

# Data Processing

Team 2

2025-11-03

```
source("00_requirements.R")
```

```
## Loading required package: tidyverse
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
```

```
## v dplyr      1.1.4      v readr      2.1.5
```

```
## v forcats    1.0.1      v stringr    1.5.2
```

```
## v ggplot2    4.0.0      v tibble     3.3.0
```

```
## v lubridate  1.9.4      v tidyr      1.3.1
```

```
## v purrr      1.1.0
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x dplyr::filter() masks stats::filter()
```

```
## x dplyr::lag()     masks stats::lag()
```

```
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
## Loading required package: broom
```

```
##
```

```
## Loading required package: GGally
```

```
##
```

```
## Loading required package: modelsummary
```

```
##
```

```
## Loading required package: knitr
```

```
##
```

```
## Loading required package: kableExtra
```

```
##
```

```
##
```

```
## Attaching package: 'kableExtra'
```

```
##
```

```
##
```

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

```
##
```

```
##      group_rows
```

```
##
```

```
##
```

```
## Loading required package: caTools
```

```
##
```

```
## Loading required package: pROC
```

```
##
```

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

```
##
```

```
##
```

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

```
##
##
## The following objects are masked from 'package:stats':
##
##     cov, smooth, var
##
##
## Loading required package: ROSE
##
## Loaded ROSE 0.0-4
```

```
data <- read.csv("00_ProstateCancer_Data.csv", header=T)
```

```
cols1 <- c("Tani_Tarihi", "Tedavi_Tarihi", "PSA_Takip_3ay", "PSA_Takip_6ay", "PSA_Takip_12ay", "BCR_Tar",
data <- data[, !(names(data) %in% cols1)]
```

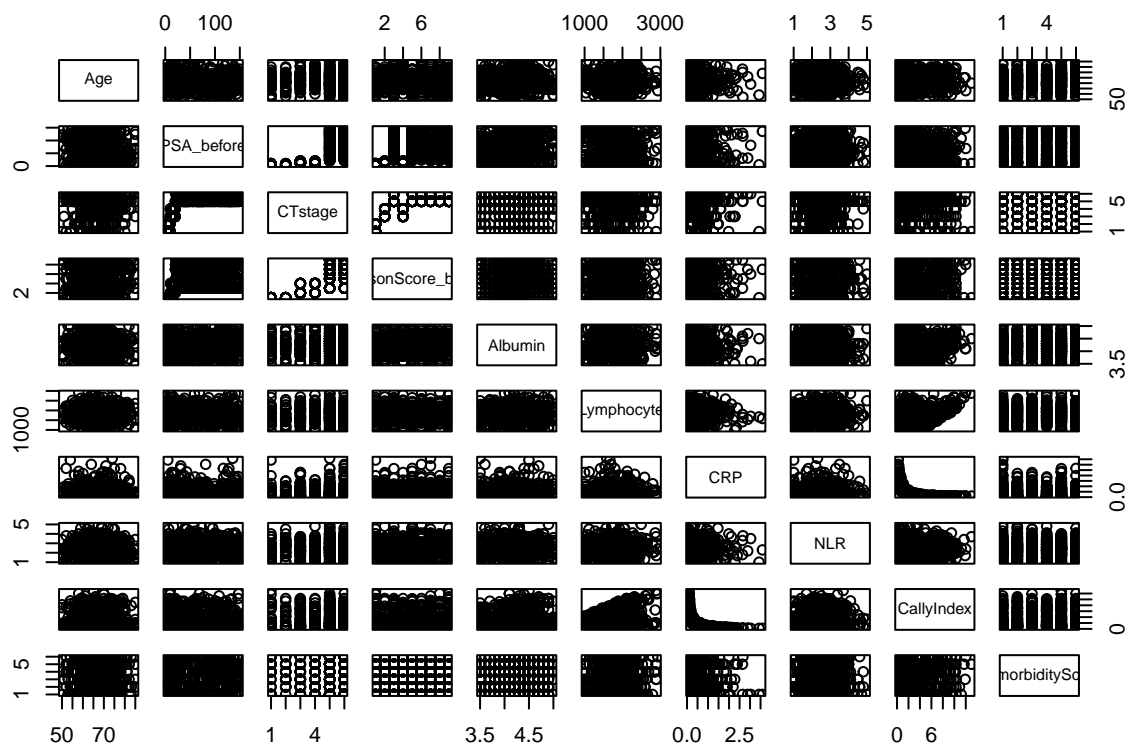
```
cols2 <- c("Klinik_Evre", "Biyopsi_Gleason", "Risk_Grubu", "Komorbidite_Skor", "Tedavi_Tipi", "ADT_Tipi",
data[cols2] <- lapply(data[cols2], as.factor)
```

```
names(data) <- c("Patient ID", "Age", "PSA_before", "CTstage", "GleasonScore_before", "RiskClass", "Alb",
```

```
data$Delta_PSA <- data$PSA_before - data$PSA_after
```

