ADS-503 Final Project

Roberto Cancel, Kyle Estaban Dalope, Nicholas Lee

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Data Import

```
## Load in Data - Convert Blank Cells to NA
patient_data <- read.csv("dataset.csv", na.strings = c("","NA"))
```

```
## Load in File Containing Varible Definitions ##
data_dictionary <- read.csv("Dataset Dictionary - updated.csv")
```

Handling Missing Data

```
summary(patient_data)
```

```
##   encounter_id      patient_id      hospital_id         age
##  Min.   :     1   Min.   :     1   Min.   :  2.0   Min.   :16.00
##  1st Qu.: 32852   1st Qu.: 32830   1st Qu.: 47.0   1st Qu.:52.00
##  Median : 65665   Median : 65413   Median :109.0   Median :65.00
##  Mean   : 65606   Mean   : 65537   Mean   :105.7   Mean   :62.31
##  3rd Qu.: 98342   3rd Qu.: 98298   3rd Qu.:161.0   3rd Qu.:75.00
##  Max.   :131051   Max.   :131051   Max.   :204.0   Max.   :89.00
##                                                    NA's   :4228
##       bmi        elective_surgery  ethnicity           gender
##  Min.   :14.85   Min.   :0.0000   Length:91713       Length:91713
##  1st Qu.:23.64   1st Qu.:0.0000   Class :character   Class :character
##  Median :27.66   Median :0.0000   Mode  :character   Mode  :character
##  Mean   :29.19   Mean   :0.1837
##  3rd Qu.:32.93   3rd Qu.:0.0000
##  Max.   :67.81   Max.   :1.0000
##  NA's   :3429
##      height      icu_admit_source       icu_id      icu_stay_type
##  Min.   :137.2   Length:91713       Min.   : 82.0   Length:91713
##  1st Qu.:162.5   Class :character   1st Qu.:369.0   Class :character
##  Median :170.1   Mode  :character   Median :504.0   Mode  :character
##  Mean   :169.6                      Mean   :508.4
##  3rd Qu.:177.8                      3rd Qu.:679.0
##  Max.   :195.6                      Max.   :927.0
##  NA's   :1334
```

```
##    icu_type          pre_icu_los_days        weight       apache_2_diagnosis
##  Length:91713       Min.   :-24.94722   Min.   : 38.60   Min.   :101.0
##  Class :character   1st Qu.:  0.03542   1st Qu.: 66.80   1st Qu.:113.0
##  Mode  :character   Median :  0.13889   Median : 80.30   Median :122.0
##                     Mean   :  0.83577   Mean   : 84.03   Mean   :185.4
##                     3rd Qu.:  0.40903   3rd Qu.: 97.10   3rd Qu.:301.0
##                     Max.   :159.09097   Max.   :186.00   Max.   :308.0
##                                         NA's   :2720     NA's   :1662
##  apache_3j_diagnosis apache_post_operative   arf_apache    gcs_eyes_apache
##  Min.   :   0.01     Min.   :0.0000        Min.   :0.000   Min.   :1.000
##  1st Qu.: 203.01     1st Qu.:0.0000        1st Qu.:0.000   1st Qu.:3.000
##  Median : 409.02     Median :0.0000        Median :0.000   Median :4.000
##  Mean   : 558.22     Mean   :0.2011        Mean   :0.028   Mean   :3.465
##  3rd Qu.: 703.03     3rd Qu.:0.0000        3rd Qu.:0.000   3rd Qu.:4.000
##  Max.   :2201.05     Max.   :1.0000        Max.   :1.000   Max.   :4.000
##  NA's   :1101                              NA's   :715     NA's   :1901
##  gcs_motor_apache gcs_unable_apache gcs_verbal_apache heart_rate_apache
##  Min.   :1.000    Min.   :0.0000    Min.   :1.000     Min.   : 30.00
##  1st Qu.:6.000    1st Qu.:0.0000    1st Qu.:4.000     1st Qu.: 86.00
##  Median :6.000    Median :0.0000    Median :5.000     Median :104.00
##  Mean   :5.471    Mean   :0.0095    Mean   :3.995     Mean   : 99.71
##  3rd Qu.:6.000    3rd Qu.:0.0000    3rd Qu.:5.000     3rd Qu.:120.00
##  Max.   :6.000    Max.   :1.0000    Max.   :5.000     Max.   :178.00
##  NA's   :1901     NA's   :1037      NA's   :1901      NA's   :878
##  intubated_apache   map_apache     resprate_apache  temp_apache
##  Min.   :0.0000   Min.   : 40.00   Min.   : 4.00   Min.   :32.10
##  1st Qu.:0.0000   1st Qu.: 54.00   1st Qu.:11.00   1st Qu.:36.20
##  Median :0.0000   Median : 67.00   Median :28.00   Median :36.50
##  Mean   :0.1512   Mean   : 88.02   Mean   :25.81   Mean   :36.41
##  3rd Qu.:0.0000   3rd Qu.:125.00   3rd Qu.:36.00   3rd Qu.:36.70
##  Max.   :1.0000   Max.   :200.00   Max.   :60.00   Max.   :39.70
##  NA's   :715      NA's   :994      NA's   :1234    NA's   :4108
##  ventilated_apache d1_diasbp_max    d1_diasbp_min   d1_diasbp_noninvasive_max
##  Min.   :0.0000    Min.   : 46.00   Min.   :13.00   Min.   : 46.00
##  1st Qu.:0.0000    1st Qu.: 75.00   1st Qu.:42.00   1st Qu.: 75.00
##  Median :0.0000    Median : 86.00   Median :50.00   Median : 87.00
##  Mean   :0.3257    Mean   : 88.49   Mean   :50.16   Mean   : 88.61
##  3rd Qu.:1.0000    3rd Qu.: 99.00   3rd Qu.:58.00   3rd Qu.: 99.00
##  Max.   :1.0000    Max.   :165.00   Max.   :90.00   Max.   :165.00
##  NA's   :715       NA's   :165      NA's   :165     NA's   :1040
##  d1_diasbp_noninvasive_min d1_heartrate_max d1_heartrate_min   d1_mbp_max
##  Min.   :13.00             Min.   : 58      Min.   :  0.00   Min.   : 60.0
##  1st Qu.:42.00             1st Qu.: 87      1st Qu.: 60.00   1st Qu.: 90.0
##  Median :50.00             Median :101      Median : 69.00   Median :102.0
##  Mean   :50.24             Mean   :103      Mean   : 70.32   Mean   :104.7
##  3rd Qu.:58.00             3rd Qu.:116      3rd Qu.: 81.00   3rd Qu.:116.0
##  Max.   :90.00             Max.   :177      Max.   :175.00   Max.   :184.0
##  NA's   :1040              NA's   :145      NA's   :145      NA's   :220
##    d1_mbp_min     d1_mbp_noninvasive_max d1_mbp_noninvasive_min d1_resprate_max
##  Min.   : 22.00   Min.   : 60.0          Min.   : 22.00         Min.   :14.00
##  1st Qu.: 55.00   1st Qu.: 90.0          1st Qu.: 55.00         1st Qu.:22.00
##  Median : 64.00   Median :102.0          Median : 64.00         Median :26.00
##  Mean   : 64.87   Mean   :104.6          Mean   : 64.94         Mean   :28.88
##  3rd Qu.: 75.00   3rd Qu.:116.0          3rd Qu.: 75.00         3rd Qu.:32.00
```

```
##  Max.   :112.00   Max.   :181.0          Max.   :112.00         Max.   :92.00
##  NA's   :220      NA's   :1479           NA's   :1479           NA's   :385
##  d1_resprate_min   d1_spo2_max      d1_spo2_min      d1_sysbp_max
##  Min.   :  0.00   Min.   :  0.00   Min.   :  0.00   Min.   : 90.0
##  1st Qu.: 10.00   1st Qu.: 99.00   1st Qu.: 89.00   1st Qu.:130.0
##  Median : 13.00   Median :100.00   Median : 92.00   Median :146.0
##  Mean   : 12.85   Mean   : 99.24   Mean   : 90.45   Mean   :148.3
##  3rd Qu.: 16.00   3rd Qu.:100.00   3rd Qu.: 95.00   3rd Qu.:164.0
##  Max.   :100.00   Max.   :100.00   Max.   :100.00   Max.   :232.0
##  NA's   :385      NA's   :333      NA's   :333      NA's   :159
##   d1_sysbp_min    d1_sysbp_noninvasive_max d1_sysbp_noninvasive_min
##  Min.   : 41.00   Min.   : 90.0            Min.   : 41.03
##  1st Qu.: 83.00   1st Qu.:130.0            1st Qu.: 84.00
##  Median : 96.00   Median :146.0            Median : 96.00
##  Mean   : 96.92   Mean   :148.2            Mean   : 96.99
##  3rd Qu.:110.00   3rd Qu.:164.0            3rd Qu.:110.00
##  Max.   :160.00   Max.   :232.0            Max.   :160.00
##  NA's   :159      NA's   :1027             NA's   :1027
##   d1_temp_max     d1_temp_min    h1_diasbp_max    h1_diasbp_min
##  Min.   :35.10   Min.   :31.89   Min.   : 37.00   Min.   : 22.00
##  1st Qu.:36.90   1st Qu.:36.10   1st Qu.: 62.00   1st Qu.: 52.00
##  Median :37.11   Median :36.40   Median : 74.00   Median : 62.00
##  Mean   :37.28   Mean   :36.27   Mean   : 75.36   Mean   : 62.84
##  3rd Qu.:37.60   3rd Qu.:36.66   3rd Qu.: 86.00   3rd Qu.: 73.00
##  Max.   :39.90   Max.   :37.80   Max.   :143.00   Max.   :113.00
##  NA's   :2324    NA's   :2324    NA's   :3619     NA's   :3619
##  h1_diasbp_noninvasive_max h1_diasbp_noninvasive_min h1_heartrate_max
##  Min.   : 37.00            Min.   : 22.00            Min.   : 46.00
##  1st Qu.: 63.00            1st Qu.: 52.00            1st Qu.: 77.00
##  Median : 74.00            Median : 62.00            Median : 90.00
##  Mean   : 75.81            Mean   : 63.27            Mean   : 92.23
##  3rd Qu.: 87.00            3rd Qu.: 74.00            3rd Qu.:106.00
##  Max.   :144.00            Max.   :114.00            Max.   :164.00
##  NA's   :7350              NA's   :7350              NA's   :2790
##  h1_heartrate_min   h1_mbp_max       h1_mbp_min    h1_mbp_noninvasive_max
##  Min.   : 36.00   Min.   : 49.00   Min.   : 32.0   Min.   : 49.00
##  1st Qu.: 69.00   1st Qu.: 77.00   1st Qu.: 66.0   1st Qu.: 77.00
##  Median : 82.00   Median : 90.00   Median : 78.0   Median : 90.00
##  Mean   : 83.66   Mean   : 91.61   Mean   : 79.4   Mean   : 91.59
##  3rd Qu.: 97.00   3rd Qu.:104.00   3rd Qu.: 92.0   3rd Qu.:104.00
##  Max.   :144.00   Max.   :165.00   Max.   :138.0   Max.   :163.00
##  NA's   :2790     NA's   :4639     NA's   :4639    NA's   :9084
##  h1_mbp_noninvasive_min h1_resprate_max h1_resprate_min   h1_spo2_max
##  Min.   : 32.00         Min.   :10.00   Min.   :  0.00   Min.   :  0.00
##  1st Qu.: 66.00         1st Qu.:18.00   1st Qu.: 14.00   1st Qu.: 97.00
##  Median : 79.00         Median :21.00   Median : 16.00   Median : 99.00
##  Mean   : 79.71         Mean   :22.63   Mean   : 17.21   Mean   : 98.05
##  3rd Qu.: 92.00         3rd Qu.:26.00   3rd Qu.: 20.00   3rd Qu.:100.00
##  Max.   :138.00         Max.   :59.00   Max.   :189.00   Max.   :100.00
##  NA's   :9084           NA's   :4357    NA's   :4357     NA's   :4185
##   h1_spo2_min      h1_sysbp_max    h1_sysbp_min   h1_sysbp_noninvasive_max
##  Min.   :  0.00   Min.   : 75.0   Min.   : 53.0   Min.   : 75.0
##  1st Qu.: 94.00   1st Qu.:113.0   1st Qu.: 98.0   1st Qu.:113.0
##  Median : 96.00   Median :131.0   Median :115.0   Median :130.0
```

```
##  Mean   : 95.17   Mean   :133.2   Mean   :116.4   Mean   :133.1
##  3rd Qu.: 99.00   3rd Qu.:150.0   3rd Qu.:134.0   3rd Qu.:150.0
##  Max.   :100.00   Max.   :223.0   Max.   :194.0   Max.   :223.0
##  NA's   :4185     NA's   :3611    NA's   :3611    NA's   :7341
##  h1_sysbp_noninvasive_min d1_glucose_max  d1_glucose_min  d1_potassium_max
##  Min.   : 53.0            Min.   : 73.0   Min.   : 33.0   Min.   :2.800
##  1st Qu.: 98.0            1st Qu.:117.0   1st Qu.: 91.0   1st Qu.:3.800
##  Median :115.0            Median :150.0   Median :107.0   Median :4.200
##  Mean   :116.5            Mean   :174.6   Mean   :114.4   Mean   :4.252
##  3rd Qu.:134.0            3rd Qu.:201.0   3rd Qu.:131.0   3rd Qu.:4.600
##  Max.   :195.0            Max.   :611.0   Max.   :288.0   Max.   :7.000
##  NA's   :7341             NA's   :5807    NA's   :5807    NA's   :9585
##  d1_potassium_min apache_4a_hospital_death_prob apache_4a_icu_death_prob
##  Min.   :2.400    Min.   :-1.000                Min.   :-1.000
##  1st Qu.:3.600    1st Qu.: 0.020                1st Qu.: 0.010
##  Median :3.900    Median : 0.050                Median : 0.020
##  Mean   :3.935    Mean   : 0.087                Mean   : 0.044
##  3rd Qu.:4.300    3rd Qu.: 0.130                3rd Qu.: 0.060
##  Max.   :5.800    Max.   : 0.990                Max.   : 0.970
##  NA's   :9585     NA's   :7947                  NA's   :7947
##       aids         cirrhosis      diabetes_mellitus hepatic_failure
##  Min.   :0e+00   Min.   :0.0000   Min.   :0.0000    Min.   :0.000
##  1st Qu.:0e+00   1st Qu.:0.0000   1st Qu.:0.0000    1st Qu.:0.000
##  Median :0e+00   Median :0.0000   Median :0.0000    Median :0.000
##  Mean   :9e-04   Mean   :0.0157   Mean   :0.2252    Mean   :0.013
##  3rd Qu.:0e+00   3rd Qu.:0.0000   3rd Qu.:0.0000    3rd Qu.:0.000
##  Max.   :1e+00   Max.   :1.0000   Max.   :1.0000    Max.   :1.000
##  NA's   :715     NA's   :715      NA's   :715       NA's   :715
##  immunosuppression    leukemia         lymphoma
##  Min.   :0.0000    Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.0000    1st Qu.:0.0000   1st Qu.:0.0000
##  Median :0.0000    Median :0.0000   Median :0.0000
##  Mean   :0.0262    Mean   :0.0071   Mean   :0.0041
##  3rd Qu.:0.0000    3rd Qu.:0.0000   3rd Qu.:0.0000
##  Max.   :1.0000    Max.   :1.0000   Max.   :1.0000
##  NA's   :715       NA's   :715      NA's   :715
##  solid_tumor_with_metastasis apache_3j_bodysystem apache_2_bodysystem
##  Min.   :0.0000              Length:91713         Length:91713
##  1st Qu.:0.0000              Class :character     Class :character
##  Median :0.0000              Mode  :character     Mode  :character
##  Mean   :0.0206
##  3rd Qu.:0.0000
##  Max.   :1.0000
##  NA's   :715
##     X           hospital_death
##  Mode:logical   Min.   :0.0000
##  NA's:91713     1st Qu.:0.0000
##                 Median :0.0000
##                 Mean   :0.0863
##                 3rd Qu.:0.0000
##                 Max.   :1.0000
##
```

```
# Obtain and Drop id Columns #
id_columns <- grep("_id", colnames(patient_data))
patient_data <- patient_data[, -id_columns]
# Convert Outcome Variable to factor #
patient_data$hospital_death <- as.factor(patient_data$hospital_death)
# Drop NAs from gender #
patient_data <- patient_data[!is.na(patient_data$gender), ]
patient_data$gender <- ifelse(patient_data$gender  == "M", "1", "0")
patient_data$gender <- as.numeric(as.character(patient_data$gender))

# Distribution of Target Variable #
table(patient_data$hospital_death)
```

```
##
##     0     1
## 83781  7907
```

```
## Roughly 8.6% of the data set is the positive class (1 = death)
```

```
# Stratified Sampling #
set.seed(100)
trainingRows <- createDataPartition(patient_data$hospital_death,
                                    p = 0.80,
                                    list = FALSE)
## Subset Data into Training and Test Sets ##
patient_train <- patient_data[trainingRows, ]
patient_test <- patient_data[-trainingRows, ]
```

```
summary(patient_train)
```

```
##       age             bmi        elective_surgery  ethnicity
##  Min.   :16.0   Min.   :14.84   Min.   :0.0000   Length:73351
##  1st Qu.:52.0   1st Qu.:23.64   1st Qu.:0.0000   Class :character
##  Median :65.0   Median :27.65   Median :0.0000   Mode  :character
##  Mean   :62.3   Mean   :29.18   Mean   :0.1833
##  3rd Qu.:75.0   3rd Qu.:32.93   3rd Qu.:0.0000
##  Max.   :89.0   Max.   :67.81   Max.   :1.0000
##  NA's   :3367   NA's   :2682
##      gender           height      icu_admit_source   icu_stay_type
##  Min.   :0.0000   Min.   :137.2   Length:73351       Length:73351
##  1st Qu.:0.0000   1st Qu.:162.5   Class :character   Class :character
##  Median :1.0000   Median :170.0   Mode  :character   Mode  :character
##  Mean   :0.5396   Mean   :169.6
##  3rd Qu.:1.0000   3rd Qu.:177.8
##  Max.   :1.0000   Max.   :195.6
##                   NA's   :1034
##    icu_type         pre_icu_los_days        weight       apache_2_diagnosis
##  Length:73351       Min.   :-24.94722   Min.   : 38.60   Min.   :101.0
##  Class :character   1st Qu.:  0.03542   1st Qu.: 66.70   1st Qu.:113.0
##  Mode  :character   Median :  0.13889   Median : 80.20   Median :122.0
##                     Mean   :  0.83731   Mean   : 84.01   Mean   :185.3
##                     3rd Qu.:  0.40903   3rd Qu.: 97.10   3rd Qu.:301.0
```

```
