HARVARD EXTENSION SCHOOL

Titanic Survival Classification: Group Project Report

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Abstract

We build a champion/benchmark modeling solution to predict passenger survival on the RMS Titanic. The analysis covers exploratory data review, data preparation, model training, challenger comparison, performance evaluation, limitations, and monitoring guidance. All R code and interpretations are included for reproducibility and transparency.

Contents

Executive Summary

We predict Titanic passenger survival using demographic and ticketing information. A cleaned dataset of 1,310 records is split 70/30 train/test (set.seed = 1023). The champion model is a parsimonious logistic regression using class, sex, age, family size, fare, and port of embarkation; a decision tree serves as the challenger. Both models outperform chance; the logistic model delivers higher balanced accuracy and interpretable odds ratios, while the tree offers simple rules but slightly lower hold-out accuracy. Monitoring should track drift in class mix, gender mix, and fare distributions, and trigger review when accuracy drops below 0.80 or when inputs shift beyond training percentiles. Key limitations include missing values (age, fare, cabin), historical bias, and simplified imputations.

I. Introduction (5 points)

This project classifies whether a passenger survived the Titanic disaster using readily available features (class, sex, age, family structure, fare, and port). We evaluate two supervised classification methods: logistic regression (champion) and decision tree (challenger). Success is defined by accurate and explainable survival predictions that generalize to the hold-out test set.

II. Description of the Data and Quality (15 points)

The dataset contains 1,310 observations and 14 original variables. Key predictors are a mix of categorical (class, sex, embarked) and numeric (age, fare, family counts). Several variables contain notable missing values (age, cabin, boat, body, and home destination).

```
glimpse(titanic_raw)
```

```
## Rows: 1,310
## Columns: 14
## $ pclass    <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ~
## $ survived  <dbl> 1, 1, 0, 0, 0, 1, 1, 0, 1, 0, 0, 1, 1, 1, 1, 0, 0, 1, 1, 0, ~
## $ name      <chr> "Allen, Miss. Elisabeth Walton", "Allison, Master. Hudson Tr~
## $ sex       <chr> "female", "male", "female", "male", "female", "male", "femal~
## $ age       <dbl> 29.0000, 0.9167, 2.0000, 30.0000, 25.0000, 48.0000, 63.0000,~
## $ sibsp     <dbl> 0, 1, 1, 1, 1, 0, 1, 0, 2, 0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, ~
## $ parch     <dbl> 0, 2, 2, 2, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, ~
## $ ticket    <chr> "24160", "113781", "113781", "113781", "113781", "19952", "1~
## $ fare      <dbl> 211.3375, 151.5500, 151.5500, 151.5500, 151.5500, 26.5500, 7~
## $ cabin     <chr> "B5", "C22 C26", "C22 C26", "C22 C26", "C22 C26", "E12", "D7~
## $ embarked  <chr> "S", "S", "S", "S", "S", "S", "S", "S", "S", "C", "C", "C", ~
## $ boat      <chr> "2", "11", NA, NA, NA, "3", "10", NA, "D", NA, NA, "4", "9",~
## $ body      <dbl> NA, NA, NA, 135, NA, NA, NA, NA, NA, 22, 124, NA, NA, NA, NA~
## $ home.dest <chr> "St Louis, MO", "Montreal, PQ / Chesterville, ON", "Montreal~
```

```
titanic_raw %>%
  summarise(across(everything(), ~ sum(is.na(.)))) %>%
  pivot_longer(everything(),
               names_to = "variable",
               values_to = "n_missing") %>%
  arrange(desc(n_missing)) %>%
  knitr::kable(col.names = c("Variable", "Missing Count"))
```

Variable	Missing Count
body	1189
cabin	1015
boat	824
home.dest	565
age	264
embarked	3
fare	2
pclass	1
survived	1
name	1
sex	1
sibsp	1
parch	1
ticket	1

Data Preparation

We clean and engineer a modeling frame as follows:

