

Treatment Effectiveness in Patients with Prostate Cancer

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Abstract

This project aims to analyze which treatment option for prostate cancer leads to the highest recovery rate among patients. Prostate cancer is one of the most common cancers among men and is ranked as the "second most frequently diagnosed cancer" (Rawla, 2019). It also remains the "fifth leading cause of death worldwide" (Rawla, 2019), making the identification of the most effective treatment essential. As research in cancer therapy continues to expand, it is imperative to compare the overall effectiveness of different treatment methods, including hormonal therapy, radiation therapy, surgery, and combination therapies, to determine whether a single or combined approach yields better recovery outcomes. This study will evaluate tumor size, initial PSA levels, and biopsy Gleason scores over a one-year period to compare patient recovery and cancer recurrence. Statistical analyses will identify patterns of effectiveness among various treatments and determine which method best improves survival rates while reducing recurrence. It is hypothesized that combination treatments will decrease survival and decrease recurrence, whereas single therapies may yield higher recurrence rates but increased survival rates. By analyzing these relationships, this project seeks to highlight how treatment choice influences recovery rates, recurrence, and long-term survival outcomes for prostate cancer patients.

1) Introduction:

The primary purpose of this analysis is to compare and quantify the long-term differential effectiveness of major treatment modalities for prostate cancer—specifically surgery, radiotherapy, hormonal therapy, and a combination of hormonal therapy with radiotherapy. The goal is to apply meticulous statistical methods and rigorous data analysis to determine which specific treatment provides the best outcomes for patient survival and recovery, as well as whether combining therapies is more effective than single-treatment approaches. This study directly addresses the central research question: "What is the differential effectiveness of primary treatment modalities on clinical survival rates and biochemical recurrence outcomes for prostate cancer patients after controlling for prognostic factors?" The analysis is designed to benefit patients by identifying treatments with the most durable effectiveness, while also assisting families and clinicians in making informed decisions based on reliable statistical evidence. By providing outcome-based comparisons, this research aims to guide more personalized treatment strategies tailored to each patient's risk profile and cancer stage. Patient-specific factors, including initial cancer stage (severity and aggressiveness), overall health status, tumor size, initial PSA levels, and biopsy Gleason scores, will be considered. A multivariable regression model will be employed to isolate the effectiveness of treatment type while controlling for these prognostic factors to test the hypothesis that significant differences exist in long-term outcomes among first-line treatments..

2) Data:

The data used for this analysis were retrieved from the Zenodo repository, a well-known open-access repository mainly used by science communities. A dataset we're using, titled "Comprehensive Clinical, Pathological and Follow-up Dataset of Prostate Cancer Patients," was collected and published by Mert Başaranoglu at

Mersin Üniversitesi Hastanesi (Mersin University Hospital) in southern Turkey. It contains detailed information on factors related to Prostate Cancer, including 30 variables spanning four broader categories: Clinical Parameters, Treatment Information, Pathological Outcomes, and Follow-up Data.

2-1) Dataset Variables:

Table 1: Initial Diagnosis Variables

Variable_Name	English_Translation	Type_of_Data
Hasta_ID	Patient ID	Categorical
Yas	Age	Discrete
Tani_Tarihi	Diagnosis Date	Date
PSA_Tani	Serum Prostate-Specific Antigen (PSA) level at diagnosis (ng/mL)	Continuous
Klinik_Evre	Clinical cT-Stage determined by pre-treatment examinations (cT1c < cT2a < cT2b < cT2c < cT3a < cT3b for increasing extent of tumor invasion)	Ordinal/Categorical
Biyopsi_Gleason	Biopsy Gleason Score (3+3 < 3+4 < 4+3 < 3+5 < 4+4 < 4+5 < 5+4 < 5+5, higher score indicates higher aggressiveness)	Ordinal/Categorical
Risk_Grubu	Risk Group Classification (1 for Low, 2 for Intermediate, 3 for High)	Ordinal/Categorical

Table 2: Risk Factors

Variable	In_English	Type_of_Data
Albumin	ASerum albumin level (g/dL). Indicator of nutritional status and systemic health	Continuous
Lenfosit	Lymphocyte (Immune system component) Count	Discrete
CRP	C-Reactive Protein (mg/L). Indicator of inflammation	Continuous
NLR	Neutrophil-to-Lymphocyte Ratio. A prognostic indicator for systemic inflammation and cancer aggressiveness.	Continuous
CALLY_Index	CALLY Index. A composite index, likely related to inflammation or blood components.	Continuous
Komorbidite_Skor	Comorbidity Score indicating the severity of other co-existing chronic diseases (0 (No comorbidities) < ... < 5 (Severe comorbidities))	Ordinal/Categorical

Treatment Information

Table 3: Treatment Information

Variable	In_English	Type_of_Data
Tedavi_Tipi	Main Treatment Type received (1 for Radical Prostatectomy, 2 for Radiotherapy/RT, 3 for Hormone Therapy, 4 for Combination of Radiotherapy and Hormone Therapy)	Categorical
Tedavi_Tarihi	Treatment Date	Date
RT_Doza	Total Radiation Dose (in Gy), if radiotherapy was performed	Continuous
ADT_Tipi	Androgen Deprivation Therapy (ADT, hormone therapy) Type used	Categorical
ADT_Suresi	ADT(hormone therapy) Duration	Continuous

Table 4: Pathological Markers

Variable	In_English	Type_of_Data
Patolojik_Evre	Final Tumor Pathological Stage determined after surgery on the removed tissue (pT2a < pT2b < pT2c < pT3a < pT3b < pT4, NaN indicates patient did not undergo surgery)	Ordinal/Categorical
Cerrahi_Sinir	Surgical Margin Status indicating if cancer cells were present at the edge of the removed tissue. Crucial for recurrence prediction (0: Negative, 1: Positive, NaN indicates patient did not undergo surgery).	Binary/Categorical
Final_Gleason	Final Gleason Score confirmed from the final excised tissue (3+3 < 3+4 < 4+3 < 3+5 < 4+4 < 4+5 < 5+4 < 5+5, higher score indicates higher aggressiveness)	Ordinal/Categorical