##                   Max.   :159.09097   Max.   :186.00   Max.   :308.0
##                                        NA's   :2138     NA's   :1330
##  apache_3j_diagnosis apache_post_operative   arf_apache     gcs_eyes_apache
##  Min.   :   0.01     Min.   :0.0000        Min.   :0.0000   Min.   :1.000
##  1st Qu.: 203.01     1st Qu.:0.0000        1st Qu.:0.0000   1st Qu.:3.000
##  Median : 409.02     Median :0.0000        Median :0.0000   Median :4.000
##  Mean   : 558.26     Mean   :0.2011        Mean   :0.0283   Mean   :3.462
##  3rd Qu.: 703.03     3rd Qu.:0.0000        3rd Qu.:0.0000   3rd Qu.:4.000
##  Max.   :2201.05     Max.   :1.0000        Max.   :1.0000   Max.   :4.000
##  NA's   :883                               NA's   :570      NA's   :1523
##  gcs_motor_apache gcs_unable_apache gcs_verbal_apache heart_rate_apache
##  Min.   :1.000    Min.   :0.0000    Min.   :1.000     Min.   : 30.00
##  1st Qu.:6.000    1st Qu.:0.0000    1st Qu.:4.000     1st Qu.: 86.00
##  Median :6.000    Median :0.0000    Median :5.000     Median :104.00
##  Mean   :5.467    Mean   :0.0096    Mean   :3.989     Mean   : 99.79
##  3rd Qu.:6.000    3rd Qu.:0.0000    3rd Qu.:5.000     3rd Qu.:120.00
##  Max.   :6.000    Max.   :1.0000    Max.   :5.000     Max.   :178.00
##  NA's   :1523     NA's   :825       NA's   :1523      NA's   :693
##  intubated_apache   map_apache     resprate_apache  temp_apache
##  Min.   :0.0000   Min.   : 40.00   Min.   : 4.00   Min.   :32.10
##  1st Qu.:0.0000   1st Qu.: 54.00   1st Qu.:11.00   1st Qu.:36.20
##  Median :0.0000   Median : 67.00   Median :28.00   Median :36.50
##  Mean   :0.1515   Mean   : 88.08   Mean   :25.81   Mean   :36.41
##  3rd Qu.:0.0000   3rd Qu.:125.00   3rd Qu.:36.00   3rd Qu.:36.70
##  Max.   :1.0000   Max.   :200.00   Max.   :60.00   Max.   :39.70
##  NA's   :570      NA's   :779      NA's   :963     NA's   :3230
##  ventilated_apache d1_diasbp_max    d1_diasbp_min   d1_diasbp_noninvasive_max
##  Min.   :0.0000    Min.   : 46.00   Min.   :13.00   Min.   : 46.00
##  1st Qu.:0.0000    1st Qu.: 75.00   1st Qu.:42.00   1st Qu.: 75.00
##  Median :0.0000    Median : 86.00   Median :50.00   Median : 87.00
##  Mean   :0.3269    Mean   : 88.49   Mean   :50.16   Mean   : 88.61
##  3rd Qu.:1.0000    3rd Qu.: 99.00   3rd Qu.:58.00   3rd Qu.: 99.00
##  Max.   :1.0000    Max.   :165.00   Max.   :90.00   Max.   :165.00
##  NA's   :570       NA's   :120      NA's   :120     NA's   :839
##  d1_diasbp_noninvasive_min d1_heartrate_max d1_heartrate_min   d1_mbp_max
##  Min.   :13.00             Min.   : 58      Min.   :  0.00   Min.   : 60.0
##  1st Qu.:42.00             1st Qu.: 87      1st Qu.: 60.00   1st Qu.: 90.0
##  Median :50.00             Median :101      Median : 70.00   Median :102.0
##  Mean   :50.25             Mean   :103      Mean   : 70.35   Mean   :104.7
##  3rd Qu.:58.00             3rd Qu.:117      3rd Qu.: 81.00   3rd Qu.:116.0
##  Max.   :90.00             Max.   :177      Max.   :160.00   Max.   :184.0
##  NA's   :839               NA's   :108      NA's   :108      NA's   :165
##    d1_mbp_min     d1_mbp_noninvasive_max d1_mbp_noninvasive_min d1_resprate_max
##  Min.   : 22.00   Min.   : 60.0          Min.   : 22.00         Min.   :14.00
##  1st Qu.: 55.00   1st Qu.: 90.0          1st Qu.: 55.00         1st Qu.:22.00
##  Median : 64.00   Median :102.0          Median : 64.00         Median :26.00
##  Mean   : 64.85   Mean   :104.6          Mean   : 64.92         Mean   :28.89
##  3rd Qu.: 75.00   3rd Qu.:116.0          3rd Qu.: 75.00         3rd Qu.:32.00
##  Max.   :112.00   Max.   :181.0          Max.   :112.00         Max.   :92.00
##  NA's   :165      NA's   :1196           NA's   :1196           NA's   :296
##  d1_resprate_min   d1_spo2_max      d1_spo2_min      d1_sysbp_max
##  Min.   :  0.00   Min.   :  0.00   Min.   :  0.00   Min.   : 90.0
##  1st Qu.: 10.00   1st Qu.: 99.00   1st Qu.: 89.00   1st Qu.:130.0
##  Median : 13.00   Median :100.00   Median : 92.00   Median :146.0
```

```
##  Mean   : 12.85   Mean   : 99.25   Mean   : 90.46   Mean   :148.3
##  3rd Qu.: 16.00   3rd Qu.:100.00   3rd Qu.: 95.00   3rd Qu.:164.0
##  Max.   :100.00   Max.   :100.00   Max.   :100.00   Max.   :232.0
##  NA's   :296      NA's   :263      NA's   :263      NA's   :116
##   d1_sysbp_min    d1_sysbp_noninvasive_max d1_sysbp_noninvasive_min
##  Min.   : 41.00   Min.   : 90.0            Min.   : 41.03
##  1st Qu.: 83.00   1st Qu.:130.0            1st Qu.: 84.00
##  Median : 96.00   Median :146.0            Median : 96.00
##  Mean   : 96.91   Mean   :148.2            Mean   : 96.99
##  3rd Qu.:110.00   3rd Qu.:164.0            3rd Qu.:110.00
##  Max.   :160.00   Max.   :232.0            Max.   :160.00
##  NA's   :116      NA's   :829              NA's   :829
##   d1_temp_max     d1_temp_min    h1_diasbp_max    h1_diasbp_min
##  Min.   :35.10   Min.   :31.89   Min.   : 37.00   Min.   : 22.00
##  1st Qu.:36.90   1st Qu.:36.10   1st Qu.: 62.00   1st Qu.: 52.00
##  Median :37.11   Median :36.40   Median : 74.00   Median : 62.00
##  Mean   :37.29   Mean   :36.27   Mean   : 75.36   Mean   : 62.81
##  3rd Qu.:37.60   3rd Qu.:36.66   3rd Qu.: 86.00   3rd Qu.: 73.00
##  Max.   :39.90   Max.   :37.80   Max.   :143.00   Max.   :113.00
##  NA's   :1815    NA's   :1815    NA's   :2885     NA's   :2885
##  h1_diasbp_noninvasive_max h1_diasbp_noninvasive_min h1_heartrate_max
##  Min.   : 37.00            Min.   : 22.00            Min.   : 46.00
##  1st Qu.: 63.00            1st Qu.: 52.00            1st Qu.: 77.00
##  Median : 74.00            Median : 62.00            Median : 90.00
##  Mean   : 75.81            Mean   : 63.24            Mean   : 92.31
##  3rd Qu.: 87.00            3rd Qu.: 74.00            3rd Qu.:106.00
##  Max.   :144.00            Max.   :114.00            Max.   :164.00
##  NA's   :5850              NA's   :5850              NA's   :2231
##  h1_heartrate_min   h1_mbp_max       h1_mbp_min     h1_mbp_noninvasive_max
##  Min.   : 36.00   Min.   : 49.00   Min.   : 32.00   Min.   : 49.00
##  1st Qu.: 69.00   1st Qu.: 77.00   1st Qu.: 66.00   1st Qu.: 77.00
##  Median : 82.00   Median : 90.00   Median : 78.00   Median : 90.00
##  Mean   : 83.72   Mean   : 91.63   Mean   : 79.37   Mean   : 91.61
##  3rd Qu.: 97.00   3rd Qu.:104.00   3rd Qu.: 92.00   3rd Qu.:104.00
##  Max.   :144.00   Max.   :165.00   Max.   :138.00   Max.   :163.00
##  NA's   :2231     NA's   :3702     NA's   :3702     NA's   :7247
##  h1_mbp_noninvasive_min h1_resprate_max h1_resprate_min   h1_spo2_max
##  Min.   : 32.00         Min.   :10.00   Min.   :  0.00   Min.   :  0.00
##  1st Qu.: 66.00         1st Qu.:18.00   1st Qu.: 14.00   1st Qu.: 97.00
##  Median : 79.00         Median :21.00   Median : 16.00   Median : 99.00
##  Mean   : 79.68         Mean   :22.64   Mean   : 17.22   Mean   : 98.05
##  3rd Qu.: 92.00         3rd Qu.:26.00   3rd Qu.: 20.00   3rd Qu.:100.00
##  Max.   :138.00         Max.   :59.00   Max.   :189.00   Max.   :100.00
##  NA's   :7247           NA's   :3450    NA's   :3450     NA's   :3329
##   h1_spo2_min      h1_sysbp_max    h1_sysbp_min   h1_sysbp_noninvasive_max
##  Min.   :  0.00   Min.   : 75.0   Min.   : 53.0   Min.   : 75.0
##  1st Qu.: 94.00   1st Qu.:113.0   1st Qu.: 98.0   1st Qu.:113.0
##  Median : 96.00   Median :131.0   Median :115.0   Median :130.0
##  Mean   : 95.19   Mean   :133.2   Mean   :116.3   Mean   :133.1
##  3rd Qu.: 99.00   3rd Qu.:150.0   3rd Qu.:134.0   3rd Qu.:150.0
##  Max.   :100.00   Max.   :223.0   Max.   :194.0   Max.   :223.0
##  NA's   :3329     NA's   :2877    NA's   :2877    NA's   :5843
##  h1_sysbp_noninvasive_min d1_glucose_max  d1_glucose_min  d1_potassium_max
##  Min.   : 53.0            Min.   : 73.0   Min.   : 33.0   Min.   :2.800
```

```
##  1st Qu.: 98.0            1st Qu.:117.0   1st Qu.: 90.0   1st Qu.:3.800
##  Median :115.0            Median :150.0   Median :107.0   Median :4.200
##  Mean   :116.5            Mean   :174.6   Mean   :114.3   Mean   :4.252
##  3rd Qu.:134.0            3rd Qu.:201.0   3rd Qu.:131.0   3rd Qu.:4.600
##  Max.   :195.0            Max.   :611.0   Max.   :288.0   Max.   :7.000
##  NA's   :5843             NA's   :4630    NA's   :4630    NA's   :7650
##  d1_potassium_min apache_4a_hospital_death_prob apache_4a_icu_death_prob
##  Min.   :2.400    Min.   :-1.000                Min.   :-1.000
##  1st Qu.:3.600    1st Qu.: 0.020                1st Qu.: 0.010
##  Median :3.900    Median : 0.050                Median : 0.020
##  Mean   :3.936    Mean   : 0.088                Mean   : 0.045
##  3rd Qu.:4.300    3rd Qu.: 0.130                3rd Qu.: 0.060
##  Max.   :5.800    Max.   : 0.980                Max.   : 0.970
##  NA's   :7650     NA's   :6356                  NA's   :6356
##       aids          cirrhosis      diabetes_mellitus hepatic_failure
##  Min.   :0e+00   Min.   :0.0000   Min.   :0.0000    Min.   :0.000
##  1st Qu.:0e+00   1st Qu.:0.0000   1st Qu.:0.0000    1st Qu.:0.000
##  Median :0e+00   Median :0.0000   Median :0.0000    Median :0.000
##  Mean   :9e-04   Mean   :0.0156   Mean   :0.2255    Mean   :0.013
##  3rd Qu.:0e+00   3rd Qu.:0.0000   3rd Qu.:0.0000    3rd Qu.:0.000
##  Max.   :1e+00   Max.   :1.0000   Max.   :1.0000    Max.   :1.000
##  NA's   :570     NA's   :570      NA's   :570       NA's   :570
##  immunosuppression    leukemia         lymphoma
##  Min.   :0.0000    Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.0000    1st Qu.:0.0000   1st Qu.:0.0000
##  Median :0.0000    Median :0.0000   Median :0.0000
##  Mean   :0.0264    Mean   :0.0071   Mean   :0.0041
##  3rd Qu.:0.0000    3rd Qu.:0.0000   3rd Qu.:0.0000
##  Max.   :1.0000    Max.   :1.0000   Max.   :1.0000
##  NA's   :570       NA's   :570      NA's   :570
##  solid_tumor_with_metastasis apache_3j_bodysystem apache_2_bodysystem
##  Min.   :0.0000              Length:73351         Length:73351
##  1st Qu.:0.0000              Class :character     Class :character
##  Median :0.0000              Mode  :character     Mode  :character
##  Mean   :0.0207
##  3rd Qu.:0.0000
##  Max.   :1.0000
##  NA's   :570
##     X           hospital_death
##  Mode:logical   0:67025
##  NA's:73351     1: 6326
##
##
##
##
##
```

```
sort(sapply(patient_train, function(x) sum(is.na(x))), decreasing = TRUE)
```

```
##                              X             d1_potassium_max
##                          73351                         7650
##              d1_potassium_min        h1_mbp_noninvasive_max
##                          7650                         7247
##        h1_mbp_noninvasive_min apache_4a_hospital_death_prob
```

```
##                          7247                          6356
##      apache_4a_icu_death_prob     h1_diasbp_noninvasive_max
##                          6356                          5850
##     h1_diasbp_noninvasive_min      h1_sysbp_noninvasive_max
##                          5850                          5843
##      h1_sysbp_noninvasive_min                d1_glucose_max
##                          5843                          4630
##                d1_glucose_min                    h1_mbp_max
##                          4630                          3702
##                    h1_mbp_min                h1_resprate_max
##                          3702                          3450
##                h1_resprate_min                           age
##                          3450                          3367
##                   h1_spo2_max                   h1_spo2_min
##                          3329                          3329
##                   temp_apache                  h1_diasbp_max
##                          3230                          2885
##                  h1_diasbp_min                  h1_sysbp_max
##                          2885                          2877
##                  h1_sysbp_min                           bmi
##                          2877                          2682
##                h1_heartrate_max              h1_heartrate_min
##                          2231                          2231
##                        weight                   d1_temp_max
##                          2138                          1815
##                   d1_temp_min              gcs_eyes_apache
##                          1815                          1523
##                gcs_motor_apache             gcs_verbal_apache
##                          1523                          1523
##             apache_2_diagnosis          apache_3j_bodysystem
##                          1330                          1330
##           apache_2_bodysystem        d1_mbp_noninvasive_max
##                          1330                          1196
##         d1_mbp_noninvasive_min                     ethnicity
##                          1196                          1103
##                        height                resprate_apache
##                          1034                           963
##           apache_3j_diagnosis     d1_diasbp_noninvasive_max
##                           883                           839
##      d1_diasbp_noninvasive_min      d1_sysbp_noninvasive_max
##                           839                           829
##      d1_sysbp_noninvasive_min             gcs_unable_apache
##                           829                           825
##                     map_apache             heart_rate_apache
##                           779                           693
##                    arf_apache              intubated_apache
##                           570                           570
##              ventilated_apache                          aids
##                           570                           570
##                     cirrhosis             diabetes_mellitus
##                           570                           570
##                hepatic_failure             immunosuppression
##                           570                           570
##                      leukemia                      lymphoma
```

```
##                           570                           570
##   solid_tumor_with_metastasis                d1_resprate_max
##                           570                           296
##                d1_resprate_min                   d1_spo2_max
##                           296                           263
##                   d1_spo2_min                    d1_mbp_max
##                           263                           165
##                    d1_mbp_min                  d1_diasbp_max
##                           165                           120
##                  d1_diasbp_min                  d1_sysbp_max
##                           120                           116
##                   d1_sysbp_min                d1_heartrate_max
##                           116                           108
##               d1_heartrate_min               icu_admit_source
##                           108                            86
##               elective_surgery                        gender
##                             0                             0
##                  icu_stay_type                     icu_type
##                             0                             0
##               pre_icu_los_days          apache_post_operative
##                             0                             0
##                 hospital_death
##                             0
```