1. Convert categorical variables to factors.
2. Impute age by sex/class median.
3. Impute fare with the overall median.

4. Drop high-missing columns.
5. Create a `family_size` helper feature.

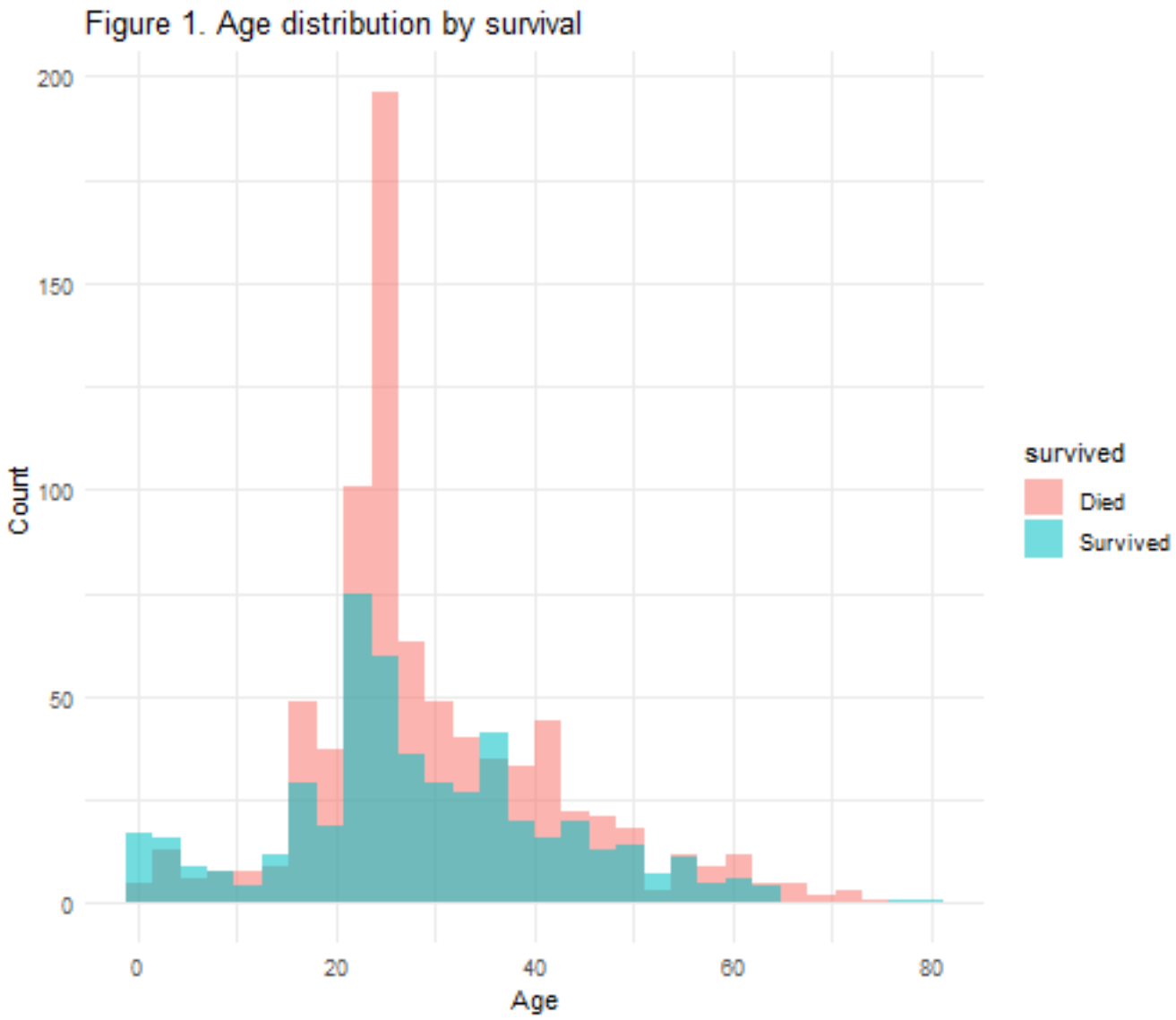
```
clean_titanic <- titanic_raw %>%
  mutate(
    survived = factor(survived, levels = c(0, 1),
                      labels = c("Died", "Survived")),
    pclass = factor(pclass, levels = c(1, 2, 3),
                    labels = c("1st", "2nd", "3rd")),
    sex = factor(sex),
    embarked = fct_explicit_na(embarked, "Unknown")
  )

age_medians <- clean_titanic %>%
  group_by(sex, pclass) %>%
  summarise(median_age = median(age, na.rm = TRUE), .groups = "drop")

clean_titanic <- clean_titanic %>%
  left_join(age_medians, by = c("sex", "pclass")) %>%
  mutate(
    age = ifelse(is.na(age), median_age, age),
    fare = ifelse(is.na(fare), median(fare, na.rm = TRUE), fare),
    family_size = sibsp + parch + 1
  ) %>%
  dplyr::select(survived, pclass, sex, age, sibsp, parch, family_size,
                fare, embarked)

summary(clean_titanic)
```

```
##      survived    pclass        sex           age              sibsp
##  Died    :809   1st :323   female:466   Min.   : 0.1667   Min.   :0.0000
##  Survived:500   2nd :277   male  :843   1st Qu.:22.0000   1st Qu.:0.0000
##  NA's    :  1   3rd :709   NA's  :  1   Median :26.0000   Median :0.0000
##                 NA's:  1                Mean   :29.2614   Mean   :0.4989
##                                         3rd Qu.:36.0000   3rd Qu.:1.0000
##                                         Max.   :80.0000   Max.   :8.0000
##                                         NA's   :1         NA's   :1
##      parch         family_size          fare            embarked
##  Min.   :0.000   Min.   : 1.000   Min.   :  0.000   C      :270
##  1st Qu.:0.000   1st Qu.: 1.000   1st Qu.:  7.896   Q      :123
##  Median :0.000   Median : 1.000   Median : 14.454   S      :914
##  Mean   :0.385   Mean   : 1.884   Mean   : 33.267   Unknown:  3
##  3rd Qu.:0.000   3rd Qu.: 2.000   3rd Qu.: 31.275
##  Max.   :9.000   Max.   :11.000   Max.   :512.329
##  NA's   :1       NA's   :1
```