## Data Analysis 0: Correlation between Variables

```
vars <- c("Age", "PSA_before", "CTstage", "GleasonScore_before", "Albumin", "Lymphocyte", "CRP", "NLR",
pairs(data[, vars])
```



## Data Analysis 1: Logistic Regression (BCR)

```
bcr_model <- glm(BCR ~ Age + PSA_before + CTstage + GleasonScore_before + Albumin + Lymphocyte + CRP + NLR + CallyIndex + ComorbidityScore + Treatment, family = binomial, data = data, na.action = na.omit)
summary(bcr_model)
```

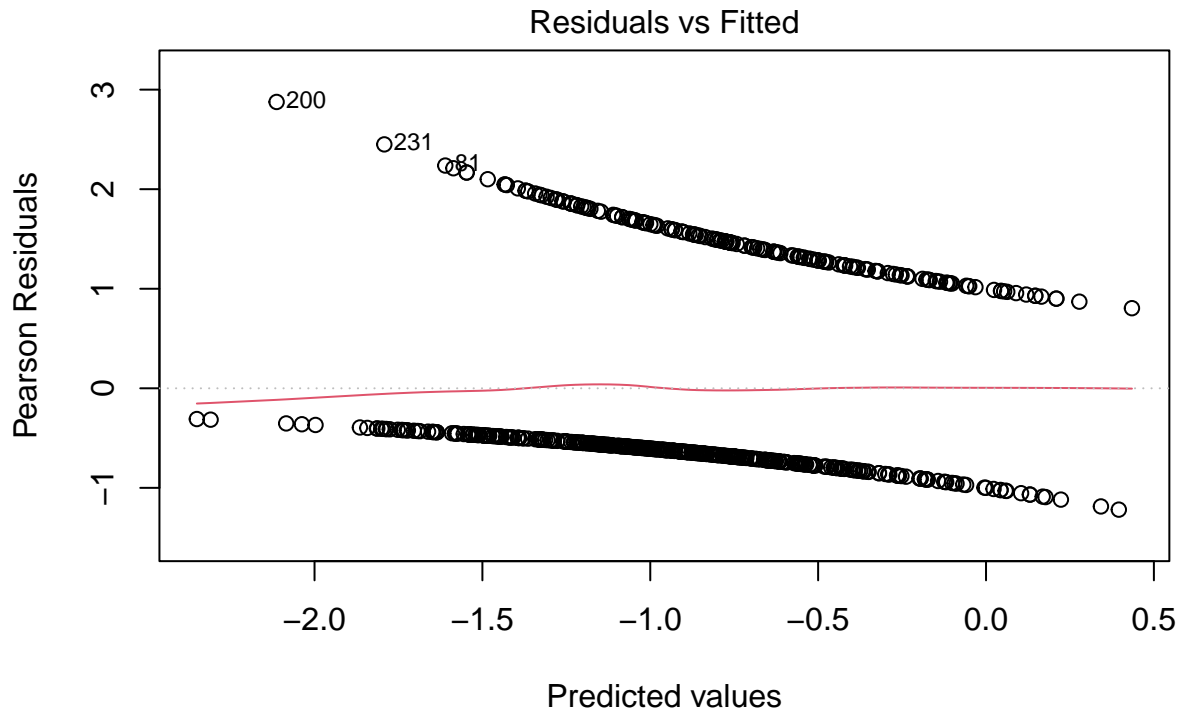
```
##
## Call:
## glm(formula = BCR ~ Age + PSA_before + CTstage + GleasonScore_before +
##       Albumin + Lymphocyte + CRP + NLR + CallyIndex + ComorbidityScore +
##       Treatment, family = binomial, data = data, na.action = na.omit)
##
## Coefficients: (2 not defined because of singularities)
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -1.081e+00  1.542e+00  -0.701   0.4833
## Age           -2.019e-02  1.311e-02  -1.541   0.1234
## PSA_before      5.780e-03  2.794e-03   2.069   0.0386 *
## CTstageT2a      2.026e-01  6.178e-01   0.328   0.7430
## CTstageT2b      3.239e-01  6.244e-01   0.519   0.6040
## CTstageT2c     -2.387e-01  5.881e-01  -0.406   0.6848
## CTstageT3a      9.524e-02  5.697e-01   0.167   0.8672
## CTstageT3b     -1.203e-01  5.755e-01  -0.209   0.8345
## GleasonScore_before3+4 -1.374e-01  4.881e-01  -0.282   0.7783
```