Given the high number of missing values, we will remove all features with more that 5% missingness. This is based on Schafer (1999) asserted that a missing rate of 5% or less is inconsequential.

```
# Remove Columns with 5% or more NA #
patient_train_r <- patient_train[, !sapply(patient_train,
                                           function(x) mean(is.na(x)) > 0.05)]
# Drop the same Columns from the Test Set #
patient_test_r <- patient_test[, colnames(patient_train_r)]
```

```
subset <- patient_train_r[is.na(patient_train_r$aids), ]
sort(colSums(is.na(subset)), decreasing = TRUE)
```

```
##                           age           apache_2_diagnosis
##                           570                          570
##          apache_3j_diagnosis                   arf_apache
##                           570                          570
##              gcs_eyes_apache             gcs_motor_apache
##                           570                          570
##            gcs_unable_apache            gcs_verbal_apache
##                           570                          570
##            heart_rate_apache             intubated_apache
##                           570                          570
##                  map_apache               resprate_apache
##                           570                          570
##                 temp_apache            ventilated_apache
##                           570                          570
##                        aids                      cirrhosis
##                           570                          570
##            diabetes_mellitus               hepatic_failure
```

```
##                         570                         570
##           immunosuppression                    leukemia
##                         570                         570
##                    lymphoma solid_tumor_with_metastasis
##                         570                         570
##        apache_3j_bodysystem         apache_2_bodysystem
##                         570                         570
##                h1_spo2_max                h1_spo2_min
##                          49                          49
##               h1_diasbp_max               h1_diasbp_min
##                          43                          43
##                h1_sysbp_max                h1_sysbp_min
##                          43                          43
##             h1_resprate_max             h1_resprate_min
##                          42                          42
##            h1_heartrate_max            h1_heartrate_min
##                          34                          34
##                         bmi                      weight
##                          23                          19
##                d1_temp_max                 d1_temp_min
##                          16                          16
##                      height      d1_mbp_noninvasive_max
##                          13                          12
##      d1_mbp_noninvasive_min   d1_diasbp_noninvasive_max
##                          12                          11
##   d1_diasbp_noninvasive_min    d1_sysbp_noninvasive_max
##                          11                          11
##    d1_sysbp_noninvasive_min                   ethnicity
##                          11                           6
##                d1_spo2_max                 d1_spo2_min
##                           6                           6
##             d1_resprate_max             d1_resprate_min
##                           5                           5
##               d1_diasbp_max               d1_diasbp_min
##                           4                           4
##            d1_heartrate_max            d1_heartrate_min
##                           4                           4
##                 d1_mbp_max                  d1_mbp_min
##                           4                           4
##                d1_sysbp_max                d1_sysbp_min
##                           4                           4
##            elective_surgery                      gender
##                           0                           0
##            icu_admit_source                icu_stay_type
##                           0                           0
##                    icu_type             pre_icu_los_days
##                           0                           0
##       apache_post_operative              hospital_death
##                           0                           0
```

Missing data appears to be related to the missingness in illness-related features.

```r
patient_train_r <- patient_train_r[!is.na(patient_train_r$aids), ]
patient_test_r <- patient_test_r[!is.na(patient_test_r$aids), ]
```

```r
#Drop the observations with missing apache_2 data
patient_train_r2 <- patient_train_r[!is.na(patient_train_r$apache_2_diagnosis), ]
patient_test_r2 <- patient_test_r[!is.na(patient_test_r$apache_2_diagnosis), ]

#Drop the observations with missing apache_3j_diagnosis
patient_train_r3 <- patient_train_r2[!is.na(patient_train_r$apache_2_diagnosis), ]
patient_test_r3 <- patient_test_r2[!is.na(patient_test_r$apache_2_diagnosis), ]
```

```r
patient_train_r3$ethnicity[is.na(patient_train_r3$ethnicity)] <- "Other/Unknown"
patient_test_r3$ethnicity[is.na(patient_test_r3$ethnicity)] <- "Other/Unknown"
```

```r
imp <- preProcess(patient_train_r3, method = c("medianImpute", "nzv", "corr"), cutoff = .8)
train_pr = predict(imp, patient_train_r3)
test_pr = predict(imp, patient_test_r3)
```

```r
train_pr <- train_pr[complete.cases(train_pr), ]
sum(is.na(train_pr))
```

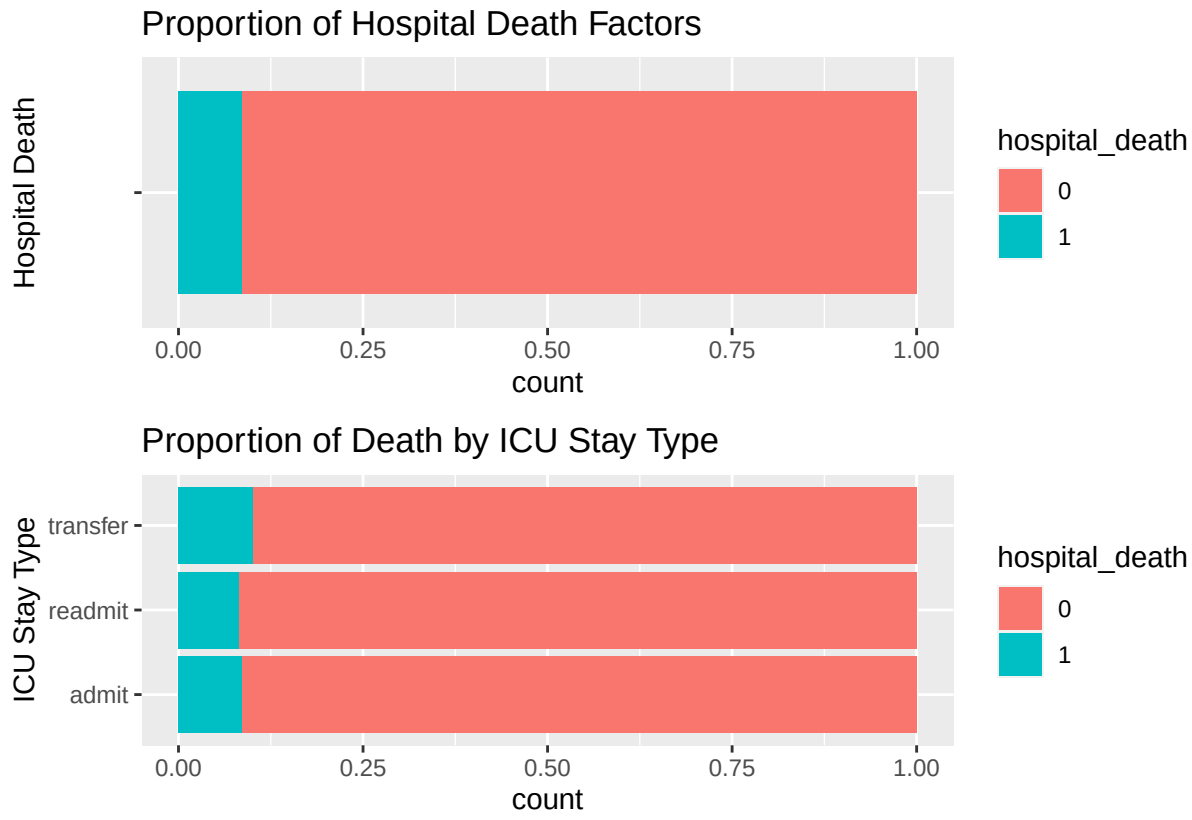
```
## [1] 0
```

```r
test_pr <- test_pr[complete.cases(test_pr), ]
sum(is.na(test_pr))
```

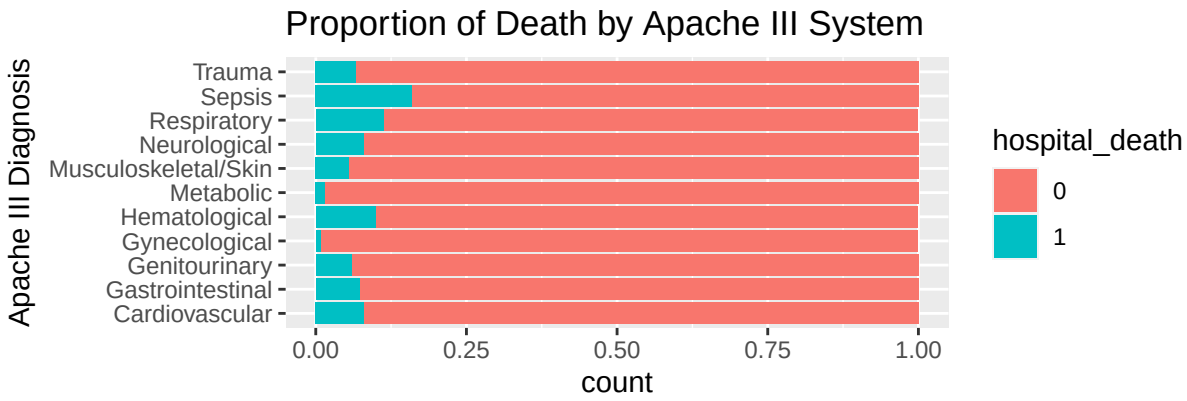
```
## [1] 0
```

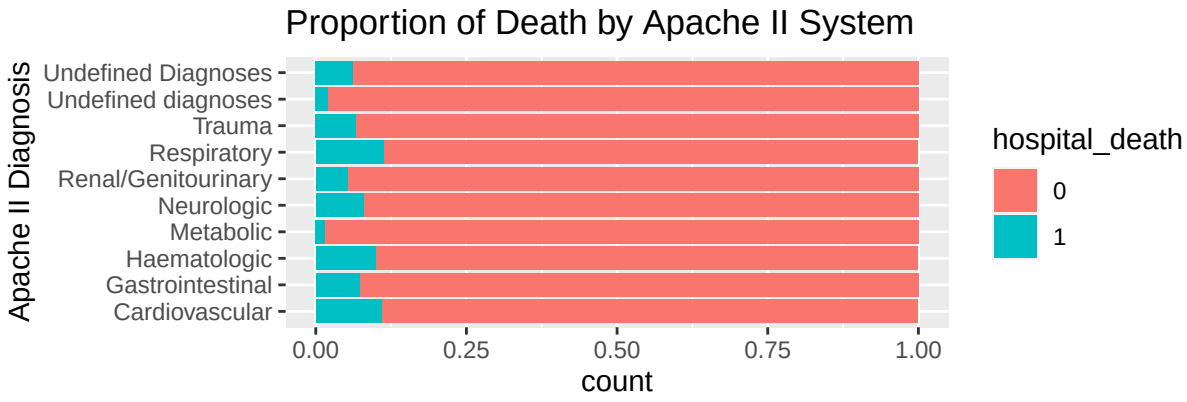
EDA

```r
p1 <- ggplot(train_pr, aes(x = '', fill = hospital_death)) +
    geom_bar(position = "fill") +
    ggtitle("Proportion of Hospital Death Factors") +
    xlab("Hospital Death") + coord_flip()

p2 <- ggplot(train_pr, aes(x = icu_stay_type, fill = hospital_death)) +
    geom_bar(position = "fill") +
    ggtitle("Proportion of Death by ICU Stay Type") +
    xlab("ICU Stay Type") + coord_flip()

p1 / p2
```

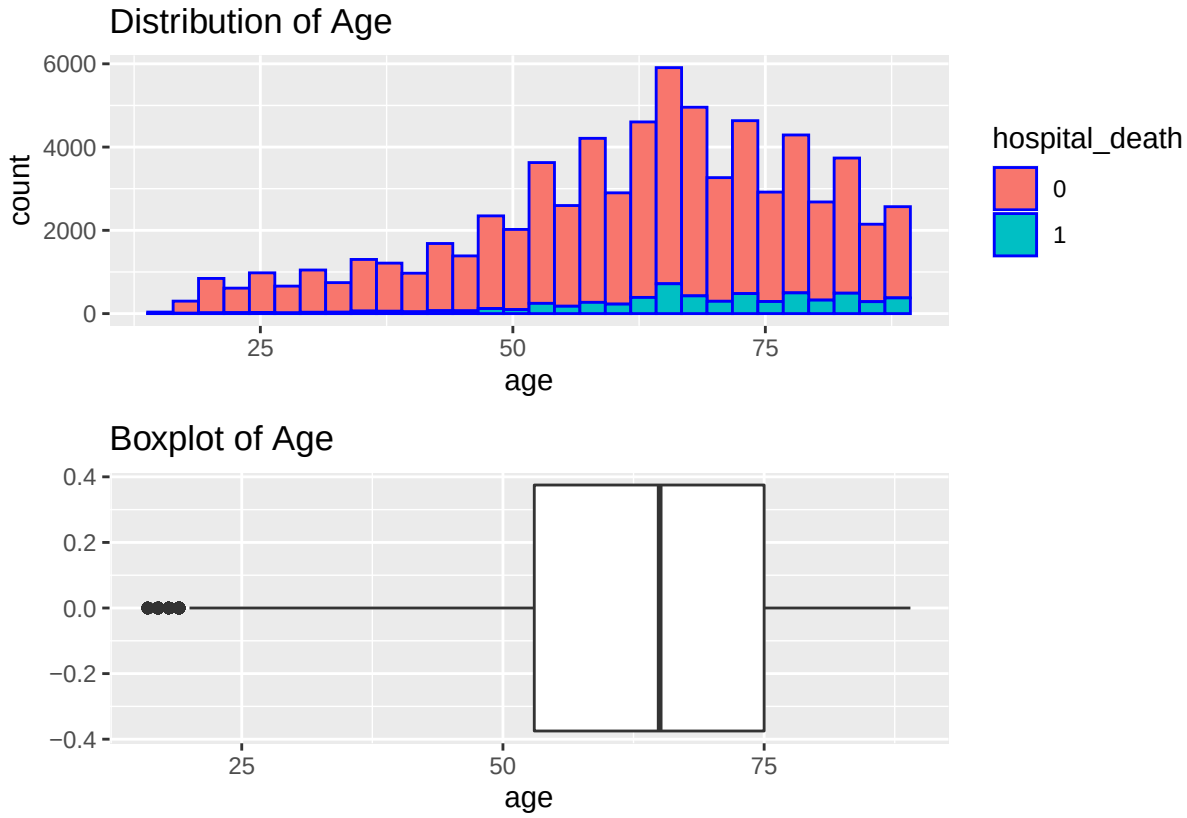



```
p3 <- ggplot(train_pr, aes(x = apache_3j_bodysystem, fill = hospital_death)) +
    geom_bar(position = "fill") +
    ggtitle("Proportion of Death by Apache III System") +
    xlab("Apache III Diagnosis") + coord_flip()

p4 <- ggplot(train_pr, aes(x = apache_2_bodysystem, fill = hospital_death)) +
    geom_bar(position = "fill") +
    ggtitle("Proportion of Death by Apache II System") +
    xlab("Apache II Diagnosis") + coord_flip()

p3 / p4
```