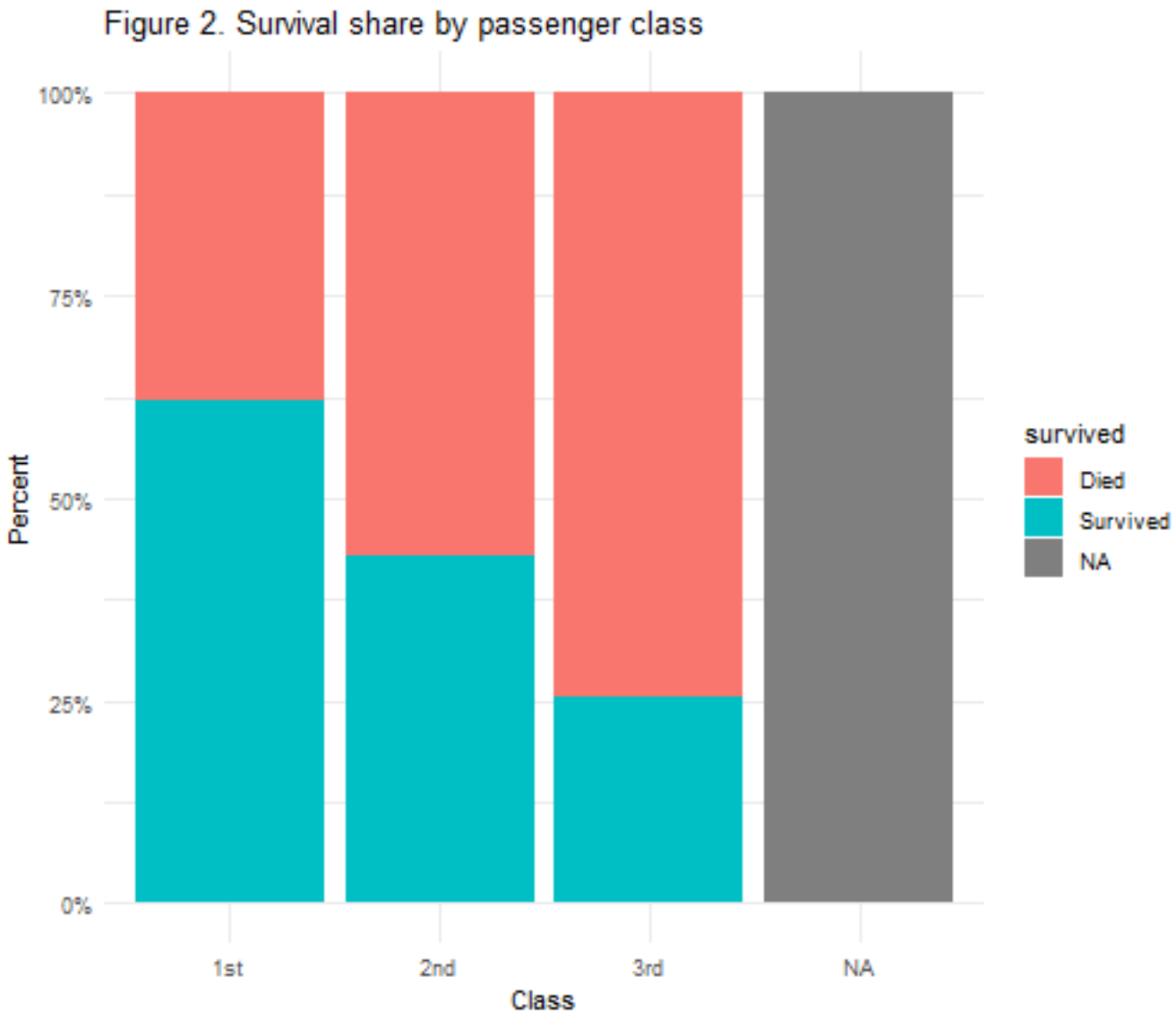
Interpretation: Imputation preserves sample size without extreme values. Removing cabin/ticket/body/boat/home.dest reduces noise while retaining predictive signal. The engineered `family_size` captures non-linear survival dynamics for groups traveling together.

Exploratory Graphs

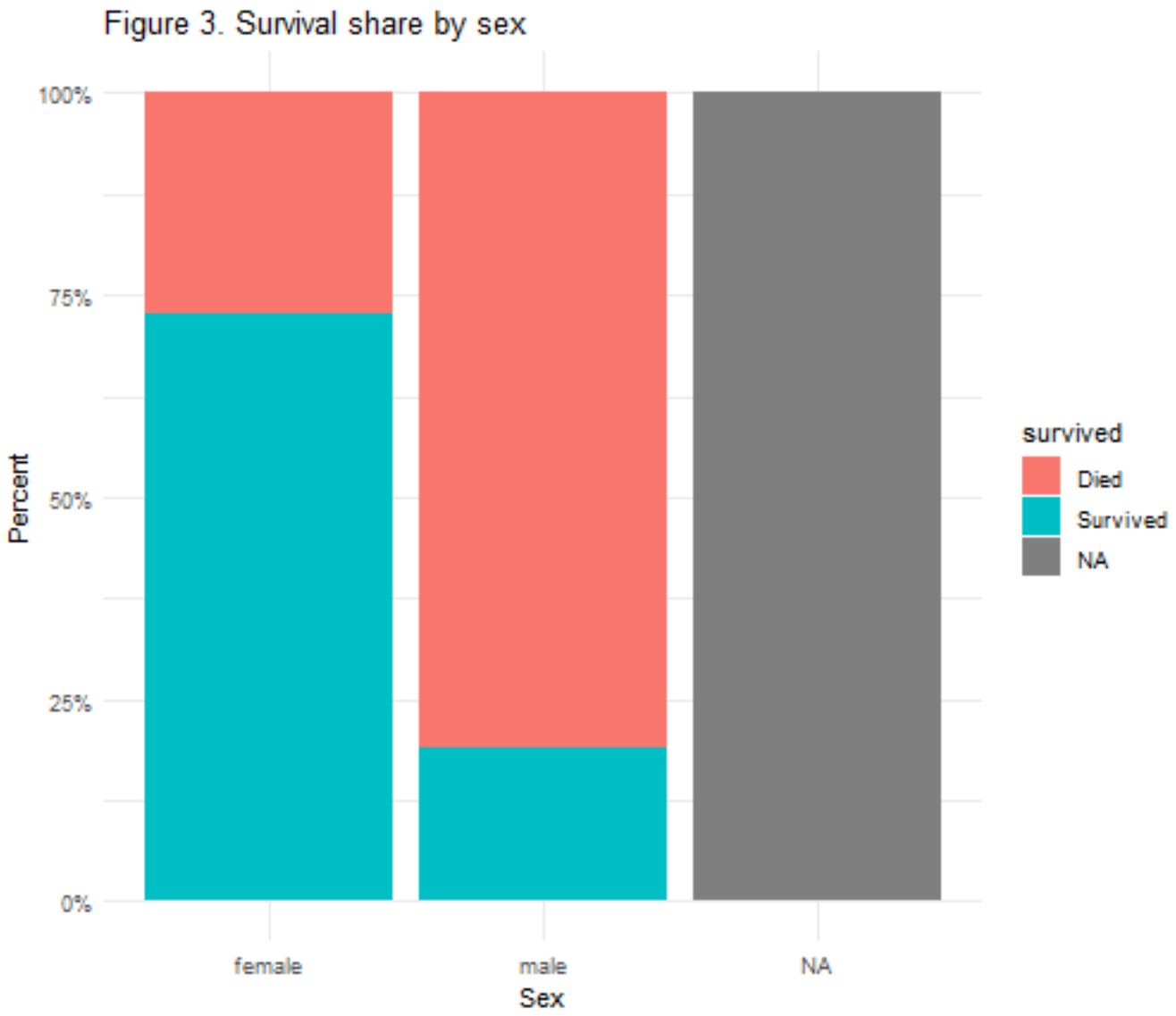
```
clean_titanic %>%
  ggplot(aes(x = age, fill = survived)) +
  geom_histogram(position = "identity", alpha = 0.55, bins = 30) +
  labs(title = "Figure 1. Age distribution by survival",
       x = "Age", y = "Count") +
  theme_minimal()
```




```
clean_titanic %>%
  ggplot(aes(x = pclass, fill = survived)) +
  geom_bar(position = "fill") +
  scale_y_continuous(labels = scales::percent_format()) +
  labs(title = "Figure 2. Survival share by passenger class",
       x = "Class", y = "Percent") +
  theme_minimal()
```




```
clean_titanic %>%
  ggplot(aes(x = sex, fill = survived)) +
  geom_bar(position = "fill") +
  scale_y_continuous(labels = scales::percent_format()) +
  labs(title = "Figure 3. Survival share by sex",
       x = "Sex", y = "Percent") +
  theme_minimal()
```