```

## GleasonScore_before3+5 -9.053e-02 3.498e-01 -0.259 0.7958
## GleasonScore_before4+3 NA NA NA NA
## GleasonScore_before4+4 -2.344e-01 3.614e-01 -0.648 0.5167
## GleasonScore_before4+5 -6.841e-02 3.788e-01 -0.181 0.8567
## GleasonScore_before5+3 2.789e-01 3.626e-01 0.769 0.4417
## GleasonScore_before5+4 9.191e-02 3.656e-01 0.251 0.8015
## GleasonScore_before5+5 NA NA NA NA
## Albumin 2.257e-01 2.477e-01 0.911 0.3621
## Lymphocyte 1.387e-04 2.624e-04 0.529 0.5970
## CRP -1.539e-01 2.462e-01 -0.625 0.5319
## NLR 8.682e-05 1.173e-01 0.001 0.9994
## CallyIndex -3.165e-02 4.543e-02 -0.697 0.4860
## ComorbidityScore1 6.865e-02 3.187e-01 0.215 0.8294
## ComorbidityScore2 -5.122e-02 3.308e-01 -0.155 0.8770
## ComorbidityScore3 -3.583e-01 3.268e-01 -1.096 0.2729
## ComorbidityScore4 2.711e-01 2.973e-01 0.912 0.3619
## ComorbidityScore5 -2.400e-03 3.301e-01 -0.007 0.9942
## Treatment2 2.849e-01 2.276e-01 1.252 0.2107
## Treatment3 6.202e-01 2.975e-01 2.084 0.0371 *
## Treatment4 2.014e-01 2.818e-01 0.715 0.4747
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 739.69 on 599 degrees of freedom
## Residual deviance: 711.93 on 573 degrees of freedom
## AIC: 765.93
##
## Number of Fisher Scoring iterations: 4

