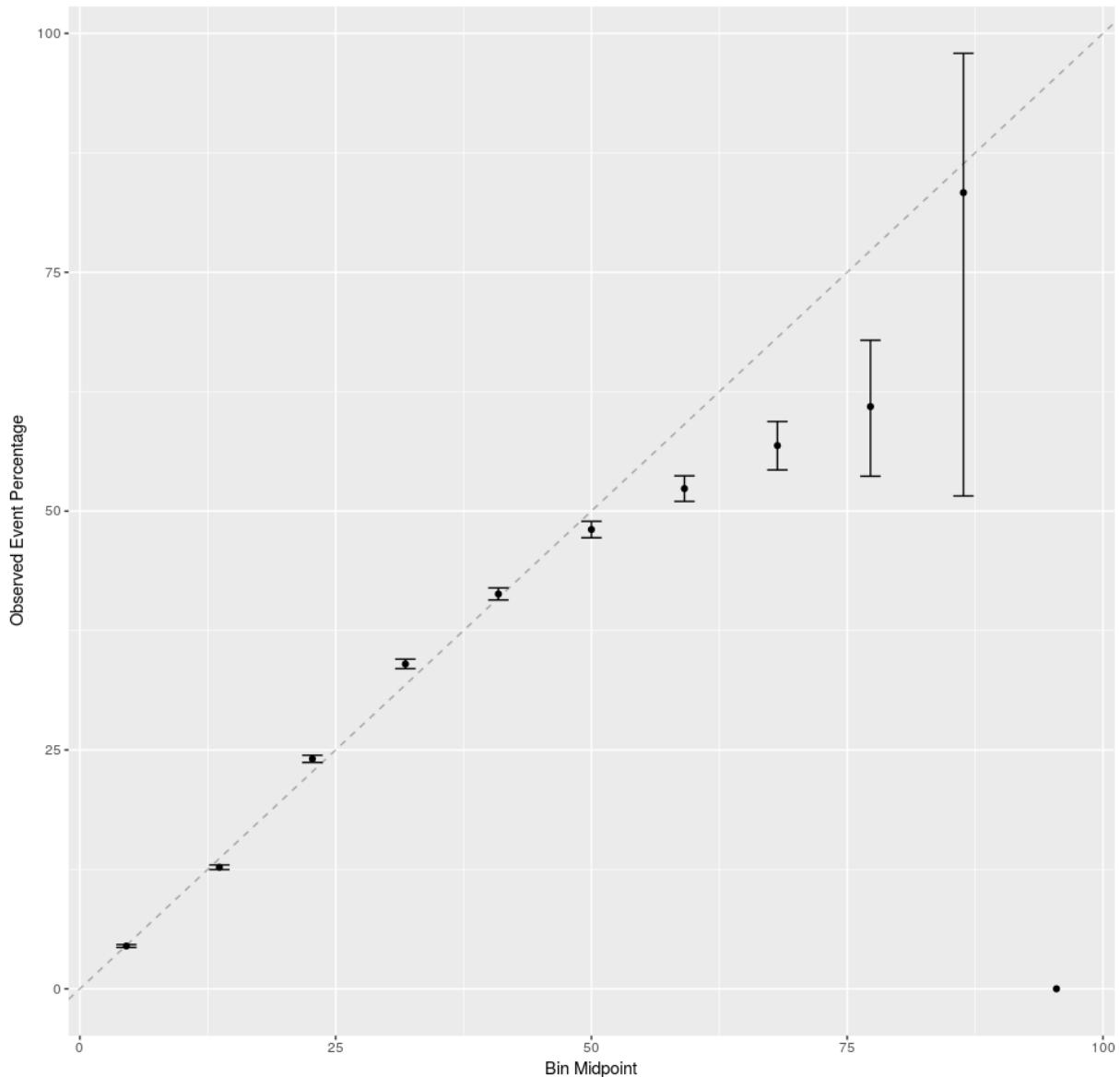
```
SIRS1ADJSepsis.Pred.roc <- roc(sepsis_outcome~SIRS1ADJSepsisPred,data=ssd_incl_te)
ci(SIRS1ADJSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7526-0.7582 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~SIRS1ADJSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of SIRS Total Sepsis Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

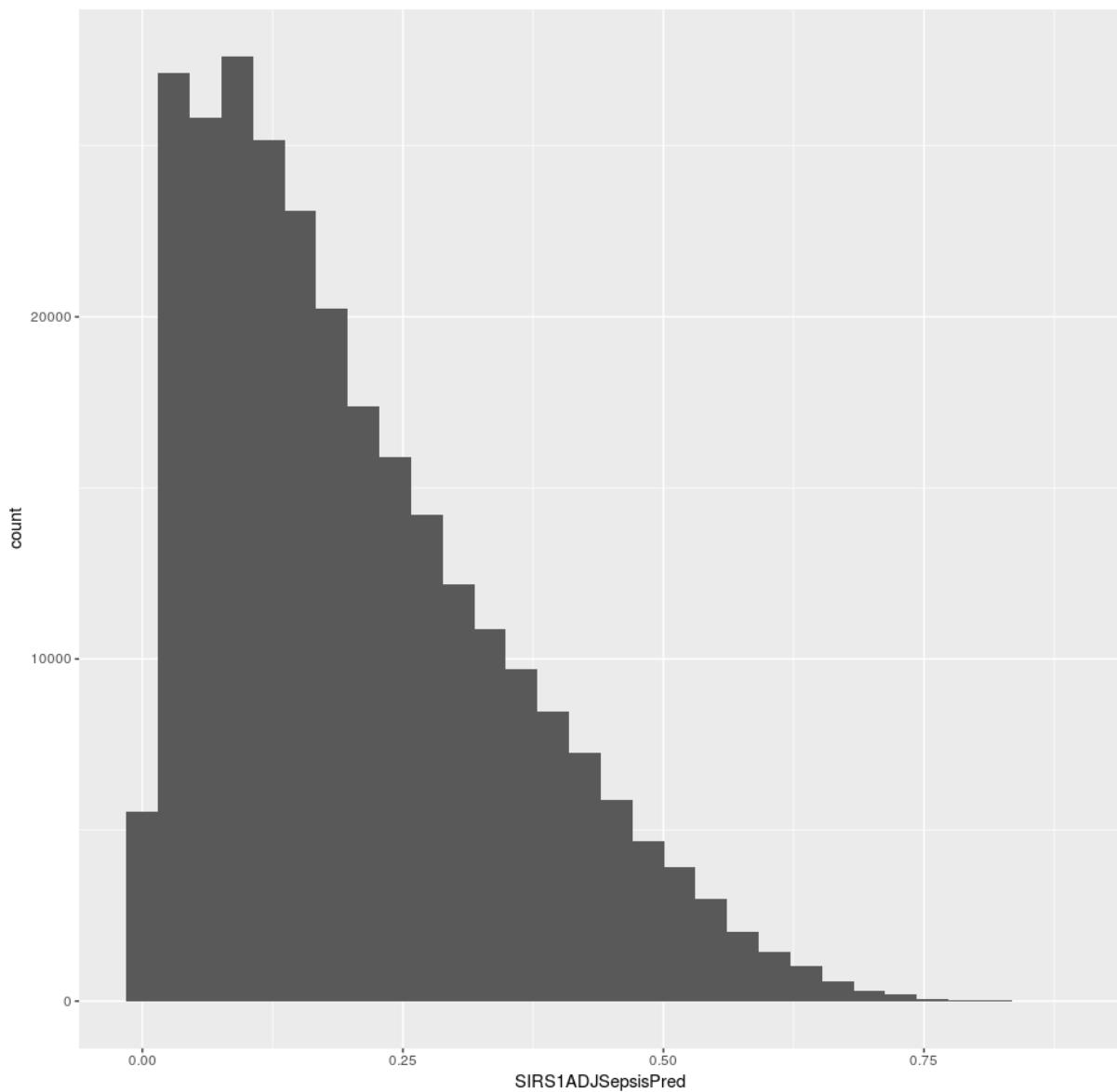
Calibration of SIRS Total Sepsis Prediction



```
qplot(SIRS1ADJSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of SIRS Total Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of SIRS Total Sepsis Predictions



```
SIRS2_ADJ_Sepsis_tr<-glm(sepsis_outcome ~ as.factor(SIRS_Positive) + age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SIRS2_ADJ_Sepsis_tr)
#sjt.glm(SIRS2_ADJ_Sepsis_tr)

#drop1(SIRS2_ADJ_Sepsis_tr,test="Chisq")

summary(SIRS2_ADJ_Sepsis_tr)
```

```

## 
## Call:
##   glm(formula = sepsis_outcome ~ as.factor(SIRS_Positive) + age_Ranges +
##     gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status +
##     hospital_size + physicianSpeciality2 + hospitaldischargeyear +
##     dialysis + aids + hepaticfailure + diabetes + immunosuppression +
##     leukemia + lymphoma + metastaticcancer + thrombolytics +
##     sofa_respiration_baseline2 + cardiovascular_baseline, family = "binomial",
##     data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q  Median      3Q     Max
## -1.9803 -0.7421 -0.4828 -0.2363  3.5802
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -1.936435  0.033653 -57.542
## as.factor(SIRS_Positive)TRUE 1.048040  0.009609 109.071
## age_Ranges(25,35]            0.162463  0.026974  6.023
## age_Ranges(35,45]            0.327205  0.025070 13.052
## age_Ranges(45,55]            0.530769  0.023195 22.883
## age_Ranges(55,65]            0.730340  0.022688 32.191
## age_Ranges(65,75]            0.789052  0.022681 34.790
## age_Ranges(75,85]            0.874976  0.022801 38.374
## age_Ranges(85,100]           1.002089  0.023981 41.787
## gender2Female                0.044010  0.006658  6.610
## gender2Other/Unknown         -1.004654  0.264674 -3.796
## ethnicity2African American   -0.092363  0.010769 -8.577
## ethnicity2Hispanic            0.414171  0.014891 27.813
## ethnicity2Asian               0.085743  0.029042  2.952
## ethnicity2Native American     0.317633  0.036965  8.593
## ethnicity2Other/Unknown        0.082246  0.014582  5.640
## BMI_Ranges(18.5,25]          -0.232734  0.014828 -15.695
## BMI_Ranges(25,35]             -0.300477  0.014528 -20.682
## BMI_Ranges(35,200]            -0.099830  0.015759 -6.335
## BMI_RangesOther/Unknown       -0.524068  0.023235 -22.555
## icu_admit_source2OR/Proc Area -1.959456  0.014380 -136.259
## icu_admit_source2Direct Admit -0.558916  0.012569 -44.469
## icu_admit_source2Emergency Department -0.271484  0.008222 -33.021
## icu_admit_source2Other         -0.190686  0.032700 -5.831
## icu_admit_source2Step-Down Unit 0.017408  0.020719  0.840
## hospital_teaching_statusf    -0.253374  0.024258 -10.445
## hospital_teaching_statust    -0.211064  0.024432 -8.639
## hospital_size<100            0.612993  0.023172 26.455
## hospital_size100-249          0.324457  0.018871 17.194
## hospital_size250-500          0.284720  0.019202 14.828
## hospital_size>500             0.150109  0.017929  8.373
## physicianSpeciality2Speciality-Other -0.573496  0.007451 -76.974
## hospitaldischargeyear2011     0.085237  0.012839  6.639
## hospitaldischargeyear2012     -0.065207  0.012465 -5.231
## hospitaldischargeyear2013     -0.077513  0.012183 -6.362
## hospitaldischargeyear2014     -0.108178  0.012091 -8.947
## hospitaldischargeyear2015-16   -0.066888  0.011965 -5.591
## dialysis1                      0.265450  0.017262 15.378
## aids1                           1.314977  0.085993 15.292
## hepaticfailureTRUE              0.168457  0.021192  7.949
## diabetes1                      -0.071153  0.008198 -8.679
## immunosuppression1              0.549108  0.019920 27.565
## leukemial                        0.436945  0.033120 13.193
## lymphomai                         0.379458  0.045234  8.389
## metastaticcancer1                0.053638  0.023601  2.273
## thrombolytics1                  -2.158174  0.060174 -35.866
## sofa_respiration_baseline2TRUE   0.433702  0.007344 59.057
## cardiovascular_baseline1        -0.040490  0.008057 -5.025
## 
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## as.factor(SIRS_Positive)TRUE < 2e-16 ***
## age_Ranges(25,35] 1.71e-09 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female 3.85e-11 ***
## gender2Other/Unknown 0.000147 ***
## ethnicity2African American < 2e-16 ***
## ethnicity2Hispanic < 2e-16 ***

```

```

## ethnicity2Asian          0.003153 **
## ethnicity2Native American < 2e-16 ***
## ethnicity2Other/Unknown  1.70e-08 ***
## BMI_Ranges(18.5,25]      < 2e-16 ***
## BMI_Ranges(25,35]        < 2e-16 ***
## BMI_Ranges(35,200]       2.38e-10 ***
## BMI_RangesOther/Unknown  < 2e-16 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other     5.50e-09 ***
## icu_admit_source2Step-Down Unit 0.400795
## hospital_teaching_statusf < 2e-16 ***
## hospital_teaching_statust < 2e-16 ***
## hospital_size<100        < 2e-16 ***
## hospital_size100-249     < 2e-16 ***
## hospital_size250-500     < 2e-16 ***
## hospital_size>500        < 2e-16 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 3.16e-11 ***
## hospitaldischargeyear2012 1.68e-07 ***
## hospitaldischargeyear2013 1.99e-10 ***
## hospitaldischargeyear2014 < 2e-16 ***
## hospitaldischargeyear2015-16 2.26e-08 ***
## dialysis1                 < 2e-16 ***
## aids1                     < 2e-16 ***
## hepaticfailureTRUE        1.88e-15 ***
## diabetes1                < 2e-16 ***
## immunosuppression1       < 2e-16 ***
## leukemial                 < 2e-16 ***
## lymphoma1                 < 2e-16 ***
## metastaticcancer1        0.023046 *
## thrombolytics1            < 2e-16 ***
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1 5.02e-07 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128 on 638756 degrees of freedom
## Residual deviance: 576168 on 638709 degrees of freedom
## AIC: 576264
##
## Number of Fisher Scoring iterations: 6

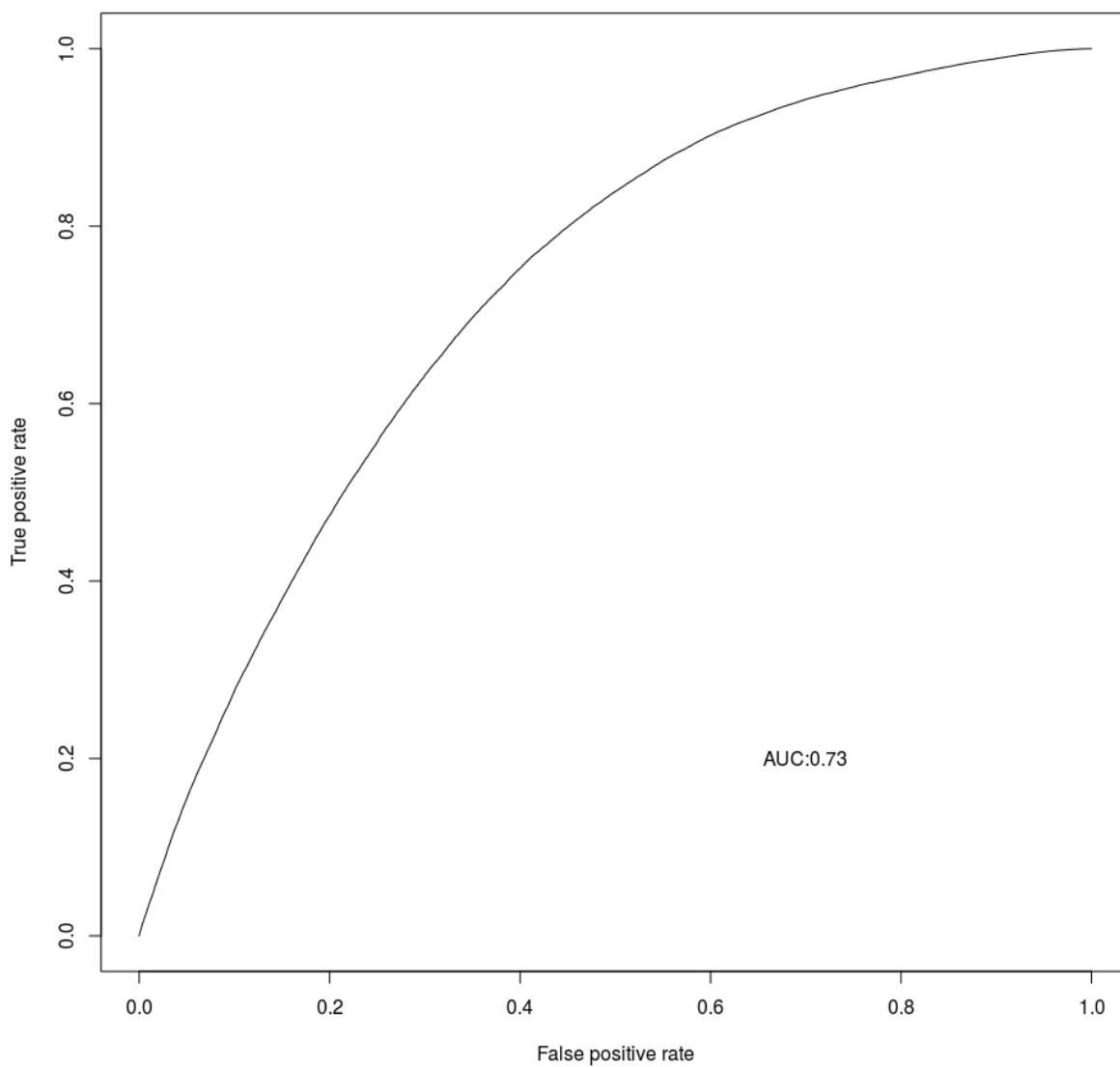
```

```

ssd_incl_te$SIRS2ADJSepsisPred <- predict(SIRS2_ADJ_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

SIRS2ADJSepsis.Pred <- prediction(ssd_incl_te$SIRS2ADJSepsisPred, ssd_incl_te$sepsis_outcome)
SIRS2ADJSepsis.Perf <- performance(SIRS2ADJSepsis.Pred, "tpr", "fpr")
plot(SIRS2ADJSepsis.Perf, main = "SIRS Positive Adjusted
Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SIRS2ADJSepsis.Pred,"auc")@y.values[[1]],3)))

```

**SIRS Positive Adjusted
Sepsis Prediction Test Model**

```
performance(SIRS2ADJSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7303764
##
## Slot "alpha.values":
## list()
```

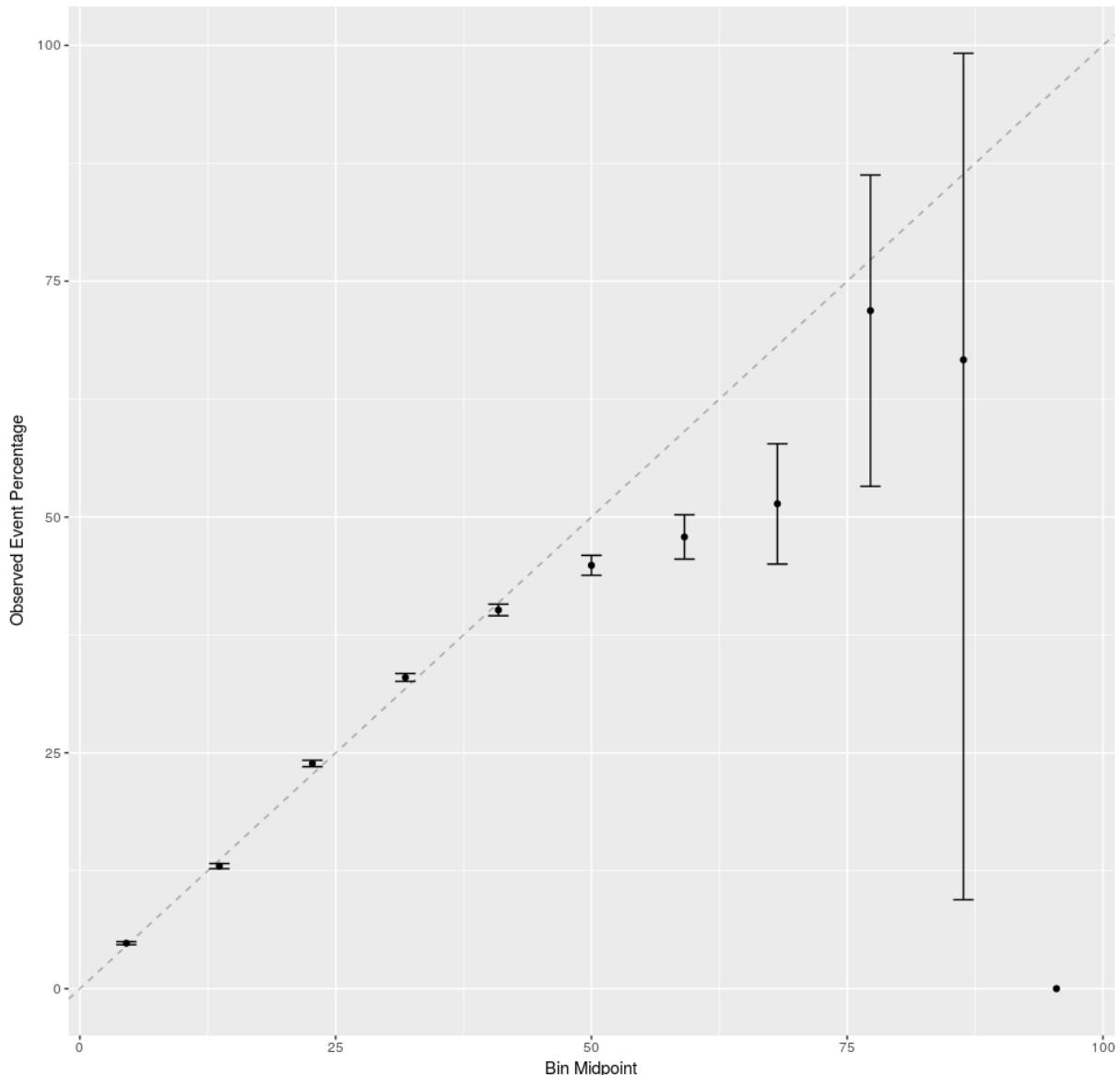
```
SIRS2ADJSepsis.Pred.roc <- roc(sepsis_outcome~SIRS2ADJSepsisPred,data=ssd_incl_te)
ci(SIRS2ADJSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7275-0.7332 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~SIRS2ADJSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of SI  
RS Positive Sepsis Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

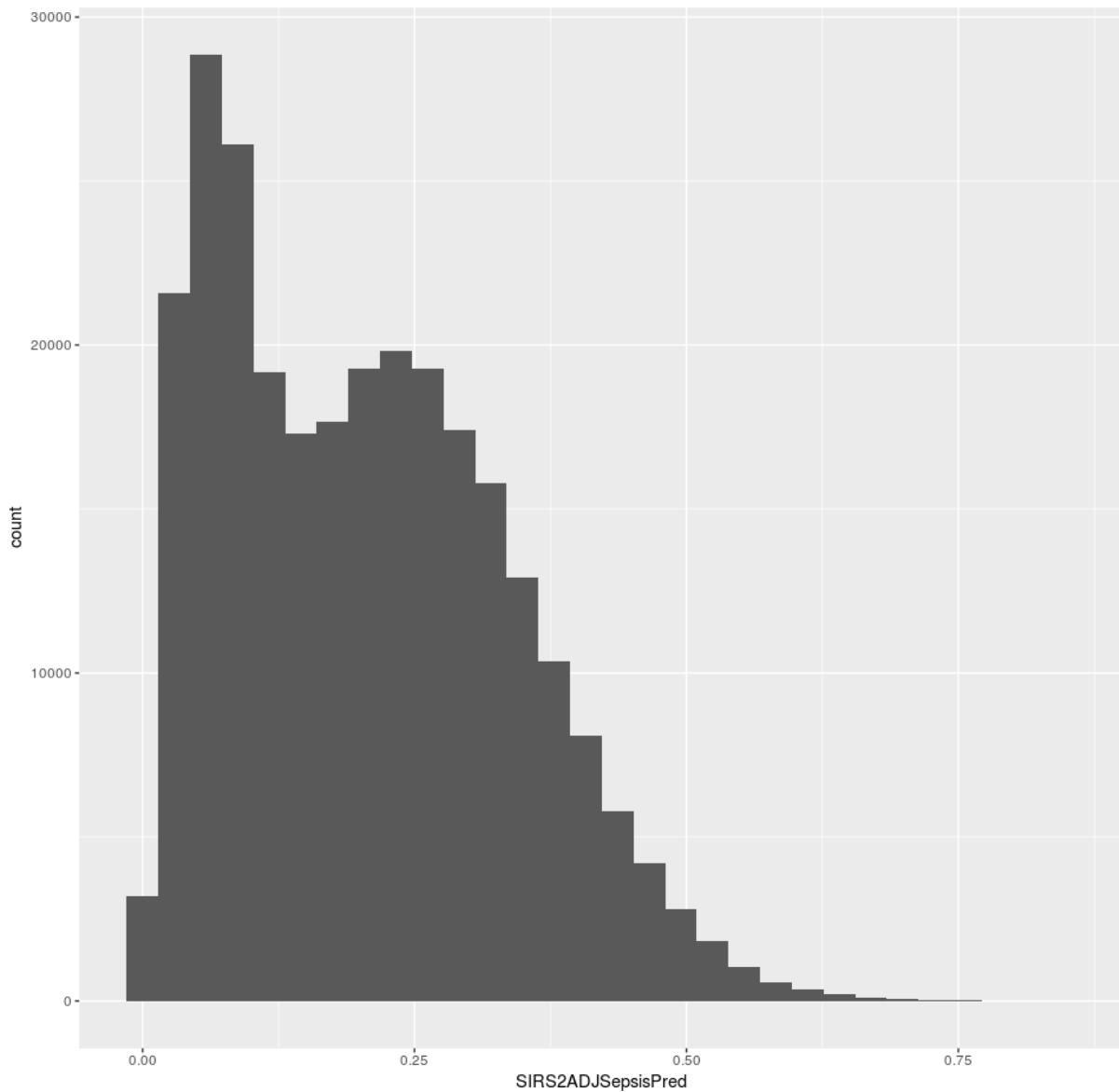
Calibration of SIRS Positive Sepsis Prediction



```
qplot(SIRS2ADJSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of SIRS Positive Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of SIRS Positive Sepsis Predictions



```
qSOFA1_ADJ_Sepsis_tr<-glm(sepsis_outcome ~ as.factor(qSOFA_total) + age_Ranges + gender2 + ethnicity2 + BMI_Range
s + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischargeyear +
dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer + throm
bolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.action = n
a.omit)

#sjp.glm(qSOFA1_ADJ_Sepsis_tr)
#sjt.glm(qSOFA1_ADJ_Sepsis_tr)

#drop1(qSOFA1_ADJ_Sepsis_tr,test="Chisq")

summary(qSOFA1_ADJ_Sepsis_tr)
```

```

## 
## Call:
##   glm(formula = sepsis_outcome ~ as.factor(qSOFA_total) + age_Ranges +
##     gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status +
##     hospital_size + physicianSpecialty2 + hospitaldischargeyear +
##     dialysis + aids + hepaticfailure + diabetes + immunosuppression +
##     leukemia + lymphoma + metastaticcancer + thrombolytics +
##     sofa_respiration_baseline2 + cardiovascular_baseline, family = "binomial",
##     data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##   Min      1Q  Median      3Q     Max
## -2.1636 -0.7142 -0.4937 -0.2294  3.4145
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                 -2.210126  0.037877 -58.349
## as.factor(qSOFA_total)1       0.644273  0.020786 30.996
## as.factor(qSOFA_total)2       1.163153  0.020020 58.098
## as.factor(qSOFA_total)3       1.772241  0.020300 87.301
## age_Ranges(25,35]            0.167541  0.027182  6.164
## age_Ranges(35,45]            0.307748  0.025266 12.180
## age_Ranges(45,55]            0.463480  0.023372 19.830
## age_Ranges(55,65]            0.637824  0.022859 27.902
## age_Ranges(65,75]            0.675474  0.022849 29.563
## age_Ranges(75,85]            0.729479  0.022964 31.767
## age_Ranges(85,100]           0.808471  0.024149 33.479
## gender2Female                0.031488  0.006702  4.698
## gender2Other/Unknown         -1.048583  0.266049 -3.941
## ethnicity2African American   -0.056398  0.010855 -5.195
## ethnicity2Hispanic            0.442768  0.014988 29.541
## ethnicity2Asian               0.088790  0.029224  3.038
## ethnicity2Native American     0.269451  0.037163  7.251
## ethnicity2Other/Unknown       0.098057  0.014689  6.675
## BMI_Ranges(18.5,25]          -0.213684  0.014944 -14.299
## BMI_Ranges(25,35]             -0.259585  0.014649 -17.721
## BMI_Ranges(35,200]            -0.059729  0.015896 -3.758
## BMI_RangesOther/Unknown       -0.518174  0.023360 -22.182
## icu_admit_source2OR/Proc Area -1.897887  0.014444 -131.398
## icu_admit_source2Direct Admit -0.543341  0.012658 -42.925
## icu_admit_source2Emergency Department -0.260007  0.008287 -31.376
## icu_admit_source2Other        -0.205693  0.032990 -6.235
## icu_admit_source2Step-Down Unit 0.002663  0.020917  0.127
## hospital_teaching_statusf    -0.336939  0.024412 -13.802
## hospital_teaching_statust    -0.305396  0.024511 -12.459
## hospital_size<100            0.775406  0.023350 33.208
## hospital_size100-249          0.444667  0.019011 23.391
## hospital_size250-500          0.390689  0.019337 20.205
## hospital_size>500             0.230553  0.017992 12.814
## physicianSpecialty2Speciality-Other -0.534023  0.007509 -71.116
## hospitaldischargeyear2011     0.064268  0.012930  4.970
## hospitaldischargeyear2012     -0.105120  0.012561 -8.369
## hospitaldischargeyear2013     -0.105697  0.012273 -8.612
## hospitaldischargeyear2014     -0.133086  0.012179 -10.928
## hospitaldischargeyear2015-16   -0.098864  0.012056 -8.200
## dialysis1                      0.234254  0.017422 13.446
## aids1                          1.322708  0.086976 15.208
## hepaticfailureTRUE              0.099746  0.021374  4.667
## diabetes1                      -0.050246  0.008274 -6.073
## immunosuppression1              0.619986  0.020126 30.806
## leukemial                       0.501722  0.033508 14.973
## lymphomai                        0.414851  0.045777  9.062
## metastaticcancer1               0.075231  0.023838  3.156
## thrombolytics1                  -2.156666  0.060254 -35.793
## sofa_respiration_baseline2TRUE  0.451352  0.007391 61.071
## cardiovascular_baseline1        -0.075059  0.008102 -9.265
##
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## as.factor(qSOFA_total)1 < 2e-16 ***
## as.factor(qSOFA_total)2 < 2e-16 ***
## as.factor(qSOFA_total)3 < 2e-16 ***
## age_Ranges(25,35] 7.11e-10 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***

```

```

## gender2Female          2.62e-06 ***
## gender2Other/Unknown   8.10e-05 ***
## ethnicity2African American 2.04e-07 ***
## ethnicity2Hispanic      < 2e-16 ***
## ethnicity2Asian         0.002380 **
## ethnicity2Native American 4.15e-13 ***
## ethnicity2Other/Unknown 2.47e-11 ***
## BMI_Ranges(18.5,25]     < 2e-16 ***
## BMI_Ranges(25,35]       < 2e-16 ***
## BMI_Ranges(35,200]      0.000172 ***
## BMI_RangesOther/Unknown < 2e-16 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other      4.52e-10 ***
## icu_admit_source2Step-Down Unit 0.898706
## hospital_teaching_statusf < 2e-16 ***
## hospital_teaching_statust < 2e-16 ***
## hospital_size<100        < 2e-16 ***
## hospital_size100-249      < 2e-16 ***
## hospital_size250-500      < 2e-16 ***
## hospital_size>500         < 2e-16 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 6.68e-07 ***
## hospitaldischargeyear2012 < 2e-16 ***
## hospitaldischargeyear2013 < 2e-16 ***
## hospitaldischargeyear2014 < 2e-16 ***
## hospitaldischargeyear2015-16 2.40e-16 ***
## dialysis1                 < 2e-16 ***
## aids1                     < 2e-16 ***
## hepaticfailureTRUE        3.06e-06 ***
## diabetes1                 1.26e-09 ***
## immunosuppression1        < 2e-16 ***
## leukemia1                 < 2e-16 ***
## lymphoma1                 < 2e-16 ***
## metastaticcancer1         0.001600 **
## thrombolytics1            < 2e-16 ***
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128  on 638756  degrees of freedom
## Residual deviance: 570280  on 638707  degrees of freedom
## AIC: 570380
##
## Number of Fisher Scoring iterations: 6

```

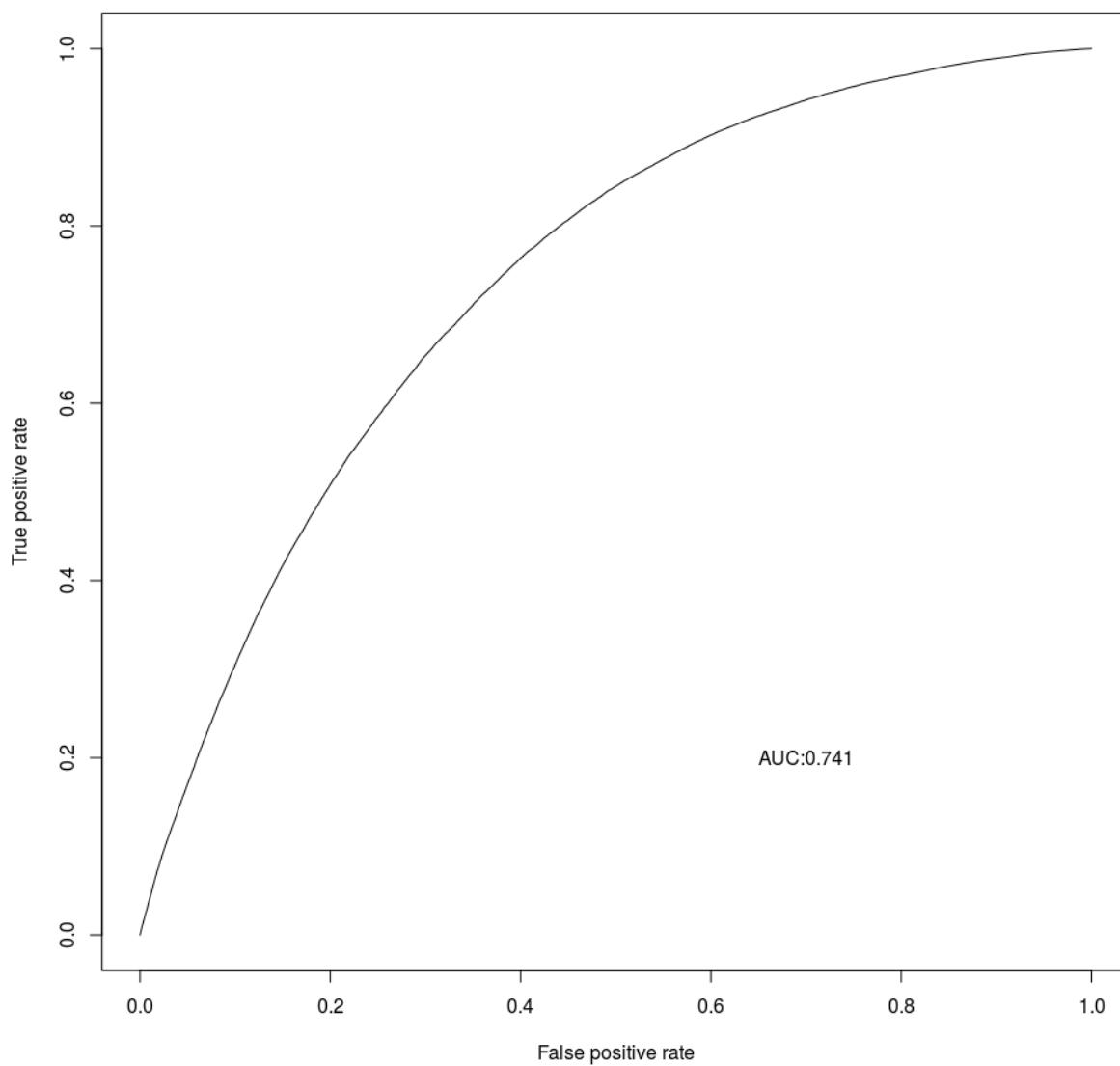
```

ssd_incl_te$qSOFA1ADJSepsisPred <- predict(qSOFA1_ADJ_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

qSOFA1ADJSepsis.Pred <- prediction(ssd_incl_te$qSOFA1ADJSepsisPred, ssd_incl_te$sepsis_outcome)
qSOFA1ADJSepsis.Perf <- performance(qSOFA1ADJSepsis.Pred, "tpr", "fpr")
plot(qSOFA1ADJSepsis.Perf, main = "qSOFA1 Total Adjusted
Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(qSOFA1ADJSepsis.Pred,"auc")@y.values[[1]],3)))

```

**qSOFA1 Total Adjusted
Sepsis Prediction Test Model**



```
performance(qSOFA1ADJSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7409462
##
## Slot "alpha.values":
## list()
```

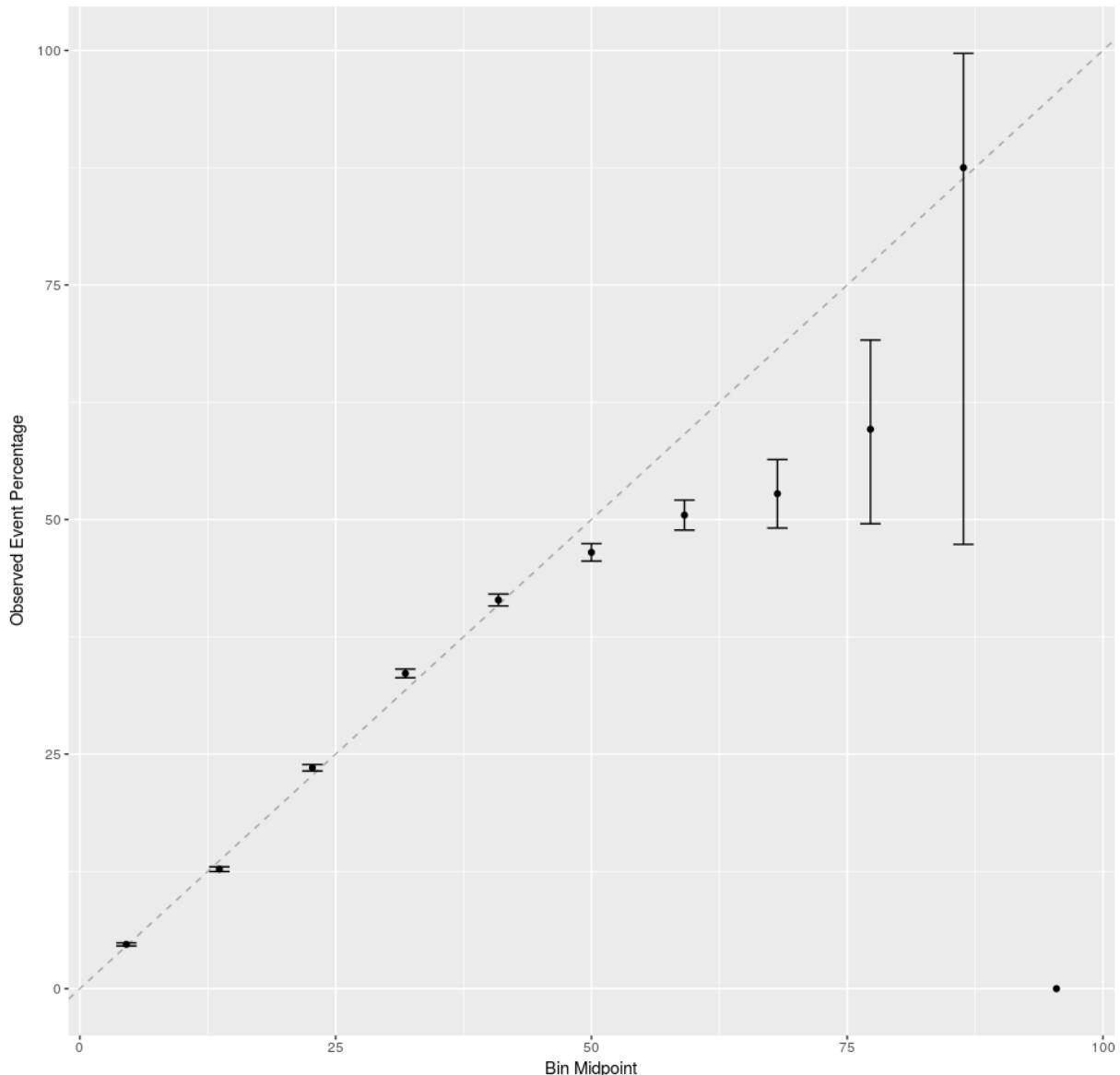
```
qSOFA1ADJSepsis.Pred.roc <- roc(sepsis_outcome~qSOFA1ADJSepsisPred,data=ssd_incl_te)
ci(qSOFA1ADJSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7381-0.7438 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~qSOFA1ADJSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of q  
SOFA Total Sepsis Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

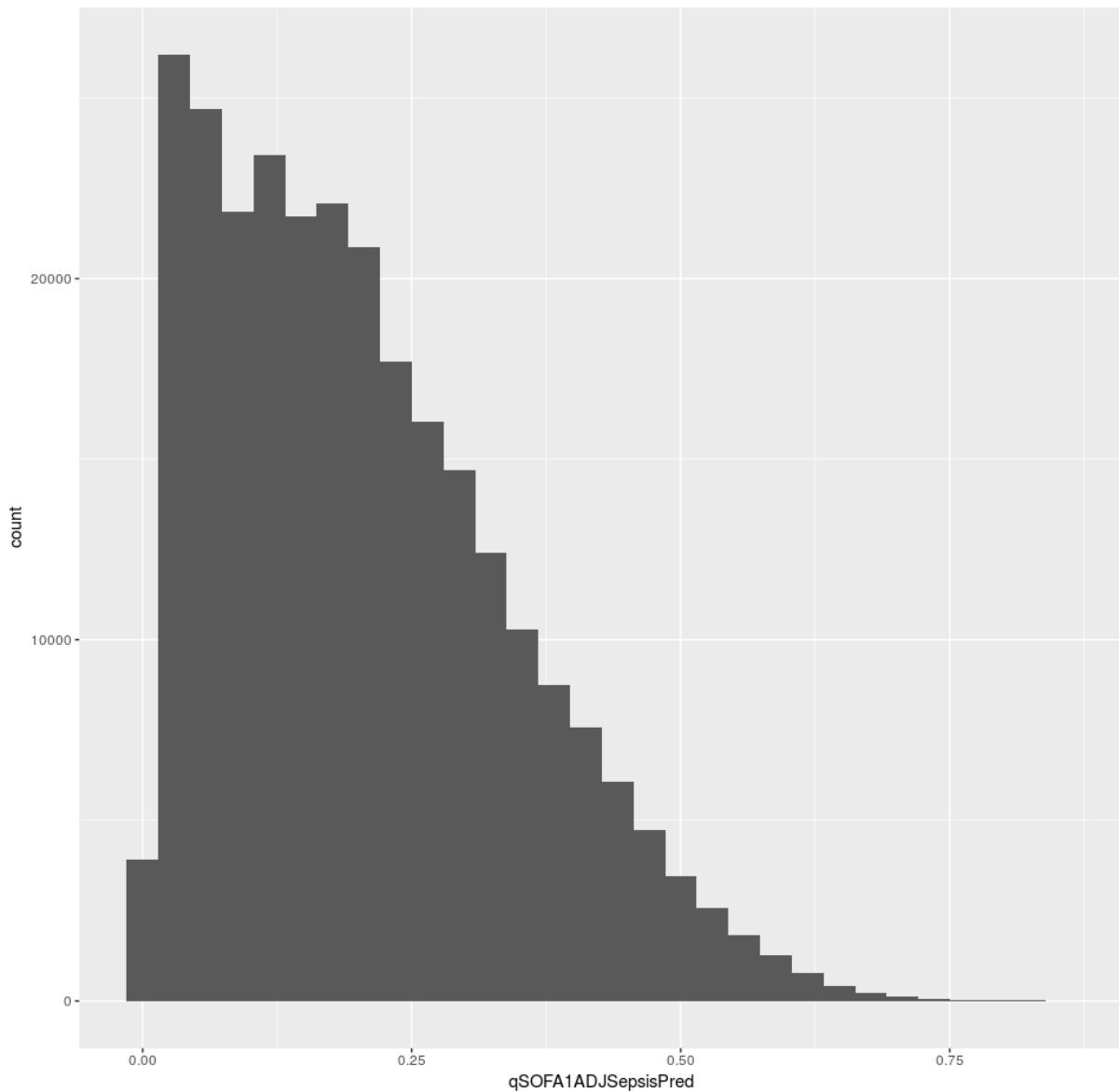
Calibration of qSOFA Total Sepsis Prediction



```
qplot(qSOFA1ADJSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of qSOFA Total Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of qSOFA Total Sepsis Predictions



```
qSOFA2_ADJ_Sepsis_tr<-glm(sepsis_outcome ~ as.factor(qSOFA_Positive) + age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischargeyea r + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(qSOFA2_ADJ_Sepsis_tr)
#sjt.glm(qSOFA2_ADJ_Sepsis_tr)

#drop1(qSOFA2_ADJ_Sepsis_tr,test="Chisq")

summary(qSOFA2_ADJ_Sepsis_tr)
```

```

## 
## Call:
##   glm(formula = sepsis_outcome ~ as.factor(qSOFA_Positive) + age_Ranges +
##     gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status +
##     hospital_size + physicianSpecialty2 + hospitaldischargeyear +
##     dialysis + aids + hepaticfailure + diabetes + immunosuppression +
##     leukemia + lymphoma + metastaticcancer + thrombolytics +
##     sofa_respiration_baseline2 + cardiovascular_baseline, family = "binomial",
##     data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##   Min      1Q  Median      3Q     Max
## -2.0393 -0.7351 -0.4970 -0.2318  3.4675
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -1.613432  0.033040 -48.833
## as.factor(qSOFA_Positive)TRUE 0.858277  0.008067 106.392
## age_Ranges(25,35]            0.166693  0.027053  6.162
## age_Ranges(35,45]            0.309178  0.025142 12.297
## age_Ranges(45,55]            0.467968  0.023255 20.124
## age_Ranges(55,65]            0.647344  0.022744 28.463
## age_Ranges(65,75]            0.689490  0.022732 30.331
## age_Ranges(75,85]            0.755401  0.022845 33.067
## age_Ranges(85,100]           0.860668  0.024010 35.846
## gender2Female                0.034811  0.006652  5.233
## gender2Other/Unknown         -0.987923  0.264232 -3.739
## ethnicity2African American   -0.057522  0.010779 -5.336
## ethnicity2Hispanic            0.429726  0.014880 28.879
## ethnicity2Asian               0.082931  0.028990  2.861
## ethnicity2Native American     0.295288  0.036883  8.006
## ethnicity2Other/Unknown       0.097719  0.014576  6.704
## BMI_Ranges(18.5,25]          -0.233284  0.014814 -15.748
## BMI_Ranges(25,35]             -0.294022  0.014518 -20.252
## BMI_Ranges(35,200]            -0.089909  0.015757 -5.706
## BMI_RangesOther/Unknown       -0.549213  0.023181 -23.692
## icu_admit_source2OR/Proc Area -1.926253  0.014386 -133.902
## icu_admit_source2Direct Admit -0.568880  0.012550 -45.330
## icu_admit_source2Emergency Department -0.281458  0.008214 -34.267
## icu_admit_source2Other        -0.195166  0.032709 -5.967
## icu_admit_source2Step-Down Unit 0.012350  0.020723  0.596
## hospital_teaching_statusf    -0.327672  0.024226 -13.526
## hospital_teaching_statust    -0.291603  0.024332 -11.984
## hospital_size<100            0.713440  0.023164 30.800
## hospital_size100-249          0.406885  0.018854 21.581
## hospital_size250-500          0.377611  0.019187 19.680
## hospital_size>500             0.222832  0.017857 12.479
## physicianSpecialty2Speciality-Other -0.574583  0.007441 -77.215
## hospitaldischargeyear2011     0.072656  0.012825  5.665
## hospitaldischargeyear2012     -0.089982  0.012458 -7.223
## hospitaldischargeyear2013     -0.098500  0.012175 -8.090
## hospitaldischargeyear2014     -0.126439  0.012083 -10.464
## hospitaldischargeyear2015-16   -0.080106  0.011959 -6.699
## dialysis1                      0.244431  0.017266 14.157
## aids1                           1.316464  0.086323 15.250
## hepaticfailureTRUE              0.133771  0.021190  6.313
## diabetes1                      -0.057409  0.008208 -6.994
## immunosuppression1              0.594927  0.019985 29.768
## leukemial                        0.493029  0.033257 14.825
## lymphomai                         0.402676  0.045354  8.878
## metastaticcancer1                0.076569  0.023661  3.236
## thrombolytics1                  -2.190913  0.060142 -36.429
## sofa_respiration_baseline2TRUE   0.460443  0.007332 62.796
## cardiovascular_baseline1        -0.081378  0.008038 -10.125
## 
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## as.factor(qSOFA_Positive)TRUE < 2e-16 ***
## age_Ranges(25,35] 7.19e-10 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female 1.67e-07 ***
## gender2Other/Unknown 0.000185 ***
## ethnicity2African American 9.48e-08 ***
## ethnicity2Hispanic < 2e-16 ***

```

```

## ethnicity2Asian          0.004227 **
## ethnicity2Native American 1.18e-15 ***
## ethnicity2Other/Unknown   2.02e-11 ***
## BMI_Ranges(18.5,25]      < 2e-16 ***
## BMI_Ranges(25,35]        < 2e-16 ***
## BMI_Ranges(35,200]       1.16e-08 ***
## BMI_RangesOther/Unknown   < 2e-16 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other     2.42e-09 ***
## icu_admit_source2Step-Down Unit 0.551192
## hospital_teaching_statusf < 2e-16 ***
## hospital_teaching_statust < 2e-16 ***
## hospital_size<100        < 2e-16 ***
## hospital_size100-249      < 2e-16 ***
## hospital_size250-500      < 2e-16 ***
## hospital_size>500        < 2e-16 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 1.47e-08 ***
## hospitaldischargeyear2012 5.08e-13 ***
## hospitaldischargeyear2013 5.95e-16 ***
## hospitaldischargeyear2014 < 2e-16 ***
## hospitaldischargeyear2015-16 2.11e-11 ***
## dialysis1                 < 2e-16 ***
## aids1                     < 2e-16 ***
## hepaticfailureTRUE        2.74e-10 ***
## diabetes1                2.67e-12 ***
## immunosuppression1        < 2e-16 ***
## leukemial                 < 2e-16 ***
## lymphoma1                 < 2e-16 ***
## metastaticcancer1         0.001212 **
## thrombolytics1            < 2e-16 ***
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1 < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128 on 638756 degrees of freedom
## Residual deviance: 577744 on 638709 degrees of freedom
## AIC: 577840
##
## Number of Fisher Scoring iterations: 6

```

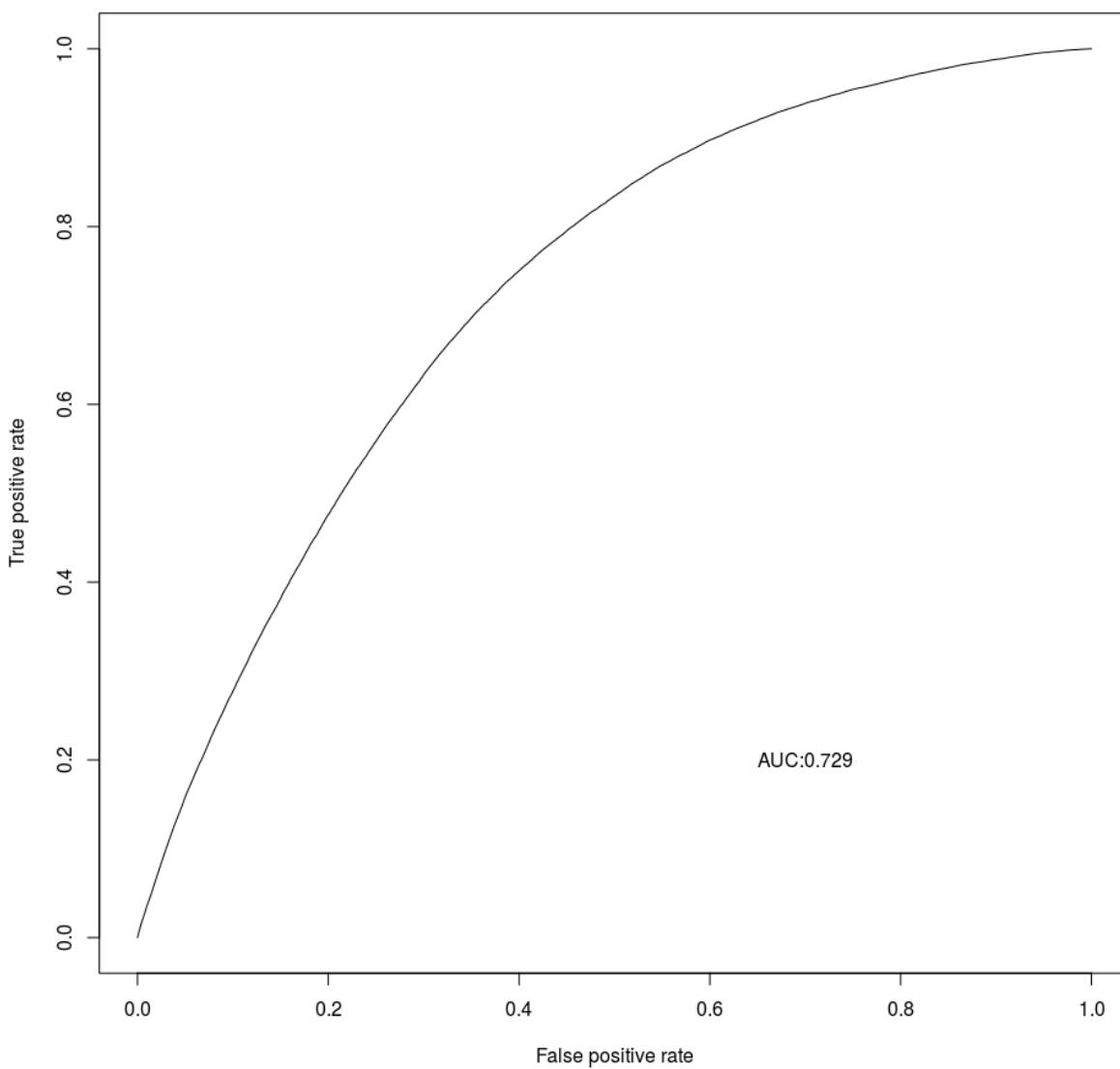
```

ssd_incl_te$qSOFA2ADJSepsisPred <- predict(qSOFA2_ADJ_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="respo
nse")
library(sjPlot)
library(ROCR)

qSOFA2ADJSepsis.Pred <- prediction(ssd_incl_te$qSOFA2ADJSepsisPred, ssd_incl_te$sepsis_outcome)
qSOFA2ADJSepsis.Perf <- performance(qSOFA2ADJSepsis.Pred, "tpr", "fpr")
plot(qSOFA2ADJSepsis.Perf, main = "qSOFA Positive Adjusted
Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(qSOFA2ADJSepsis.Pred,"auc")@y.values[[1]],3)))

```

**qSOFA Positive Adjusted
Sepsis Prediction Test Model**



```
performance(qSOFA2ADJSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7291955
##
## Slot "alpha.values":
## list()
```

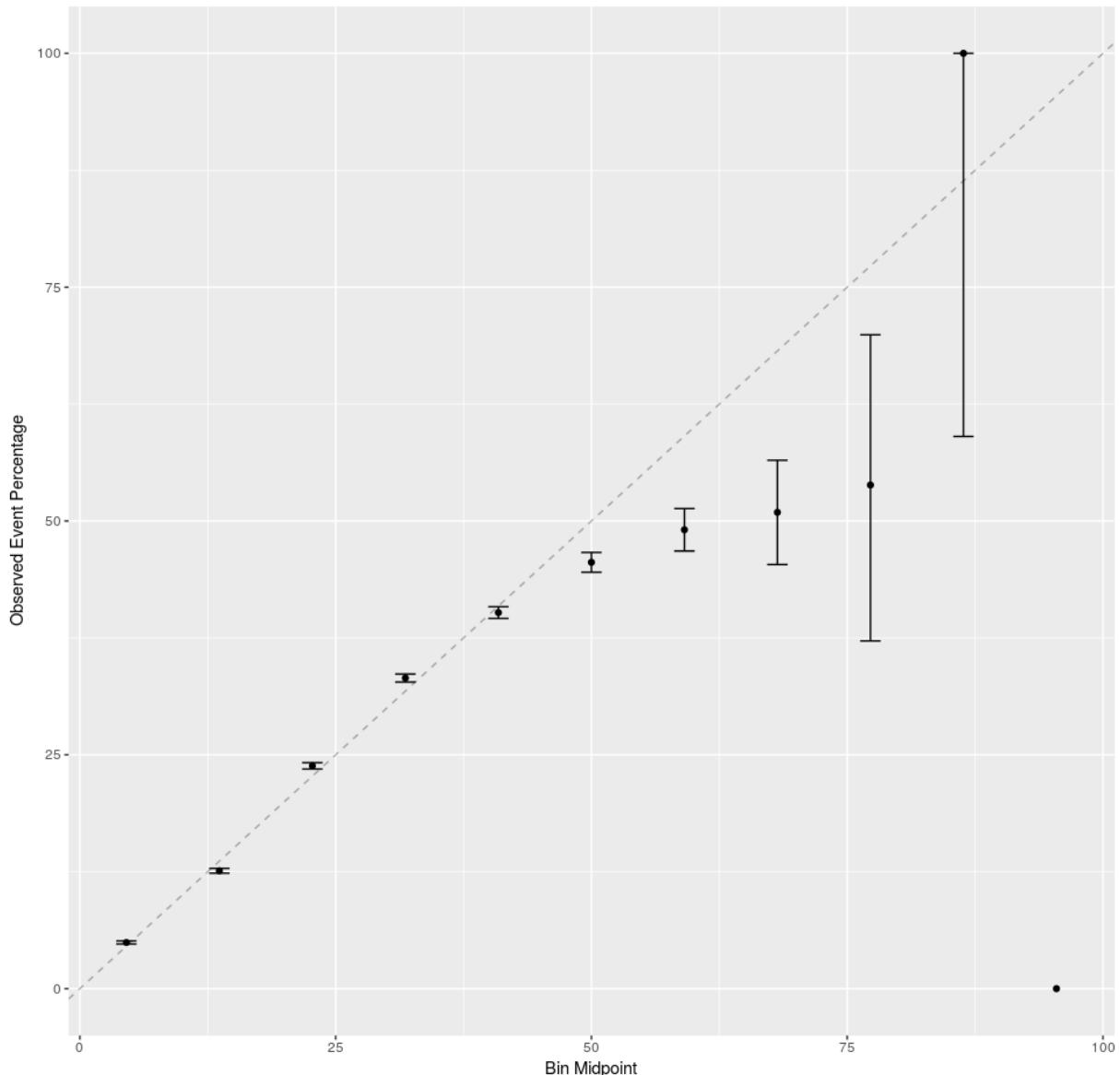
```
qSOFA2ADJSepsis.Pred.roc <- roc(sepsis_outcome~qSOFA2ADJSepsisPred,data=ssd_incl_te)
ci(qSOFA2ADJSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7263-0.7321 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~qSOFA2ADJSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of q  
SOFA Positive Sepsis Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

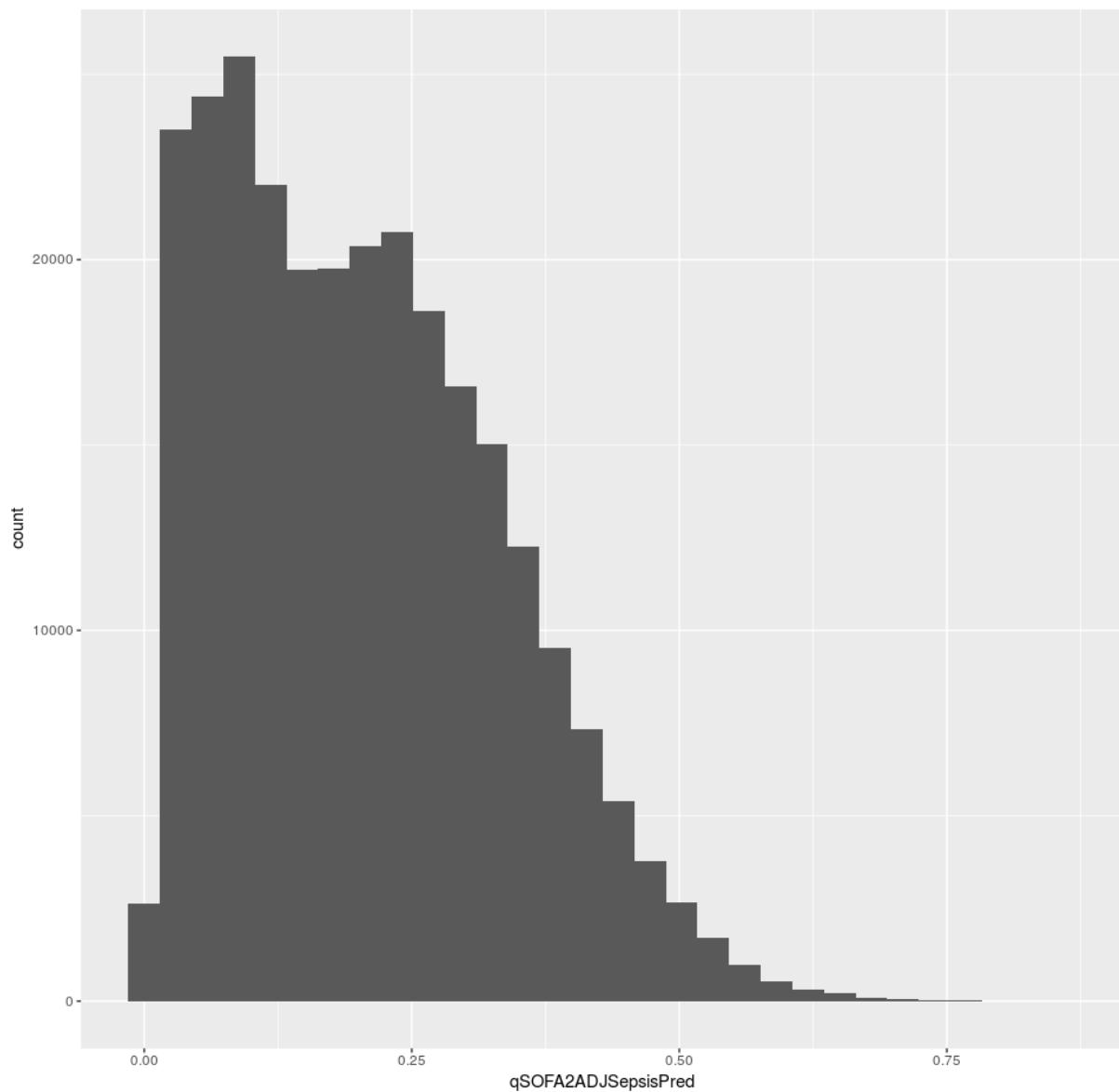
Calibration of qSOFA Positive Sepsis Prediction



```
qplot(qSOFA2ADJSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of qSOFA Positive Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of qSOFA Positive Sepsis Predictions



```
SOFA1_ADJ_Sepsis_tr<-glm(sepsis_outcome ~ as.factor(SOFA_Change) + age_Ranges + gender2 + ethnicity2 + BMI_Ranges
+ icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischargeyear + d
ialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer + thromb
olytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.action = n
a.omit)

#sjp.glm(SOFA1_ADJ_Sepsis_tr)
#sjt.glm(SOFA1_ADJ_Sepsis_tr)

#drop1(SOFA1_ADJ_Sepsis_tr,test="Chisq")

summary(SOFA1_ADJ_Sepsis_tr)
```

```

## 
## Call:
## glm(formula = sepsis_outcome ~ as.factor(SOFA_Change) + age_Ranges +
##      gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status +
##      hospital_size + physicianSpecialty2 + hospitaldischargeyear +
##      dialysis + aids + hepaticfailure + diabetes + immunosuppression +
##      leukemia + lymphoma + metastaticcancer + thrombolytics +
##      sofa_respiration_baseline2 + cardiovascular_baseline, family = "binomial",
##      data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.1484 -0.6904 -0.4485 -0.1961  3.6099
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -2.2974474  0.0374927 -61.277
## as.factor(SOFA_Change) 1       0.3815506  0.0195444  19.522
## as.factor(SOFA_Change) 2       0.7749043  0.0198496  39.039
## as.factor(SOFA_Change) 3       1.1701393  0.0196310  59.607
## as.factor(SOFA_Change) 4       1.3627618  0.0197353  69.052
## as.factor(SOFA_Change) 5       1.5448495  0.0201691  76.595
## as.factor(SOFA_Change) 6       1.8229743  0.0209532  87.002
## as.factor(SOFA_Change) 7       1.9324285  0.0217400  88.888
## as.factor(SOFA_Change) 8       2.0646047  0.0233577  88.391
## as.factor(SOFA_Change) 9       2.2093509  0.0254045  86.967
## as.factor(SOFA_Change)10      2.3112344  0.0280222  82.479
## as.factor(SOFA_Change)11      2.3462752  0.0312230  75.146
## as.factor(SOFA_Change)12      2.4894621  0.0362115  68.748
## as.factor(SOFA_Change)13      2.6173961  0.0422963  61.882
## as.factor(SOFA_Change)14      2.6895330  0.0511733  52.557
## as.factor(SOFA_Change)15      2.8433938  0.0621335  45.763
## as.factor(SOFA_Change)16      2.9439344  0.0789525  37.287
## as.factor(SOFA_Change)17      2.9272520  0.1085591  26.965
## as.factor(SOFA_Change)[18,23] 3.3159140  0.1113884  29.769
## age_Ranges[25,35]             0.1229100  0.0276502  4.445
## age_Ranges[35,45]             0.2329097  0.0257154  9.057
## age_Ranges(45,55]             0.3447512  0.0237784  14.499
## age_Ranges(55,65]             0.4805564  0.0232537  20.666
## age_Ranges(65,75]             0.4982811  0.0232423  21.439
## age_Ranges(75,85]             0.5414234  0.0233603  23.177
## age_Ranges(85,100]            0.6497776  0.0245559  26.461
## gender2Female                0.1271904  0.0068417  18.591
## gender2Other/Unknown          -1.0727793  0.2680879 -4.002
## ethnicity2African American   -0.1476021  0.0110779 -13.324
## ethnicity2Hispanic            0.3656723  0.0152937  23.910
## ethnicity2Asian               0.0024908  0.0298339  0.083
## ethnicity2Native American     0.1088718  0.0380294  2.863
## ethnicity2Other/Unknown        0.0042039  0.0149839  0.281
## BMI_Ranges[18.5,25]           -0.2257829  0.0151932 -14.861
## BMI_Ranges(25,35]              -0.3092834  0.0148901 -20.771
## BMI_Ranges(35,200]             -0.1599401  0.0161740 -9.889
## BMI_RangesOther/Unknown        -0.5402381  0.0237741 -22.724
## icu_admit_source2OR/Proc Area -1.9657000  0.0146192 -134.460
## icu_admit_source2Direct Admit -0.5749002  0.0129442 -44.414
## icu_admit_source2Emergency Department -0.2114964  0.0084562 -25.011
## icu_admit_source2Other         -0.2096404  0.0336959 -6.222
## icu_admit_source2Step-Down Unit -0.0002818  0.0213110 -0.013
## hospital_teaching_statusf     -0.1461240  0.0249314 -5.861
## hospital_teaching_statust     -0.1006492  0.0251522 -4.002
## hospital_size<100             0.7137552  0.0237263 30.083
## hospital_size100-249           0.3137806  0.0193616 16.206
## hospital_size250-500           0.2302913  0.0197074 11.686
## hospital_size>500              0.0771523  0.0184306  4.186
## physicianSpecialty2Speciality-Other -0.4624119  0.0076889 -60.140
## hospitaldischargeyear2011      0.0978542  0.0131609  7.435
## hospitaldischargeyear2012      -0.0269191  0.0127768 -2.107
## hospitaldischargeyear2013      -0.0013943  0.0124847 -0.112
## hospitaldischargeyear2014      -0.0355241  0.0123910 -2.867
## hospitaldischargeyear2015-16    -0.0187272  0.0122673 -1.527
## dialysis1                      0.4040387  0.0177082 22.816
## aids1                           1.2901577  0.0892030 14.463
## hepaticfailureTRUE              -0.1266740  0.0216698 -5.846
## diabetes1                       -0.0546649  0.0084230 -6.490
## immunosuppression1              0.5625198  0.0206016 27.305
## leukemial                        0.2855345  0.0343888  8.303
## lymphomai                        0.3310231  0.0469236  7.055
## metastaticcancer1               0.0610930  0.0244262  2.501