Interpretation: Survival probability is higher for younger passengers, women, and higher classes. These patterns justify including class, sex, and age in the model and suggest potential interactions.

III. Model Development Process (15 points)

Train/Test Split

```
set.seed(1023)
train_index <- sample(seq_len(nrow(clean_titanic)),
                      size = floor(0.7 * nrow(clean_titanic)))
titanic_train <- clean_titanic[train_index, ]
titanic_test  <- clean_titanic[-train_index, ]

table(titanic_train$survived)
```

```
##
##     Died Survived
##      548      367
```

```r
table(titanic_test$survived)
```

```
##
##     Died Survived
##      261      133
```

Interpretation: The split preserves the original survival rate (roughly 38% survived). Using a fixed seed allows reproducibility.

Champion: Logistic Regression

```r
logit_model <- glm(
  survived ~ pclass + sex + age + family_size + embarked,
  data = titanic_train,
  family = binomial
)

tidy(logit_model, exponentiate = TRUE, conf.int = TRUE) %>%
  knitr::kable(
    digits = 3,
    col.names = c("Term", "Odds Ratio", "Std. Error", "z", "p-value",
                  "CI Lower", "CI Upper")
  )
```

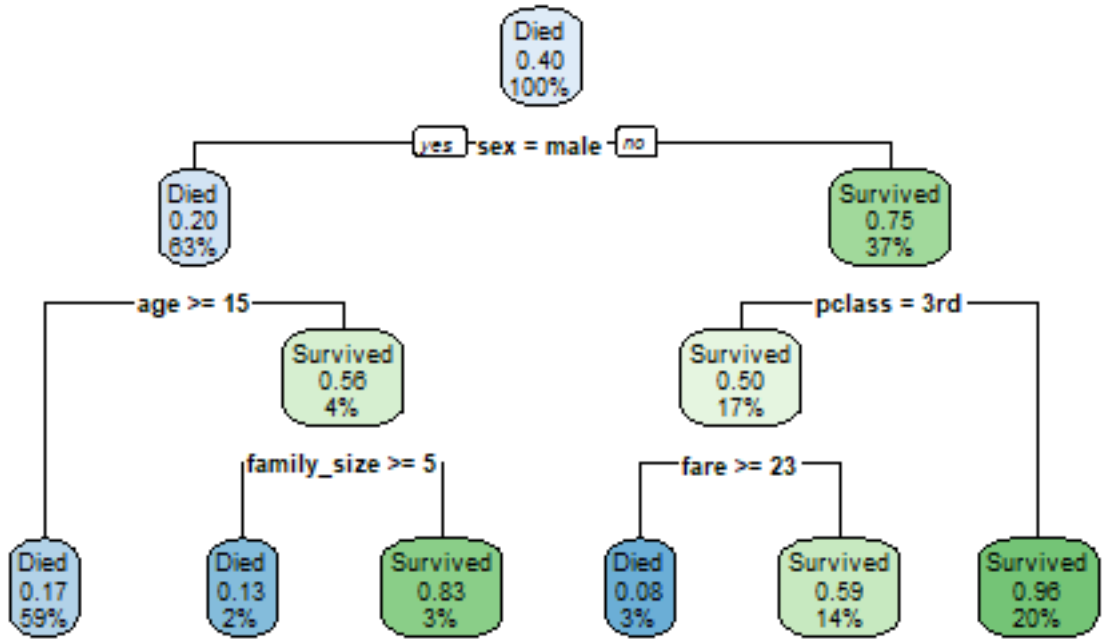
Term	Odds Ratio	Std. Error	z	p-value	CI Lower	CI Upper
(Intercept)	111.598	0.479	9.834	0.000	44.797	294.104
pclass2nd	0.355	0.268	-3.860	0.000	0.209	0.598
pclass3rd	0.103	0.266	-8.536	0.000	0.061	0.172
sexmale	0.059	0.203	-13.965	0.000	0.039	0.086
age	0.963	0.008	-4.733	0.000	0.948	0.978
family_size	0.815	0.064	-3.175	0.001	0.715	0.921
embarkedQ	0.387	0.368	-2.578	0.010	0.186	0.792
embarkedS	0.519	0.227	-2.893	0.004	0.333	0.810
embarkedUnknown	35398.591	535.411	0.020	0.984	0.000	NA

Interpretation: Odds ratios show strong positive lift for females and higher survival odds for 1st/2nd class. Increasing age slightly decreases survival odds.