```

```
plot(bcr_model, which = 1)
```

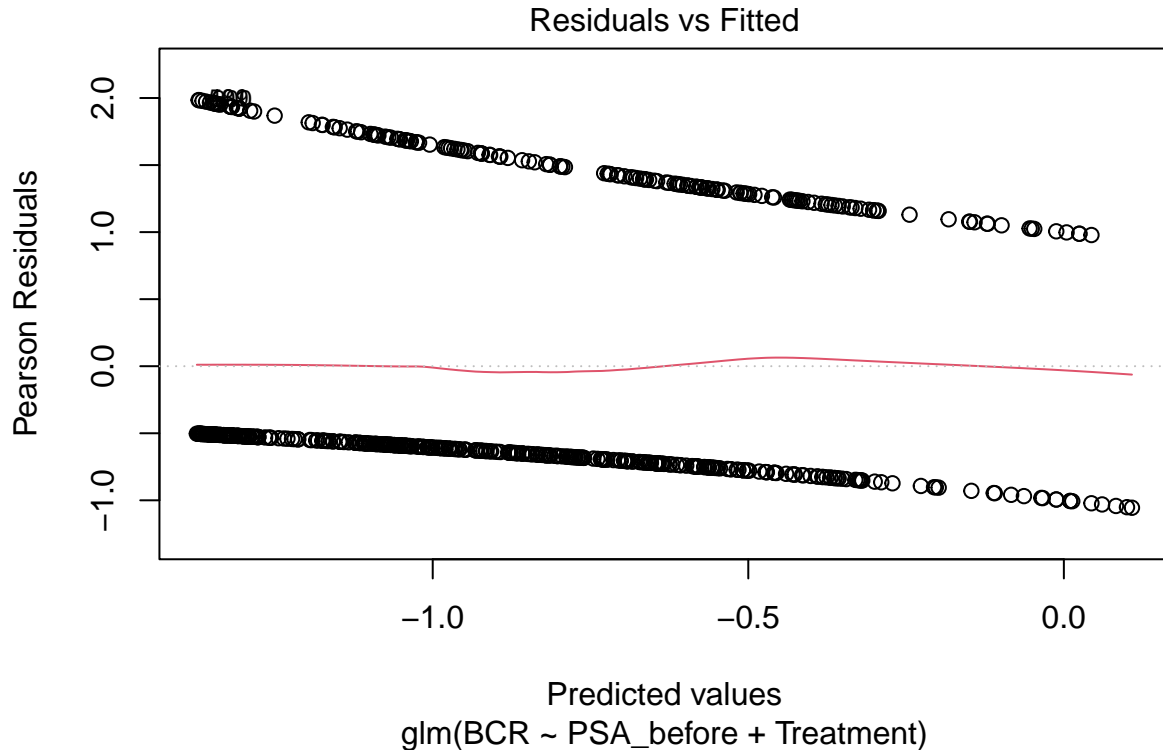


glm(BCR ~ Age + PSA\_before + CTstage + GleasonScore\_before + Albumin + Lymph

```
bcr_model <- glm(BCR ~ PSA_before + Treatment, data = data, family = binomial, na.action = na.omit)
summary(bcr_model)
```

```
##
## Call:
## glm(formula = BCR ~ PSA_before + Treatment, family = binomial,
##      data = data, na.action = na.omit)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.387813   0.186466  -7.443 9.86e-14 ***
## PSA_before   0.005629   0.001964   2.867  0.00415 **
## Treatment2   0.254127   0.216914   1.172  0.24137
## Treatment3   0.655230   0.285619   2.294  0.02179 *
## Treatment4   0.185449   0.269549   0.688  0.49145
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 739.69  on 599  degrees of freedom
## Residual deviance: 722.69  on 595  degrees of freedom
## AIC: 732.69
##
## Number of Fisher Scoring iterations: 4
```

```
plot(bcr_model, which = 1)
```



## Data Analysis 2: Logistic Regression (Survival)

```
survival_model <- glm(Survival ~ Age + PSA_before + CTstage + GleasonScore_before + Albumin + Lymphocyte
summary(survival_model)
```