Table 5: Follow-up & Outcomes

Variable	In_English	Type_of_Data
PSA_Nadir	The lowest PSA level reached after treatment (ng/mL). A lower nadir generally indicates better treatment success	Continuous
PSA_Takip_3ay / 6ay / 12ay	Follow-up PSA levels (ng/mL) measured at 3/6/12 Months	Continuous
BCR_Durum	Biochemical Recurrence (BCR) Status whether the PSA level rise above a recurrence threshold? (True for Recurrence occurred, False for no Recurrence occurred)	Binary/Categorical

BCR_Tarihi	Date when biochemical recurrence was confirmed	Date
Metastaz_Durum	Metastasis Status whether distant metastasis occur during follow-up? (0 for No, 1 for Yes)	Binary/Categorical
Metastaz_Tarihi	Date when metastasis was confirmed	Date
Son_Durum	Patient's Survival Status at the last follow-up (0 for Alive, 1 for Deceased)	Binary/Categorical
Son_Takip_Tarihi	Date of the last recorded patient information.	Date

2-2) Data Cleaning

To make data sets more consistent, we then decided to delete unnecessary information by removing the corresponding columns. Afterward, converting all categorical variables into factor type was required to ensure that our program, R(Studio), correctly interprets them as discrete categories rather than as continuous values or even strings. Moreover, this foreign data set has named its critical variables in another language that we need to rename in English. Lastly, addressing missing variables and visualizing were involved in each of them in various forms. These process allow us to observe that missing values were only found for the Hormone Type (ADT_Tipi) variable in patients who did not receive Hormone Therapy (as it is not applicable). Also, information is only present for the specific treatment a patient received (e.g., Radiation Dose is missing for surgery patients and vise versa).

3) Visualization:

We use preliminary visualizations and numerical summaries in order to prepare and interpreting the two multivariate logistic regression models and one linear regression, as this step is essential for diagnosing data quality, identifying confounding factors, and assessing the signal strength before the formal statistical analysis begins. We've established a few bar graphs on the frequency of treatment type, frequency of biochemical recurrence status, survival status, and risk factors. The box plots on PSA level at diagnosis and after treatment will be used to directly confound our numerical data among different treatment groups, as well as interpreting information from risk factors through our numerical summary.

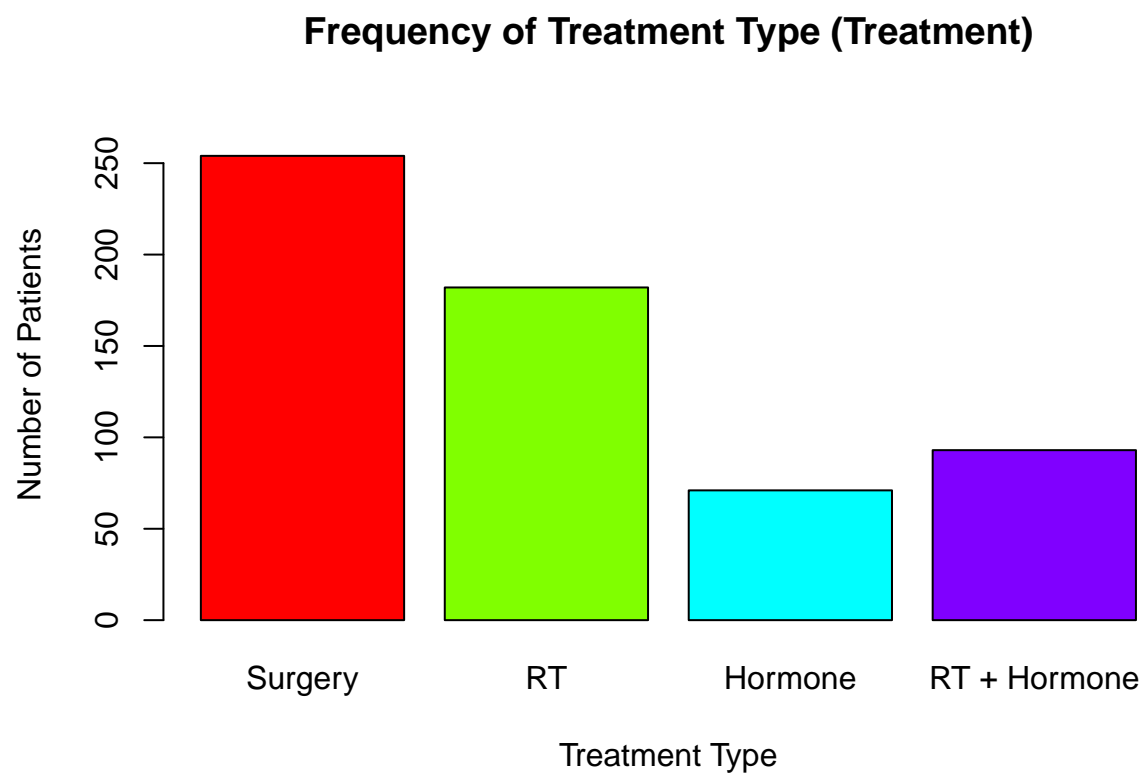


Figure 1: Illustration of distribution of the four main treatment groups across the patient cohort.