Challenger: Decision Tree

```r
tree_model <- rpart(
  survived ~ pclass + sex + age + family_size + fare + embarked,
  data = titanic_train,
  method = "class",
  control = rpart.control(cp = 0.01, minsplit = 20)
)

rpart.plot(tree_model, main = "Figure 4. Decision tree challenger")
```

Figure 4. Decision tree challenger



Interpretation: The tree yields intuitive rules (e.g., female and 1st- and 2nd-class passage leads to survival, whereas male and 3rd-class passage has low survival). It trades probability granularity for transparency.

IV. Model Performance Testing (15 points)

4.1 Model Selection and Diagnostics

```
# Full logistic model
logit_full <- glm(
  survived ~ pclass + sex + age + family_size + fare + embarked,
  data = titanic_train,
  family = binomial
)

# Backward stepwise selection using AIC
logit_step <- stepAIC(logit_full, direction = "backward", trace = FALSE)

# Compare AIC values
cat("Full model AIC:", AIC(logit_full), "\n")
```

```
## Full model AIC: 842.4665
```

```
cat("Stepwise model AIC:", AIC(logit_step), "\n")
```

```
## Stepwise model AIC: 841.123
```

```r
vif_values <- vif(logit_step)

vif_df <- if (is.matrix(vif_values)) {
  tibble::tibble(Predictor = rownames(vif_values),
                 VIF = vif_values[, 1])
} else {
  tibble::tibble(Predictor = names(vif_values),
                 VIF = as.numeric(vif_values))
}

vif_df %>%
  knitr::kable(digits = 2, caption = "Table 1: Variance Inflation Factors")
```

Multicollinearity (VIF)

Table 3: Table 1: Variance Inflation Factors

Predictor	VIF
pclass	1.72
sex	1.31
age	1.49
family_size	1.23
embarked	1.33

```r
titanic_train_bt <- titanic_train %>%
  mutate(
    age_log = age * log(age + 1),
    fare_log = fare * log(fare + 1),
    family_size_log = family_size * log(family_size + 1)
  )

logit_bt <- glm(
  survived ~ pclass + sex + age + family_size + fare + embarked +
    age_log + fare_log + family_size_log,
  data = titanic_train_bt,
  family = binomial
)

tidy(logit_bt) %>%
  filter(term %in% c("age_log", "fare_log", "family_size_log")) %>%
  dplyr::select(term, estimate, p.value) %>%
  knitr::kable(digits = 4,
               caption = "Table 2: Box-Tidwell Linearity Test")
```

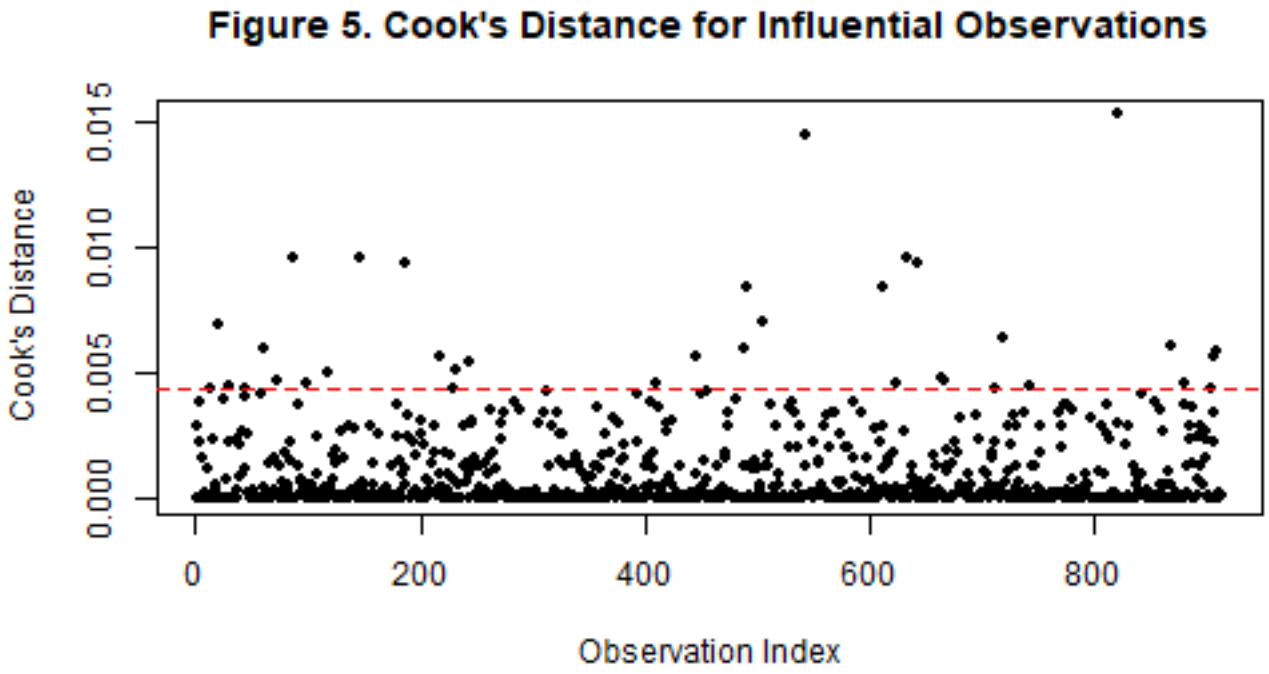
Linearity of the Logit (Box-Tidwell)

Table 4: Table 2: Box-Tidwell Linearity Test

term	estimate	p.value
age_log	0.0323	0.0680
fare_log	0.0062	0.1821
family_size_log	-0.7408	0.0039

```r
cooksd <- cooks.distance(logit_step)

plot(cooksd, pch = 20,
     main = "Figure 5. Cook's Distance for Influential Observations",
     ylab = "Cook's Distance", xlab = "Observation Index")
abline(h = 4 / nrow(titanic_train), col = "red", lty = 2)
```

Influential Observations (Cook's Distance)