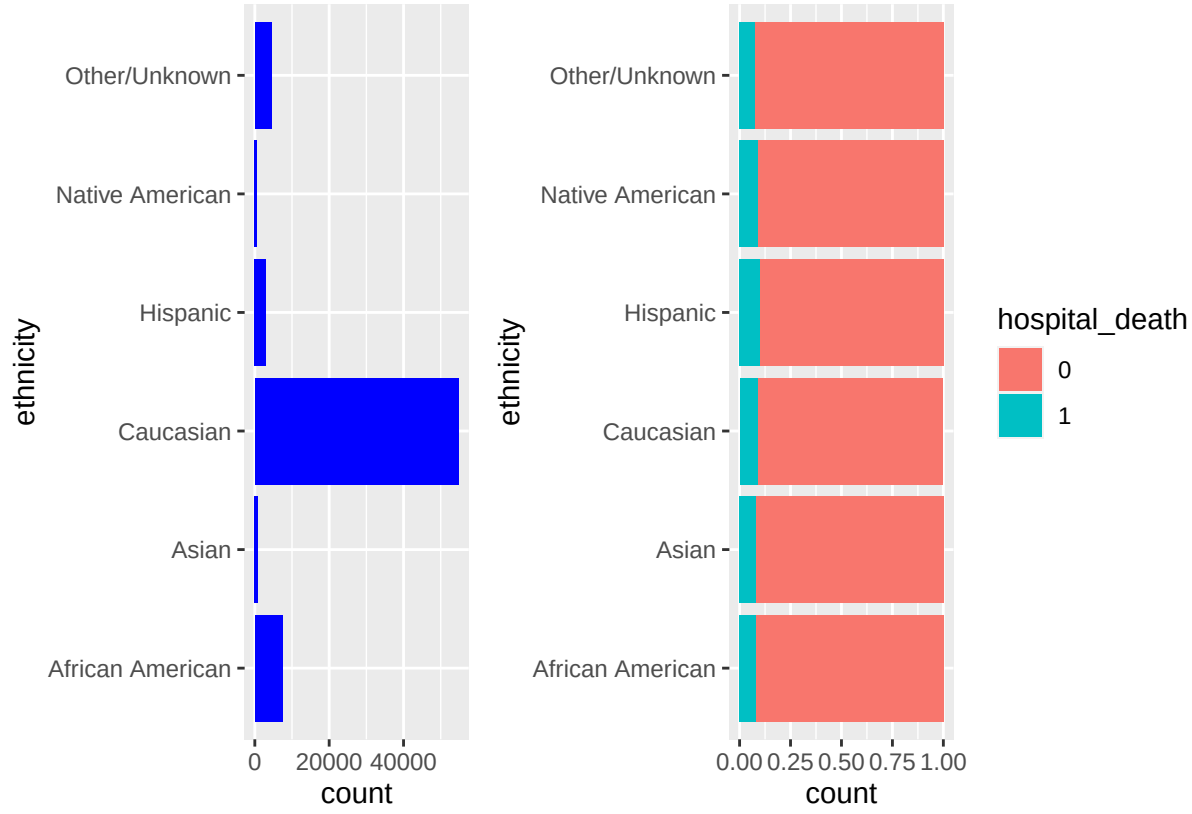




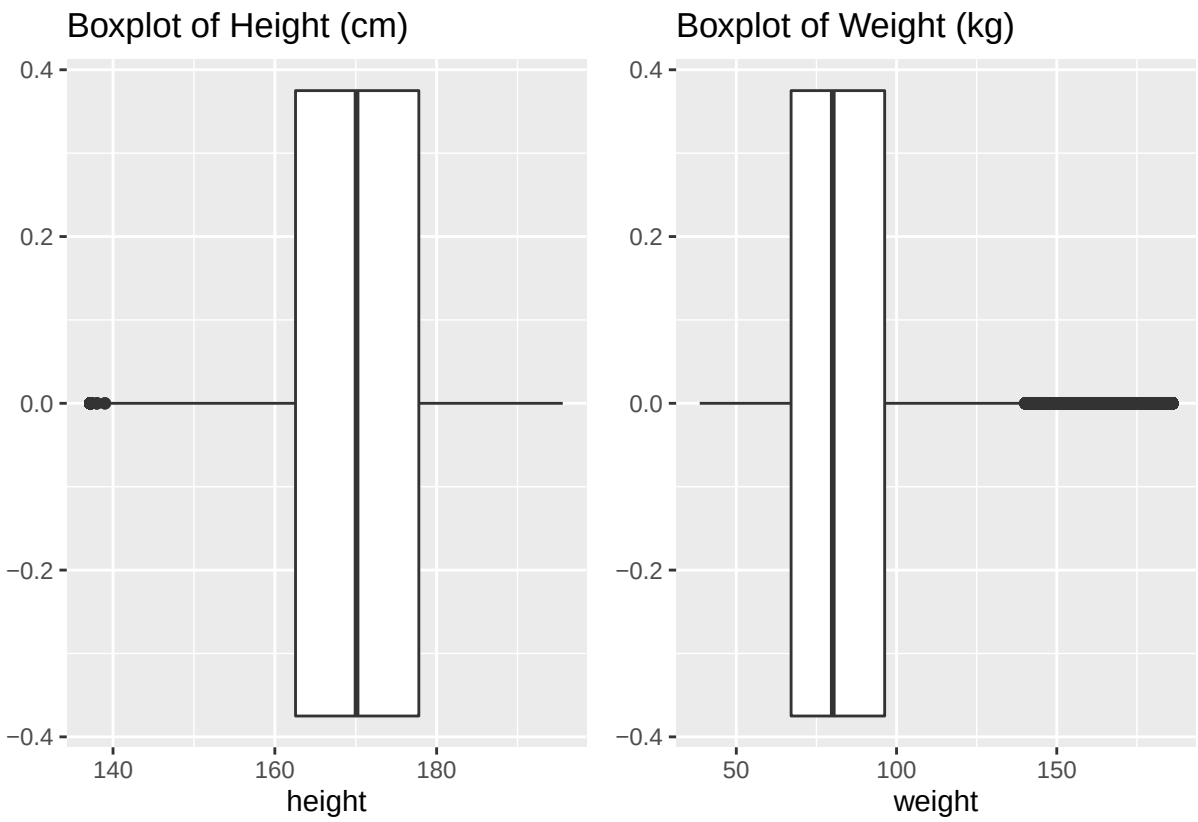

```
p5 <- ggplot(train_pr, aes(x = age)) +
  geom_histogram(aes(fill = hospital_death), color = "blue") +
  ggtitle("Distribution of Age")
p6 <- ggplot(train_pr, aes(x = age)) + geom_boxplot() +
  ggtitle("Boxplot of Age")
p5 / p6
```



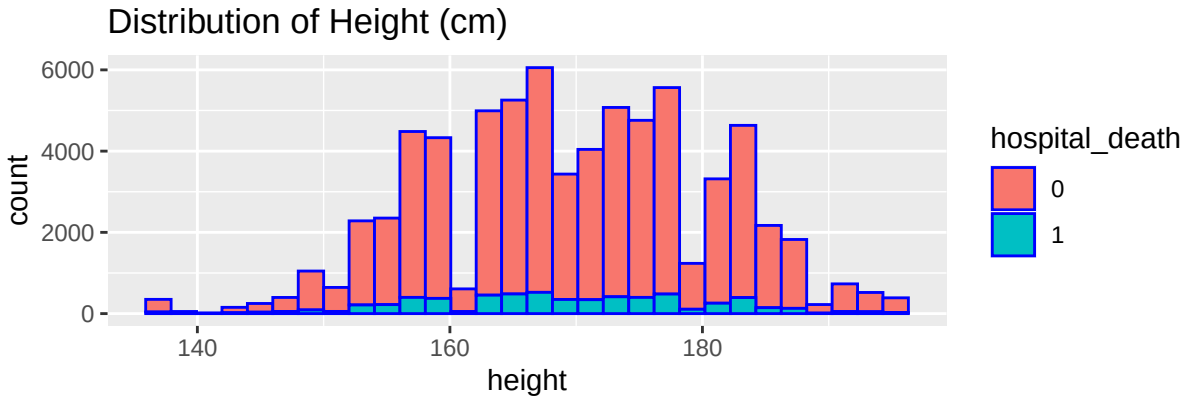

```
p7 <- ggplot(train_pr, aes(x = ethnicity)) +
  geom_bar(fill = "blue") + coord_flip()
p8 <- ggplot(train_pr, aes(x = ethnicity, fill = hospital_death)) +
  geom_bar(position = "fill") + coord_flip()

p7 + p8
```

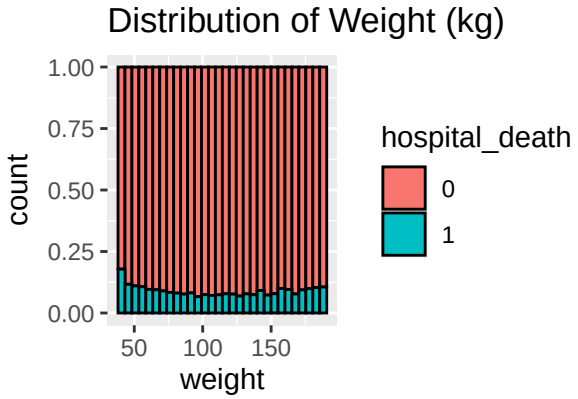


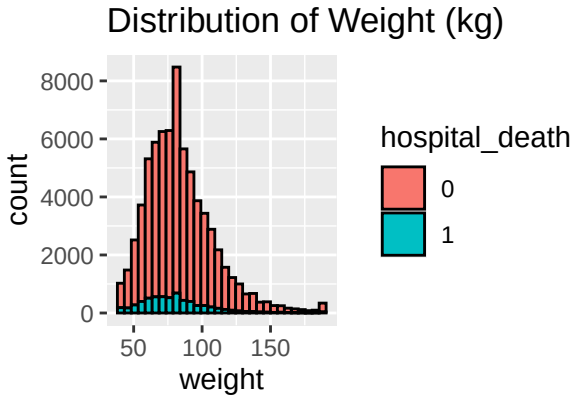

```
p9 <- ggplot(train_pr, aes(x = height)) + geom_boxplot() +
  ggtitle("Boxplot of Height (cm)")
p10 <- ggplot(train_pr, aes(x = weight)) + geom_boxplot() +
  ggtitle("Boxplot of Weight (kg)")

p11 <- ggplot(train_pr, aes(x = height)) +
  geom_histogram(aes(fill = hospital_death), color = "blue") +
  ggtitle("Distribution of Height (cm)")
p12 <- ggplot(train_pr, aes(x = weight)) +
  geom_histogram(aes(fill = hospital_death), color = "black", position = "fill") +
  ggtitle("Distribution of Weight (kg)")
p13 <- ggplot(train_pr, aes(x = weight)) +
  geom_histogram(aes(fill = hospital_death), color = "black") +
  ggtitle("Distribution of Weight (kg)")

p9 + p10
```


Boxplot of Height (cm)
0.4
0.2
0.0
−0.2
−0.4
140
160
180
height
Boxplot of Weight (kg)
0.4
0.2
0.0
−0.2
−0.4
50
100
150
weight

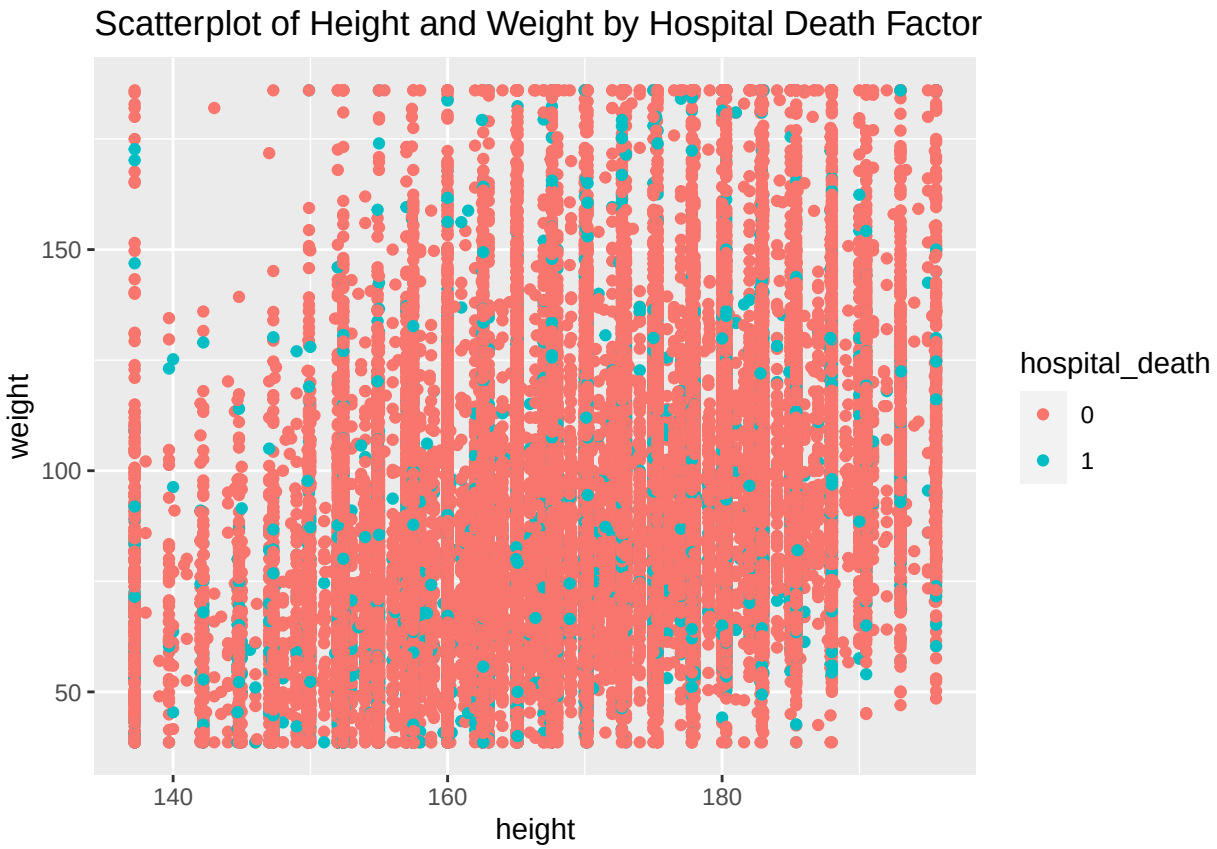
```
p11 / (p12 + p13)
```








```
ggplot(train_pr, aes(x = height, y = weight, color = hospital_death)) +
  geom_point() +
  ggtitle("Scatterplot of Height and Weight by Hospital Death Factor")
```



Feature Handling - Downsampling and Dummy Variables

```
set.seed(100)
#Due to our severely class imbalance, we've chosen to downsample the minority class
downsampledTrain <- downSample(x = subset(train_pr, select = -hospital_death),
                               y = train_pr$hospital_death,
                               yname = "hospital_death")
dim(train_pr)
```

```
## [1] 71195    44
```

```
dim(downsampledTrain)
```

```
## [1] 12332    44
```

```
table(downsampledTrain$hospital_death)
```

```
##
##    0    1
## 6166 6166
```

```
X_train <- subset(downsampledTrain, select = -hospital_death)
y_train <- downsampledTrain$hospital_death
X_test <- subset(test_pr, select = -hospital_death)
```

```
y_test <- test_pr$hospital_death
#Dummy Variables
character_features_train <- X_train[, sapply(X_train, class) == "character"]
dummy_variables_train <- fastDummies::dummy_cols(character_features_train, remove_first_dummy = TRUE)
character_features_test <- X_test[, sapply(X_test, class) == "character"]
dummy_variables_test <- fastDummies::dummy_cols(character_features_test, remove_first_dummy = TRUE)
```

Feature Extraction

```
# Drop the original 7 features #
dummy_variables_train <- dummy_variables_train[, -c(1:6)]
dummy_variables_test <- dummy_variables_test[, -c(1:6)]

# Combine Dummy Variables with DataFrame #
## Drop y-variable and merge with dummy variables ##
train_withdummies <- data.frame(X_train, dummy_variables_train)
test_withdummies <- data.frame(X_test, dummy_variables_test)

## Drop Non-Dummy Encoded Variables ##
train_withdummies <- train_withdummies[, sapply(train_withdummies, class) != "character"]
test_withdummies <- test_withdummies[, sapply(test_withdummies, class) != "character"]
```

```
linear = findLinearCombos(train_withdummies)
#linear # suggests removing 66 67 68 69 71 72
print("Columns to be removed:")
```

```
## [1] "Columns to be removed:"
```

```
colnames(train_withdummies[, c(66, 67, 68, 69, 71, 72)])
```

```
## [1] "apache_2_bodysystem_Gastrointestinal"
## [2] "apache_2_bodysystem_Haematologic"
## [3] "apache_2_bodysystem_Metabolic"
## [4] "apache_2_bodysystem_Neurologic"
## [5] "apache_2_bodysystem_Respiratory"
## [6] "apache_2_bodysystem_Trauma"
```

```
cat("  \n")
```

```
print("Columns to be retained")
```

```
## [1] "Columns to be retained"
```

```
colnames(train_withdummies[, c(56, 59, 60, 62, 63, 65)])
```

```
## [1] "apache_3j_bodysystem_Gastrointestinal"
## [2] "apache_3j_bodysystem_Hematological"
```

```
## [3] "apache_3j_bodysystem_Metabolic"
## [4] "apache_3j_bodysystem_Neurological"
## [5] "apache_3j_bodysystem_Respiratory"
## [6] "apache_3j_bodysystem_Trauma"
```

```
train_withdummies_r <- train_withdummies[,-linear$remove]
test_withdummies_r <- test_withdummies[,-linear$remove]
```

```
levels(y_train) <- c("no_death", "death")
levels(y_test) <- c("no_death", "death")

y_train <- factor(y_train, levels=rev(levels(y_train)))
y_test <- factor(y_test, levels=rev(levels(y_test)))

# Visualize Weight of Classes #
table(y_train)
```

```
## y_train
##    death no_death
##     6166     6166
```

```
table(y_test)
```

```
## y_test
##    death no_death
##     1536    16260
```