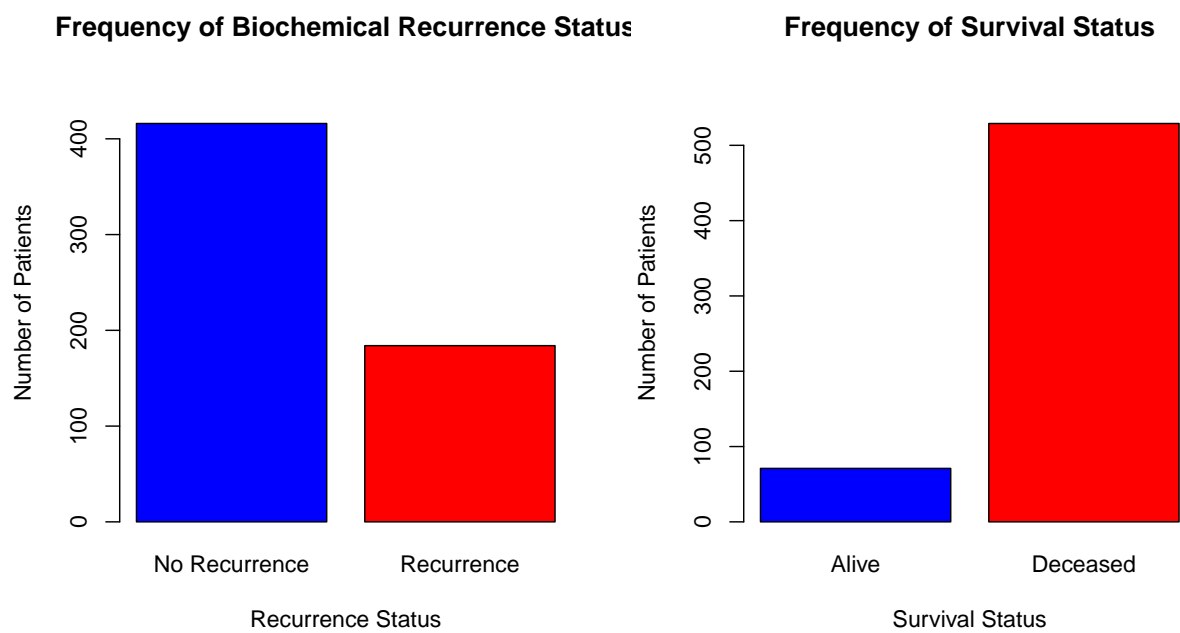


Figure 2: Side-by-side bar plots for Biochemical Recurrence (BCR) and Survival Status to display the main outcomes.

As shown in Figure 2, the data exhibit a low overall recurrence rate of Biochemical Recurrence (BCR), with the majority of patients (69.3%) successfully avoiding recurrence, which is represented as 'False'. However, the surprising and ironic cohort is Survival Status, where 0 = Alive and 1 = Deceased, showing that the survival rate is significantly low, with only 11.8% alive.

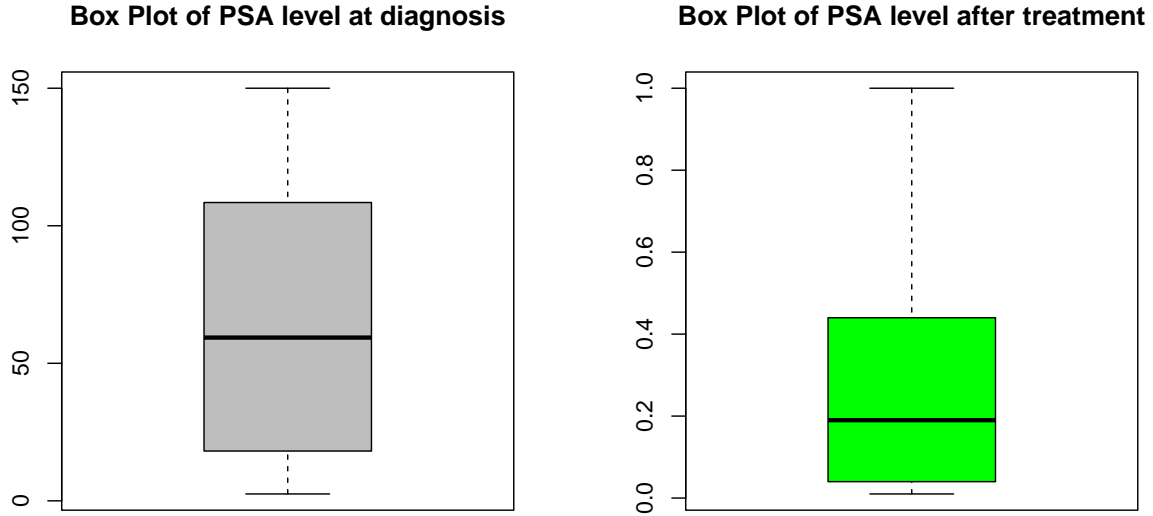


Figure 3: Comparison of PSA level before and after treatment on Diagnosis

Figure 3 displays the distributions and central tendencies of Prostate-Specific Antigen (PSA) levels at the time of diagnosis and after primary treatment. The box plots and numerical summaries illustrate a significant and positive effect of the treatment modalities on reducing PSA levels in the cohort. Before treatment (PSA_before), the median PSA level was 59.35 ng/mL, with values ranging up to 150.00 ng/mL. Following treatment (PSA_after), the median level dropped dramatically to just 0.1900 ng/mL, with most values lying significantly below the pre-treatment range. This substantial decrease in both the median and quartiles (as evidenced by the significant drop from the 1st Quartile of 18.10 to 0.0400 indicates that the treatments were immediately successful in reducing the primary tumor burden and systemic PSA activity in the majority of patients. This observation aligns with clinical expectations, in which successful treatment should drive PSA levels to near-undetectable levels (nadir).

4) Analysis aims:

PART A) TEST

4-1) Chi-squared Test on Treatment vs. BCR

A Chi-squared test was performed to examine the association between Biochemical Recurrence (BCR) and treatment type.

- Null Hypothesis (H0): Treatment Type and Biochemical Recurrence (BCR) Status are independent (The recurrence rate is the same across all treatment groups.)
- Alternative Hypothesis (Ha): Treatment Type and Biochemical Recurrence (BCR) Status are not independent (The recurrence rate is significantly different for at least one treatment group.)