```

```

## thrombolytics1          -2.1415436  0.0608640 -35.186
## sofa_respiration_baseline2TRUE 0.6184497  0.0075956  81.422
## cardiovascular_baseline1   -0.1408438  0.0082414 -17.090
##
## (Intercept)                < 2e-16 ***
## as.factor(SOFA_Change) 1    < 2e-16 ***
## as.factor(SOFA_Change) 2    < 2e-16 ***
## as.factor(SOFA_Change) 3    < 2e-16 ***
## as.factor(SOFA_Change) 4    < 2e-16 ***
## as.factor(SOFA_Change) 5    < 2e-16 ***
## as.factor(SOFA_Change) 6    < 2e-16 ***
## as.factor(SOFA_Change) 7    < 2e-16 ***
## as.factor(SOFA_Change) 8    < 2e-16 ***
## as.factor(SOFA_Change) 9    < 2e-16 ***
## as.factor(SOFA_Change)10   < 2e-16 ***
## as.factor(SOFA_Change)11   < 2e-16 ***
## as.factor(SOFA_Change)12   < 2e-16 ***
## as.factor(SOFA_Change)13   < 2e-16 ***
## as.factor(SOFA_Change)14   < 2e-16 ***
## as.factor(SOFA_Change)15   < 2e-16 ***
## as.factor(SOFA_Change)16   < 2e-16 ***
## as.factor(SOFA_Change)17   < 2e-16 ***
## as.factor(SOFA_Change)[18,23] < 2e-16 ***
## age_Ranges(25,35]           8.78e-06 ***
## age_Ranges(35,45]           < 2e-16 ***
## age_Ranges(45,55]           < 2e-16 ***
## age_Ranges(55,65]           < 2e-16 ***
## age_Ranges(65,75]           < 2e-16 ***
## age_Ranges(75,85]           < 2e-16 ***
## age_Ranges(85,100]          < 2e-16 ***
## gender2Female                < 2e-16 ***
## gender2Other/Unknown        6.29e-05 ***
## ethnicity2African American  < 2e-16 ***
## ethnicity2Hispanic          < 2e-16 ***
## ethnicity2Asian              0.93346
## ethnicity2Native American   0.00420 **
## ethnicity2Other/Unknown     0.77905
## BMI_Ranges(18.5,25]         < 2e-16 ***
## BMI_Ranges(25,35]           < 2e-16 ***
## BMI_Ranges(35,200]          < 2e-16 ***
## BMI_RangesOther/Unknown     < 2e-16 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other      4.92e-10 ***
## icu_admit_source2Step-Down Unit 0.98945
## hospital_teaching_statusf  4.60e-09 ***
## hospital_teaching_statust  6.29e-05 ***
## hospital_size<100          < 2e-16 ***
## hospital_size100-249        < 2e-16 ***
## hospital_size250-500        < 2e-16 ***
## hospital_size>500          2.84e-05 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011  1.04e-13 ***
## hospitaldischargeyear2012  0.03513 *
## hospitaldischargeyear2013  0.91108
## hospitaldischargeyear2014  0.00414 **
## hospitaldischargeyear2015-16 0.12686
## dialysis1                   < 2e-16 ***
## aids1                       < 2e-16 ***
## hepaticfailureTRUE          5.05e-09 ***
## diabetes1                  8.59e-11 ***
## immunosuppression1          < 2e-16 ***
## leukemia1                  < 2e-16 ***
## lymphoma1                  1.73e-12 ***
## metastaticcancer1          0.01238 *
## thrombolytics1               < 2e-16 ***
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1    < 2e-16 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128  on 638756  degrees of freedom
## Residual deviance: 551351  on 638692  degrees of freedom
## AIC: 551481

```

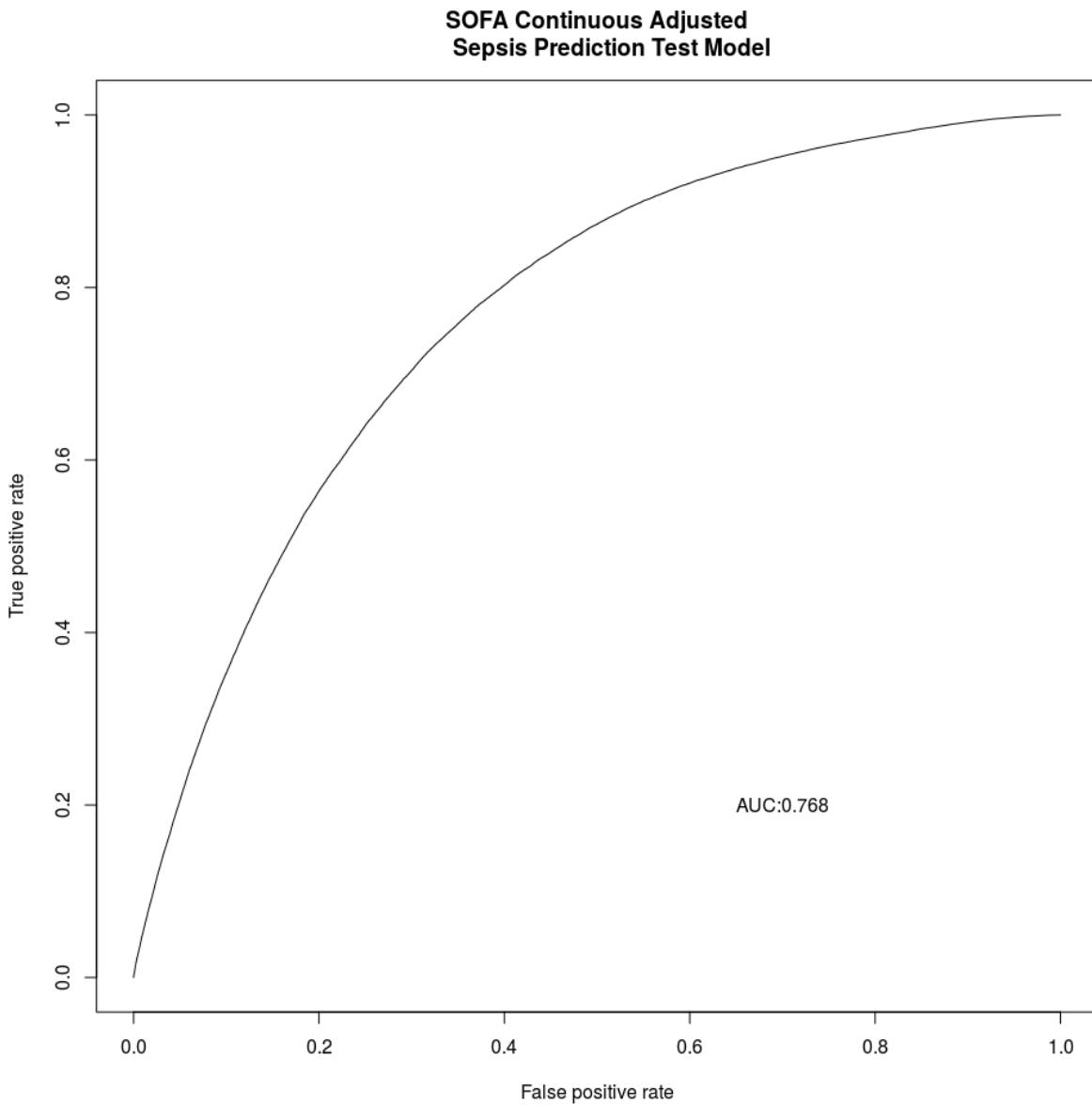
```

## 
## Number of Fisher Scoring iterations: 6

ssd_incl_te$SOFA1ADJSepsisPred <- predict(SOFA1_ADJ_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

SOFA1ADJSepsis.Pred <- prediction(ssd_incl_te$SOFA1ADJSepsisPred, ssd_incl_te$sepsis_outcome)
SOFA1ADJSepsis.Perf <- performance(SOFA1ADJSepsis.Pred, "tpr", "fpr")
plot(SOFA1ADJSepsis.Perf, main = "SOFA Continuous Adjusted Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA1ADJSepsis.Pred,"auc")@y.values[[1]],3)))

```



```
performance(SOFA1ADJSepsis.Pred, "auc")
```

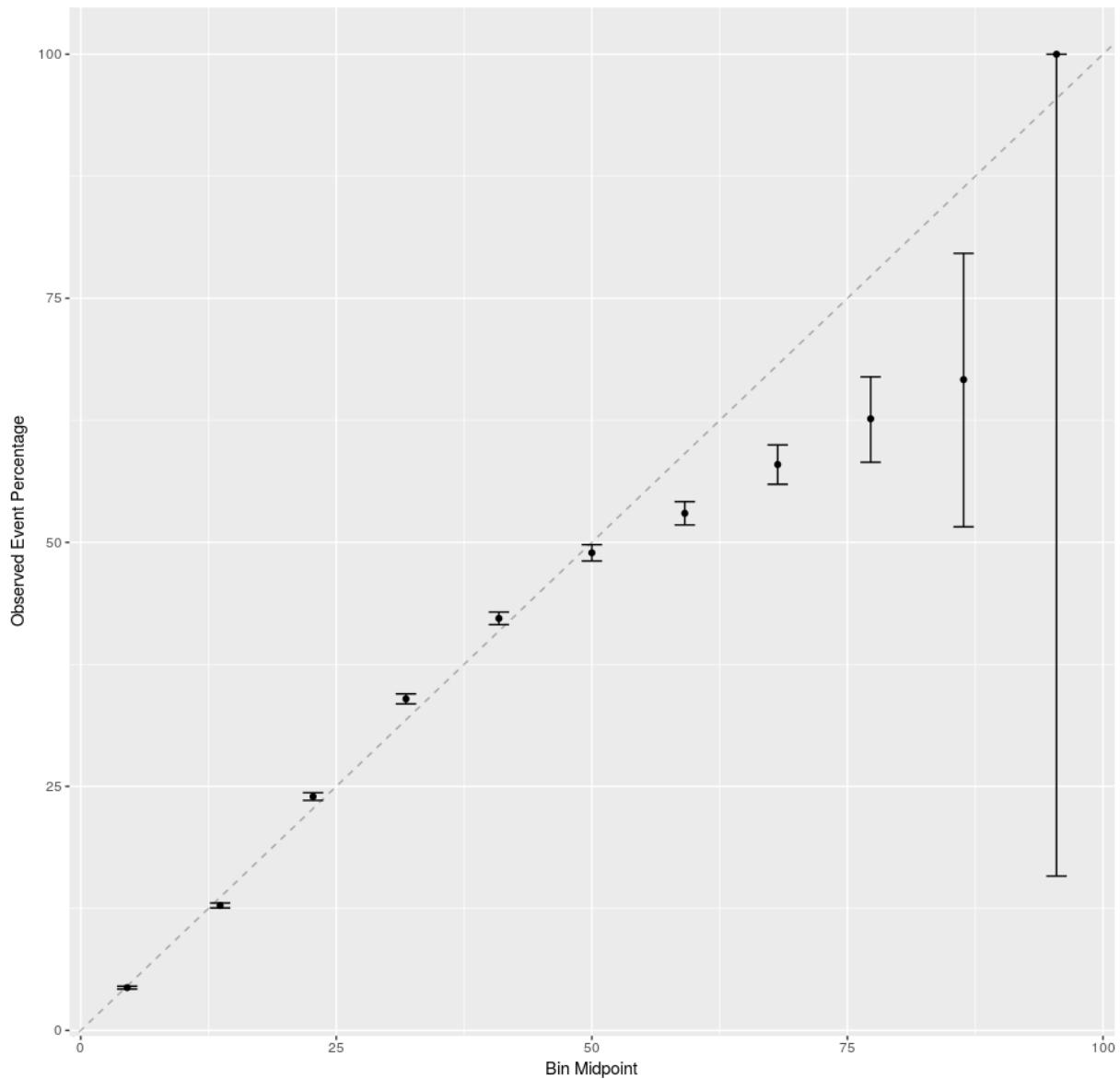
```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7678386
##
##
## Slot "alpha.values":
## list()
```

```
SOFA1ADJSepsis.Pred.roc <- roc(sepsis_outcome~SOFA1ADJSepsisPred,data=ssd_incl_te)
ci(SOFA1ADJSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7651-0.7706 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~SOFA1ADJSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of SO
FA Total Sepsis Prediction")
```

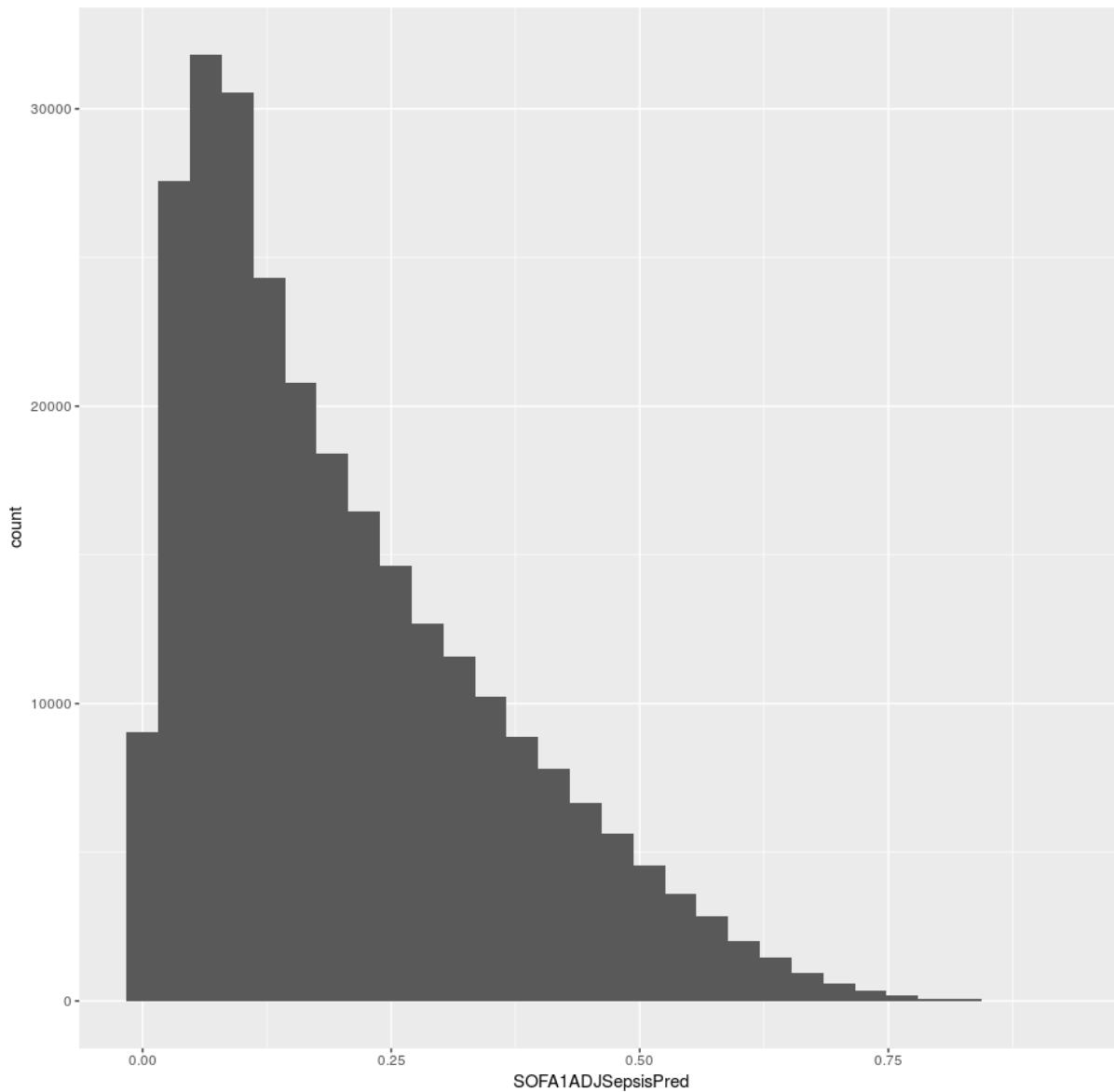
Calibration of SOFA Total Sepsis Prediction



```
qplot(SOFA1ADJSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of SOFA Total Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of SOFA Total Sepsis Predictions



```
SOFA2_ADJ_Sepsis_tr<-glm(sepsis_outcome ~ as.factor(SOFA_Positive) + age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SOFA2_ADJ_Sepsis_tr)
#sjt.glm(SOFA2_ADJ_Sepsis_tr)

#drop1(SOFA2_ADJ_Sepsis_tr,test="Chisq")

summary(SOFA2_ADJ_Sepsis_tr)
```

```

## 
## Call:
## glm(formula = sepsis_outcome ~ as.factor(SOFA_Positive) + age_Ranges +
##     gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status +
##     hospital_size + physicianSpeciality2 + hospitaldischargeyear +
##     dialysis + aids + hepaticfailure + diabetes + immunosuppression +
##     leukemia + lymphoma + metastaticcancer + thrombolytics +
##     sofa_respiration_baseline2 + cardiovascular_baseline, family = "binomial",
##     data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -2.0192   -0.7443   -0.4524   -0.2092   3.5876
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -1.866539  0.033429 -55.836
## as.factor(SOFA_Positive)TRUE 1.164883  0.008868 131.351
## age_Ranges(25,35]            0.137449  0.027266  5.041
## age_Ranges(35,45]            0.274264  0.025343 10.822
## age_Ranges(45,55]            0.412183  0.023445 17.581
## age_Ranges(55,65]            0.565255  0.022934 24.647
## age_Ranges(65,75]            0.581553  0.022928 25.364
## age_Ranges(75,85]            0.616061  0.023045 26.733
## age_Ranges(85,100]           0.705917  0.024213 29.154
## gender2Female                0.095499  0.006697 14.261
## gender2Other/Unknown         -0.942238  0.264427 -3.563
## ethnicity2African American   -0.110263  0.010823 -10.188
## ethnicity2Hispanic            0.396282  0.014972 26.468
## ethnicity2Asian                0.046724  0.029111  1.605
## ethnicity2Native American     0.237499  0.037012  6.417
## ethnicity2Other/Unknown       0.054637  0.014656  3.728
## BMI_Ranges(18.5,25]          -0.244758  0.014907 -16.419
## BMI_Ranges(25,35]             -0.318271  0.014606 -21.790
## BMI_Ranges(35,200]            -0.137382  0.015857 -8.664
## BMI_RangesOther/Unknown       -0.558014  0.023324 -23.924
## icu_admit_source2OR/Proc Area -1.953553  0.014426 -135.421
## icu_admit_source2Direct Admit -0.571572  0.012627 -45.267
## icu_admit_source2Emergency Department -0.267005  0.008265 -32.306
## icu_admit_source2Other         -0.192005  0.032909 -5.834
## icu_admit_source2Step-Down Unit 0.008125  0.020835  0.390
## hospital_teaching_statusf     -0.204197  0.024402 -8.368
## hospital_teaching_statust     -0.169205  0.024587 -6.882
## hospital_size<100              0.628172  0.023346 26.907
## hospital_size100-249           0.304835  0.018999 16.045
## hospital_size250-500           0.257730  0.019331 13.333
## hospital_size>500              0.111995  0.018061  6.201
## physicianSpeciality2Speciality-Other -0.550969  0.007502 -73.439
## hospitaldischargeyear2011      0.097619  0.012887  7.575
## hospitaldischargeyear2012      -0.034698  0.012515 -2.773
## hospitaldischargeyear2013      -0.021472  0.012235 -1.755
## hospitaldischargeyear2014      -0.054462  0.012142 -4.486
## hospitaldischargeyear2015-16    -0.015746  0.012015 -1.310
## dialysis1                      0.315902  0.017433 18.121
## aids1                           1.312983  0.086851 15.118
## hepaticfailureTRUE               0.003690  0.021156  0.174
## diabetes1                      -0.088014  0.008260 -10.655
## immunosuppression1              0.573149  0.020116 28.492
## leukemial                        0.407810  0.033338 12.233
## lymphomai                         0.379349  0.045566  8.325
## metastaticcancer1                0.074469  0.023833  3.125
## thrombolytics1                  -2.080211  0.060319 -34.487
## sofa_respiration_baseline2TRUE   0.516772  0.007399 69.843
## cardiovascular_baseline1        -0.117735  0.008087 -14.559
## 
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## as.factor(SOFA_Positive)TRUE < 2e-16 ***
## age_Ranges(25,35] 4.63e-07 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female < 2e-16 ***
## gender2Other/Unknown 0.000366 ***
## ethnicity2African American < 2e-16 ***
## ethnicity2Hispanic < 2e-16 ***

```

```

## ethnicity2Asian          0.108479
## ethnicity2Native American 1.39e-10 ***
## ethnicity2Other/Unknown   0.000193 ***
## BMI_Ranges(18.5,25]       < 2e-16 ***
## BMI_Ranges(25,35]         < 2e-16 ***
## BMI_Ranges(35,200]        < 2e-16 ***
## BMI_RangesOther/Unknown   < 2e-16 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other      5.40e-09 ***
## icu_admit_source2Step-Down Unit 0.696569
## hospital_teaching_statusf < 2e-16 ***
## hospital_teaching_statust 5.91e-12 ***
## hospital_size<100          < 2e-16 ***
## hospital_size100-249        < 2e-16 ***
## hospital_size250-500        < 2e-16 ***
## hospital_size>500          5.61e-10 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 3.60e-14 ***
## hospitaldischargeyear2012 0.005562 **
## hospitaldischargeyear2013 0.079263 .
## hospitaldischargeyear2014 7.27e-06 ***
## hospitaldischargeyear2015-16 0.190031
## dialysis1                  < 2e-16 ***
## aids1                      < 2e-16 ***
## hepaticfailureTRUE          0.861542
## diabetes1                  < 2e-16 ***
## immunosuppression1          < 2e-16 ***
## leukemial                   < 2e-16 ***
## lymphoma1                   < 2e-16 ***
## metastaticcancer1          0.001781 **
## thrombolytics1              < 2e-16 ***
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1    < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128 on 638756 degrees of freedom
## Residual deviance: 569984 on 638709 degrees of freedom
## AIC: 570080
##
## Number of Fisher Scoring iterations: 6

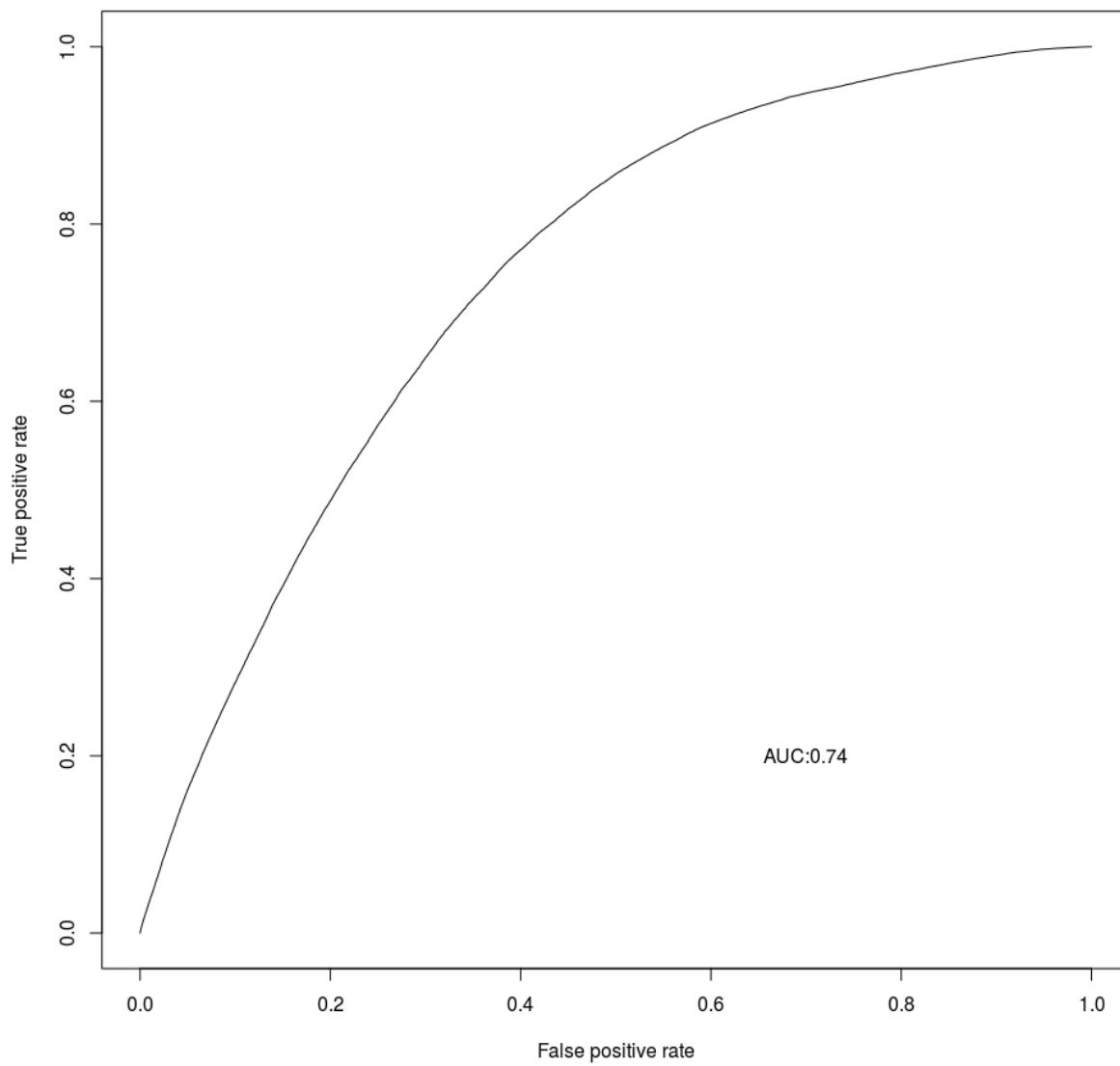
```

```

ssd_incl_te$SOFA2ADJSepsisPred <- predict(SOFA2_ADJ_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

SOFA2ADJSepsis.Pred <- prediction(ssd_incl_te$SOFA2ADJSepsisPred, ssd_incl_te$sepsis_outcome)
SOFA2ADJSepsis.Perf <- performance(SOFA2ADJSepsis.Pred, "tpr", "fpr")
plot(SOFA2ADJSepsis.Perf, main = "SOFA Positive Adjusted Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA2ADJSepsis.Pred,"auc")@y.values[[1]],3)))

```

SOFA Positive Adjusted Sepsis Prediction Test Model

```
performance(SOFA2ADJSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7398636
##
## Slot "alpha.values":
## list()
```

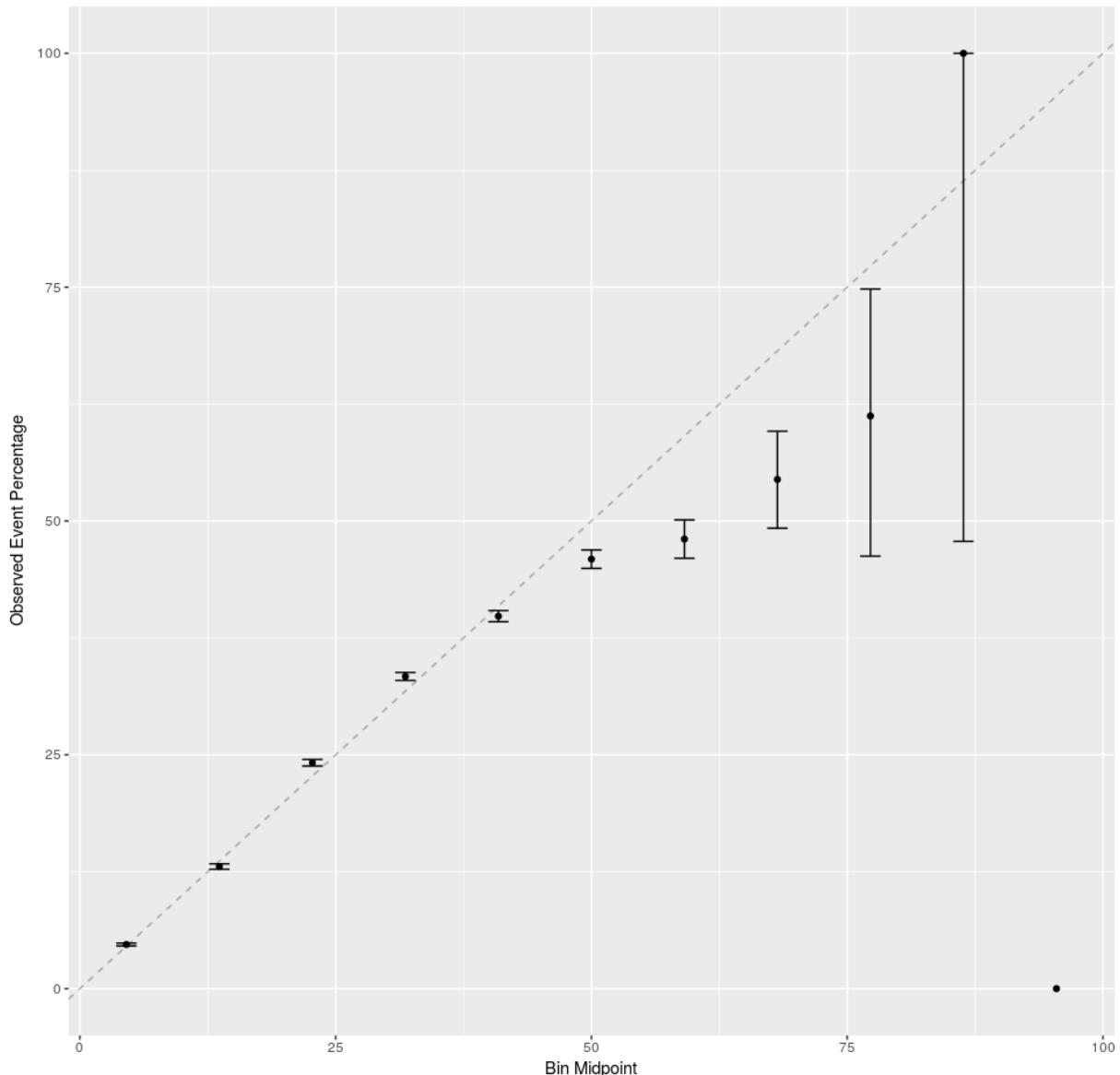
```
SOFA2ADJSepsis.Pred.roc <- roc(sepsis_outcome~SOFA2ADJSepsisPred,data=ssd_incl_te)
ci(SOFA2ADJSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7371-0.7427 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~SOFA2ADJSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of SOFA Positive Sepsis Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

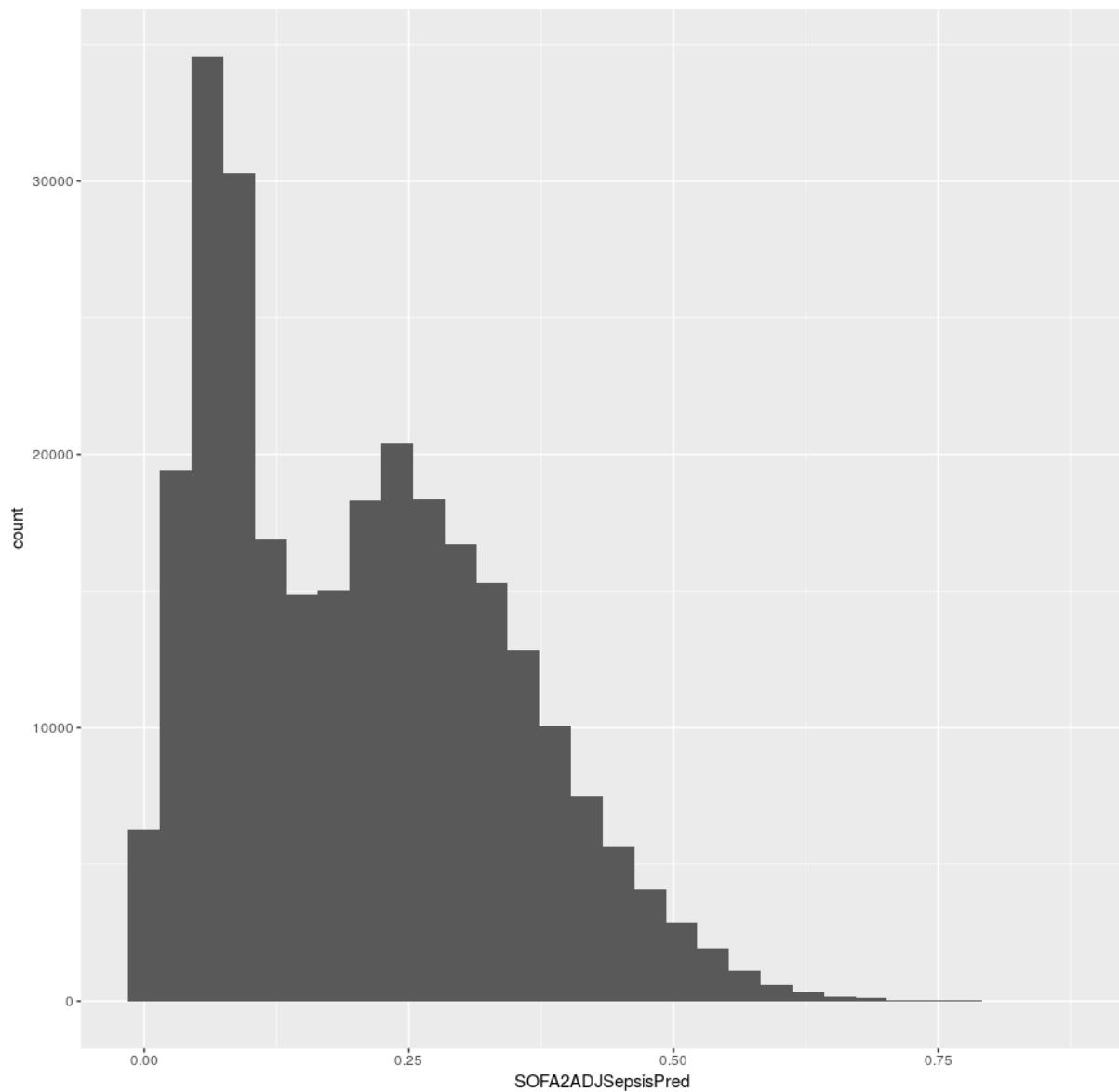
Calibration of SOFA Positive Sepsis Prediction



```
qplot(SOFA2ADJSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of SOFA Positive Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of SOFA Positive Sepsis Predictions



SOFA Score w/o Baseline SOFA

```

SOFA3_ADJ_Sepsis_tr<-glm(sepsis_outcome ~ as.factor(SOFA_Positive2) + age_Ranges + gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischargeyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcancer + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SOFA3_ADJ_Sepsis_tr)
#sjt.glm(SOFA3_ADJ_Sepsis_tr)

#drop1(SOFA3_ADJ_Sepsis_tr,test="Chisq")

summary(SOFA3_ADJ_Sepsis_tr)

```

```

## 
## Call:
##   glm(formula = sepsis_outcome ~ as.factor(SOFA_Positive2) + age_Ranges +
##     gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status +
##     hospital_size + physicianSpeciality2 + hospitaldischargeyear +
##     dialysis + aids + hepaticfailure + diabetes + immunosuppression +
##     leukemia + lymphoma + metastaticcancer + thrombolytics +
##     sofa_respiration_baseline2 + cardiovascular_baseline, family = "binomial",
##     data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##   Min      1Q  Median      3Q     Max
## -2.0136 -0.7503 -0.4458 -0.2054  3.5975
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -1.914544  0.033544 -57.076
## as.factor(SOFA_Positive2)TRUE 1.224253  0.009377 130.565
## age_Ranges(25,35]            0.130401  0.027284  4.779
## age_Ranges(35,45]            0.266394  0.025362 10.504
## age_Ranges(45,55]            0.406306  0.023462 17.317
## age_Ranges(55,65]            0.560699  0.022951 24.430
## age_Ranges(65,75]            0.579444  0.022944 25.254
## age_Ranges(75,85]            0.615448  0.023060 26.689
## age_Ranges(85,100]           0.705471  0.024228 29.118
## gender2Female               0.093724  0.006695 14.000
## gender2Other/Unknown         -0.960428  0.264839 -3.626
## ethnicity2African American  -0.114321  0.010813 -10.572
## ethnicity2Hispanic           0.387527  0.014970 25.887
## ethnicity2Asian              0.045671  0.029083  1.570
## ethnicity2Native American    0.243562  0.036956  6.591
## ethnicity2Other/Unknown       0.052189  0.014652  3.562
## BMI_Ranges(18.5,25]          -0.245088  0.014904 -16.445
## BMI_Ranges(25,35]             -0.317553  0.014603 -21.745
## BMI_Ranges(35,200]            -0.140167  0.015853 -8.841
## BMI_RangesOther/Unknown       -0.557646  0.023327 -23.906
## icu_admit_source2OR/Proc Area -1.950075  0.014424 -135.194
## icu_admit_source2Direct Admit -0.569207  0.012622 -45.098
## icu_admit_source2Emergency Department -0.265782  0.008261 -32.173
## icu_admit_source2Other        -0.183132  0.032888 -5.568
## icu_admit_source2Step-Down Unit 0.011418  0.020819  0.548
## hospital_teaching_statusf    -0.203830  0.024390 -8.357
## hospital_teaching_statust    -0.168029  0.024579 -6.836
## hospital_size<100            0.626015  0.023351 26.809
## hospital_size100-249          0.301889  0.018988 15.899
## hospital_size250-500          0.259083  0.019320 13.410
## hospital_size>500             0.110670  0.018054  6.130
## physicianSpeciality2Speciality-Other -0.546170  0.007503 -72.790
## hospitaldischargeyear2011     0.097124  0.012885  7.538
## hospitaldischargeyear2012     -0.034913  0.012512 -2.790
## hospitaldischargeyear2013     -0.024620  0.012231 -2.013
## hospitaldischargeyear2014     -0.056569  0.012138 -4.661
## hospitaldischargeyear2015-16   -0.018383  0.012011 -1.530
## dialysis1                      0.028401  0.017084  1.662
## aids1                           1.325191  0.086796 15.268
## hepaticfailureTRUE              -0.003968  0.021092 -0.188
## diabetes1                      -0.086506  0.008253 -10.482
## immunosuppression1              0.568214  0.020114 28.250
## leukemial                        0.414446  0.033304 12.444
## lymphomai                         0.383929  0.045572  8.425
## metastaticcancer1                0.076147  0.023836  3.195
## thrombolytics1                  -2.069251  0.060320 -34.305
## sofa_respiration_baseline2TRUE   0.482563  0.007387 65.326
## cardiovascular_baseline1        -0.118644  0.008078 -14.688
## 
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## as.factor(SOFA_Positive2)TRUE 1.76e-06 ***
## age_Ranges(25,35] < 2e-16 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female < 2e-16 ***
## gender2Other/Unknown 0.000287 ***
## ethnicity2African American < 2e-16 ***
## ethnicity2Hispanic < 2e-16 ***

```

```

## ethnicity2Asian          0.116327
## ethnicity2Native American 4.38e-11 ***
## ethnicity2Other/Unknown   0.000368 ***
## BMI_Ranges(18.5,25]       < 2e-16 ***
## BMI_Ranges(25,35]         < 2e-16 ***
## BMI_Ranges(35,200]        < 2e-16 ***
## BMI_RangesOther/Unknown   < 2e-16 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other      2.57e-08 ***
## icu_admit_source2Step-Down Unit 0.583380
## hospital_teaching_statusf < 2e-16 ***
## hospital_teaching_statust 8.13e-12 ***
## hospital_size<100          < 2e-16 ***
## hospital_size100-249        < 2e-16 ***
## hospital_size250-500        < 2e-16 ***
## hospital_size>500          8.78e-10 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 4.78e-14 ***
## hospitaldischargeyear2012 0.005264 **
## hospitaldischargeyear2013 0.044123 *
## hospitaldischargeyear2014 3.15e-06 ***
## hospitaldischargeyear2015-16 0.125897
## dialysis1                  0.096429 .
## aids1                      < 2e-16 ***
## hepaticfailureTRUE          0.850790
## diabetes1                  < 2e-16 ***
## immunosuppression1          < 2e-16 ***
## leukemial                   < 2e-16 ***
## lymphoma1                   < 2e-16 ***
## metastaticcancer1          0.001400 **
## thrombolytics1              < 2e-16 ***
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1    < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128 on 638756 degrees of freedom
## Residual deviance: 569775 on 638709 degrees of freedom
## AIC: 569871
##
## Number of Fisher Scoring iterations: 6

```

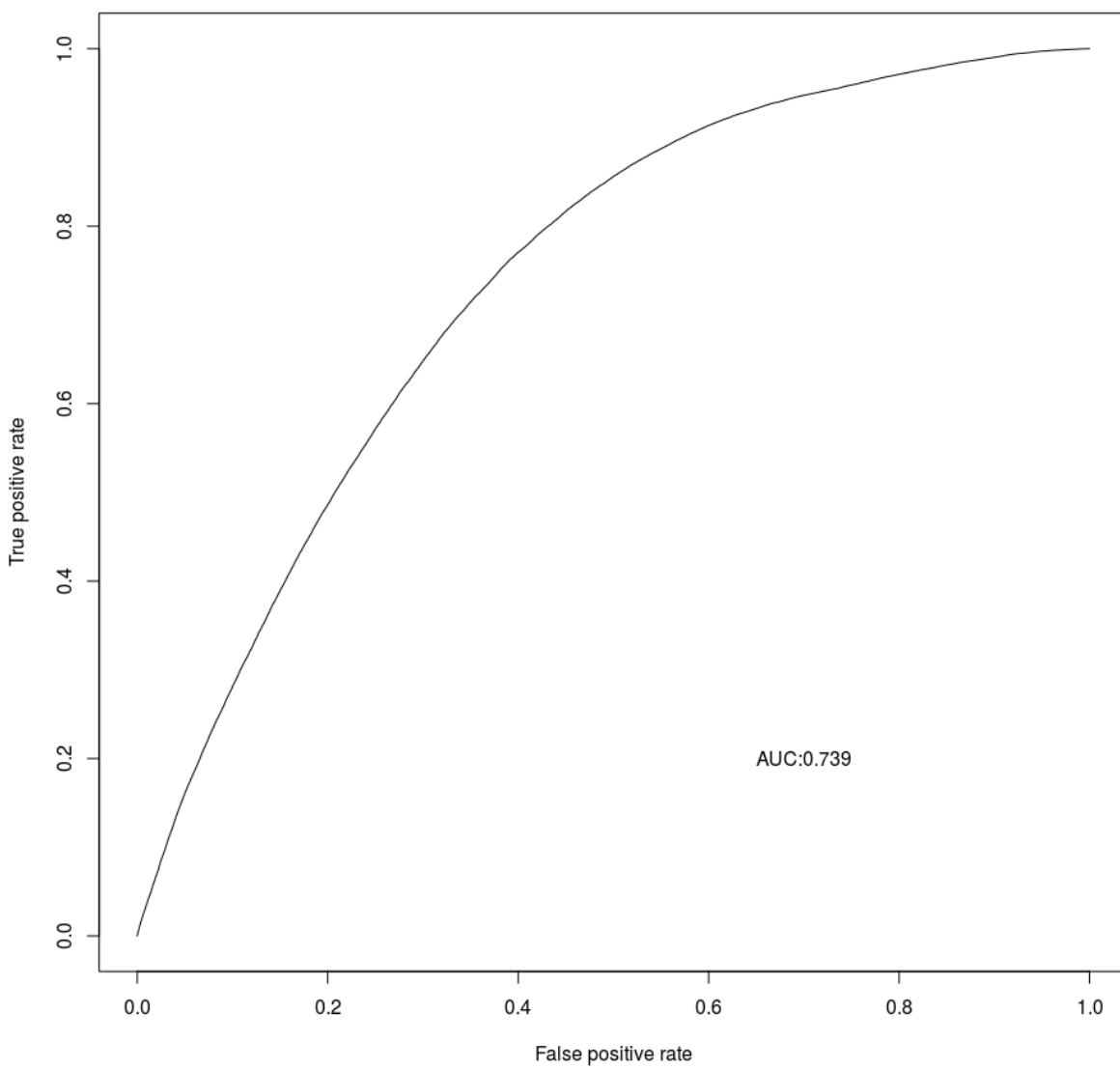
```

ssd_incl_te$SOFA3ADJSepsisPred <- predict(SOFA3_ADJ_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

SOFA3ADJSepsis.Pred <- prediction(ssd_incl_te$SOFA3ADJSepsisPred, ssd_incl_te$sepsis_outcome)
SOFA3ADJSepsis.Perf <- performance(SOFA3ADJSepsis.Pred, "tpr", "fpr")
plot(SOFA3ADJSepsis.Perf, main = "SOFA Positive w/o Baseline Adjusted Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA3ADJSepsis.Pred, "auc")@y.values[[1]],3)))

```

SOFA Positive w/o Baseline Adjusted Sepsis Prediction Test Model



```
performance(SOFA3ADJSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7393518
##
## Slot "alpha.values":
## list()
```

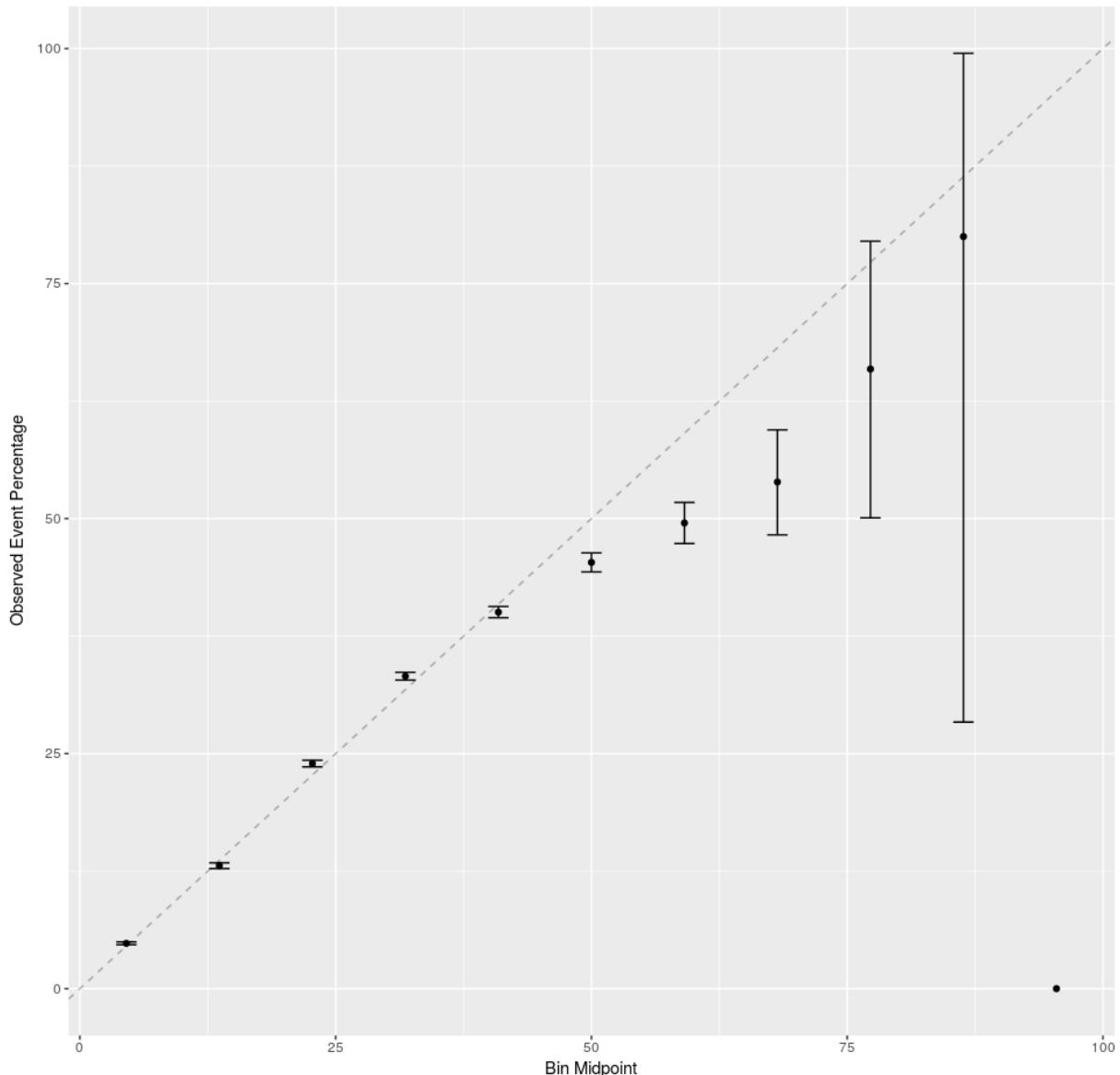
```
SOFA3ADJSepsis.Pred.roc <- roc(sepsis_outcome~SOFA3ADJSepsisPred,data=ssd_incl_te)
ci(SOFA3ADJSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.7366-0.7421 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~SOFA3ADJSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of SOFA Positive w/o Baseline Sepsis Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

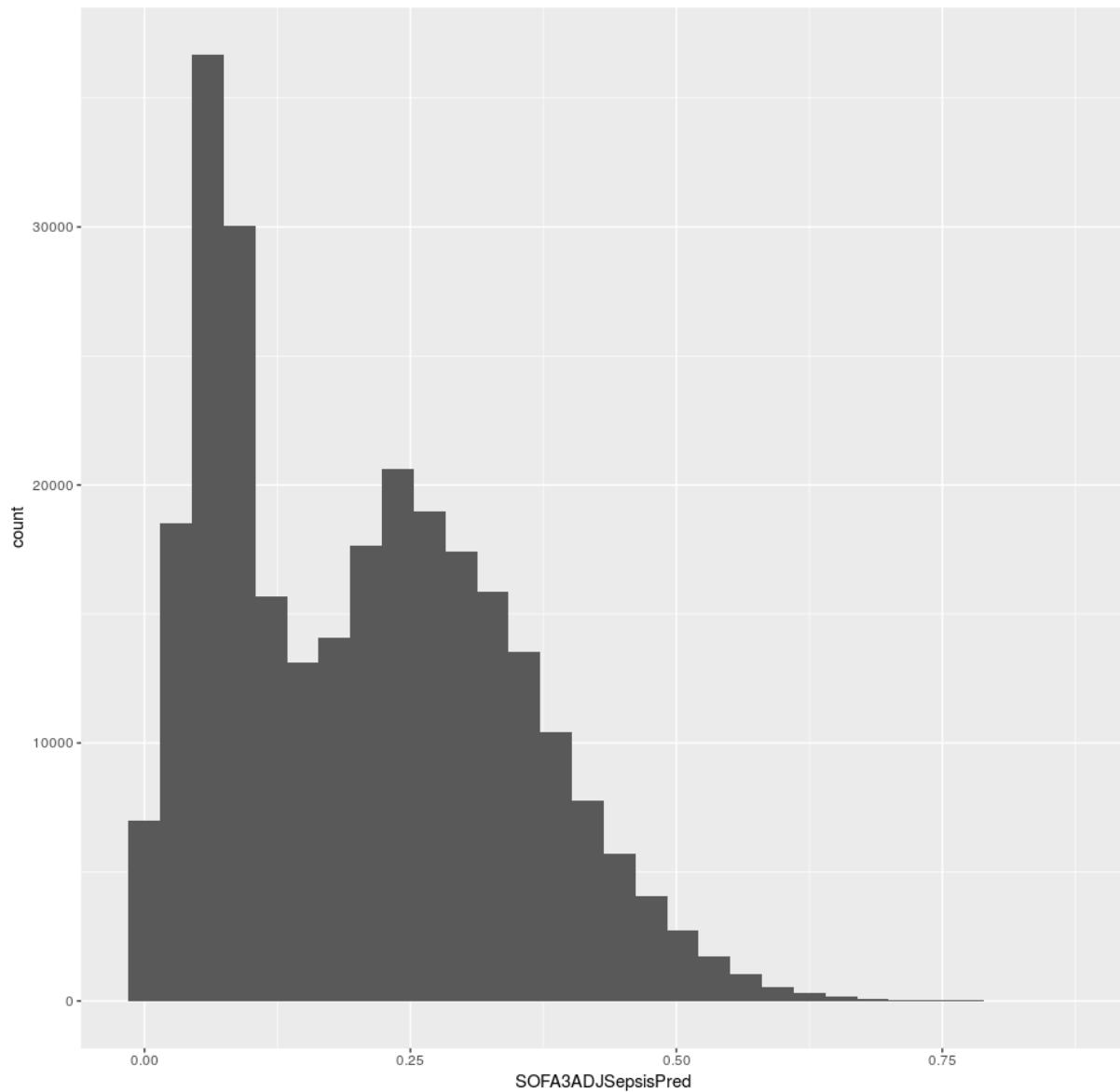
Calibration of SOFA Positive w/o Baseline Sepsis Prediction



```
qplot(SOFA3ADJSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of SOFA Positive w/o Baseline Sepsis Prediction")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of SOFA Positive w/o Baseline Sepsis Predictions



```
FuzzyLogic_ADJ_Sepsis_tr<-glm(sepsis_outcome ~ (SepsisFuzzyLogicPositive) + age_Ranges + gender2 + ethnicity2 + B
MI_Ranges + icu_admit_source2 + hospital_teaching_status + hospital_size + physicianSpeciality2 + hospitaldischar
geyear + dialysis + aids + hepaticfailure + diabetes + immunosuppression + leukemia + lymphoma + metastaticcance
r + thrombolytics + sofa_respiration_baseline2 + cardiovascular_baseline, data=ssd_incl_tr,family="binomial",na.a
ction = na.omit)

#sjp.glm(FuzzyLogic_ADJ_Sepsis_tr)
#sjt.glm(FuzzyLogic_ADJ_Sepsis_tr)

#drop1(FuzzyLogic_ADJ_Sepsis_tr,test="Chisq")

summary(FuzzyLogic_ADJ_Sepsis_tr)
```

```

## 
## Call:
## glm(formula = sepsis_outcome ~ (SepsisFuzzyLogicPositive) + age_Ranges +
##     gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status +
##     hospital_size + physicianSpecialty2 + hospitaldischargeyear +
##     dialysis + aids + hepaticfailure + diabetes + immunosuppression +
##     leukemia + lymphoma + metastaticcancer + thrombolytics +
##     sofa_respiration_baseline2 + cardiovascular_baseline, family = "binomial",
##     data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.0787 -0.7206 -0.4234 -0.1814  3.6169
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                 -2.124152  0.033816 -62.815
## SepsisFuzzyLogicPositiveTRUE 1.494644  0.007929 188.497
## age_Ranges(25,35]              0.200047  0.027507  7.272
## age_Ranges(35,45]              0.380838  0.025582 14.887
## age_Ranges(45,55]              0.539099  0.023648 22.797
## age_Ranges(55,65]              0.710904  0.023120 30.748
## age_Ranges(65,75]              0.744332  0.023110 32.209
## age_Ranges(75,85]              0.822203  0.023233 35.390
## age_Ranges(85,100]             0.957012  0.024461 39.125
## gender2Female                  0.036346  0.006828  5.323
## gender2Other/Unknown           -1.078963  0.267177 -4.038
## ethnicity2African American     -0.029079  0.011073 -2.626
## ethnicity2Hispanic              0.399012  0.015308 26.065
## ethnicity2Asian                 0.110971  0.029812  3.722
## ethnicity2Native American       0.266320  0.037867  7.033
## ethnicity2Other/Unknown         0.046935  0.014927  3.144
## BMI_Ranges(18.5,25]            -0.220140  0.015229 -14.455
## BMI_Ranges(25,35]              -0.286701  0.014915 -19.222
## BMI_Ranges(35,200]              -0.114540  0.016172 -7.083
## BMI_RangesOther/Unknown        -0.465796  0.023828 -19.548
## icu_admit_source2OR/Proc Area -1.996615  0.014573 -137.012
## icu_admit_source2Direct Admit -0.459874  0.012939 -35.543
## icu_admit_source2Emergency Department -0.280337  0.008454 -33.161
## icu_admit_source2Other          -0.107824  0.033765 -3.193
## icu_admit_source2Step-Down Unit 0.055622  0.021391  2.600
## hospital_teaching_statusf     -0.240214  0.024886 -9.652
## hospital_teaching_statust     -0.207117  0.025137 -8.240
## hospital_size<100              0.621431  0.023826 26.082
## hospital_size100-249           0.311101  0.019367 16.063
## hospital_size250-500           0.262875  0.019696 13.346
## hospital_size>500              0.108788  0.018436  5.901
## physicianSpecialty2Speciality-Other -0.501852  0.007684 -65.313
## hospitaldischargeyear2011       0.092410  0.013172  7.016
## hospitaldischargeyear2012       0.039503  0.012781 -3.091
## hospitaldischargeyear2013       0.038688  0.012491 -3.097
## hospitaldischargeyear2014       0.059266  0.012397 -4.781
## hospitaldischargeyear2015-16    -0.019868  0.012269 -1.619
## dialysis1                      0.270859  0.017788 15.227
## aids1                           1.331422  0.089546 14.869
## hepaticfailureTRUE              -0.029653  0.021485 -1.380
## diabetes1                       0.044792  0.008428  5.315
## immunosuppression1              0.526333  0.020537 25.628
## leukemia1                        0.399091  0.034129 11.694
## lymphoma1                        0.345324  0.046675  7.399
## metastaticcancer1               0.019801  0.024233  0.817
## thrombolytics1                  -2.110673  0.060512 -34.880
## sofa_respiration_baseline2TRUE   0.392935  0.007544  52.086
## cardiovascular_baseline1        -0.072916  0.008255 -8.833
## 
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## SepsisFuzzyLogicPositiveTRUE < 2e-16 ***
## age_Ranges(25,35] 3.53e-13 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female 1.02e-07 ***
## gender2Other/Unknown 5.38e-05 ***
## ethnicity2African American 0.008635 **
## ethnicity2Hispanic < 2e-16 ***

```

```

## ethnicity2Asian          0.000197 ***
## ethnicity2Native American 2.02e-12 ***
## ethnicity2Other/Unknown   0.001665 **
## BMI_Ranges(18.5,25]      < 2e-16 ***
## BMI_Ranges(25,35]        < 2e-16 ***
## BMI_Ranges(35,200]       1.41e-12 ***
## BMI_RangesOther/Unknown   < 2e-16 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other      0.001406 **
## icu_admit_source2Step-Down Unit 0.009314 **
## hospital_teaching_statusf < 2e-16 ***
## hospital_teaching_statust < 2e-16 ***
## hospital_size<100         < 2e-16 ***
## hospital_size100-249       < 2e-16 ***
## hospital_size250-500       < 2e-16 ***
## hospital_size>500         3.61e-09 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 2.29e-12 ***
## hospitaldischargeyear2012 0.001996 **
## hospitaldischargeyear2013 0.001952 **
## hospitaldischargeyear2014 1.75e-06 ***
## hospitaldischargeyear2015-16 0.105359
## dialysis1                  < 2e-16 ***
## aids1                      < 2e-16 ***
## hepaticfailureTRUE         0.167532
## diabetes1                 1.07e-07 ***
## immunosuppression1        < 2e-16 ***
## leukemial                  < 2e-16 ***
## lymphoma1                  1.38e-13 ***
## metastaticcancer1         0.413868
## thrombolytics1             < 2e-16 ***
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1  < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128 on 638756 degrees of freedom
## Residual deviance: 548492 on 638709 degrees of freedom
## AIC: 548588
##
## Number of Fisher Scoring iterations: 6

```

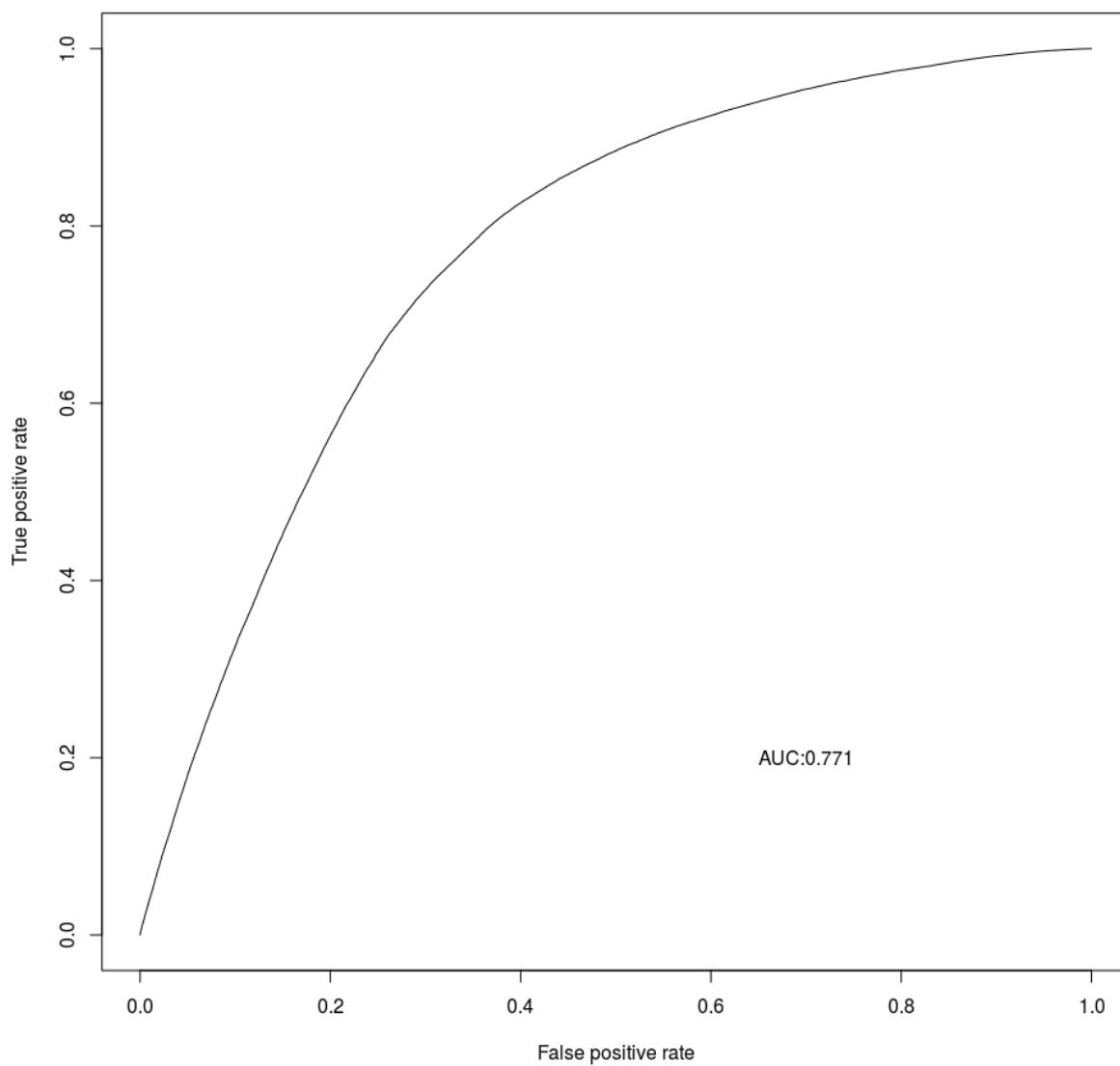
```

ssd_incl_te$FuzzyLogicADJSepsisPred <- predict(FuzzyLogic_ADJ_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,typ
e="response")
library(sjPlot)
library(ROCR)

FuzzyLogicADJSepsis.Pred <- prediction(ssd_incl_te$FuzzyLogicADJSepsisPred, ssd_incl_te$sepsis_outcome)
FuzzyLogicADJSepsis.Perf <- performance(FuzzyLogicADJSepsis.Pred, "tpr", "fpr")
plot(FuzzyLogicADJSepsis.Perf, main = "FuzzyLogic Positive Adjusted Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(FuzzyLogicADJSepsis.Pred,"auc")@y.values[[1]],3)))

```

FuzzyLogic Positive Adjusted Sepsis Prediction Test Model



```
performance(FuzzyLogicADJSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.7706897
##
## Slot "alpha.values":
## list()
```

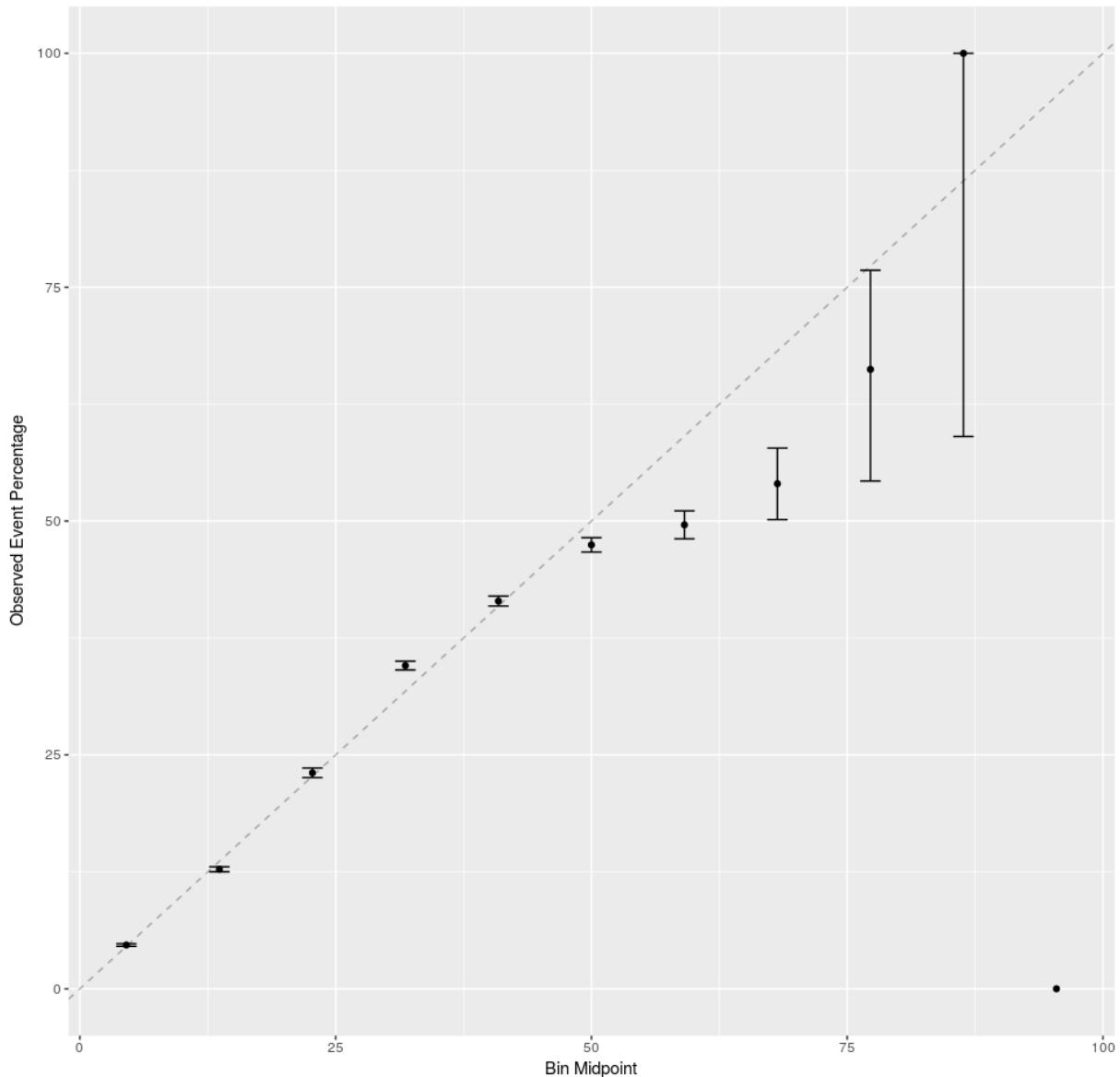
```
FuzzyLogicADJSepsis.Pred.roc <- roc(sepsis_outcome~FuzzyLogicADJSepsisPred,data=ssd_incl_te)
ci(FuzzyLogicADJSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.768–0.7734 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~FuzzyLogicADJSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of FuzzyLogic Positive Sepsis Prediction")
```

```
## Warning: Removed 1 rows containing missing values (geom_errorbar).
```

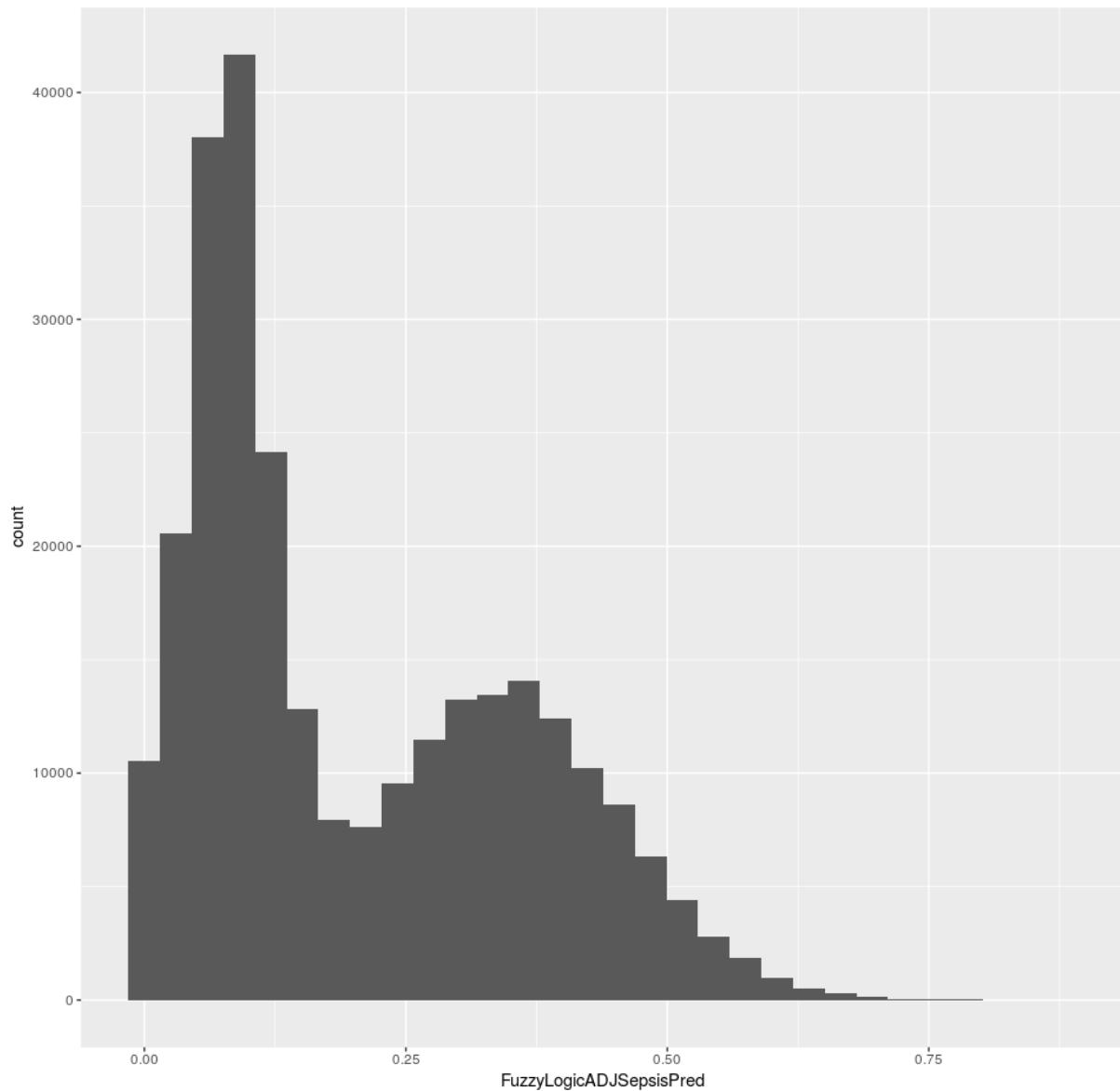
Calibration of FuzzyLogic Positive Sepsis Prediction