Models

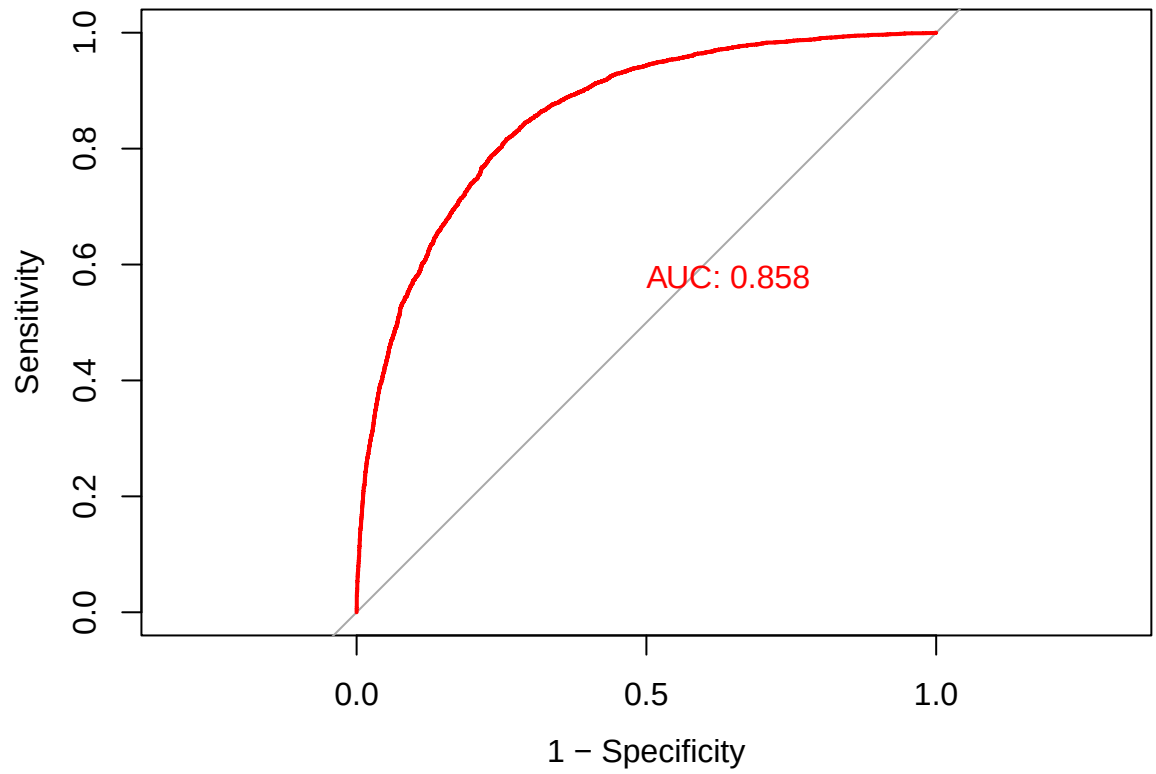
Logistic Regression Model

```
# Train Control Settings #
ctrl <- trainControl(method = "cv", #Cross-validation
                     summaryFunction = twoClassSummary, #for binary classification
                     classProbs = TRUE, #note class probabilities
                     savePredictions = TRUE)

## Logistic Regression Model #
set.seed(100)
lrFit <- train(x = train_withdummies_r,
               y = y_train,
               method = "glm",
               preProc = c("center","scale"),
               metric = "ROC", #best metric for classification
               trControl = ctrl)
lrFit
```

```
## Generalized Linear Model
##
```

```
## 12332 samples
##    68 predictor
##     2 classes: 'death', 'no_death'
##
## Pre-processing: centered (68), scaled (68)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 11099, 11098, 11099, 11100, 11099, 11100, ...
## Resampling results:
##
##   ROC        Sens      Spec
##   0.8579017  0.768256  0.7829987
```

```
#lrFit$finalModel
## Save ROC curve for the hold-out set
lrRoc <- roc(response = lrFit$pred$obs,
             predictor = lrFit$pred$death,
             levels = rev(levels(lrFit$pred$obs)))
plot(lrRoc, type = "s", col = 'red',
     legacy.axes = TRUE, print.auc = TRUE, print.auc.y = .6)
```




```
testResults <- data.frame(obs = y_test,
                          LR = predict(lrFit, test_withdummies_r))

confusionMatrix(testResults$LR, testResults$obs, positive = "death")
```

```
## Confusion Matrix and Statistics
```

```
##
##           Reference
## Prediction death no_death
##   death     1169     3297
##   no_death   367    12963
##
##                Accuracy : 0.7941
##                  95% CI : (0.7881, 0.8)
##     No Information Rate : 0.9137
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.2996
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.76107
##             Specificity : 0.79723
##          Pos Pred Value : 0.26176
##          Neg Pred Value : 0.97247
##              Prevalence : 0.08631
##          Detection Rate : 0.06569
##    Detection Prevalence : 0.25096
##       Balanced Accuracy : 0.77915
##
##        'Positive' Class : death
##
```

Penalized Logistic Regression Model

```
glmnGrid <- expand.grid(alpha = c(0, .2, .4, .6, 1),
                        lambda = seq(.01, .2, length = 2))

set.seed(100)
glmnFit <- train(x = train_withdummies_r,
                 y = y_train,
                 method = "glmnet",   #method is glmnet for penalized logistic regression
                 tuneGrid = glmnGrid,
                 metric = "ROC",
                 trControl = ctrl)
glmnFit
```

```
## glmnet
##
## 12332 samples
##    68 predictor
##     2 classes: 'death', 'no_death'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 11099, 11098, 11099, 11100, 11099, 11100, ...
## Resampling results across tuning parameters:
##
```

```
##   alpha  lambda  ROC        Sens       Spec
##   0.0    0.01    0.8575896  0.7677703  0.7805682
##   0.0    0.20    0.8529863  0.7533354  0.7812159
##   0.2    0.01    0.8576383  0.7612844  0.7834860
##   0.2    0.20    0.8393270  0.7202485  0.7893286
##   0.4    0.01    0.8571936  0.7611229  0.7834865
##   0.4    0.20    0.7986893  0.6711099  0.7617601
##   0.6    0.01    0.8566126  0.7616094  0.7810544
##   0.6    0.20    0.7831474  0.6782436  0.7293223
##   1.0    0.01    0.8547255  0.7577159  0.7833232
##   1.0    0.20    0.5000000  0.8000000  0.2000000
##
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were alpha = 0.2 and lambda = 0.01.
```

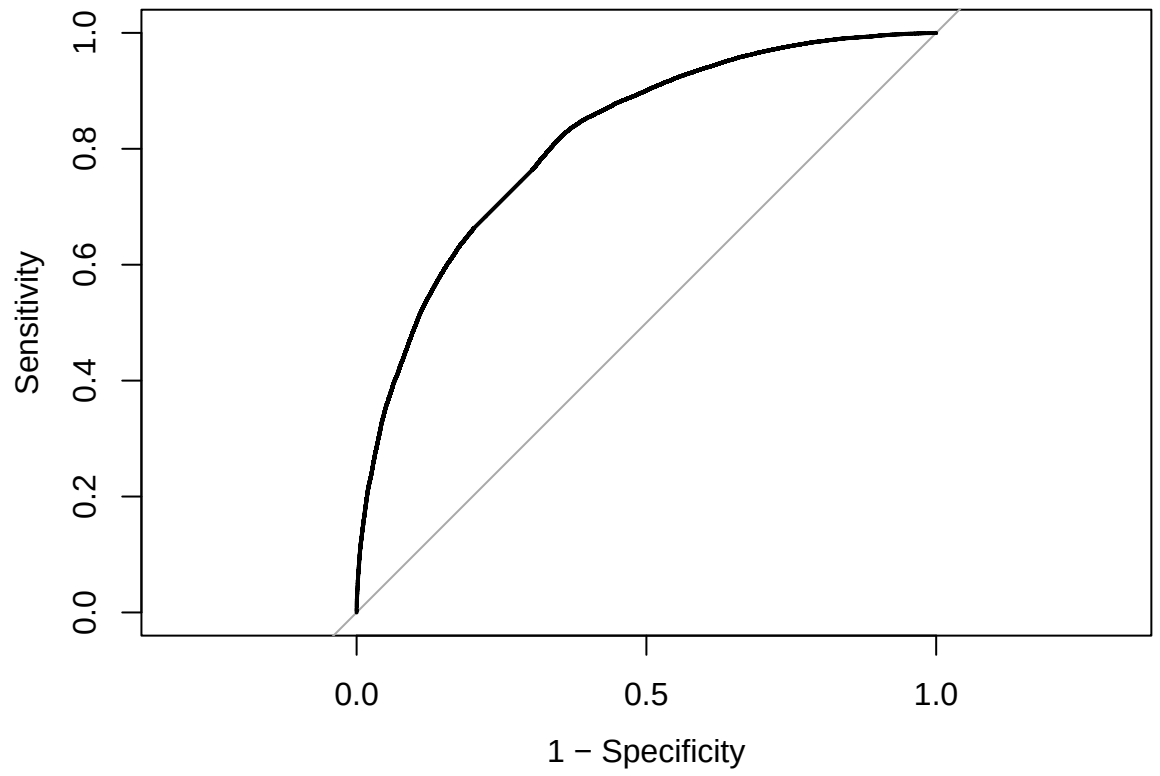
```
glmnFit$results   #View results for each hyperparamater combination
```

```
##    alpha lambda       ROC      Sens      Spec       ROCSD     SensSD
## 1    0.0   0.01 0.8575896 0.7677703 0.7805682 0.006129892 0.02004755
## 2    0.0   0.20 0.8529863 0.7533354 0.7812159 0.006735173 0.02083116
## 3    0.2   0.01 0.8576383 0.7612844 0.7834860 0.006144798 0.02211895
## 4    0.2   0.20 0.8393270 0.7202485 0.7893286 0.010314350 0.01657460
## 5    0.4   0.01 0.8571936 0.7611229 0.7834865 0.006194961 0.02245604
## 6    0.4   0.20 0.7986893 0.6711099 0.7617601 0.015437975 0.01660620
## 7    0.6   0.01 0.8566126 0.7616094 0.7810544 0.006337836 0.02143141
## 8    0.6   0.20 0.7831474 0.6782436 0.7293223 0.016649144 0.01348821
## 9    1.0   0.01 0.8547255 0.7577159 0.7833232 0.006529745 0.02154028
## 10   1.0   0.20 0.5000000 0.8000000 0.2000000 0.000000000 0.42163702
##         SpecSD
## 1  0.010092702
## 2  0.009740332
## 3  0.010159039
## 4  0.013340922
## 5  0.009882179
## 6  0.016104997
## 7  0.008492177
## 8  0.015066643
## 9  0.009395132
## 10 0.421637021
```

```
glmnetCM <- confusionMatrix(glmnFit, norm = "none")
glmnetCM
```

```
## Cross-Validated (10 fold) Confusion Matrix
##
## (entries are un-normalized aggregated counts)
##
##           Reference
## Prediction death no_death
##   death     4694     1335
##   no_death  1472     4831
##
##  Accuracy (average) : 0.7724
```

```
## Plot the ROC curve for the hold-out set
glmRoc <- roc(response = glmnFit$pred$obs,
              predictor = glmnFit$pred$death,
              levels = rev(levels(glmnFit$pred$obs)))

plot(glmRoc, legacy.axes = TRUE)
```




```
testResults <- data.frame(obs = y_test,
                          GLM = predict(glmnFit, test_withdummies_r))

confusionMatrix(testResults$GLM, testResults$obs, positive = "death")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction death no_death
##   death     1164     3282
##   no_death   372    12978
##
##                Accuracy : 0.7947
##                  95% CI : (0.7887, 0.8006)
##     No Information Rate : 0.9137
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.2993
```

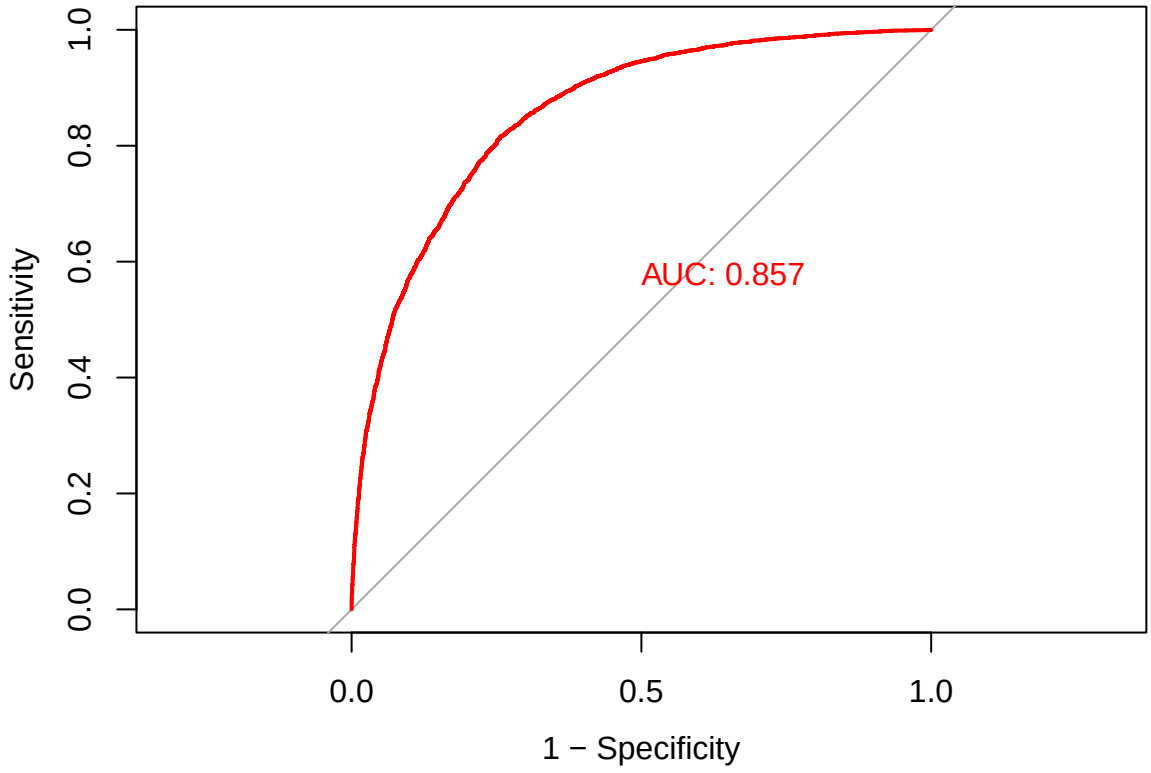
```
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.75781
##             Specificity : 0.79815
##          Pos Pred Value : 0.26181
##          Neg Pred Value : 0.97213
##              Prevalence : 0.08631
##          Detection Rate : 0.06541
##    Detection Prevalence : 0.24983
##       Balanced Accuracy : 0.77798
##
##        'Positive' Class : death
##
```

LDA Model

```
set.seed(100)
ldaFit <- train(x = train_withdummies_r,
                y = y_train,
                method = "lda",
                trControl = ctrl,
                preProcess=c("center", "scale","BoxCox"),
                metric="ROC")
ldaFit
```

```
## Linear Discriminant Analysis
##
## 12332 samples
##    68 predictor
##     2 classes: 'death', 'no_death'
##
## Pre-processing: centered (68), scaled (68), Box-Cox transformation (25)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 11099, 11098, 11099, 11100, 11099, 11100, ...
## Resampling results:
##
##   ROC        Sens       Spec
##   0.8574246  0.7624198  0.7847834
```

```
#Training performance: ROC =0.861, Sens = 0.793, Spec = 0.757

## Save ROC curve for the hold-out set
ldaRoc <- roc(response = ldaFit$pred$obs,
            predictor = ldaFit$pred$death,
            levels = rev(levels(ldaFit$pred$obs)))

plot(ldaRoc, type = "s", col = 'red', legacy.axes = TRUE, print.auc = TRUE, print.auc.y = .6)
```




```
testResults$LDA = predict(ldaFit, test_withdummies_r)
confusionMatrix(testResults$LDA, testResults$obs, positive = "death")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction death no_death
##   death     1157     3266
##   no_death   379    12994
##
##                Accuracy : 0.7952
##                  95% CI : (0.7892, 0.8011)
##     No Information Rate : 0.9137
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.2984
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.75326
##             Specificity : 0.79914
##          Pos Pred Value : 0.26159
##          Neg Pred Value : 0.97166
##              Prevalence : 0.08631
##          Detection Rate : 0.06501
```

```
##    Detection Prevalence : 0.24854
##       Balanced Accuracy : 0.77620
##
##        'Positive' Class : death
##
```

```
#Test performance: Sens = 0.766, Spec = 0.794 (3370 no deaths classified as deaths)
varImp(ldaFit)
```

```
## ROC curve variable importance
##
##   only 20 most important variables shown (out of 68)
##
##                      Importance
## d1_sysbp_min             100.00
## gcs_verbal_apache         97.35
## ventilated_apache         97.12
## gcs_motor_apache          90.87
## gcs_eyes_apache           90.18
## d1_diasbp_min             83.62
## h1_sysbp_min              71.16
## d1_spo2_min               69.47
## d1_resprate_max           64.41
## h1_diasbp_min             63.10
## heart_rate_apache         60.22
## h1_resprate_max           59.10
## intubated_apache          56.53
## d1_temp_min               56.50
## apache_3j_diagnosis       53.67
## apache_2_diagnosis        53.26
## age                       53.13
## h1_resprate_min           52.75
## temp_apache               51.09
## map_apache                45.30
```