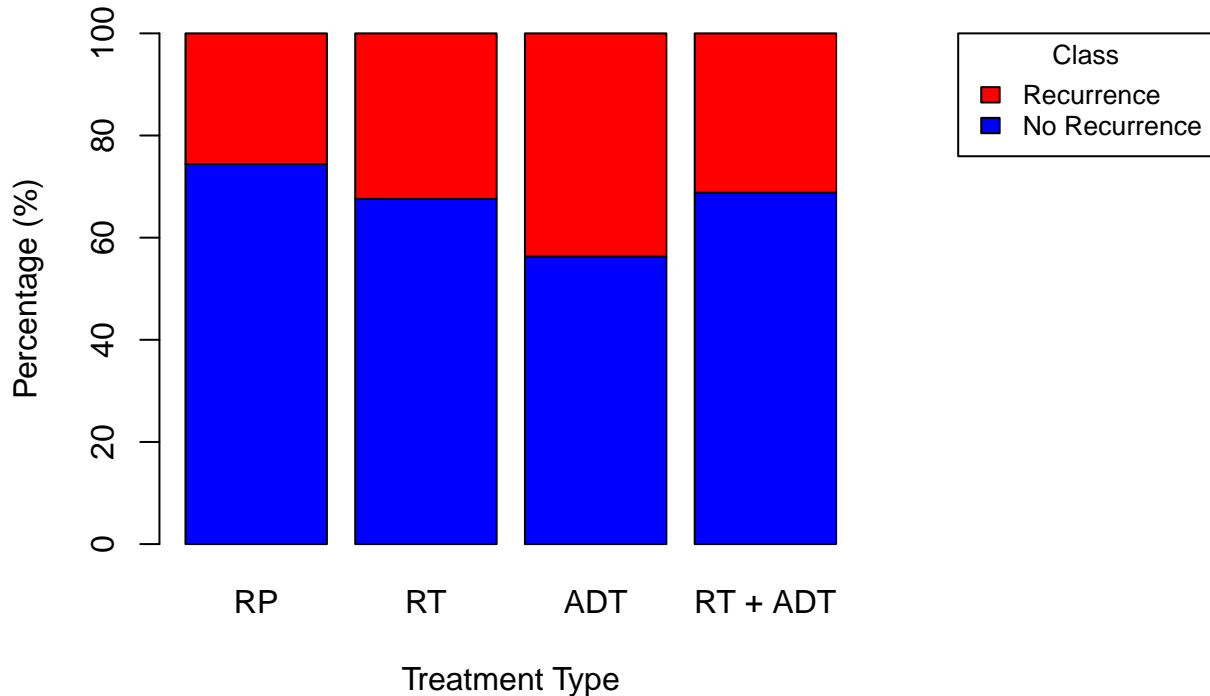
Table 6: 4.1 Association between Treatment Type and Biochemical Recurrence (BCR)

	Treatment Type	Recurrence Count (False)	Recurrence Count (True)	No Recurrence (%) (False)	Recurrence (%) (True)
Radical Prostatectomy	Radical Prostatectomy	189	65	74.4	25.6
Radiotherapy (RT)	Radiotherapy (RT)	123	59	67.6	32.4
Hormone Monotherapy	Hormone Monotherapy	40	31	56.3	43.7
Combination (RT + Hormone)	Combination (RT + Hormone)	64	29	68.8	31.2

Chi-squared = 8.9915, df = 3, p-value = 0.0294

The Chi-squared test yielded a test statistic of $\chi^2 = 8.9915$ with a corresponding p-value of 0.0294. Since the p-value is less than the significance level ($\alpha = 0.05$), we reject the null hypothesis. There is a statistically significant association between the type of treatment a patient receives and the likelihood of experiencing Biochemical Recurrence (BCR).

Biochemical Recurrence (BCR) Rate by Treatment Type



Hormone Monotherapy had the highest recurrence rate at 43.7%, while Radical Prostatectomy had the lowest at 25.6%. The bar plot visually confirms this, with the red recurrence portion for Hormone Monotherapy (ADT) notably larger and the recurrence portion for Radical Prostatectomy (RP) noticeably smaller compared to other treatment methods.

4-2) Chi-squared Test on Treatment vs. Survival

A Chi-squared test was performed to examine the association between Biochemical Recurrence (BCR) and treatment type.

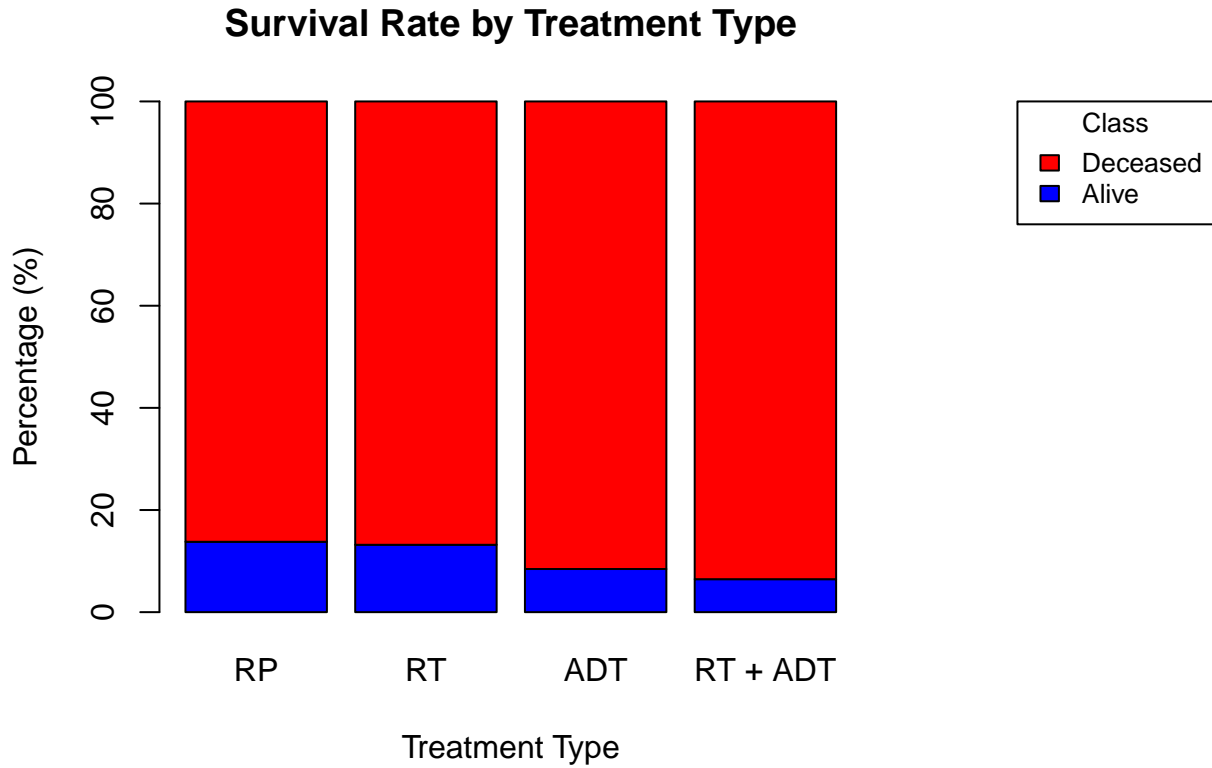
- Null Hypothesis (H_0): Treatment Type and Biochemical Recurrence (BCR) Status are independent (The survival rate is the same across all treatment groups.)
- Alternative Hypothesis (H_a): Treatment Type and Biochemical Recurrence (BCR) Status are not independent (The survival rate is significantly different for at least one treatment group.)