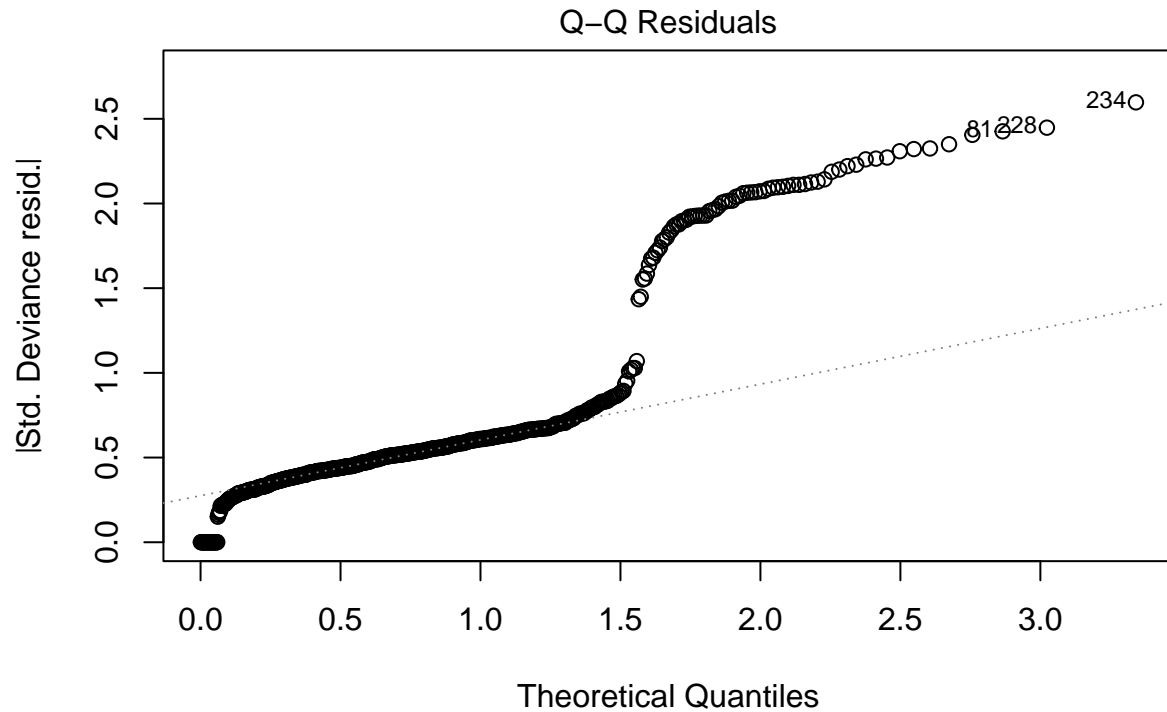
```
##
## Call:
## glm(formula = Survival ~ Age + PSA_before + CTstage + GleasonScore_before +
##      Albumin + Lymphocyte + CRP + NLR + CallyIndex + ComorbidityScore +
##      Treatment, family = binomial, data = data, na.action = na.omit)
##
## Coefficients: (2 not defined because of singularities)
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    2.137e+00  2.305e+00   0.927   0.3539
## Age            -1.432e-02  1.926e-02  -0.744   0.4571
## PSA_before     -5.326e-03  4.009e-03  -1.328   0.1840
## CTstageT2a      1.501e+01  7.183e+02   0.021   0.9833
## CTstageT2b     -5.715e-01  9.402e-01  -0.608   0.5433
## CTstageT2c     -6.360e-01  8.983e-01  -0.708   0.4790
## CTstageT3a     -5.481e-01  9.238e-01  -0.593   0.5529
```

```

## CTstagecT3b          -1.775e-01  9.300e-01  -0.191  0.8486
## GleasonScore_before3+4 -4.216e-01  6.089e-01  -0.692  0.4887
## GleasonScore_before3+5  1.017e-01  5.329e-01   0.191  0.8486
## GleasonScore_before4+3          NA          NA          NA          NA
## GleasonScore_before4+4 -3.853e-01  5.071e-01  -0.760  0.4474
## GleasonScore_before4+5  2.886e-01  6.112e-01   0.472  0.6368
## GleasonScore_before5+3 -2.008e-01  5.348e-01  -0.375  0.7074
## GleasonScore_before5+4 -5.629e-01  5.175e-01  -1.088  0.2767
## GleasonScore_before5+5          NA          NA          NA          NA
## Albumin              1.316e-01  3.595e-01   0.366  0.7144
## Lymphocyte           6.403e-04  3.878e-04   1.651  0.0987
## CRP                  4.782e-01  4.251e-01   1.125  0.2606
## NLR                  -1.478e-01  1.679e-01  -0.880  0.3788
## CallyIndex           2.322e-02  6.964e-02   0.333  0.7389
## ComorbidityScore1     -2.827e-01  4.637e-01  -0.610  0.5421
## ComorbidityScore2     -4.300e-01  4.675e-01  -0.920  0.3577
## ComorbidityScore3      8.570e-02  4.905e-01   0.175  0.8613
## ComorbidityScore4     -1.129e-01  4.612e-01  -0.245  0.8066
## ComorbidityScore5     -4.427e-01  4.752e-01  -0.932  0.3516
## Treatment2            1.879e-01  3.009e-01   0.624  0.5324
## Treatment3            8.841e-01  4.861e-01   1.819  0.0690
## Treatment4            1.040e+00  4.756e-01   2.188  0.0287 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##    Null deviance: 436.31  on 599  degrees of freedom
## Residual deviance: 403.52  on 573  degrees of freedom
## AIC: 457.52
##
## Number of Fisher Scoring iterations: 16