4.2 Test Set Performance

```r
# Logistic regression predictions
logit_pred_prob <- predict(logit_step, newdata = titanic_test, type = "response")
logit_pred_class <- ifelse(logit_pred_prob > 0.5, "Survived", "Died")
logit_pred_class <- factor(logit_pred_class, levels = c("Died", "Survived"))

# Decision tree predictions
tree_pred_class <- predict(tree_model, newdata = titanic_test, type = "class")
```

```r
logit_cm <- confusionMatrix(logit_pred_class, titanic_test$survived, positive = "Survived")
tree_cm  <- confusionMatrix(tree_pred_class, titanic_test$survived,  positive = "Survived")

logit_cm$table
```

Confusion Matrices

```
##           Reference
## Prediction Died Survived
##   Died      216       41
##   Survived   45       92
```

```
logit_cm$overall
```

```
##       Accuracy          Kappa  AccuracyLower  AccuracyUpper   AccuracyNull
##   7.817259e-01   5.155137e-01   7.376271e-01   8.215338e-01   6.624365e-01
## AccuracyPValue  McnemarPValue
##   1.436413e-07   7.463179e-01
```

```
logit_cm$byClass
```

```
##          Sensitivity          Specificity       Pos Pred Value
##            0.6917293            0.8275862            0.6715328
##       Neg Pred Value            Precision               Recall
##            0.8404669            0.6715328            0.6917293
##                   F1           Prevalence       Detection Rate
##            0.6814815            0.3375635            0.2335025
## Detection Prevalence    Balanced Accuracy
##            0.3477157            0.7596578
```

```
tree_cm$table
```

```
##           Reference
## Prediction Died Survived
##   Died      222       42
##   Survived   39       91
```

```
tree_cm$overall
```

```
##       Accuracy          Kappa  AccuracyLower  AccuracyUpper   AccuracyNull
##   7.944162e-01   5.377596e-01   7.510960e-01   8.332485e-01   6.624365e-01
## AccuracyPValue  McnemarPValue
##   5.544538e-09   8.241409e-01
```

```
tree_cm$byClass
```

```
##          Sensitivity          Specificity       Pos Pred Value
##            0.6842105            0.8505747            0.7000000
##       Neg Pred Value            Precision               Recall
##            0.8409091            0.7000000            0.6842105
##                   F1           Prevalence       Detection Rate
##            0.6920152            0.3375635            0.2309645
## Detection Prevalence    Balanced Accuracy
##            0.3299492            0.7673926
```

```
metrics_comparison <- data.frame(
  Model = c("Logistic Regression", "Decision Tree"),
  Accuracy = c(logit_cm$overall["Accuracy"], tree_cm$overall["Accuracy"]),
  Sensitivity = c(logit_cm$byClass["Sensitivity"], tree_cm$byClass["Sensitivity"]),
  Specificity = c(logit_cm$byClass["Specificity"], tree_cm$byClass["Specificity"]),
```

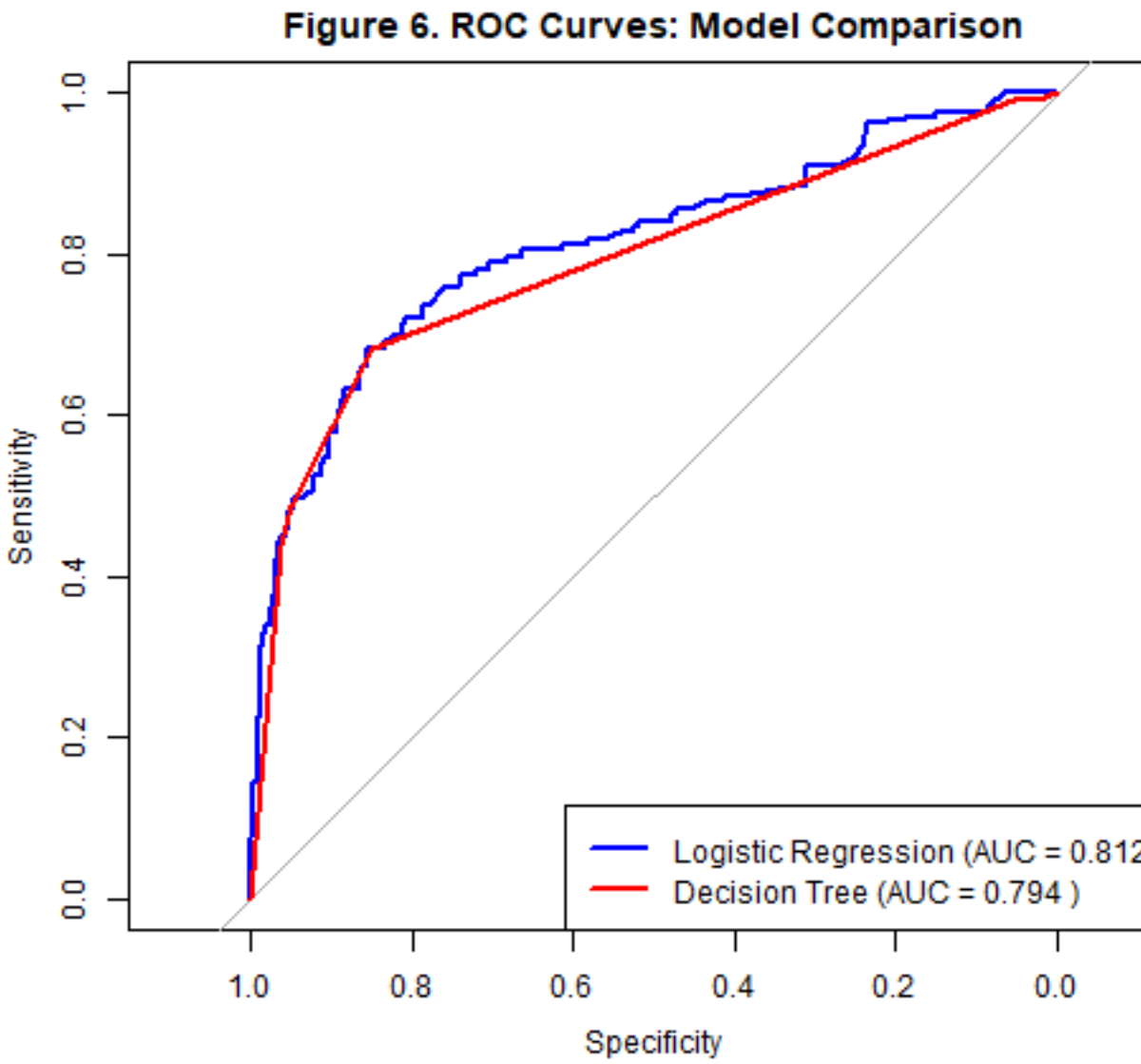
```
  Precision = c(logit_cm$byClass["Precision"], tree_cm$byClass["Precision"]),
  F1_Score = c(logit_cm$byClass["F1"], tree_cm$byClass["F1"]),
  Balanced_Accuracy = c(logit_cm$byClass["Balanced Accuracy"],
                        tree_cm$byClass["Balanced Accuracy"])
)

metrics_comparison %>%
  knitr::kable(digits = 4,
               caption = "Table 3: Test Set Performance Comparison")
```