Table 7: Table 4.2: Association between Treatment Type and Survival Status

	Treatment Type	Count (Alive)	Count (Deceased)	Survival (%)	Mortality (%)
Radical Prostatectomy	Radical Prostatectomy	35	219	13.8	86.2
Radiotherapy (RT)	Radiotherapy (RT)	24	158	13.2	86.8
Hormone Monotherapy	Hormone Monotherapy	6	65	8.5	91.5
Combination (RT + Hormone)	Combination (RT + Hormone)	6	87	6.5	93.5

Chi-squared = 4.6021, df = 3, p-value = 0.2034

The Chi-squared test yielded a test statistic of $\chi^2 = 4.6021$ with a corresponding p-value of 0.2034. Since the p-value is greater than the significance level ($\alpha = 0.05$), we fail to reject the null hypothesis (H_0). Therefore, we can conclude that there is no statistically significant association between the type of treatment a patient receives and the likelihood of their Survival Status (Alive vs. Deceased). The bar plot also supports this conclusion, showing that the distribution of survival rates is not substantially different across the four treatment types.



The bar plot also supports this conclusion, showing that the survival rate distribution is not substantially different across the four treatment types.

4-3) ANOVA Test, Treatment vs PSA Difference

An ANOVA was conducted to compare mean PSA at diagnosis (PSA_before) across the four Treatment Type groups.

- Null Hypothesis (H_0): PSA at diagnosis is the same across all four Treatment Type groups
- Alternative Hypothesis (H_a): Alternative Hypothesis (H_1) PSA at diagnosis is significantly different for at least one treatment group

Table 8: Table 4.5: Tukey's HSD Post-Hoc Test for Delta PSA

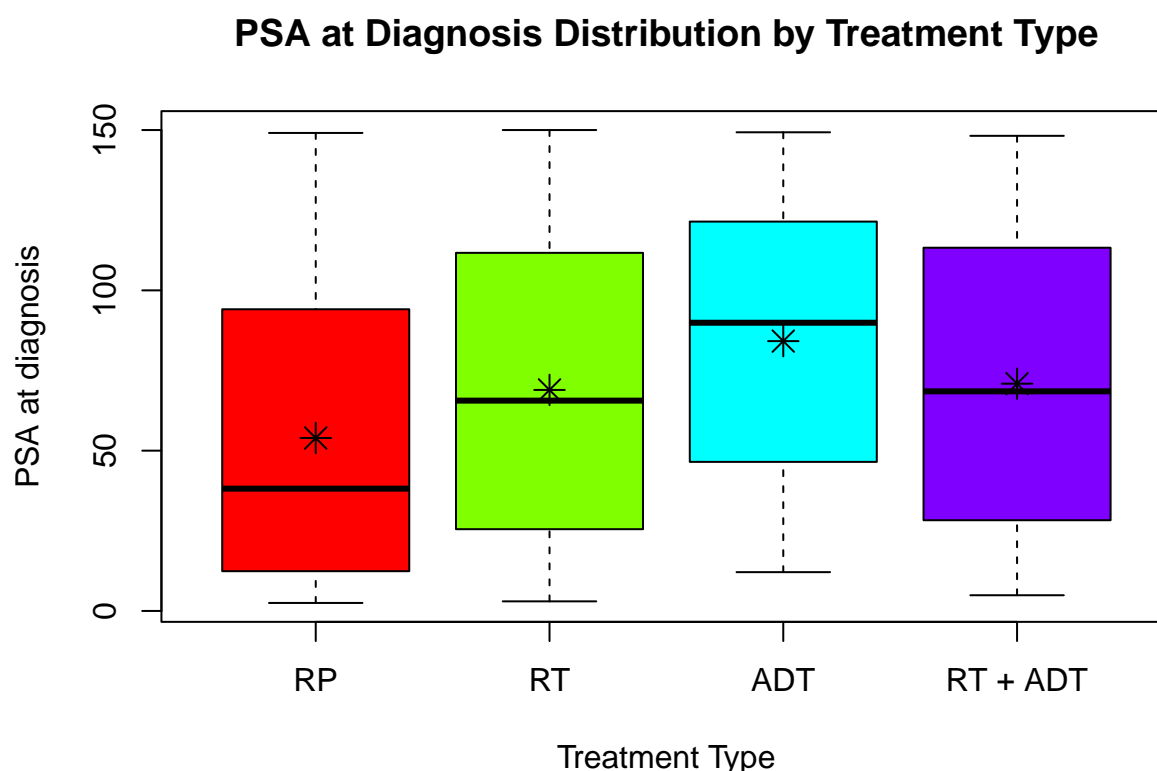
Group 1	Group 2	Mean Diff.	p-value	Sig. (p < 0.05)
Radical Prostatectomy	Radiotherapy (RT)	14.598	0.0056	Yes
Radical Prostatectomy	Hormone Monotherapy	29.754	0.0000	Yes
Radical Prostatectomy	Combination (RT + Hormone)	16.523	0.0151	Yes
Radiotherapy (RT)	Hormone Monotherapy	15.157	0.0821	No
Radiotherapy (RT)	Combination (RT + Hormone)	1.925	0.9874	No

Hormone Monotherapy	Combination (RT + Hormone)	-13.232	0.2536	No
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The ANOVA test yielded a p-value of 1.6e-6 (0.0000016). Since the p-value is much less than the significance level ($\alpha = 0.05$), we reject the null hypothesis (H_0). Thus, there is a statistically significant difference in the mean PSA at diagnosis (PSA_before) among the different treatment groups.