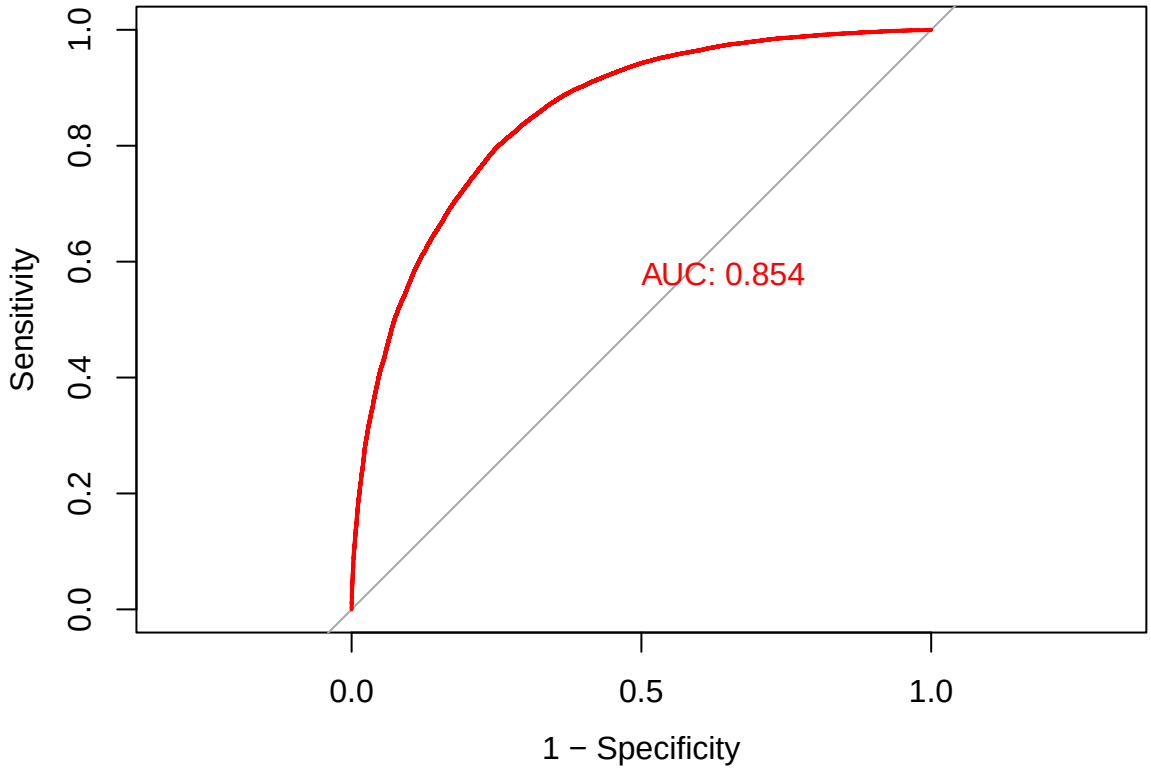
PLSDA Model

```
set.seed(100)
plsGrid = expand.grid(.ncomp = 1:10)

plsdaFit <- train(x = train_withdummies_r,
                  y = y_train,
                  method = "pls",
                  tuneGrid = plsGrid,
                  preProc = c("center","scale"),
                  metric = "ROC",
                  trControl = ctrl)
plsdaFit
```

```
## Partial Least Squares
##
```

```
## 12332 samples
##    68 predictor
##     2 classes: 'death', 'no_death'
##
## Pre-processing: centered (68), scaled (68)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 11099, 11098, 11099, 11100, 11099, 11100, ...
## Resampling results across tuning parameters:
##
##   ncomp  ROC        Sens       Spec
##    1     0.8382861  0.7265718  0.7834858
##    2     0.8504667  0.7363073  0.7948394
##    3     0.8544708  0.7580408  0.7799183
##    4     0.8557215  0.7562549  0.7829998
##    5     0.8558596  0.7601468  0.7849452
##    6     0.8561790  0.7578767  0.7834844
##    7     0.8564196  0.7585263  0.7849452
##    8     0.8564527  0.7590141  0.7846203
##    9     0.8564918  0.7606356  0.7842967
##   10     0.8564199  0.7588520  0.7833237
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was ncomp = 9.
```

```r
#Training performance: ROC =0.861, Sens = 0.793, Spec = 0.758

## Save ROC curve for the hold-out set
plsdaRoc <- roc(response = plsdaFit$pred$obs,
            predictor = plsdaFit$pred$death,
            levels = rev(levels(plsdaFit$pred$obs)))

plot(plsdaRoc, type = "s", col = 'red', legacy.axes = TRUE, print.auc = TRUE, print.auc.y = .6)
```




```
testResults$plsLDA = predict(plsdaFit, test_withdummies_r)
confusionMatrix(testResults$plsLDA, testResults$obs, positive = "death")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction death no_death
##   death     1153     3276
##   no_death   383    12984
##
##                Accuracy : 0.7944
##                  95% CI : (0.7884, 0.8003)
##     No Information Rate : 0.9137
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.2964
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.75065
##             Specificity : 0.79852
##          Pos Pred Value : 0.26033
##          Neg Pred Value : 0.97135
##              Prevalence : 0.08631
##          Detection Rate : 0.06479
```

```
##    Detection Prevalence : 0.24888
##       Balanced Accuracy : 0.77459
##
##        'Positive' Class : death
##
```

```
#Test performance: Sens = 0.764, Spec = 0.794 (3385 no deaths classified as deaths)
varImp(plsdaFit)
```

```
## pls variable importance
##
##   only 20 most important variables shown (out of 68)
##
##                                             Overall
## ventilated_apache                            100.00
## gcs_verbal_apache                             91.24
## gcs_eyes_apache                               90.91
## gcs_motor_apache                              88.72
## d1_sysbp_min                                  83.99
## d1_diasbp_min                                 72.74
## intubated_apache                              65.87
## d1_spo2_min                                   61.32
## d1_temp_min                                   61.22
## h1_sysbp_min                                  60.99
## h1_diasbp_min                                 53.78
## age                                           53.53
## h1_resprate_max                               48.42
## temp_apache                                   48.39
## apache_3j_bodysystem_Metabolic                48.01
## h1_resprate_min                               44.02
## heart_rate_apache                             43.89
## d1_resprate_max                               43.84
## apache_3j_diagnosis                           43.83
## icu_admit_source_Operating.Room...Recovery    43.23
```

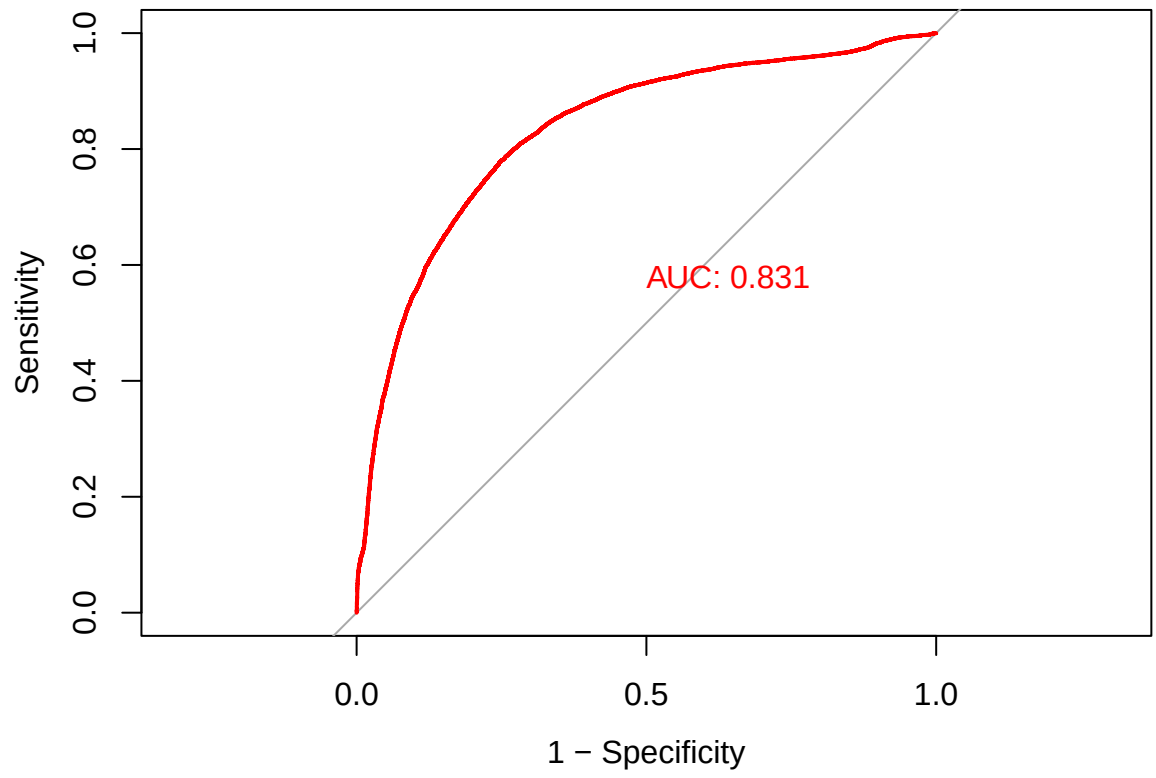
MDA Model

```
set.seed(100)

mdaFit <- train(x = train_withdummies_r,
                y = y_train,
                method = "mda",
                tuneGrid = expand.grid(subclasses=1:3),
                preProc = c("center","scale"),
                metric = "ROC",
                trControl = ctrl)

mdaFit
```

```
## Mixture Discriminant Analysis
##
```

```
## 12332 samples
##    68 predictor
##     2 classes: 'death', 'no_death'
##
## Pre-processing: centered (68), scaled (68)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 11099, 11098, 11099, 11100, 11099, 11100, ...
## Resampling results across tuning parameters:
##
##   subclasses  ROC        Sens       Spec
##   1           0.8558741  0.7587521  0.7835600
##   2           0.8259244  0.7317263  0.7822951
##   3           0.8254666  0.7286608  0.7858990
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was subclasses = 1.
```

```
## Save ROC curve for the hold-out set
mdaRoc <- roc(response = mdaFit$pred$obs,
              predictor = mdaFit$pred$death,
              levels = rev(levels(mdaFit$pred$obs)))

plot(mdaRoc, type = "s", col = 'red', legacy.axes = TRUE, print.auc = TRUE, print.auc.y = .6)
```



```r
testResults$MDA = predict(mdaFit, test_withdummies_r)
confusionMatrix(testResults$MDA, testResults$obs, positive = "death")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction death no_death
##   death     1154     3270
##   no_death   382    12990
##
##                Accuracy : 0.7948
##                  95% CI : (0.7888, 0.8007)
##     No Information Rate : 0.9137
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.2972
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.75130
##             Specificity : 0.79889
##          Pos Pred Value : 0.26085
##          Neg Pred Value : 0.97143
##              Prevalence : 0.08631
##          Detection Rate : 0.06485
##    Detection Prevalence : 0.24860
##       Balanced Accuracy : 0.77510
##
##        'Positive' Class : death
##
```

```r
varImp(mdaFit)
```

```
## ROC curve variable importance
##
##   only 20 most important variables shown (out of 68)
##
##                      Importance
## d1_sysbp_min             100.00
## gcs_verbal_apache         97.35
## ventilated_apache         97.12
## gcs_motor_apache          90.87
## gcs_eyes_apache           90.18
## d1_diasbp_min             83.62
## h1_sysbp_min              71.16
## d1_spo2_min               69.47
## d1_resprate_max           64.41
## h1_diasbp_min             63.10
## heart_rate_apache         60.22
## h1_resprate_max           59.10
## intubated_apache          56.53
## d1_temp_min               56.50
```

```
## apache_3j_diagnosis      53.67
## apache_2_diagnosis       53.26
## age                      53.13
## h1_resprate_min          52.75
## temp_apache              51.09
## map_apache               45.30
```

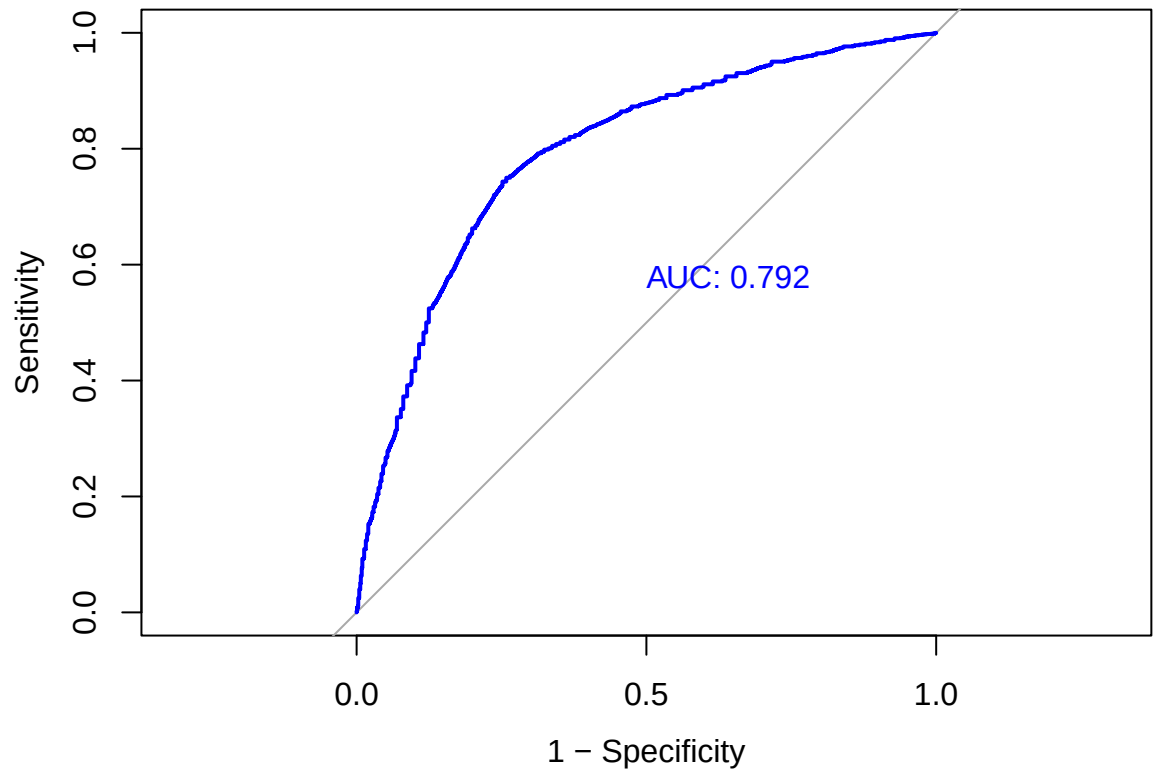
(CART) Decision Tree Model

```
# Change Character Variables to Factors #
x_tree_train <- X_train
x_tree_test <- X_test
x_tree_train[sapply(x_tree_train, is.character)] <- lapply(
  x_tree_train[sapply(x_tree_train, is.character)], as.factor)
x_tree_test[sapply(x_tree_test, is.character)] <- lapply(
  x_tree_test[sapply(x_tree_test, is.character)], as.factor)


set.seed(100)
dtree <- train(x = x_tree_train, y = y_train,
               method = "rpart", metric = "ROC",
               trControl = ctrl, tuneLength = 30)

dtree #Optimal cp = 0.0008108985
```

```
## CART
##
## 12332 samples
##    43 predictor
##     2 classes: 'death', 'no_death'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 11099, 11098, 11099, 11100, 11099, 11100, ...
## Resampling results across tuning parameters:
##
##   cp            ROC        Sens       Spec
##   0.0004865391  0.8069706  0.7531731  0.7388895
##   0.0005405990  0.8076738  0.7554442  0.7374298
##   0.0005676289  0.8114755  0.7586894  0.7440801
##   0.0005946589  0.8104424  0.7614491  0.7429466
##   0.0006487188  0.8134832  0.7614494  0.7461915
##   0.0007298086  0.8160897  0.7616128  0.7504044
##   0.0008108985  0.8167127  0.7633954  0.7499187
##   0.0008919883  0.8154879  0.7630723  0.7478123
##   0.0009730782  0.8153405  0.7658202  0.7476539
##   0.0010271381  0.8149172  0.7633869  0.7508961
##   0.0010541680  0.8140427  0.7641973  0.7478146
##   0.0011352579  0.8136765  0.7638766  0.7461878
##   0.0012163477  0.8102481  0.7659864  0.7453740
##   0.0012974376  0.8110857  0.7637174  0.7487821
##   0.0013785274  0.8111028  0.7633930  0.7494306
```

```
##   0.0016217970  0.8094707  0.7671178  0.7442416
##   0.0016623419  0.8019248  0.7609545  0.7491039
##   0.0019461563  0.7851467  0.7651674  0.7372614
##   0.0020434642  0.7830323  0.7632228  0.7395312
##   0.0021083360  0.7792465  0.7672812  0.7346637
##   0.0022705157  0.7774414  0.7667931  0.7345011
##   0.0028381447  0.7689627  0.7643657  0.7330469
##   0.0030814142  0.7686326  0.7682592  0.7268852
##   0.0037301330  0.7680229  0.7593343  0.7314311
##   0.0068115472  0.7681263  0.7543110  0.7275374
##   0.0129743756  0.7688547  0.7419813  0.7366199
##   0.0201913720  0.7517048  0.7048362  0.7534796
##   0.0277327279  0.7295409  0.6154721  0.8122008
##   0.0317872202  0.7030948  0.6355780  0.7525253
##   0.3848524165  0.5905218  0.7357638  0.4452798
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was cp = 0.0008108985.
```

```
#ROC = 0.8167127, Sens. = 0.7633954, Spec. = 0.7499187
#dtree$finalModel
dtreeRoc <- roc(response = dtree$pred$obs,
           predictor = dtree$pred$death,
           levels = rev(levels(dtree$pred$obs)))
plot(dtreeRoc, type = "s", col = 'blue',
     legacy.axes = TRUE, print.auc = TRUE, print.auc.y = .6)
```



```
testResults$DecisionTree <- c(predict(dtree, x_tree_test))

confusionMatrix(testResults$DecisionTree, testResults$obs, positive = "death")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction death no_death
##   death     1157     3988
##   no_death   379    12272
##
##                Accuracy : 0.7546
##                  95% CI : (0.7482, 0.7609)
##     No Information Rate : 0.9137
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.2461
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.75326
##             Specificity : 0.75474
##          Pos Pred Value : 0.22488
##          Neg Pred Value : 0.97004
##              Prevalence : 0.08631
##          Detection Rate : 0.06501
##    Detection Prevalence : 0.28911
##       Balanced Accuracy : 0.75400
##
##        'Positive' Class : death
##
```

Random Forest Model

```
# Recommended values of mtry: sqrt(p) = sqrt(43) ~ 6 or 7
mtryvalues <- c(7)

set.seed(100)
randforest <- train(x = x_tree_train, y = y_train,
               method = "rf", metric = "ROC",
               trControl = ctrl,
               tuneGrid = data.frame(mtry = mtryvalues),
               ntree = 50)

randforest
```