```
qplot(FuzzyLogicADJSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of FuzzyLogic Positive Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of FuzzyLogic Positive Sepsis Predictions



```
SIRS1_Crude_Sepsis_tr<-glm(sepsis_outcome ~ (SIRS_total), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SIRS1_Crude_Sepsis_tr)
#sjt.glm(SIRS1_Crude_Sepsis_tr)

#drop1(SIRS1_Crude_Sepsis_tr,test="Chisq")

summary(SIRS1_Crude_Sepsis_tr)
```

```

## 
## Call:
##   glm(formula = sepsis_outcome ~ (SIRS_total), family = "binomial",
##       data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q  Median      3Q     Max
## -0.9790 -0.7802 -0.6119 -0.3651  2.3415
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.674538  0.008932 -299.4 <2e-16 ***
## SIRS_total    0.547049  0.003252   168.2 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128  on 638756  degrees of freedom
## Residual deviance: 616197  on 638755  degrees of freedom
## AIC: 616201
##
## Number of Fisher Scoring iterations: 4

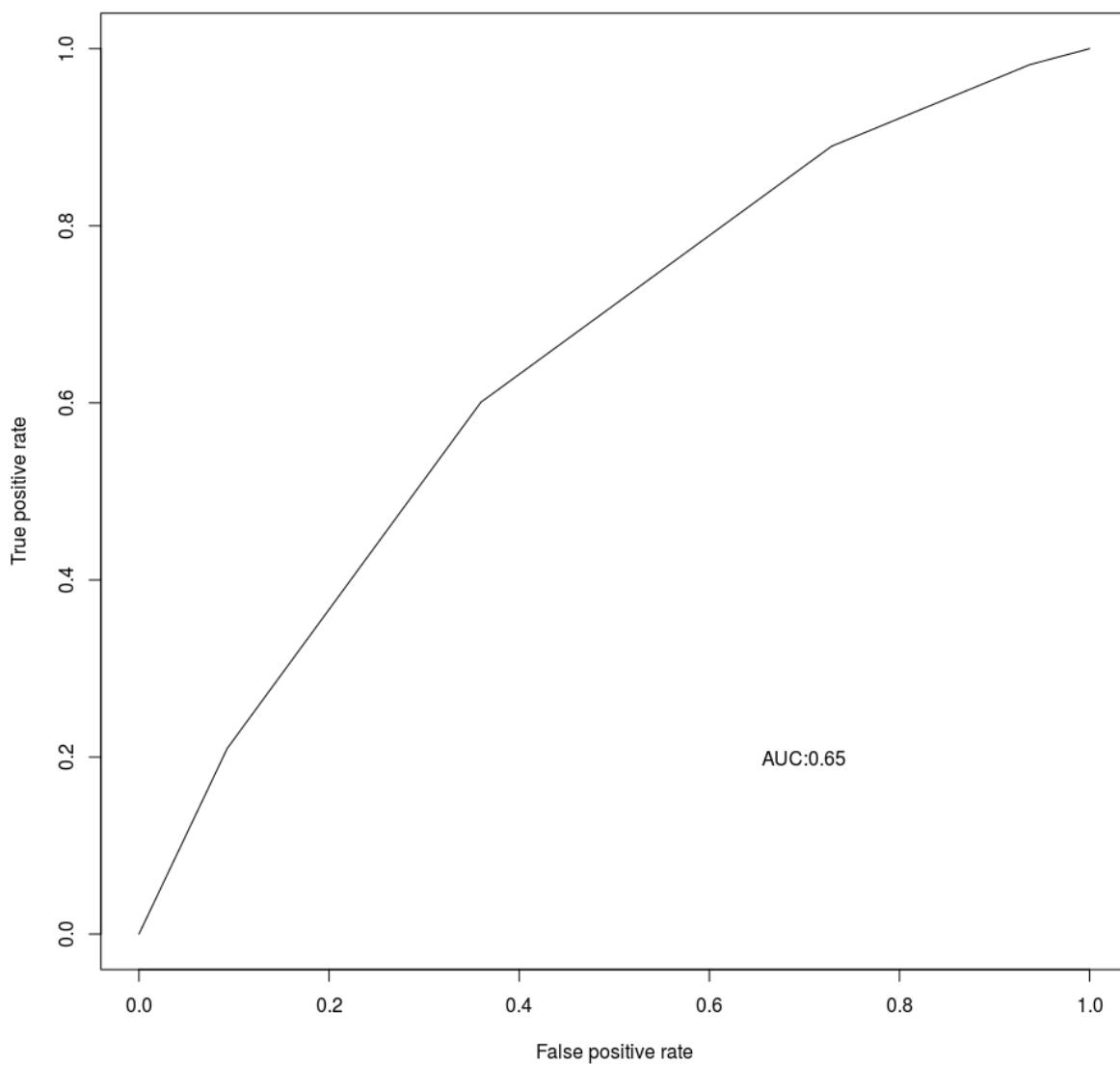
```

```

ssd_incl_te$SIRS1CrudeSepsisPred <- predict(SIRS1_Crude_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

SIRS1CrudeSepsis.Pred <- prediction(ssd_incl_te$SIRS1CrudeSepsisPred, ssd_incl_te$sepsis_outcome)
SIRS1CrudeSepsis.Perf <- performance(SIRS1CrudeSepsis.Pred, "tpr", "fpr")
plot(SIRS1CrudeSepsis.Perf, main = "SIRS Total Crude Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SIRS1CrudeSepsis.Pred,"auc")@y.values[[1]],3)))

```

SIRS Total Crude Sepsis Prediction Test Model

```
performance(SIRS1CrudeSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.6502231
##
## Slot "alpha.values":
## list()
```

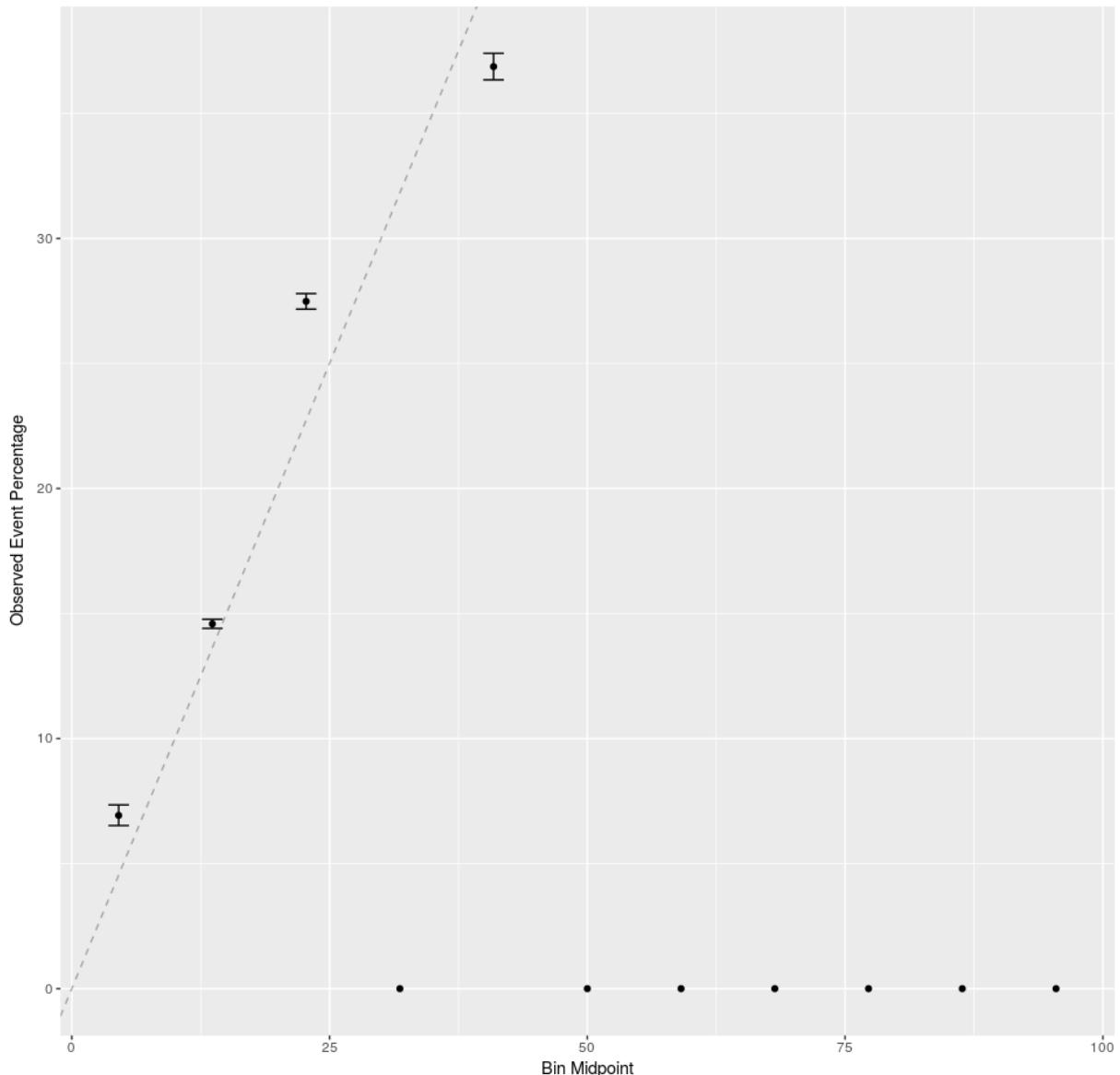
```
SIRS1CrudeSepsis.Pred.roc <- roc(sepsis_outcome~SIRS1CrudeSepsisPred,data=ssd_incl_te)
ci(SIRS1CrudeSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.6471-0.6534 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~SIRS1CrudeSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of SIRS Total Sepsis Prediction")
```

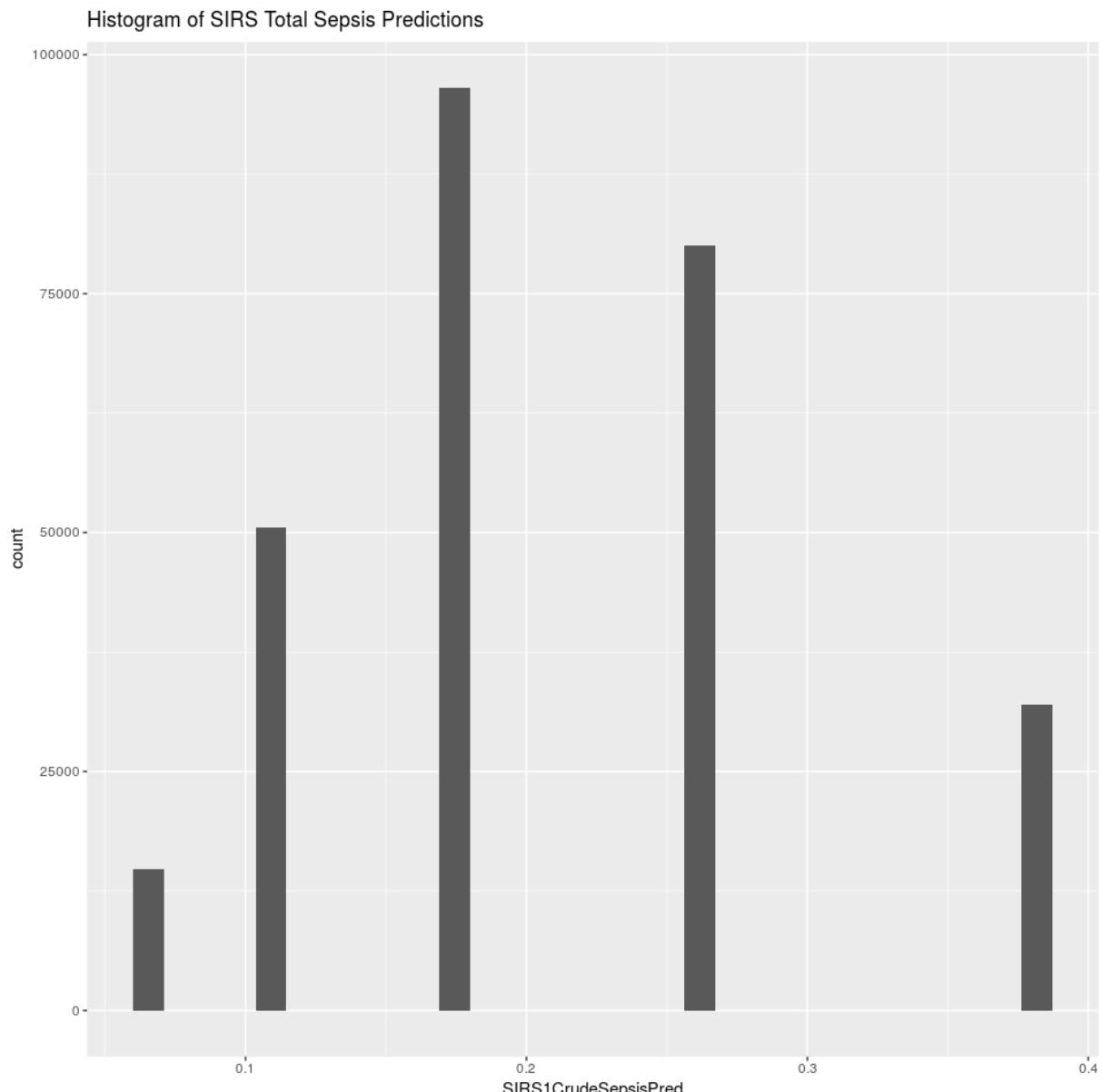
```
## Warning: Removed 7 rows containing missing values (geom_errorbar).
```

Calibration of SIRS Total Sepsis Prediction



```
qplot(SIRS1CrudeSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of SIRS Total Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



```
SIRS2_Crude_Sepsis_tr<-glm(sepsis_outcome ~ (SIRS_Positive), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SIRS2_Crude_Sepsis_tr)
#sjt.glm(SIRS2_Crude_Sepsis_tr)

#drop1(SIRS2_Crude_Sepsis_tr,test="Chisq")

summary(SIRS2_Crude_Sepsis_tr)
```

```

## 
## Call:
##   glm(formula = sepsis_outcome ~ (SIRS_Positive), family = "binomial",
##       data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q  Median      3Q     Max
## -0.7387 -0.7387 -0.7387 -0.4491  2.1653
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -2.243447   0.008668 -258.8 <2e-16 ***
## SIRS_PositiveTRUE 1.084204   0.009299   116.6 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128  on 638756  degrees of freedom
## Residual deviance: 630537  on 638755  degrees of freedom
## AIC: 630541
##
## Number of Fisher Scoring iterations: 4

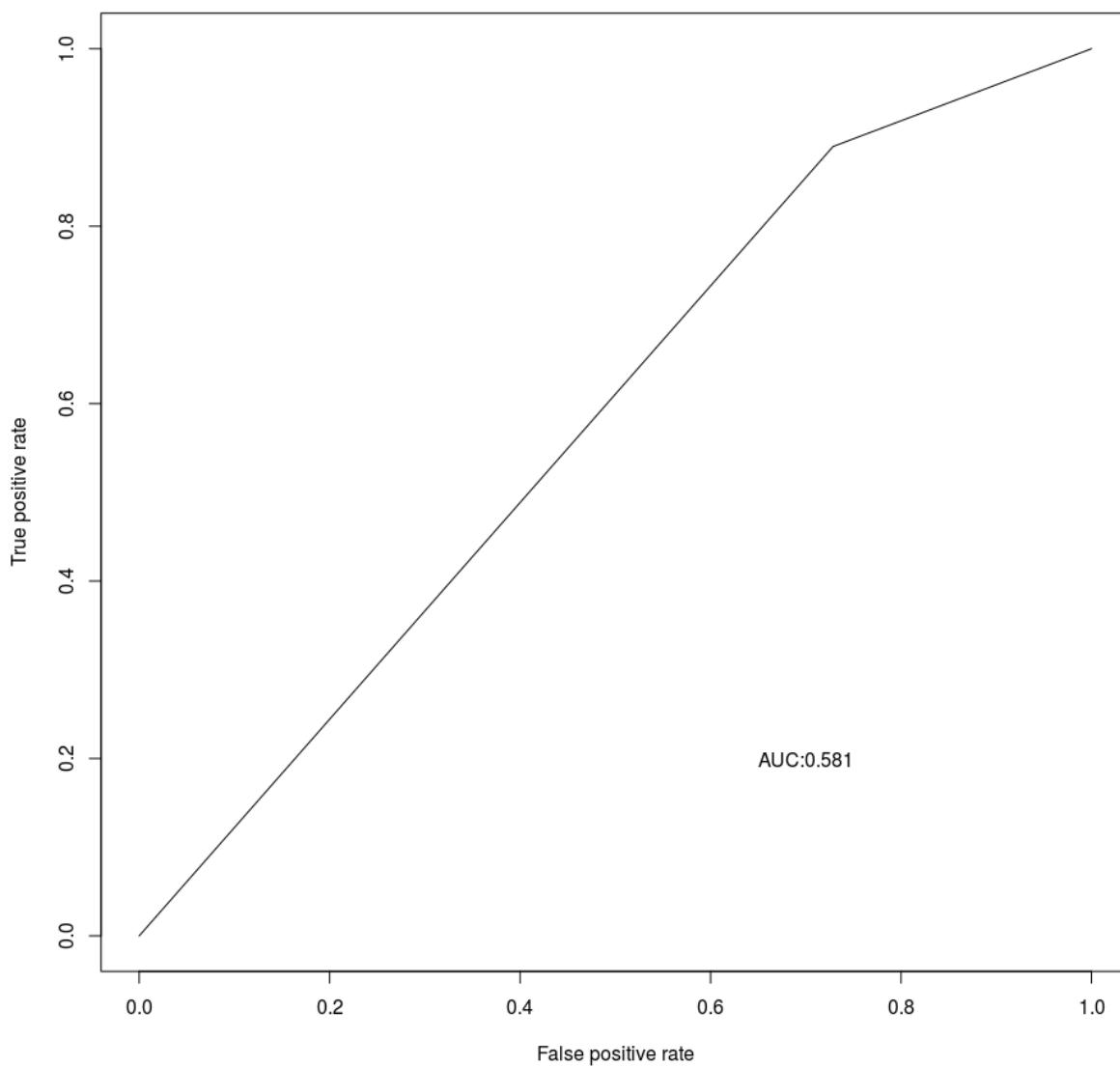
```

```

ssd_incl_te$SIRS2CrudeSepsisPred <- predict(SIRS2_Crude_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

SIRS2CrudeSepsis.Pred <- prediction(ssd_incl_te$SIRS2CrudeSepsisPred, ssd_incl_te$sepsis_outcome)
SIRS2CrudeSepsis.Perf <- performance(SIRS2CrudeSepsis.Pred, "tpr", "fpr")
plot(SIRS2CrudeSepsis.Perf, main = "SIRS Positive Crude Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SIRS2CrudeSepsis.Pred,"auc")@y.values[[1]],3)))

```

SIRS Positive Crude Sepsis Prediction Test Model

```
performance(SIRS2CrudeSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.5805731
##
## Slot "alpha.values":
## list()
```

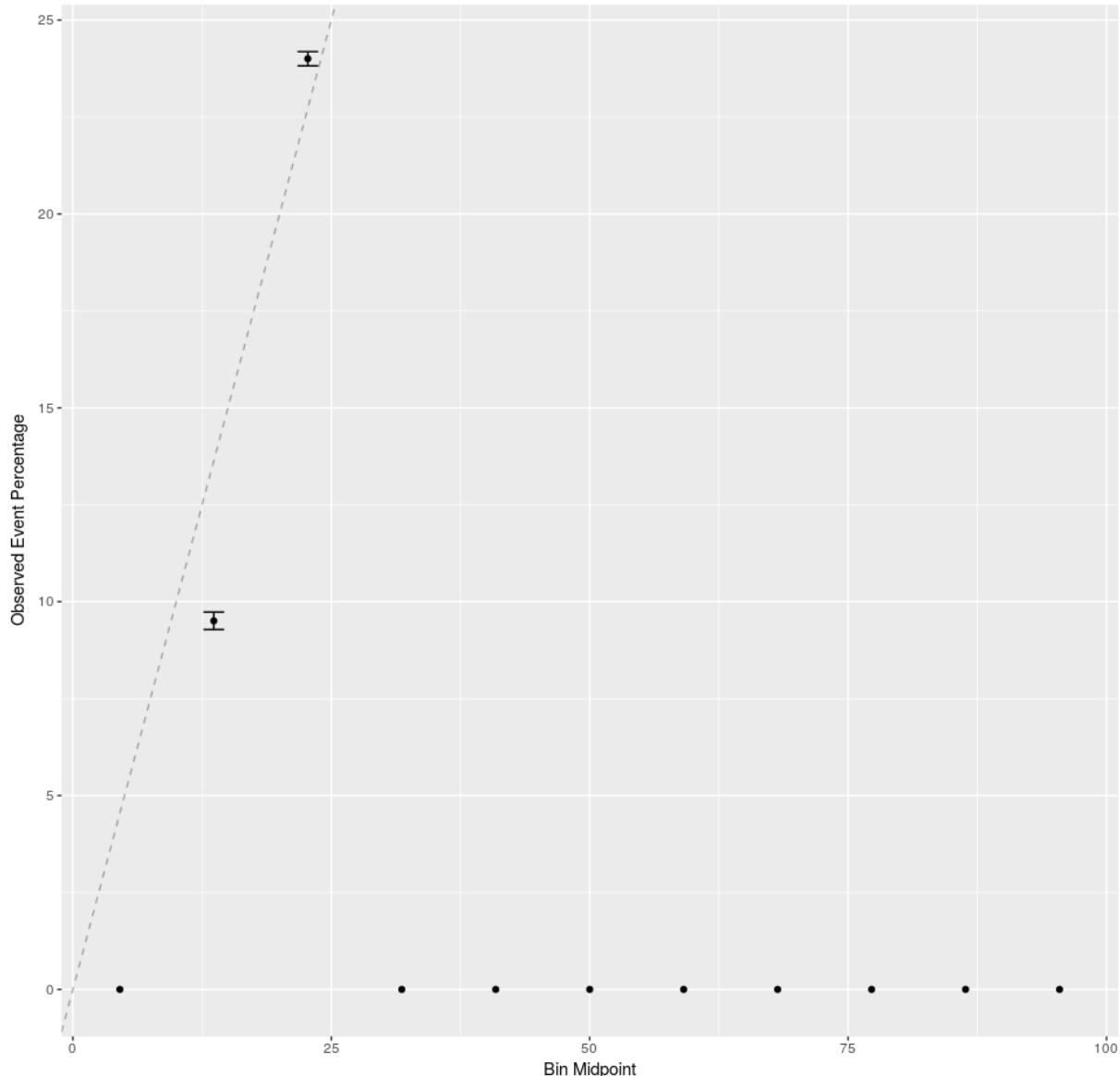
```
SIRS2CrudeSepsis.Pred.roc <- roc(sepsis_outcome~SIRS2CrudeSepsisPred,data=ssd_incl_te)
ci(SIRS2CrudeSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.5785-0.5827 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~SIRS2CrudeSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of SIRS Positive Sepsis Prediction")
```

```
## Warning: Removed 9 rows containing missing values (geom_errorbar).
```

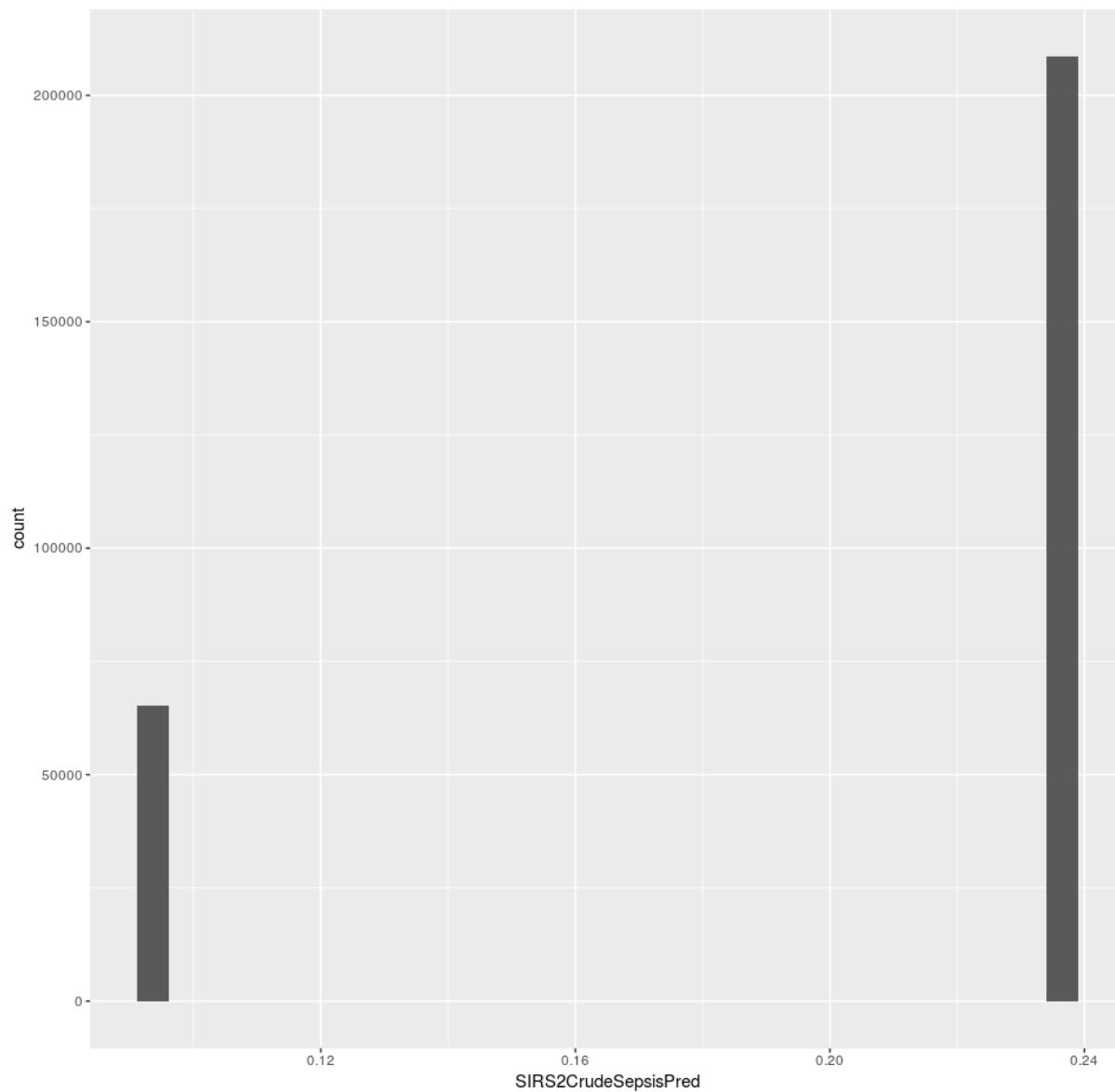
Calibration of SIRS Positive Sepsis Prediction



```
qplot(SIRS2CrudeSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of SIRS Positive Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of SIRS Positive Sepsis Predictions



```
qSOFA1_Crude_Sepsis_tr<-glm(sepsis_outcome ~ (qSOFA_total), data=ssd_incl_tr,family="binomial",na.action = na.omit)
#sjp.glm(qSOFA1_Crude_Sepsis_tr)
#sjt.glm(qSOFA1_Crude_Sepsis_tr)

#drop1(qSOFA1_Crude_Sepsis_tr,test="Chisq")
summary(qSOFA1_Crude_Sepsis_tr)
```

```

## 
## Call:
##   glm(formula = sepsis_outcome ~ (qSOFA_total), family = "binomial",
##       data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q     Median      3Q      Max
## -0.8922 -0.6807 -0.6807 -0.3782  2.3123
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.601940  0.009022 -288.4 <2e-16 ***
## qSOFA_total  0.628731  0.004012  156.7 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128  on 638756  degrees of freedom
## Residual deviance: 620004  on 638755  degrees of freedom
## AIC: 620008
##
## Number of Fisher Scoring iterations: 4

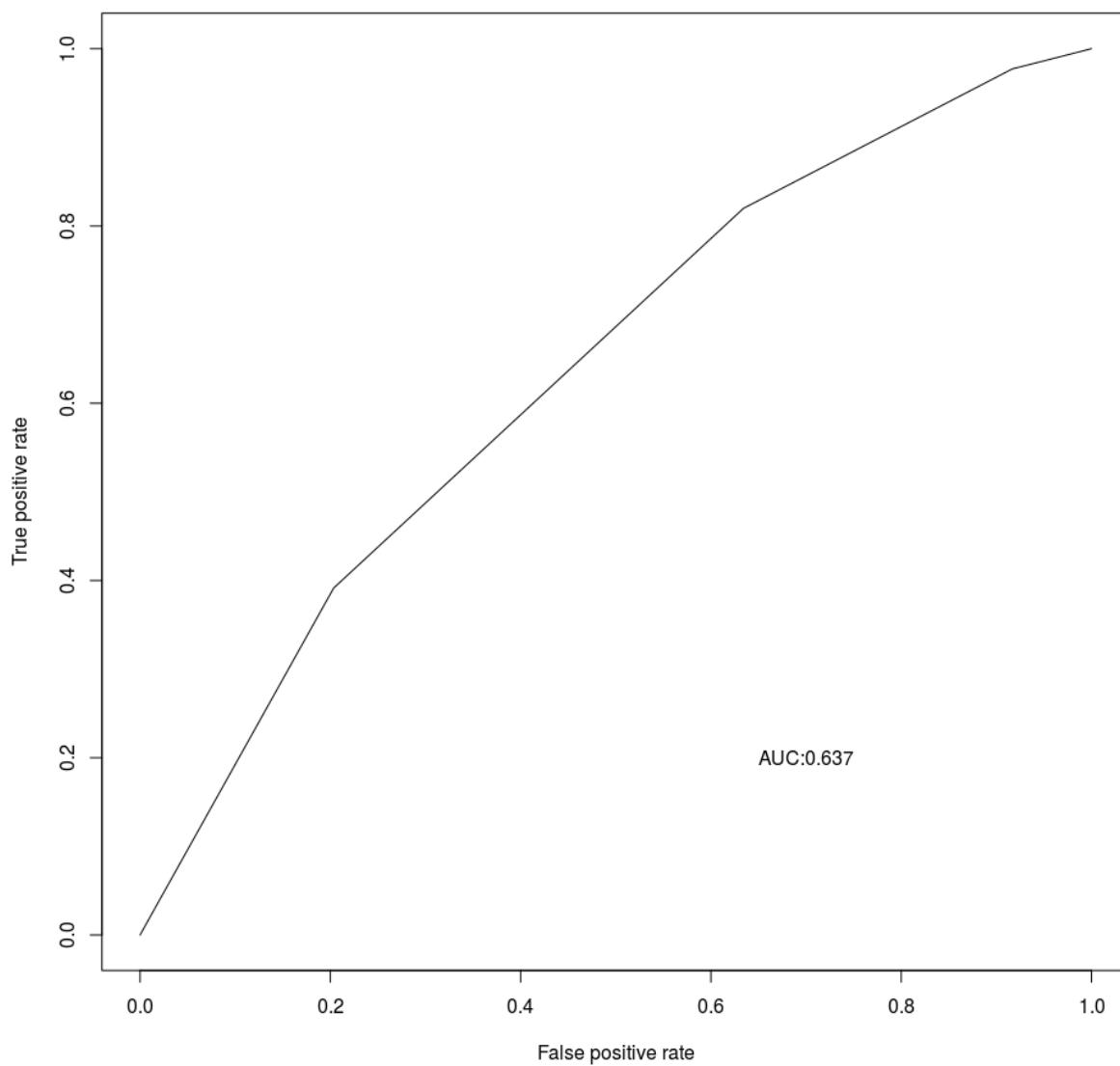
```

```

ssd_incl_te$qSOFA1CrudeSepsisPred <- predict(qSOFA1_Crude_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

qSOFA1CrudeSepsis.Pred <- prediction(ssd_incl_te$qSOFA1CrudeSepsisPred, ssd_incl_te$sepsis_outcome)
qSOFA1CrudeSepsis.Perf <- performance(qSOFA1CrudeSepsis.Pred, "tpr", "fpr")
plot(qSOFA1CrudeSepsis.Perf, main = "qSOFA1 Total Crude Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(qSOFA1CrudeSepsis.Pred,"auc")@y.values[[1]],3)))

```

qSOFA1 Total Crude Sepsis Prediction Test Model

```
performance(qSOFA1CrudeSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.6368558
##
## Slot "alpha.values":
## list()
```

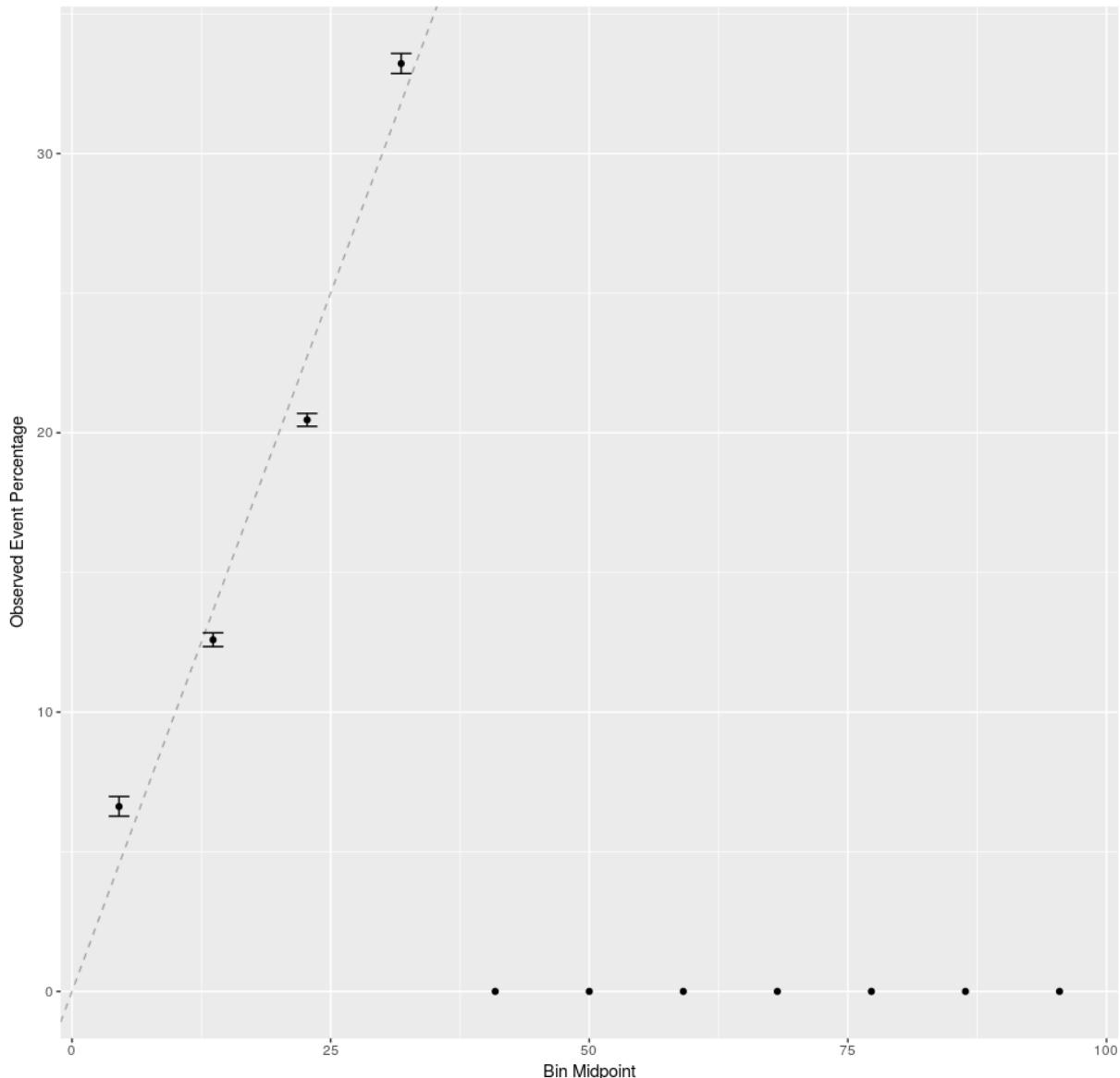
```
qSOFA1CrudeSepsis.Pred.roc <- roc(sepsis_outcome~qSOFA1CrudeSepsisPred,data=ssd_incl_te)
ci(qSOFA1CrudeSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.6338-0.6399 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~qSOFA1CrudeSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of qSOFA Total Sepsis Prediction")
```

```
## Warning: Removed 7 rows containing missing values (geom_errorbar).
```

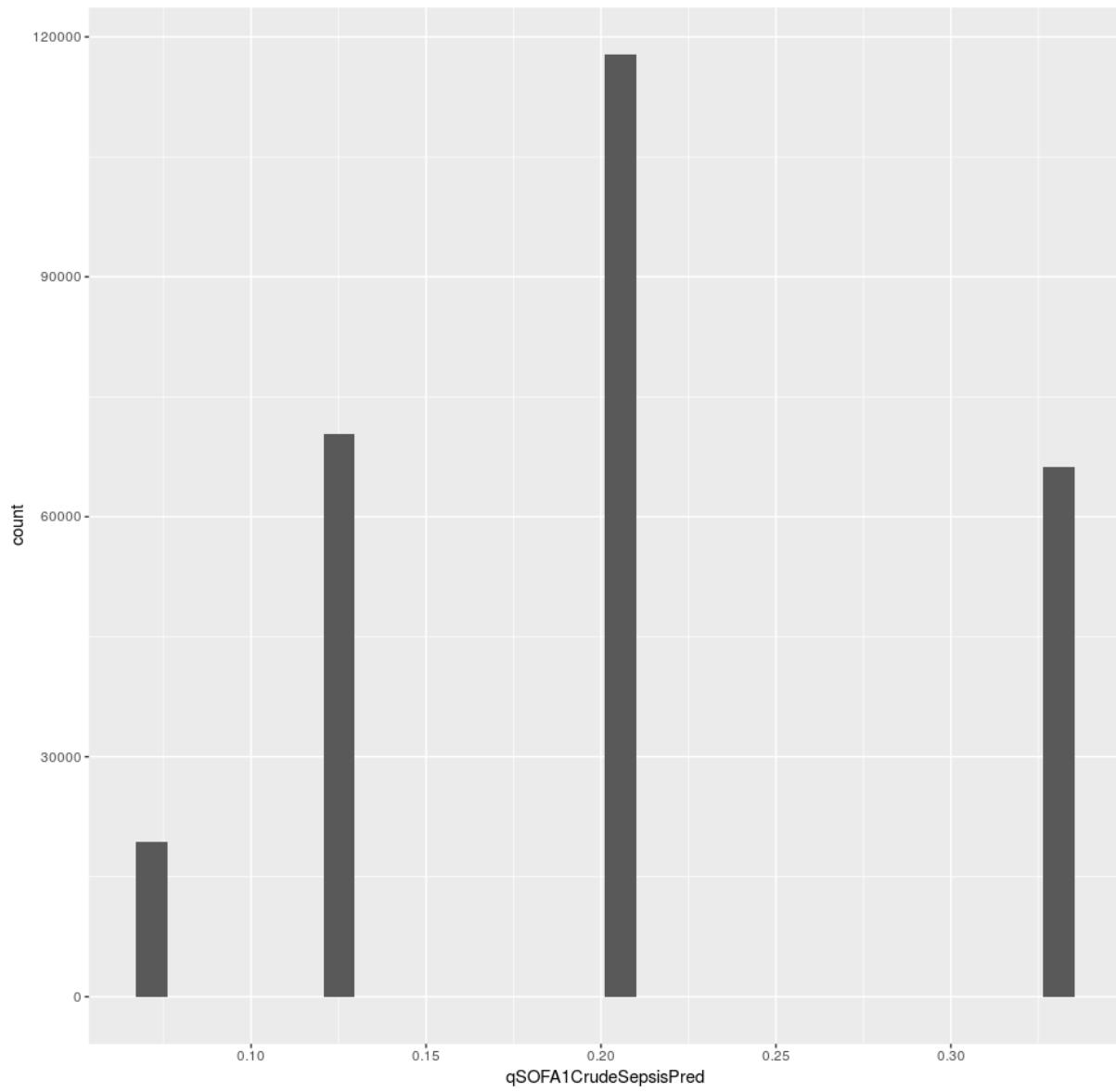
Calibration of qSOFA Total Sepsis Prediction



```
qplot(qSOFA1CrudeSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of qSOFA Total Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of qSOFA Total Sepsis Predictions



```
qSOFA2_Crude_Sepsis_tr<-glm(sepsis_outcome ~ (qSOFA_Positive), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(qSOFA2_Crude_Sepsis_tr)
#sjt.glm(qSOFA2_Crude_Sepsis_tr)

#drop1(qSOFA2_Crude_Sepsis_tr,test="Chisq")

summary(qSOFA2_Crude_Sepsis_tr)
```

```

## 
## Call:
##   glm(formula = sepsis_outcome ~ (qSOFA_Positive), family = "binomial",
##       data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q  Median      3Q     Max
## -0.7565 -0.7565 -0.7565 -0.4915  2.0849
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -2.052644  0.006875 -298.6 <2e-16 ***
## qSOFA_PositiveTRUE 0.947849  0.007729  122.6 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128  on 638756  degrees of freedom
## Residual deviance: 630027  on 638755  degrees of freedom
## AIC: 630031
##
## Number of Fisher Scoring iterations: 4

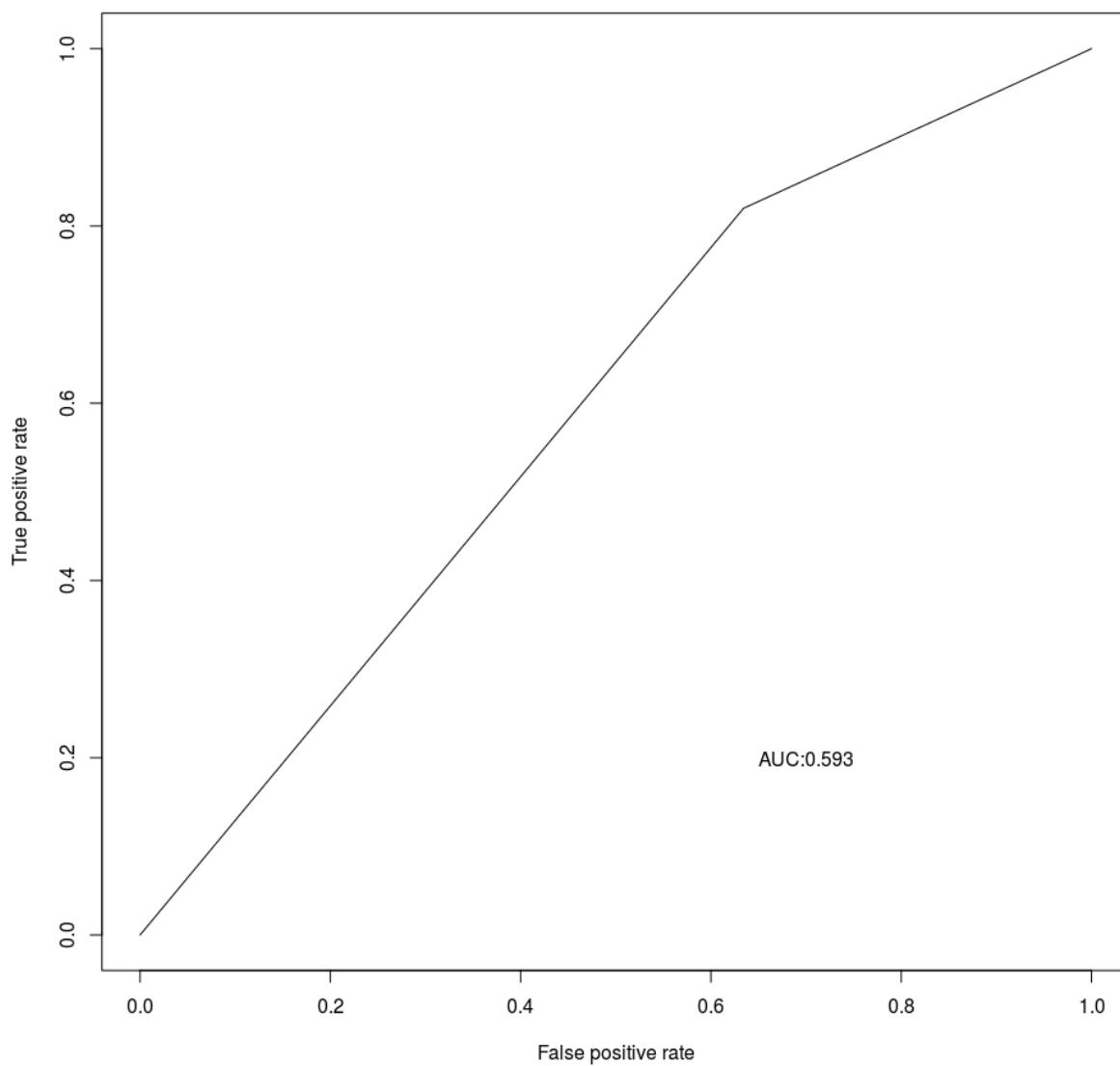
```

```

ssd_incl_te$qSOFA2CrudeSepsisPred <- predict(qSOFA2_Crude_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

qSOFA2CrudeSepsis.Pred <- prediction(ssd_incl_te$qSOFA2CrudeSepsisPred, ssd_incl_te$sepsis_outcome)
qSOFA2CrudeSepsis.Perf <- performance(qSOFA2CrudeSepsis.Pred, "tpr", "fpr")
plot(qSOFA2CrudeSepsis.Perf, main = "qSOFA Positive Crude Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(qSOFA2CrudeSepsis.Pred,"auc")@y.values[[1]],3)))

```

qSOFA Positive Crude Sepsis Prediction Test Model

```
performance(qSOFA2CrudeSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.5928223
##
## Slot "alpha.values":
## list()
```

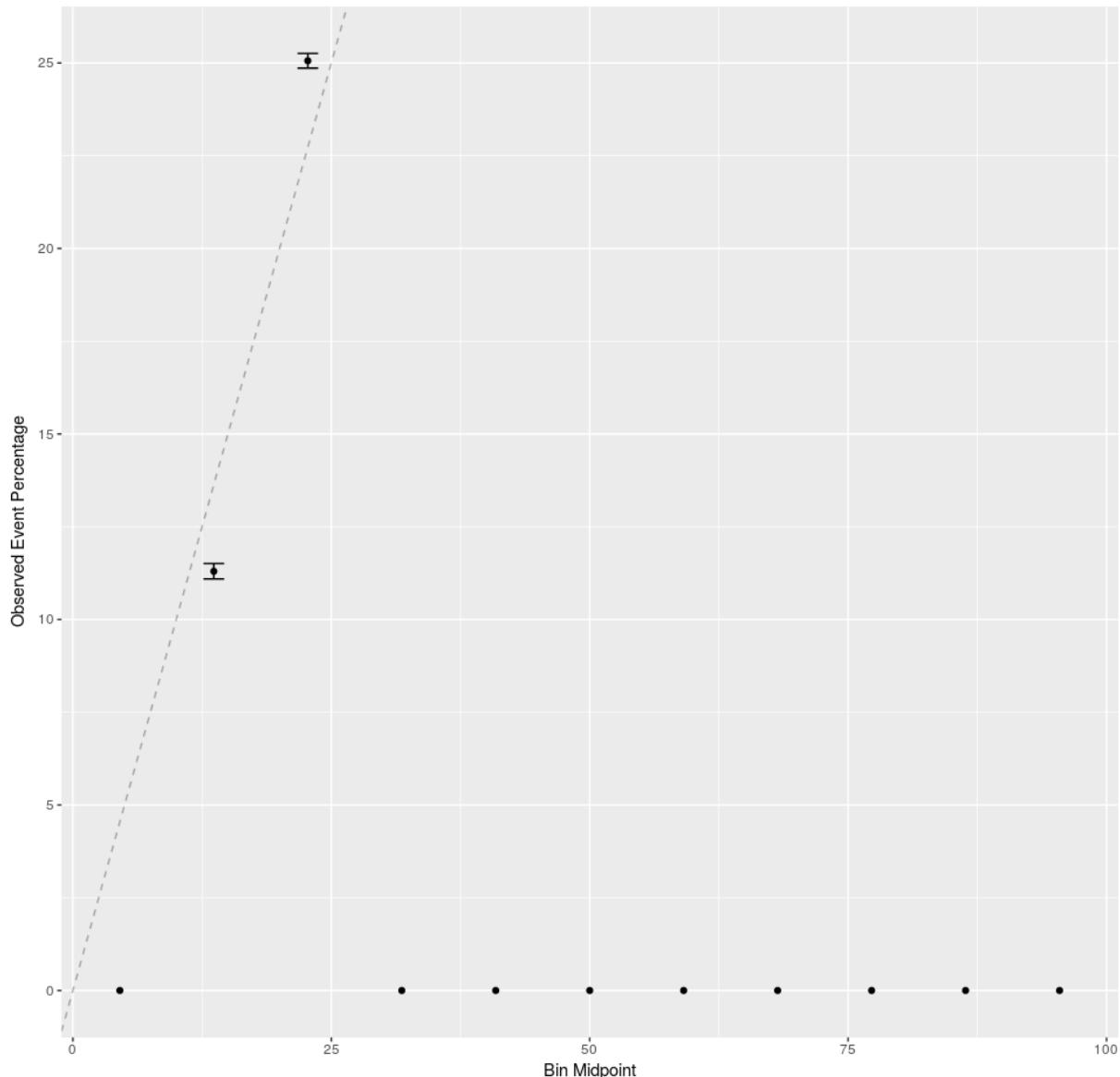
```
qSOFA2CrudeSepsis.Pred.roc <- roc(sepsis_outcome~qSOFA2CrudeSepsisPred,data=ssd_incl_te)
ci(qSOFA2CrudeSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.5903-0.5953 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~qSOFA2CrudeSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of qSOFA Positive Sepsis Prediction")
```

```
## Warning: Removed 9 rows containing missing values (geom_errorbar).
```

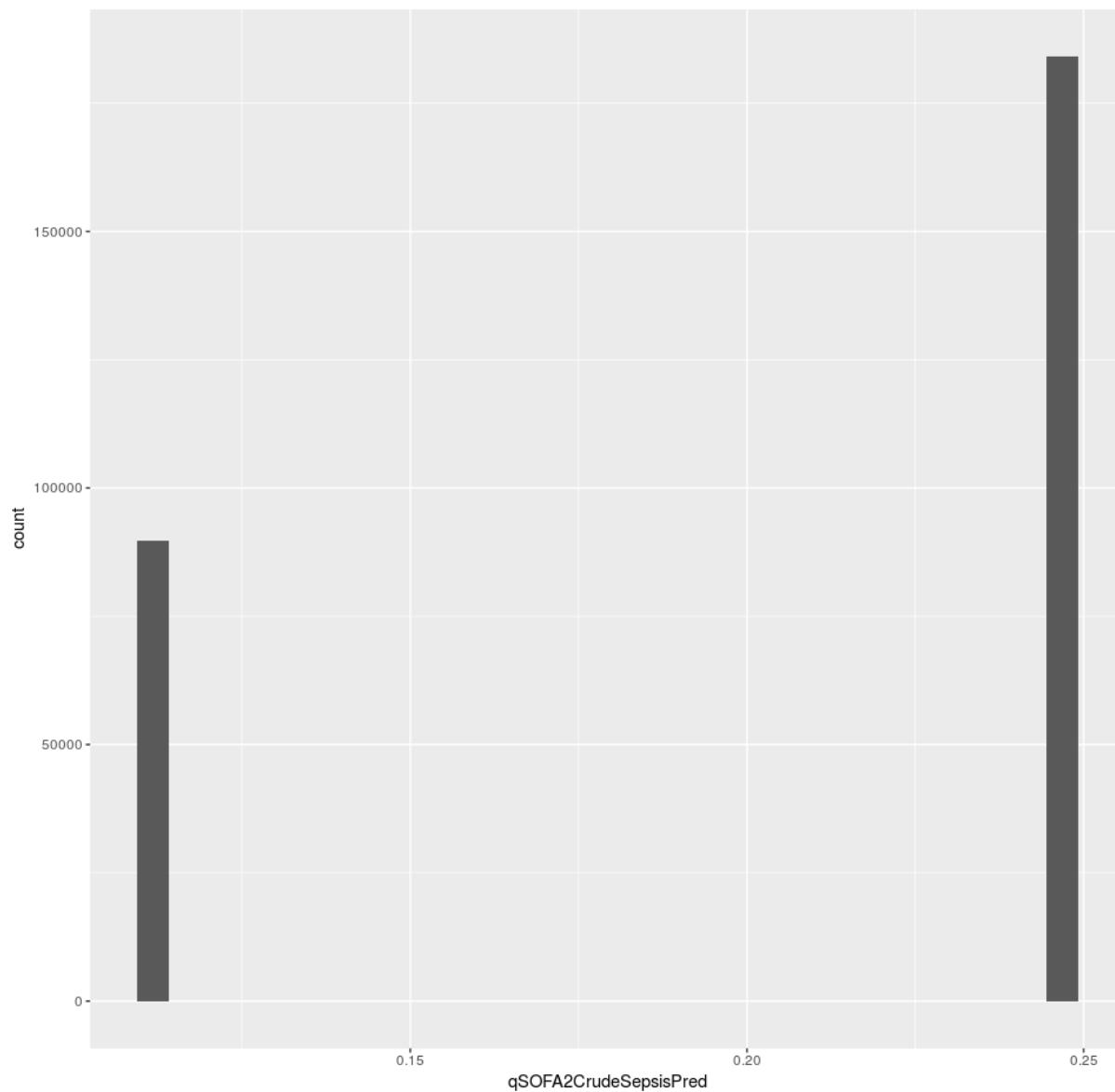
Calibration of qSOFA Positive Sepsis Prediction



```
qplot(qSOFA2CrudeSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of qSOFA Positive Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of qSOFA Positive Sepsis Predictions



```
SOFA1_Crude_Sepsis_tr<-glm(sepsis_outcome ~ as.factor(SOFA_Change), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SOFA1_Crude_Sepsis_tr)
#sjt.glm(SOFA1_Crude_Sepsis_tr)

#drop1(SOFA1_Crude_Sepsis_tr,test="Chisq")

summary(SOFA1_Crude_Sepsis_tr)
```

```

## 
## Call:
##   glm(formula = sepsis_outcome ~ as.factor(SOFA_Change), family = "binomial",
##       data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q  Median      3Q     Max
## -1.4096 -0.7412 -0.5635 -0.3790  2.3105
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)                -2.59739  0.01702 -152.61 <2e-16 ***
## as.factor(SOFA_Change) 1    0.40363  0.01913  21.10 <2e-16 ***
## as.factor(SOFA_Change) 2    0.83756  0.01933  43.32 <2e-16 ***
## as.factor(SOFA_Change) 3    1.25489  0.01909  65.75 <2e-16 ***
## as.factor(SOFA_Change) 4    1.44584  0.01915  75.50 <2e-16 ***
## as.factor(SOFA_Change) 5    1.59643  0.01951  81.82 <2e-16 ***
## as.factor(SOFA_Change) 6    1.84006  0.02015  91.32 <2e-16 ***
## as.factor(SOFA_Change) 7    1.91239  0.02084  91.78 <2e-16 ***
## as.factor(SOFA_Change) 8    2.01564  0.02226  90.55 <2e-16 ***
## as.factor(SOFA_Change) 9    2.12645  0.02408  88.30 <2e-16 ***
## as.factor(SOFA_Change)10   2.20521  0.02644  83.40 <2e-16 ***
## as.factor(SOFA_Change)11   2.25783  0.02949  76.57 <2e-16 ***
## as.factor(SOFA_Change)12   2.38680  0.03413  69.94 <2e-16 ***
## as.factor(SOFA_Change)13   2.50214  0.03973  62.97 <2e-16 ***
## as.factor(SOFA_Change)14   2.55797  0.04808  53.20 <2e-16 ***
## as.factor(SOFA_Change)15   2.74004  0.05891  46.51 <2e-16 ***
## as.factor(SOFA_Change)16   2.78495  0.07437  37.45 <2e-16 ***
## as.factor(SOFA_Change)17   2.82860  0.10323  27.40 <2e-16 ***
## as.factor(SOFA_Change)[18,23] 3.12842  0.10532  29.70 <2e-16 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128  on 638756  degrees of freedom
## Residual deviance: 604543  on 638738  degrees of freedom
## AIC: 604581
##
## Number of Fisher Scoring iterations: 5

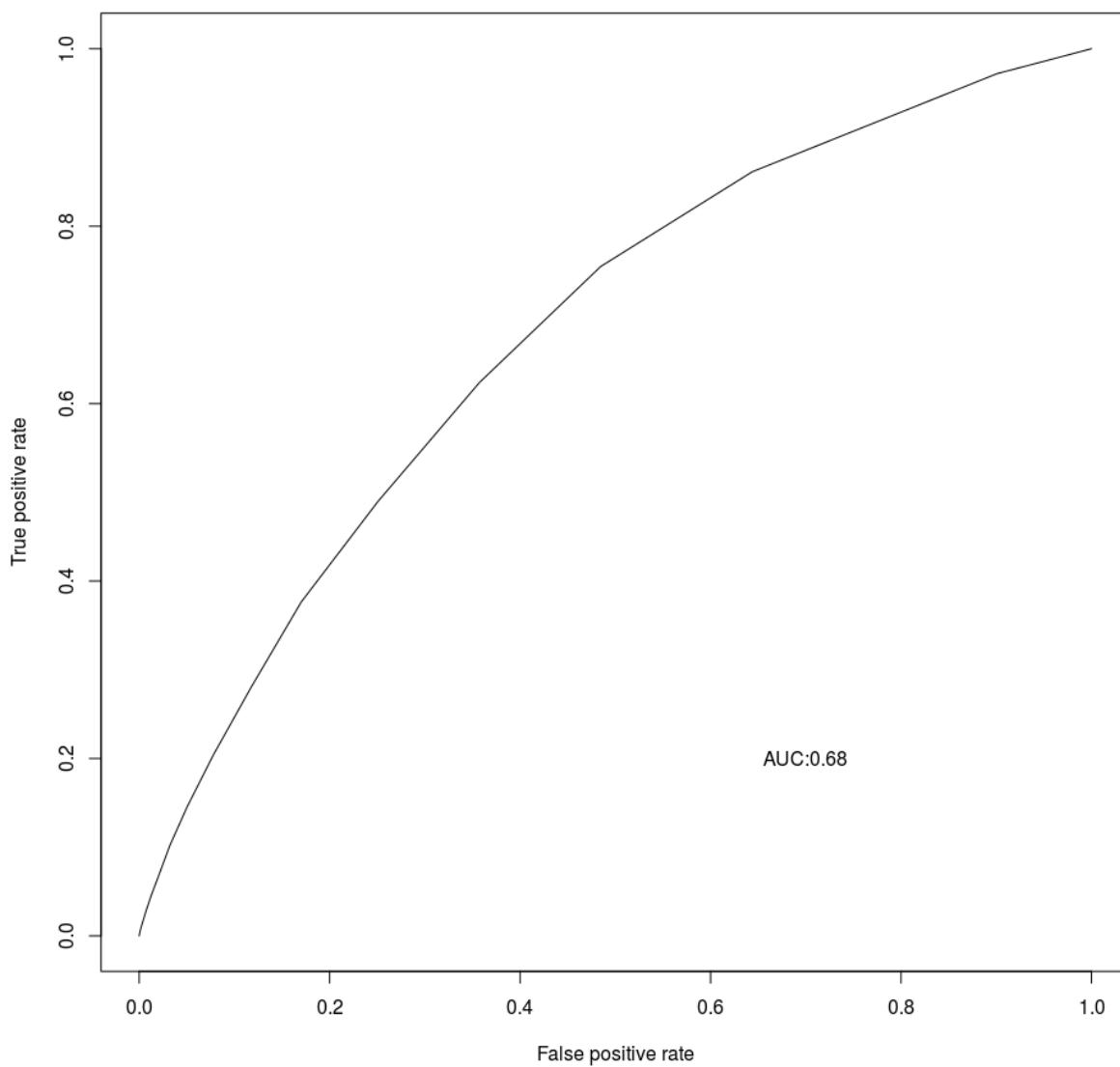
```

```

ssd_incl_te$SOFA1CrudeSepsisPred <- predict(SOFA1_Crude_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

SOFA1CrudeSepsis.Pred <- prediction(ssd_incl_te$SOFA1CrudeSepsisPred, ssd_incl_te$sepsis_outcome)
SOFA1CrudeSepsis.Perf <- performance(SOFA1CrudeSepsis.Pred, "tpr", "fpr")
plot(SOFA1CrudeSepsis.Perf, main = "SOFA Continuous Crude Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA1CrudeSepsis.Pred,"auc")@y.values[[1]],3)))

```

SOFA Continuous Crude Sepsis Prediction Test Model

```
performance(SOFA1CrudeSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.6796153
##
## Slot "alpha.values":
## list()
```

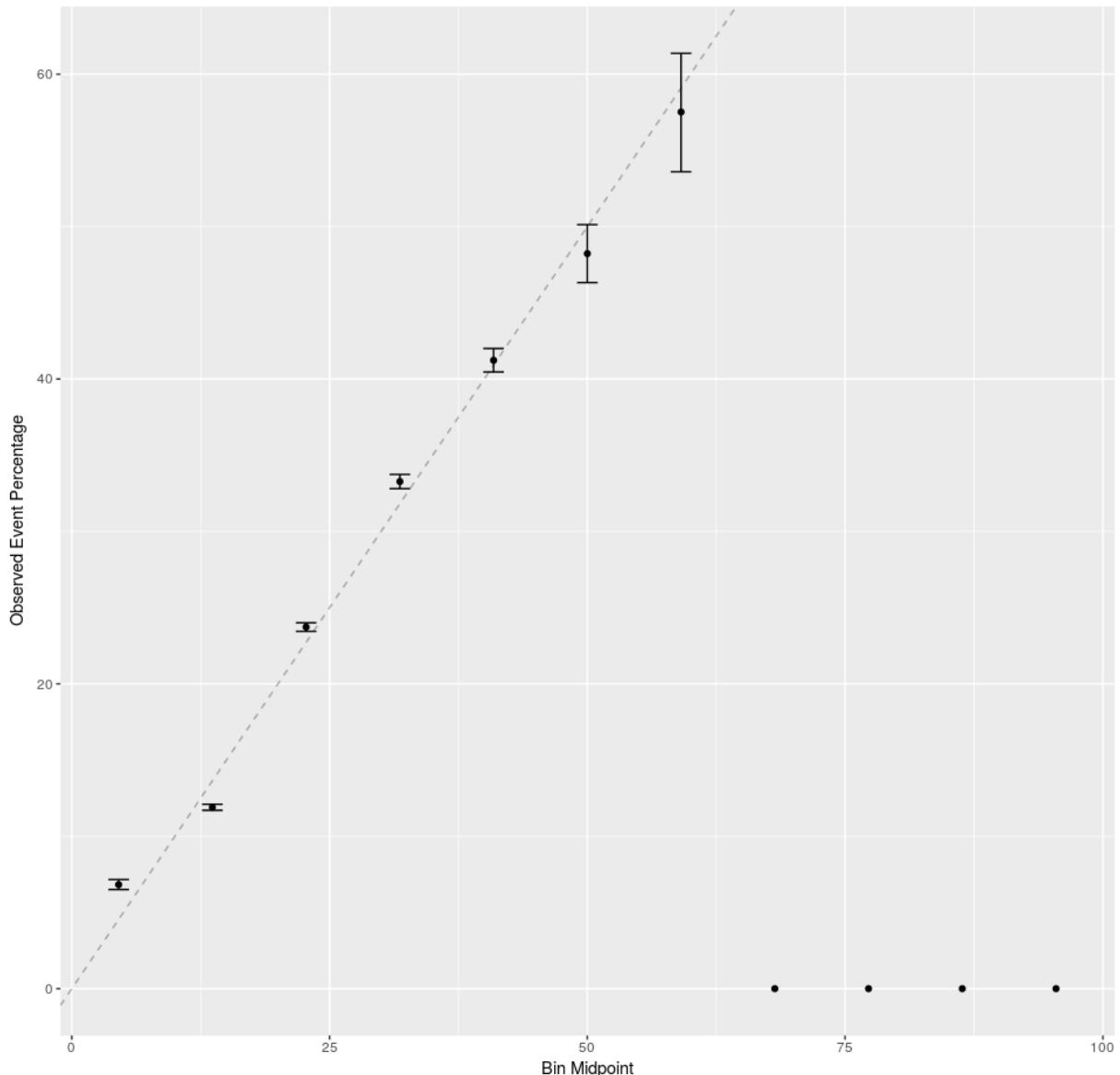
```
SOFA1CrudeSepsis.Pred.roc <- roc(sepsis_outcome~SOFA1CrudeSepsisPred,data=ssd_incl_te)
ci(SOFA1CrudeSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.6764-0.6828 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~SOFA1CrudeSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of SOFA Total Sepsis Prediction")
```

```
## Warning: Removed 4 rows containing missing values (geom_errorbar).
```

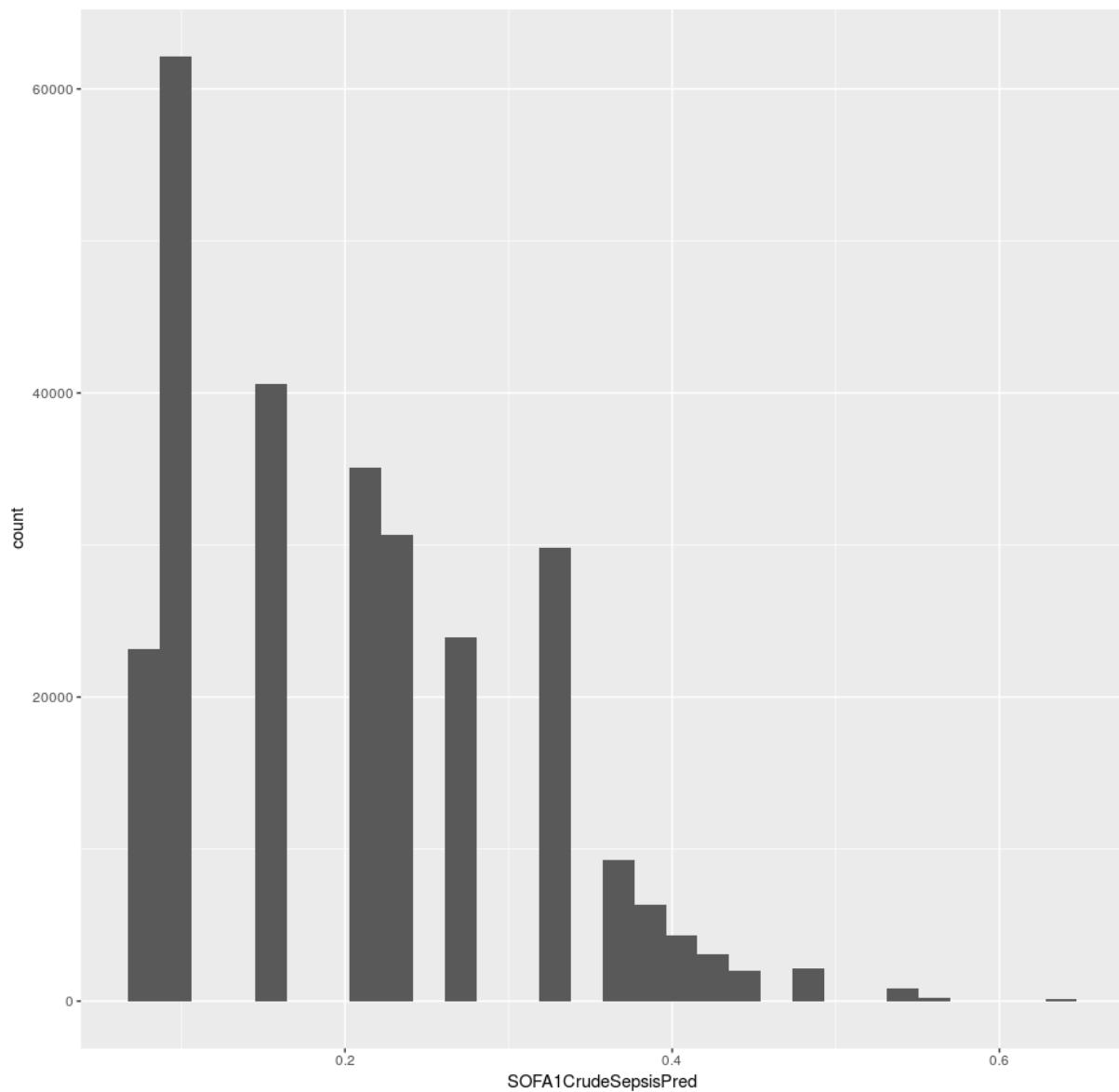
Calibration of SOFA Total Sepsis Prediction



```
qplot(SOFA1CrudeSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of SOFA Total Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of SOFA Total Sepsis Predictions



```
SOFA2_Crude_Sepsis_tr<-glm(sepsis_outcome ~ as.factor(SOFA_Positive), data=ssd_incl_tr,family="binomial",na.action=n = na.omit)

#sjp.glm(SOFA2_Crude_Sepsis_tr)
#sjt.glm(SOFA2_Crude_Sepsis_tr)

#drop1(SOFA2_Crude_Sepsis_tr,test="Chisq")

summary(SOFA2_Crude_Sepsis_tr)
```

```

## Call:
## glm(formula = sepsis_outcome ~ as.factor(SOFA_Positive), family = "binomial",
##      data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min      1Q   Median      3Q     Max
## -0.7680 -0.7680 -0.7680 -0.4393  2.1846
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)           -2.289758   0.007755 -295.3 <2e-16 ***
## as.factor(SOFA_Positive)TRUE 1.219750   0.008491   143.7 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128  on 638756  degrees of freedom
## Residual deviance: 621940  on 638755  degrees of freedom
## AIC: 621944
##
## Number of Fisher Scoring iterations: 4