Since the ANOVA test confirmed a significant difference, a Tukey HSD post hoc test was performed to identify which specific pairs of groups differ significantly.

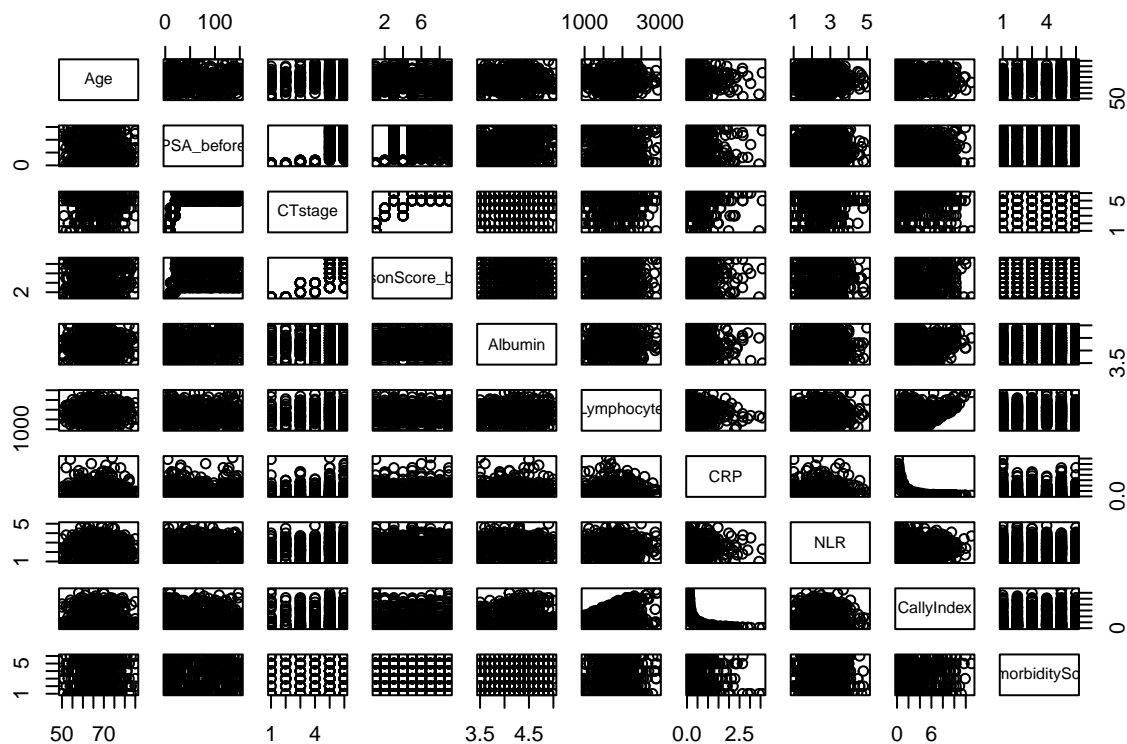
The mean PSA at diagnosis for the Radical Prostatectomy (Treatment 1) group is significantly lower than that for all other treatment groups (Treatment 2, 3, and 4). There is no significant difference in the mean PSA at diagnosis among the three non-surgical groups (Treatment 2, 3, and 4) in their pairwise comparisons. The comparison between Hormone Therapy Monotherapy (Treatment 3) and Radical Prostatectomy (Treatment 1) showed the most considerable mean difference ($\text{diff} = 30.21$). This indicates that the Treatment 3 group had the highest average PSA at diagnosis, whereas the Treatment 1 group had the lowest.



The box plot visually confirms these findings: the PSA distribution for the Radical Prostatectomy (RP) group is noticeably lower than that of all other groups, and its mean value (often marked by a symbol) is the lowest. Conversely, the distribution and mean value for the Hormone Monotherapy (ADT) group are distinctly higher than those for the RP group, visually confirming that patients selected for RP had the lowest initial PSA levels at diagnosis.