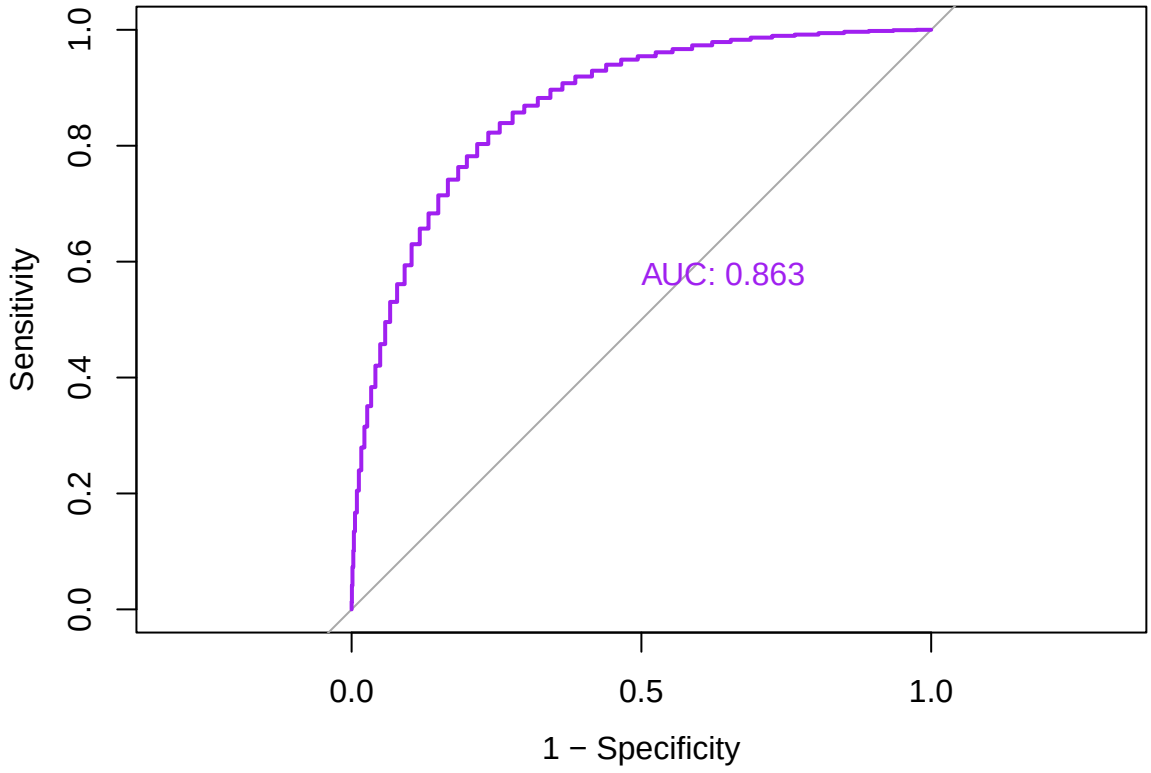
```
## Random Forest
##
## 12332 samples
##    43 predictor
##     2 classes: 'death', 'no_death'
```

```
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 11099, 11098, 11099, 11100, 11099, 11100, ...
## Resampling results:
##
##   ROC        Sens       Spec
##   0.8633535  0.7955027  0.7698633
##
## Tuning parameter 'mtry' was held constant at a value of 7
```

```
#ROC = 0.8633535, Sens. = 0.7955027, Spec. = 0.7698633
## Compared to Baseline Decision Tree, ROC and Sens. increased, Spec. decreased slightly
randforest$finalModel #OOB estimate of error rate: 22.64%
```

```
##
## Call:
##  randomForest(x = x, y = y, ntree = 50, mtry = min(param$mtry,      ncol(x)))
##                Type of random forest: classification
##                      Number of trees: 50
## No. of variables tried at each split: 7
##
##         OOB estimate of  error rate: 22.64%
## Confusion matrix:
##          death no_death class.error
## death     4818     1348   0.2186182
## no_death  1444     4722   0.2341875
```

```
randforestROC <- roc(response = randforest$pred$obs,
            predictor = randforest$pred$death,
            levels = rev(levels(randforest$pred$obs)))
plot(randforestROC, type = "s", col = 'purple',
     legacy.axes = TRUE, print.auc = TRUE, print.auc.y = .6)
```




```
testResults$RandomForest <- c(predict(randforest, x_tree_test))
#testResults$RandomForest <- as.factor(ifelse(testResults$RandomForest == 2, "no_death", "death"))

confusionMatrix(testResults$RandomForest, testResults$obs, positive = "death")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction death no_death
##   death     1227     3614
##   no_death   309    12646
##
##                Accuracy : 0.7796
##                  95% CI : (0.7734, 0.7856)
##     No Information Rate : 0.9137
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.292
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.79883
##             Specificity : 0.77774
##          Pos Pred Value : 0.25346
##          Neg Pred Value : 0.97615
```

```
##              Prevalence : 0.08631
##          Detection Rate : 0.06895
##    Detection Prevalence : 0.27203
##       Balanced Accuracy : 0.78828
##
##        'Positive' Class : death
##
```

Boosted Tree Model

```
gbmGrid <- expand.grid(interaction.depth = c(5),
                       n.trees = (1:20)*5,
                       shrinkage = c(.01, .1),
                       n.minobsinnode = 5)

set.seed(100)
boost_tree <- train(x = x_tree_train, y = y_train,
                method = "gbm", tuneGrid = gbmGrid,
                verbose = FALSE, metric = "ROC",
                trControl = ctrl)
boost_tree
```

```
## Stochastic Gradient Boosting
##
## 12332 samples
##    43 predictor
##     2 classes: 'death', 'no_death'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 11099, 11098, 11099, 11100, 11099, 11100, ...
## Resampling results across tuning parameters:
##
##   shrinkage  n.trees  ROC        Sens       Spec
##   0.01         5      0.7969763  0.7528495  0.7246153
##   0.01        10      0.8061954  0.7479849  0.7359732
##   0.01        15      0.8115177  0.7377744  0.7484598
##   0.01        20      0.8151833  0.7280355  0.7620843
##   0.01        25      0.8169332  0.7333918  0.7633819
##   0.01        30      0.8196914  0.7286864  0.7667850
##   0.01        35      0.8217036  0.7322555  0.7697044
##   0.01        40      0.8236841  0.7322542  0.7706753
##   0.01        45      0.8250887  0.7350115  0.7718114
##   0.01        50      0.8264713  0.7356603  0.7713244
##   0.01        55      0.8276595  0.7377689  0.7719729
##   0.01        60      0.8292226  0.7384185  0.7716491
##   0.01        65      0.8307137  0.7395543  0.7716491
##   0.01        70      0.8320329  0.7411761  0.7706745
##   0.01        75      0.8335434  0.7445800  0.7682410
##   0.01        80      0.8346083  0.7484748  0.7666197
##   0.01        85      0.8357148  0.7491233  0.7666192
##   0.01        90      0.8367413  0.7528537  0.7643489
```

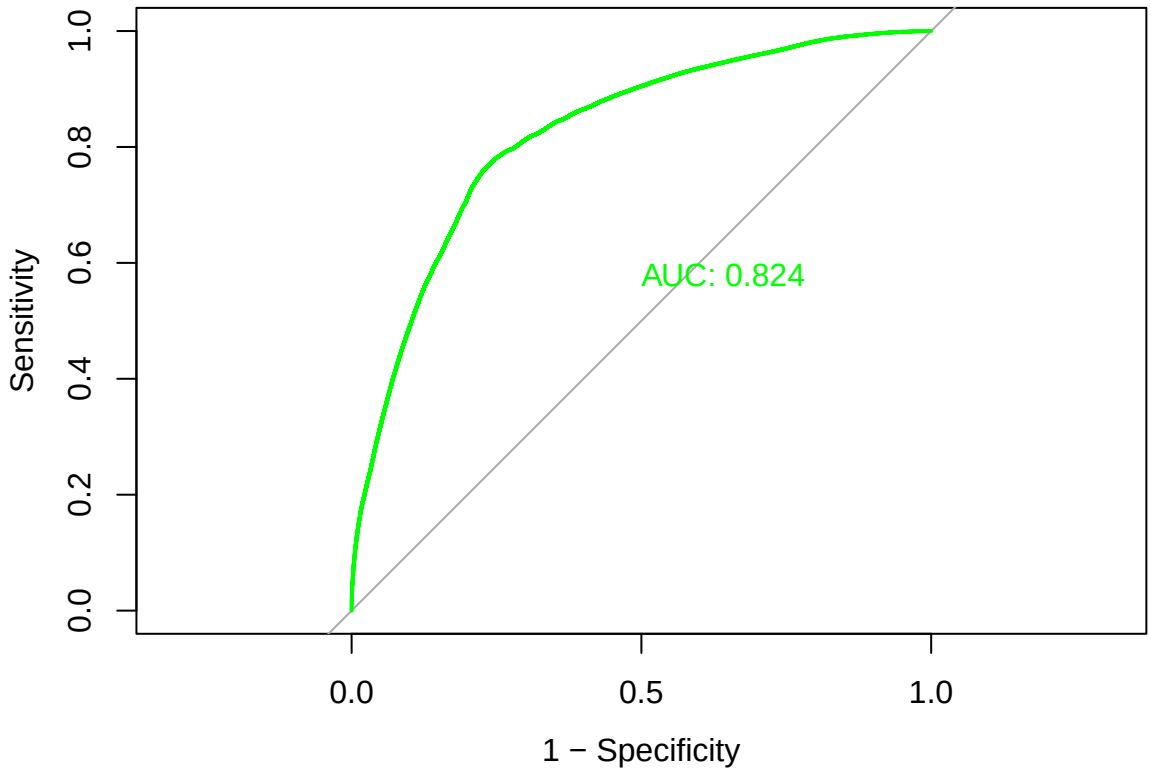
```
##   0.01        95      0.8378904  0.7556100  0.7625658
##   0.01       100      0.8389130  0.7575562  0.7614313
##   0.10         5      0.8181994  0.7465272  0.7552745
##   0.10        10      0.8351199  0.7539898  0.7585137
##   0.10        15      0.8457670  0.7672849  0.7632183
##   0.10        20      0.8525161  0.7745819  0.7661367
##   0.10        25      0.8572740  0.7791242  0.7714891
##   0.10        30      0.8608624  0.7825291  0.7732722
##   0.10        35      0.8637478  0.7847997  0.7765163
##   0.10        40      0.8657817  0.7878815  0.7757041
##   0.10        45      0.8672010  0.7873953  0.7773248
##   0.10        50      0.8689191  0.7886945  0.7795952
##   0.10        55      0.8702337  0.7896659  0.7797559
##   0.10        60      0.8710704  0.7916126  0.7826772
##   0.10        65      0.8718519  0.7914506  0.7825146
##   0.10        70      0.8726666  0.7933960  0.7831621
##   0.10        75      0.8733420  0.7946942  0.7820263
##   0.10        80      0.8734793  0.7942064  0.7815401
##   0.10        85      0.8738232  0.7948557  0.7820260
##   0.10        90      0.8741476  0.7951796  0.7828359
##   0.10        95      0.8745928  0.7955037  0.7851062
##   0.10       100      0.8745278  0.7933957  0.7852699
##
## Tuning parameter 'interaction.depth' was held constant at a value of 5
##
## Tuning parameter 'n.minobsinnode' was held constant at a value of 5
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were n.trees = 95, interaction.depth =
##  5, shrinkage = 0.1 and n.minobsinnode = 5.
```

```
# Shrinkage = 0.1, n.tree = 5
# ROC = 0.8745928, Sens. = 0.7955037, Spec. = 0.7851062

#boost_tree$finalModel

confusionMatrix(boost_tree, norm = "none")
```

```
## Cross-Validated (10 fold) Confusion Matrix
##
## (entries are un-normalized aggregated counts)
##
##           Reference
## Prediction death no_death
##   death     4905     1325
##   no_death  1261     4841
##
##  Accuracy (average) : 0.7903
```

```
## Plot the ROC curve for the hold-out set
boost_treeRoc <- roc(response = boost_tree$pred$obs,
              predictor = boost_tree$pred$death,
              levels = rev(levels(boost_tree$pred$obs)))
```

```
plot(boost_treeRoc, type = "s", col = 'green',
     legacy.axes = TRUE, print.auc = TRUE, print.auc.y = .6)
```




```
testResults$BoostedTree <- c(predict(boost_tree, x_tree_test))
#testResults$BoostedTree <- as.factor(ifelse(testResults$BoostedTree == 2, "no_death", "death"))

confusionMatrix(testResults$BoostedTree, testResults$obs, positive = "death",
                mode = "everything")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction death no_death
##   death     1216     3252
##   no_death   320    13008
##
##                Accuracy : 0.7993
##                  95% CI : (0.7933, 0.8051)
##     No Information Rate : 0.9137
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.3174
##
##  Mcnemar's Test P-Value : <2e-16
##
```

```
##             Sensitivity : 0.79167
##             Specificity : 0.80000
##          Pos Pred Value : 0.27216
##          Neg Pred Value : 0.97599
##               Precision : 0.27216
##                  Recall : 0.79167
##                      F1 : 0.40506
##              Prevalence : 0.08631
##          Detection Rate : 0.06833
##    Detection Prevalence : 0.25107
##       Balanced Accuracy : 0.79583
##
##        'Positive' Class : death
##
```

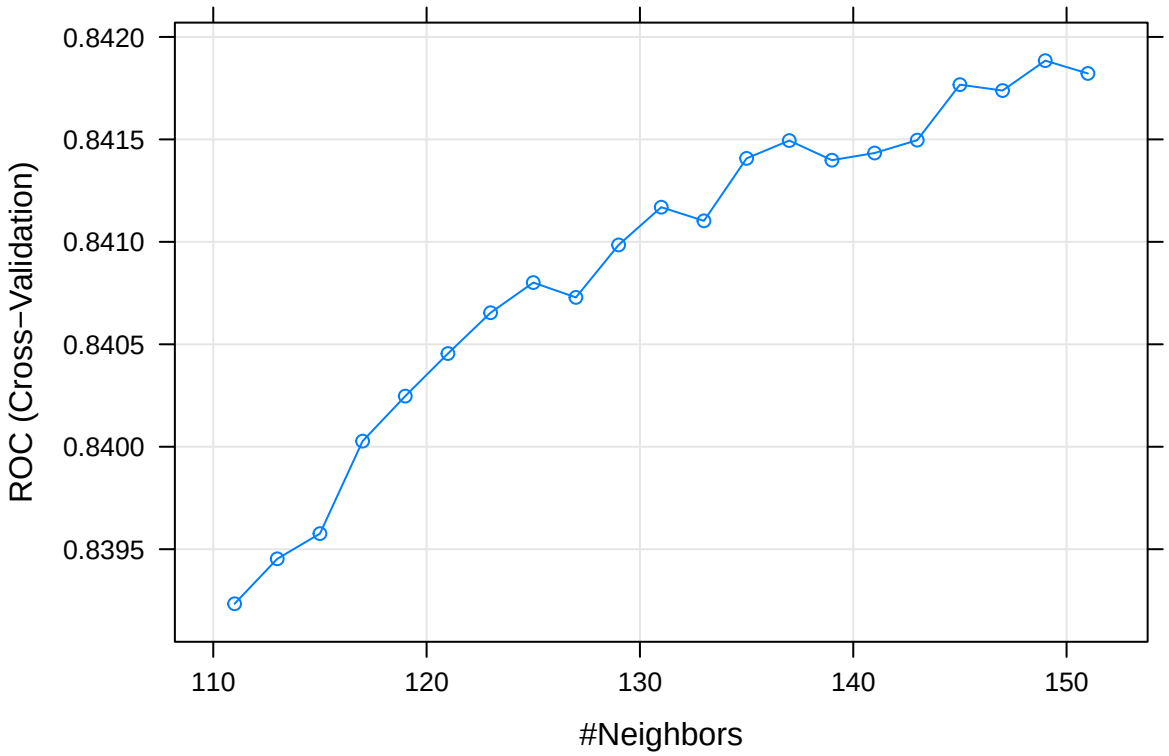
KNN Model

```
set.seed(100)
knnTune <- train(x = train_withdummies_r, y = y_train,
                 method = "knn", metric = "ROC",
                 preProc = c("center", "scale"),  #measuring distances, keep on the same scale and cent
                 tuneGrid = data.frame(k = seq(111, 151, by=2)),   #see which k-value performms the bes
                 trControl = ctrl)
knnTune
```