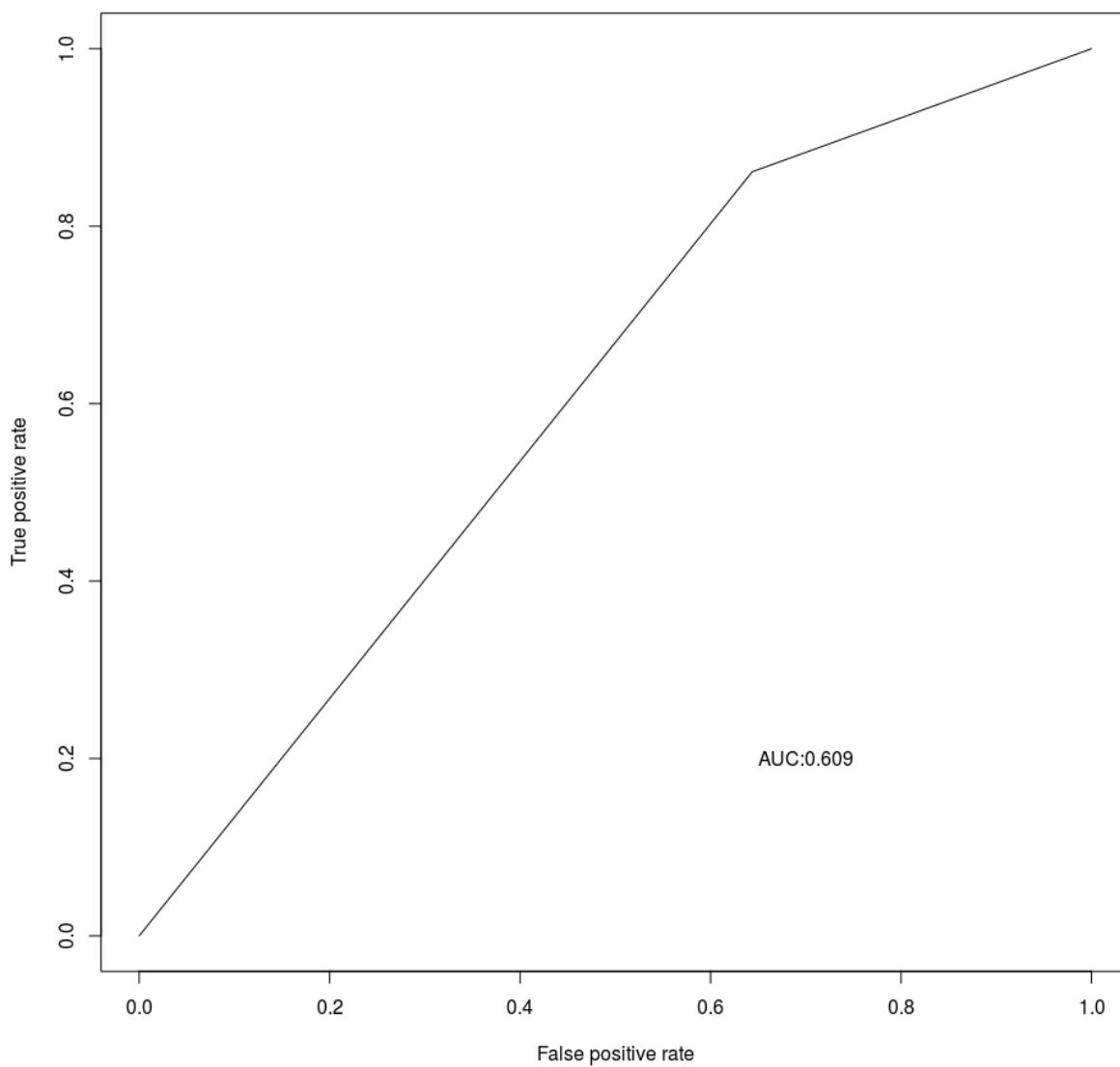
```

```

ssd_incl_te$SOFA2CrudeSepsisPred <- predict(SOFA2_Crude_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

SOFA2CrudeSepsis.Pred <- prediction(ssd_incl_te$SOFA2CrudeSepsisPred, ssd_incl_te$sepsis_outcome)
SOFA2CrudeSepsis.Perf <- performance(SOFA2CrudeSepsis.Pred, "tpr", "fpr")
plot(SOFA2CrudeSepsis.Perf, main = "SOFA Positive Crude Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA2CrudeSepsis.Pred,"auc")@y.values[[1]],3)))

```

SOFA Positive Crude Sepsis Prediction Test Model

```
performance(SOFA2CrudeSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.6087716
##
## Slot "alpha.values":
## list()
```

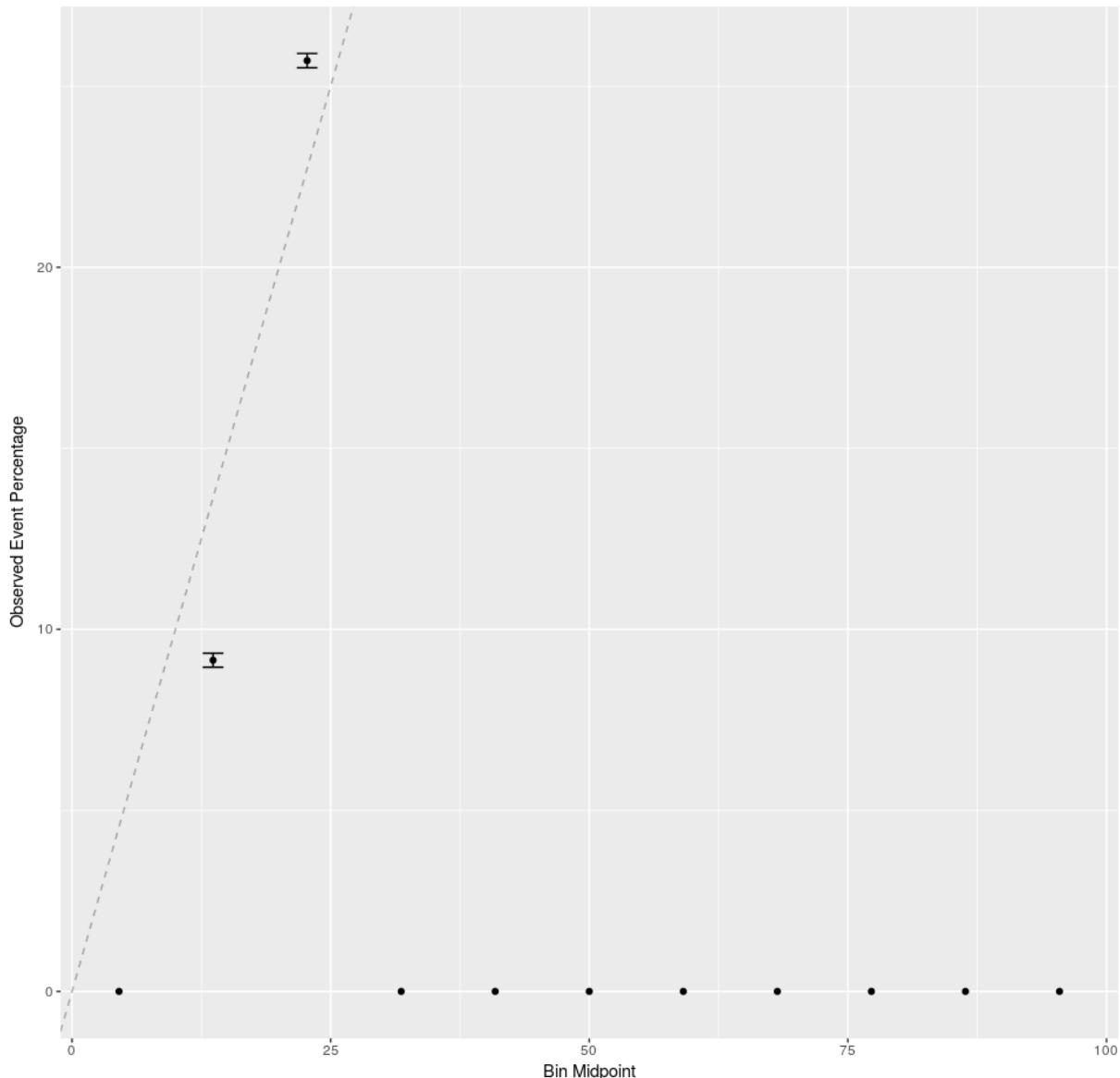
```
SOFA2CrudeSepsis.Pred.roc <- roc(sepsis_outcome~SOFA2CrudeSepsisPred,data=ssd_incl_te)
ci(SOFA2CrudeSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.6065-0.6111 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~SOFA2CrudeSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of SOFA Positive Sepsis Prediction")
```

```
## Warning: Removed 9 rows containing missing values (geom_errorbar).
```

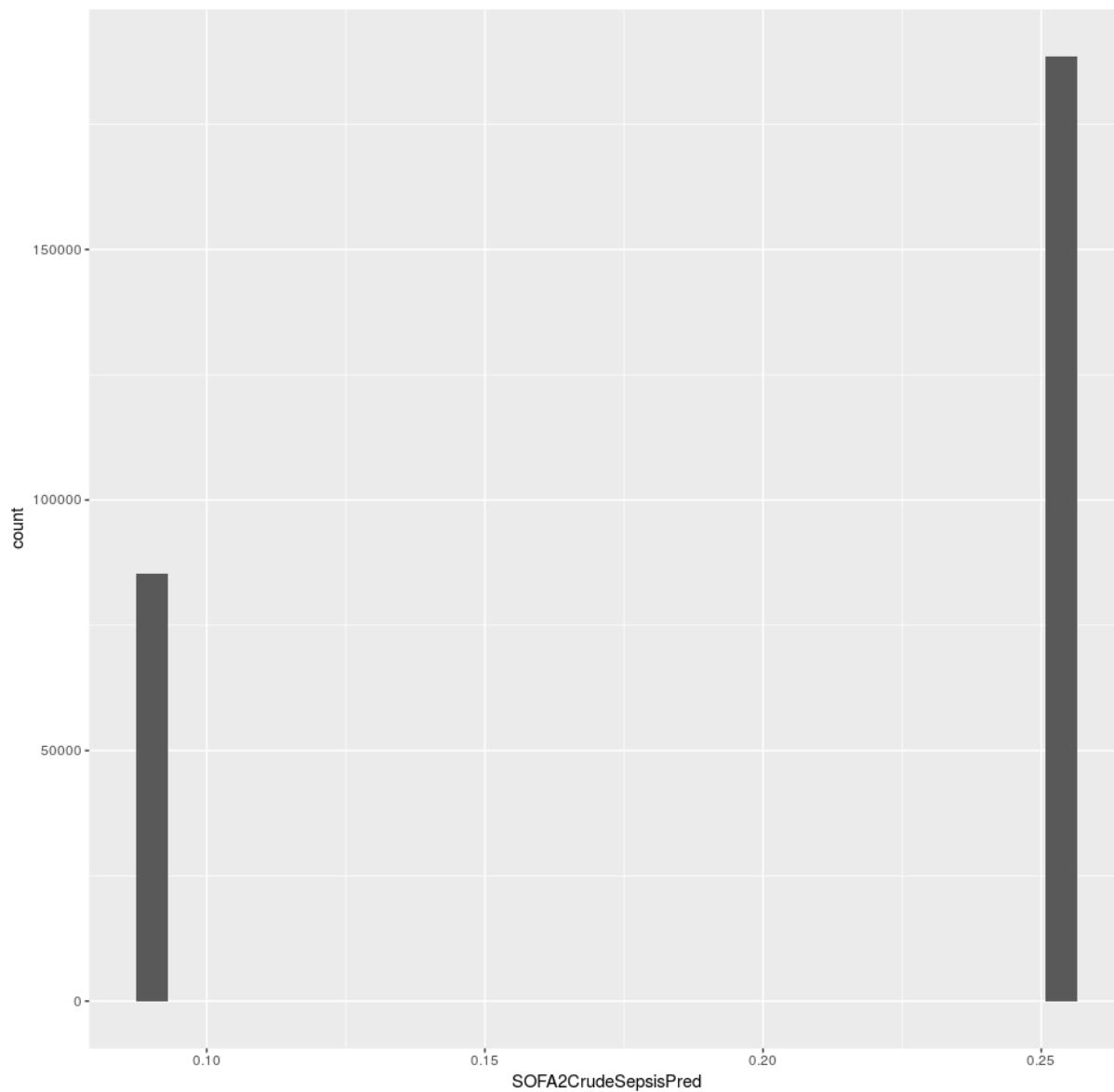
Calibration of SOFA Positive Sepsis Prediction



```
qplot(SOFA2CrudeSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of SOFA Positive Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of SOFA Positive Sepsis Predictions



```
SOFA3_Crude_Sepsis_tr<-glm(sepsis_outcome ~ as.factor(SOFA_Positive2), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(SOFA3_Crude_Sepsis_tr)
#sjt.glm(SOFA3_Crude_Sepsis_tr)

#drop1(SOFA3_Crude_Sepsis_tr,test="Chisq")

summary(SOFA3_Crude_Sepsis_tr)
```

```

## Call:
## glm(formula = sepsis_outcome ~ as.factor(SOFA_Positive2), family = "binomial",
##      data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##       Min     1Q   Median     3Q    Max
## -0.7663 -0.7663 -0.7663 -0.4193  2.2250
##
## Coefficients:
##                               Estimate Std. Error z value Pr(>|z|)
## (Intercept)             -2.387468  0.008324 -286.8 <2e-16 ***
## as.factor(SOFA_Positive2)TRUE 1.312243  0.008998  145.8 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128  on 638756  degrees of freedom
## Residual deviance: 620236  on 638755  degrees of freedom
## AIC: 620240
##
## Number of Fisher Scoring iterations: 5

```

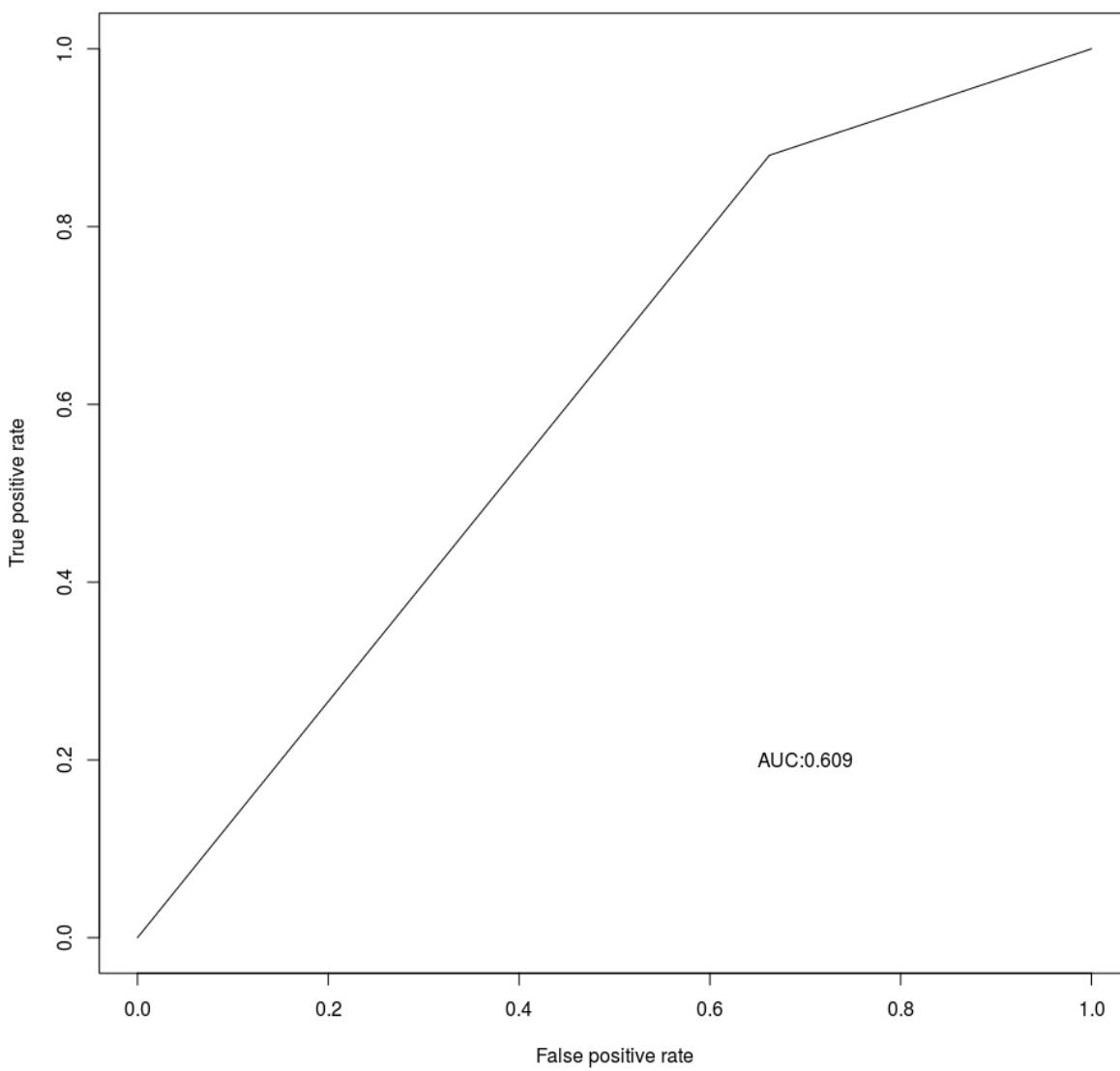
```

ssd_incl_te$SOFA3CrudeSepsisPred <- predict(SOFA3_Crude_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

SOFA3CrudeSepsis.Pred <- prediction(ssd_incl_te$SOFA3CrudeSepsisPred, ssd_incl_te$sepsis_outcome)
SOFA3CrudeSepsis.Perf <- performance(SOFA3CrudeSepsis.Pred, "tpr", "fpr")
plot(SOFA3CrudeSepsis.Perf, main = "SOFA Positive w/o Baseline
Crude Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(SOFA3CrudeSepsis.Pred,"auc")@y.values[[1]],3)))

```

**SOFA Positive w/o Baseline
Crude Sepsis Prediction Test Model**



```
performance(SOFA3CrudeSepsis.Pred, "auc")
```

```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.6088949
##
## Slot "alpha.values":
## list()
```

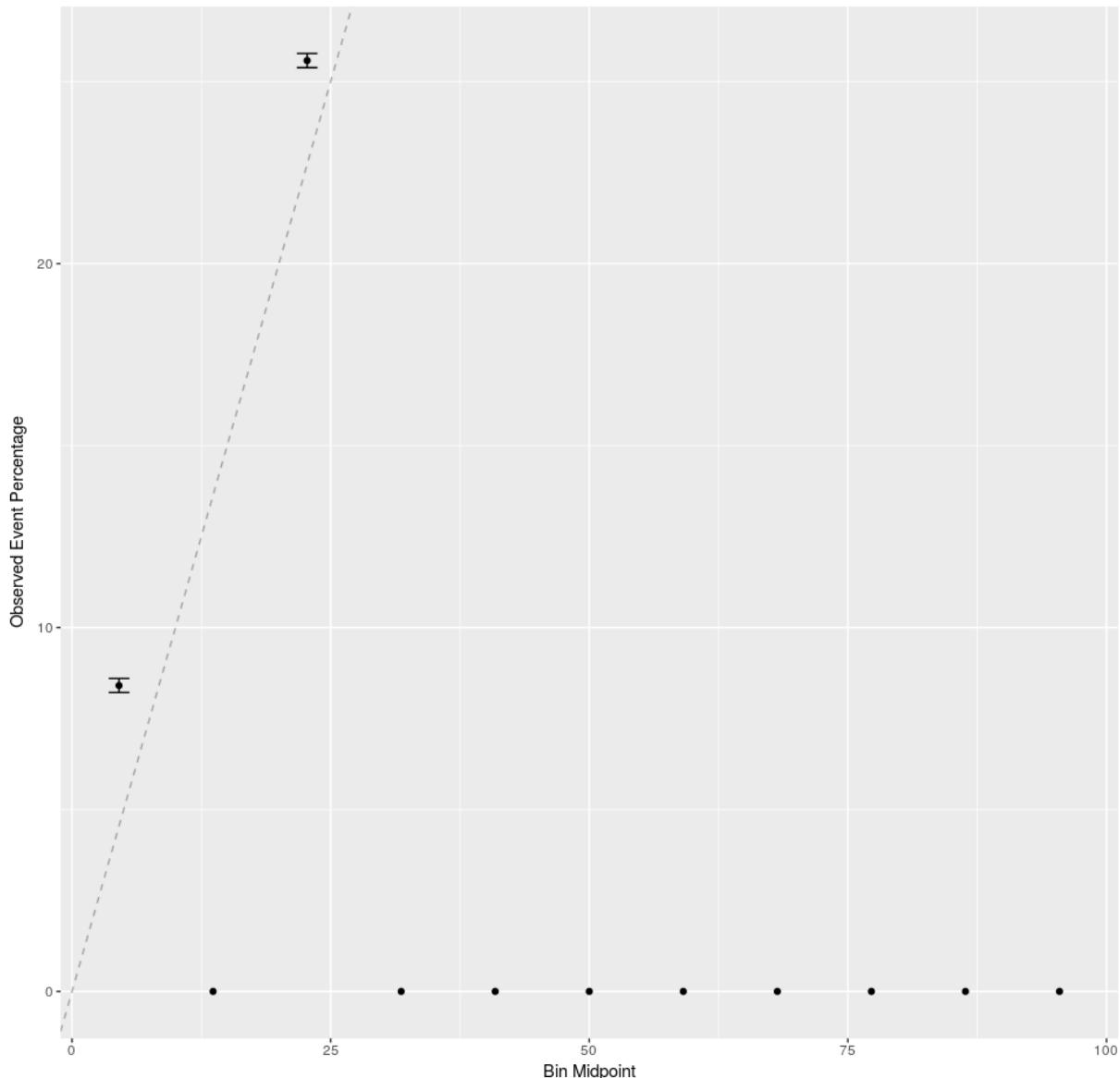
```
SOFA3CrudeSepsis.Pred.roc <- roc(sepsis_outcome~SOFA3CrudeSepsisPred,data=ssd_incl_te)
ci(SOFA3CrudeSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.6067-0.6111 (DeLong)
```

```
ggplot(calibration(as.factor(!sepsis_outcome)~SOFA3CrudeSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of SOFA Positive w/o Baseline Sepsis Prediction")
```

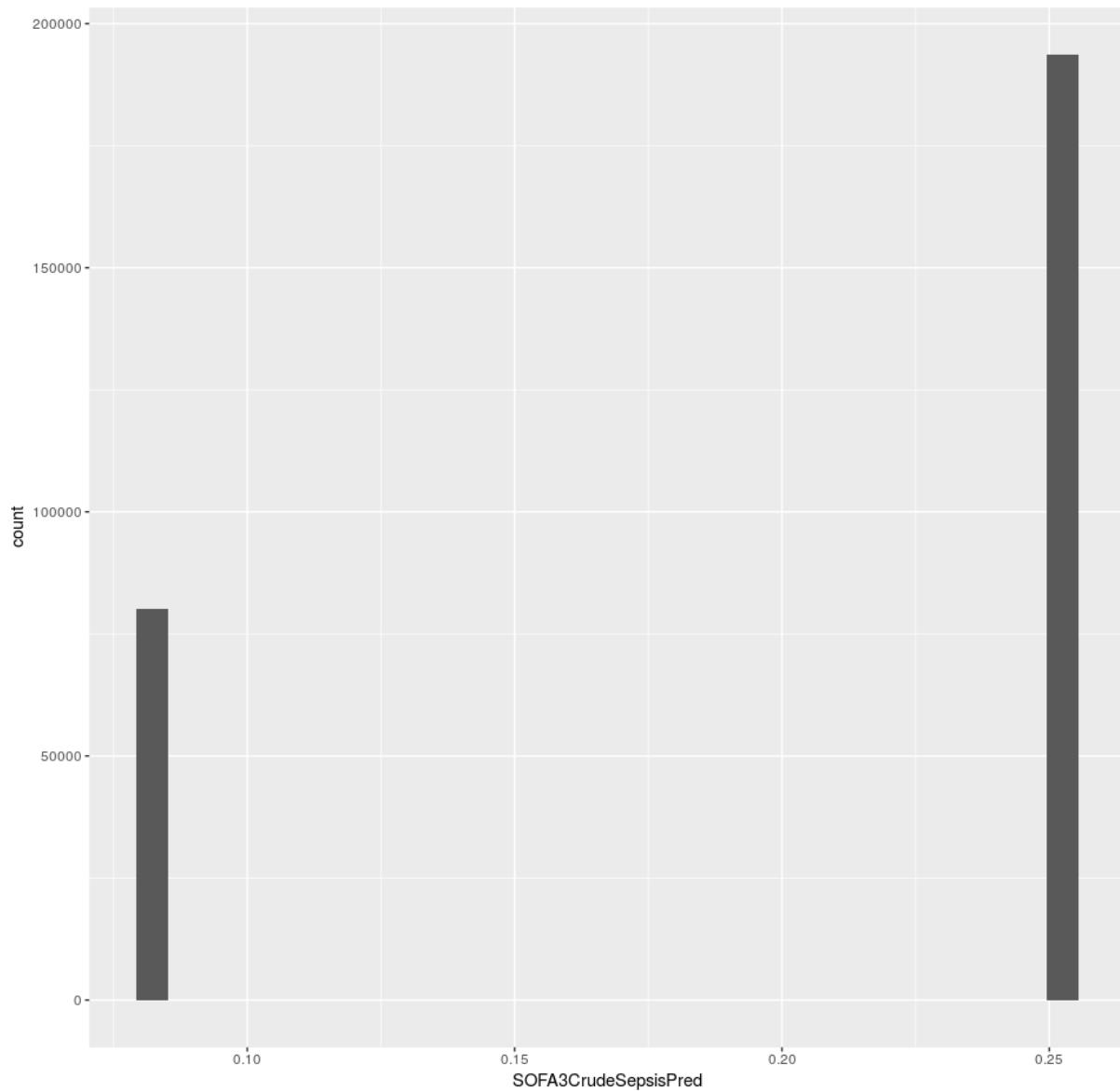
```
## Warning: Removed 9 rows containing missing values (geom_errorbar).
```

Calibration of SOFA Positive w/o Baseline Sepsis Prediction



```
qplot(SOFA3CrudeSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of SOFA Positive w/o Baseline Sepsis Predictions")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of SOFA Positive w/o Baseline Sepsis Predictions

```
FuzzyLogic_Crude_Sepsis_tr<-glm(sepsis_outcome ~ (SepsisFuzzyLogicPositive), data=ssd_incl_tr,family="binomial",na.action = na.omit)

#sjp.glm(FuzzyLogic_ADJ_Sepsis_tr)
#sjt.glm(FuzzyLogic_ADJ_Sepsis_tr)

#drop1(FuzzyLogic_ADJ_Sepsis_tr,test="Chisq")

summary(FuzzyLogic_ADJ_Sepsis_tr)
```

```

## 
## Call:
##   glm(formula = sepsis_outcome ~ (SepsisFuzzyLogicPositive) + age_Ranges +
##     gender2 + ethnicity2 + BMI_Ranges + icu_admit_source2 + hospital_teaching_status +
##     hospital_size + physicianSpeciality2 + hospitaldischargeyear +
##     dialysis + aids + hepaticfailure + diabetes + immunosuppression +
##     leukemia + lymphoma + metastaticcancer + thrombolytics +
##     sofa_respiration_baseline2 + cardiovascular_baseline, family = "binomial",
##     data = ssd_incl_tr, na.action = na.omit)
##
## Deviance Residuals:
##   Min      1Q  Median      3Q     Max
## -2.0787 -0.7206 -0.4234 -0.1814  3.6169
##
## Coefficients:
##                               Estimate Std. Error z value
## (Intercept)                -2.124152  0.033816 -62.815
## SepsisFuzzyLogicPositiveTRUE 1.494644  0.007929 188.497
## age_Ranges(25,35]            0.200047  0.027507  7.272
## age_Ranges(35,45]            0.380838  0.025582 14.887
## age_Ranges(45,55]            0.539099  0.023648 22.797
## age_Ranges(55,65]            0.710904  0.023120 30.748
## age_Ranges(65,75]            0.744332  0.023110 32.209
## age_Ranges(75,85]            0.822203  0.023233 35.390
## age_Ranges(85,100]           0.957012  0.024461 39.125
## gender2Female                0.036346  0.006828  5.323
## gender2Other/Unknown         -1.078963  0.267177 -4.038
## ethnicity2African American   -0.029079  0.011073 -2.626
## ethnicity2Hispanic            0.399012  0.015308 26.065
## ethnicity2Asian               0.110971  0.029812  3.722
## ethnicity2Native American    0.266320  0.037867  7.033
## ethnicity2Other/Unknown       0.046935  0.014927  3.144
## BMI_Ranges(18.5,25]          -0.220140  0.015229 -14.455
## BMI_Ranges(25,35]             -0.286701  0.014915 -19.222
## BMI_Ranges(35,200]            -0.114540  0.016172 -7.083
## BMI_RangesOther/Unknown       -0.465796  0.023828 -19.548
## icu_admit_source2OR/Proc Area -1.996615  0.014573 -137.012
## icu_admit_source2Direct Admit -0.459874  0.012939 -35.543
## icu_admit_source2Emergency Department -0.280337  0.008454 -33.161
## icu_admit_source2Other         -0.107824  0.033765 -3.193
## icu_admit_source2Step-Down Unit 0.055622  0.021391  2.600
## hospital_teaching_statusf    -0.240214  0.024886 -9.652
## hospital_teaching_statust    -0.207117  0.025137 -8.240
## hospital_size<100            0.621431  0.023826 26.082
## hospital_size100-249          0.311101  0.019367 16.063
## hospital_size250-500          0.262875  0.019696 13.346
## hospital_size>500             0.108788  0.018436  5.901
## physicianSpeciality2Speciality-Other -0.501852  0.007684 -65.313
## hospitaldischargeyear2011     0.092410  0.013172  7.016
## hospitaldischargeyear2012     -0.039503  0.012781 -3.091
## hospitaldischargeyear2013     -0.038688  0.012491 -3.097
## hospitaldischargeyear2014     -0.059266  0.012397 -4.781
## hospitaldischargeyear2015-16   -0.019868  0.012269 -1.619
## dialysis1                      0.270859  0.017788 15.227
## aids1                           1.331422  0.089546 14.869
## hepaticfailureTRUE              -0.029653  0.021485 -1.380
## diabetes1                       0.044792  0.008428  5.315
## immunosuppression1              0.526333  0.020537 25.628
## leukemial                        0.399091  0.034129 11.694
## lymphomai                         0.345324  0.046675  7.399
## metastaticcancer1                0.019801  0.024233  0.817
## thrombolytics1                  -2.110673  0.060512 -34.880
## sofa_respiration_baseline2TRUE   0.392935  0.007544  52.086
## cardiovascular_baseline1        -0.072916  0.008255 -8.833
## 
## Pr(>|z|)
## (Intercept) < 2e-16 ***
## SepsisFuzzyLogicPositiveTRUE < 2e-16 ***
## age_Ranges(25,35] 3.53e-13 ***
## age_Ranges(35,45] < 2e-16 ***
## age_Ranges(45,55] < 2e-16 ***
## age_Ranges(55,65] < 2e-16 ***
## age_Ranges(65,75] < 2e-16 ***
## age_Ranges(75,85] < 2e-16 ***
## age_Ranges(85,100] < 2e-16 ***
## gender2Female 1.02e-07 ***
## gender2Other/Unknown 5.38e-05 ***
## ethnicity2African American 0.008635 **
## ethnicity2Hispanic < 2e-16 ***

```

```

## ethnicity2Asian          0.000197 ***
## ethnicity2Native American 2.02e-12 ***
## ethnicity2Other/Unknown   0.001665 **
## BMI_Ranges(18.5,25]      < 2e-16 ***
## BMI_Ranges(25,35]        < 2e-16 ***
## BMI_Ranges(35,200]       1.41e-12 ***
## BMI_RangesOther/Unknown   < 2e-16 ***
## icu_admit_source2OR/Proc Area < 2e-16 ***
## icu_admit_source2Direct Admit < 2e-16 ***
## icu_admit_source2Emergency Department < 2e-16 ***
## icu_admit_source2Other     0.001406 **
## icu_admit_source2Step-Down Unit 0.009314 **
## hospital_teaching_statusf < 2e-16 ***
## hospital_teaching_statust < 2e-16 ***
## hospital_size<100        < 2e-16 ***
## hospital_size100-249      < 2e-16 ***
## hospital_size250-500      < 2e-16 ***
## hospital_size>500        3.61e-09 ***
## physicianSpeciality2Speciality-Other < 2e-16 ***
## hospitaldischargeyear2011 2.29e-12 ***
## hospitaldischargeyear2012 0.001996 **
## hospitaldischargeyear2013 0.001952 **
## hospitaldischargeyear2014 1.75e-06 ***
## hospitaldischargeyear2015-16 0.105359
## dialysis1                 < 2e-16 ***
## aids1                      < 2e-16 ***
## hepaticfailureTRUE         0.167532
## diabetes1                 1.07e-07 ***
## immunosuppression1        < 2e-16 ***
## leukemial                  < 2e-16 ***
## lymphoma1                  1.38e-13 ***
## metastaticcancer1         0.413868
## thrombolytics1            < 2e-16 ***
## sofa_respiration_baseline2TRUE < 2e-16 ***
## cardiovascular_baseline1  < 2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 647128 on 638756 degrees of freedom
## Residual deviance: 548492 on 638709 degrees of freedom
## AIC: 548588
##
## Number of Fisher Scoring iterations: 6

```

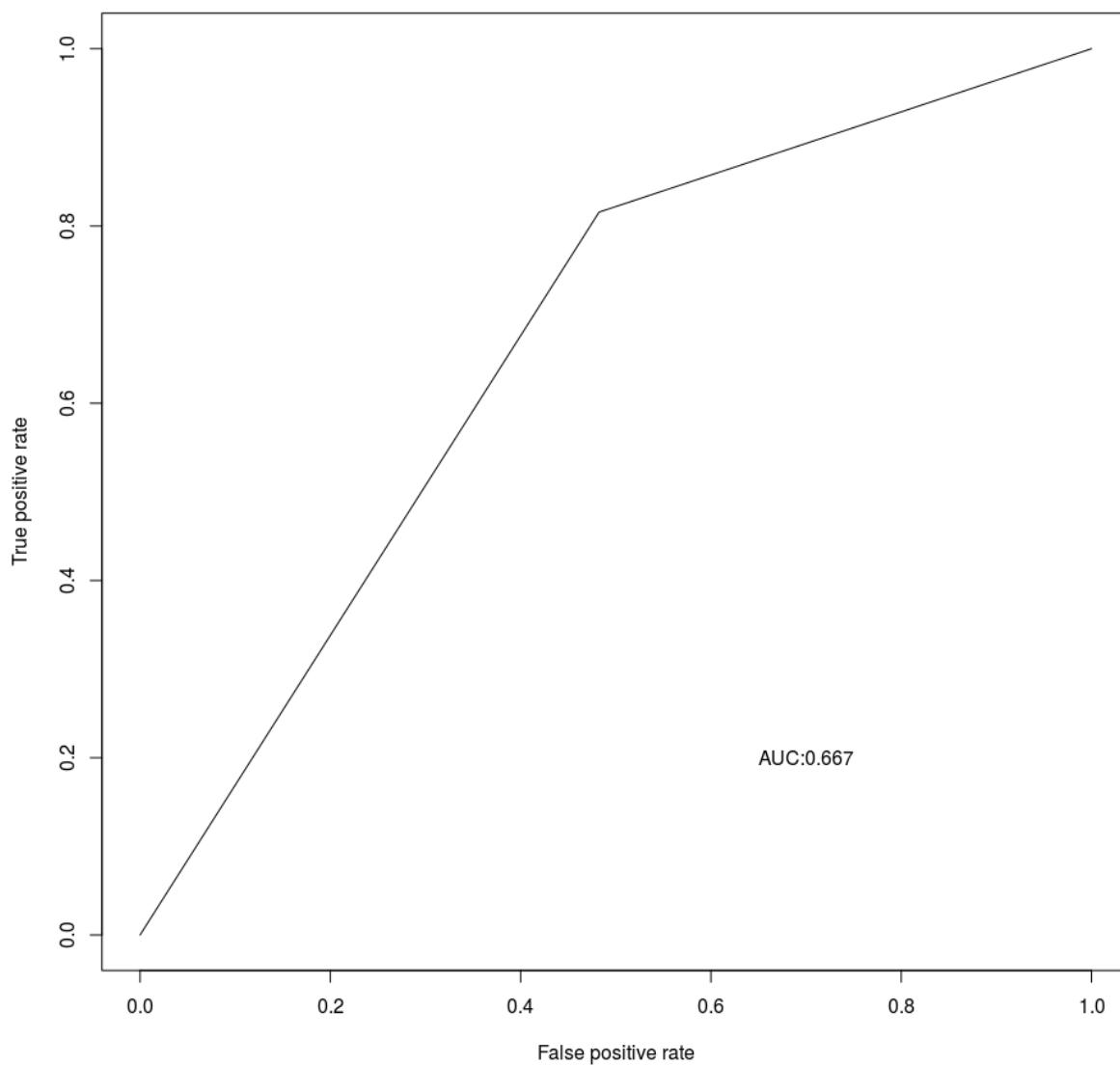
```

ssd_incl_te$FuzzyLogicCrudeSepsisPred <- predict(FuzzyLogic_Crude_Sepsis_tr,newdata=ssd_incl_te,na.action=na.pass,type="response")
library(sjPlot)
library(ROCR)

FuzzyLogicCrudeSepsis.Pred <- prediction(ssd_incl_te$FuzzyLogicCrudeSepsisPred, ssd_incl_te$sepsis_outcome)
FuzzyLogicCrudeSepsis.Perf <- performance(FuzzyLogicCrudeSepsis.Pred, "tpr", "fpr")
plot(FuzzyLogicCrudeSepsis.Perf, main = "FuzzyLogic Positive Crude Sepsis Prediction Test Model")
text(0.7,0.2,label=paste0("AUC:",round(performance(FuzzyLogicCrudeSepsis.Pred,"auc")@y.values[[1]],3)))

```

FuzzyLogic Positive Crude Sepsis Prediction Test Model



```
performance(FuzzyLogicCrudeSepsis.Pred, "auc")
```

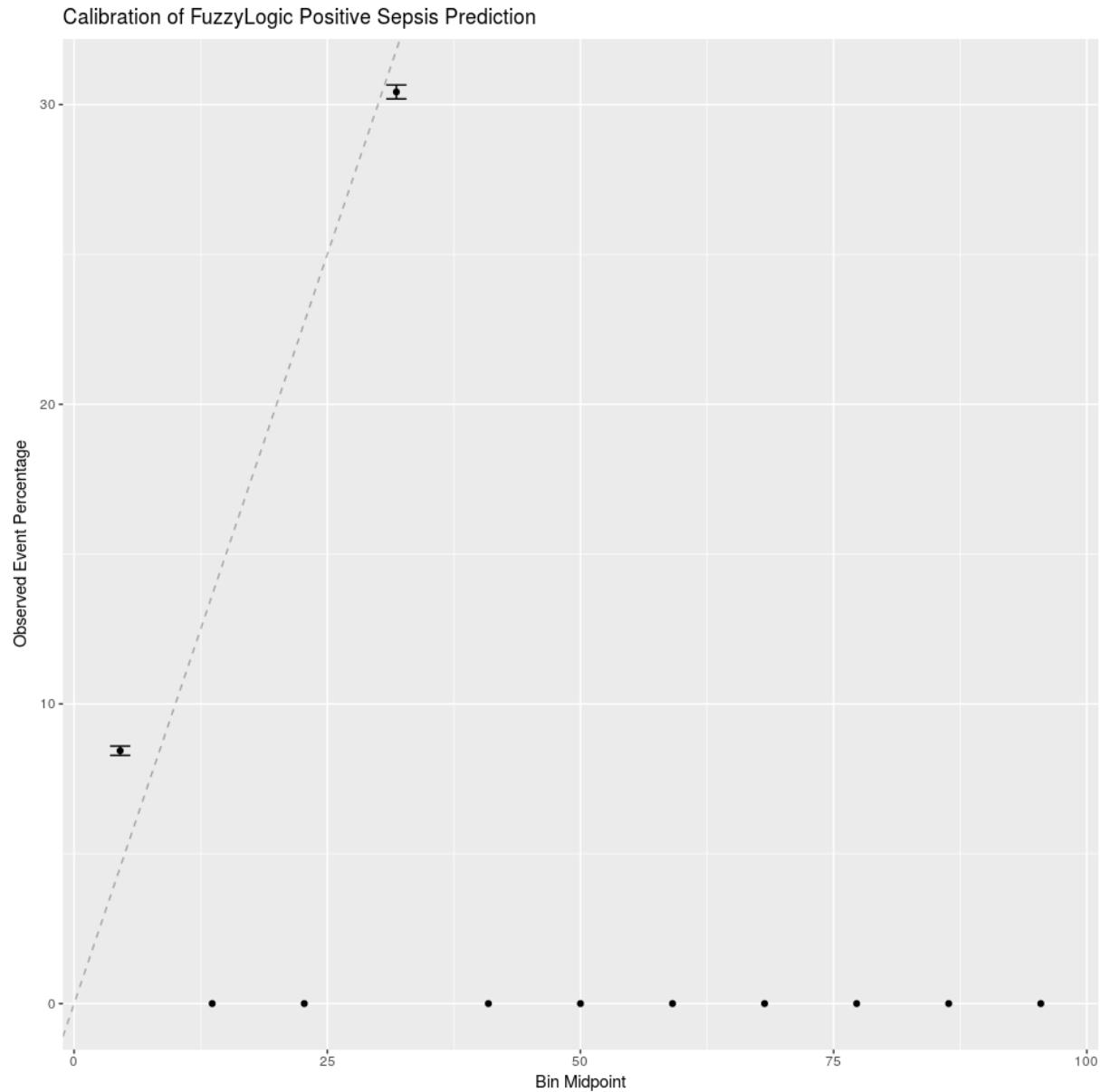
```
## An object of class "performance"
## Slot "x.name":
## [1] "None"
##
## Slot "y.name":
## [1] "Area under the ROC curve"
##
## Slot "alpha.name":
## [1] "none"
##
## Slot "x.values":
## list()
##
## Slot "y.values":
## [[1]]
## [1] 0.6665731
##
## Slot "alpha.values":
## list()
```

```
FuzzyLogicCrudeSepsis.Pred.roc <- roc(sepsis_outcome~FuzzyLogicCrudeSepsisPred,data=ssd_incl_te)
ci(FuzzyLogicCrudeSepsis.Pred.roc, conf.level=0.99)
```

```
## 99% CI: 0.6641-0.6691 (DeLong)

ggplot(calibration(as.factor(!sepsis_outcome)~FuzzyLogicCrudeSepsisPred, data = ssd_incl_te))+ggtitle("Calibration of FuzzyLogic Positive Sepsis Prediction")

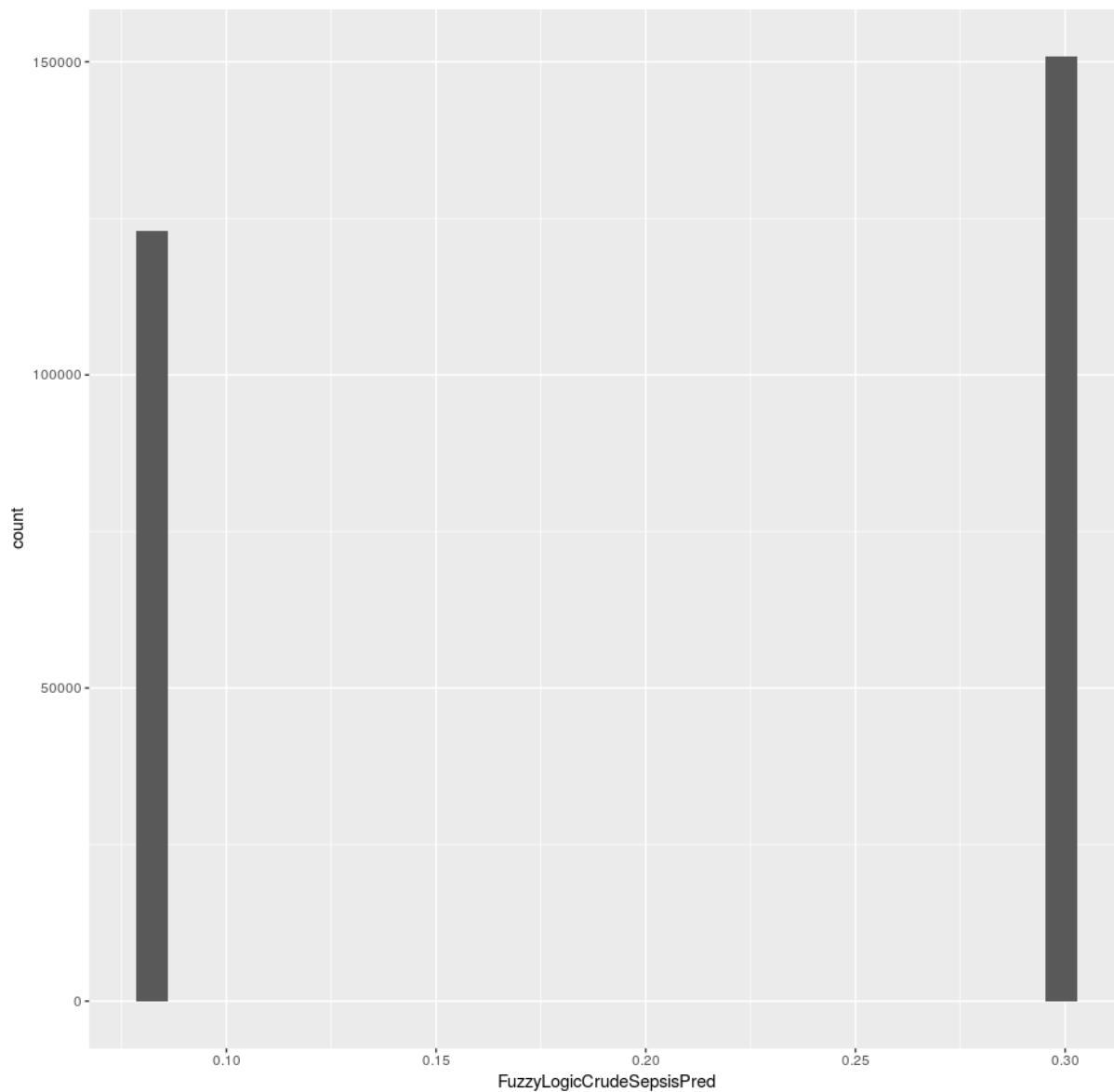
## Warning: Removed 9 rows containing missing values (geom_errorbar).
```



```
qplot(FuzzyLogicCrudeSepsisPred, data = ssd_incl_te)+ggtitle("Histogram of FuzzyLogic Positive Sepsis Predictions")

## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

Histogram of FuzzyLogic Positive Sepsis Predictions



23 Setting up variables to analyze interactions

```
ssd_incl_te <- ssd_incl_te %>% mutate(SIRS2TruthSepsis=interaction (SIRS_Positive,sepsis_outcome))
ssd_incl_te <- ssd_incl_te %>% mutate(qSOFA2TruthSepsis=interaction (qSOFA_Positive,sepsis_outcome))
ssd_incl_te <- ssd_incl_te %>% mutate(SOFA2TruthSepsis=interaction (SOFA_Positive,sepsis_outcome))
ssd_incl_te <- ssd_incl_te %>% mutate(FuzzyLogicTruthSepsis=interaction (SepsisFuzzyLogicPositive,sepsis_outcome))
```

```

vars5 <- c("age_Ranges", "gender2", "ethnicity2", "BMI_Ranges", "physicianSpeciality2", "icu_admit_source2", "icu_disch_location2", "hospitaldischargeyear", "dischargelocation", "dialysis", "aids", "hepaticfailure", "diabetes", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baseline2", "sofa_liver_baseline2", "sofa_renal_baseline2", "cardiovascular_baseline", "group" )

library(dplyr); library(Hmisc); library(ggplot2); #library(sjPlot)

if(!(tableone %in% rownames(installed.packages()))){
  install.packages("tableone")
}
library(dplyr); library(Hmisc); library(ggplot2); #library(sjPlot)
library(tableone)

CreateTableOne(data=ssd_incl_te ,vars=vars5,strata="SIRS2TruthSepsis",test=FALSE, includeNA=TRUE
) %>% print(nonnnormal= c("sofa_respiration_baseline", "sofa_liver_baseline", "sofa_renal_baseline"),minMax=TRUE,
printToggle      = FALSE,
showAllLevels   = TRUE,
cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="SIRS positive negative sepsis outcome")

```

SIRS positive negative sepsis outcome

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
n		59019	158477	6200	50056
age_Ranges (%)	(0,25]	1497 (2.5)	6467 (4.1)	50 (0.8)	1037 (2.1)
	(25,35]	2487 (4.2)	9392 (5.9)	150 (2.4)	2031 (4.1)
	(35,45]	3958 (6.7)	13094 (8.3)	246 (4.0)	3030 (6.1)
	(45,55]	8810 (14.9)	24376 (15.4)	803 (13.0)	6540 (13.1)
	(55,65]	12717 (21.5)	32813 (20.7)	1288 (20.8)	10286 (20.5)
	(65,75]	13662 (23.1)	33702 (21.3)	1517 (24.5)	11725 (23.4)
	(75,85]	11188 (19.0)	26913 (17.0)	1418 (22.9)	10103 (20.2)
	(85,100]	4700 (8.0)	11720 (7.4)	728 (11.7)	5304 (10.6)
gender2 (%)	Male	33335 (56.5)	85328 (53.8)	3126 (50.4)	25113 (50.2)
	Female	25670 (43.5)	73095 (46.1)	3074 (49.6)	24931 (49.8)
	Other/Unknown	14 (0.0)	54 (0.0)	0 (0.0)	12 (0.0)
ethnicity2 (%)	Caucasian	44895 (76.1)	121150 (76.4)	4622 (74.5)	38021 (76.0)
	African American	6653 (11.3)	18953 (12.0)	674 (10.9)	5449 (10.9)
	Hispanic	2668 (4.5)	6357 (4.0)	410 (6.6)	2850 (5.7)
	Asian	761 (1.3)	2024 (1.3)	84 (1.4)	664 (1.3)
	Native American	407 (0.7)	1151 (0.7)	53 (0.9)	401 (0.8)
	Other/Unknown	3635 (6.2)	8842 (5.6)	357 (5.8)	2671 (5.3)
BMI_Ranges (%)	(0,18.5]	2204 (3.7)	7542 (4.8)	331 (5.3)	3371 (6.7)
	(18.5,25]	15631 (26.5)	44539 (28.1)	1693 (27.3)	15012 (30.0)
	(25,35]	29041 (49.2)	72828 (46.0)	2588 (41.7)	20755 (41.5)
	(35,200]	9515 (16.1)	28123 (17.7)	1352 (21.8)	9467 (18.9)
	Other/Unknown	2628 (4.5)	5445 (3.4)	236 (3.8)	1451 (2.9)
physicianSpeciality2 (%)	Critical Care	11115 (18.8)	47303 (29.8)	2028 (32.7)	19849 (39.7)
	Speciality-Other	47904 (81.2)	111174 (70.2)	4172 (67.3)	30207 (60.3)
icu_admit_source2 (%)	Floor	7769 (13.2)	24660 (15.6)	1460 (23.5)	12545 (25.1)
	OR/Proc Area	11280 (19.1)	38657 (24.4)	279 (4.5)	2715 (5.4)
	Direct Admit	7535 (12.8)	16746 (10.6)	483 (7.8)	4707 (9.4)
	Emergency Department	31279 (53.0)	73813 (46.6)	3755 (60.6)	27827 (55.6)

Combined Code Near Final

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	Other	361 (0.6)	1361 (0.9)	55 (0.9)	583 (1.2)
	Step-Down Unit	795 (1.3)	3240 (2.0)	168 (2.7)	1679 (3.4)
icu_disch_location2 (%)	Floor	41911 (71.0)	117529 (74.2)	4876 (78.6)	35103 (70.1)
	Death	775 (1.3)	10088 (6.4)	309 (5.0)	7183 (14.3)
	Home	11221 (19.0)	13662 (8.6)	330 (5.3)	1470 (2.9)
	SNF/Rehab	653 (1.1)	1995 (1.3)	195 (3.1)	1415 (2.8)
	Other	1545 (2.6)	5027 (3.2)	197 (3.2)	2036 (4.1)
	Other Hospital	1223 (2.1)	3434 (2.2)	144 (2.3)	1355 (2.7)
	Step-Down Unit	1691 (2.9)	6742 (4.3)	149 (2.4)	1494 (3.0)
hospitaldischargeyear (%)	-2010	8182 (13.9)	18265 (11.5)	797 (12.9)	6104 (12.2)
	2011	8248 (14.0)	20448 (12.9)	938 (15.1)	7180 (14.3)
	2012	9659 (16.4)	26048 (16.4)	950 (15.3)	8153 (16.3)
	2013	10589 (17.9)	29524 (18.6)	1097 (17.7)	9052 (18.1)
	2014	11459 (19.4)	31504 (19.9)	1231 (19.9)	9357 (18.7)
	2015-16	10882 (18.4)	32688 (20.6)	1187 (19.1)	10210 (20.4)
dischargelocation (mean (sd))		5.23 (1.68)	5.30 (1.86)	5.01 (1.73)	5.43 (2.05)
dialysis (%)	0	57032 (96.6)	153514 (96.9)	5861 (94.5)	48087 (96.1)
	1	1987 (3.4)	4963 (3.1)	339 (5.5)	1969 (3.9)
aids (%)	0	58999 (100.0)	158392 (99.9)	6187 (99.8)	49911 (99.7)
	1	20 (0.0)	85 (0.1)	13 (0.2)	145 (0.3)
hepaticfailure (%)	FALSE	58024 (98.3)	155221 (97.9)	6031 (97.3)	48795 (97.5)
	TRUE	995 (1.7)	3256 (2.1)	169 (2.7)	1261 (2.5)
diabetes (%)	0	46071 (78.1)	123897 (78.2)	4557 (73.5)	39395 (78.7)
	1	12948 (21.9)	34580 (21.8)	1643 (26.5)	10661 (21.3)
immunosuppression (%)	0	58280 (98.7)	155067 (97.8)	6026 (97.2)	48013 (95.9)
	1	739 (1.3)	3410 (2.2)	174 (2.8)	2043 (4.1)
leukemia (%)	0	58808 (99.6)	157498 (99.4)	6156 (99.3)	49352 (98.6)
	1	211 (0.4)	979 (0.6)	44 (0.7)	704 (1.4)
lymphoma (%)	0	58868 (99.7)	157942 (99.7)	6177 (99.6)	49735 (99.4)
	1	151 (0.3)	535 (0.3)	23 (0.4)	321 (0.6)
metastaticcancer (%)	0	58219 (98.6)	155333 (98.0)	6102 (98.4)	48792 (97.5)
	1	800 (1.4)	3144 (2.0)	98 (1.6)	1264 (2.5)
thrombolytics (%)	0	57043 (96.7)	155581 (98.2)	6193 (99.9)	49967 (99.8)
	1	1976 (3.3)	2896 (1.8)	7 (0.1)	89 (0.2)
sofa_respiration_baseline2 (%)	FALSE	48496 (82.2)	122329 (77.2)	3953 (63.8)	33230 (66.4)
	TRUE	10523 (17.8)	36148 (22.8)	2247 (36.2)	16826 (33.6)
sofa_liver_baseline2 (%)	FALSE	58024 (98.3)	155221 (97.9)	6031 (97.3)	48795 (97.5)
	TRUE	995 (1.7)	3256 (2.1)	169 (2.7)	1261 (2.5)
sofa_renal_baseline2 (%)	FALSE	57032 (96.6)	153514 (96.9)	5861 (94.5)	48087 (96.1)
	TRUE	1987 (3.4)	4963 (3.1)	339 (5.5)	1969 (3.9)
cardiovascular_baseline (%)	0	44589 (75.6)	124723 (78.7)	4265 (68.8)	38284 (76.5)
	1	14430 (24.4)	33754 (21.3)	1935 (31.2)	11772 (23.5)
group (%)	Cardiovascular	26820 (45.4)	55465 (35.0)	830 (13.4)	5248 (10.5)
	Gastrointestinal	5558 (9.4)	19470 (12.3)	348 (5.6)	3168 (6.3)
	Gynaecological	103 (0.2)	579 (0.4)	2 (0.0)	31 (0.1)
	Hematological	396 (0.7)	1383 (0.9)	33 (0.5)	274 (0.5)

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	Metabolic	5526 (9.4)	15086 (9.5)	297 (4.8)	1552 (3.1)
	Muscoskeletal/Skin disease	649 (1.1)	2130 (1.3)	77 (1.2)	602 (1.2)
	Neurological	10203 (17.3)	23845 (15.0)	457 (7.4)	2332 (4.7)
	Renal/Genitourinary	1340 (2.3)	3749 (2.4)	231 (3.7)	1256 (2.5)
	Respiratory	4715 (8.0)	22238 (14.0)	1629 (26.3)	12276 (24.5)
	Sepsis	360 (0.6)	3890 (2.5)	2249 (36.3)	22838 (45.6)
	Trauma	2883 (4.9)	8928 (5.6)	28 (0.5)	286 (0.6)
	Undefined	466 (0.8)	1714 (1.1)	19 (0.3)	193 (0.4)

```
library(tidyr)
ssd_incl_te %>% group_by(hospitaldischargeyear, SIRS2TruthSepsis) %>% summarise(n=n()) %>% spread(SIRS2TruthSepsis, n) %
>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

hospitaldischargeyear	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
-2010	8182	18265	797	6104	0.8845095	0.3093735
2011	8248	20448	938	7180	0.8844543	0.2874268
2012	9659	26048	950	8153	0.8956388	0.2705072
2013	10589	29524	1097	9052	0.8919105	0.2639793
2014	11459	31504	1231	9357	0.8837363	0.2667179
2015-16	10882	32688	1187	10210	0.8958498	0.2497590

```
ssd_incl_te %>% group_by(hospitaldischargeyear, SIRS2TruthSepsis) %>% summarise(n=n()) %>% spread(SIRS2TruthSepsis, n) %
>% head()
```

```
## # A tibble: 6 x 5
## # Groups: hospitaldischargeyear [6]
##   hospitaldischargeyear FALSE.FALSE TRUE.FALSE FALSE.TRUE TRUE.TRUE
##   <chr>           <int>       <int>     <int>      <int>
## 1 -2010            8182       18265     797       6104
## 2 2011             8248       20448     938       7180
## 3 2012             9659       26048     950       8153
## 4 2013            10589      29524    1097      9052
## 5 2014            11459      31504    1231      9357
## 6 2015-16          10882      32688    1187     10210
```

```
ssd_incl_te %>% group_by(age_Ranges, SIRS2TruthSepsis) %>% summarise(n=n()) %>% spread(SIRS2TruthSepsis, n) %>% mutate(SEN
S=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

age_Ranges	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
(0,25]	1497	6467	50	1037	0.9540018	0.1879709
(25,35]	2487	9392	150	2031	0.9312242	0.2093611
(35,45]	3958	13094	246	3030	0.9249084	0.2321135
(45,55]	8810	24376	803	6540	0.8906442	0.2654734
(55,65]	12717	32813	1288	10286	0.8887161	0.2793103
(65,75]	13662	33702	1517	11725	0.8854403	0.2884469
(75,85]	11188	26913	1418	10103	0.8769204	0.2936406
(85,100]	4700	11720	728	5304	0.8793103	0.2862363

```
ssd_incl_te %>% group_by(BMI_Ranges, SIRS2TruthSepsis) %>% summarise(n=n()) %>% spread(SIRS2TruthSepsis, n) %>% mutate(SEN
S=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

BMI_Ranges	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
(0,18.5]	2204	7542	331	3371	0.9105889	0.2261441
(18.5,25]	15631	44539	1693	15012	0.8986531	0.2597806
(25,35]	29041	72828	2588	20755	0.8891316	0.2850818

BMI_Ranges	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
(35,200]	9515	28123	1352	9467	0.8750347	0.2528030
Other/Unknown	2628	5445	236	1451	0.8601067	0.3255295

```
ssd_incl_te %>% group_by(icu_admit_source2, SIRS2TruthSepsis) %>% summarise(n=n()) %>% spread(SIRS2TruthSepsis, n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

icu_admit_source2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Floor	7769	24660	1460	12545	0.8957515	0.2395695
OR/Proc Area	11280	38657	279	2715	0.9068136	0.2258846
Direct Admit	7535	16746	483	4707	0.9069364	0.3103249
Emergency Department	31279	73813	3755	27827	0.8811032	0.2976345
Other	361	1361	55	583	0.9137931	0.2096400
Step-Down Unit	795	3240	168	1679	0.9090417	0.1970260

```
ssd_incl_te %>% group_by(ethnicity2, SIRS2TruthSepsis) %>% summarise(n=n()) %>% spread(SIRS2TruthSepsis, n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

ethnicity2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Caucasian	44895	121150	4622	38021	0.8916118	0.2703785
African American	6653	18953	674	5449	0.8899232	0.2598219
Hispanic	2668	6357	410	2850	0.8742331	0.2956233
Asian	761	2024	84	664	0.8877005	0.2732496
Native American	407	1151	53	401	0.8832599	0.2612323
Other/Unknown	3635	8842	357	2671	0.8821004	0.2913361

```
ssd_incl_te %>% group_by(physicianSpeciality2, SIRS2TruthSepsis) %>% summarise(n=n()) %>% spread(SIRS2TruthSepsis, n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

physicianSpeciality2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Critical Care	11115	47303	2028	19849	0.9072999	0.1902667
Speciality-Other	47904	111174	4172	30207	0.8786468	0.3011353

```
vars5 <- c("age_Ranges", "gender2", "ethnicity2", "BMI_Ranges", "physicianSpeciality2", "icu_admit_source2", "icu_disch_location2", "hospitaldischargeyear", "dischargelocation", "dialysis", "aids", "hepatictfailure", "diabetes", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baseline2", "sofa_liver_baseline2", "sofa_renal_baseline2", "cardiovascular_baseline", "group" )
```

```
library(dplyr); library(Hmisc); library(ggplot2); #library(sjPlot)
library(tableone)

if(!("tableone" %in% rownames(installed.packages()))){
  install.packages("tableone")
}
library(dplyr); library(Hmisc); library(ggplot2); #library(sjPlot)
library(tableone)

CreateTableOne(data=ssd_incl_te ,vars=vars5,strata="qSOFA2TruthSepsis",test=FALSE, includeNA=TRUE
) %>% print(nonnormals= c("sofa_respiration_baseline", "sofa_liver_baseline", "sofa_renal_baseline"),minMax=TRUE,
  printToggle      = FALSE,
  showAllLevels   = TRUE,
  cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="qSOFA positive negative sepsis_outcome")
```

qSOFA positive negative sepsis_outcome

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
---------------	-------	-------------	------------	------------	-----------

Combined Code Near Final

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
n		79553	137943	10133	46123
age_Ranges (%)	(0,25]	3156 (4.0)	4808 (3.5)	247 (2.4)	840 (1.8)
	(25,35]	4835 (6.1)	7044 (5.1)	511 (5.0)	1670 (3.6)
	(35,45]	7038 (8.8)	10014 (7.3)	716 (7.1)	2560 (5.6)
	(45,55]	12932 (16.3)	20254 (14.7)	1460 (14.4)	5883 (12.8)
	(55,65]	17115 (21.5)	28415 (20.6)	2222 (21.9)	9352 (20.3)
	(65,75]	17013 (21.4)	30351 (22.0)	2375 (23.4)	10867 (23.6)
	(75,85]	12777 (16.1)	25324 (18.4)	1842 (18.2)	9679 (21.0)
	(85,100]	4687 (5.9)	11733 (8.5)	760 (7.5)	5272 (11.4)
gender2 (%)	Male	45645 (57.4)	73018 (52.9)	5252 (51.8)	22987 (49.8)
	Female	33886 (42.6)	64879 (47.0)	4880 (48.2)	23125 (50.1)
	Other/Unknown	22 (0.0)	46 (0.0)	1 (0.0)	11 (0.0)
ethnicity2 (%)	Caucasian	58577 (73.6)	107468 (77.9)	7447 (73.5)	35196 (76.3)
	African American	10487 (13.2)	15119 (11.0)	1199 (11.8)	4924 (10.7)
	Hispanic	3745 (4.7)	5280 (3.8)	682 (6.7)	2578 (5.6)
	Asian	959 (1.2)	1826 (1.3)	138 (1.4)	610 (1.3)
	Native American	562 (0.7)	996 (0.7)	73 (0.7)	381 (0.8)
	Other/Unknown	5223 (6.6)	7254 (5.3)	594 (5.9)	2434 (5.3)
BMI_Ranges (%)	(0,18.5]	2961 (3.7)	6785 (4.9)	542 (5.3)	3160 (6.9)
	(18.5,25]	20564 (25.8)	39606 (28.7)	2685 (26.5)	14020 (30.4)
	(25,35]	38762 (48.7)	63107 (45.7)	4337 (42.8)	19006 (41.2)
	(35,200]	14063 (17.7)	23575 (17.1)	2212 (21.8)	8607 (18.7)
	Other/Unknown	3203 (4.0)	4870 (3.5)	357 (3.5)	1330 (2.9)
physicianSpeciality2 (%)	Critical Care	16452 (20.7)	41966 (30.4)	3171 (31.3)	18706 (40.6)
	Speciality-Other	63101 (79.3)	95977 (69.6)	6962 (68.7)	27417 (59.4)
icu_admit_source2 (%)	Floor	10198 (12.8)	22231 (16.1)	2449 (24.2)	11556 (25.1)
	OR/Proc Area	17853 (22.4)	32084 (23.3)	626 (6.2)	2368 (5.1)
	Direct Admit	9294 (11.7)	14987 (10.9)	794 (7.8)	4396 (9.5)
	Emergency Department	40542 (51.0)	64550 (46.8)	5938 (58.6)	25644 (55.6)
	Other	518 (0.7)	1204 (0.9)	91 (0.9)	547 (1.2)
	Step-Down Unit	1148 (1.4)	2887 (2.1)	235 (2.3)	1612 (3.5)
icu_disch_location2 (%)	Floor	58038 (73.0)	101402 (73.5)	8150 (80.4)	31829 (69.0)
	Death	1085 (1.4)	9778 (7.1)	467 (4.6)	7025 (15.2)
	Home	13244 (16.6)	11639 (8.4)	531 (5.2)	1269 (2.8)
	SNF/Rehab	754 (0.9)	1894 (1.4)	198 (2.0)	1412 (3.1)
	Other	1972 (2.5)	4600 (3.3)	299 (3.0)	1934 (4.2)
	Other Hospital	1487 (1.9)	3170 (2.3)	248 (2.4)	1251 (2.7)
	Step-Down Unit	2973 (3.7)	5460 (4.0)	240 (2.4)	1403 (3.0)
hospitaldischargeyear (%)	-2010	11213 (14.1)	15234 (11.0)	1373 (13.5)	5528 (12.0)
	2011	10956 (13.8)	17740 (12.9)	1466 (14.5)	6652 (14.4)
	2012	12705 (16.0)	23002 (16.7)	1526 (15.1)	7577 (16.4)
	2013	14050 (17.7)	26063 (18.9)	1728 (17.1)	8421 (18.3)
	2014	15404 (19.4)	27559 (20.0)	2024 (20.0)	8564 (18.6)
	2015-16	15225 (19.1)	28345 (20.5)	2016 (19.9)	9381 (20.3)
dischargelocation (mean (sd))		5.15 (1.67)	5.35 (1.89)	4.91 (1.66)	5.49 (2.07)
dialysis (%)	0	76924 (96.7)	133622 (96.9)	9715 (95.9)	44233 (95.9)

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	1	2629 (3.3)	4321 (3.1)	418 (4.1)	1890 (4.1)
aids (%)	0	79514 (100.0)	137877 (100.0)	10100 (99.7)	45998 (99.7)
	1	39 (0.0)	66 (0.0)	33 (0.3)	125 (0.3)
hepaticfailure (%)	FALSE	78337 (98.5)	134908 (97.8)	9912 (97.8)	44914 (97.4)
	TRUE	1216 (1.5)	3035 (2.2)	221 (2.2)	1209 (2.6)
diabetes (%)	0	61305 (77.1)	108663 (78.8)	7670 (75.7)	36282 (78.7)
	1	18248 (22.9)	29280 (21.2)	2463 (24.3)	9841 (21.3)
immunosuppression (%)	0	78204 (98.3)	135143 (98.0)	9724 (96.0)	44315 (96.1)
	1	1349 (1.7)	2800 (2.0)	409 (4.0)	1808 (3.9)
leukemia (%)	0	79172 (99.5)	137134 (99.4)	10005 (98.7)	45503 (98.7)
	1	381 (0.5)	809 (0.6)	128 (1.3)	620 (1.3)
lymphoma (%)	0	79345 (99.7)	137465 (99.7)	10083 (99.5)	45829 (99.4)
	1	208 (0.3)	478 (0.3)	50 (0.5)	294 (0.6)
metastaticcancer (%)	0	78252 (98.4)	135300 (98.1)	9908 (97.8)	44986 (97.5)
	1	1301 (1.6)	2643 (1.9)	225 (2.2)	1137 (2.5)
thrombolytics (%)	0	77364 (97.2)	135260 (98.1)	10117 (99.8)	46043 (99.8)
	1	2189 (2.8)	2683 (1.9)	16 (0.2)	80 (0.2)
sofa_respiration_baseline2 (%)	FALSE	64499 (81.1)	106326 (77.1)	6459 (63.7)	30724 (66.6)
	TRUE	15054 (18.9)	31617 (22.9)	3674 (36.3)	15399 (33.4)
sofa_liver_baseline2 (%)	FALSE	78337 (98.5)	134908 (97.8)	9912 (97.8)	44914 (97.4)
	TRUE	1216 (1.5)	3035 (2.2)	221 (2.2)	1209 (2.6)
sofa_renal_baseline2 (%)	FALSE	76924 (96.7)	133622 (96.9)	9715 (95.9)	44233 (95.9)
	TRUE	2629 (3.3)	4321 (3.1)	418 (4.1)	1890 (4.1)
cardiovascular_baseline (%)	0	63290 (79.6)	106022 (76.9)	7729 (76.3)	34820 (75.5)
	1	16263 (20.4)	31921 (23.1)	2404 (23.7)	11303 (24.5)
group (%)	Cardiovascular	32493 (40.8)	49792 (36.1)	1221 (12.0)	4857 (10.5)
	Gastrointestinal	9231 (11.6)	15797 (11.5)	722 (7.1)	2794 (6.1)
	Gynaecological	270 (0.3)	412 (0.3)	6 (0.1)	27 (0.1)
	Hematological	736 (0.9)	1043 (0.8)	77 (0.8)	230 (0.5)
	Metabolic	7826 (9.8)	12786 (9.3)	435 (4.3)	1414 (3.1)
	Muscoskeletal/Skin disease	1066 (1.3)	1713 (1.2)	141 (1.4)	538 (1.2)
	Neurological	11556 (14.5)	22492 (16.3)	464 (4.6)	2325 (5.0)
	Renal/Genitourinary	1860 (2.3)	3229 (2.3)	336 (3.3)	1151 (2.5)
	Respiratory	8318 (10.5)	18635 (13.5)	2640 (26.1)	11265 (24.4)
	Sepsis	748 (0.9)	3502 (2.5)	3989 (39.4)	21098 (45.7)
	Trauma	4584 (5.8)	7227 (5.2)	58 (0.6)	256 (0.6)
	Undefined	865 (1.1)	1315 (1.0)	44 (0.4)	168 (0.4)

```
ssd_incl_te %>% group_by(hospitaldischargeyear,qSOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(qSOFA2TruthSepsis, n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr:::kable()
```

hospitaldischargeyear	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
-2010	11213	15234	1373	5528	0.8010433	0.4239800
2011	10956	17740	1466	6652	0.8194136	0.3817954
2012	12705	23002	1526	7577	0.8323630	0.3558126
2013	14050	26063	1728	8421	0.8297369	0.3502605
2014	15404	27559	2024	8564	0.8088402	0.3585411

hospitaldischargeyear	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
2015-16	15225	28345	2016	9381	0.8231113	0.3494377

```
ssd_incl_te %>% group_by(age_Ranges,qSOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(qSOFA2TruthSepsis,n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE),SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

age_Ranges	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
(0,25]	3156	4808	247	840	0.7727691	0.3962833
(25,35]	4835	7044	511	1670	0.7657038	0.4070208
(35,45]	7038	10014	716	2560	0.7814408	0.4127375
(45,55]	12932	20254	1460	5883	0.8011712	0.3896824
(55,65]	17115	28415	2222	9352	0.8080180	0.3759060
(65,75]	17013	30351	2375	10867	0.8206464	0.3591969
(75,85]	12777	25324	1842	9679	0.8401180	0.3353455
(85,100]	4687	11733	760	5272	0.8740053	0.2854446