PART B) MODELING

Data Analysis 0: Correlation between Variables



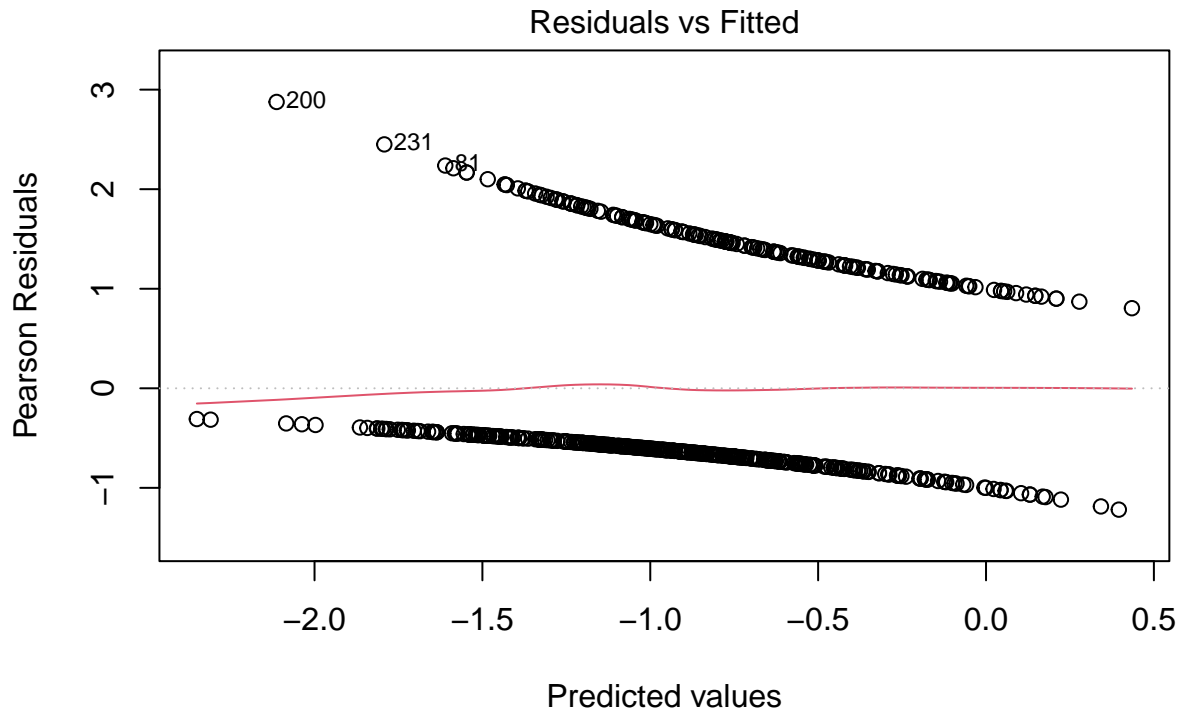
Data Analysis 1: Logistic Regression (BCR)

```
##
## 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 *
## CTstagecT2a    2.026e-01  6.178e-01   0.328   0.7430
## CTstagecT2b    3.239e-01  6.244e-01   0.519   0.6040
## CTstagecT2c   -2.387e-01  5.881e-01  -0.406   0.6848
## CTstagecT3a    9.524e-02  5.697e-01   0.167   0.8672
## CTstagecT3b   -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
```

```

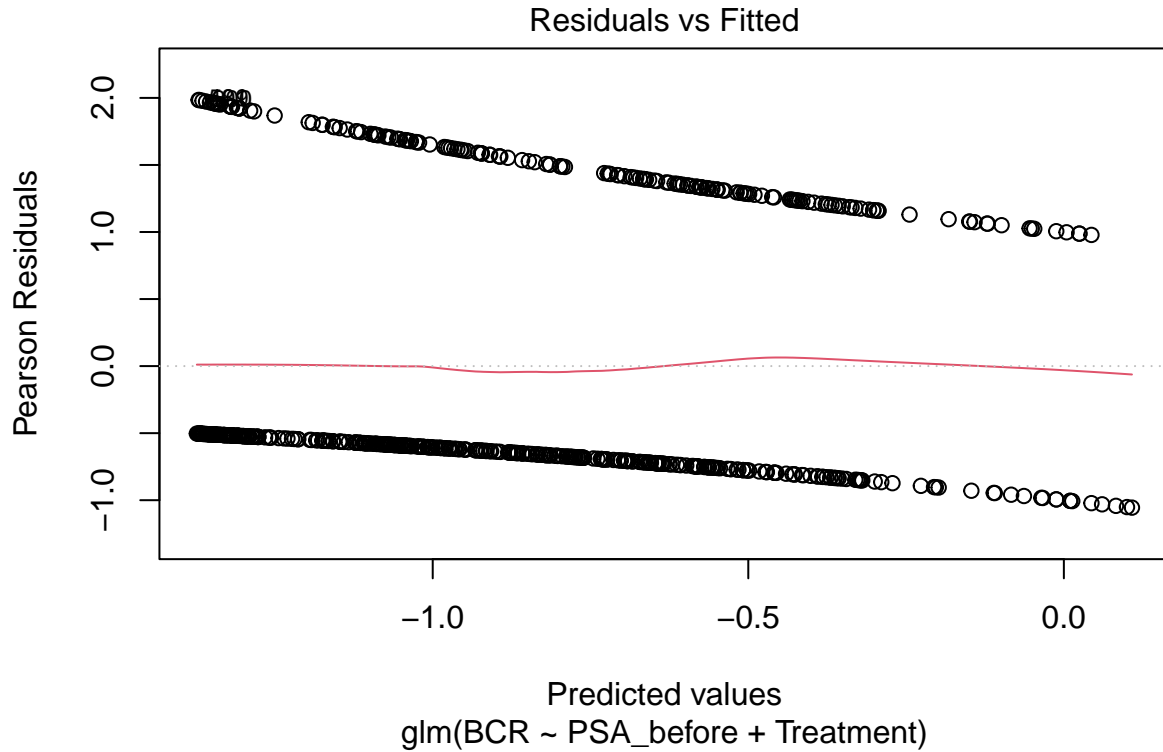
## GleasonScore_before4+4 -2.344e-01 3.614e-01 -0.648 0.5167
## GleasonScore_before4+5 -6.841e-02 3.788e-01 -0.181 0.8567
## GleasonScore_before5+3 2.789e-01 3.626e-01 0.769 0.4417
## GleasonScore_before5+4 9.191e-02 3.656e-01 0.251 0.8015
## GleasonScore_before5+5 NA NA NA NA
## Albumin 2.257e-01 2.477e-01 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