```

```
plot(survival_model, which= 2)
```



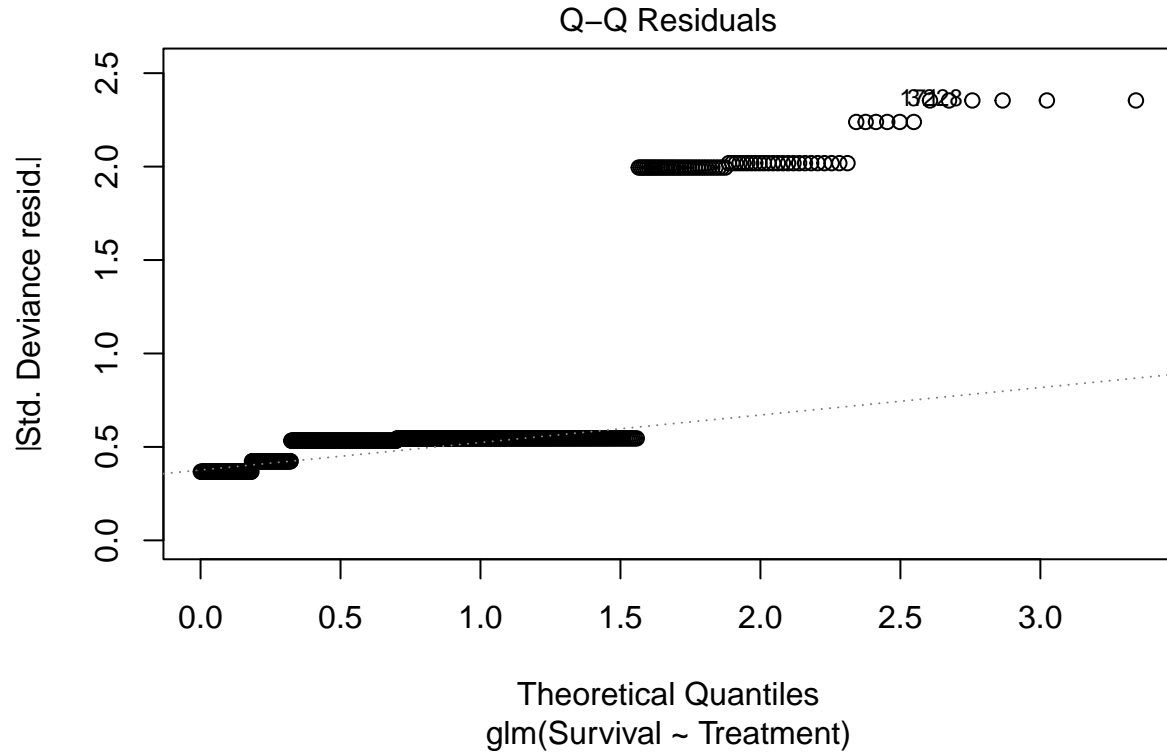
glm(Survival ~ Age + PSA\_before + CTstage + GleasonScore\_before + Albumin + ..

```
survival_model <- glm(Survival ~ Treatment, data = data, family = binomial, na.action = na.omit)
summary(survival_model)
```

```
##
## Call:
## glm(formula = Survival ~ Treatment, family = binomial, data = data,
##      na.action = na.omit)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  1.83372    0.18204  10.073  <2e-16 ***
## Treatment2   0.05082    0.28484   0.178   0.8584
## Treatment3   0.54890    0.46388   1.183   0.2367
## Treatment4   0.84042    0.45967   1.828   0.0675 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##    Null deviance: 436.31  on 599  degrees of freedom
## Residual deviance: 431.23  on 596  degrees of freedom
## AIC: 439.23
##
## Number of Fisher Scoring iterations: 5
```



```
plot(survival_model, which = 2)
```