```
ssd_incl_te %>% group_by(BMI_Ranges,qSOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(qSOFA2TruthSepsis,n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE),SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

BMI_Ranges	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
(0,18.5]	2961	6785	542	3160	0.8535927	0.3038170
(18.5,25]	20564	39606	2685	14020	0.8392697	0.3417650
(25,35]	38762	63107	4337	19006	0.8142055	0.3805083
(35,200]	14063	23575	2212	8607	0.7955449	0.3736383
Other/Unknown	3203	4870	357	1330	0.7883817	0.3967546

```
ssd_incl_te %>% group_by(icu_admit_source2,qSOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(qSOFA2TruthSepsis,n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE),SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

icu_admit_source2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Floor	10198	22231	2449	11556	0.8251339	0.3144716
OR/Proc Area	17853	32084	626	2368	0.7909152	0.3575105
Direct Admit	9294	14987	794	4396	0.8470135	0.3827684
Emergency Department	40542	64550	5938	25644	0.8119815	0.3857763
Other	518	1204	91	547	0.8573668	0.3008130
Step-Down Unit	1148	2887	235	1612	0.8727666	0.2845105

```
ssd_incl_te %>% group_by(ethnicity2,qSOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(qSOFA2TruthSepsis,n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE),SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

ethnicity2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Caucasian	58577	107468	7447	35196	0.8253641	0.3527779
African American	10487	15119	1199	4924	0.8041810	0.4095524
Hispanic	3745	5280	682	2578	0.7907975	0.4149584
Asian	959	1826	138	610	0.8155080	0.3443447
Native American	562	996	73	381	0.8392070	0.3607189
Other/Unknown	5223	7254	594	2434	0.8038309	0.4186102

```
ssd_incl_te %>% group_by(physicianSpeciality2,qSOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(qSOFA2TruthSepsis,n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE),SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

physicianSpeciality2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Critical Care	16452	41966	3171	18706	0.8550533	0.2816255

physicianSpeciality2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Speciality-Other	63101	95977	6962	27417	0.7974927	0.3966670

```

vars5 <- c("age_Ranges", "gender2", "ethnicity2", "BMI_Ranges", "physicianSpeciality2", "icu_admit_source2", "icu_disch_location2", "hospitaldischargeyear", "dischargelocation", "dialysis", "aids", "hepaticfailure", "diabetes", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baseline2", "sofa_liver_baseline2", "sofa_renal_baseline2", "cardiovascular_baseline", "group" )

library(dplyr); library(Hmisc); library(ggplot2); #library(sjPlot)

if(!(tableone %in% rownames(installed.packages()))){
  install.packages("tableone")
}
library(dplyr); library(Hmisc); library(ggplot2); #library(sjPlot)
library(tableone)

CreateTableOne(data=ssd_incl_te ,vars=vars5,strata="SOFA2TruthSepsis",test=FALSE, includeNA=TRUE
) %>% print(nonnormal= c("sofa_respiration_baseline", "sofa_liver_baseline", "sofa_renal_baseline"),minMax=TRUE,
printToggle      = FALSE,
showAllLevels   = TRUE,
cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="SOFA positive negative sepsis outcome")

```

SOFA positive negative sepsis outcome

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
n		77471	140025	7800	48456
age_Ranges (%)	(0,25]	3772 (4.9)	4192 (3.0)	262 (3.4)	825 (1.7)
	(25,35]	5346 (6.9)	6533 (4.7)	501 (6.4)	1680 (3.5)
	(35,45]	7772 (10.0)	9280 (6.6)	609 (7.8)	2667 (5.5)
	(45,55]	13955 (18.0)	19231 (13.7)	1226 (15.7)	6117 (12.6)
	(55,65]	16991 (21.9)	28539 (20.4)	1753 (22.5)	9821 (20.3)
	(65,75]	15326 (19.8)	32038 (22.9)	1762 (22.6)	11480 (23.7)
	(75,85]	10459 (13.5)	27642 (19.7)	1194 (15.3)	10327 (21.3)
	(85,100]	3850 (5.0)	12570 (9.0)	493 (6.3)	5539 (11.4)
gender2 (%)	Male	40185 (51.9)	78478 (56.0)	3557 (45.6)	24682 (50.9)
	Female	37275 (48.1)	61490 (43.9)	4241 (54.4)	23764 (49.0)
	Other/Unknown	11 (0.0)	57 (0.0)	2 (0.0)	10 (0.0)
ethnicity2 (%)	Caucasian	59028 (76.2)	107017 (76.4)	5981 (76.7)	36662 (75.7)
	African American	9154 (11.8)	16452 (11.7)	823 (10.6)	5300 (10.9)
	Hispanic	3263 (4.2)	5762 (4.1)	447 (5.7)	2813 (5.8)
	Asian	944 (1.2)	1841 (1.3)	95 (1.2)	653 (1.3)
	Native American	504 (0.7)	1054 (0.8)	50 (0.6)	404 (0.8)
	Other/Unknown	4578 (5.9)	7899 (5.6)	404 (5.2)	2624 (5.4)
BMI_Ranges (%)	(0,18.5]	3175 (4.1)	6571 (4.7)	566 (7.3)	3136 (6.5)
	(18.5,25]	20829 (26.9)	39341 (28.1)	2330 (29.9)	14375 (29.7)
	(25,35]	36732 (47.4)	65137 (46.5)	3094 (39.7)	20249 (41.8)
	(35,200]	13439 (17.3)	24199 (17.3)	1535 (19.7)	9284 (19.2)
	Other/Unknown	3296 (4.3)	4777 (3.4)	275 (3.5)	1412 (2.9)
physicianSpeciality2 (%)	Critical Care	14837 (19.2)	43581 (31.1)	2551 (32.7)	19326 (39.9)
	Speciality-Other	62634 (80.8)	96444 (68.9)	5249 (67.3)	29130 (60.1)
icu_admit_source2 (%)	Floor	9714 (12.5)	22715 (16.2)	1941 (24.9)	12064 (24.9)

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	OR/Proc Area	15485 (20.0)	34452 (24.6)	389 (5.0)	2605 (5.4)
	Direct Admit	9236 (11.9)	15045 (10.7)	492 (6.3)	4698 (9.7)
	Emergency Department	41469 (53.5)	63623 (45.4)	4696 (60.2)	26886 (55.5)
	Other	486 (0.6)	1236 (0.9)	84 (1.1)	554 (1.1)
	Step-Down Unit	1081 (1.4)	2954 (2.1)	198 (2.5)	1649 (3.4)
icu_disch_location2 (%)	Floor	56350 (72.7)	103090 (73.6)	6344 (81.3)	33635 (69.4)
	Death	572 (0.7)	10291 (7.3)	258 (3.3)	7234 (14.9)
	Home	14248 (18.4)	10635 (7.6)	453 (5.8)	1347 (2.8)
	SNF/Rehab	557 (0.7)	2091 (1.5)	126 (1.6)	1484 (3.1)
	Other	1944 (2.5)	4628 (3.3)	259 (3.3)	1974 (4.1)
	Other Hospital	1459 (1.9)	3198 (2.3)	170 (2.2)	1329 (2.7)
	Step-Down Unit	2341 (3.0)	6092 (4.4)	190 (2.4)	1453 (3.0)
hospitaldischargeyear (%)	-2010	9187 (11.9)	17260 (12.3)	794 (10.2)	6107 (12.6)
	2011	9895 (12.8)	18801 (13.4)	1004 (12.9)	7114 (14.7)
	2012	12512 (16.2)	23195 (16.6)	1199 (15.4)	7904 (16.3)
	2013	14808 (19.1)	25305 (18.1)	1453 (18.6)	8696 (17.9)
	2014	15818 (20.4)	27145 (19.4)	1636 (21.0)	8952 (18.5)
	2015-16	15251 (19.7)	28319 (20.2)	1714 (22.0)	9683 (20.0)
dischargelocation (mean (sd))		5.23 (1.68)	5.31 (1.89)	4.89 (1.64)	5.46 (2.06)
dialysis (%)	0	74624 (96.3)	135922 (97.1)	7395 (94.8)	46553 (96.1)
	1	2847 (3.7)	4103 (2.9)	405 (5.2)	1903 (3.9)
aids (%)	0	77438 (100.0)	139953 (99.9)	7775 (99.7)	48323 (99.7)
	1	33 (0.0)	72 (0.1)	25 (0.3)	133 (0.3)
hepaticfailure (%)	FALSE	76815 (99.2)	136430 (97.4)	7727 (99.1)	47099 (97.2)
	TRUE	656 (0.8)	3595 (2.6)	73 (0.9)	1357 (2.8)
diabetes (%)	0	61213 (79.0)	108755 (77.7)	6161 (79.0)	37791 (78.0)
	1	16258 (21.0)	31270 (22.3)	1639 (21.0)	10665 (22.0)
immunosuppression (%)	0	76228 (98.4)	137119 (97.9)	7500 (96.2)	46539 (96.0)
	1	1243 (1.6)	2906 (2.1)	300 (3.8)	1917 (4.0)
leukemia (%)	0	77222 (99.7)	139084 (99.3)	7746 (99.3)	47762 (98.6)
	1	249 (0.3)	941 (0.7)	54 (0.7)	694 (1.4)
lymphoma (%)	0	77301 (99.8)	139509 (99.6)	7770 (99.6)	48142 (99.4)
	1	170 (0.2)	516 (0.4)	30 (0.4)	314 (0.6)
metastaticcancer (%)	0	76182 (98.3)	137370 (98.1)	7638 (97.9)	47256 (97.5)
	1	1289 (1.7)	2655 (1.9)	162 (2.1)	1200 (2.5)
thrombolytics (%)	0	74789 (96.5)	137835 (98.4)	7793 (99.9)	48367 (99.8)
	1	2682 (3.5)	2190 (1.6)	7 (0.1)	89 (0.2)
sofa_respiration_baseline2 (%)	FALSE	61018 (78.8)	109807 (78.4)	4142 (53.1)	33041 (68.2)
	TRUE	16453 (21.2)	30218 (21.6)	3658 (46.9)	15415 (31.8)
sofa_liver_baseline2 (%)	FALSE	76815 (99.2)	136430 (97.4)	7727 (99.1)	47099 (97.2)
	TRUE	656 (0.8)	3595 (2.6)	73 (0.9)	1357 (2.8)
sofa_renal_baseline2 (%)	FALSE	74624 (96.3)	135922 (97.1)	7395 (94.8)	46553 (96.1)
	TRUE	2847 (3.7)	4103 (2.9)	405 (5.2)	1903 (3.9)
cardiovascular_baseline (%)	0	63736 (82.3)	105576 (75.4)	6152 (78.9)	36397 (75.1)
	1	13735 (17.7)	34449 (24.6)	1648 (21.1)	12059 (24.9)
group (%)	Cardiovascular	30306 (39.1)	51979 (37.1)	817 (10.5)	5261 (10.9)

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	Gastrointestinal	7801 (10.1)	17227 (12.3)	407 (5.2)	3109 (6.4)
	Gynaecological	261 (0.3)	421 (0.3)	5 (0.1)	28 (0.1)
	Hematological	455 (0.6)	1324 (0.9)	33 (0.4)	274 (0.6)
	Metabolic	8310 (10.7)	12302 (8.8)	274 (3.5)	1575 (3.3)
	Muscoskeletal/Skin disease	1086 (1.4)	1693 (1.2)	127 (1.6)	552 (1.1)
	Neurological	12518 (16.2)	21530 (15.4)	292 (3.7)	2497 (5.2)
	Renal/Genitourinary	886 (1.1)	4203 (3.0)	109 (1.4)	1378 (2.8)
	Respiratory	9883 (12.8)	17070 (12.2)	2882 (36.9)	11023 (22.7)
	Sepsis	787 (1.0)	3463 (2.5)	2783 (35.7)	22304 (46.0)
	Trauma	4145 (5.4)	7666 (5.5)	31 (0.4)	283 (0.6)
	Undefined	1033 (1.3)	1147 (0.8)	40 (0.5)	172 (0.4)

```
library(tidyr)

ssd_incl_te %>% group_by(hospitaldischargeyear, SOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(SOFA2TruthSepsis, n) %>%
  mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

hospitaldischargeyear	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
-2010	9187	17260	794	6107	0.8849442	0.3473740
2011	9895	18801	1004	7114	0.8763242	0.3448216
2012	12512	23195	1199	7904	0.8682852	0.3504075
2013	14808	25305	1453	8696	0.8568332	0.3691571
2014	15818	27145	1636	8952	0.8454855	0.3681773
2015-16	15251	28319	1714	9683	0.8496095	0.3500344

```
ssd_incl_te %>% group_by(age_Ranges, SOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(SOFA2TruthSepsis, n) %>%
  mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

age_Ranges	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
(0,25]	3772	4192	262	825	0.7589696	0.4736313
(25,35]	5346	6533	501	1680	0.7702889	0.4500379
(35,45]	7772	9280	609	2667	0.8141026	0.4557823
(45,55]	13955	19231	1226	6117	0.8330383	0.4205086
(55,65]	16991	28539	1753	9821	0.8485398	0.3731825
(65,75]	15326	32038	1762	11480	0.8669385	0.3235791
(75,85]	10459	27642	1194	10327	0.8963632	0.2745072
(85,100]	3850	12570	493	5539	0.9182692	0.2344702

```
ssd_incl_te %>% group_by(BMI_Ranges, SOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(SOFA2TruthSepsis, n) %>%
  mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

BMI_Ranges	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
(0,18.5]	3175	6571	566	3136	0.8471097	0.3257747
(18.5,25]	20829	39341	2330	14375	0.8605208	0.3461692
(25,35]	36732	65137	3094	20249	0.8674549	0.3605807
(35,200]	13439	24199	1535	9284	0.8581200	0.3570594
Other/Unknown	3296	4777	275	1412	0.8369887	0.4082745

```
ssd_incl_te %>% group_by(icu_admit_source2, SOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(SOFA2TruthSepsis, n) %>%
  mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

icu_admit_source2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Floor	9714	22715	1941	12064	0.8614066	0.2995467
OR/Proc Area	15485	34452	389	2605	0.8700735	0.3100907
Direct Admit	9236	15045	492	4698	0.9052023	0.3803797
Emergency Department	41469	63623	4696	26886	0.8513077	0.3945971
Other	486	1236	84	554	0.8683386	0.2822300
Step-Down Unit	1081	2954	198	1649	0.8927991	0.2679058

```
ssd_incl_te %>% group_by(ethnicity2, SOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(SOFA2TruthSepsis, n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

ethnicity2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Caucasian	59028	107017	5981	36662	0.8597425	0.3554940
African American	9154	16452	823	5300	0.8655888	0.3574943
Hispanic	3263	5762	447	2813	0.8628834	0.3615512
Asian	944	1841	95	653	0.8729947	0.3389587
Native American	504	1054	50	404	0.8898678	0.3234917
Other/Unknown	4578	7899	404	2624	0.8665786	0.3669151

```
ssd_incl_te %>% group_by(physicianSpeciality2, SOFA2TruthSepsis) %>% summarise(n=n()) %>% spread(SOFA2TruthSepsis, n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr::kable()
```

physicianSpeciality2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Critical Care	14837	43581	2551	19326	0.8833935	0.2539799
Specialty-Other	62634	96444	5249	29130	0.8473196	0.3937314

```
vars5 <- c("age_Ranges", "gender2", "ethnicity2", "BMI_Ranges", "physicianSpeciality2", "icu_admit_source2", "icu_disch_location2", "hospitaldischargeyear", "dischargelocation", "dialysis", "aids", "hepaticfailure", "diabetess", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baseline2", "sofa_liver_baseline2", "sofa_renal_baseline2", "cardiovascular_baseline", "group" )

library(dplyr); library(Hmisc); library(ggplot2); #library(sjPlot)

if(!( "tableone" %in% rownames(installed.packages()))){
  install.packages("tableone")
}
library(dplyr); library(Hmisc); library(ggplot2); #library(sjPlot)
library(tableone)

CreateTableOne(data=ssd_incl_te ,vars=vars5,strata="FuzzyLogicTruthSepsis",test=FALSE, includeNA=TRUE
) %>% print(nonnormal= c("sofa_respiration_baseline", "sofa_liver_baseline", "sofa_renal_baseline"),minMax=TRUE,
  printToggle      = FALSE,
  showAllLevels   = TRUE,
  cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="FuzzyLogic positive negative sepsis outcome")
```

FuzzyLogic positive negative sepsis outcome

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
n		112558	104938	10372	45884
age_Ranges (%)	(0,25]	3831 (3.4)	4133 (3.9)	192 (1.9)	895 (2.0)
	(25,35]	6258 (5.6)	5621 (5.4)	407 (3.9)	1774 (3.9)
	(35,45]	9317 (8.3)	7735 (7.4)	622 (6.0)	2654 (5.8)
	(45,55]	17833 (15.8)	15353 (14.6)	1381 (13.3)	5962 (13.0)
	(55,65]	23682 (21.0)	21848 (20.8)	2171 (20.9)	9403 (20.5)

Combined Code Near Final

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	(65,75]	24038 (21.4)	23326 (22.2)	2475 (23.9)	10767 (23.5)
	(75,85]	19205 (17.1)	18896 (18.0)	2085 (20.1)	9436 (20.6)
	(85,100]	8394 (7.5)	8026 (7.6)	1039 (10.0)	4993 (10.9)
gender2 (%)	Male	62445 (55.5)	56218 (53.6)	5331 (51.4)	22908 (49.9)
	Female	50090 (44.5)	48675 (46.4)	5038 (48.6)	22967 (50.1)
	Other/Unknown	23 (0.0)	45 (0.0)	3 (0.0)	9 (0.0)
ethnicity2 (%)	Caucasian	84661 (75.2)	81384 (77.6)	7718 (74.4)	34925 (76.1)
	African American	14257 (12.7)	11349 (10.8)	1321 (12.7)	4802 (10.5)
	Hispanic	4791 (4.3)	4234 (4.0)	608 (5.9)	2652 (5.8)
	Asian	1526 (1.4)	1259 (1.2)	117 (1.1)	631 (1.4)
	Native American	805 (0.7)	753 (0.7)	79 (0.8)	375 (0.8)
	Other/Unknown	6518 (5.8)	5959 (5.7)	529 (5.1)	2499 (5.4)
BMI_Ranges (%)	(0,18.5]	4542 (4.0)	5204 (5.0)	593 (5.7)	3109 (6.8)
	(18.5,25]	30572 (27.2)	29598 (28.2)	2894 (27.9)	13811 (30.1)
	(25,35]	53815 (47.8)	48054 (45.8)	4301 (41.5)	19042 (41.5)
	(35,200]	18893 (16.8)	18745 (17.9)	2195 (21.2)	8624 (18.8)
	Other/Unknown	4736 (4.2)	3337 (3.2)	389 (3.8)	1298 (2.8)
physicianSpeciality2 (%)	Critical Care	23765 (21.1)	34653 (33.0)	3459 (33.3)	18418 (40.1)
	Speciality-Other	88793 (78.9)	70285 (67.0)	6913 (66.7)	27466 (59.9)
icu_admit_source2 (%)	Floor	15639 (13.9)	16790 (16.0)	2919 (28.1)	11086 (24.2)
	OR/Proc Area	22390 (19.9)	27547 (26.3)	589 (5.7)	2405 (5.2)
	Direct Admit	14914 (13.3)	9367 (8.9)	1063 (10.2)	4127 (9.0)
	Emergency Department	56909 (50.6)	48183 (45.9)	5225 (50.4)	26357 (57.4)
	Other	862 (0.8)	860 (0.8)	156 (1.5)	482 (1.1)
	Step-Down Unit	1844 (1.6)	2191 (2.1)	420 (4.0)	1427 (3.1)
icu_disch_location2 (%)	Floor	82010 (72.9)	77430 (73.8)	8231 (79.4)	31748 (69.2)
	Death	1594 (1.4)	9269 (8.8)	389 (3.8)	7103 (15.5)
	Home	18696 (16.6)	6187 (5.9)	536 (5.2)	1264 (2.8)
	SNF/Rehab	1207 (1.1)	1441 (1.4)	269 (2.6)	1341 (2.9)
	Other	3233 (2.9)	3339 (3.2)	361 (3.5)	1872 (4.1)
	Other Hospital	2217 (2.0)	2440 (2.3)	249 (2.4)	1250 (2.7)
	Step-Down Unit	3601 (3.2)	4832 (4.6)	337 (3.2)	1306 (2.8)
hospitaldischargeyear (%)	-2010	13636 (12.1)	12811 (12.2)	1155 (11.1)	5746 (12.5)
	2011	14634 (13.0)	14062 (13.4)	1365 (13.2)	6753 (14.7)
	2012	18350 (16.3)	17357 (16.5)	1581 (15.2)	7522 (16.4)
	2013	20936 (18.6)	19177 (18.3)	1906 (18.4)	8243 (18.0)
	2014	22558 (20.0)	20405 (19.4)	2090 (20.2)	8498 (18.5)
	2015-16	22444 (19.9)	21126 (20.1)	2275 (21.9)	9122 (19.9)
dischargelocation (mean (sd))		5.22 (1.70)	5.34 (1.93)	4.99 (1.70)	5.47 (2.07)
dialysis (%)	0	108683 (96.6)	101863 (97.1)	9843 (94.9)	44105 (96.1)
	1	3875 (3.4)	3075 (2.9)	529 (5.1)	1779 (3.9)
aids (%)	0	112497 (99.9)	104894 (100.0)	10332 (99.6)	45766 (99.7)
	1	61 (0.1)	44 (0.0)	40 (0.4)	118 (0.3)
hepaticfailure (%)	FALSE	111225 (98.8)	102020 (97.2)	10184 (98.2)	44642 (97.3)
	TRUE	1333 (1.2)	2918 (2.8)	188 (1.8)	1242 (2.7)
diabetes (%)	0	85076 (75.6)	84892 (80.9)	7122 (68.7)	36830 (80.3)

Combined Code Near Final

variable_name	level	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE
	1	27482 (24.4)	20046 (19.1)	3250 (31.3)	9054 (19.7)
immunosuppression (%)	0	110806 (98.4)	102541 (97.7)	9998 (96.4)	44041 (96.0)
	1	1752 (1.6)	2397 (2.3)	374 (3.6)	1843 (4.0)
leukemia (%)	0	112074 (99.6)	104232 (99.3)	10244 (98.8)	45264 (98.6)
	1	484 (0.4)	706 (0.7)	128 (1.2)	620 (1.4)
lymphoma (%)	0	112246 (99.7)	104564 (99.6)	10321 (99.5)	45591 (99.4)
	1	312 (0.3)	374 (0.4)	51 (0.5)	293 (0.6)
metastaticcancer (%)	0	110816 (98.5)	102736 (97.9)	10162 (98.0)	44732 (97.5)
	1	1742 (1.5)	2202 (2.1)	210 (2.0)	1152 (2.5)
thrombolytics (%)	0	109282 (97.1)	103342 (98.5)	10356 (99.8)	45804 (99.8)
	1	3276 (2.9)	1596 (1.5)	16 (0.2)	80 (0.2)
sofa_respiration_baseline2 (%)	FALSE	91478 (81.3)	79347 (75.6)	6619 (63.8)	30564 (66.6)
	TRUE	21080 (18.7)	25591 (24.4)	3753 (36.2)	15320 (33.4)
sofa_liver_baseline2 (%)	FALSE	111225 (98.8)	102020 (97.2)	10184 (98.2)	44642 (97.3)
	TRUE	1333 (1.2)	2918 (2.8)	188 (1.8)	1242 (2.7)
sofa_renal_baseline2 (%)	FALSE	108683 (96.6)	101863 (97.1)	9843 (94.9)	44105 (96.1)
	TRUE	3875 (3.4)	3075 (2.9)	529 (5.1)	1779 (3.9)
cardiovascular_baseline (%)	0	88247 (78.4)	81065 (77.3)	7585 (73.1)	34964 (76.2)
	1	24311 (21.6)	23873 (22.7)	2787 (26.9)	10920 (23.8)
group (%)	Cardiovascular	45657 (40.6)	36628 (34.9)	1376 (13.3)	4702 (10.2)
	Gastrointestinal	10269 (9.1)	14759 (14.1)	576 (5.6)	2940 (6.4)
	Gynaecological	241 (0.2)	441 (0.4)	7 (0.1)	26 (0.1)
	Hematological	810 (0.7)	969 (0.9)	64 (0.6)	243 (0.5)
	Metabolic	10717 (9.5)	9895 (9.4)	429 (4.1)	1420 (3.1)
	Muscoskeletal/Skin disease	1404 (1.2)	1375 (1.3)	150 (1.4)	529 (1.2)
	Neurological	22038 (19.6)	12010 (11.4)	796 (7.7)	1993 (4.3)
	Renal/Genitourinary	2428 (2.2)	2661 (2.5)	363 (3.5)	1124 (2.4)
	Respiratory	11009 (9.8)	15944 (15.2)	3127 (30.1)	10778 (23.5)
	Sepsis	949 (0.8)	3301 (3.1)	3370 (32.5)	21717 (47.3)
	Trauma	5862 (5.2)	5949 (5.7)	63 (0.6)	251 (0.5)
	Undefined	1174 (1.0)	1006 (1.0)	51 (0.5)	161 (0.4)

```
library(tidyverse)
ssd_incl_te %>% group_by(hospitaldischargeyear,FuzzyLogicTruthSepsis) %>% summarise(n=n()) %>% spread(FuzzyLogicTruthSepsis,n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE),SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr:::kable()
```

hospitaldischargeyear	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
-2010	13636	12811	1155	5746	0.8326330	0.5155972
2011	14634	14062	1365	6753	0.8318551	0.5099665
2012	18350	17357	1581	7522	0.8263210	0.5139048
2013	20936	19177	1906	8243	0.8121982	0.5219256
2014	22558	20405	2090	8498	0.8026067	0.5250564
2015-16	22444	21126	2275	9122	0.8003861	0.5151251

```
ssd_incl_te %>% group_by(age_Ranges,FuzzyLogicTruthSepsis) %>% summarise(n=n()) %>% spread(FuzzyLogicTruthSepsis,n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE),SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr:::kable()
```

age_Ranges	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
(0,25]	3831	4133	192	895	0.8233671	0.4810397
(25,35]	6258	5621	407	1774	0.8133884	0.5268120
(35,45]	9317	7735	622	2654	0.8101343	0.5463875
(45,55]	17833	15353	1381	5962	0.8119297	0.5373652
(55,65]	23682	21848	2171	9403	0.8124244	0.5201406
(65,75]	24038	23326	2475	10767	0.8130947	0.5075163
(75,85]	19205	18896	2085	9436	0.8190261	0.5040550
(85,100]	8394	8026	1039	4993	0.8277520	0.5112058

```
ssd_incl_te %>% group_by(BMI_Ranges, FuzzyLogicTruthSepsis) %>% summarise(n=n()) %>% spread(FuzzyLogicTruthSepsis, n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr:::kable()
```

BMI_Ranges	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
(0,18.5]	4542	5204	593	3109	0.8398163	0.4660373
(18.5,25]	30572	29598	2894	13811	0.8267585	0.5080937
(25,35]	53815	48054	4301	19042	0.8157478	0.5282765
(35,200]	18893	18745	2195	8624	0.7971162	0.5019661
Other/Unknown	4736	3337	389	1298	0.7694132	0.5866468

```
ssd_incl_te %>% group_by(icu_admit_source2, FuzzyLogicTruthSepsis) %>% summarise(n=n()) %>% spread(FuzzyLogicTruthSepsis, n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr:::kable()
```

icu_admit_source2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Floor	15639	16790	2919	11086	0.7915744	0.4822535
OR/Proc Area	22390	27547	589	2405	0.8032732	0.4483649
Direct Admit	14914	9367	1063	4127	0.7951830	0.6142251
Emergency Department	56909	48183	5225	26357	0.8345577	0.5415160
Other	862	860	156	482	0.7554859	0.5005807
Step-Down Unit	1844	2191	420	1427	0.7726042	0.4570012

```
ssd_incl_te %>% group_by(ethnicity2, FuzzyLogicTruthSepsis) %>% summarise(n=n()) %>% spread(FuzzyLogicTruthSepsis, n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr:::kable()
```

ethnicity2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Caucasian	84661	81384	7718	34925	0.8190090	0.5098678
African American	14257	11349	1321	4802	0.7842561	0.5567836
Hispanic	4791	4234	608	2652	0.8134969	0.5308587
Asian	1526	1259	117	631	0.8435829	0.5479354
Native American	805	753	79	375	0.8259912	0.5166881
Other/Unknown	6518	5959	529	2499	0.8252972	0.5224012

```
ssd_incl_te %>% group_by(physicianSpeciality2, FuzzyLogicTruthSepsis) %>% summarise(n=n()) %>% spread(FuzzyLogicTruthSepsis, n) %>% mutate(SENS=TRUE.TRUE/(TRUE.TRUE+FALSE.TRUE), SPEC=FALSE.FALSE/(FALSE.FALSE+TRUE.FALSE)) %>% knitr:::kable()
```

physicianSpeciality2	FALSE.FALSE	TRUE.FALSE	FALSE.TRUE	TRUE.TRUE	SENS	SPEC
Critical Care	23765	34653	3459	18418	0.8418887	0.4068095
Speciality-Other	88793	70285	6913	27466	0.7989179	0.5581727

24 Table 1 Before inclusion/exclusion

```

varsTable1 <- c("age", "gender2", "ethnicity2", "BMI_Ranges", "icu_admit_source2", "physicianSpeciality2", "hospitaldischargeyear", "hospital_teaching_status", "hospital_size", "hospital_region2", "dialysis", "aids", "hepatitis", "diabetes", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baseline2", "cardiovascular_baseline", "SIRS_Positive", "qSOFA_Positive", "SOFA_Positive", "SepsisFuzzyLogi_cPositive", "apacheiva", "hospital_mortality_ultimate", "icu_mortality", "hospital_los", "icu_los", "sepsis_outcome", "group")

library(dplyr); library(Hmisc); library(ggplot2); library(sjPlot)

if(!("tableone" %in% rownames(installed.packages()))){
  install.packages("tableone")
}

library(tableone)

CreateTableOne(data=ssd ,vars=varsTable1,strata="hospital_mortality_ultimate",test=TRUE, includeNA=TRUE
) %>% print(nonnormals= c("icu_mortality", "sepsis_outcome", "hospital_teaching_status"),minMax=TRUE,
printToggle      = FALSE,
showAllLevels   = TRUE,
cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption= "Demographic, Severity of Illness, Diagnostic, and Outcome Data")

```

Demographic, Severity of Illness, Diagnostic, and Outcome Data

variable_name	level	0	1	p	test
n		2200750	236690		
age (mean (sd))		61.97 (17.51)	69.72 (15.00)	<0.001	
gender2 (%)	Male	1185691 (53.9)	125568 (53.1)	<0.001	
	Female	1011585 (46.0)	110708 (46.8)		
	Other/Unknown	3474 (0.2)	414 (0.2)		
ethnicity2 (%)	Caucasian	1662178 (75.5)	179335 (75.8)	<0.001	
	African American	241932 (11.0)	25446 (10.8)		
	Hispanic	109661 (5.0)	11284 (4.8)		
	Asian	34728 (1.6)	4497 (1.9)		
	Native American	17674 (0.8)	1689 (0.7)		
	Other/Unknown	134577 (6.1)	14439 (6.1)		
BMI_Ranges (%)	(0,18.5]	99308 (4.5)	17010 (7.2)	<0.001	
	(18.5,25]	607267 (27.6)	74018 (31.3)		
	(25,35]	981253 (44.6)	90336 (38.2)		
	(35,200]	371204 (16.9)	33388 (14.1)		
	Other/Unknown	141718 (6.4)	21938 (9.3)		
icu_admit_source2 (%)	Floor	353263 (16.1)	68254 (28.8)	<0.001	
	OR/Proc Area	451553 (20.5)	19077 (8.1)		
	Direct Admit	209313 (9.5)	23747 (10.0)		
	Emergency Department	1078676 (49.0)	108740 (45.9)		
	Other	63717 (2.9)	8765 (3.7)		
	Step-Down Unit	44228 (2.0)	8107 (3.4)		
physicianSpeciality2 (%)	Critical Care	411995 (18.7)	61205 (25.9)	<0.001	
	Speciality-Other	1788755 (81.3)	175485 (74.1)		
hospitaldischargeyear (%)	-2010	752801 (34.2)	83469 (35.3)	<0.001	
	2011	227837 (10.4)	24579 (10.4)		
	2012	260187 (11.8)	27611 (11.7)		
	2013	277559 (12.6)	29612 (12.5)		

Combined Code Near Final

variable_name	level	0	1	p	test
	2014	294619 (13.4)	30288 (12.8)		
	2015-16	387747 (17.6)	41131 (17.4)		
hospital_teaching_status (%)		439931 (20.0)	41136 (17.4)	<0.001	
	f	1304606 (59.3)	138608 (58.6)		
	t	456213 (20.7)	56946 (24.1)		
hospital_size (%)		509771 (23.2)	48616 (20.5)	<0.001	
	<100	111324 (5.1)	8921 (3.8)		
	100-249	431572 (19.6)	40995 (17.3)		
	250-500	376455 (17.1)	41401 (17.5)		
	>500	771628 (35.1)	96757 (40.9)		
hospital_region2 (%)	Midwest	622551 (28.3)	64551 (27.3)	<0.001	
	Northeast	124015 (5.6)	17161 (7.3)		
	South	565828 (25.7)	69791 (29.5)		
	West	395017 (17.9)	38840 (16.4)		
	Unknown	493339 (22.4)	46347 (19.6)		
dialysis (%)	0	2124367 (96.5)	224664 (94.9)	NaN	
	1	76383 (3.5)	12026 (5.1)		
	NA	0 (0.0)	0 (0.0)		
aids (%)	0	2198348 (99.9)	236188 (99.8)	NaN	
	1	2402 (0.1)	502 (0.2)		
	NA	0 (0.0)	0 (0.0)		
hepaticfailure (%)	FALSE	2159154 (98.1)	228258 (96.4)	NaN	
	TRUE	41596 (1.9)	8432 (3.6)		
	NA	0 (0.0)	0 (0.0)		
diabetes (%)	0	1724302 (78.4)	191474 (80.9)	NaN	
	1	476448 (21.6)	45216 (19.1)		
	NA	0 (0.0)	0 (0.0)		
immunosuppression (%)	0	2155928 (98.0)	226667 (95.8)	NaN	
	1	44822 (2.0)	10023 (4.2)		
	NA	0 (0.0)	0 (0.0)		
leukemia (%)	0	2187388 (99.4)	233115 (98.5)	NaN	
	1	13362 (0.6)	3575 (1.5)		
	NA	0 (0.0)	0 (0.0)		
lymphoma (%)	0	2192810 (99.6)	235019 (99.3)	NaN	
	1	7940 (0.4)	1671 (0.7)		
	NA	0 (0.0)	0 (0.0)		
metastaticcancer (%)	0	2164132 (98.3)	227609 (96.2)	NaN	
	1	36618 (1.7)	9081 (3.8)		
	NA	0 (0.0)	0 (0.0)		
thrombolytics (%)	0	2163227 (98.3)	233398 (98.6)	NaN	
	1	37523 (1.7)	3292 (1.4)		
	NA	0 (0.0)	0 (0.0)		
sofa_respiration_baseline2 (%)	FALSE	1725862 (78.4)	174443 (73.7)	<0.001	
	TRUE	474888 (21.6)	62247 (26.3)		
cardiovascular_baseline (%)	0	1743486 (79.2)	174973 (73.9)	<0.001	
	1	457264 (20.8)	61717 (26.1)		

Combined Code Near Final

variable_name	level	0	1	p	test
SIRS_Positive (%)	FALSE	662262 (30.1)	29711 (12.6)	<0.001	
	TRUE	1538488 (69.9)	206979 (87.4)		
qSOFA_Positive (%)	FALSE	905481 (41.1)	42305 (17.9)	<0.001	
	TRUE	1295269 (58.9)	194385 (82.1)		
SOFA_Positive (%)	FALSE	833502 (37.9)	24965 (10.5)	<0.001	
	TRUE	1367248 (62.1)	211725 (89.5)		
SepsisFuzzyLogicPositive (%)	FALSE	1156340 (52.5)	49013 (20.7)	<0.001	
	TRUE	1044410 (47.5)	187677 (79.3)		
apacheiva (mean (sd))		49.53 (23.88)	82.85 (35.21)	<0.001	
hospital_mortality_ultimate (%)	0	2200750 (100.0)	0 (0.0)	NaN	
	1	0 (0.0)	236690 (100.0)		
	NA	0 (0.0)	0 (0.0)		
icu_mortality (%)	0	2197818 (99.9)	97253 (41.1)	<0.001	
	1	2560 (0.1)	139399 (58.9)		
	NA	372 (0.0)	38 (0.0)		
hospital_los (mean (sd))		8.70 (51.35)	10.40 (100.12)	<0.001	
icu_los (mean (sd))		2.84 (4.10)	4.27 (6.37)	<0.001	
sepsis_outcome (%)	FALSE	1654616 (75.2)	127568 (53.9)	<0.001	
	TRUE	371469 (16.9)	83856 (35.4)		
	NA	174665 (7.9)	25266 (10.7)		
group (%)	Cardiovascular	717129 (32.6)	66498 (28.1)	<0.001	
	Gastrointestinal	227007 (10.3)	21653 (9.1)		
	Gynaecological	6498 (0.3)	100 (0.0)		
	Hematological	15625 (0.7)	1911 (0.8)		
	Metabolic	181200 (8.2)	3691 (1.6)		
	Muscoskeletal/Skin disease	32042 (1.5)	1584 (0.7)		
	Neurological	275981 (12.5)	27757 (11.7)		
	Renal/Genitourinary	54223 (2.5)	4372 (1.8)		
	Respiratory	307334 (14.0)	47033 (19.9)		
	Sepsis	260337 (11.8)	52266 (22.1)		
Trauma	Trauma	98345 (4.5)	7363 (3.1)	<0.001	
	Undefined	17322 (0.8)	2275 (1.0)		
	NA	7707 (0.4)	187 (0.1)		

```
CreateTableOne(data=ssd ,vars=varsTable1,strata="sepsis_outcome",test=TRUE, includeNA=TRUE
) %>% print(nonnormals= c("hospital_mortality_ultimate", "icu_mortality", "hospital_teaching_status"),minMax=TRUE,
printToggle      = FALSE,
showAllLevels   = TRUE,
cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption= "Demographic, Severity of Illness, Diagnostic, and Outcome Data")
```

Demographic, Severity of Illness, Diagnostic, and Outcome Data

variable_name	level	FALSE	TRUE	p	test
n		1906183	485158		
age (mean (sd))		62.00 (17.62)	65.33 (16.30)	<0.001	

Combined Code Near Final

variable_name	level	FALSE	TRUE	p	test
gender2 (%)	Male	1041537 (54.6)	247071 (50.9)	<0.001	
	Female	862802 (45.3)	237856 (49.0)		
	Other/Unknown	1844 (0.1)	231 (0.0)		
ethnicity2 (%)	Caucasian	1440415 (75.6)	362535 (74.7)	<0.001	
	African American	209919 (11.0)	54731 (11.3)		
	Hispanic	89531 (4.7)	28114 (5.8)		
	Asian	30883 (1.6)	8136 (1.7)		
	Native American	15141 (0.8)	4412 (0.9)		
BMI_Ranges (%)	Other/Unknown	120294 (6.3)	27230 (5.6)	<0.001	
	(0,18.5]	82448 (4.3)	32315 (6.7)		
	(18.5,25]	527106 (27.7)	143582 (29.6)		
	(25,35]	864803 (45.4)	194894 (40.2)		
	(35,200]	312118 (16.4)	89639 (18.5)		
icu_admit_source2 (%)	Other/Unknown	119708 (6.3)	24728 (5.1)	<0.001	
	Floor	274569 (14.4)	118755 (24.5)		
	OR/Proc Area	435146 (22.8)	24784 (5.1)		
	Direct Admit	187226 (9.8)	35055 (7.2)		
	Emergency Department	881068 (46.2)	263433 (54.3)		
physicianSpeciality2 (%)	Other	71673 (3.8)	22718 (4.7)	<0.001	
	Step-Down Unit	56501 (3.0)	20413 (4.2)		
	Critical Care	319996 (16.8)	120000 (24.7)		
	Speciality-Other	1586187 (83.2)	365158 (75.3)		
	-2010	639409 (33.5)	127734 (26.3)		
hospitaldischargeyear (%)	2011	201908 (10.6)	55907 (11.5)	<0.001	
	2012	232782 (12.2)	63074 (13.0)		
	2013	247893 (13.0)	69668 (14.4)		
	2014	261515 (13.7)	74955 (15.4)		
	2015-16	322676 (16.9)	93820 (19.3)		
hospital_teaching_status (%)		381796 (20.0)	81424 (16.8)	<0.001	
	f	1134725 (59.5)	293910 (60.6)		
	t	389662 (20.4)	109824 (22.6)		
hospital_size (%)		443992 (23.3)	95727 (19.7)	<0.001	
	<100	80363 (4.2)	30002 (6.2)		
	100-249	366501 (19.2)	91993 (19.0)		
	250-500	314346 (16.5)	95797 (19.7)		
	>500	700981 (36.8)	171639 (35.4)		
hospital_region2 (%)	Midwest	527381 (27.7)	123262 (25.4)	<0.001	
	Northeast	94132 (4.9)	48266 (9.9)		
	South	500396 (26.3)	127715 (26.3)		
	West	343530 (18.0)	95658 (19.7)		
	Unknown	440744 (23.1)	90257 (18.6)		
dialysis (%)	0	1721090 (90.3)	433406 (89.3)	<0.001	
	1	61094 (3.2)	21919 (4.5)		
	NA	123999 (6.5)	29833 (6.1)		
aids (%)	0	1781020 (93.4)	453749 (93.5)	<0.001	
	1	1164 (0.1)	1576 (0.3)		

Combined Code Near Final

variable_name	level	FALSE	TRUE	p	test
	NA	123999 (6.5)	29833 (6.1)		
hepaticfailure (%)	FALSE	1747642 (91.7)	442751 (91.3)	<0.001	
	TRUE	34542 (1.8)	12574 (2.6)		
	NA	123999 (6.5)	29833 (6.1)		
diabetes (%)	0	1393143 (73.1)	351921 (72.5)	<0.001	
	1	389041 (20.4)	103404 (21.3)		
	NA	123999 (6.5)	29833 (6.1)		
immunosuppression (%)	0	1748852 (91.7)	437507 (90.2)	<0.001	
	1	33332 (1.7)	17818 (3.7)		
	NA	123999 (6.5)	29833 (6.1)		
leukemia (%)	0	1772097 (93.0)	449469 (92.6)	<0.001	
	1	10087 (0.5)	5856 (1.2)		
	NA	123999 (6.5)	29833 (6.1)		
lymphoma (%)	0	1776216 (93.2)	452286 (93.2)	<0.001	
	1	5968 (0.3)	3039 (0.6)		
	NA	123999 (6.5)	29833 (6.1)		
metastaticcancer (%)	0	1750410 (91.8)	444166 (91.6)	<0.001	
	1	31774 (1.7)	11159 (2.3)		
	NA	123999 (6.5)	29833 (6.1)		
thrombolytics (%)	0	1744509 (91.5)	454375 (93.7)	<0.001	
	1	37675 (2.0)	950 (0.2)		
	NA	123999 (6.5)	29833 (6.1)		
sofa_respiration_baseline2 (%)	FALSE	1519390 (79.7)	324930 (67.0)	<0.001	
	TRUE	386793 (20.3)	160228 (33.0)		
cardiovascular_baseline (%)	0	1500867 (78.7)	370111 (76.3)	<0.001	
	1	405316 (21.3)	115047 (23.7)		
SIRS_Positive (%)	FALSE	604594 (31.7)	67054 (13.8)	<0.001	
	TRUE	1301589 (68.3)	418104 (86.2)		
qSOFA_Positive (%)	FALSE	824832 (43.3)	117284 (24.2)	<0.001	
	TRUE	1081351 (56.7)	367874 (75.8)		
SOFA_Positive (%)	FALSE	763287 (40.0)	85809 (17.7)	<0.001	
	TRUE	1142896 (60.0)	399349 (82.3)		
SepsisFuzzyLogicPositive (%)	FALSE	1064503 (55.8)	108422 (22.3)	<0.001	
	TRUE	841680 (44.2)	376736 (77.7)		
apacheiva (mean (sd))		49.62 (24.87)	67.19 (28.91)	<0.001	
hospital_mortality_ultimate (%)	0	1654616 (86.8)	371469 (76.6)	<0.001	
	1	127568 (6.7)	83856 (17.3)		
	NA	123999 (6.5)	29833 (6.1)		
icu_mortality (%)	0	1825421 (95.8)	430566 (88.7)	<0.001	
	1	80536 (4.2)	54546 (11.2)		
	NA	226 (0.0)	46 (0.0)		
hospital_los (mean (sd))		7.91 (60.18)	12.00 (35.87)	<0.001	
icu_los (mean (sd))		2.66 (3.89)	4.05 (5.37)	<0.001	
sepsis_outcome (%)	FALSE	1906183 (100.0)	0 (0.0)	NaN	
	TRUE	0 (0.0)	485158 (100.0)		
	NA	0 (0.0)	0 (0.0)		

variable_name	level	FALSE	TRUE	p	test
group (%)	Cardiovascular	731047 (38.4)	53266 (11.0)	<0.001	
	Gastrointestinal	217852 (11.4)	30809 (6.4)		
	Gynaecological	6226 (0.3)	287 (0.1)		
	Hematological	14624 (0.8)	2823 (0.6)		
	Metabolic	170040 (8.9)	15144 (3.1)		
	Muscoskeletal/Skin disease	26906 (1.4)	6003 (1.2)		
	Neurological	278905 (14.6)	24108 (5.0)		
	Renal/Genitourinary	45496 (2.4)	12549 (2.6)		
	Respiratory	236310 (12.4)	116604 (24.0)		
	Sepsis	52258 (2.7)	218627 (45.1)		
	Trauma	102234 (5.4)	3019 (0.6)		
	Undefined	17802 (0.9)	1838 (0.4)		
	NA	6483 (0.3)	81 (0.0)		

25 Table 1 ALL After Inclusion/Exclusion

```

varsTable1 <- c("age", "gender2", "ethnicity2", "BMI_Ranges", "icu_admit_source2", "physicianSpeciality2", "hospi_taldischargeyear", "hospital_teaching_status", "hospital_size", "hospital_region2", "dialysis", "aids", "hepaticfa ilure", "diabetes", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baseline2", "cardiovascular_baseline", "SIRS_Positive", "qSOFA_Positive", "SOFA_Positive", "SepsisFuzzyLog icPositive", "apacheiva", "hospital_mortality_ultimate", "icu_mortality", "hospital_los", "icu_los", "sepsis_outcome", "group")

library(dplyr); library(Hmisc); library(ggplot2); library(sjPlot)

if(!("tableone" %in% rownames(installed.packages())))
  install.packages("tableone")
}

library(tableone)

CreateTableOne(data=ssd_incl ,vars=varsTable1,strata="hospital_mortality_ultimate",test=TRUE, includeNA=TRUE)
) %>% print(nonnormals= c("icu_mortality", "sepsis_outcome", "hospital_teaching_status"),minMax=TRUE,
  printToggle      = FALSE,
  showAllLevels   = TRUE,
  cramVars        = "kon"
) %>%
{
  data.frame(
    variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
    row.names         = NULL,
    check.names       = FALSE,
    stringsAsFactors = FALSE)} %>%
knitr::kable(caption="Demographic, Severity of Illness, Diagnostic, and Outcome Data")

```

Demographic, Severity of Illness, Diagnostic, and Outcome Data

variable_name	level	0	1	p	test
n		826290	86219		
age (mean (sd))		62.26 (17.20)	69.51 (15.00)	<0.001	
gender2 (%)	Male	444766 (53.8)	45767 (53.1)	<0.001	
	Female	381402 (46.2)	40346 (46.8)		
	Other/Unknown	122 (0.0)	106 (0.1)		
ethnicity2 (%)	Caucasian	629231 (76.2)	66136 (76.7)	<0.001	
	African American	96168 (11.6)	9124 (10.6)		
	Hispanic	37359 (4.5)	4034 (4.7)		
	Asian	10468 (1.3)	1227 (1.4)		
	Native American	6085 (0.7)	680 (0.8)		
	Other/Unknown	46979 (5.7)	5018 (5.8)		

Combined Code Near Final

variable_name	level	0	1	p	test
BMI_Ranges (%)	(0,18.5]	37672 (4.6)	6337 (7.3)	<0.001	
	(18.5,25]	230063 (27.8)	27575 (32.0)		
	(25,35]	381728 (46.2)	34794 (40.4)		
	(35,200]	148643 (18.0)	13411 (15.6)		
	Other/Unknown	28184 (3.4)	4102 (4.8)		
icu_admit_source2 (%)	Floor	131068 (15.9)	23568 (27.3)	<0.001	
	OR/Proc Area	169828 (20.6)	6615 (7.7)		
	Direct Admit	87805 (10.6)	10233 (11.9)		
	Emergency Department	415282 (50.3)	41193 (47.8)		
	Other	6616 (0.8)	1147 (1.3)		
	Step-Down Unit	15691 (1.9)	3463 (4.0)		
physicianSpeciality2 (%)	Critical Care	235008 (28.4)	32228 (37.4)	<0.001	
	Speciality-Other	591282 (71.6)	53991 (62.6)		
hospitaldischargeyear (%)	-2010	100104 (12.1)	11426 (13.3)	<0.001	
	2011	109790 (13.3)	12246 (14.2)		
	2012	134912 (16.3)	14257 (16.5)		
	2013	151717 (18.4)	15581 (18.1)		
	2014	162398 (19.7)	15789 (18.3)		
	2015-16	167369 (20.3)	16920 (19.6)		
hospital_teaching_status (%)		34473 (4.2)	3442 (4.0)	<0.001	
	f	543349 (65.8)	54693 (63.4)		
	t	248468 (30.1)	28084 (32.6)		
hospital_size (%)		66107 (8.0)	6571 (7.6)	<0.001	
	<100	34747 (4.2)	2025 (2.3)		
	100-249	190062 (23.0)	17055 (19.8)		
	250-500	151081 (18.3)	16032 (18.6)		
	>500	384293 (46.5)	44536 (51.7)		
hospital_region2 (%)	Midwest	352325 (42.6)	30750 (35.7)	<0.001	
	Northeast	63922 (7.7)	9601 (11.1)		
	South	256647 (31.1)	27340 (31.7)		
	West	102962 (12.5)	13821 (16.0)		
	Unknown	50434 (6.1)	4707 (5.5)		
dialysis (%)	0	799492 (96.8)	82383 (95.6)	<0.001	
	1	26798 (3.2)	3836 (4.4)		
aids (%)	0	825524 (99.9)	86095 (99.9)	<0.001	
	1	766 (0.1)	124 (0.1)		
hepaticfailure (%)	FALSE	810457 (98.1)	82987 (96.3)	<0.001	
	TRUE	15833 (1.9)	3232 (3.7)		
diabetes (%)	0	642502 (77.8)	70191 (81.4)	<0.001	
	1	183788 (22.2)	16028 (18.6)		
immunosuppression (%)	0	808507 (97.8)	82621 (95.8)	<0.001	
	1	17783 (2.2)	3598 (4.2)		
leukemia (%)	0	820977 (99.4)	84948 (98.5)	<0.001	
	1	5313 (0.6)	1271 (1.5)		
lymphoma (%)	0	823248 (99.6)	85647 (99.3)	<0.001	
	1	3042 (0.4)	572 (0.7)		

Combined Code Near Final

variable_name	level	0	1	p	test
metastaticcancer (%)	0	812021 (98.3)	82981 (96.2)	<0.001	
	1	14269 (1.7)	3238 (3.8)		
thrombolytics (%)	0	810938 (98.1)	84836 (98.4)	<0.001	
	1	15352 (1.9)	1383 (1.6)		
sofa_respiration_baseline2 (%)	FALSE	630876 (76.4)	61776 (71.7)	<0.001	
	TRUE	195414 (23.6)	24443 (28.3)		
cardiovascular_baseline (%)	0	642985 (77.8)	62318 (72.3)	<0.001	
	1	183305 (22.2)	23901 (27.7)		
SIRS_Positive (%)	FALSE	212707 (25.7)	5948 (6.9)	<0.001	
	TRUE	613583 (74.3)	80271 (93.1)		
qSOFA_Positive (%)	FALSE	291347 (35.3)	8146 (9.4)	<0.001	
	TRUE	534943 (64.7)	78073 (90.6)		
SOFA_Positive (%)	FALSE	279544 (33.8)	4749 (5.5)	<0.001	
	TRUE	546746 (66.2)	81470 (94.5)		
SepsisFuzzyLogicPositive (%)	FALSE	398466 (48.2)	11535 (13.4)	<0.001	
	TRUE	427824 (51.8)	74684 (86.6)		
apacheiva (mean (sd))		51.90 (22.17)	90.36 (31.77)	<0.001	
hospital_mortality_ultimate (%)	0	826290 (100.0)	0 (0.0)		
	1	0 (0.0)	86219 (100.0)		
icu_mortality (%)	0	826246 (100.0)	24853 (28.8)	<0.001	
	1	0 (0.0)	61357 (71.2)		
	NA	44 (0.0)	9 (0.0)		
hospital_los (mean (sd))		7.69 (9.37)	7.97 (11.80)	<0.001	
icu_los (mean (sd))		2.93 (3.85)	4.49 (5.84)		
sepsis_outcome (%)	FALSE	674037 (81.6)	51602 (59.8)	<0.001	
	TRUE	152253 (18.4)	34617 (40.2)		
group (%)	Cardiovascular	270546 (32.7)	24802 (28.8)	<0.001	
	Gastrointestinal	87106 (10.5)	7567 (8.8)		
	Gynaecological	2381 (0.3)	29 (0.0)		
	Hematological	6220 (0.8)	599 (0.7)		
	Metabolic	73481 (8.9)	1384 (1.6)		
	Muscoskeletal/Skin disease	10969 (1.3)	486 (0.6)		
	Neurological	111809 (13.5)	11101 (12.9)		
	Renal/Genitourinary	20549 (2.5)	1576 (1.8)		
	Respiratory	118873 (14.4)	17182 (19.9)		
	Sepsis	79999 (9.7)	17599 (20.4)		
Trauma		37405 (4.5)	3090 (3.6)		
	Undefined	6952 (0.8)	804 (0.9)		

```
CreateTableOne(data=ssd_incl ,vars=varsTable1,strata="sepsis_outcome",test=TRUE, includeNA=TRUE
) %>% print(nonnnormal= c("hospital_mortality_ultimate", "icu_mortality", "hospital_teaching_status"),minMax=TRUE,
printToggle      = FALSE,
showAlllevels   = TRUE,
cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="Demographic, Severity of Illness, Diagnostic, and Outcome Data")
```

Demographic, Severity of Illness, Diagnostic, and Outcome Data

variable_name	level	FALSE	TRUE	p	test
n		725639	186870		
age (mean (sd))		62.23 (17.30)	65.70 (16.18)	<0.001	
gender2 (%)	Male	395985 (54.6)	94548 (50.6)	<0.001	
	Female	329455 (45.4)	92293 (49.4)		
	Other/Unknown	199 (0.0)	29 (0.0)		
ethnicity2 (%)	Caucasian	553821 (76.3)	141546 (75.7)	<0.001	
	African American	84902 (11.7)	20390 (10.9)		
	Hispanic	30536 (4.2)	10857 (5.8)		
	Asian	9221 (1.3)	2474 (1.3)		
	Native American	5248 (0.7)	1517 (0.8)		
	Other/Unknown	41911 (5.8)	10086 (5.4)		
BMI_Ranges (%)	(0,18.5]	31764 (4.4)	12245 (6.6)	<0.001	
	(18.5,25]	202170 (27.9)	55468 (29.7)		
	(25,35]	338933 (46.7)	77589 (41.5)		
	(35,200]	125888 (17.3)	36166 (19.4)		
	Other/Unknown	26884 (3.7)	5402 (2.9)		
icu_admit_source2 (%)	Floor	107913 (14.9)	46723 (25.0)	<0.001	
	OR/Proc Area	166553 (23.0)	9890 (5.3)		
	Direct Admit	80562 (11.1)	17476 (9.4)		
	Emergency Department	351730 (48.5)	104745 (56.1)		
	Other	5693 (0.8)	2070 (1.1)		
	Step-Down Unit	13188 (1.8)	5966 (3.2)		
physicianSpeciality2 (%)	Critical Care	194821 (26.8)	72415 (38.8)	<0.001	
	Speciality-Other	530818 (73.2)	114455 (61.2)		
hospitaldischargeyear (%)	-2010	88588 (12.2)	22942 (12.3)	<0.001	
	2011	95007 (13.1)	27029 (14.5)		
	2012	119084 (16.4)	30085 (16.1)		
	2013	133576 (18.4)	33722 (18.0)		
	2014	142947 (19.7)	35240 (18.9)		
	2015-16	146437 (20.2)	37852 (20.3)		
hospital_teaching_status (%)		30704 (4.2)	7211 (3.9)	<0.001	
	f	476998 (65.7)	121044 (64.8)		
	t	217937 (30.0)	58615 (31.4)		
hospital_size (%)		58989 (8.1)	13689 (7.3)	<0.001	
	<100	26993 (3.7)	9779 (5.2)		
	100-249	163833 (22.6)	43284 (23.2)		
	250-500	131717 (18.2)	35396 (18.9)		

variable_name	level	FALSE	TRUE	p	test
	>500	344107 (47.4)	84722 (45.3)		
hospital_region2 (%)	Midwest	313401 (43.2)	69674 (37.3)	<0.001	
	Northeast	46163 (6.4)	27360 (14.6)		
	South	229437 (31.6)	54550 (29.2)		
	West	90846 (12.5)	25937 (13.9)		
	Unknown	45792 (6.3)	9349 (5.0)		
dialysis (%)	0	702756 (96.8)	179119 (95.9)	<0.001	
	1	22883 (3.2)	7751 (4.1)		
aids (%)	0	725221 (99.9)	186398 (99.7)	<0.001	
	1	418 (0.1)	472 (0.3)		
hepaticfailure (%)	FALSE	711408 (98.0)	182036 (97.4)	<0.001	
	TRUE	14231 (2.0)	4834 (2.6)		
diabetes (%)	0	566573 (78.1)	146120 (78.2)	0.288	
	1	159066 (21.9)	40750 (21.8)		
immunosuppression (%)	0	711733 (98.1)	179395 (96.0)	<0.001	
	1	13906 (1.9)	7475 (4.0)		
leukemia (%)	0	721482 (99.4)	184443 (98.7)	<0.001	
	1	4157 (0.6)	2427 (1.3)		
lymphoma (%)	0	723226 (99.7)	185669 (99.4)	<0.001	
	1	2413 (0.3)	1201 (0.6)		
metastaticcancer (%)	0	712655 (98.2)	182347 (97.6)	<0.001	
	1	12984 (1.8)	4523 (2.4)		
thrombolytics (%)	0	709288 (97.7)	186486 (99.8)	<0.001	
	1	16351 (2.3)	384 (0.2)		
sofa_respiration_baseline2 (%)	FALSE	569370 (78.5)	123282 (66.0)	<0.001	
	TRUE	156269 (21.5)	63588 (34.0)		
cardiovascular_baseline (%)	0	564204 (77.8)	141099 (75.5)	<0.001	
	1	161435 (22.2)	45771 (24.5)		
SIRS_Positive (%)	FALSE	197738 (27.3)	20917 (11.2)	<0.001	
	TRUE	527901 (72.7)	165953 (88.8)		
qSOFA_Positive (%)	FALSE	265487 (36.6)	34006 (18.2)	<0.001	
	TRUE	460152 (63.4)	152864 (81.8)		
SOFA_Positive (%)	FALSE	258188 (35.6)	26105 (14.0)	<0.001	
	TRUE	467451 (64.4)	160765 (86.0)		
SepsisFuzzyLogicPositive (%)	FALSE	375201 (51.7)	34800 (18.6)	<0.001	
	TRUE	350438 (48.3)	152070 (81.4)		
apacheiva (mean (sd))		51.95 (23.95)	69.47 (28.02)	<0.001	
hospital_mortality_ultimate (%)	0	674037 (92.9)	152253 (81.5)	<0.001	
	1	51602 (7.1)	34617 (18.5)		
icu_mortality (%)	0	689161 (95.0)	161938 (86.7)	<0.001	
	1	36436 (5.0)	24921 (13.3)		
	NA	42 (0.0)	11 (0.0)		
hospital_los (mean (sd))		7.05 (8.71)	10.31 (12.24)	<0.001	
icu_los (mean (sd))		2.79 (3.75)	4.20 (5.13)	<0.001	
sepsis_outcome (%)	FALSE	725639 (100.0)	0 (0.0)	<0.001	
	TRUE	0 (0.0)	186870 (100.0)		

variable_name	level	FALSE	TRUE	p	test
group (%)	Cardiovascular	275329 (37.9)	20019 (10.7)	<0.001	
	Gastrointestinal	83127 (11.5)	11546 (6.2)		
	Gynaecological	2293 (0.3)	117 (0.1)		
	Hematological	5761 (0.8)	1058 (0.6)		
	Metabolic	68815 (9.5)	6050 (3.2)		
	Muscoskeletal/Skin disease	9185 (1.3)	2270 (1.2)		
	Neurological	113662 (15.7)	9248 (4.9)		
	Renal/Genitourinary	17170 (2.4)	4955 (2.7)		
	Respiratory	89707 (12.4)	46348 (24.8)		
	Sepsis	14033 (1.9)	83565 (44.7)		
	Trauma	39475 (5.4)	1020 (0.5)		
	Undefined	7082 (1.0)	674 (0.4)		

26 Table 1 Test Dataset

```

varsTable1 <- c("age", "gender2", "ethnicity2", "BMI_Ranges", "icu_admit_source2","physicianSpeciality2", "hospital_admissionyear", "hospital_teaching_status", "hospital_size", "hospital_region2","dialysis", "aids", "hepatitisfai lure", "diabetes", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baseline2", "cardiovascular_baseline","SIRS_Positive", "qSOFA_Positive", "SOFA_Positive", "SepsisFuzzyLogi cPositive","apacheiva", "hospital_mortality_ultimate", "icu_mortality", "hospital_los", "icu_los","sepsis_outcom e", "group")

library(dplyr); library(Hmisc); library(ggplot2); library(sjPlot)

if(!("tableone" %in% rownames(installed.packages()))){
  install.packages("tableone")
}

library(tableone)

CreateTableOne(data=ssd_incl_te ,vars=varsTable1,strata="hospital_mortality_ultimate",test=TRUE, includeNA=TRUE
) %>% print(nonnnormal= c("icu_mortality", "sepsis_outcome", "hospital_teaching_status"),minMax=TRUE,
printToggle      = FALSE,
showAlllevels   = TRUE,
cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="Demographic, Severity of Illness, Diagnostic, and Outcome Data")

```

Demographic, Severity of Illness, Diagnostic, and Outcome Data

variable_name	level	FALSE	TRUE	p	test
n		247887	25865		
age (mean (sd))		62.23 (17.23)	69.63 (14.92)	<0.001	
gender2 (%)	Male	133288 (53.8)	13614 (52.6)	<0.001	
	Female	114558 (46.2)	12212 (47.2)		
	Other/Unknown	41 (0.0)	39 (0.2)		
ethnicity2 (%)	Caucasian	188789 (76.2)	19899 (76.9)	<0.001	
	African American	28950 (11.7)	2779 (10.7)		
	Hispanic	11097 (4.5)	1188 (4.6)		
	Asian	3171 (1.3)	362 (1.4)		
	Native American	1834 (0.7)	178 (0.7)		
	Other/Unknown	14046 (5.7)	1459 (5.6)		
BMI_Ranges (%)	(0,18.5]	11536 (4.7)	1912 (7.4)	<0.001	

variable_name	level	FALSE	TRUE	p	test
	(18.5,25]	68576 (27.7)	8299 (32.1)		
	(25,35]	114763 (46.3)	10449 (40.4)		
	(35,200]	44499 (18.0)	3958 (15.3)		
	Other/Unknown	8513 (3.4)	1247 (4.8)		
icu_admit_source2 (%)	Floor	39313 (15.9)	7121 (27.5)	<0.001	
	OR/Proc Area	50962 (20.6)	1969 (7.6)		
	Direct Admit	26416 (10.7)	3055 (11.8)		
	Emergency Department	124404 (50.2)	12270 (47.4)		
	Other	1995 (0.8)	365 (1.4)		
	Step-Down Unit	4797 (1.9)	1085 (4.2)		
physicianSpeciality2 (%)	Critical Care	70540 (28.5)	9755 (37.7)	<0.001	
	Speciality-Other	177347 (71.5)	16110 (62.3)		
hospitaldischargeyear (%)	-2010	29982 (12.1)	3366 (13.0)	<0.001	
	2011	33134 (13.4)	3680 (14.2)		
	2012	40551 (16.4)	4259 (16.5)		
	2013	45509 (18.4)	4753 (18.4)		
	2014	48843 (19.7)	4708 (18.2)		
	2015-16	49868 (20.1)	5099 (19.7)		
hospital_teaching_status (%)		10370 (4.2)	1051 (4.1)	<0.001	
	f	162894 (65.7)	16377 (63.3)		
	t	74623 (30.1)	8437 (32.6)		
hospital_size (%)		19895 (8.0)	1985 (7.7)	<0.001	
	<100	10464 (4.2)	614 (2.4)		
	100-249	56948 (23.0)	5071 (19.6)		
	250-500	45347 (18.3)	4859 (18.8)		
	>500	115233 (46.5)	13336 (51.6)		
hospital_region2 (%)	Midwest	105735 (42.7)	9171 (35.5)	<0.001	
	Northeast	19043 (7.7)	2962 (11.5)		
	South	77072 (31.1)	8209 (31.7)		
	West	30786 (12.4)	4083 (15.8)		
	Unknown	15251 (6.2)	1440 (5.6)		
dialysis (%)	0	239806 (96.7)	24688 (95.4)	<0.001	
	1	8081 (3.3)	1177 (4.6)		
aids (%)	0	247657 (99.9)	25832 (99.9)	0.107	
	1	230 (0.1)	33 (0.1)		
hepatictfailure (%)	FALSE	243163 (98.1)	24908 (96.3)	<0.001	
	TRUE	4724 (1.9)	957 (3.7)		
diabetes (%)	0	192864 (77.8)	21056 (81.4)	<0.001	
	1	55023 (22.2)	4809 (18.6)		
immunosuppression (%)	0	242591 (97.9)	24795 (95.9)	<0.001	
	1	5296 (2.1)	1070 (4.1)		
leukemia (%)	0	246333 (99.4)	25481 (98.5)	<0.001	
	1	1554 (0.6)	384 (1.5)		
lymphoma (%)	0	247024 (99.7)	25698 (99.4)	<0.001	
	1	863 (0.3)	167 (0.6)		
metastaticcancer (%)	0	243535 (98.2)	24911 (96.3)	<0.001	

variable_name	level	FALSE	TRUE	p	test
	1	4352 (1.8)	954 (3.7)		
thrombolytics (%)	0	243323 (98.2)	25461 (98.4)	0.001	
	1	4564 (1.8)	404 (1.6)		
sofa_respiration_baseline2 (%)	FALSE	189447 (76.4)	18561 (71.8)	<0.001	
	TRUE	58440 (23.6)	7304 (28.2)		
cardiovascular_baseline (%)	0	193108 (77.9)	18753 (72.5)	<0.001	
	1	54779 (22.1)	7112 (27.5)		
SIRS_Positive (%)	FALSE	63427 (25.6)	1792 (6.9)	<0.001	
	TRUE	184460 (74.4)	24073 (93.1)		
qSOFA_Positive (%)	FALSE	87257 (35.2)	2429 (9.4)	<0.001	
	TRUE	160630 (64.8)	23436 (90.6)		
SOFA_Positive (%)	FALSE	83807 (33.8)	1464 (5.7)	<0.001	
	TRUE	164080 (66.2)	24401 (94.3)		
SepsisFuzzyLogicPositive (%)	FALSE	119438 (48.2)	3492 (13.5)	<0.001	
	TRUE	128449 (51.8)	22373 (86.5)		
apacheiva (mean (sd))		51.90 (22.21)	90.36 (31.62)	<0.001	
hospital_mortality_ultimate (%)	FALSE	247887 (100.0)	0 (0.0)	<0.001	
	TRUE	0 (0.0)	25865 (100.0)		
icu_mortality (%)	0	247870 (100.0)	7507 (29.0)	<0.001	
	1	0 (0.0)	18355 (71.0)		
	NA	17 (0.0)	3 (0.0)		
hospital_los (mean (sd))		7.74 (10.56)	7.96 (10.32)	0.001	
icu_los (mean (sd))		2.94 (3.90)	4.46 (5.87)	<0.001	
sepsis_outcome (%)	FALSE	202080 (81.5)	15416 (59.6)	<0.001	
	TRUE	45807 (18.5)	10449 (40.4)		
group (%)	Cardiovascular	80965 (32.7)	7398 (28.6)	<0.001	
	Gastrointestinal	26265 (10.6)	2279 (8.8)		
	Gynaecological	706 (0.3)	9 (0.0)		
	Hematological	1915 (0.8)	171 (0.7)		
	Metabolic	22029 (8.9)	432 (1.7)		
	Muscoskeletal/Skin disease	3332 (1.3)	126 (0.5)		
	Neurological	33500 (13.5)	3337 (12.9)		
	Renal/Genitourinary	6101 (2.5)	475 (1.8)		
	Respiratory	35716 (14.4)	5142 (19.9)		
	Sepsis	24033 (9.7)	5304 (20.5)		
	Trauma	11196 (4.5)	929 (3.6)		
	Undefined	2129 (0.9)	263 (1.0)		

```
CreateTableOne(data=ssd_incl_te ,vars=varsTable1,strata="sepsis_outcome",test=TRUE, includeNA=TRUE
) %>% print(nonnornormal= c("hospital_mortality_ultimate", "icu_mortality", "hospital_teaching_status"),minMax=TRUE,
printToggle      = FALSE,
showAllLevels   = TRUE,
cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="Demographic, Severity of Illness, Diagnostic, and Outcome Data")
```