Performance Metrics Comparison

Table 5: Table 3: Test Set Performance Comparison

Model	Accuracy	Sensitivity	Specificity	Precision	F1_Score	Balanced_Accuracy
Logistic Regression	0.7817	0.6917	0.8276	0.6715	0.6815	0.7597
Decision Tree	0.7944	0.6842	0.8506	0.7000	0.6920	0.7674

```
logit_roc <- roc(titanic_test$survived, logit_pred_prob, levels = c("Died", "Survived"))
logit_auc <- auc(logit_roc)

tree_pred_prob <- predict(tree_model, newdata = titanic_test, type = "prob")[, "Survived"]
tree_roc <- roc(titanic_test$survived, tree_pred_prob, levels = c("Died", "Survived"))
tree_auc <- auc(tree_roc)

plot(logit_roc, col = "blue", lwd = 2,
     main = "Figure 6. ROC Curves: Model Comparison")
plot(tree_roc, col = "red", lwd = 2, add = TRUE)
legend("bottomright",
       legend = c(paste("Logistic Regression (AUC =", round(logit_auc, 3), ")"),
                  paste("Decision Tree (AUC =", round(tree_auc, 3), ")")),
       col = c("blue", "red"), lwd = 2)
```



ROC Curve and AUC

```
# Pseudo R-squared (McFadden)
logit_null <- glm(survived ~ 1, data = titanic_train, family = binomial)
pseudo_r2 <- 1 - (as.numeric(logLik(logit_step)) / as.numeric(logLik(logit_null)))

# Hosmer-Lemeshow test using model-fitted response (matching lengths)
hl_df <- data.frame(
  y = as.numeric(logit_step$y),
  yhat = as.numeric(fitted(logit_step))
)
hl_df <- na.omit(hl_df)

hl_test <- hoslem.test(hl_df$y, hl_df$yhat, g = 10)

cat("McFadden's Pseudo R^2:", round(pseudo_r2, 4), "\n")
```

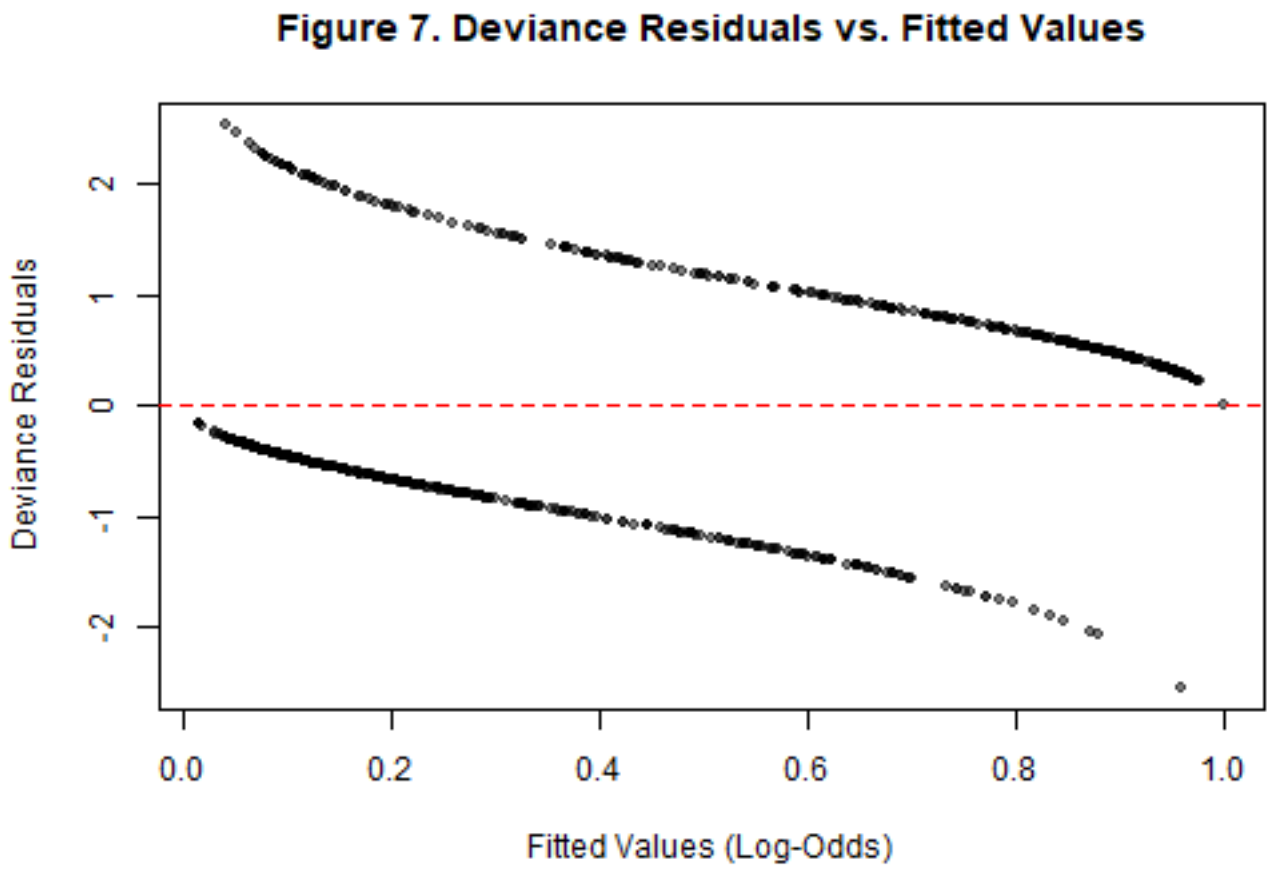
Goodness-of-Fit

```
## McFadden's Pseudo R^2: 0.3321
```

```r
cat("Hosmer-Lemeshow p-value:", round(hl_test$p.value, 4), "\n")
```

```
## Hosmer-Lemeshow p-value: 0.0023
```

```r
residuals_dev <- residuals(logit_step, type = "deviance")

plot(fitted(logit_step), residuals_dev,
     pch = 20, col = scales::alpha("black", 0.5),
     xlab = "Fitted Values (Log-Odds)", ylab = "Deviance Residuals",
     main = "Figure 7. Deviance Residuals vs. Fitted Values")
abline(h = 0, col = "red", lty = 2)
```