### Model Interpretation 1: Logistic Regression (BCR ~ Treatment)

```
data$Treatment <- relevel(data$Treatment, ref = 3)

bcr_model_t3 <- glm(BCR ~ PSA_before + Treatment, data = data, family = binomial, na.action = na.omit)

summary(bcr_model_t3)
```

```
##
## Call:
## glm(formula = BCR ~ PSA_before + Treatment, family = binomial,
##      data = data, na.action = na.omit)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.732583   0.293763  -2.494  0.01264 *
## PSA_before   0.005629   0.001964   2.867  0.00415 **
## Treatment1  -0.655230   0.285619  -2.294  0.02179 *
## Treatment2  -0.401103   0.290011  -1.383  0.16665
## Treatment4  -0.469781   0.330558  -1.421  0.15526
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##    Null deviance: 739.69  on 599  degrees of freedom
## Residual deviance: 722.69  on 595  degrees of freedom
## AIC: 732.69
##
## Number of Fisher Scoring iterations: 4
```

## Model Interpretation 2: Logistic Regression (BCR ~ Combination)

```
data$Combination <- ifelse(data$Treatment == 4, "Yes", "No")
data$Combination <- as.factor(data$Combination)

bcr_model_2 <- glm(BCR ~ PSA_before + Combination, data = data, family = binomial, na.action = na.omit)

summary(bcr_model_2)
```

```
##
## Call:
## glm(formula = BCR ~ PSA_before + Combination, family = binomial,
##      data = data, na.action = na.omit)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -1.250651   0.163902  -7.630 2.34e-14 ***
## PSA_before     0.006496   0.001914   3.394 0.00069 ***
## CombinationYes -0.017033   0.246312  -0.069 0.94487
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##    Null deviance: 739.69  on 599  degrees of freedom
## Residual deviance: 728.04  on 597  degrees of freedom
## AIC: 734.04
##
## Number of Fisher Scoring iterations: 4
```