Demographic, Severity of Illness, Diagnostic, and Outcome Data

variable_name	level	FALSE	TRUE	p	test
n		217496	56256		
age (mean (sd))		62.21 (17.32)	65.70 (16.27)	<0.001	
gender2 (%)	Male	118663 (54.6)	28239 (50.2)	<0.001	
	Female	98765 (45.4)	28005 (49.8)		
	Other/Unknown	68 (0.0)	12 (0.0)		
ethnicity2 (%)	Caucasian	166045 (76.3)	42643 (75.8)	<0.001	
	African American	25606 (11.8)	6123 (10.9)		
	Hispanic	9025 (4.1)	3260 (5.8)		
	Asian	2785 (1.3)	748 (1.3)		
	Native American	1558 (0.7)	454 (0.8)		
	Other/Unknown	12477 (5.7)	3028 (5.4)		
BMI_Ranges (%)	(0,18.5]	9746 (4.5)	3702 (6.6)	<0.001	
	(18.5,25]	60170 (27.7)	16705 (29.7)		
	(25,35]	101869 (46.8)	23343 (41.5)		
	(35,200]	37638 (17.3)	10819 (19.2)		
	Other/Unknown	8073 (3.7)	1687 (3.0)		
icu_admit_source2 (%)	Floor	32429 (14.9)	14005 (24.9)	<0.001	
	OR/Proc Area	49937 (23.0)	2994 (5.3)		
	Direct Admit	24281 (11.2)	5190 (9.2)		
	Emergency Department	105092 (48.3)	31582 (56.1)		
	Other	1722 (0.8)	638 (1.1)		
	Step-Down Unit	4035 (1.9)	1847 (3.3)		
physicianSpeciality2 (%)	Critical Care	58418 (26.9)	21877 (38.9)	<0.001	
	Speciality-Other	159078 (73.1)	34379 (61.1)		
hospitaldischargeyear (%)	-2010	26447 (12.2)	6901 (12.3)	<0.001	
	2011	28696 (13.2)	8118 (14.4)		
	2012	35707 (16.4)	9103 (16.2)		
	2013	40113 (18.4)	10149 (18.0)		
	2014	42963 (19.8)	10588 (18.8)		
	2015-16	43570 (20.0)	11397 (20.3)		
hospital_teaching_status (%)		9199 (4.2)	2222 (3.9)	<0.001	
	f	143044 (65.8)	36227 (64.4)		
	t	65253 (30.0)	17807 (31.7)		
hospital_size (%)		17716 (8.1)	4164 (7.4)	<0.001	
	<100	8157 (3.8)	2921 (5.2)		
	100-249	48999 (22.5)	13020 (23.1)		
	250-500	39608 (18.2)	10598 (18.8)		
	>500	103016 (47.4)	25553 (45.4)		
hospital_region2 (%)	Midwest	93946 (43.2)	20960 (37.3)	<0.001	
	Northeast	13710 (6.3)	8295 (14.7)		
	South	68820 (31.6)	16461 (29.3)		
	West	27201 (12.5)	7668 (13.6)		
	Unknown	13819 (6.4)	2872 (5.1)		
dialysis (%)	0	210546 (96.8)	53948 (95.9)	<0.001	
	1	6950 (3.2)	2308 (4.1)		

variable_name	level	FALSE	TRUE	p	test
aids (%)	0	217391 (100.0)	56098 (99.7)	<0.001	
	1	105 (0.0)	158 (0.3)		
hepaticfailure (%)	FALSE	213245 (98.0)	54826 (97.5)	<0.001	
	TRUE	4251 (2.0)	1430 (2.5)		
diabetes (%)	0	169968 (78.1)	43952 (78.1)	0.927	
	1	47528 (21.9)	12304 (21.9)		
immunosuppression (%)	0	213347 (98.1)	54039 (96.1)	<0.001	
	1	4149 (1.9)	2217 (3.9)		
leukemia (%)	0	216306 (99.5)	55508 (98.7)	<0.001	
	1	1190 (0.5)	748 (1.3)		
lymphoma (%)	0	216810 (99.7)	55912 (99.4)	<0.001	
	1	686 (0.3)	344 (0.6)		
metastaticcancer (%)	0	213552 (98.2)	54894 (97.6)	<0.001	
	1	3944 (1.8)	1362 (2.4)		
thrombolytics (%)	0	212624 (97.8)	56160 (99.8)	<0.001	
	1	4872 (2.2)	96 (0.2)		
sofa_respiration_baseline2 (%)	FALSE	170825 (78.5)	37183 (66.1)	<0.001	
	TRUE	46671 (21.5)	19073 (33.9)		
cardiovascular_baseline (%)	0	169312 (77.8)	42549 (75.6)	<0.001	
	1	48184 (22.2)	13707 (24.4)		
SIRS_Positive (%)	FALSE	59019 (27.1)	6200 (11.0)	<0.001	
	TRUE	158477 (72.9)	50056 (89.0)		
qSOFA_Positive (%)	FALSE	79553 (36.6)	10133 (18.0)	<0.001	
	TRUE	137943 (63.4)	46123 (82.0)		
SOFA_Positive (%)	FALSE	77471 (35.6)	7800 (13.9)	<0.001	
	TRUE	140025 (64.4)	48456 (86.1)		
SepsisFuzzyLogicPositive (%)	FALSE	112558 (51.8)	10372 (18.4)	<0.001	
	TRUE	104938 (48.2)	45884 (81.6)		
apacheiva (mean (sd))		51.93 (23.93)	69.48 (28.13)	<0.001	
hospital_mortality_ultimate (%)	FALSE	202080 (92.9)	45807 (81.4)	<0.001	
	TRUE	15416 (7.1)	10449 (18.6)		
icu_mortality (%)	0	206618 (95.0)	48759 (86.7)	<0.001	
	1	10863 (5.0)	7492 (13.3)		
	NA	15 (0.0)	5 (0.0)		
hospital_los (mean (sd))		7.08 (9.34)	10.38 (13.93)	<0.001	
icu_los (mean (sd))		2.79 (3.78)	4.22 (5.20)	<0.001	
sepsis_outcome (%)	FALSE	217496 (100.0)	0 (0.0)	<0.001	
	TRUE	0 (0.0)	56256 (100.0)		
group (%)	Cardiovascular	82285 (37.8)	6078 (10.8)	<0.001	
	Gastrointestinal	25028 (11.5)	3516 (6.2)		
	Gynaecological	682 (0.3)	33 (0.1)		
	Hematological	1779 (0.8)	307 (0.5)		
	Metabolic	20612 (9.5)	1849 (3.3)		
	Muscoskeletal/Skin disease	2779 (1.3)	679 (1.2)		
	Neurological	34048 (15.7)	2789 (5.0)		
	Renal/Genitourinary	5089 (2.3)	1487 (2.6)		

variable_name	level	FALSE	TRUE	p	test
	Respiratory	26953 (12.4)	13905 (24.7)		
	Sepsis	4250 (2.0)	25087 (44.6)		
	Trauma	11811 (5.4)	314 (0.6)		
	Undefined	2180 (1.0)	212 (0.4)		

27 Table 1 Train Dataset

```

varsTable1 <- c("age", "gender2", "ethnicity2", "BMI_Ranges", "icu_admit_source2", "physicianSpeciality2", "hospitaldischargeyear", "hospital_teaching_status", "hospital_size", "hospital_region2", "dialysis", "aids", "hepatitis", "diabetes", "immunosuppression", "leukemia", "lymphoma", "metastaticcancer", "thrombolytics", "sofa_respiration_baseline2", "cardiovascular_baseline", "SIRS_Positive", "qSOFA_Positive", "SOFA_Positive", "SepsisFuzzyLogicPositive", "apacheiva", "hospital_mortality_ultimate", "icu_mortality", "hospital_los", "icu_los", "sepsis_outcome", "group")

library(dplyr); library(Hmisc); library(ggplot2); library(sjPlot)

if(!(tableone %in% rownames(installed.packages())))
  install.packages("tableone")
}

library(tableone)

CreateTableOne(data=ssd_incl_tr ,vars=varsTable1,strata="hospital_mortality_ultimate",test=TRUE, includeNA=TRUE
) %>% print(nonnormals= c("icu_mortality", "hospital_teaching_status"),minMax=TRUE,
printToggle      = FALSE,
showAllLevels   = TRUE,
cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE), ,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="Demographic, Severity of Illness, Diagnostic, and Outcome Data")

```

Demographic, Severity of Illness, Diagnostic, and Outcome Data

variable_name	level	0	1	p	test
n		578403	60354		
age (mean (sd))		62.27 (17.19)	69.45 (15.04)	<0.001	
gender2 (%)	Male	311478 (53.9)	32153 (53.3)	<0.001	
	Female	266844 (46.1)	28134 (46.6)		
	Other/Unknown	81 (0.0)	67 (0.1)		
ethnicity2 (%)	Caucasian	440442 (76.1)	46237 (76.6)	<0.001	
	African American	67218 (11.6)	6345 (10.5)		
	Hispanic	26262 (4.5)	2846 (4.7)		
	Asian	7297 (1.3)	865 (1.4)		
	Native American	4251 (0.7)	502 (0.8)		
	Other/Unknown	32933 (5.7)	3559 (5.9)		
BMI_Ranges (%)	(0,18.5]	26136 (4.5)	4425 (7.3)	<0.001	
	(18.5,25]	161487 (27.9)	19276 (31.9)		
	(25,35]	266965 (46.2)	24345 (40.3)		
	(35,200]	104144 (18.0)	9453 (15.7)		
	Other/Unknown	19671 (3.4)	2855 (4.7)		
icu_admit_source2 (%)	Floor	91755 (15.9)	16447 (27.3)	<0.001	
	OR/Proc Area	118866 (20.6)	4646 (7.7)		
	Direct Admit	61389 (10.6)	7178 (11.9)		
	Emergency Department	290878 (50.3)	28923 (47.9)		

Combined Code Near Final

variable_name	level	0	1	p	test
	Other	4621 (0.8)	782 (1.3)		
	Step-Down Unit	10894 (1.9)	2378 (3.9)		
physicianSpeciality2 (%)	Critical Care	164468 (28.4)	22473 (37.2)	<0.001	
	Speciality-Other	413935 (71.6)	37881 (62.8)		
hospitaldischargeyear (%)	-2010	70122 (12.1)	8060 (13.4)	<0.001	
	2011	76656 (13.3)	8566 (14.2)		
	2012	94361 (16.3)	9998 (16.6)		
	2013	106208 (18.4)	10828 (17.9)		
	2014	113555 (19.6)	11081 (18.4)		
	2015-16	117501 (20.3)	11821 (19.6)		
hospital_teaching_status (%)		24103 (4.2)	2391 (4.0)	<0.001	
	f	380455 (65.8)	38316 (63.5)		
	t	173845 (30.1)	19647 (32.6)		
hospital_size (%)		46212 (8.0)	4586 (7.6)	<0.001	
	<100	24283 (4.2)	1411 (2.3)		
	100-249	133114 (23.0)	11984 (19.9)		
	250-500	105734 (18.3)	11173 (18.5)		
	>500	269060 (46.5)	31200 (51.7)		
hospital_region2 (%)	Midwest	246590 (42.6)	21579 (35.8)	<0.001	
	Northeast	44879 (7.8)	6639 (11.0)		
	South	179575 (31.0)	19131 (31.7)		
	West	72176 (12.5)	9738 (16.1)		
	Unknown	35183 (6.1)	3267 (5.4)		
dialysis (%)	0	559686 (96.8)	57695 (95.6)	<0.001	
	1	18717 (3.2)	2659 (4.4)		
aids (%)	0	577867 (99.9)	60263 (99.8)	<0.001	
	1	536 (0.1)	91 (0.2)		
hepaticfailure (%)	FALSE	567294 (98.1)	58079 (96.2)	<0.001	
	TRUE	11109 (1.9)	2275 (3.8)		
diabetes (%)	0	449638 (77.7)	49135 (81.4)	<0.001	
	1	128765 (22.3)	11219 (18.6)		
immunosuppression (%)	0	565916 (97.8)	57826 (95.8)	<0.001	
	1	12487 (2.2)	2528 (4.2)		
leukemia (%)	0	574644 (99.4)	59467 (98.5)	<0.001	
	1	3759 (0.6)	887 (1.5)		
lymphoma (%)	0	576224 (99.6)	59949 (99.3)	<0.001	
	1	2179 (0.4)	405 (0.7)		
metastaticcancer (%)	0	568486 (98.3)	58070 (96.2)	<0.001	
	1	9917 (1.7)	2284 (3.8)		
thrombolytics (%)	0	567615 (98.1)	59375 (98.4)	<0.001	
	1	10788 (1.9)	979 (1.6)		
sofa_respiration_baseline2 (%)	FALSE	441429 (76.3)	43215 (71.6)	<0.001	
	TRUE	136974 (23.7)	17139 (28.4)		
cardiovascular_baseline (%)	0	449877 (77.8)	43565 (72.2)	<0.001	
	1	128526 (22.2)	16789 (27.8)		
SIRS_Positive (%)	FALSE	149280 (25.8)	4156 (6.9)	<0.001	

Combined Code Near Final

variable_name	level	0	1	p	test
	TRUE	429123 (74.2)	56198 (93.1)		
qSOFA_Positive (%)	FALSE	204090 (35.3)	5717 (9.5)	<0.001	
	TRUE	374313 (64.7)	54637 (90.5)		
SOFA_Positive (%)	FALSE	195737 (33.8)	3285 (5.4)	<0.001	
	TRUE	382666 (66.2)	57069 (94.6)		
SepsisFuzzyLogicPositive (%)	FALSE	279028 (48.2)	8043 (13.3)	<0.001	
	TRUE	299375 (51.8)	52311 (86.7)		
apacheiva (mean (sd))		51.91 (22.15)	90.36 (31.83)	<0.001	
hospital_mortality_ultimate (%)	0	578403 (100.0)	0 (0.0)	<0.001	
	1	0 (0.0)	60354 (100.0)		
icu_mortality (%)	0	578376 (100.0)	17346 (28.7)	<0.001	
	1	0 (0.0)	43002 (71.2)		
	NA	27 (0.0)	6 (0.0)		
hospital_los (mean (sd))		7.67 (8.82)	7.97 (12.38)	<0.001	
icu_los (mean (sd))		2.93 (3.83)	4.50 (5.83)	<0.001	
sepsis_outcome (%)	FALSE	471957 (81.6)	36186 (60.0)	<0.001	
	TRUE	106446 (18.4)	24168 (40.0)		
group (%)	Cardiovascular	189581 (32.8)	17404 (28.8)	<0.001	
	Gastrointestinal	60841 (10.5)	5288 (8.8)		
	Gynaecological	1675 (0.3)	20 (0.0)		
	Hematological	4305 (0.7)	428 (0.7)		
	Metabolic	51452 (8.9)	952 (1.6)		
	Muscoskeletal/Skin disease	7637 (1.3)	360 (0.6)		
	Neurological	78309 (13.5)	7764 (12.9)		
	Renal/Genitourinary	14448 (2.5)	1101 (1.8)		
	Respiratory	83157 (14.4)	12040 (19.9)		
	Sepsis	55966 (9.7)	12295 (20.4)		
	Trauma	26209 (4.5)	2161 (3.6)		
	Undefined	4823 (0.8)	541 (0.9)		

```
CreateTableOne(data=ssd_incl_tr ,vars=varsTable1,strata="sepsis_outcome",test=TRUE, includeNA=TRUE
) %>% print(nonnormals= c("hospital_mortality_ultimate", "icu_mortality", "hospital_teaching_status"),minMax=TRUE,
printToggle      = FALSE,
showAllLevels   = TRUE,
cramVars        = "kon"
) %>%
{data.frame(
  variable_name      = gsub(" ", " ", rownames(.), fixed = TRUE),.,
  row.names         = NULL,
  check.names       = FALSE,
  stringsAsFactors = FALSE)} %>%
knitr::kable(caption="Demographic, Severity of Illness, Diagnostic, and Outcome Data")
```

Demographic, Severity of Illness, Diagnostic, and Outcome Data

variable_name	level	FALSE	TRUE	p	test
n		508143	130614		
age (mean (sd))		62.24 (17.30)	65.70 (16.15)	<0.001	
gender2 (%)	Male	277322 (54.6)	66309 (50.8)	<0.001	
	Female	230690 (45.4)	64288 (49.2)		
	Other/Unknown	131 (0.0)	17 (0.0)		
ethnicity2 (%)	Caucasian	387776 (76.3)	98903 (75.7)	<0.001	

variable_name	level	FALSE	TRUE	p	test
	African American	59296 (11.7)	14267 (10.9)		
	Hispanic	21511 (4.2)	7597 (5.8)		
	Asian	6436 (1.3)	1726 (1.3)		
	Native American	3690 (0.7)	1063 (0.8)		
	Other/Unknown	29434 (5.8)	7058 (5.4)		
BMI_Ranges (%)	(0,18.5]	22018 (4.3)	8543 (6.5)	<0.001	
	(18.5,25]	142000 (27.9)	38763 (29.7)		
	(25,35]	237064 (46.7)	54246 (41.5)		
	(35,200]	88250 (17.4)	25347 (19.4)		
	Other/Unknown	18811 (3.7)	3715 (2.8)		
icu_admit_source2 (%)	Floor	75484 (14.9)	32718 (25.0)	<0.001	
	OR/Proc Area	116616 (22.9)	6896 (5.3)		
	Direct Admit	56281 (11.1)	12286 (9.4)		
	Emergency Department	246638 (48.5)	73163 (56.0)		
	Other	3971 (0.8)	1432 (1.1)		
	Step-Down Unit	9153 (1.8)	4119 (3.2)		
physicianSpeciality2 (%)	Critical Care	136403 (26.8)	50538 (38.7)	<0.001	
	Speciality-Other	371740 (73.2)	80076 (61.3)		
hospitaldischargeyear (%)	-2010	62141 (12.2)	16041 (12.3)	<0.001	
	2011	66311 (13.0)	18911 (14.5)		
	2012	83377 (16.4)	20982 (16.1)		
	2013	93463 (18.4)	23573 (18.0)		
	2014	99984 (19.7)	24652 (18.9)		
	2015-16	102867 (20.2)	26455 (20.3)		
hospital_teaching_status (%)		21505 (4.2)	4989 (3.8)	<0.001	
	f	333954 (65.7)	84817 (64.9)		
	t	152684 (30.0)	40808 (31.2)		
hospital_size (%)		41273 (8.1)	9525 (7.3)	<0.001	
	<100	18836 (3.7)	6858 (5.3)		
	100-249	114834 (22.6)	30264 (23.2)		
	250-500	92109 (18.1)	24798 (19.0)		
	>500	241091 (47.4)	59169 (45.3)		
hospital_region2 (%)	Midwest	219455 (43.2)	48714 (37.3)	<0.001	
	Northeast	32453 (6.4)	19065 (14.6)		
	South	160617 (31.6)	38089 (29.2)		
	West	63645 (12.5)	18269 (14.0)		
	Unknown	31973 (6.3)	6477 (5.0)		
dialysis (%)	0	492210 (96.9)	125171 (95.8)	<0.001	
	1	15933 (3.1)	5443 (4.2)		
aids (%)	0	507830 (99.9)	130300 (99.8)	<0.001	
	1	313 (0.1)	314 (0.2)		
hepaticfailure (%)	FALSE	498163 (98.0)	127210 (97.4)	<0.001	
	TRUE	9980 (2.0)	3404 (2.6)		
diabetes (%)	0	396605 (78.0)	102168 (78.2)	0.183	
	1	111538 (22.0)	28446 (21.8)		
immunosuppression (%)	0	498386 (98.1)	125356 (96.0)	<0.001	

variable_name	level	FALSE	TRUE	p	test
	1	9757 (1.9)	5258 (4.0)		
leukemia (%)	0	505176 (99.4)	128935 (98.7)	<0.001	
	1	2967 (0.6)	1679 (1.3)		
lymphoma (%)	0	506416 (99.7)	129757 (99.3)	<0.001	
	1	1727 (0.3)	857 (0.7)		
metastaticcancer (%)	0	499103 (98.2)	127453 (97.6)	<0.001	
	1	9040 (1.8)	3161 (2.4)		
thrombolytics (%)	0	496664 (97.7)	130326 (99.8)	<0.001	
	1	11479 (2.3)	288 (0.2)		
sofa_respiration_baseline2 (%)	FALSE	398545 (78.4)	86099 (65.9)	<0.001	
	TRUE	109598 (21.6)	44515 (34.1)		
cardiovascular_baseline (%)	0	394892 (77.7)	98550 (75.5)	<0.001	
	1	113251 (22.3)	32064 (24.5)		
SIRS_Positive (%)	FALSE	138719 (27.3)	14717 (11.3)	<0.001	
	TRUE	369424 (72.7)	115897 (88.7)		
qSOFA_Positive (%)	FALSE	185934 (36.6)	23873 (18.3)	<0.001	
	TRUE	322209 (63.4)	106741 (81.7)		
SOFA_Positive (%)	FALSE	180717 (35.6)	18305 (14.0)	<0.001	
	TRUE	327426 (64.4)	112309 (86.0)		
SepsisFuzzyLogicPositive (%)	FALSE	262643 (51.7)	24428 (18.7)	<0.001	
	TRUE	245500 (48.3)	106186 (81.3)		
apacheiva (mean (sd))		51.96 (23.96)	69.47 (27.97)	<0.001	
hospital_mortality_ultimate (%)	0	471957 (92.9)	106446 (81.5)	<0.001	
	1	36186 (7.1)	24168 (18.5)		
icu_mortality (%)	0	482543 (95.0)	113179 (86.7)	<0.001	
	1	25573 (5.0)	17429 (13.3)		
	NA	27 (0.0)	6 (0.0)		
hospital_los (mean (sd))		7.03 (8.42)	10.28 (11.44)	<0.001	
icu_los (mean (sd))		2.79 (3.73)	4.19 (5.11)	<0.001	
sepsis_outcome (%)	FALSE	508143 (100.0)	0 (0.0)	<0.001	
	TRUE	0 (0.0)	130614 (100.0)		
group (%)	Cardiovascular	193044 (38.0)	13941 (10.7)	<0.001	
	Gastrointestinal	58099 (11.4)	8030 (6.1)		
	Gynaecological	1611 (0.3)	84 (0.1)		
	Hematological	3982 (0.8)	751 (0.6)		
	Metabolic	48203 (9.5)	4201 (3.2)		
	Muscoskeletal/Skin disease	6406 (1.3)	1591 (1.2)		
	Neurological	79614 (15.7)	6459 (4.9)		
	Renal/Genitourinary	12081 (2.4)	3468 (2.7)		
	Respiratory	62754 (12.3)	32443 (24.8)		
	Sepsis	9783 (1.9)	58478 (44.8)		
	Trauma	27664 (5.4)	706 (0.5)		
	Undefined	4902 (1.0)	462 (0.4)		

28 Table 2 Between Groups

```
roc.test(SIRS1ADJSepsis.Pred.roc,qSOFA1ADJSepsis.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SIRS1ADJSepsis.Pred.roc and qSOFA1ADJSepsis.Pred.roc
## Z = 18.208, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7553989 0.7409462

```

```
roc.test(SIRS1ADJSepsis.Pred.roc, SOFA1ADJSepsis.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SIRS1ADJSepsis.Pred.roc and SOFA1ADJSepsis.Pred.roc
## Z = -13.586, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7553989 0.7678386

```

```
roc.test(SOFA1ADJSepsis.Pred.roc, qSOFA1ADJSepsis.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SOFA1ADJSepsis.Pred.roc and qSOFA1ADJSepsis.Pred.roc
## Z = 35.98, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7678386 0.7409462

```

```
roc.test(qSOFA2ADJSepsis.Pred.roc, SIRS2ADJSepsis.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: qSOFA2ADJSepsis.Pred.roc and SIRS2ADJSepsis.Pred.roc
## Z = -1.7694, p-value = 0.07683
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7291955 0.7303764

```

```
roc.test(SOFA2ADJSepsis.Pred.roc, SIRS2ADJSepsis.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SOFA2ADJSepsis.Pred.roc and SIRS2ADJSepsis.Pred.roc
## Z = 11.937, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7398636 0.7303764

```

```
roc.test(FuzzyLogicADJSepsis.Pred.roc, SIRS2ADJSepsis.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: FuzzyLogicADJSepsis.Pred.roc and SIRS2ADJSepsis.Pred.roc
## Z = 52.772, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7706897 0.7303764

```

```
roc.test(FuzzyLogicADJSepsis.Pred.roc,qSOFA2ADJSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
## 
## data: FuzzyLogicADJSepsis.Pred.roc and qSOFA2ADJSepsis.Pred.roc
## Z = 50.241, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
##      0.7706897    0.7291955
```

```
roc.test(FuzzyLogicADJSepsis.Pred.roc,SOFA2ADJSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
## 
## data: FuzzyLogicADJSepsis.Pred.roc and SOFA2ADJSepsis.Pred.roc
## Z = 36.222, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
##      0.7706897    0.7398636
```

```
roc.test(SOFA2ADJSepsis.Pred.roc,qSOFA2ADJSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
## 
## data: SOFA2ADJSepsis.Pred.roc and qSOFA2ADJSepsis.Pred.roc
## Z = 15.33, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
##      0.7398636    0.7291955
```

```
roc.test(SIRS1CrudeSepsis.Pred.roc,qSOFAlCrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
## 
## data: SIRS1CrudeSepsis.Pred.roc and qSOFAlCrudeSepsis.Pred.roc
## Z = 9.6054, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
##      0.6502231    0.6368558
```

```
roc.test(SIRS1CrudeSepsis.Pred.roc,SOFAlCrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
## 
## data: SIRS1CrudeSepsis.Pred.roc and SOFAlCrudeSepsis.Pred.roc
## Z = -19.427, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
##      0.6502231    0.6796153
```

```
roc.test(SOFAlCrudeSepsis.Pred.roc,qSOFAlCrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
## 
## data: SOFA1CrudeSepsis.Pred.roc and qSOFA1CrudeSepsis.Pred.roc
## Z = 34.588, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6796153 0.6368558
```

```
roc.test(qSOFA2CrudeSepsis.Pred.roc,SIRS2CrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
## 
## data: qSOFA2CrudeSepsis.Pred.roc and SIRS2CrudeSepsis.Pred.roc
## Z = 11.434, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.5928223 0.5805731
```

```
roc.test(SOFA2CrudeSepsis.Pred.roc,SIRS2CrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
## 
## data: SOFA2CrudeSepsis.Pred.roc and SIRS2CrudeSepsis.Pred.roc
## Z = 24.43, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6087716 0.5805731
```

```
roc.test(FuzzyLogicCrudeSepsis.Pred.roc,SIRS2CrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
## 
## data: FuzzyLogicCrudeSepsis.Pred.roc and SIRS2CrudeSepsis.Pred.roc
## Z = 83.266, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6665731 0.5805731
```

```
roc.test(FuzzyLogicCrudeSepsis.Pred.roc,qSOFA2CrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
## 
## data: FuzzyLogicCrudeSepsis.Pred.roc and qSOFA2CrudeSepsis.Pred.roc
## Z = 61.41, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6665731 0.5928223
```

```
roc.test(FuzzyLogicCrudeSepsis.Pred.roc,SOFA2CrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
## 
## data: FuzzyLogicCrudeSepsis.Pred.roc and SOFA2CrudeSepsis.Pred.roc
## Z = 49.06, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6665731 0.6087716
```

```
roc.test(SOFA2CrudeSepsis.Pred.roc,qSOFA2CrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
##
## data: SOFA2CrudeSepsis.Pred.roc and qSOFA2CrudeSepsis.Pred.roc
## Z = 14.701, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6087716 0.5928223
```

```
roc.test(SIRS2ADJSepsis.Pred.roc,SIRS2CrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
##
## data: SIRS2ADJSepsis.Pred.roc and SIRS2CrudeSepsis.Pred.roc
## Z = 145.5, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7303764 0.5805731
```

```
roc.test(SOFA2ADJSepsis.Pred.roc,SOFA2CrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
##
## data: SOFA2ADJSepsis.Pred.roc and SOFA2CrudeSepsis.Pred.roc
## Z = 134.85, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7398636 0.6087716
```

```
roc.test(FuzzyLogicADJSepsis.Pred.roc,FuzzyLogicCrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
##
## data: FuzzyLogicADJSepsis.Pred.roc and FuzzyLogicCrudeSepsis.Pred.roc
## Z = 124.58, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7706897 0.6665731
```

```
roc.test(FuzzyLogicCrudeSepsis.Pred.roc,qSOFA2CrudeSepsis.Pred.roc)
```

```
## 
## DeLong's test for two correlated ROC curves
##
## data: FuzzyLogicCrudeSepsis.Pred.roc and qSOFA2CrudeSepsis.Pred.roc
## Z = 61.41, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6665731 0.5928223
```

```
roc.test(FuzzyLogicCrudeSepsis.Pred.roc,SOFA2CrudeSepsis.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: FuzzyLogicCrudeSepsis.Pred.roc and SOFA2CrudeSepsis.Pred.roc
## Z = 49.06, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6665731 0.6087716

```

```
roc.test(SOFA2CrudeSepsis.Pred.roc,qSOFA2CrudeSepsis.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SOFA2CrudeSepsis.Pred.roc and qSOFA2CrudeSepsis.Pred.roc
## Z = 14.701, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6087716 0.5928223

```

```
roc.test(SIRS1ADJMort.Pred.roc,qSOFAlADJMort.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SIRS1ADJMort.Pred.roc and qSOFAlADJMort.Pred.roc
## Z = 3.0026, p-value = 0.002677
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7814890 0.7777231

```

```
roc.test(SIRS1ADJMort.Pred.roc,SOFAlADJMort.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SIRS1ADJMort.Pred.roc and SOFAlADJMort.Pred.roc
## Z = -46.605, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7814890 0.8472926

```

```
roc.test(SOFAlADJMort.Pred.roc,qSOFAlADJMort.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SOFAlADJMort.Pred.roc and qSOFAlADJMort.Pred.roc
## Z = 55.425, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.8472926 0.7777231

```

```
roc.test(qSOFAlADJMort.Pred.roc,SIRS2ADJMort.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: qSOFAlADJMort.Pred.roc and SIRS2ADJMort.Pred.roc
## Z = 7.8843, p-value = 3.163e-15
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.7505584 0.7423965

```

```
roc.test(SOFA2ADJMort.Pred.roc,SIRS2ADJMort.Pred.roc)
```

```
##  
## DeLong's test for two correlated ROC curves  
##  
## data: SOFA2ADJMort.Pred.roc and SIRS2ADJMort.Pred.roc  
## Z = 14.999, p-value < 2.2e-16  
## alternative hypothesis: true difference in AUC is not equal to 0  
## sample estimates:  
## AUC of roc1 AUC of roc2  
## 0.7592311 0.7423965
```

```
roc.test(FuzzyLogicADJMort.Pred.roc,SIRS2ADJMort.Pred.roc)
```

```
##  
## DeLong's test for two correlated ROC curves  
##  
## data: FuzzyLogicADJMort.Pred.roc and SIRS2ADJMort.Pred.roc  
## Z = 30.923, p-value < 2.2e-16  
## alternative hypothesis: true difference in AUC is not equal to 0  
## sample estimates:  
## AUC of roc1 AUC of roc2  
## 0.7767738 0.7423965
```

```
roc.test(FuzzyLogicADJMort.Pred.roc,qSOFA2ADJMort.Pred.roc)
```

```
##  
## DeLong's test for two correlated ROC curves  
##  
## data: FuzzyLogicADJMort.Pred.roc and qSOFA2ADJMort.Pred.roc  
## Z = 21.591, p-value < 2.2e-16  
## alternative hypothesis: true difference in AUC is not equal to 0  
## sample estimates:  
## AUC of roc1 AUC of roc2  
## 0.7767738 0.7505584
```

```
roc.test(FuzzyLogicADJMort.Pred.roc,SOFA2ADJMort.Pred.roc)
```

```
##  
## DeLong's test for two correlated ROC curves  
##  
## data: FuzzyLogicADJMort.Pred.roc and SOFA2ADJMort.Pred.roc  
## Z = 14.737, p-value < 2.2e-16  
## alternative hypothesis: true difference in AUC is not equal to 0  
## sample estimates:  
## AUC of roc1 AUC of roc2  
## 0.7767738 0.7592311
```

```
roc.test(SOFA2ADJMort.Pred.roc,qSOFA2ADJMort.Pred.roc)
```

```
##  
## DeLong's test for two correlated ROC curves  
##  
## data: SOFA2ADJMort.Pred.roc and qSOFA2ADJMort.Pred.roc  
## Z = 8.3814, p-value < 2.2e-16  
## alternative hypothesis: true difference in AUC is not equal to 0  
## sample estimates:  
## AUC of roc1 AUC of roc2  
## 0.7592311 0.7505584
```

```
roc.test(SIRS1CrudeMort.Pred.roc,qSOFAlCrudeMort.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SIRS1CrudeMort.Pred.roc and qSOFA1CrudeMort.Pred.roc
## Z = -6.7101, p-value = 1.945e-11
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6959156 0.7080340

```

```
roc.test(SIRS1CrudeMort.Pred.roc,qSOFA1CrudeMort.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SIRS1CrudeMort.Pred.roc and SOFA1CrudeMort.Pred.roc
## Z = -58.592, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6959156 0.8037549

```

```
roc.test(SOFA1CrudeMort.Pred.roc,qSOFA1CrudeMort.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SOFA1CrudeMort.Pred.roc and qSOFA1CrudeMort.Pred.roc
## Z = 61.582, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.8037549 0.7080340

```

```
roc.test(qSOFA2CrudeMort.Pred.roc,SIRS2CrudeMort.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: qSOFA2CrudeMort.Pred.roc and SIRS2CrudeMort.Pred.roc
## Z = 30.418, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6290462 0.5932939

```

```
roc.test(SOFA2CrudeMort.Pred.roc,SIRS2CrudeMort.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: SOFA2CrudeMort.Pred.roc and SIRS2CrudeMort.Pred.roc
## Z = 39.722, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6407420 0.5932939

```

```
roc.test(FuzzyLogicCrudeMort.Pred.roc,SIRS2CrudeMort.Pred.roc)
```

```

## 
## DeLong's test for two correlated ROC curves
##
## data: FuzzyLogicCrudeMort.Pred.roc and SIRS2CrudeMort.Pred.roc
## Z = 65.688, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6734078 0.5932939

```

```
roc.test(FuzzyLogicCrudeMort.Pred.roc,qSOFA2CrudeMort.Pred.roc)

##
## DeLong's test for two correlated ROC curves
##
## data: FuzzyLogicCrudeMort.Pred.roc and qSOFA2CrudeMort.Pred.roc
## Z = 31.809, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6734078 0.6290462
```

```
roc.test(FuzzyLogicCrudeMort.Pred.roc,SOFA2CrudeMort.Pred.roc)
```

```
##
## DeLong's test for two correlated ROC curves
##
## data: FuzzyLogicCrudeMort.Pred.roc and SOFA2CrudeMort.Pred.roc
## Z = 24.679, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6734078 0.6407420
```

```
roc.test(SOFA2CrudeMort.Pred.roc,qSOFA2CrudeMort.Pred.roc)
```

```
##
## DeLong's test for two correlated ROC curves
##
## data: SOFA2CrudeMort.Pred.roc and qSOFA2CrudeMort.Pred.roc
## Z = 10.147, p-value < 2.2e-16
## alternative hypothesis: true difference in AUC is not equal to 0
## sample estimates:
## AUC of roc1 AUC of roc2
## 0.6407420 0.6290462
```

29 Table 3 Mortality Outcome

```
options(dplyr.width=Inf)
SIRSmortality_Table3 <- ssd_incl_te %>% group_by(BaselineDec, SIRS_Positive) %>% summarise(n=n(),nMortality=sum(hospital_mortality_ultimate), propMortality=mean(hospital_mortality_ultimate), Oddsmortality=propMortality/(1-prop.Mortality))
options(dplyr.width=Inf)
SIRSmortality_Table3 %>% filter(!SIRS_Positive) %>% rename(lt2SIRS=SIRS_Positive) %>% inner_join(SIRSmortality_Table3 %>% filter(SIRS_Positive) %>% rename(gt2SIRS=SIRS_Positive),by="BaselineDec")%>%mutate(Ratio=propMortality.y/propMortality.x)%>%knitr::kable()
```

BaselineDec	lt2SIRS	n.x	nMortality.x	propMortality.x	Oddsmortality.x	gt2SIRS	n.y	nMortality.y	propMortality.y	Oddsmortality.y	Ratio
[0.00359,0.0284)	FALSE	6003	20	0.0033317	0.0033428	TRUE	21380	509	0.0238073	0.0243879	7.145760
[0.02839,0.0400)	FALSE	6581	35	0.0053183	0.0053468	TRUE	20806	833	0.0400365	0.0417063	7.528011
[0.03996,0.0516)	FALSE	6745	68	0.0100815	0.0101842	TRUE	20613	1065	0.0516664	0.0544813	5.124850
[0.05164,0.0644)	FALSE	7113	95	0.0133558	0.0135366	TRUE	20260	1477	0.0729023	0.0786349	5.458462
[0.06437,0.0788)	FALSE	7438	132	0.0177467	0.0180673	TRUE	19939	1729	0.0867145	0.0949478	4.886229
[0.07885,0.0956)	FALSE	7196	171	0.0237632	0.0243416	TRUE	20195	2273	0.1125526	0.1268274	4.736425
[0.09557,0.1154)	FALSE	7021	213	0.0303376	0.0312867	TRUE	20338	2675	0.1315272	0.1514465	4.335451
[0.11543,0.1411)	FALSE	6392	272	0.0425532	0.0444444	TRUE	20983	3445	0.1641805	0.1964306	3.858242
[0.14115,0.1821)	FALSE	5831	352	0.0603670	0.0642453	TRUE	21544	4145	0.1923970	0.2382321	3.187121
[0.18207,0.7473]	FALSE	4899	434	0.0885895	0.0972004	TRUE	22475	5922	0.2634928	0.3577599	2.974311

```
qSOFAmortality_Table3 <- ssd_incl_te %>% group_by(BaselineDec, qSOFA_Positive) %>% summarise(n=n(), nMortality=sum(hospital_mortality_ultimate), propMortality=mean(hospital_mortality_ultimate), Oddsmortality=propMortality/(1-propMortality))
options(dplyr.width=Inf)
qSOFAmortality_Table3 %>% filter(!qSOFA_Positive) %>% rename(lt2qSOFA=qSOFA_Positive) %>% inner_join(qSOFAmortality_Table3 %>% filter(qSOFA_Positive) %>% rename(gt2qSOFA=qSOFA_Positive), by="BaselineDec") %>% mutate(Ratio=propMortality.y/propMortality.x) %>% knitr::kable()
```

BaselineDec	lt2qSOFA	n.x	nMortality.x	propMortality.x	Oddsmortality.x	gt2qSOFA	n.y	nMortality.y	propMortality.y	Oddsmortality.y	F
[0.00359,0.0284)	FALSE	11150	54	0.0048430	0.0048666	TRUE	16233	475	0.0292614	0.0301434	6.0
[0.02839,0.0400)	FALSE	10438	86	0.0082391	0.0083076	TRUE	16949	782	0.0461384	0.0483701	5.5
[0.03996,0.0516)	FALSE	10215	121	0.0118453	0.0119873	TRUE	17143	1012	0.0590328	0.0627363	4.9
[0.05164,0.0644)	FALSE	10130	148	0.0146101	0.0148267	TRUE	17243	1424	0.0825842	0.0900183	5.6
[0.06437,0.0788)	FALSE	9842	198	0.0201179	0.0205309	TRUE	17535	1663	0.0948389	0.1047757	4.7
[0.07885,0.0956)	FALSE	9242	259	0.0280242	0.0288322	TRUE	18149	2185	0.1203923	0.1368705	4.2
[0.09557,0.1154)	FALSE	8586	300	0.0349406	0.0362056	TRUE	18773	2588	0.1378576	0.1599011	3.9
[0.11543,0.1411)	FALSE	7737	351	0.0453664	0.0475223	TRUE	19638	3366	0.1714024	0.2068584	3.7
[0.14115,0.1821)	FALSE	6724	393	0.0584474	0.0620755	TRUE	20651	4104	0.1987313	0.2480208	3.4
[0.18207,0.7473]	FALSE	5622	519	0.0923159	0.1017049	TRUE	21752	5837	0.2683431	0.3667609	2.9

```
SOFAmortality_Table3 <- ssd_incl_te %>% group_by(BaselineDec, SOFA_Positive) %>% summarise(n=n(), nMortality=sum(hospital_mortality_ultimate), propMortality=mean(hospital_mortality_ultimate), Oddsmortality=propMortality/(1-propMortality))
options(dplyr.width=Inf)
SOFAmortality_Table3 %>% filter(!SOFA_Positive) %>% rename(lt2SOFA=SOFA_Positive) %>% inner_join(SOFAmortality_Table3 %>% filter(SOFA_Positive) %>% rename(gt2SOFA=SOFA_Positive), by="BaselineDec") %>% mutate(Ratio=propMortality.y/propMortality.x) %>% knitr::kable()
```

BaselineDec	lt2SOFA	n.x	nMortality.x	propMortality.x	Oddsmortality.x	gt2SOFA	n.y	nMortality.y	propMortality.y	Oddsmortality.y	F
[0.00359,0.0284)	FALSE	12149	21	0.0017285	0.0017315	TRUE	15234	508	0.0333465	0.0344968	19.29
[0.02839,0.0400)	FALSE	10095	31	0.0030708	0.0030803	TRUE	17292	837	0.0484039	0.0508660	15.76
[0.03996,0.0516)	FALSE	9963	48	0.0048178	0.0048411	TRUE	17395	1085	0.0623742	0.0665236	12.94
[0.05164,0.0644)	FALSE	9901	66	0.0066660	0.0067107	TRUE	17472	1506	0.0861951	0.0943254	12.93
[0.06437,0.0788)	FALSE	9577	119	0.0124256	0.0125819	TRUE	17800	1742	0.0978652	0.1084818	7.87
[0.07885,0.0956)	FALSE	8554	156	0.0182371	0.0185759	TRUE	18837	2288	0.1214631	0.1382561	6.66
[0.09557,0.1154)	FALSE	7782	158	0.0203033	0.0207240	TRUE	19577	2730	0.1394494	0.1620467	6.86
[0.11543,0.1411)	FALSE	6785	227	0.0334562	0.0346142	TRUE	20590	3490	0.1694998	0.2040936	5.06
[0.14115,0.1821)	FALSE	5856	254	0.0433743	0.0453409	TRUE	21519	4243	0.1971746	0.2456008	4.54
[0.18207,0.7473]	FALSE	4609	384	0.0833153	0.0908876	TRUE	22765	5972	0.2623325	0.3556244	3.14

```
FuzzyLogicmortality_Table3 <- ssd_incl_te %>% group_by(BaselineDec, SepsisFuzzyLogicPositive) %>% summarise(n=n(), nMortality=sum(hospital_mortality_ultimate), propMortality=mean(hospital_mortality_ultimate), Oddsmortality=propMortality/(1-propMortality))
options(dplyr.width=Inf)
FuzzyLogicmortality_Table3 %>% filter(!SepsisFuzzyLogicPositive) %>% rename(lt2FuzzyLogic=SepsisFuzzyLogicPositive) %>% inner_join(FuzzyLogicmortality_Table3 %>% filter(SepsisFuzzyLogicPositive) %>% rename(gt2FuzzyLogic=SepsisFuzzyLogicPositive), by="BaselineDec") %>% mutate(Ratio=propMortality.y/propMortality.x) %>% knitr::kable()
```

BaselineDec	lt2FuzzyLogic	n.x	nMortality.x	propMortality.x	Oddsmortality.x	gt2FuzzyLogic	n.y	nMortality.y	propMortality.y	Oddsmorta
[0.00359,0.0284)	FALSE	13638	51	0.0037396	0.0037536	TRUE	13745	478	0.0347763	0.0361
[0.02839,0.0400)	FALSE	13374	91	0.0068042	0.0068509	TRUE	14013	777	0.0554485	0.058
[0.03996,0.0516)	FALSE	13338	129	0.0096716	0.0097661	TRUE	14020	1004	0.0716120	0.077
[0.05164,0.0644)	FALSE	13377	199	0.0148763	0.0151009	TRUE	13996	1373	0.0980995	0.108
[0.06437,0.0788)	FALSE	13568	272	0.0200472	0.0204573	TRUE	13809	1589	0.1150699	0.130
[0.07885,0.0956)	FALSE	12865	351	0.0272833	0.0280486	TRUE	14526	2093	0.1440865	0.168
[0.09557,0.1154)	FALSE	12301	408	0.0331680	0.0343059	TRUE	15058	2480	0.1646965	0.197

BaselineDec	lt2FuzzyLogic	n.x	nMortality.x	propMortality.x	Odds mortality.x	gt2FuzzyLogic	n.y	nMortality.y	propMortality.y	Odds morta
[0.11543,0.1411)	FALSE	11311	541	0.0478295	0.0502321	TRUE	16064	3176	0.1977092	0.246
[0.14115,0.1821)	FALSE	10409	617	0.0592756	0.0630106	TRUE	16966	3880	0.2286927	0.296
[0.18207,0.7473]	FALSE	8749	833	0.0952109	0.1052299	TRUE	18625	5523	0.2965369	0.421

30 Table 3 Sepsis Outcome

```
SIRSsepsis_Table3 <- ssd_incl_te %>% group_by(BaselineDec, SIRS_Positive) %>% summarise(n=n(),nsepsis=sum(sepsis_outcome), propsepsis=mean(sepsis_outcome),Oddssepsis=propsepsis/(1-propsepsis))
options(dplyr.width=Inf)
SIRSsepsis_Table3 %>% filter(!SIRS_Positive) %>% rename(lt2SIRS=SIRS_Positive) %>% inner_join(SIRSsepsis_Table3 %>% filter(SIRS_Positive) %>% rename(gt2SIRS=SIRS_Positive),by="BaselineDec")%>%mutate(Ratio=propsepsis.y/propsepsis.x)%>%knitr::kable()
```

BaselineDec	lt2SIRS	n.x	nsepsis.x	propsepsis.x	Oddssepsis.x	gt2SIRS	n.y	nsepsis.y	propsepsis.y	Oddssepsis.y	Ratio
[0.00359,0.0284)	FALSE	6003	152	0.0253207	0.0259785	TRUE	21380	1679	0.0785313	0.0852241	3.101471
[0.02839,0.0400)	FALSE	6581	274	0.0416350	0.0434438	TRUE	20806	2392	0.1149668	0.1299012	2.761302
[0.03996,0.0516)	FALSE	6745	398	0.0590067	0.0627068	TRUE	20613	3148	0.1527192	0.1802462	2.588168
[0.05164,0.0644)	FALSE	7113	523	0.0735273	0.0793627	TRUE	20260	3960	0.1954590	0.2429448	2.658318
[0.06437,0.0788)	FALSE	7438	635	0.0853724	0.0933412	TRUE	19939	4663	0.2338633	0.3052501	2.739331
[0.07885,0.0956)	FALSE	7196	711	0.0988049	0.1096376	TRUE	20195	5426	0.2686804	0.3673912	2.719302
[0.09557,0.1154)	FALSE	7021	834	0.1187865	0.1347988	TRUE	20338	6019	0.2959485	0.4203506	2.491432
[0.11543,0.1411)	FALSE	6392	820	0.1282854	0.1471644	TRUE	20983	6694	0.3190202	0.4684723	2.486801
[0.14115,0.1821)	FALSE	5831	852	0.1461156	0.1711187	TRUE	21544	7450	0.3458039	0.5285937	2.366646
[0.18207,0.7473]	FALSE	4899	1001	0.2043274	0.2567984	TRUE	22475	8625	0.3837597	0.6227437	1.878161

```
qSOFAsepsis_Table3 <- ssd_incl_te %>% group_by(BaselineDec, qSOFA_Positive) %>% summarise(n=n(),nsepsis=sum(sepsis_outcome), propsepsis=mean(sepsis_outcome), Oddssepsis=propsepsis/(1-propsepsis))
options(dplyr.width=Inf)
qSOFAsepsis_Table3 %>% filter(!qSOFA_Positive) %>% rename(lt2qSOFA=qSOFA_Positive) %>% inner_join(qSOFAsepsis_Table3 %>% filter(qSOFA_Positive) %>% rename(gt2qSOFA=qSOFA_Positive),by="BaselineDec")%>%mutate(Ratio=propsepsis.y/propsepsis.x)%>%knitr::kable()
```

BaselineDec	lt2qSOFA	n.x	nsepsis.x	propsepsis.x	Oddssepsis.x	gt2qSOFA	n.y	nsepsis.y	propsepsis.y	Oddssepsis.y	Ratio
[0.00359,0.0284)	FALSE	11150	497	0.0445740	0.0466535	TRUE	16233	1334	0.0821783	0.0895362	1.843637
[0.02839,0.0400)	FALSE	10438	675	0.0646676	0.0691386	TRUE	16949	1991	0.1174701	0.1331060	1.816522
[0.03996,0.0516)	FALSE	10215	858	0.0839941	0.0916961	TRUE	17143	2688	0.1567987	0.1859564	1.866782
[0.05164,0.0644)	FALSE	10130	990	0.0977295	0.1083151	TRUE	17243	3493	0.2025750	0.2540364	2.072812
[0.06437,0.0788)	FALSE	9842	1096	0.1113595	0.1253144	TRUE	17535	4202	0.2396350	0.3151579	2.151905
[0.07885,0.0956)	FALSE	9242	1208	0.1307076	0.1503610	TRUE	18149	4929	0.2715852	0.3728442	2.077807
[0.09557,0.1154)	FALSE	8586	1268	0.1476823	0.1732714	TRUE	18773	5585	0.2975017	0.4234911	2.014471
[0.11543,0.1411)	FALSE	7737	1205	0.1557451	0.1844764	TRUE	19638	6309	0.3212649	0.4733288	2.062761
[0.14115,0.1821)	FALSE	6724	1125	0.1673111	0.2009287	TRUE	20651	7177	0.3475376	0.5326555	2.077194
[0.18207,0.7473]	FALSE	5622	1211	0.2154038	0.2745409	TRUE	21752	8415	0.3868610	0.6309515	1.795980

```
SOFAssepsis_Table3 <- ssd_incl_te %>% group_by(BaselineDec, SOFA_Positive) %>% summarise(n=n(),nsepsis=sum(sepsis_outcome), propsepsis=mean(sepsis_outcome), Oddssepsis=propsepsis/(1-propsepsis))
options(dplyr.width=Inf)
SOFAssepsis_Table3 %>% filter(!SOFA_Positive) %>% rename(lt2SOFA=SOFA_Positive) %>% inner_join(SOFAssepsis_Table3 %>% filter(SOFA_Positive) %>% rename(gt2SOFA=SOFA_Positive),by="BaselineDec")%>%mutate(Ratio=propsepsis.y/propsepsis.x)%>%knitr::kable()
```

BaselineDec	lt2SOFA	n.x	nsepsis.x	propsepsis.x	Oddssepsis.x	gt2SOFA	n.y	nsepsis.y	propsepsis.y	Oddssepsis.y	Ratio
[0.00359,0.0284)	FALSE	12149	445	0.0366285	0.0380212	TRUE	15234	1386	0.0909807	0.1000867	2.483875
[0.02839,0.0400)	FALSE	10095	533	0.0527984	0.0557415	TRUE	17292	2133	0.1233518	0.1407085	2.336279
[0.03996,0.0516)	FALSE	9963	742	0.0744756	0.0804685	TRUE	17395	2804	0.1611957	0.1921733	2.164411

BaselineDec	lt2SOFA	n.x	nsepsis.x	propsepsis.x	Oddssepsis.x	gt2SOFA	n.y	nsepsis.y	propsepsis.y	Oddssepsis.y	Ratio
[0.05164,0.0644)	FALSE	9901	741	0.0748409	0.0808952	TRUE	17472	3742	0.2141712	0.2725419	2.861686
[0.06437,0.0788)	FALSE	9577	854	0.0891720	0.0979021	TRUE	17800	4444	0.2496629	0.3327344	2.799791
[0.07885,0.0956)	FALSE	8554	866	0.1012392	0.1126431	TRUE	18837	5271	0.2798216	0.3885449	2.763966
[0.09557,0.1154)	FALSE	7782	922	0.1184785	0.1344023	TRUE	19577	5931	0.3029576	0.4346329	2.557067
[0.11543,0.1411)	FALSE	6785	916	0.1350037	0.1560743	TRUE	20590	6598	0.3204468	0.4715552	2.373615
[0.14115,0.1821)	FALSE	5856	898	0.1533470	0.1811214	TRUE	21519	7404	0.3440680	0.5245484	2.243722
[0.18207,0.7473]	FALSE	4609	883	0.1915817	0.2369834	TRUE	22765	8743	0.3840545	0.6235202	2.004651

```
FuzzyLogicsepsis_Table3 <- ssd_incl_te %>% group_by(BaselineDec, SepsisFuzzyLogicPositive) %>% summarise(n=n(),nsepsis=sum(sepsis_outcome), propsepsis=mean(sepsis_outcome), Oddssepsis=propsepsis/(1-propsepsis))
FuzzyLogicsepsis_Table3 %>% filter(!SepsisFuzzyLogicPositive) %>% rename(lt2FuzzyLogic=SepsisFuzzyLogicPositive)
%>% inner_join(FuzzyLogicsepsis_Table3 %>% filter(SepsisFuzzyLogicPositive) %>% rename(gt2FuzzyLogic=SepsisFuzzyLogicPositive),by="BaselineDec")%>%mutate (Ratio=propsepsis.y/propsepsis.x)%>%kable()
```

BaselineDec	lt2FuzzyLogic	n.x	nsepsis.x	propsepsis.x	Oddssepsis.x	gt2FuzzyLogic	n.y	nsepsis.y	propsepsis.y	Oddssepsis.y	Ratio
[0.00359,0.0284)	FALSE	13638	395	0.0289632	0.0298271	TRUE	13745	1436	0.1044744	0.1166626	3.60714:
[0.02839,0.0400)	FALSE	13374	542	0.0405264	0.0422382	TRUE	14013	2124	0.1515735	0.1786525	3.74011:
[0.03996,0.0516)	FALSE	13338	719	0.0539061	0.0569776	TRUE	14020	2827	0.2016405	0.2525686	3.74058:
[0.05164,0.0644)	FALSE	13377	899	0.0672049	0.0720468	TRUE	13996	3584	0.2560732	0.3442182	3.81033:
[0.06437,0.0788)	FALSE	13568	1054	0.0776828	0.0842257	TRUE	13809	4244	0.3073358	0.4437010	3.95629:
[0.07885,0.0956)	FALSE	12865	1130	0.0878352	0.0962931	TRUE	14526	5007	0.3446923	0.5260006	3.92430:
[0.09557,0.1154)	FALSE	12301	1324	0.1076335	0.1206158	TRUE	15058	5529	0.3671802	0.5802288	3.41139:
[0.11543,0.1411)	FALSE	11311	1351	0.1194413	0.1356426	TRUE	16064	6163	0.3836529	0.6224624	3.21206:
[0.14115,0.1821)	FALSE	10409	1397	0.1342108	0.1550155	TRUE	16966	6905	0.4069905	0.6863135	3.03247:
[0.18207,0.7473]	FALSE	8749	1561	0.1784204	0.2171675	TRUE	18625	8065	0.4330201	0.7637311	2.426961

```

options(dplyr.width=Inf)

ORSIRSmort_Table3 <- SIRSmortality_Table3 %>% filter(!SIRS_Positive) %>% rename(lt2SIRS=SIRS_Positive) %>% inner_join(SIRSmortality_Table3 %>% filter(SIRS_Positive) %>% rename(gt2SIRS=SIRS_Positive), by="BaselineDec") %>% mutate(OddsRatio=Oddsmortality.y/Oddsmortality.x) %>% mutate(a=nMortality.x, b=nMortality.y, c=n.x, d=n.y, se=sqrt(1/a+1/b+1/c+1/d), LL=exp(log(OddsRatio)-qnorm(0.995)*se), UL=exp(log(OddsRatio)+qnorm(0.995)*se)) %>% mutate(type="SIRS")

ORqSOFAmort_Table3 <- qSOFAmortality_Table3 %>% filter(!qSOFA_Positive) %>% rename(lt2qSOFA=qSOFA_Positive) %>% inner_join(qSOFAmortality_Table3 %>% filter(qSOFA_Positive) %>% rename(gt2qSOFA=qSOFA_Positive), by="BaselineDec") %>% mutate(OddsRatio=Oddsmortality.y/Oddsmortality.x) %>% mutate(a=nMortality.x, b=nMortality.y, c=n.x, d=n.y, se=sqrt(1/a+1/b+1/c+1/d), LL=exp(log(OddsRatio)-qnorm(0.995)*se), UL=exp(log(OddsRatio)+qnorm(0.995)*se)) %>% mutate(type="qSOFA")

ORSOFAmort_Table3 <- SOFAmortality_Table3 %>% filter(!SOFA_Positive) %>% rename(lt2SOFA=SOFA_Positive) %>% inner_join(SOFAmortality_Table3 %>% filter(SOFA_Positive) %>% rename(gt2SOFA=SOFA_Positive), by="BaselineDec") %>% mutate(OddsRatio=Oddsmortality.y/Oddsmortality.x) %>% mutate(a=nMortality.x, b=nMortality.y, c=n.x, d=n.y, se=sqrt(1/a+1/b+1/c+1/d), LL=exp(log(OddsRatio)-qnorm(0.995)*se), UL=exp(log(OddsRatio)+qnorm(0.995)*se)) %>% mutate(type="SOFA")

ORFuzzyLogicmort_Table3 <- FuzzyLogicmortality_Table3 %>% filter(!SepsisFuzzyLogicPositive) %>% rename(lt2FuzzyLogic=SepsisFuzzyLogicPositive) %>% inner_join(FuzzyLogicmortality_Table3 %>% filter(SepsisFuzzyLogicPositive) %>% rename(gt2FuzzyLogic=SepsisFuzzyLogicPositive), by="BaselineDec") %>% mutate(OddsRatio=Oddsmortality.y/Oddsmortality.x) %>% mutate(a=nMortality.x, b=nMortality.y, c=n.x-a, d=n.y, se=sqrt(1/a+1/b+1/c+1/d), LL=exp(log(OddsRatio)-qnorm(0.995)*se), UL=exp(log(OddsRatio)+qnorm(0.995)*se)) %>% mutate(type="Fuzzy Logic")

ORSIRSsepsis_Table3 <- SIRSsepsis_Table3 %>% filter(!SIRS_Positive) %>% rename(lt2SIRS=SIRS_Positive) %>% inner_join(SIRSsepsis_Table3 %>% filter(SIRS_Positive) %>% rename(gt2SIRS=SIRS_Positive), by="BaselineDec") %>% mutate(OddsRatio=Oddssepsis.y/Oddssepsis.x) %>% mutate(a=nsepsis.x, b=nsepsis.y, c=n.x, d=n.y, se=sqrt(1/a+1/b+1/c+1/d), LL=exp(log(OddsRatio)-qnorm(0.995)*se), UL=exp(log(OddsRatio)+qnorm(0.995)*se)) %>% mutate(type="SIRS")

ORqSOFAsepsis_Table3 <- qSOFAsepsis_Table3 %>% filter(!qSOFA_Positive) %>% rename(lt2qSOFA=qSOFA_Positive) %>% inner_join(qSOFAsepsis_Table3 %>% filter(qSOFA_Positive) %>% rename(gt2qSOFA=qSOFA_Positive), by="BaselineDec") %>% mutate(OddsRatio=Oddssepsis.y/Oddssepsis.x) %>% mutate(a=nsepsis.x, b=nsepsis.y, c=n.x, d=n.y, se=sqrt(1/a+1/b+1/c+1/d), LL=exp(log(OddsRatio)-qnorm(0.995)*se), UL=exp(log(OddsRatio)+qnorm(0.995)*se)) %>% mutate(type="qSOFA")

ORSOFAsepsis_Table3 <- SOFAsepsis_Table3 %>% filter(!SOFA_Positive) %>% rename(lt2SOFA=SOFA_Positive) %>% inner_join(SOFAsepsis_Table3 %>% filter(SOFA_Positive) %>% rename(gt2SOFA=SOFA_Positive), by="BaselineDec") %>% mutate(OddsRatio=Oddssepsis.y/Oddssepsis.x) %>% mutate(a=nsepsis.x, b=nsepsis.y, c=n.x, d=n.y, se=sqrt(1/a+1/b+1/c+1/d), LL=exp(log(OddsRatio)-qnorm(0.995)*se), UL=exp(log(OddsRatio)+qnorm(0.995)*se)) %>% mutate(type="SOFA")

ORFuzzyLogicsepsis_Table3 <- FuzzyLogicsepsis_Table3 %>% filter(!SepsisFuzzyLogicPositive) %>% rename(lt2FuzzyLogic=SepsisFuzzyLogicPositive) %>% inner_join(FuzzyLogicsepsis_Table3 %>% filter(SepsisFuzzyLogicPositive), by="BaselineDec") %>% rename(gt2FuzzyLogic=SepsisFuzzyLogicPositive) %>% mutate(OddsRatio=Oddssepsis.y/Oddssepsis.x) %>% mutate(a=nsepsis.x, b=nsepsis.y, c=n.x-a, d=n.y, se=sqrt(1/a+1/b+1/c+1/d), LL=exp(log(OddsRatio)-qnorm(0.995)*se), UL=exp(log(OddsRatio)+qnorm(0.995)*se)) %>% mutate(type="Fuzzy Logic")

```

31 Plots for Table 3

```

library(ggplot2)

levels(ORFuzzyLogicsepsis_Table3$BaselineDec)<-seq(1,10)
levels(ORSOFAsepsis_Table3$BaselineDec)<-seq(1,10)
levels(ORqSOFAsepsis_Table3$BaselineDec)<-seq(1,10)
levels(ORSIRSsepsis_Table3$BaselineDec)<-seq(1,10)

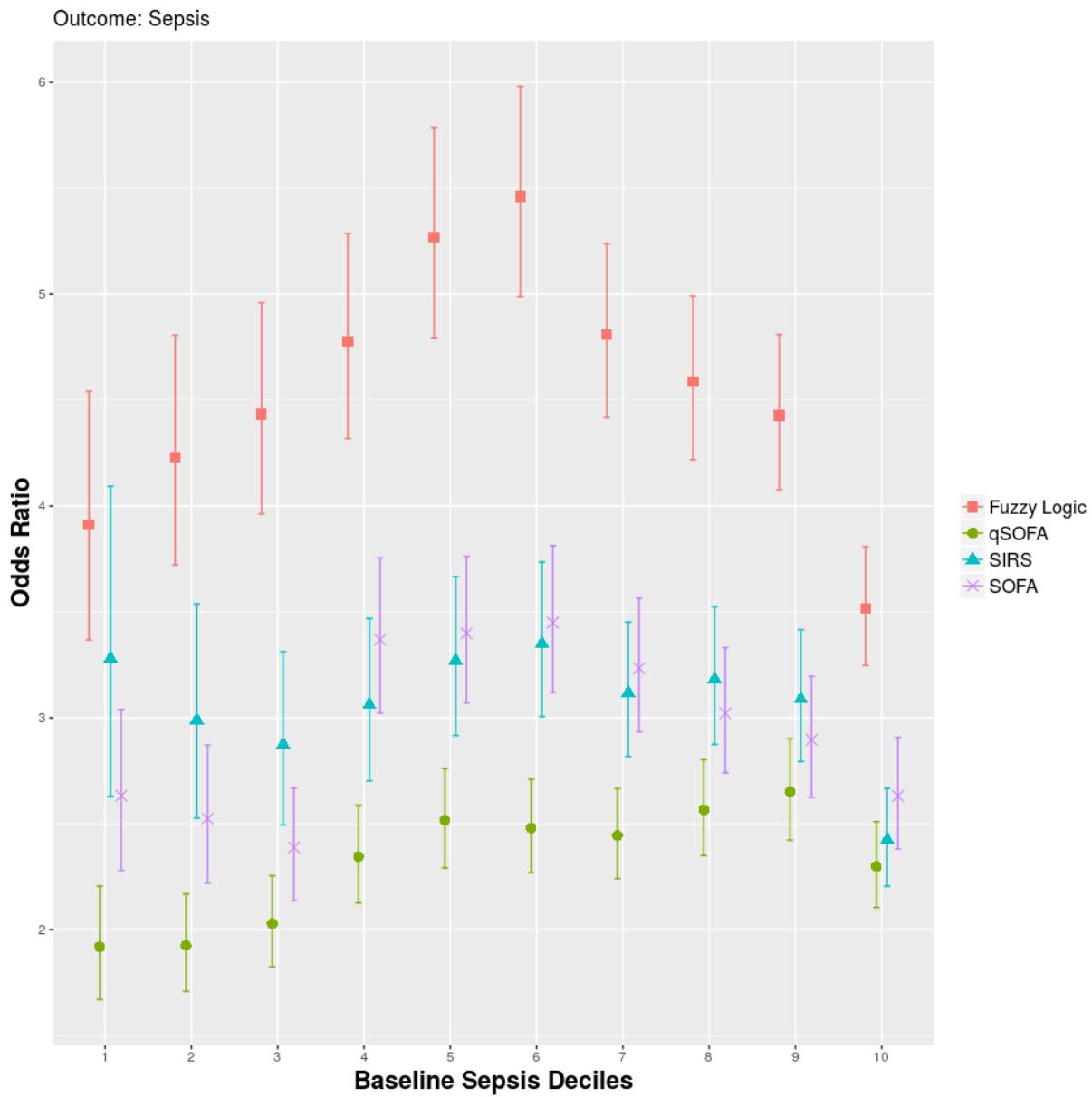
ORTable3<-ORFuzzyLogicsepsis_Table3 %>% bind_rows(ORSOFAsepsis_Table3) %>% bind_rows(ORqSOFAsepsis_Table3) %>% bind_rows(ORSIRSsepsis_Table3)

postscript(file="deciles_sepsis_nolog_orig.eps")
ggplot(ORTable3,aes(BaselineDec,OddsRatio, group=type,type)) + geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Sepsis Deciles") + ylab("Odds Ratio") + theme(legend.title=element_blank()) + theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12)) + ggtitle("Outcome: Sepsis") + scale_shape_manual(values=c(15, 16, 17,4))
dev.off()

## png
## 2

```

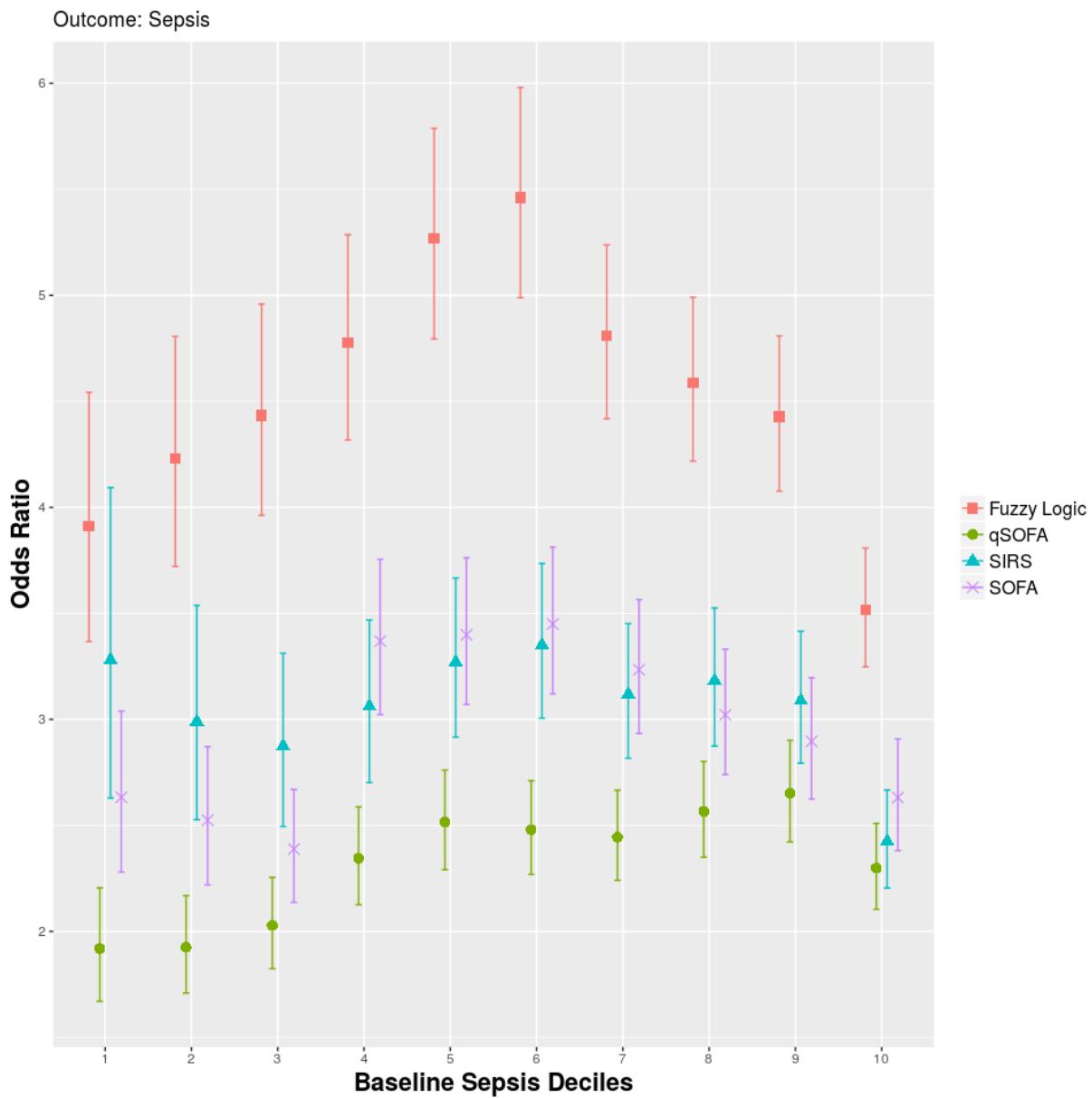
```
ggplot(ORTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Sepsis Deciles")+ylab("Odds Ratio")+ theme(legend.title=element_blank())+ theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12)) +ggtitle("Outcome: Sepsis") + scale_shape_manual(values=c(15, 16, 17,4))
```



```
postscript(file="deciles_sepsis_nolog_newszie.eps")
ggplot(ORTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Sepsis Deciles")+ylab("Odds Ratio")+ggtitle("Outcome: Sepsis") + theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12)) + scale_shape_manual(values=c(15, 16, 17,4))
dev.off()
```

```
## png
## 2
```