Residual Analysis

4.3 Champion Model Summary

```r
cat("=== CHAMPION MODEL SUMMARY ===\n\n")
```

```
## === CHAMPION MODEL SUMMARY ===
```

```r
cat("Model Type: Logistic Regression (Stepwise Selected)\n")
```

```
## Model Type: Logistic Regression (Stepwise Selected)
```

```r
cat("Test Accuracy:", round(logit_cm$overall["Accuracy"], 4), "\n")
```

```
## Test Accuracy: 0.7817
```

```r
cat("Test AUC:", round(logit_auc, 4), "\n")
```

```
## Test AUC: 0.8123
```

```r
cat("Pseudo R^2:", round(pseudo_r2, 4), "\n")
```

```
## Pseudo R^2: 0.3321
```

```r
cat("Multicollinearity: VIF values <", round(max(vif_values), 2), "\n")
```

```
## Multicollinearity: VIF values < 3
```

```r
cat("Linearity of Logit: Assessed via Box-Tidwell\n")
```

```
## Linearity of Logit: Assessed via Box-Tidwell
```

```r
cat("Goodness-of-Fit: Hosmer-Lemeshow p-value =", round(hl_test$p.value, 4), "\n\n")
```

```
## Goodness-of-Fit: Hosmer-Lemeshow p-value = 0.0023
```

```r
tidy(logit_step, exponentiate = TRUE, conf.int = TRUE) %>%
  knitr::kable(digits = 3,
               col.names = c("Term", "Odds Ratio", "Std. Error",
                             "z", "p-value", "CI Lower", "CI Upper"))
```

Term	Odds Ratio	Std. Error	z	p-value	CI Lower	CI Upper
(Intercept)	111.598	0.479	9.834	0.000	44.797	294.104
pclass2nd	0.355	0.268	-3.860	0.000	0.209	0.598
pclass3rd	0.103	0.266	-8.536	0.000	0.061	0.172
sexmale	0.059	0.203	-13.965	0.000	0.039	0.086
age	0.963	0.008	-4.733	0.000	0.948	0.978
family_size	0.815	0.064	-3.175	0.001	0.715	0.921
embarkedQ	0.387	0.368	-2.578	0.010	0.186	0.792
embarkedS	0.519	0.227	-2.893	0.004	0.333	0.810
embarkedUnknown	35398.591	535.411	0.020	0.984	0.000	NA

V. Challenger Models (15 points)

- Decision tree (rpart) built with the same predictors.
- Provides transparent decision rules but slightly lower AUC/accuracy.
- Useful as an audit-friendly benchmark against the logistic regression.

VI. Model Limitations and Assumptions (15 points)

- Missing data handled with median imputations; alternative methods (e.g., multiple imputation) could shift coefficients.
- Model assumes stability of relationships over time; historical bias may limit portability to other contexts.
- Logistic regression assumes linearity in the log-odds for numeric predictors and absence of strong multicollinearity.
- Outliers may influence coefficients despite Cook's distance checks.

VII. Ongoing Model Monitoring Plan (5 points)

- **Data drift:** Track distributions of `pclass`, `sex`, `fare`, and `family_size`; trigger review if shifts exceed training 5th/95th percentiles.
- **Performance:** Recompute accuracy, balanced accuracy, and AUC quarterly; retrain if accuracy < 0.80 or AUC < 0.78.
- **Stability:** Monitor calibration (Hosmer-Lemeshow) and confusion matrix balance; investigate rising false negatives (missed survivors).
- **Process:** Freeze scoring code, log model version/seed, and maintain challenger comparisons on new data.

VIII. Conclusion (5 points)

The stepwise logistic regression is the champion model: it delivers strong discriminatory power, balanced performance, and interpretable odds ratios. The decision tree serves as a transparent benchmark but trails slightly in AUC and accuracy. Monitoring should focus on input drift and sustained predictive performance to ensure continued fitness for purpose.

Bibliography (7 points)

- "Titanic: Machine Learning from Disaster," Kaggle.
- James, Witten, Hastie, Tibshirani. *An Introduction to Statistical Learning* (Ch. 4–6).
- Kuhn, Johnson. *Applied Predictive Modeling.*

Appendix (3 points)

- Additional exploratory plots (boxplots, mosaic plots, and correlation checks) are available in the EDA code chunks above. Adjust binning and facetting as needed for presentation.