## Model Evaluation:

### Model Fitting and Predicting

#### Evaluating: AUC (Area Under the Curve)

```
## Setting levels: control = False, case = True

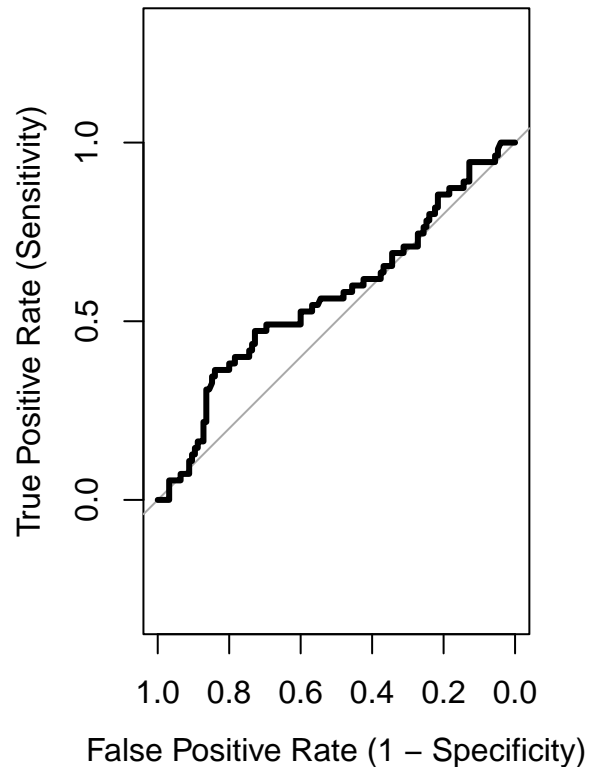
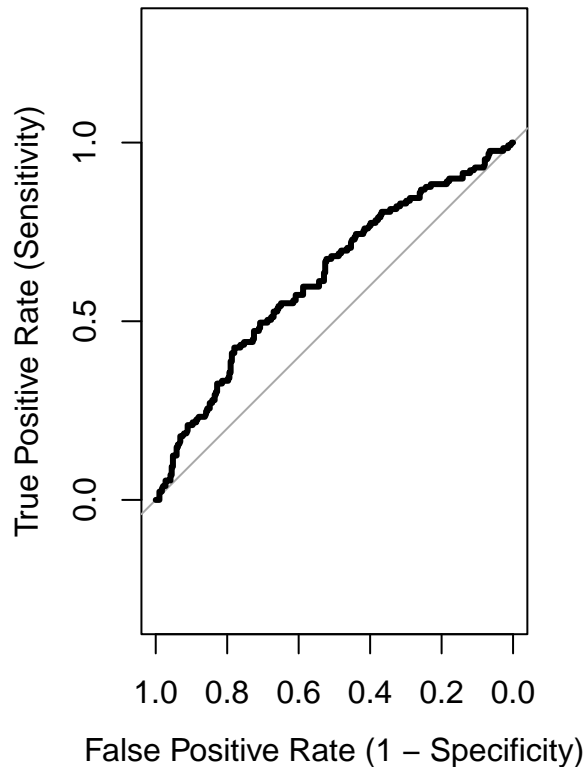
## Setting direction: controls < cases

## AUC (Area Under the Curve, Train Set): 0.6229
```

```
## Setting levels: control = False, case = True
## Setting direction: controls < cases
```

```
## AUC (Area Under the Curve): 0.5685
```

## OC Curve for Training Set (Oversamurve for BCR Prediction Model (Ove



## Confusion Matrix (Threshold 0.5)

```
test_predictions <- ifelse(test_probabilities > 0.5, "True", "False")
conf_matrix <- table(Predicted = test_predictions, Actual = test_set$BCR)
conf_matrix <- conf_matrix[, c("False", "True")]

cat("Confusion Matrix (Threshold 0.5):\n")
```

```
## Confusion Matrix (Threshold 0.5):
```

```
print(conf_matrix)
```

```
##           Actual
## Predicted False True
##      False    72   26
##      True     53   29
```

```
accuracy <- sum(diag(conf_matrix)) / sum(conf_matrix)
sensitivity <- conf_matrix["True", "True"] / sum(conf_matrix[, "True"])
specificity <- conf_matrix["False", "False"] / sum(conf_matrix[, "False"])

cat(sprintf("    Accuracy: %.4f\n", accuracy))
```

```
##    Accuracy: 0.5611
```

```
cat(sprintf("    Sensitivity: %.4f\n", sensitivity))
```

```
##    Sensitivity: 0.5273
```

```
cat(sprintf("    Specificity: %.4f\n", specificity))
```

```
##    Specificity: 0.5760
```