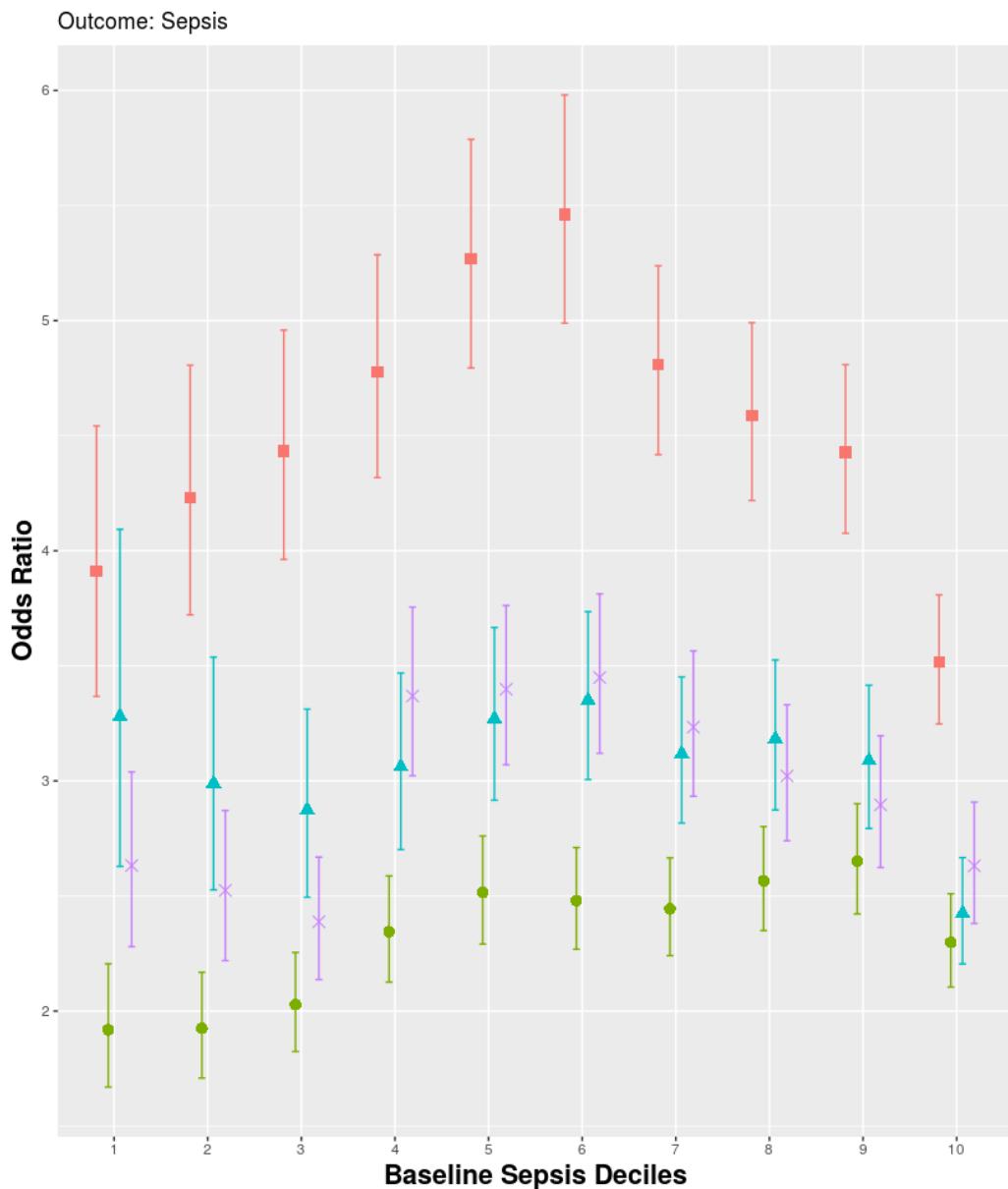
```
ggplot(ORTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Sepsis Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank())+ theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12)) +ggtitle("Outcome: Sepsis") + scale_shape_manual(values=c(15, 16, 17,4))
```



```
postscript(file="deciles_sepsis_nolog_orig.eps")
ggplot(ORTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Sepsis Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank())+ theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12))+ ggtitle("Outcome: Sepsis") + scale_y_log10() + scale_shape_manual(values=c(15, 16, 17,4))
dev.off()
```

```
## png
## 2
```

```
ggplot(ORTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Sepsis Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank())+ theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12))+ggtitle("Outcome: Sepsis") + scale_y_log10() + scale_shape_manual(values=c(15, 16, 17,4))
```

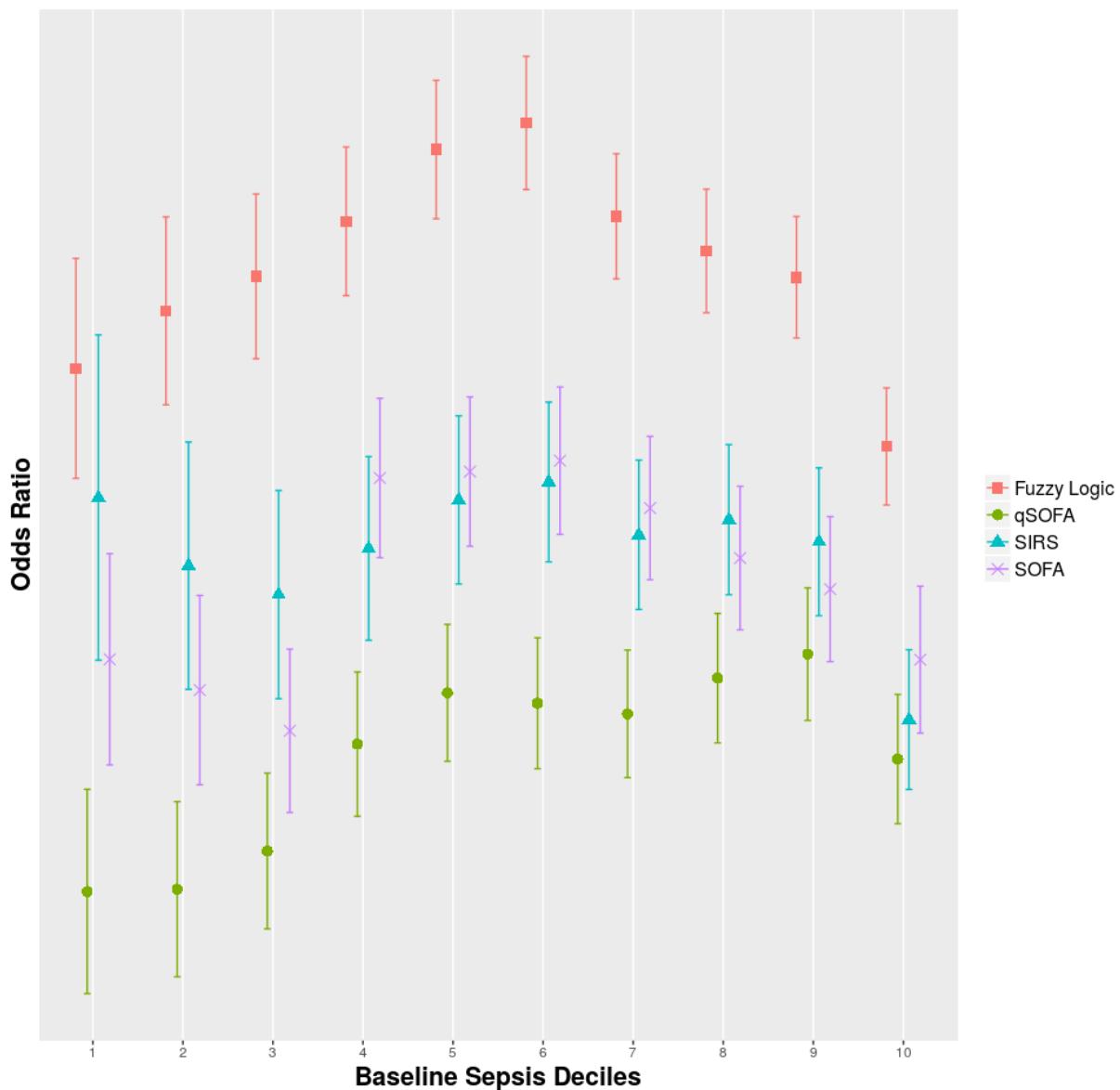


```
postscript(file="deciles_sepsis_nolog_newsize.eps")
ggplot(ORTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Sepsis Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank())+ theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12))+ggtitle("Outcome: Sepsis") + theme(axis.title=element_text(size=16,face="bold")) + scale_shape_manual(values=c(15, 16, 17,4))
dev.off()
```

```
## png
## 2
```

```
ggplot(ORTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Sepsis Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank())+ theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12))+ggtitle("Outcome: Sepsis") + theme(axis.title=element_text(size=16,face="bold")) + scale_y_log10() + scale_shape_manual(values=c(15, 16, 17,4))
```

Outcome: Sepsis



```

levels(ORFuzzyLogicmort_Table3$BaselineDec)<-seq(1,10)
levels(ORSOFAmort_Table3$BaselineDec)<-seq(1,10)
levels(ORqSOFAmort_Table3$BaselineDec)<-seq(1,10)
levels(ORSIRSmort_Table3$BaselineDec)<-seq(1,10)

ORMortTable3<-ORFuzzyLogicmort_Table3%>%bind_rows(ORSOFAmort_Table3)%>%bind_rows(ORqSOFAmort_Table3)%>%bind_rows
(ORSIRSmort_Table3)

postscript(file="deciles_mort_nolog_newsize.eps")

ggplot(ORMortTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position =
position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.
5))+xlab("Baseline Mortality Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank())+ theme(axis.title
=element_text(size=16,face="bold"),legend.text=element_text(size=12)) + ggtitle("Outcome: Mortality") + scale_sh
ape_manual(values=c(15, 16, 17,4))
dev.off()

```

```

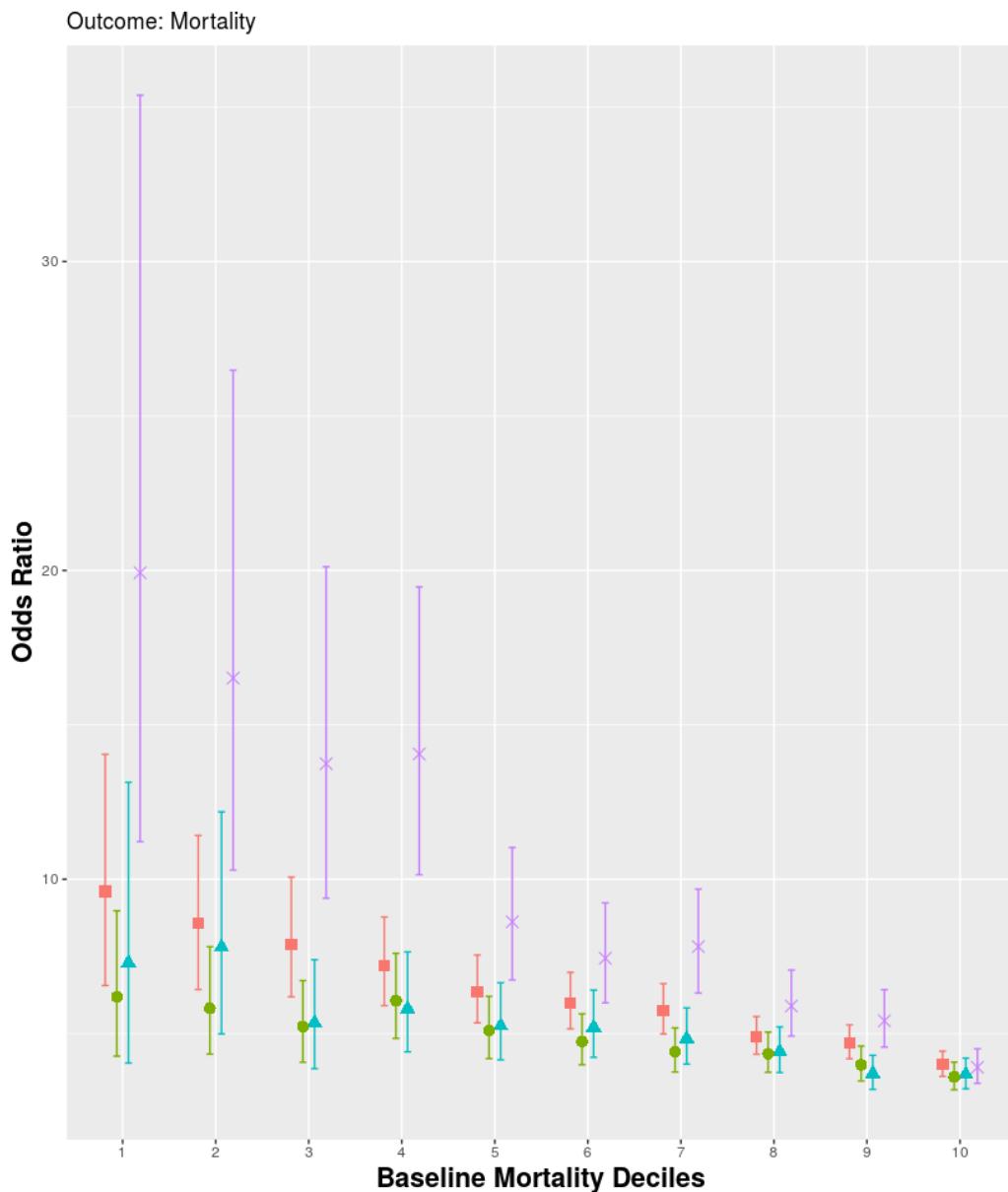
## png
## 2

```

```

ggplot(ORMortTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position =
position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position dodge(width = 0.
5))+xlab("Baseline Mortality Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank())+ theme(axis.title
=element_text(size=16,face="bold"),legend.text=element_text(size=12)) + ggtitle("Outcome: Mortality") + scale_sh
ape_manual(values=c(15, 16, 17,4))

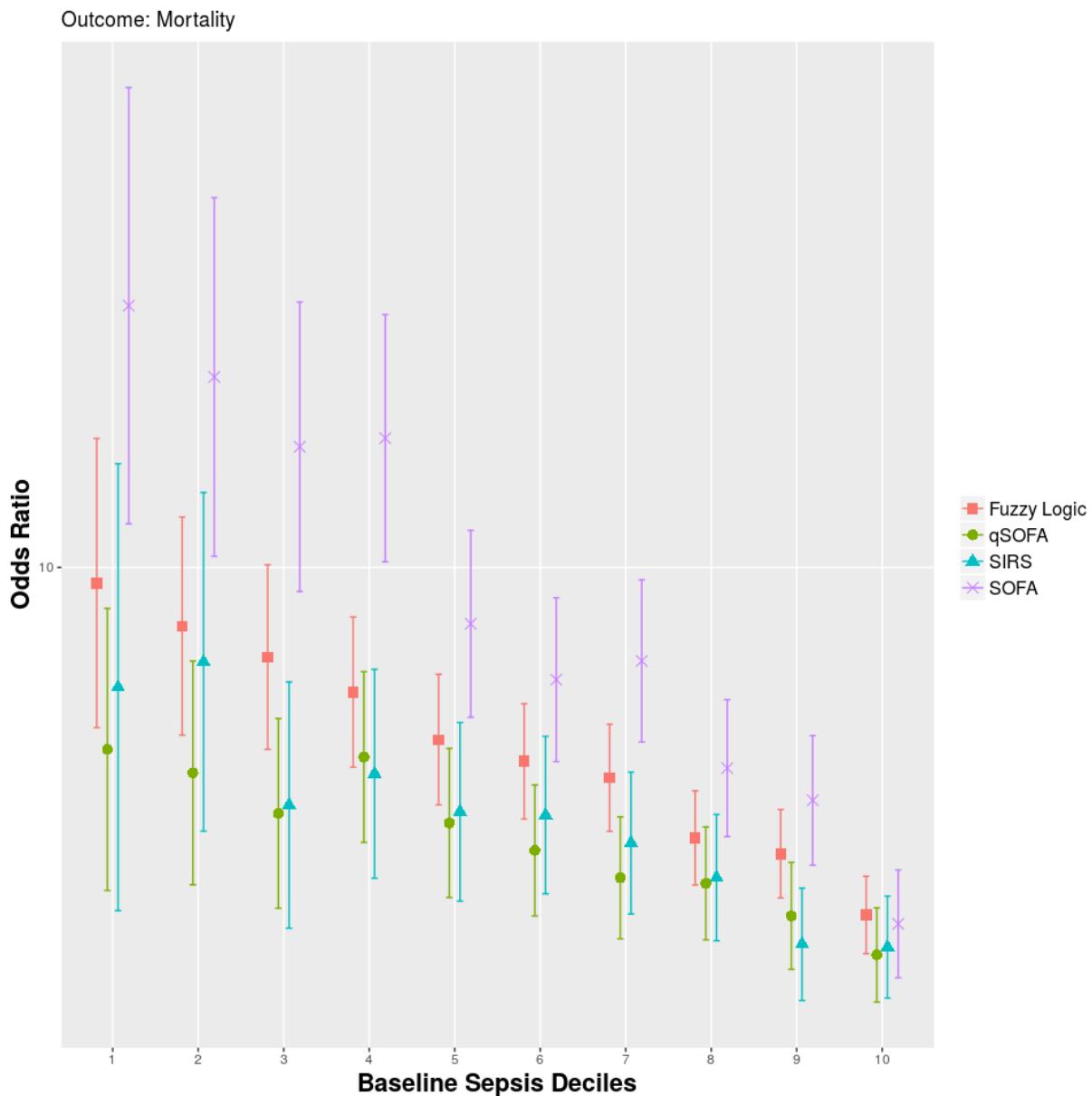
```



```
postscript(file="deciles_mort_log_newsize.eps")
ggplot(ORMortTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Mortality Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank())+ theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12))+ggtitle("Outcome: Mortality") + scale_y_log10() + scale_shape_manual(values=c(15, 16, 17,4))
dev.off()
```

```
## png
## 2
```

```
ggplot(ORMortTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Sepsis Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank())+ theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12))+ggtitle("Outcome: Mortality") + scale_y_log10() + scale_shape_manual(values=c(15, 16, 17,4))
```



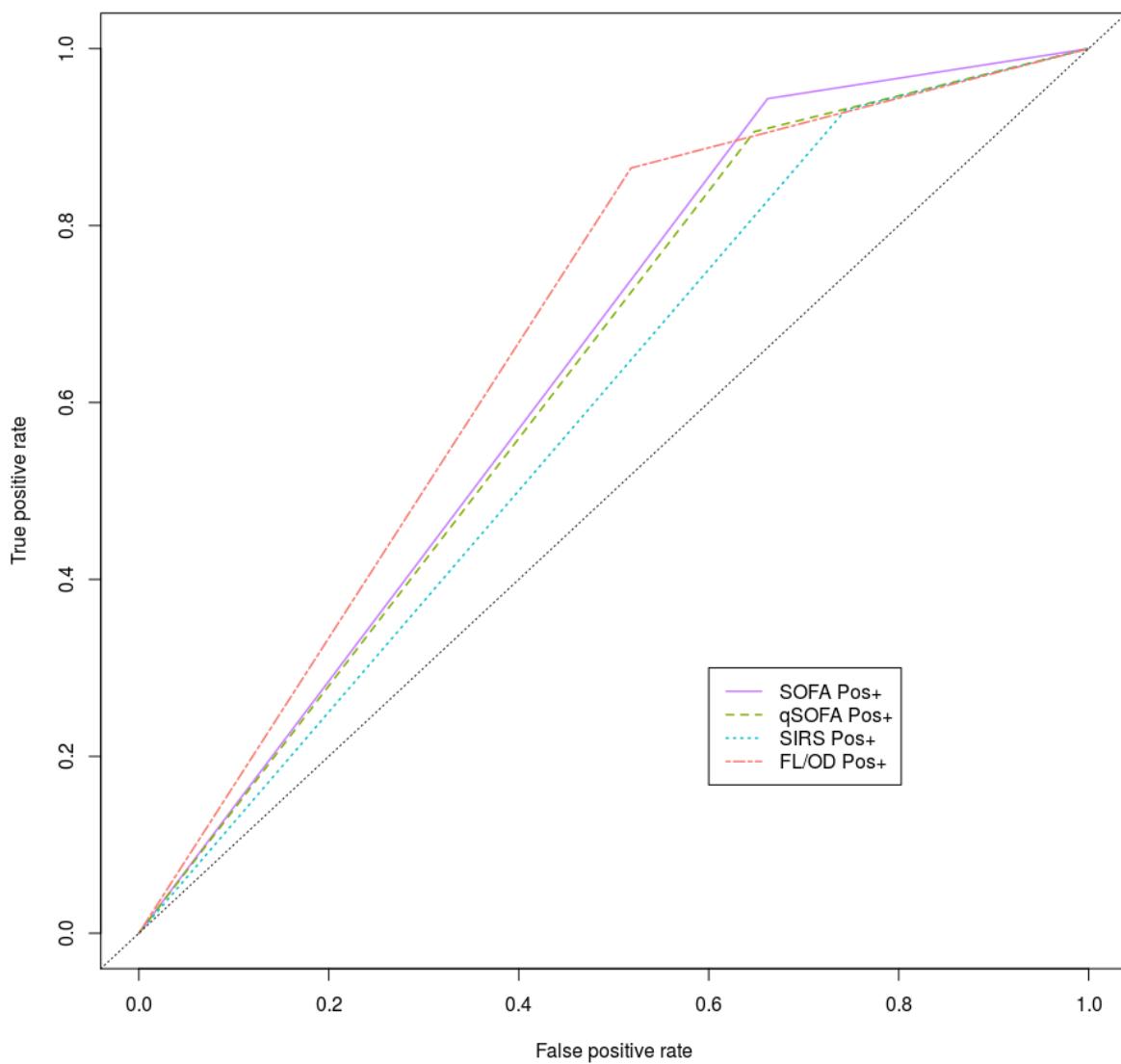
32 Plots for Table 2

```

plot(SOFA2CrudeMort.Perf, main = "Comparison of Positive Scores
Mortality Crude Prediction", col="#C77cff", lty=1, lwd=1.5)
plot(qSOFA2CrudeMort.Perf, add = TRUE, col="#7cae00", lty=2, lwd=1.5)
plot(SIRS2CrudeMort.Perf, add = TRUE, col="#00bfc4", lty=3, lwd=1.5)
plot(FuzzyLogicCrudeMort.Perf, add=TRUE, col="#F8766d", lty=6, lwd=1.5)
abline(0,1,lty=3)
#legend(.6,.3,lty = c(1,1,1),col=c("black","red","springgreen","blue"),c("SOFA Pos+","qSOFA Pos+","SIRS Pos+","FL/OD Pos+"))
legend(.6,.3,lty = c(1,2,3,6),col=c("#C77cff","#7cae00","#00bfc4","#F8766d"),c("SOFA Pos+","qSOFA Pos+","SIRS Pos+","FL/OD Pos+"),lwd=1.5)

```

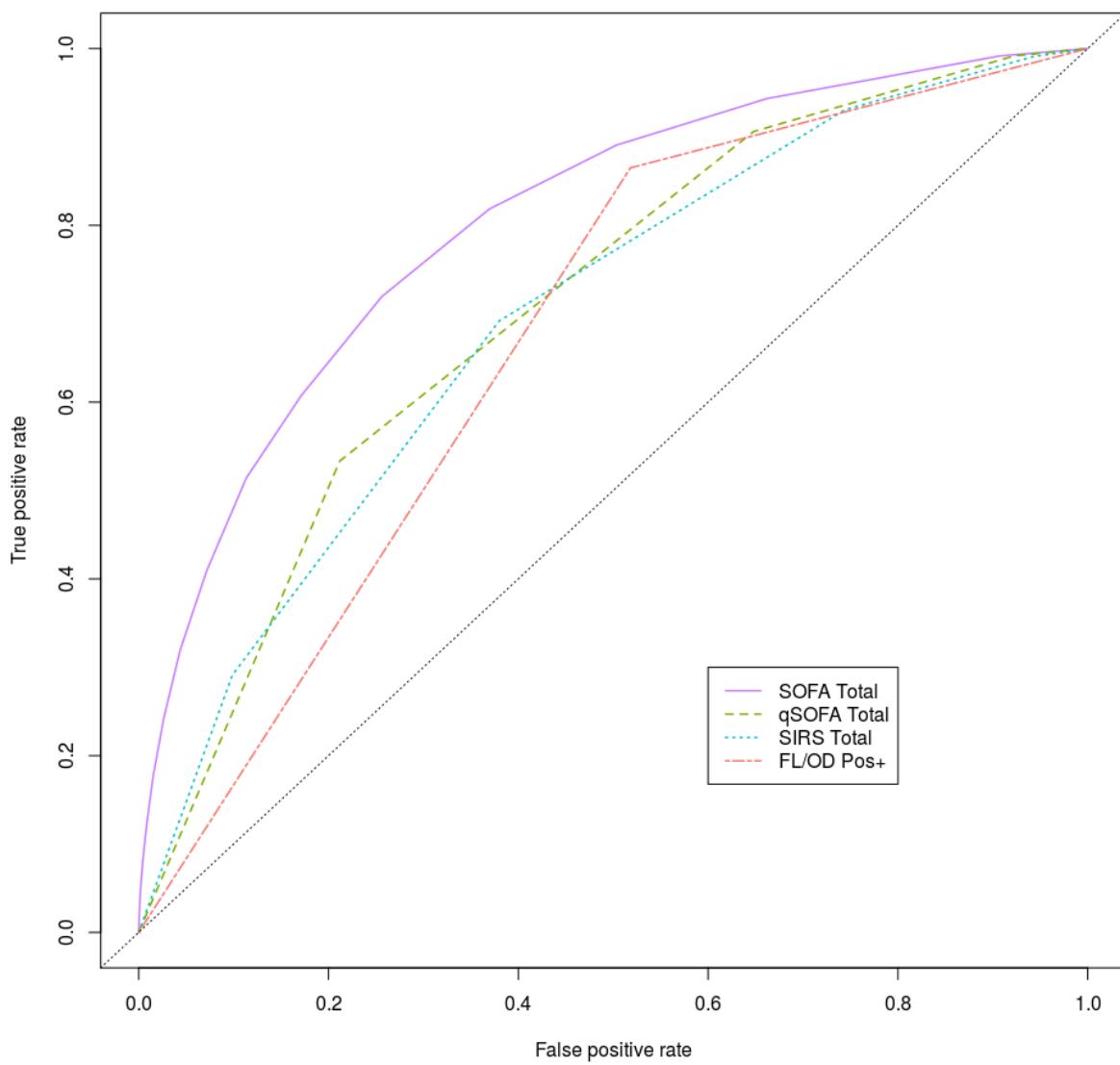
Comparison of Positive Scores Mortality Crude Prediction



```

plot(SOFA1CrudeMort.Perf, main = "Comparison of Total Scores versus
Fuzzy Logic Positive Mortality Crude Prediction", col="#C77CF", lty=1,lwd=1.5)
plot(qSOFA1CrudeMort.Perf, add = TRUE, col="#7CAE00", lty=2,lwd=1.5)
plot(SIRS1CrudeMort.Perf, add = TRUE,col="#00BFC4", lty=3,lwd=1.5)
plot(FuzzyLogicCrudeMort.Perf, add=TRUE,col="#F8766D", lty=6,lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,3,6),col=c("#C77CF","#7CAE00","#00BFC4","#F8766D"),c("SOFA Total","qSOFA Total","SIRS T
otal", "FL/OD Pos+"),lwd=1.5)
    
```

**Comparison of Total Scores versus
Fuzzy Logic Positive Mortality Crude Prediction**

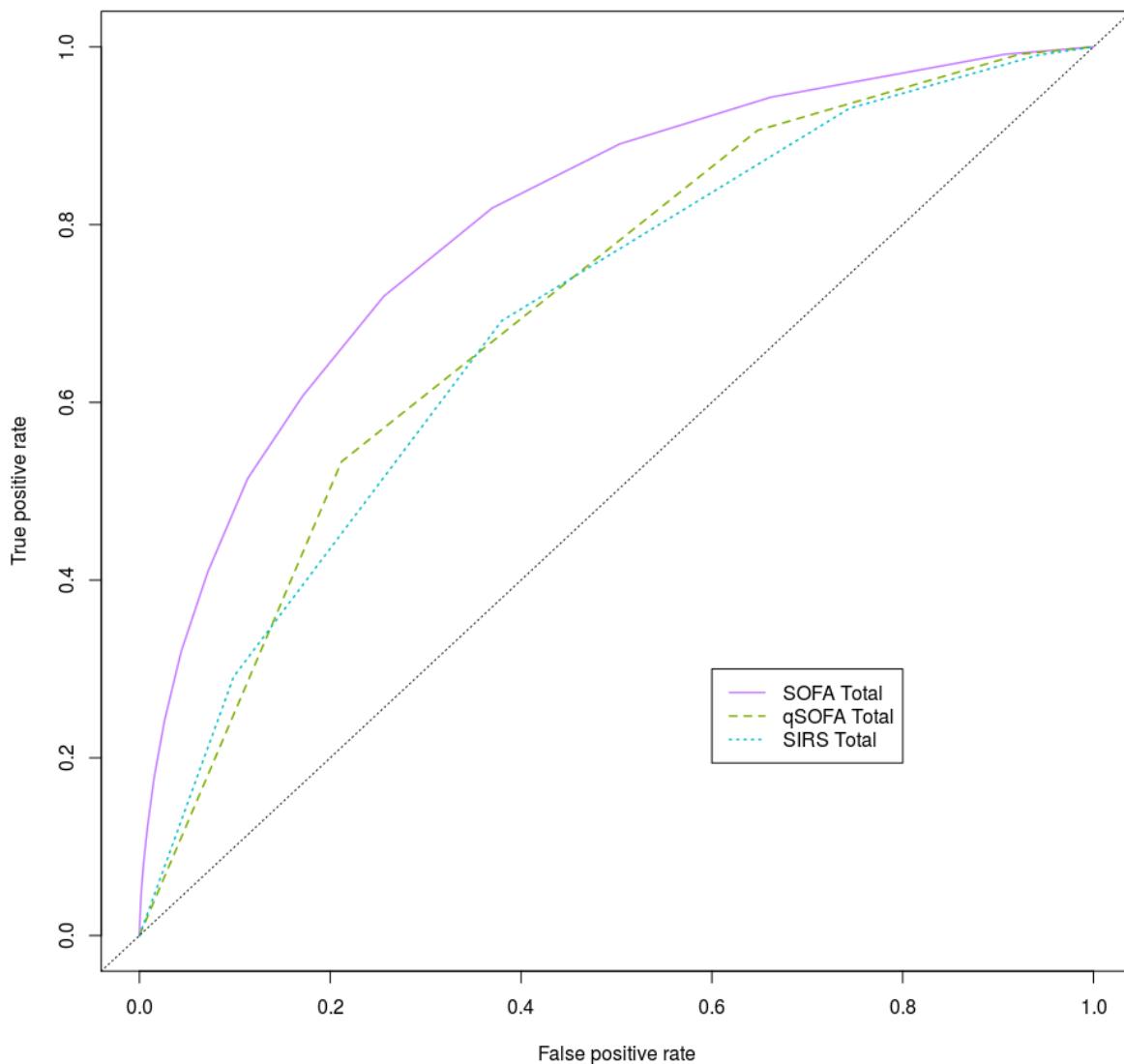


```

plot(SOFA1CrudeMort.Perf, main = "Comparison of Total Scores
Mortality Crude Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(qSOFA1CrudeMort.Perf, add = TRUE, col="#7CAE00", lty=2, lwd=1.5)
plot(SIRS1CrudeMort.Perf, add = TRUE,col="#00BFC4", lty=3,lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,3),c("SOFA Total","qSOFA Total","SIRS Total"),lwd=1.5,col=c("#C77CFF","#7CAE00","#00BFC
4"))

```

Comparison of Total Scores Mortality Crude Prediction

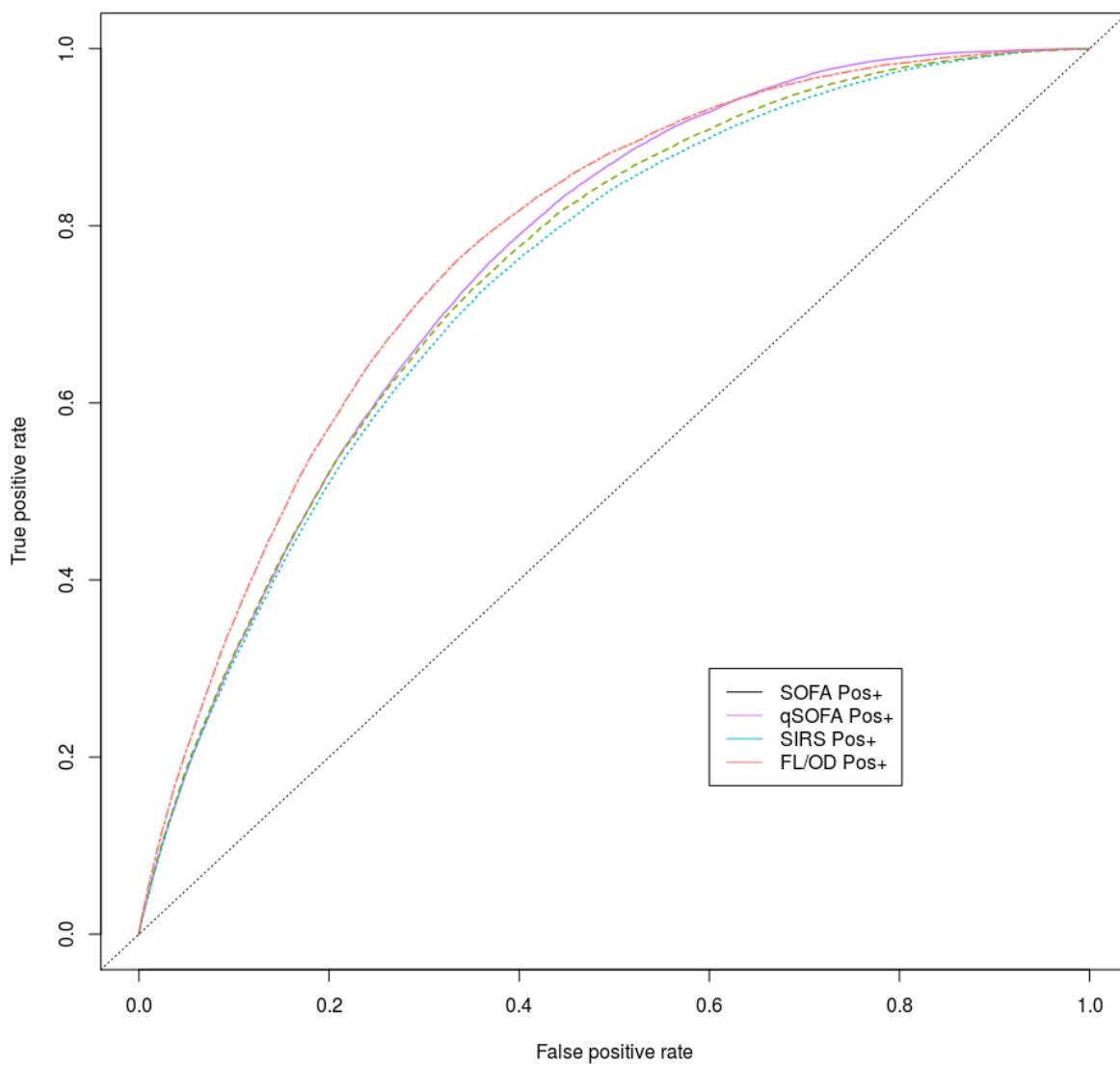


```

plot(SOFA2ADJMort.Perf, main = "Comparison of Positive Scores
Mortality Adjusted Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(qSOFA2ADJMort.Perf, add = TRUE,col="#7CAE00",lty=2,lwd=1.5)
plot(SIRS2ADJMort.Perf , add = TRUE,col="#00BFC4", lty=3,lwd=1.5)
plot(FuzzyLogicADJMort.Perf, add=TRUE,col="#F8766D", lty=6,lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,1,1),col=c("black","#C77CFF","#00BFC4","#F8766D"),c("SOFA Pos+","qSOFA Pos+","SIRS Pos+","FL/OD Pos+"))

```

Comparison of Positive Scores Mortality Adjusted Prediction

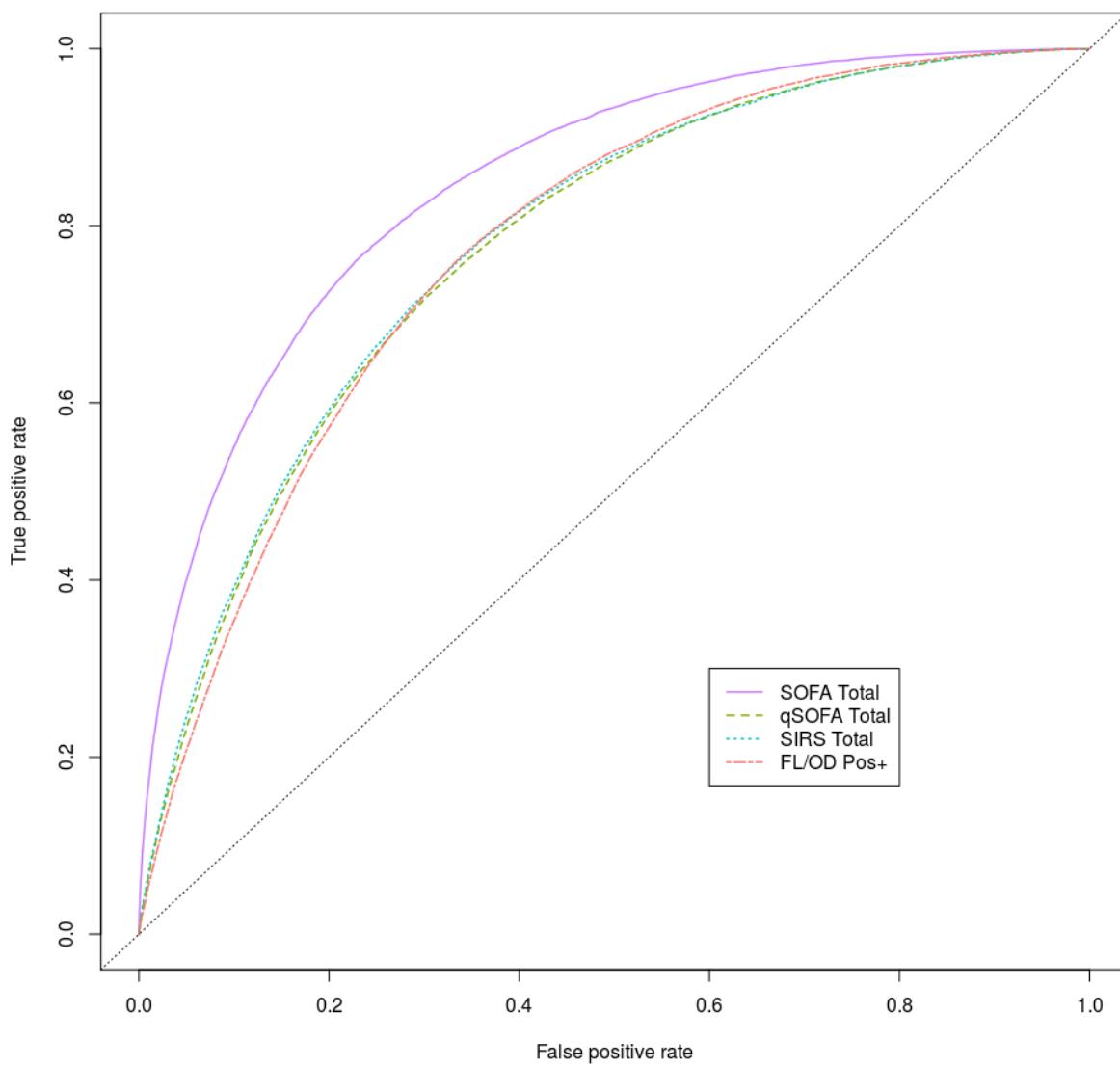


```

plot(SOFA1ADJMort.Perf, main = "Comparison of Total Scores versus
Fuzzy Logic Positive Mortality Adjusted Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(qSOFA1ADJMort.Perf, add = TRUE, col="#7CAE00", lty=2, lwd=1.5)
plot(SIRS1ADJMort.Perf, add = TRUE, col="#00BFC4", lty=3, lwd=1.5)
plot(FuzzyLogicADJMort.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,3,6),col=c("#C77CFF","#7CAE00","#00BFC4","#F8766D"),c("SOFA Total","qSOFA Total","SIRS T
otal", "FL/OD Pos+"),lwd=1.5)

```

**Comparison of Total Scores versus
Fuzzy Logic Positive Mortality Adjusted Prediction**

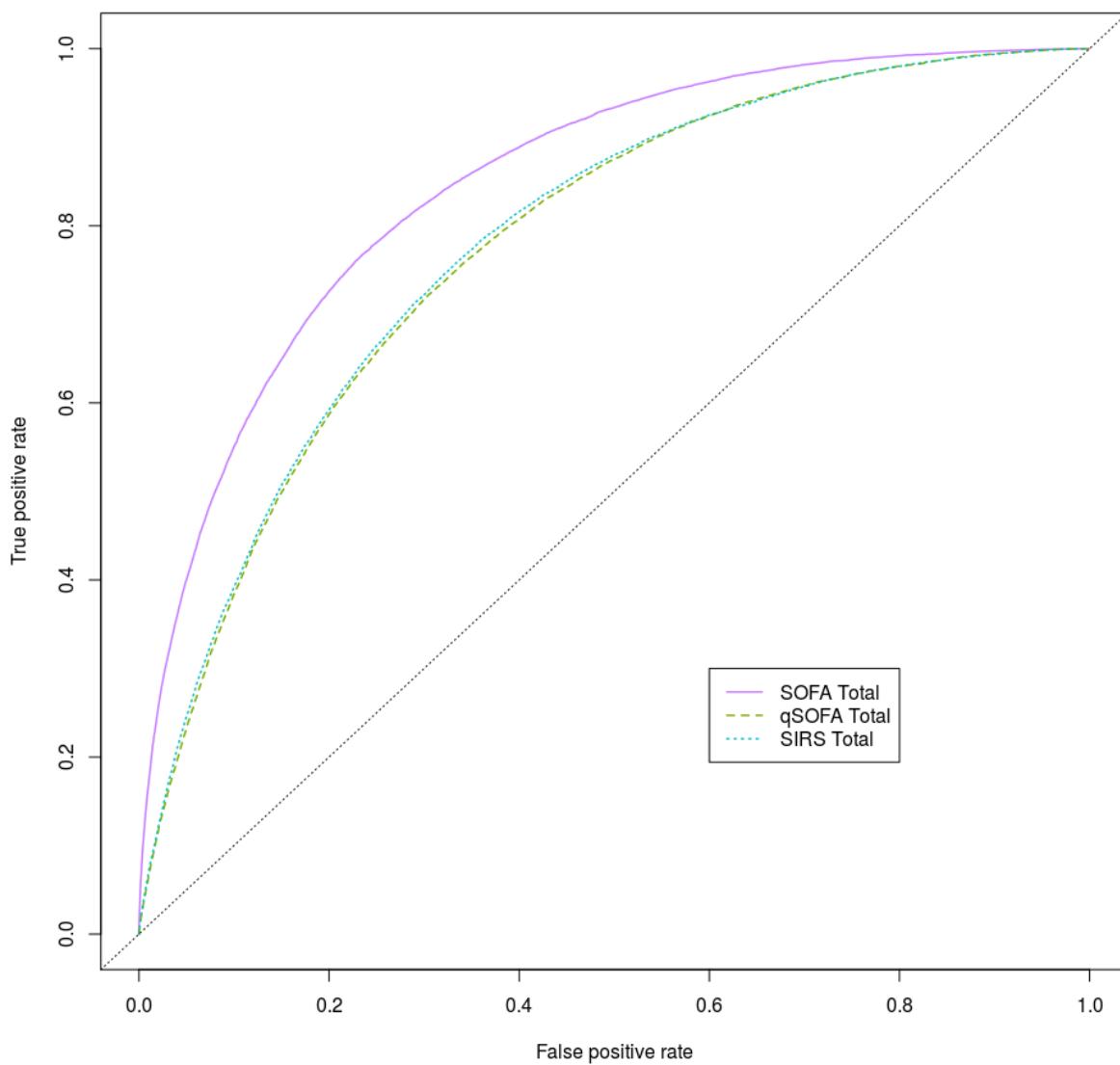


```

plot(SOFA1ADJMort.Perf, main = "Comparison of Total Scores
Mortality Adjusted Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(qSOFA1ADJMort.Perf, add = TRUE, col="#7CAE00", lty=2, lwd=1.5)
plot(SIRS1ADJMort.Perf, add = TRUE, col="#00BFC4", lty=3, lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,3),col=c("#C77CFF","#7CAE00","#00BFC4"),c("SOFA Total","qSOFA Total","SIRS Total"),lwd=1.5)

```

Comparison of Total Scores Mortality Adjusted Prediction

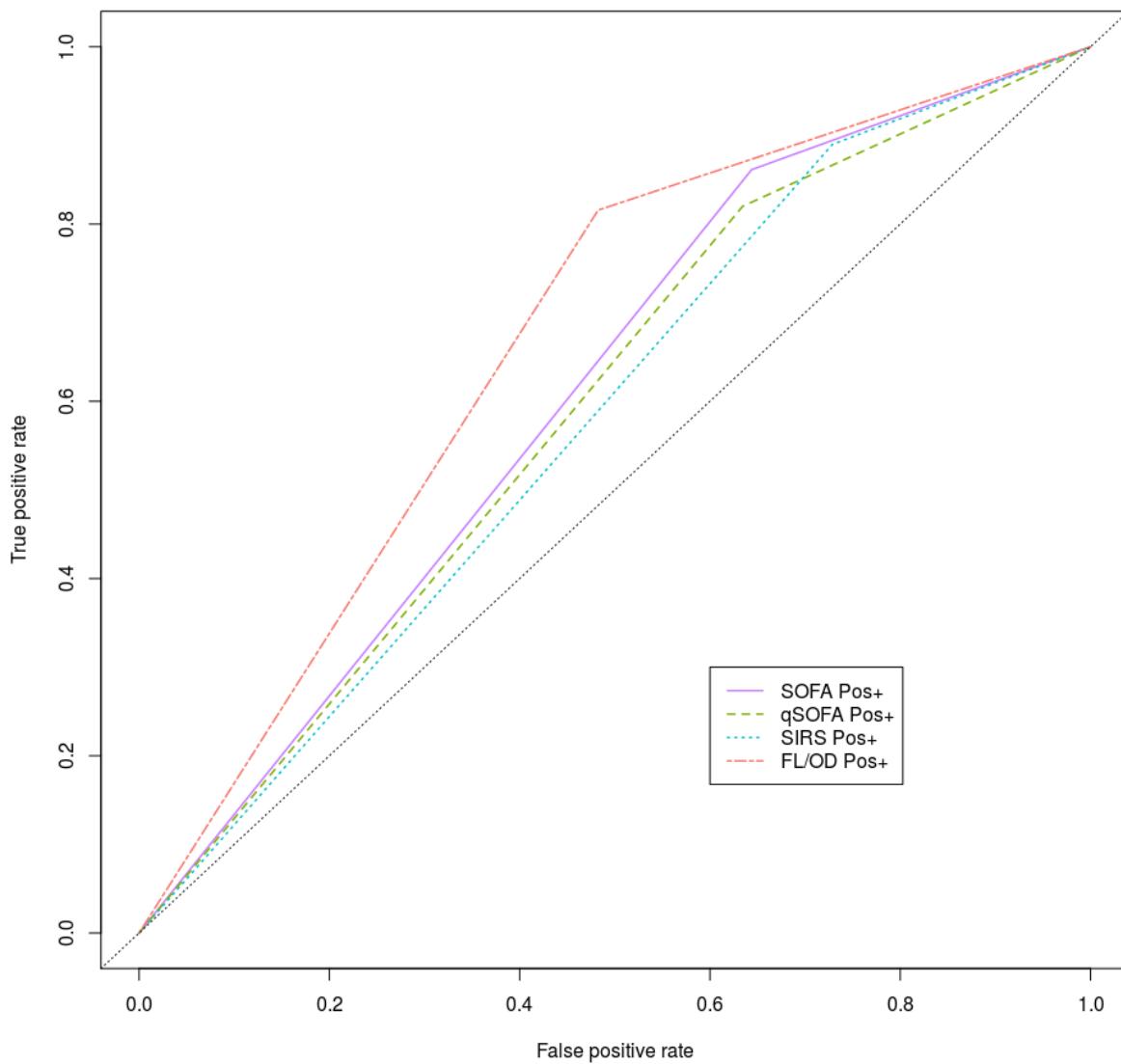


```

plot(SOFA2CrudeSepsis.Perf, main = "Comparison of Positive Scores
Sepsis Crude Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(qSOFA2CrudeSepsis.Perf, add = TRUE, col="#7CAE00", lty=2, lwd=1.5)
plot(SIRS2CrudeSepsis.Perf, add = TRUE, col="#00BFC4", lty=3, lwd=1.5)
plot(FuzzyLogicCrudeSepsis.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,3,6),col=c("#C77CFF","#7CAE00","#00BFC4","#F8766D"),c("SOFA Pos+","qSOFA Pos+","SIRS Pos+","FL/OD Pos+"),lwd=1.5)

```

Comparison of Positive Scores Sepsis Crude Prediction

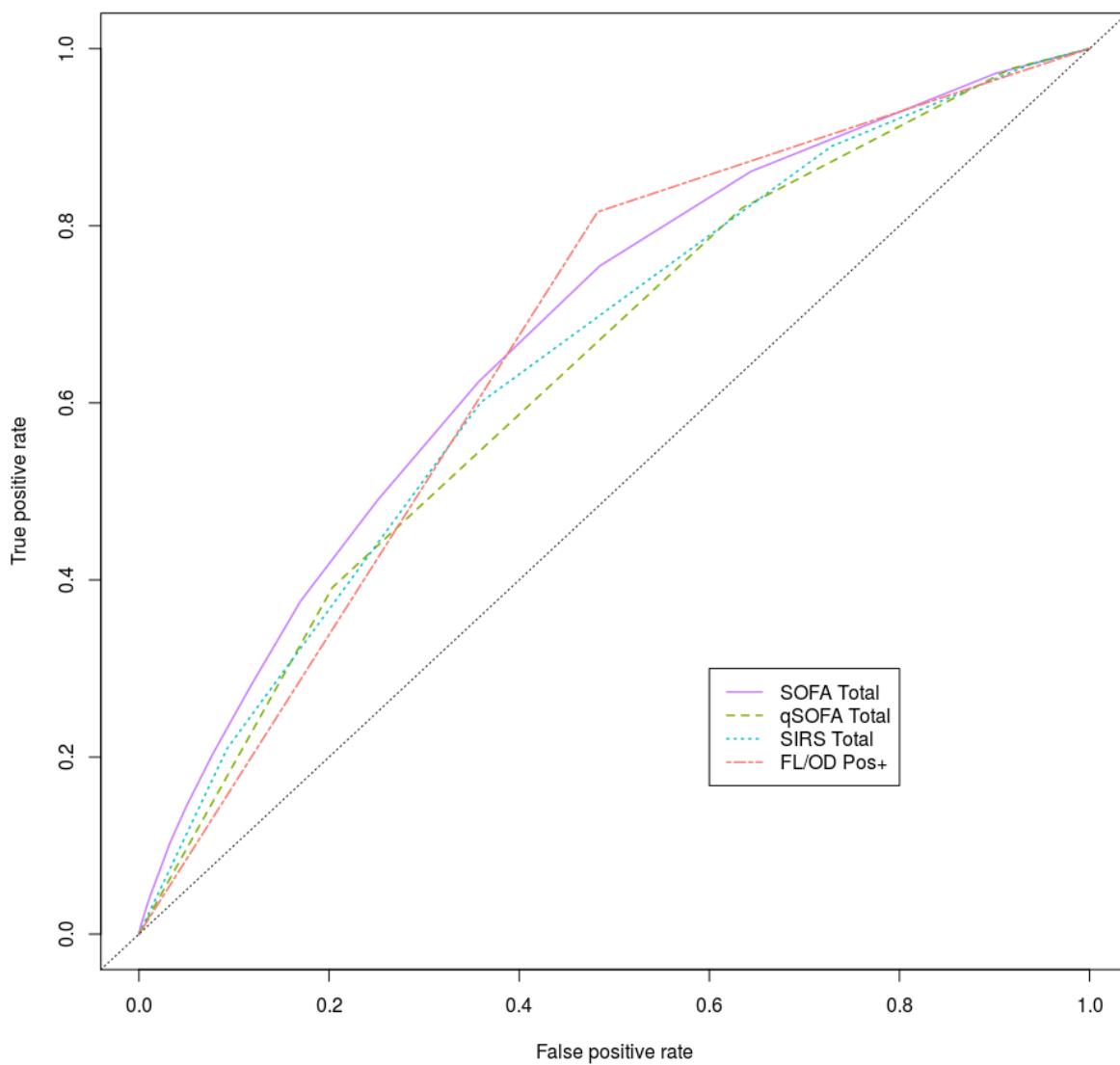


```

plot(SOFA1CrudeSepsis.Perf, main = "Comparison of Total Scores versus
Fuzzy Logic Positive Sepsis Crude Prediction", col="#C77CFF",lty=1,lwd=1.5)
plot(qSOFA1CrudeSepsis.Perf, add = TRUE,col="#7CAE00",lty=2,lwd=1.5)
plot(SIRS1CrudeSepsis.Perf, add = TRUE,col="#00BFC4", lty=3,lwd=1.5)
plot(FuzzyLogicCrudeSepsis.Perf, add=TRUE,col="#F8766D", lty=6,lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,3,6),col=c("#C77CFF","#7CAE00","#00BFC4", "#F8766D"),c("SOFA Total","qSOFA Total","SIRS
Total", "FL/OD Pos+"),lwd=1.5)

```

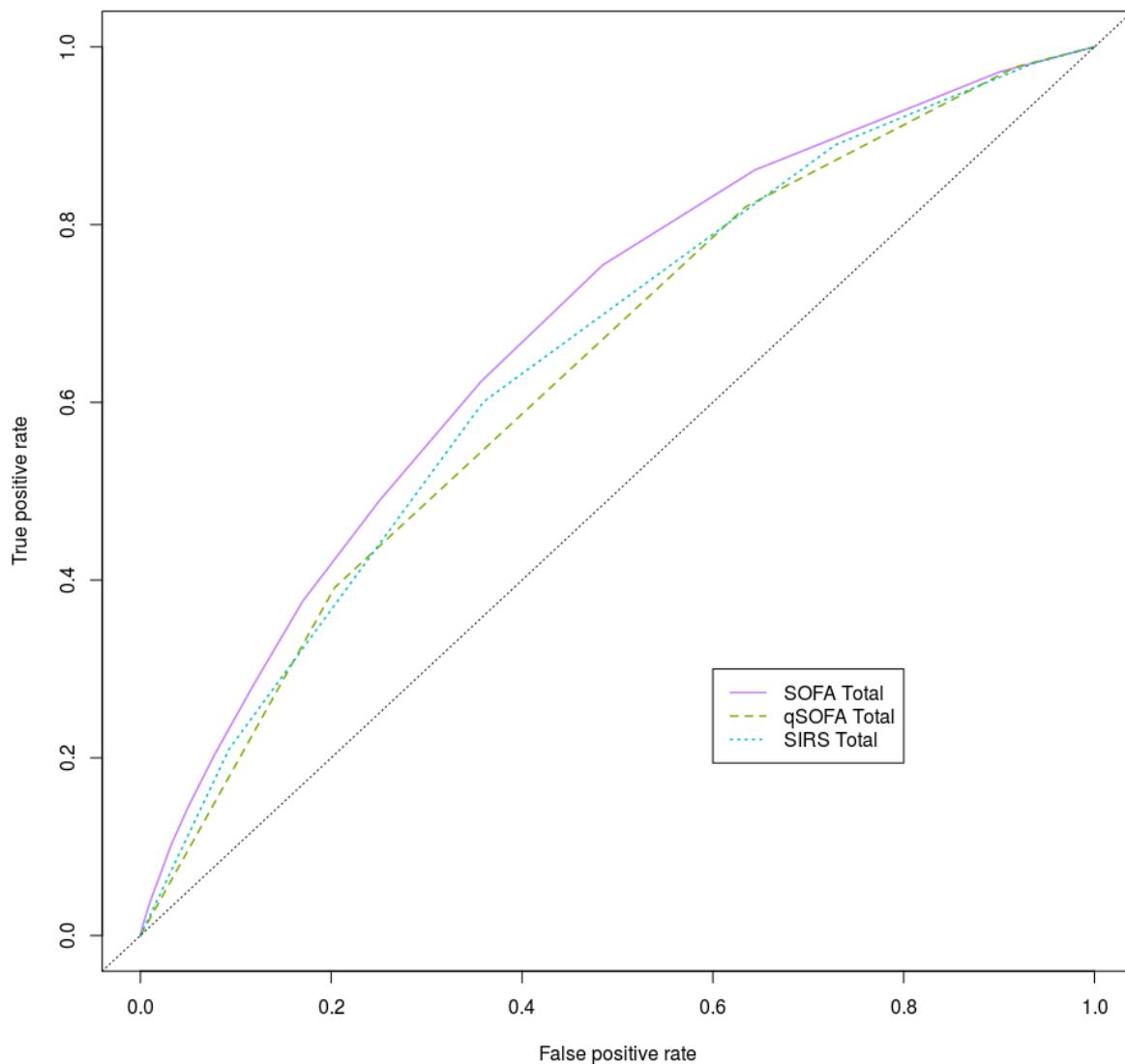
Comparison of Total Scores versus Fuzzy Logic Positive Sepsis Crude Prediction



```

plot(SOFA1CrudeSepsis.Perf, main = "Comparison of Total Scores Sepsis Crude Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(qSOFA1CrudeSepsis.Perf, add = TRUE,col="#7CAE00",lty=2,lwd=1.5)
plot(SIRS1CrudeSepsis.Perf, add = TRUE,col="#00BFC4", lty=3,lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,3,6),col=c("#C77CFF","#7CAE00","#00BFC4", "#F8766D"),c("SOFA Total","qSOFA Total","SIRS Total"),lwd=1.5)

```

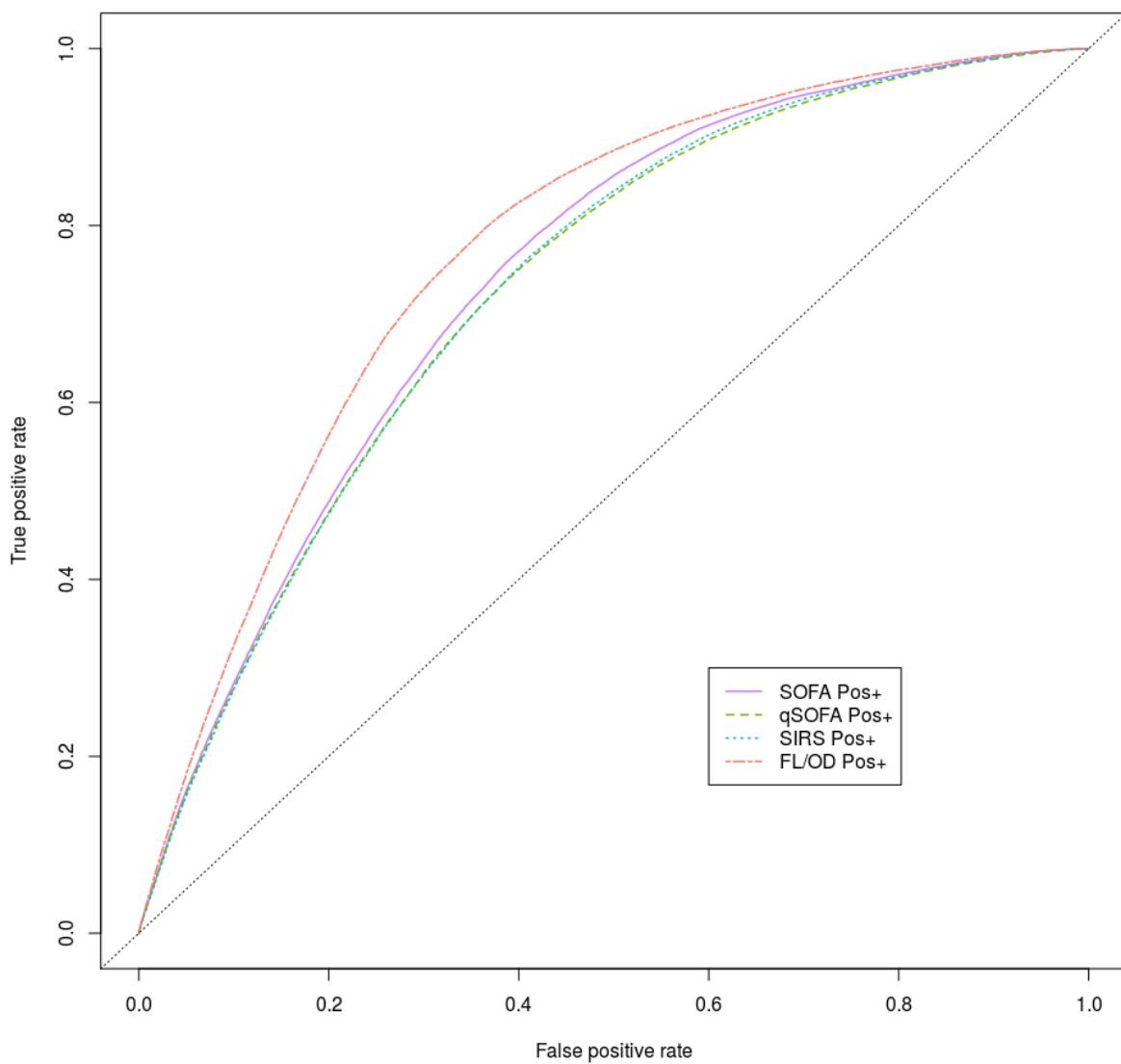
Comparison of Total Scores Sepsis Crude Prediction

```

plot(SOFA2ADJSepsis.Perf, main = "Comparison of Positive Scores
Sepsis Adjusted Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(qSOFA2ADJSepsis.Perf, add = TRUE, col="#7CAE00", lty=2, lwd=1.5)
plot(SIRS2ADJSepsis.Perf, add = TRUE, col="#00BFC4", lty=3, lwd=1.5)
plot(FuzzyLogicADJSepsis.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,3,6),col=c("#C77CFF","#7CAE00","#00BFC4", "#F8766D"),c("SOFA Pos+","qSOFA Pos+","SIRS Po
s+","FL/OD Pos+"),lwd=1.5)

```

Comparison of Positive Scores Sepsis Adjusted Prediction

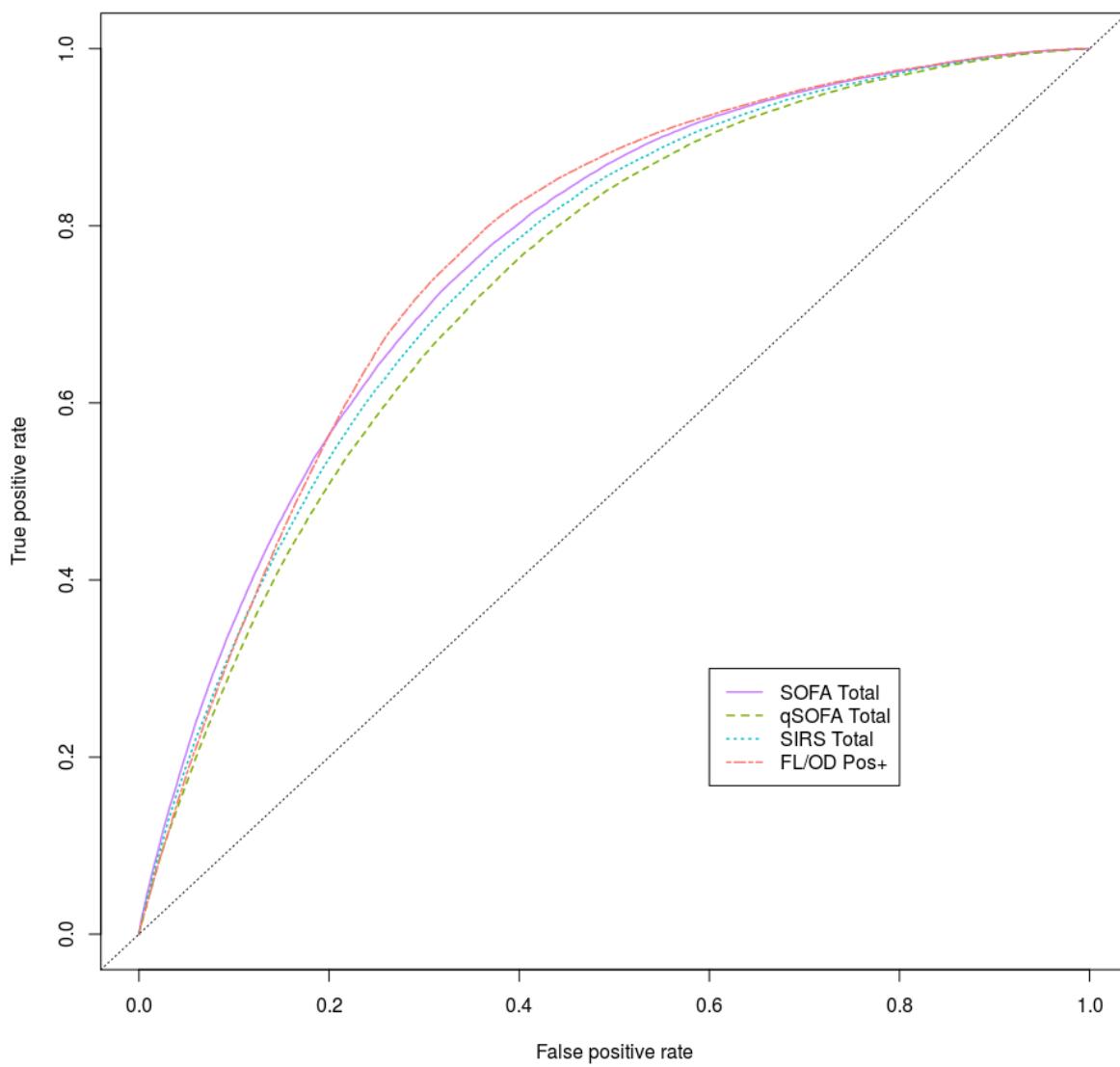


```

plot(SOFA1ADJSepsis.Perf, main = "Comparison of Total Scores versus
Fuzzy Logic Positive Sepsis Adjusted Prediction", col="#C77CF", lty=1,lwd=1.5)
plot(qSOFA1ADJSepsis.Perf, add = TRUE,col="#7CAE00",lty=2,lwd=1.5)
plot(SIRS1ADJSepsis.Perf, add = TRUE ,col="#00BFC4", lty=3,lwd=1.5)
plot(FuzzyLogicADJSepsis.Perf, add=TRUE,col="#F8766D", lty=6,lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,3,6),col=c("#C77CF","#7CAE00","#00BFC4", "#F8766D"),c("SOFA Total","qSOFA Total","SIRS
Total","FL/OD Pos+"),lwd=1.5)

```

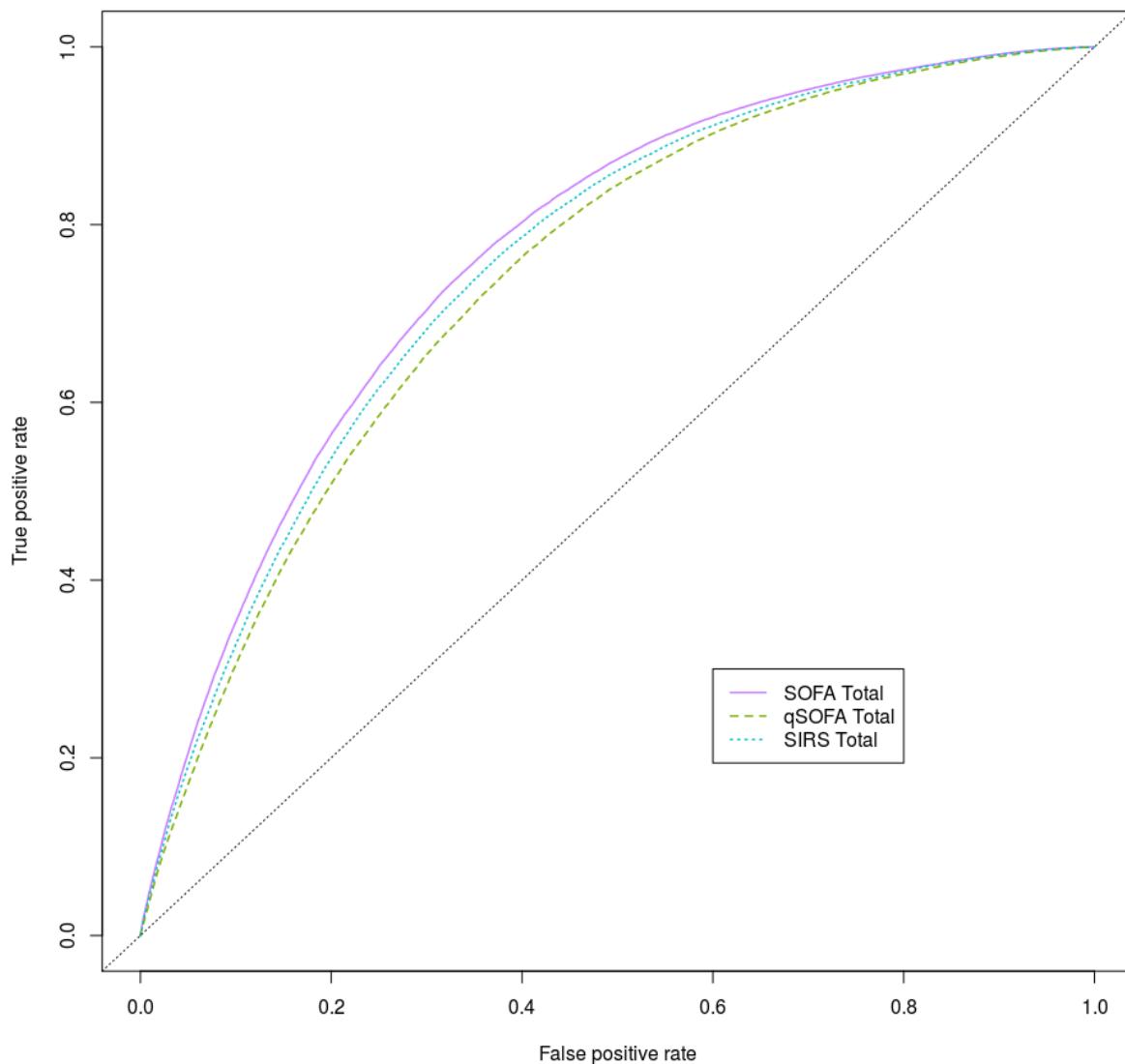
**Comparison of Total Scores versus
Fuzzy Logic Positive Sepsis Adjusted Prediction**