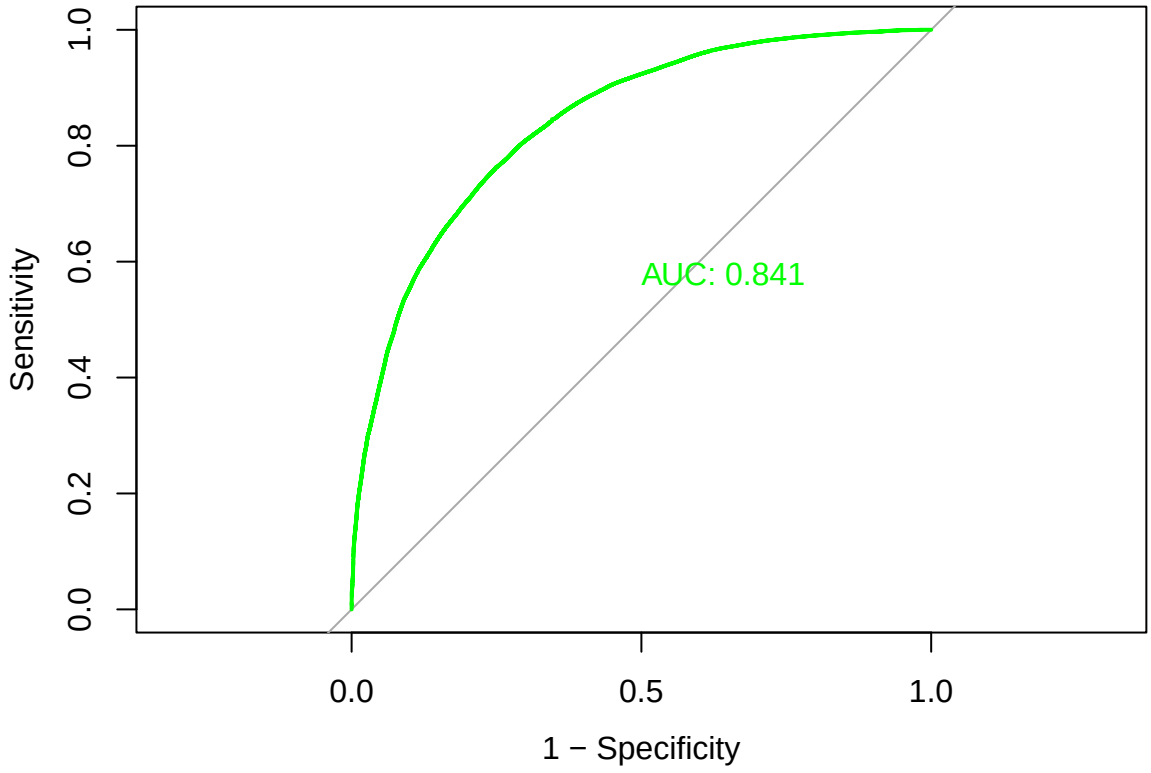
```
## k-Nearest Neighbors
##
## 12332 samples
##    68 predictor
##     2 classes: 'death', 'no_death'
##
## Pre-processing: centered (68), scaled (68)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 11099, 11098, 11099, 11100, 11099, 11100, ...
## Resampling results across tuning parameters:
##
##   k    ROC        Sens       Spec
##   111  0.8392338  0.5973145  0.8743057
##   113  0.8394531  0.5976394  0.8741436
##   115  0.8395760  0.5995851  0.8743057
##   117  0.8400274  0.5997487  0.8765784
##   119  0.8402472  0.5989378  0.8764150
##   121  0.8404548  0.5974789  0.8777129
##   123  0.8406540  0.5969935  0.8773880
##   125  0.8408012  0.5978030  0.8772262
##   127  0.8407288  0.5960197  0.8775503
##   129  0.8409849  0.5958582  0.8781989
##   131  0.8411691  0.5950457  0.8785230
##   133  0.8411024  0.5965049  0.8780371
##   135  0.8414073  0.5960179  0.8786856
##   137  0.8414942  0.5947192  0.8798217
##   139  0.8413985  0.5943953  0.8804703
```

```
##   141  0.8414334  0.5929345  0.8804692
##   143  0.8414963  0.5921228  0.8796591
##   145  0.8417672  0.5917984  0.8803077
##   147  0.8417383  0.5908249  0.8824162
##   149  0.8418843  0.5919602  0.8820923
##   151  0.8418216  0.5916361  0.8817692
##
## ROC was used to select the optimal model using the largest value.
## The final value used for the model was k = 149.
```

```
plot(knnTune)
```




```
## Plot the ROC curve for the hold-out set
knnRoc <- roc(response = knnTune$pred$obs,
              predictor = knnTune$pred$death,
              levels = rev(levels(knnTune$pred$obs)))

plot(knnRoc, type = "s", col = 'green',
     legacy.axes = TRUE, print.auc = TRUE, print.auc.y = .6)
```




```
testResults$Knn <- predict(knnTune, test_withdummies_r[, names(train_withdummies_r)])
confusionMatrix(testResults$Knn, testResults$obs, positive = "death",
                mode = "everything")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction death no_death
##   death      915     1856
##   no_death   621    14404
##
##                Accuracy : 0.8608
##                  95% CI : (0.8556, 0.8659)
##     No Information Rate : 0.9137
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.353
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.59570
##             Specificity : 0.88585
##          Pos Pred Value : 0.33021
##          Neg Pred Value : 0.95867
##               Precision : 0.33021
```

```
##                  Recall : 0.59570
##                      F1 : 0.42489
##              Prevalence : 0.08631
##          Detection Rate : 0.05142
##    Detection Prevalence : 0.15571
##       Balanced Accuracy : 0.74078
##
##        'Positive' Class : death
##
```

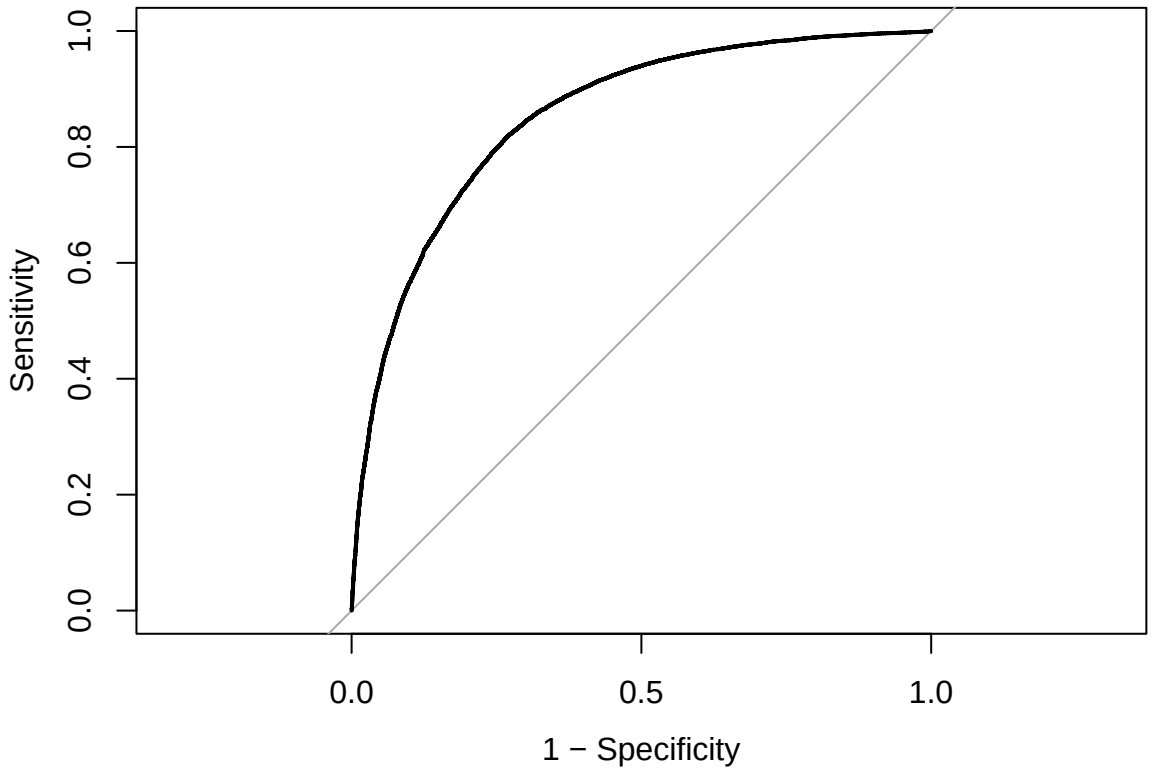
Neural Net Model

```
set.seed(100)
nnetGrid <- expand.grid(size=1:2, decay=c(0,0.1,1))
nnetFit <- train(x = train_withdummies_r,
                 y = y_train,
                 method = "nnet",
                 metric = "ROC",
                 tuneGrid = nnetGrid,
                 preProc = c("center","scale"),
                 trControl = ctrl,
                 maxit = 100,
                 trace = FALSE)

nnetFit
```

```
## Neural Network
##
## 12332 samples
##    68 predictor
##     2 classes: 'death', 'no_death'
##
## Pre-processing: centered (68), scaled (68)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 11099, 11098, 11099, 11100, 11099, 11100, ...
## Resampling results across tuning parameters:
##
##   size  decay  ROC        Sens       Spec
##   1     0.0    0.8563365  0.7799354  0.7687286
##   1     0.1    0.8566597  0.7825265  0.7656465
##   1     1.0    0.8570569  0.7833416  0.7680774
##   2     0.0    0.8479542  0.7943619  0.7439117
##   2     0.1    0.8512042  0.7674656  0.7692043
##   2     1.0    0.8560697  0.7904755  0.7607824
##
## ROC was used to select the optimal model using the largest value.
## The final values used for the model were size = 1 and decay = 1.
```

```
nnetRoc <- roc(response = nnetFit$pred$obs,
            predictor = nnetFit$pred$death,
            levels = rev(levels(nnetFit$pred$obs)))
```

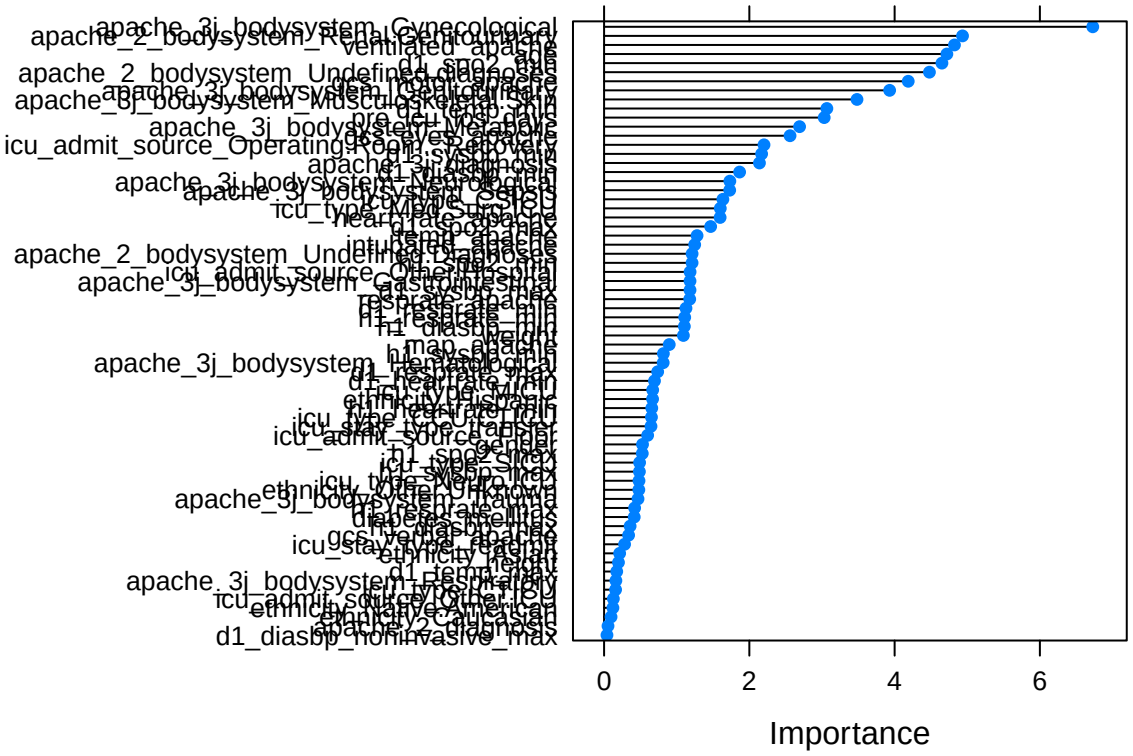
```
plot(nnetRoc, legacy.axes = TRUE)
```




```
nnetRoc$auc
```

```
## Area under the curve: 0.8522
```

```
nnetImp <- varImp(nnetFit, scale = FALSE)
plot(nnetImp)
```



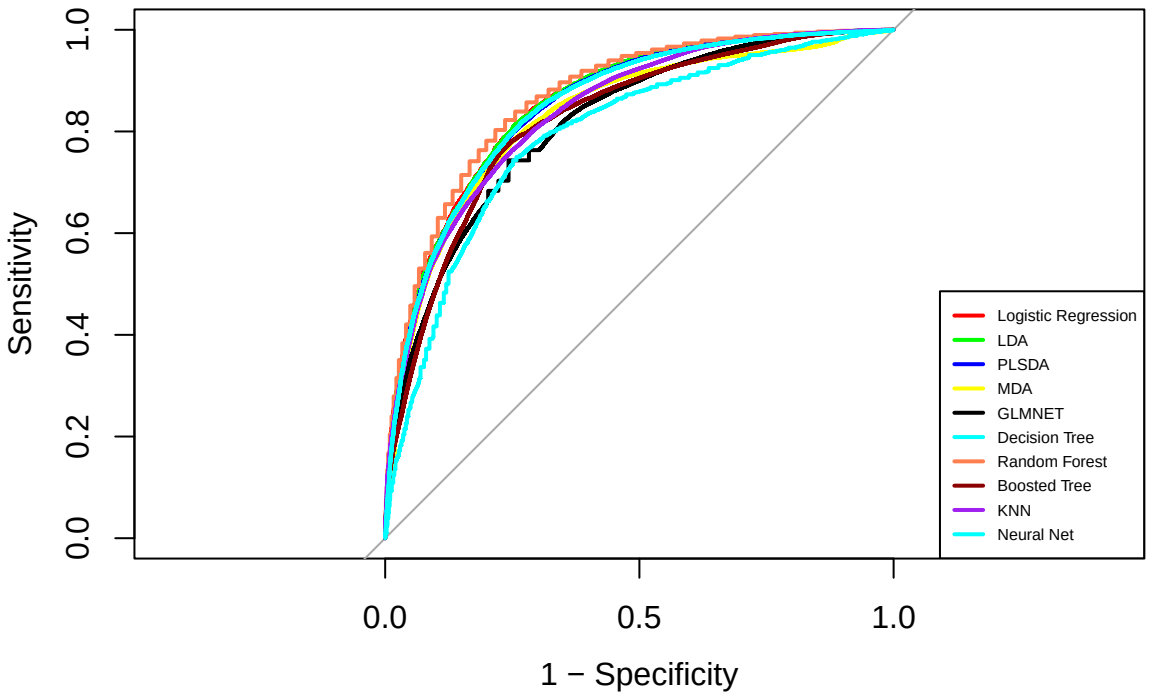

```
testResults$NN <- predict(nnetFit, test_withdummies_r)

confusionMatrix(testResults$NN, testResults$obs, positive = "death")
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction death no_death
##   death     1215     3723
##   no_death   321    12537
##
##                Accuracy : 0.7728
##                  95% CI : (0.7665, 0.7789)
##     No Information Rate : 0.9137
##     P-Value [Acc > NIR] : 1
##
##                   Kappa : 0.2806
##
##  Mcnemar's Test P-Value : <2e-16
##
##             Sensitivity : 0.79102
##             Specificity : 0.77103
##          Pos Pred Value : 0.24605
##          Neg Pred Value : 0.97503
##              Prevalence : 0.08631
```

```
##          Detection Rate : 0.06827
##    Detection Prevalence : 0.27748
##       Balanced Accuracy : 0.78102
##
##        'Positive' Class : death
##
```

Final Model Selection

```
par(oma=c(0,0,2,0))
## Plot ROC Curves ##
plot(lrRoc, type = "s", col = 'red', legacy.axes = TRUE)
plot(ldaRoc, type = "s", add = TRUE, col = 'green', legacy.axes = TRUE)
plot(plsdaRoc, type = "s", add = TRUE, col = "blue", legacy.axes = TRUE)
plot(mdaRoc, type = "s", add = TRUE, col = 'yellow', legacy.axes = TRUE)
plot(glmRoc, type = "s", add = TRUE, col = "black",legacy.axes = TRUE)
plot(dtreeRoc, type = "s", add = TRUE, col = "cyan",legacy.axes = TRUE)
plot(randforestROC, type = "s", add = TRUE, col = "coral",legacy.axes = TRUE)
plot(boost_treeRoc, type = "s", add = TRUE, col = "darkred",legacy.axes = TRUE)
plot(knnRoc, type = "s", add = TRUE, col = "purple",legacy.axes = TRUE)
plot(nnetRoc, type = "s", add = TRUE, col = "cyan",legacy.axes = TRUE)

legend("bottomright", legend = c("Logistic Regression", "LDA", "PLSDA", "MDA",
                                 "GLMNET", "Decision Tree", "Random Forest", "Boosted Tree", "KNN",
                                 "Neural Net"),
       col = c("red", "green", "blue", "yellow", "black", "cyan", "coral", "darkred", "purple", "cyan")
       lwd = 2, cex = 0.5)
title(main = "ROC Curves By Model", outer = TRUE)
```




```
# Performance Metric Table #
final_metric_table <- data.frame(
  "Models" = c("Logistic Regression", "Penalized Logistic Regression", "LDA", "PLSDA",
               "MDA", "Decision Tree", "Random Forest", "Boosted Tree", "KNN", "Neural Net"),
  "ROC- Train" = c(0.8579, 0.8576, 0.8574, 0.8565, 0.8559,
                           0.8167, 0.8634, 0.8746, 0.8401, 0.8571),
  "Sens. - Train" = c(0.7683, 0.7613, 0.7624, 0.7606, 0.7588,
                                  0.7634, 0.7955, 0.7955, 0.5981, 0.7833),
  "Spec. - Train" = c(0.7830, 0.7835, 0.7848, 0.7843, 0.7836,
                                  0.7499, 0.7699, 0.7851, 0.8766, 0.7681),
  "Sens. - Test" = c(0.7611, 0.7578, 0.7533, 0.7507, 0.7513,
                             0.7533, 0.7988, 0.7917, 0.6030, 0.7910),
  "Spec. - Test" = c(0.7972, 0.7982, 0.7991, 0.7985, 0.7989,
                             0.7547, 0.7777, 0.8000, 0.8795, 0.7710))
kable(final_metric_table)
```

Models	ROC..Train	Sens....Train	Spec....Train	Sens....Test	Spec....Test
Logistic Regression	0.8579	0.7683	0.7830	0.7611	0.7972
Penalized Logistic Regression	0.8576	0.7613	0.7835	0.7578	0.7982
LDA	0.8574	0.7624	0.7848	0.7533	0.7991
PLSDA	0.8565	0.7606	0.7843	0.7507	0.7985
MDA	0.8559	0.7588	0.7836	0.7513	0.7989
Decision Tree	0.8167	0.7634	0.7499	0.7533	0.7547
Random Forest	0.8634	0.7955	0.7699	0.7988	0.7777

Models	ROC..Train	Sens....Train	Spec....Train	Sens....Test	Spec....Test
Boosted Tree	0.8746	0.7955	0.7851	0.7917	0.8000
KNN	0.8401	0.5981	0.8766	0.6030	0.8795
Neural Net	0.8571	0.7833	0.7681	0.7910	0.7710