```



glm(BCR ~ Age + PSA_before + CTstage + GleasonScore_before + Albumin + Lymph

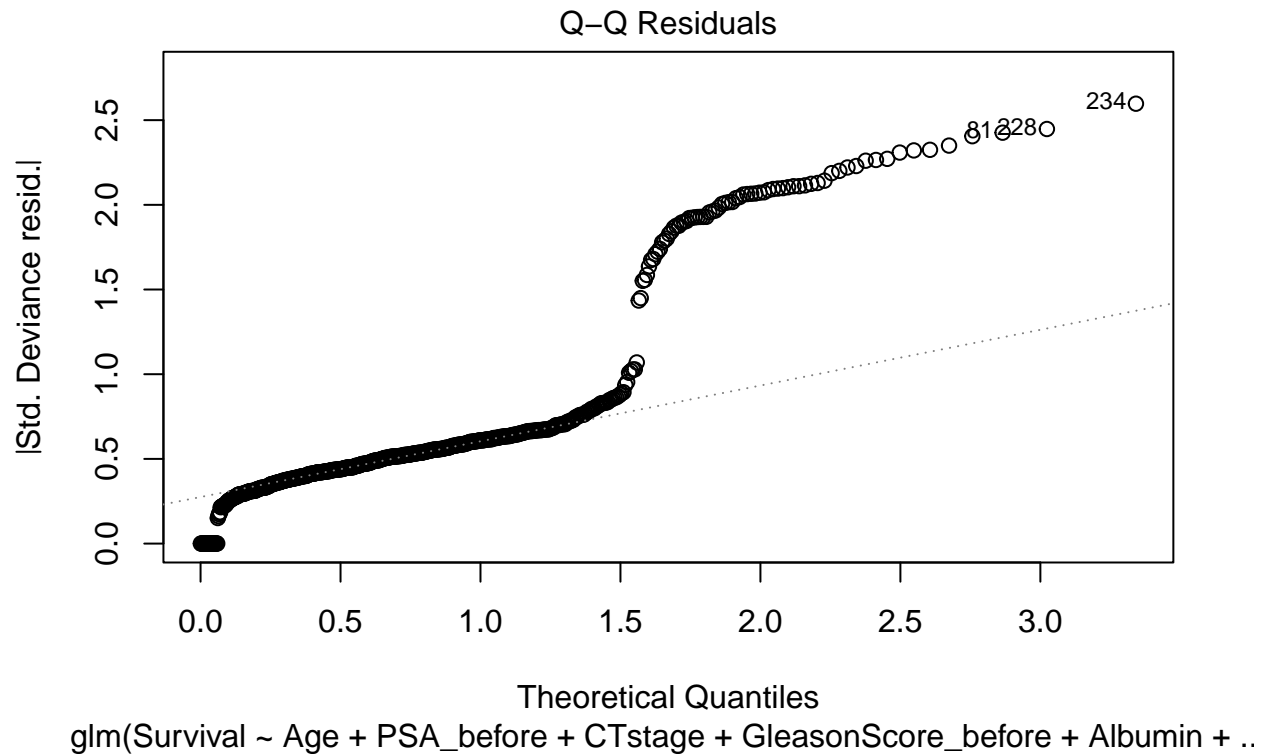
```
##
## Call:
## glm(formula = BCR ~ PSA_before + Treatment, family = binomial,
##      data = data, na.action = na.omit)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -1.387813   0.186466  -7.443 9.86e-14 ***
## PSA_before   0.005629   0.001964   2.867  0.00415 **
## 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
```



Data Analysis 2: Logistic Regression (Survival)

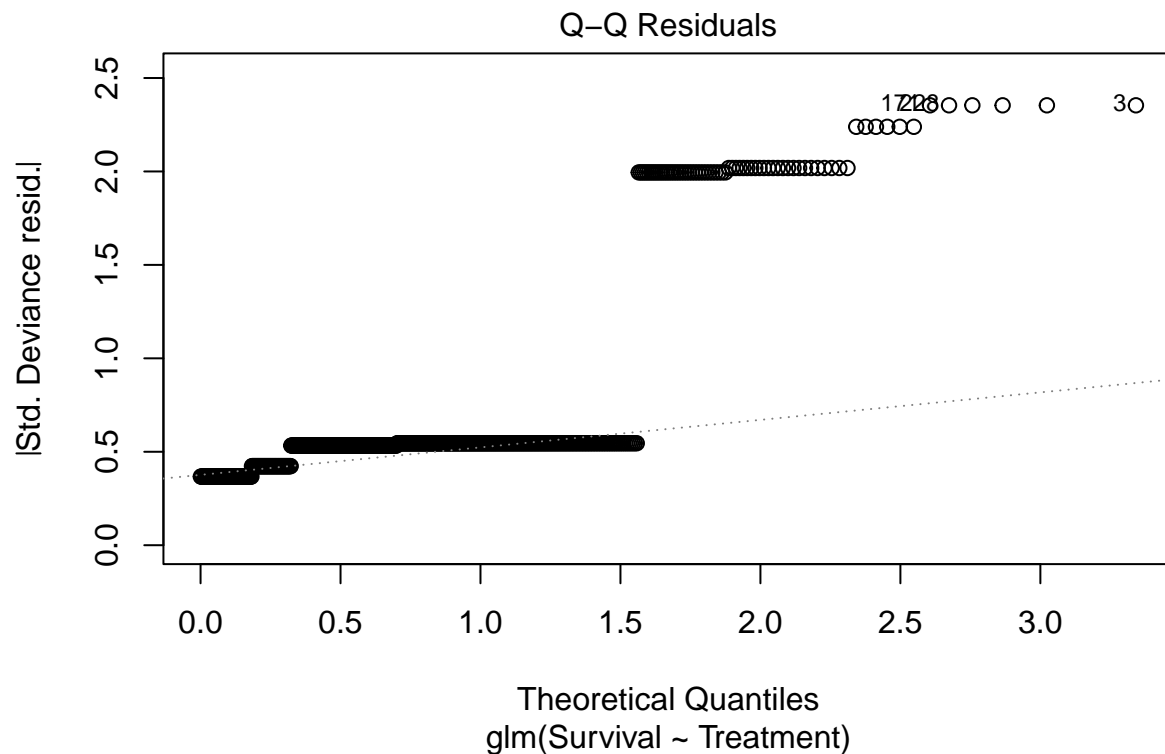
```
##
## Call:
## glm(formula = Survival ~ Age + PSA_before + CTstage + GleasonScore_before +
##       Albumin + Lymphocyte + CRP + NLR + CallyIndex + ComorbidityScore +
##       Treatment, family = binomial, data = data, na.action = na.omit)
##
## Coefficients: (2 not defined because of singularities)
##              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
## CTstagecT2a     1.501e+01  7.183e+02   0.021  0.9833
## CTstagecT2b    -5.715e-01  9.402e-01  -0.608  0.5433
## CTstagecT2c    -6.360e-01  8.983e-01  -0.708  0.4790
## CTstagecT3a    -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
```



```
##
```

```
## 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
```



Model Interpretation 1: Logistic Regression (BCR ~ Treatment)

```
##
## 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)

```
##
## 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): 0.5685

Confusion Matrix (Threshold 0.5)

Confusion Matrix (Threshold 0.5):

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

Accuracy: 0.5611

Sensitivity: 0.5273

Specificity: 0.5760

5) Conclusion:

Work Cited (Used in Abstract)

Rawla P. (2019). Epidemiology of Prostate Cancer. World journal of oncology, 10(2), 63–89. <https://doi.org/10.14740/wjon1191>