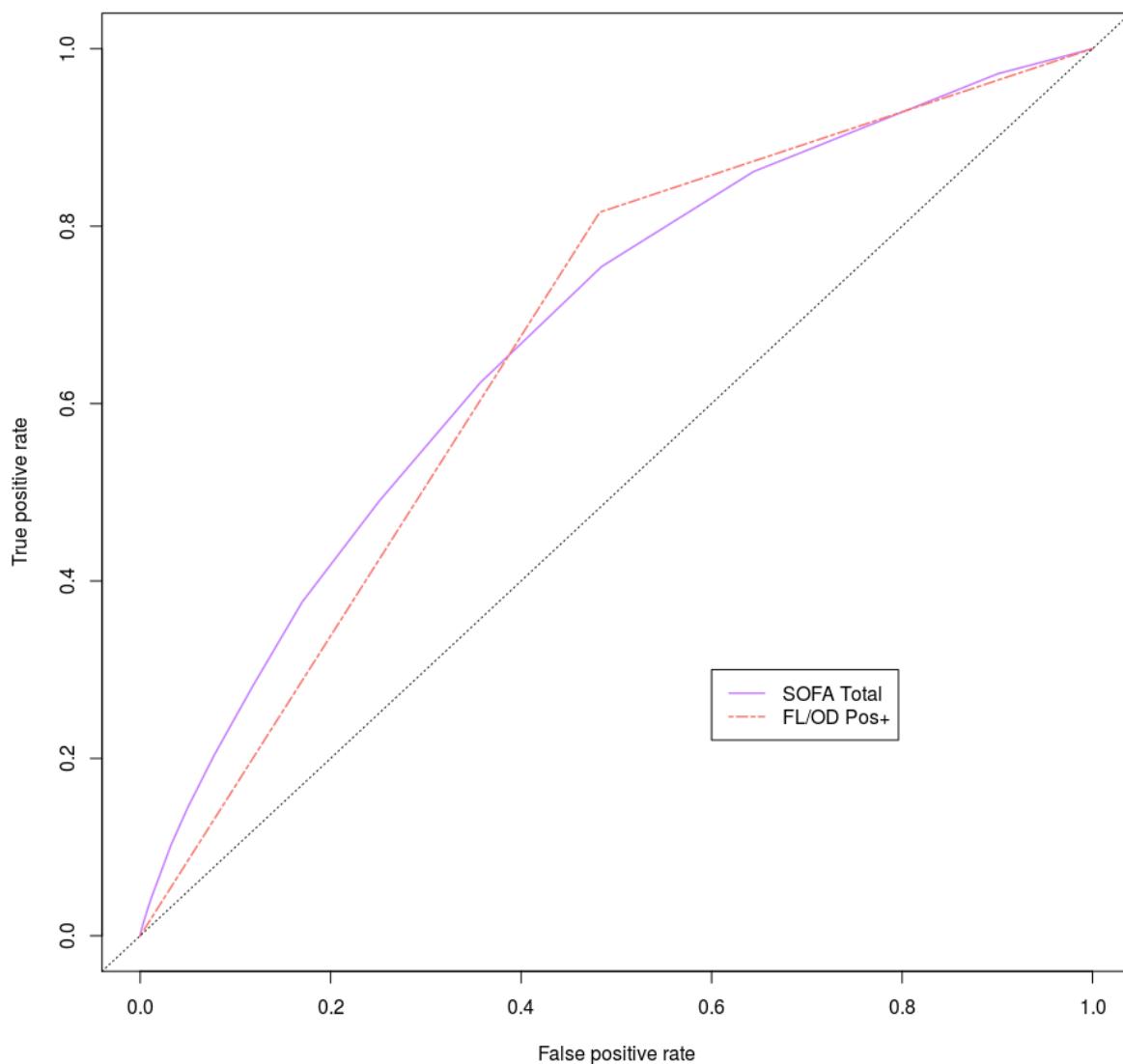
```

plot(SOFA1ADJSepsis.Perf, main = "Comparison of Total Scores Sepsis Adjusted Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(qSOFA1ADJSepsis.Perf, add = TRUE,col="#7CAE00",lty=2,lwd=1.5)
plot(SIRS1ADJSepsis.Perf, add = TRUE ,col="#00BFC4", lty=3,lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,3),col=c("#C77CFF","#7CAE00","#00BFC4","blue"),c("SOFA Total","qSOFA Total","SIRS Total"),lwd=1.5)

```

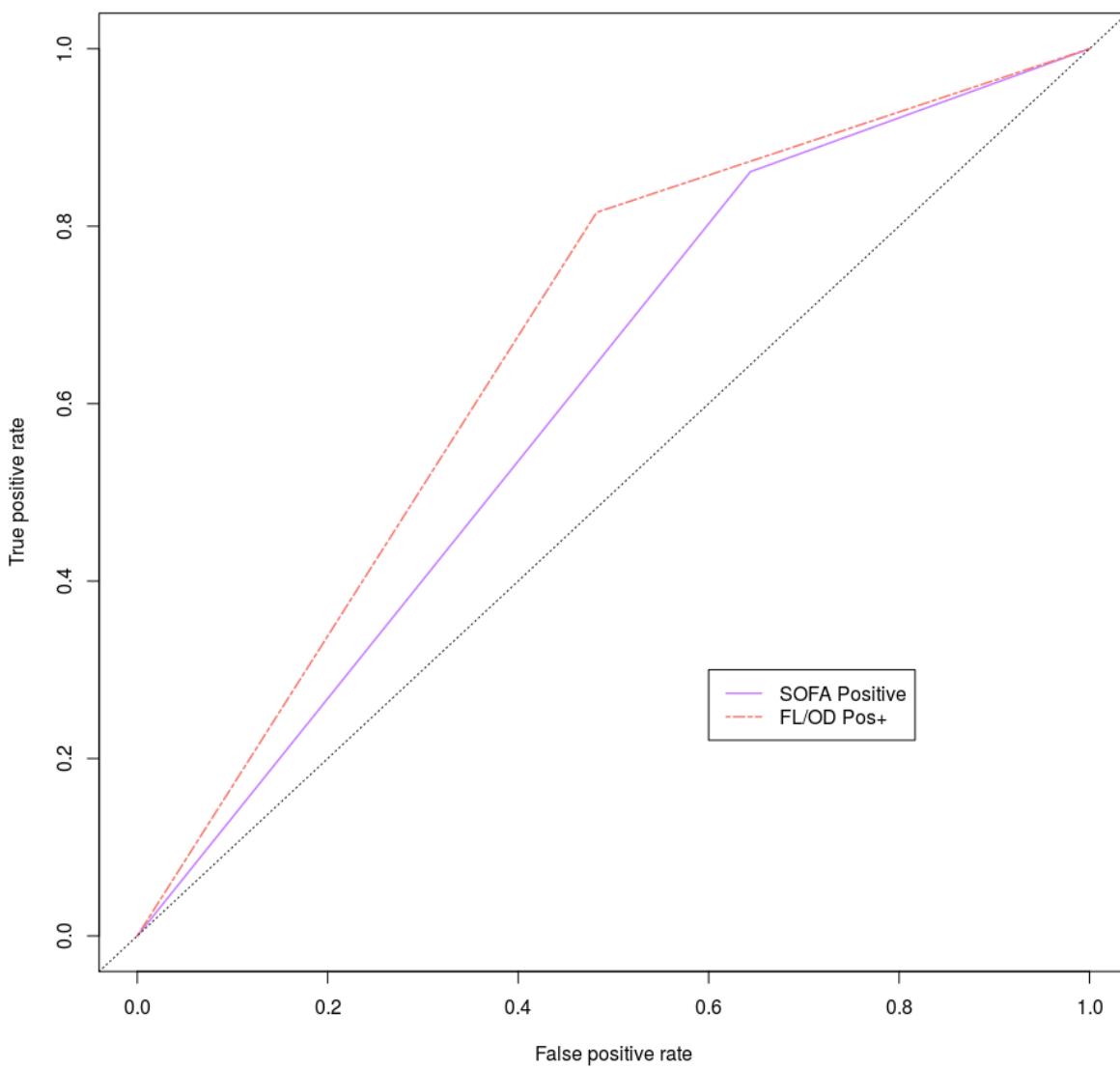
Comparison of Total Scores Sepsis Adjusted Prediction

```
plot(SOFA1CrudeSepsis.Perf, main = "Comparison of SOFA Total Score versus  
Fuzzy Logic Criteria Met Sepsis Crude Prediction", col="#C77CFF", lty=1, lwd=1.5)  
plot(FuzzyLogicCrudeSepsis.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)  
abline(0,1,lty=3)  
legend(.6,.3,lty = c(1,6),col=c("#C77CFF","#F8766D"),c("SOFA Total", "FL/OD Pos+"),lwd=1.5)
```

**Comparison of SOFA Total Score versus
Fuzzy Logic Criteria Met Sepsis Crude Prediction**

```
plot(SOFA2CrudeSepsis.Perf, main = "Comparison of SOFA Positive Score versus  
Fuzzy Logic Criteria Met Sepsis Crude Prediction", col="#C77CFF", lty=1, lwd=1.5)  
plot(FuzzyLogicCrudeSepsis.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)  
abline(0,1,lty=3)  
legend(.6,.3,lty = c(1,6),col=c("#C77CFF","#F8766D"),c("SOFA Positive", "FL/OD Pos+"),lwd=1.5)
```

Comparison of SOFA Positive Score versus Fuzzy Logic Criteria Met Sepsis Crude Prediction

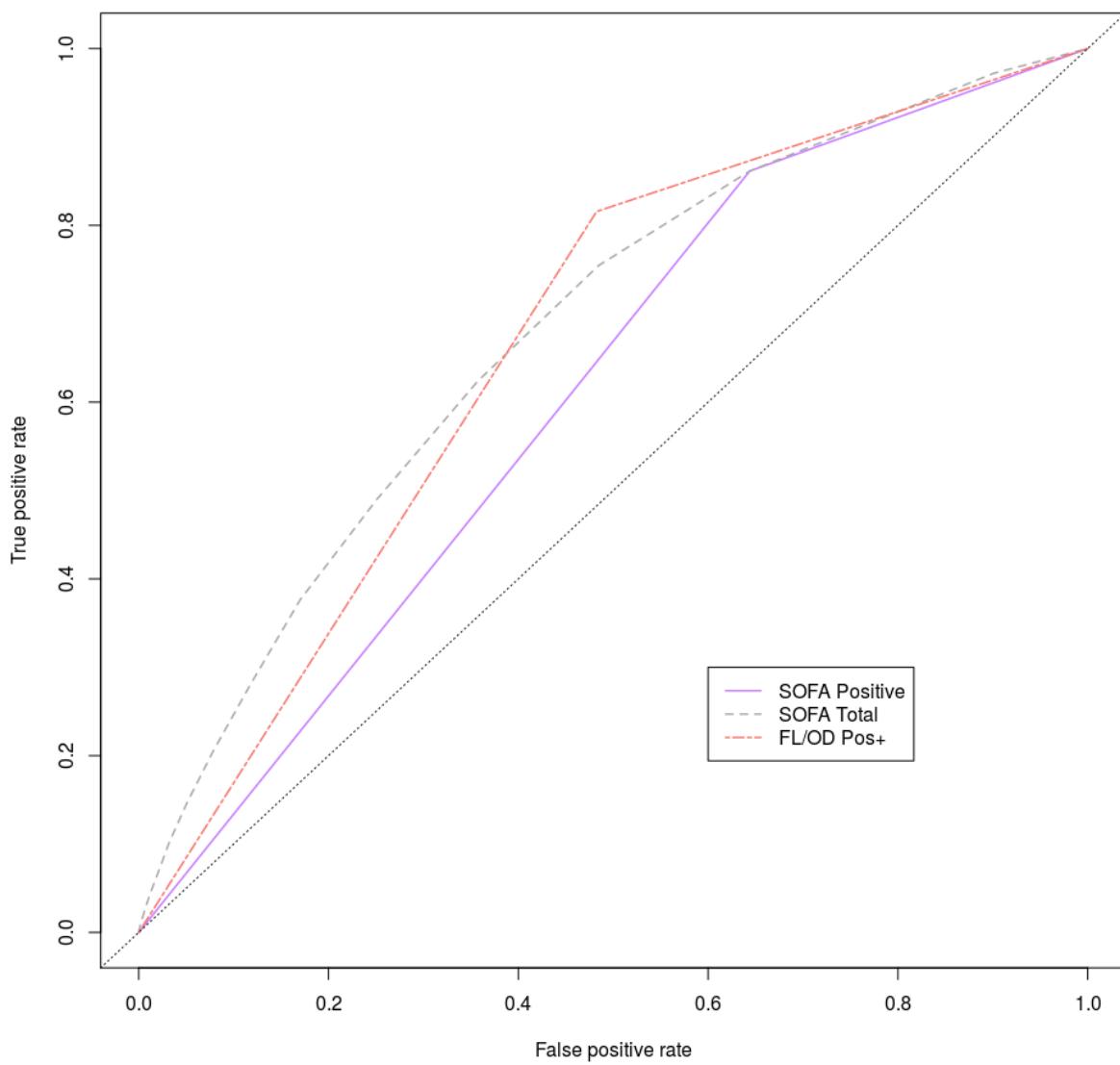


```

plot(SOFA2CrudeSepsis.Perf, main = "Comparison of SOFA Scores versus
  Fuzzy Logic Criteria Met Sepsis Crude Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(SOFA1CrudeSepsis.Perf, add=TRUE, col= "darkgrey", lty=2, lwd=1.5)
plot(FuzzyLogicCrudeSepsis.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,6),col=c("#C77CFF", "darkgrey", "#F8766D"),c("SOFA Positive", "SOFA Total", "FL/OD Pos+"),lwd=1.5)

```

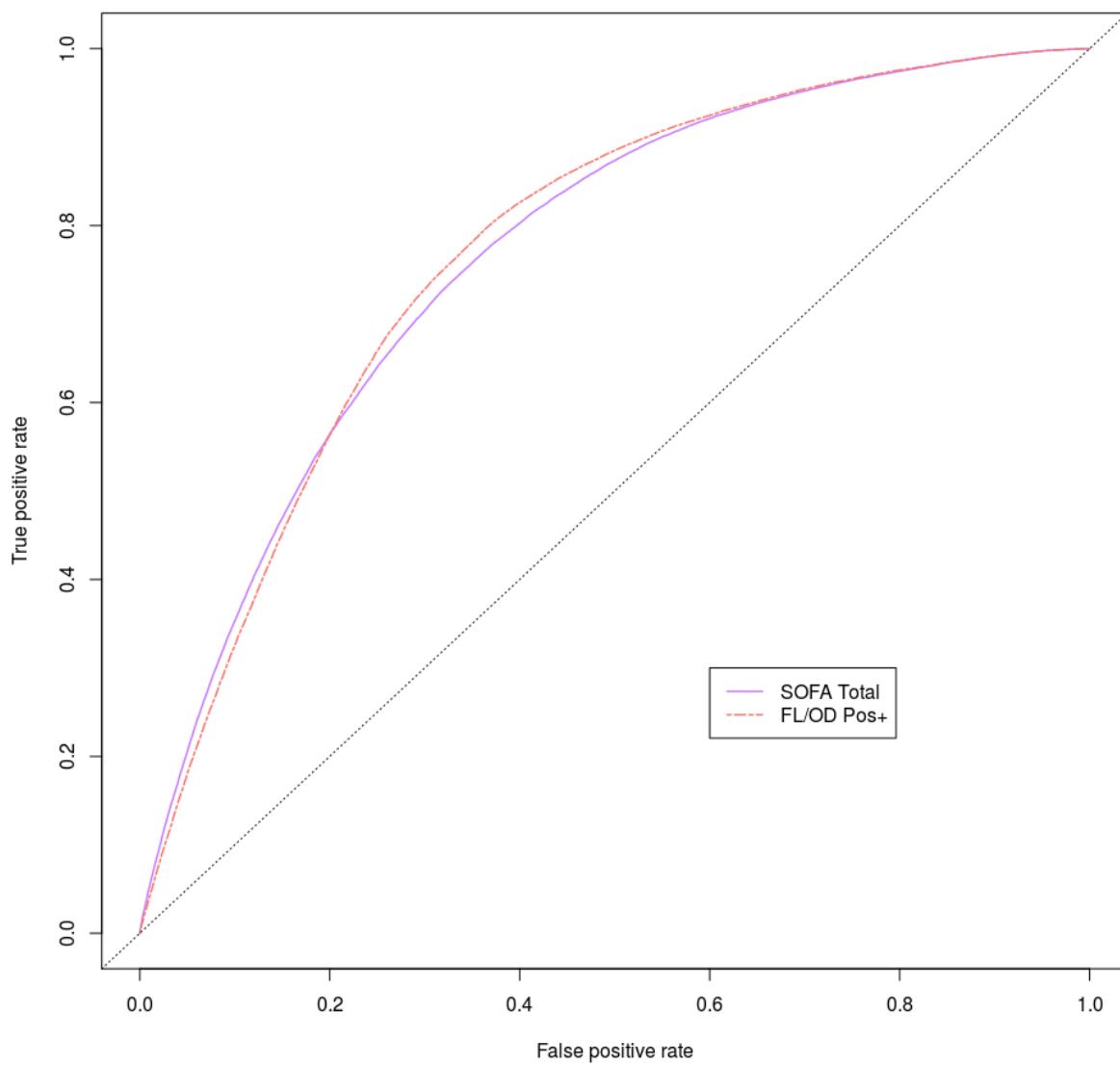
**Comparison of SOFA Scores versus
Fuzzy Logic Criteria Met Sepsis Crude Prediction**



```

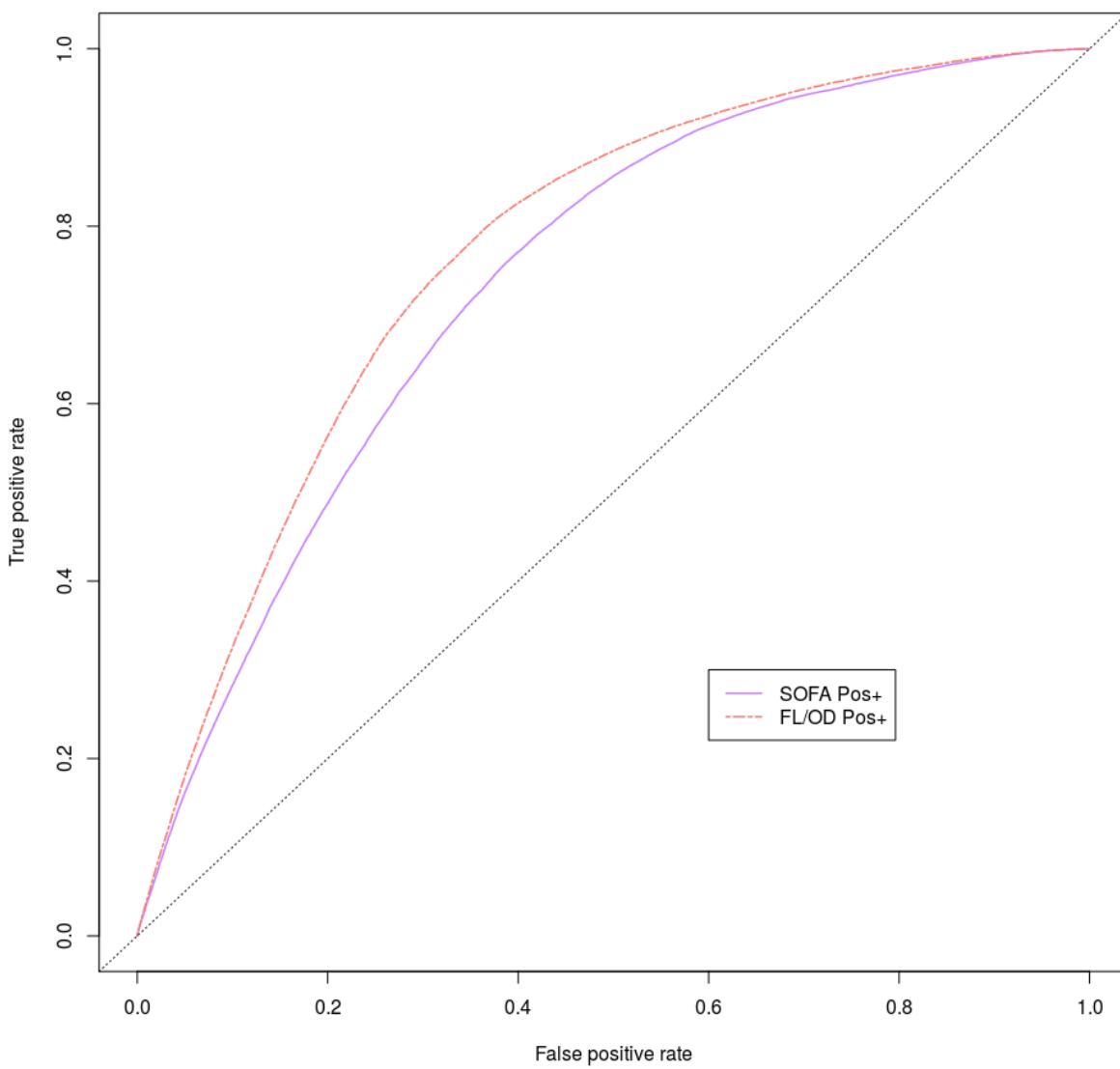
plot(SOFA1ADJSepsis.Perf, main = "Comparison of Total SOFA Score versus
    Fuzzy Logic Criteria Met Sepsis Adjusted Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(FuzzyLogicADJSepsis.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,6),col=c("#C77CFF","#F8766D"),c("SOFA Total","FL/OD Pos+"),lwd=1.5)

```

**Comparison of Total SOFA Score versus
Fuzzy Logic Criteria Met Sepsis Adjusted Prediction**

```
plot(SOFA2ADJSepsis.Perf, main = "Comparison of Positive SOFA Score versus  
Fuzzy Logic Criteria Met Sepsis Adjusted Prediction", col="#C77CFF", lty=1, lwd=1.5)  
plot(FuzzyLogicADJSepsis.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)  
abline(0,1,lty=3)  
legend(.6,.3,lty = c(1,6),col=c("#C77CFF","#F8766D"),c("SOFA Pos+","FL/OD Pos+"),lwd=1.5)
```

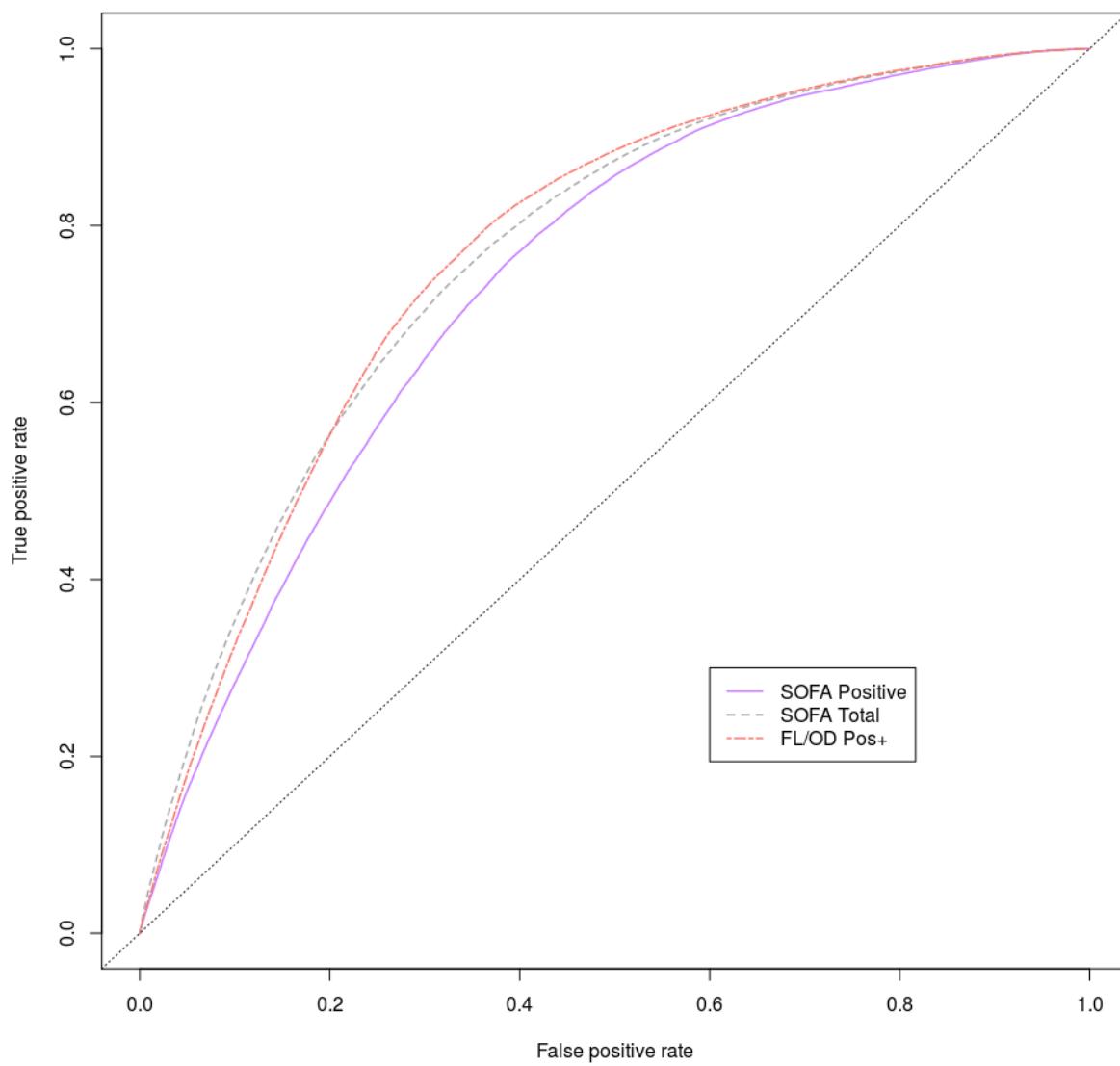
**Comparison of Positive SOFA Score versus
Fuzzy Logic Criteria Met Sepsis Adjusted Prediction**



```

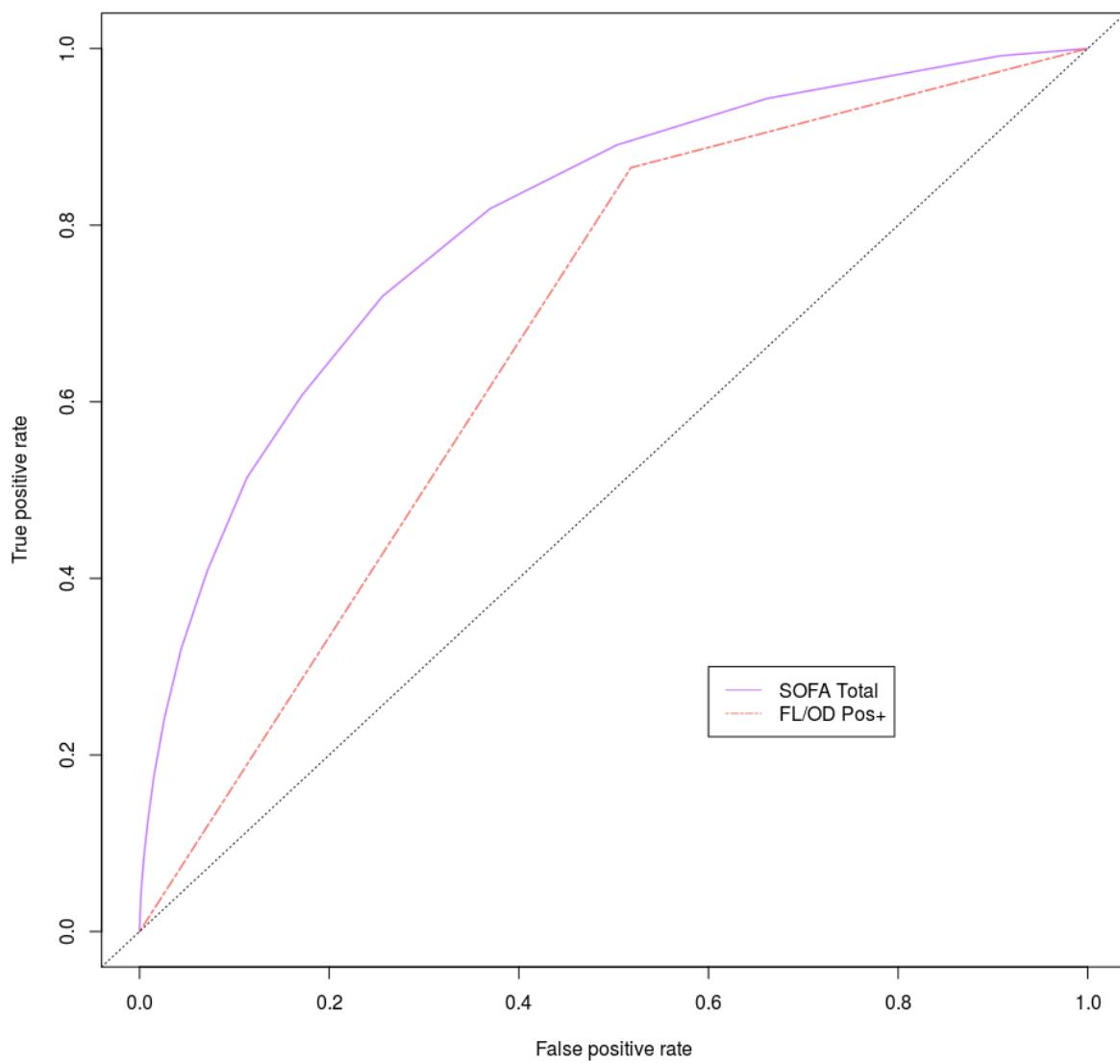
plot(SOFA2ADJSepsis.Perf, main = "Comparison of SOFA Scores versus
      Fuzzy Logic Criteria Met Sepsis Adjusted Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(SOFA1ADJSepsis.Perf, add=TRUE, col= "darkgrey", lty=2, lwd=1.5)
plot(FuzzyLogicADJSepsis.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,6),col=c("#C77CFF", "darkgrey", "#F8766D"),c("SOFA Positive", "SOFA Total", "FL/OD Pos
+"),lwd=1.5)

```

**Comparison of SOFA Scores versus
Fuzzy Logic Criteria Met Sepsis Adjusted Prediction**

```
plot(SOFA1CrudeMort.Perf, main = "Comparison of SOFA Total Scores versus  
Fuzzy Logic Criteria Met Mortality Crude Prediction", col="#C77CFF", lty=1,lwd=1.5)  
plot(FuzzyLogicCrudeMort.Perf, add=TRUE, col="#F8766D", lty=6,lwd=1.5)  
abline(0,1,lty=3)  
legend(.6,.3,lty = c(1,6),col=c("#C77CFF","#F8766D"),c("SOFA Total", "FL/OD Pos+"))
```

**Comparison of SOFA Total Scores versus
Fuzzy Logic Criteria Met Mortality Crude Prediction**

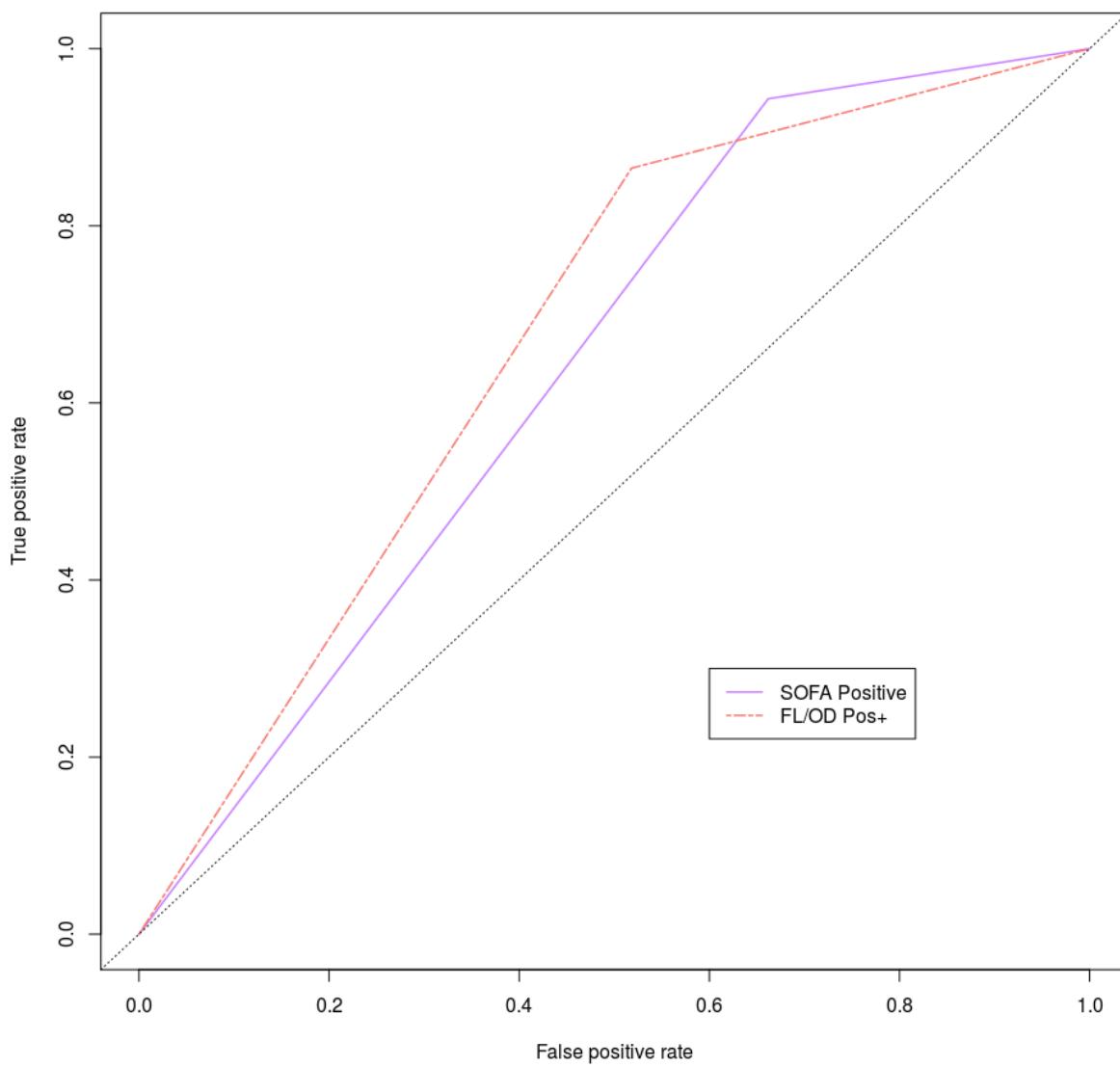


```

plot(SOFA2CrudeMort.Perf, main = "Comparison of SOFA Positive Score versus
      Fuzzy Logic Criteria Met Mortality Crude Prediction", col="#C77CFF", lty=1,lwd=1.5)
plot(FuzzyLogicCrudeMort.Perf, add=TRUE, col="#F8766D", lty=6,lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,6),col=c("#C77CFF","#F8766D"),c("SOFA Positive", "FL/OD Pos+"),lwd=1.5)

```

**Comparison of SOFA Positive Score versus
Fuzzy Logic Criteria Met Mortality Crude Prediction**

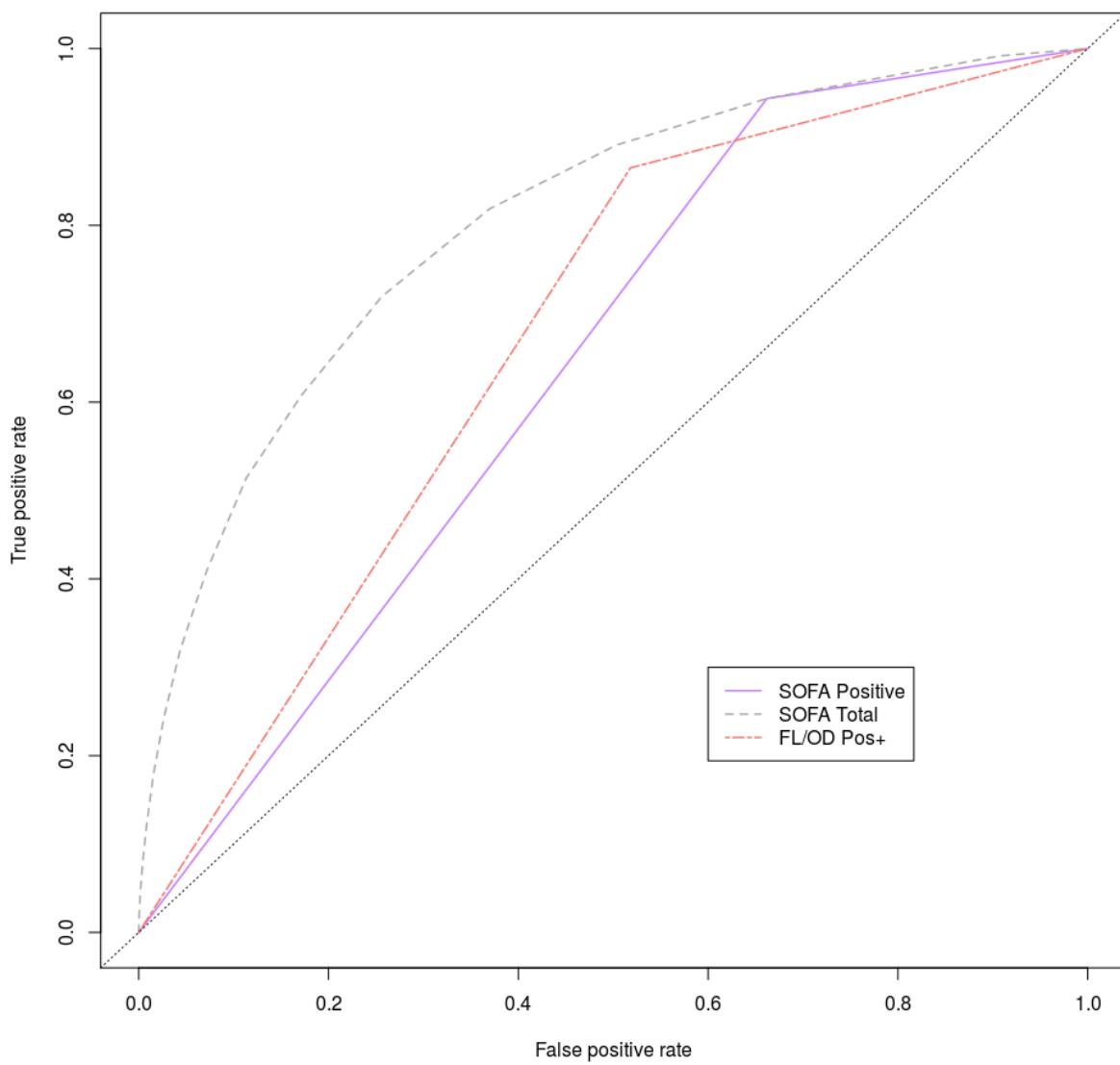


```

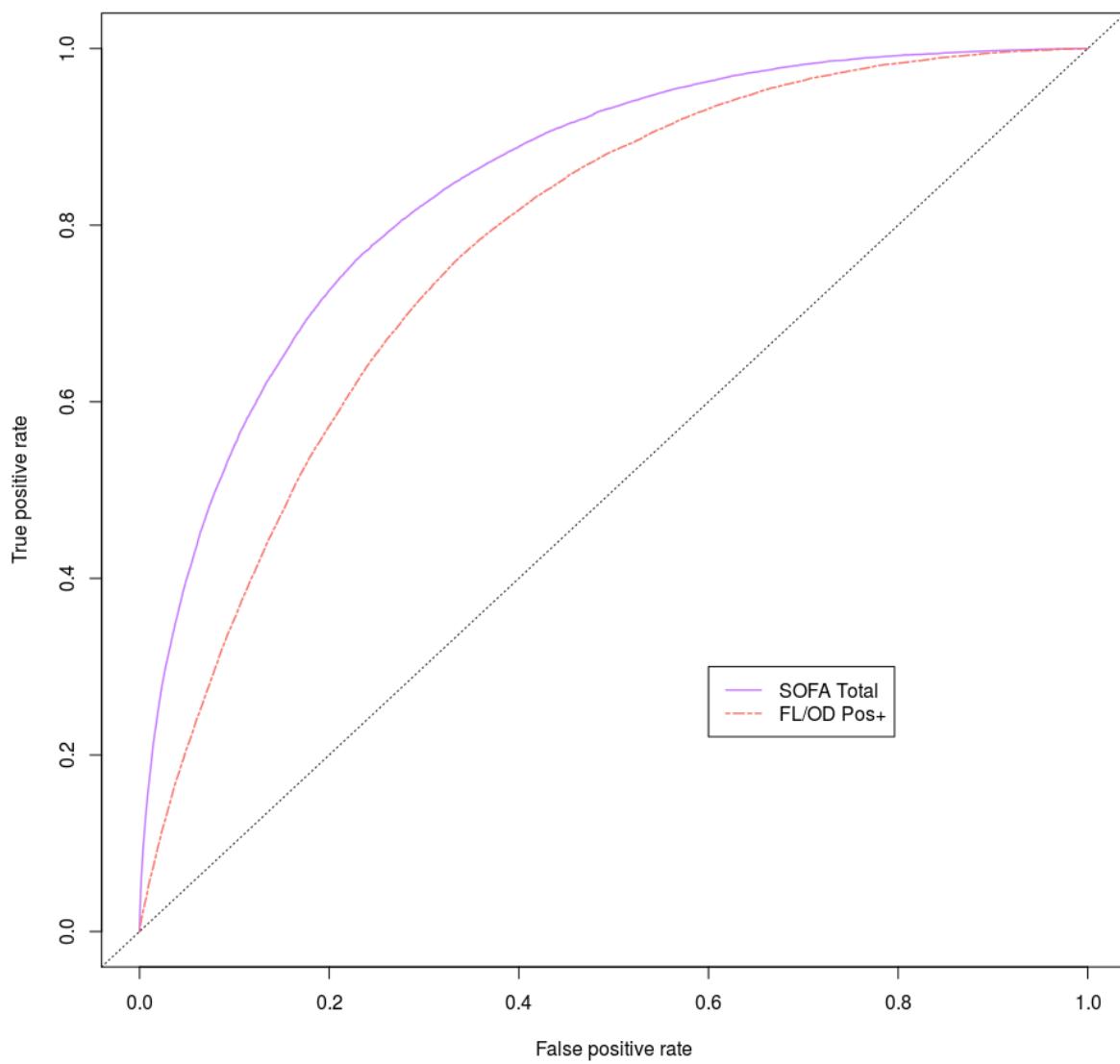
plot(SOFA2CrudeMort.Perf, main = "Comparison of SOFA Scores versus
      Fuzzy Logic Criteria Met Mortality Crude Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(SOFA1CrudeMort.Perf, add=TRUE, col= "darkgrey", lty=2, lwd=1.5)
plot(FuzzyLogicCrudeMort.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,6),col=c("#C77CFF", "darkgrey", "#F8766D"),c("SOFA Positive", "SOFA Total", "FL/OD Pos+
+"),lwd=1.5)

```

**Comparison of SOFA Scores versus
Fuzzy Logic Criteria Met Mortality Crude Prediction**

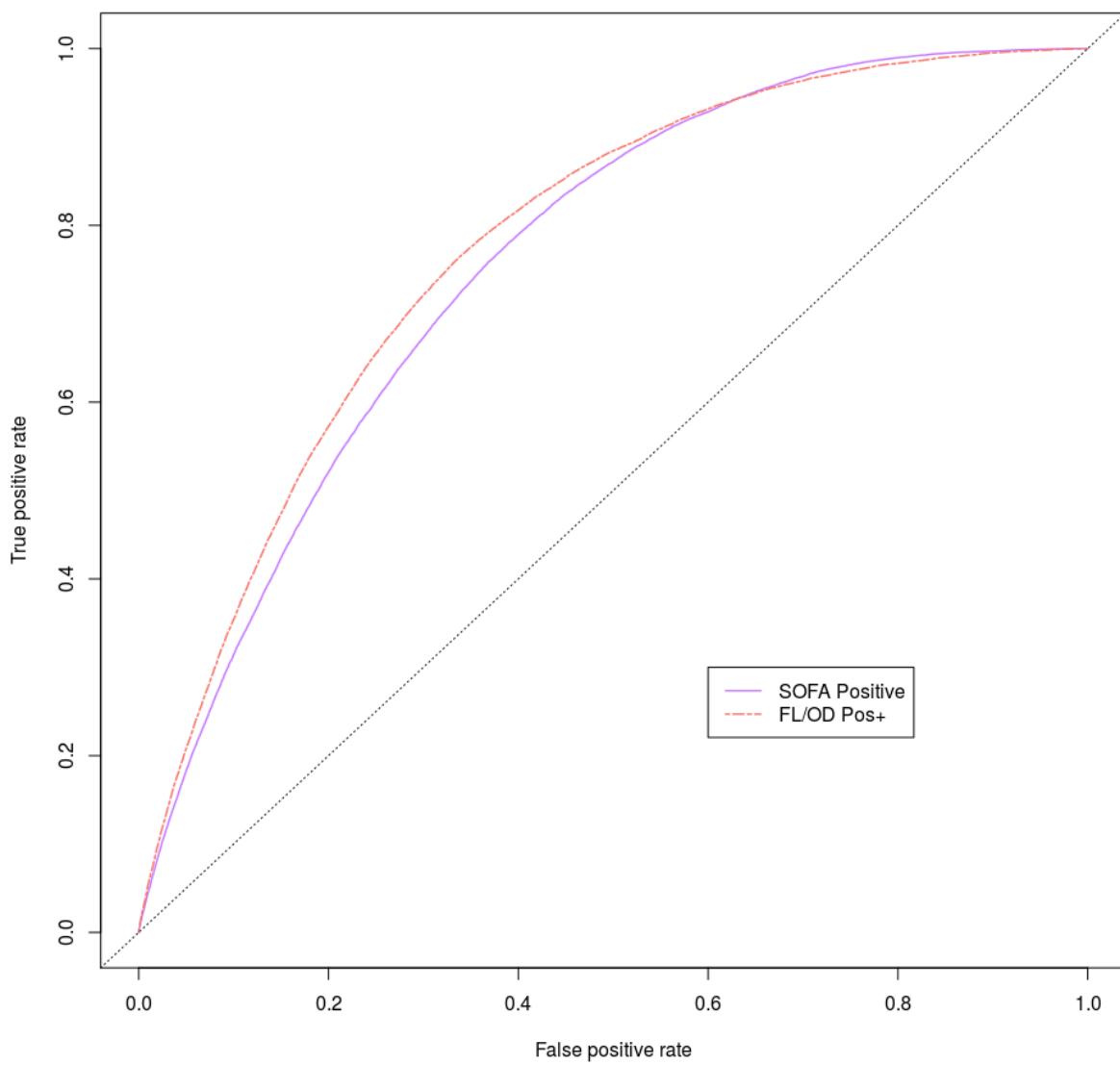


```
plot(SOFA1ADJMort.Perf, main = "Comparison of SOFA Total Score versus  
Fuzzy Logic Criteria Met Mortality Adjusted Prediction", col="#C77CFF", lty=1, lwd=1.5)  
plot(FuzzyLogicADJMort.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)  
abline(0,1,lty=3)  
legend(.6,.3,lty = c(1,6),col=c("#C77CFF", "#F8766D"),c("SOFA Total", "FL/OD Pos+"),lwd=1.5)
```

**Comparison of SOFA Total Score versus
Fuzzy Logic Criteria Met Mortality Adjusted Prediction**

```
plot(SOFA2ADJMort.Perf, main = "Comparison of SOFA Positive Scores versus  
Fuzzy Logic Criteria Met Mortality Adjusted Prediction", col="#C77CFF", lty=1, lwd=1.5)  
plot(FuzzyLogicADJMort.Perf, add=TRUE, col="#F8766D", lty=6, lwd=1.5)  
abline(0,1,lty=3)  
legend(.6,.3,lty = c(1,6),col=c("#C77CFF", "#F8766D"),c("SOFA Positive", "FL/OD Pos+"),lwd=1.5)
```

**Comparison of SOFA Positive Scores versus
Fuzzy Logic Criteria Met Mortality Adjusted Prediction**

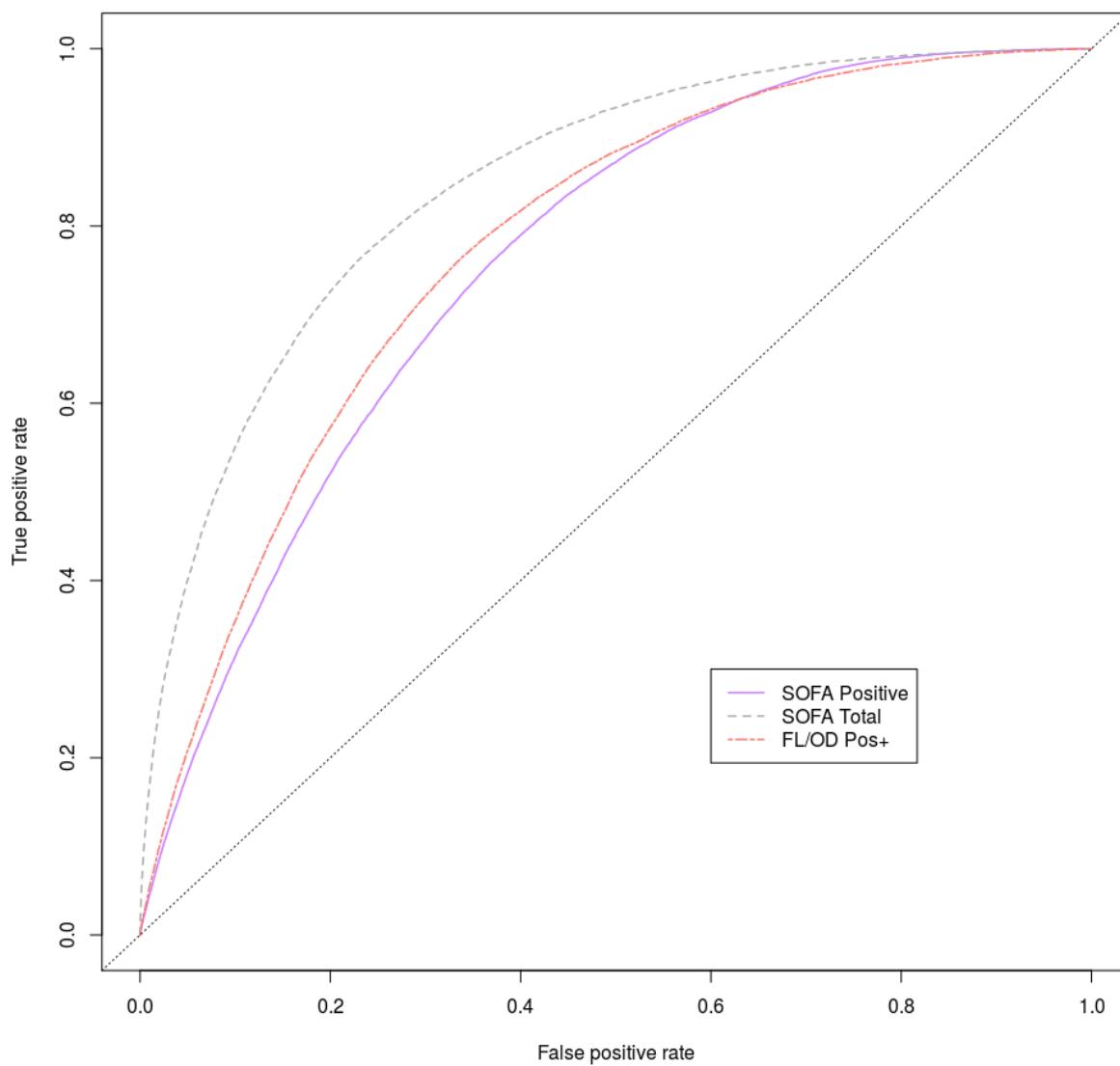


```

plot(SOFA2ADJMort.Perf, main = "Comparison of SOFA Scores versus
Fuzzy Logic Criteria Met Mortality Adjusted Prediction", col="#C77CFF", lty=1, lwd=1.5)
plot(SOFA1ADJMort.Perf, add=TRUE, col= "darkgrey", lty=2, lwd=1.5)
plot(FuzzyLogicADJMort.Perf, add=TRUE, col="#F8766D", lty=6,lwd=1.5)
abline(0,1,lty=3)
legend(.6,.3,lty = c(1,2,6),col=c("#C77CFF", "darkgrey", "#F8766D"),c("SOFA Positive", "SOFA Total", "FL/OD Pos
+"),lwd=1.5)

```

Comparison of SOFA Scores versus Fuzzy Logic Criteria Met Mortality Adjusted Prediction



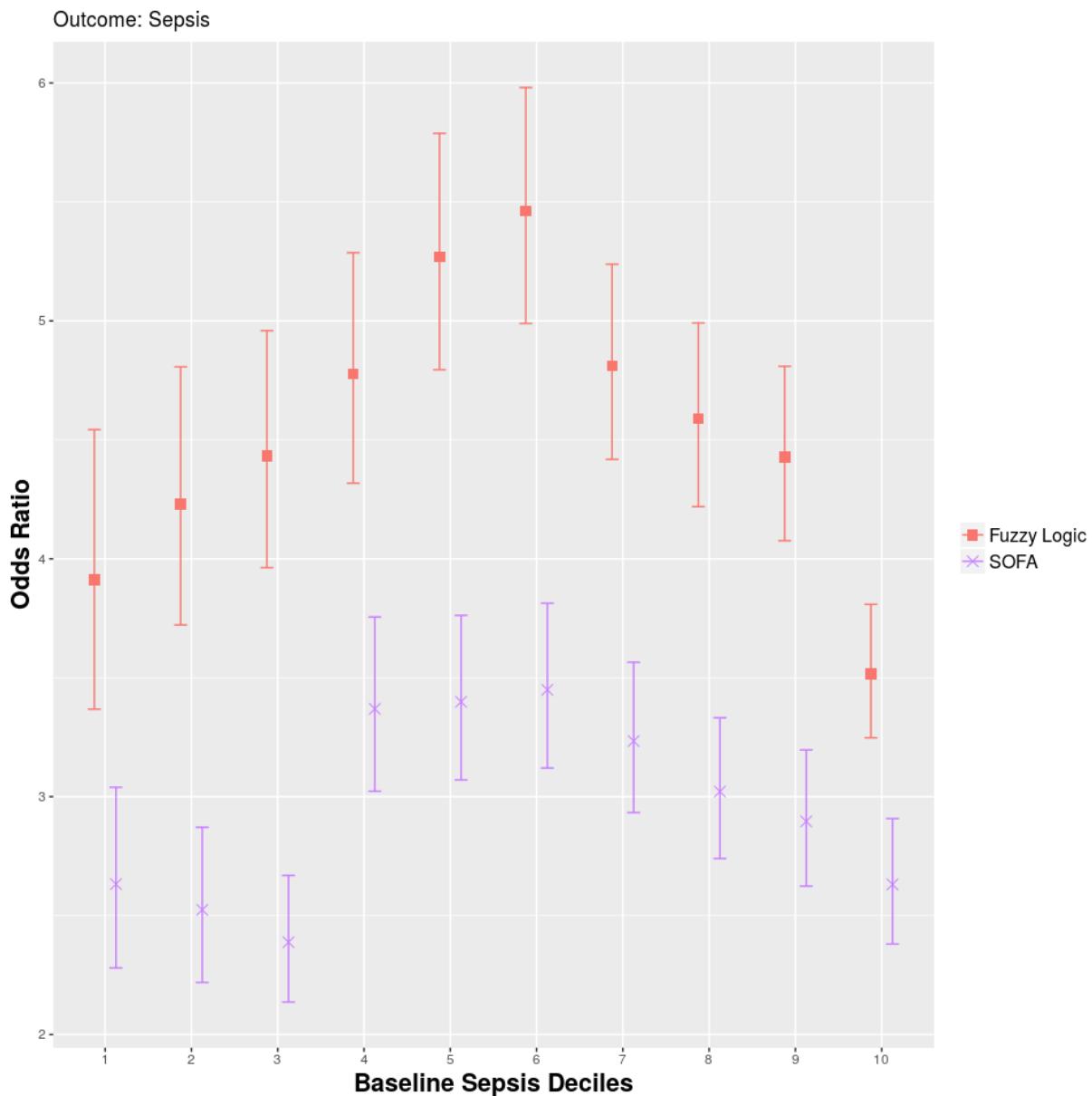
```

library(ggplot2)

levels(ORFuzzyLogicsepsis_Table3$BaselineDec)<-seq(1,10)
levels(ORSOFAsepsis_Table3$BaselineDec)<-seq(1,10)

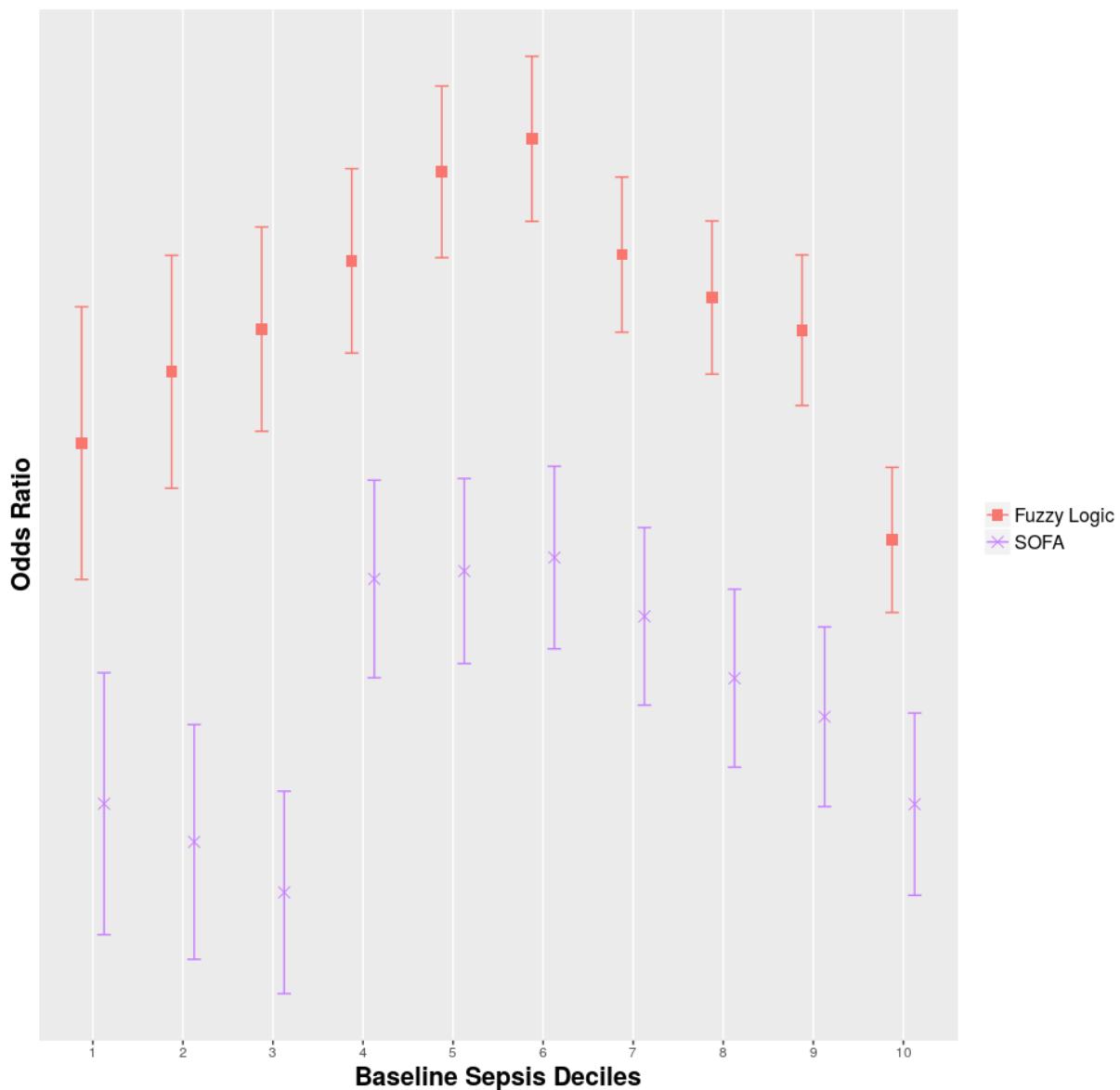
ORTable3<-ORFuzzyLogicsepsis_Table3%>%bind_rows(ORSOFAsepsis_Table3)
ggplot(ORTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Sepsis Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank()) + theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12))+ggtitle("Outcome: Sepsis") + scale_color_manual(values=c("#F8766D", "#C77cff")) + scale_shape_manual(values=c(15,4))

```



```
ORTable3<-ORFuzzyLogicsepsis_Table3%>%bind_rows(ORSOFAsepsis_Table3)
ggplot(ORTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Sepsis Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank()) + theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12))+ggtitle("Outcome: Sepsis") + scale_color_manual(values=c("#F8766D", "#C77CFF")) + scale_y_log10() + scale_shape_manual(values=c(15,4))
```

Outcome: Sepsis

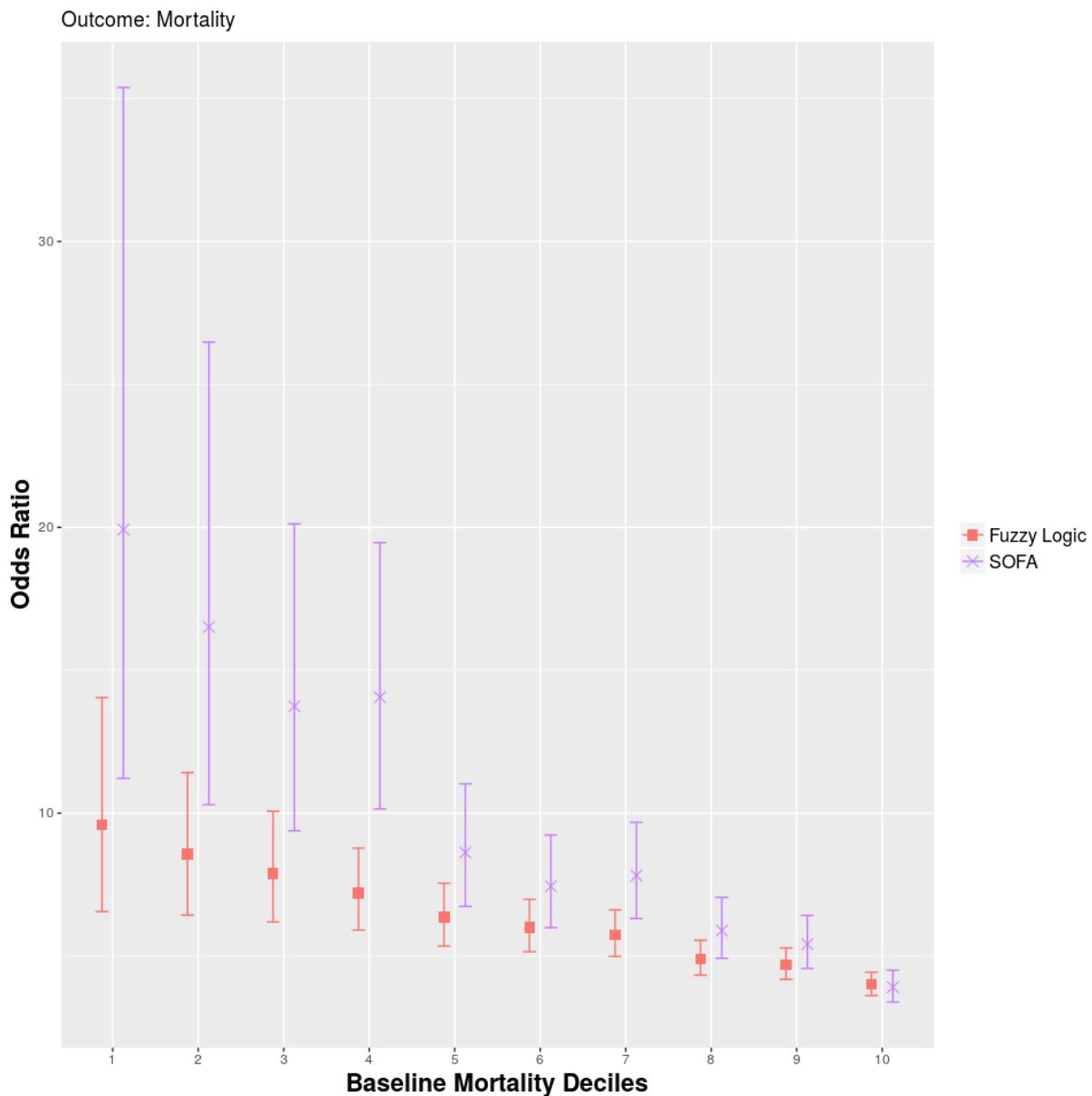


```

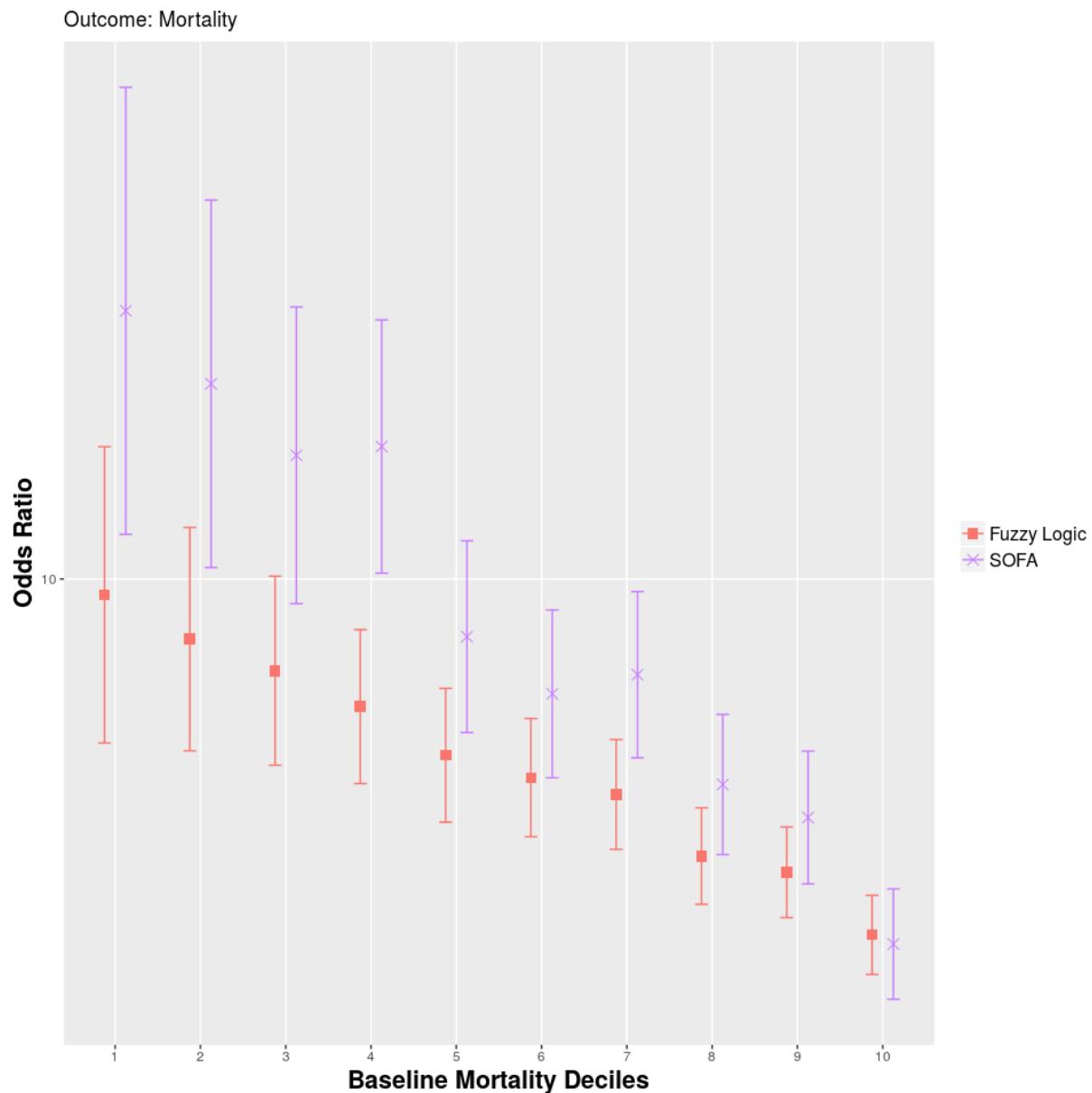
levels(ORFuzzyLogicmort_Table3$BaselineDec)<-seq(1,10)
levels(ORSOFAmort_Table3$BaselineDec)<-seq(1,10)

ORMortTable3<-ORFuzzyLogicmort_Table3%>%bind_rows(ORSOFAmort_Table3)
ggplot(ORMortTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Mortality Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank()) + theme(axis.title=element_text(size=16,face="bold"),legend.text=element_text(size=12)) +ggtitle("Outcome: Mortality") +
  scale_color_manual(values=c("#F8766D", "#C77CFF")) + scale_shape_manual(values=c(15,4))

```



```
ORMortTable3<-ORFuzzyLogicmort_Table3%>%bind_rows(ORSOFAMort_Table3)
ggplot(ORMortTable3,aes(BaselineDec,OddsRatio, group=type,col=type))+geom_point(aes(shape=type),size=3,position = position_dodge(width = 0.5))+geom_errorbar(aes(ymax=UL, ymin=LL),width=0.3,position = position_dodge(width = 0.5))+xlab("Baseline Mortality Deciles")+ylab("Odds Ratio")+
  theme(legend.title=element_blank()) + theme(axis.title.e=element_text(size=16,face="bold"),legend.text=element_text(size=12)) + ggtitle("Outcome: Mortality") + scale_y_log10() +scale_color_manual(values=c("#F8766D", "#C77CFF")) + scale_shape_manual(values=c(15,4))
```



```
#save.image("PaperImageComplete.rdata")
```