

Appendix

Phebe Chen

2024-11-15

```
# Load Libraries  
library(readxl)  
library(tidyjson)
```

```
##  
## Attaching package: 'tidyjson'  
  
## The following object is masked from 'package:stats':  
##  
##     filter
```

```
library(corrplot)
```

```
## corrplot 0.95 loaded
```

```
library(reshape2)  
library(ggplot2)  
library(caret)
```

```
## Loading required package: lattice
```

```
library(randomForest)
```

```
## randomForest 4.7-1.2
```

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

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

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

```
library(gbm)
```

```
## Loaded gbm 2.2.2
```

```
## This version of gbm is no longer under development. Consider transitioning to gbm3, https://github.com
```

```
library(Metrics)
```

```
##
```

```
## Attaching package: 'Metrics'
```

```
## The following objects are masked from 'package:caret':
```

```
##
```

```
##      precision, recall
```

```
library(tidyr)
```

```
##
```

```
## Attaching package: 'tidyr'
```

```
## The following object is masked from 'package:reshape2':
```

```
##
```

```
##      smiths
```

```
# Section 1: Data Cleaning
```

```
file_path <- "seasonDataset.xlsx"
```

```
sheets <- excel_sheets(file_path)
```

```
data <- lapply(sheets, function(sheet) read_excel(file_path, sheet = sheet))
```

```
nhl_data <- bind_rows(data)
```

```
# Select only numeric columns and drop "GP"
```

```
numeric_data <- nhl_data[, sapply(nhl_data, is.numeric)]
```

```
numeric_data <- numeric_data[, setdiff(names(numeric_data), "GP")]
```

```
# Section 2: Correlation Analysis
```

```
cor_matrix <- cor(numeric_data)
```

```
cor_pts <- cor_matrix[, "PTS"]
```

```
# Drop redundant variables & filter
```

```
columns_to_keep <- c("PTS", "AvAge", "SOS", "PPp", "PKp", "oPIMpG", "Sp", "SVp",  
                    "PDO", "CFp", "FFp", "axDiff", "SCFp", "HDFp", "HDCp", "HDCOp")
```

```
nhl_data_filtered <- nhl_data[, columns_to_keep]
```

```
# Visualize Correlation Matrix
```

```
cor_matrix_filtered <- cor(nhl_data_filtered)
```

```
melted_cor <- melt(cor_matrix_filtered)
```

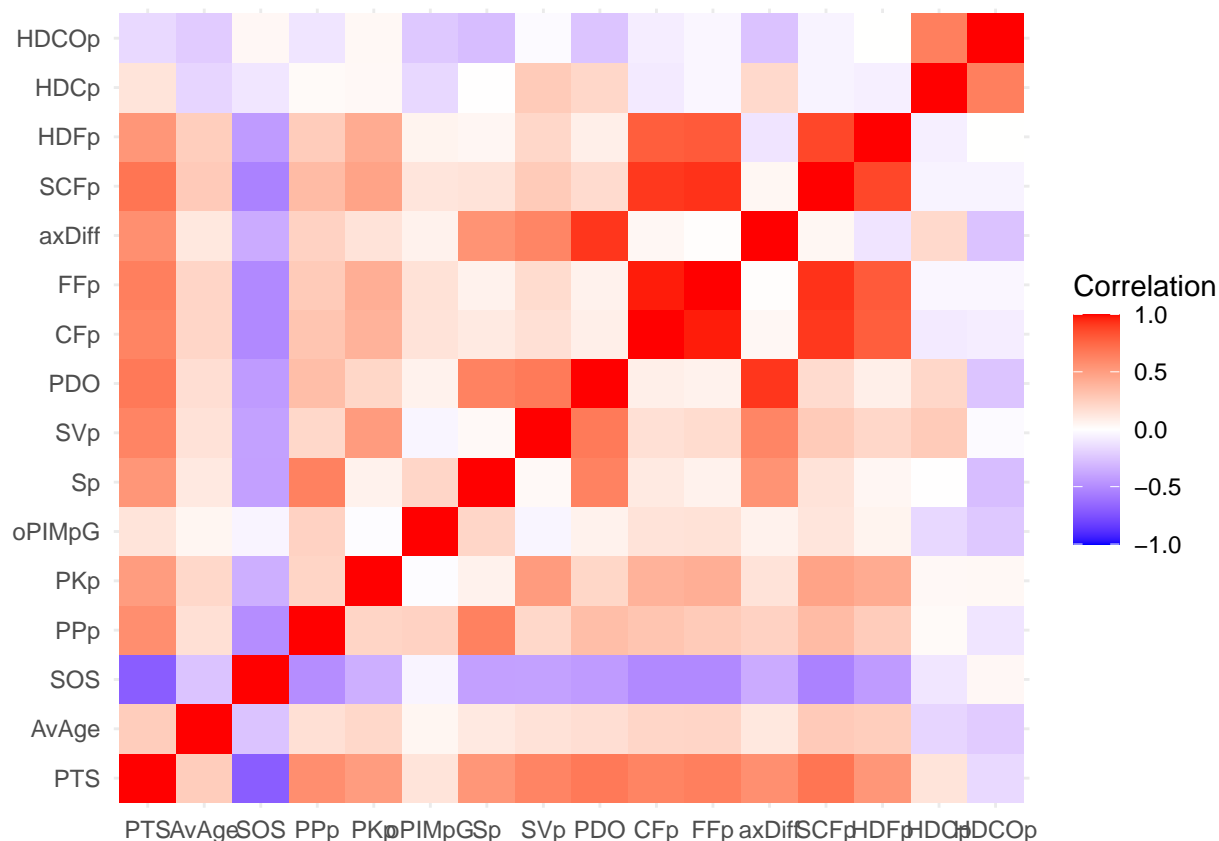
```
ggplot(data = melted_cor, aes(x = Var1, y = Var2, fill = value)) +
```

```
  geom_tile() +
```

```
  scale_fill_gradient2(low = "blue", high = "red", limit = c(-1, 1), name = "Correlation") +
```

```
  theme_minimal() +
```

```
  theme(axis.title.x = element_blank(), axis.title.y = element_blank())
```



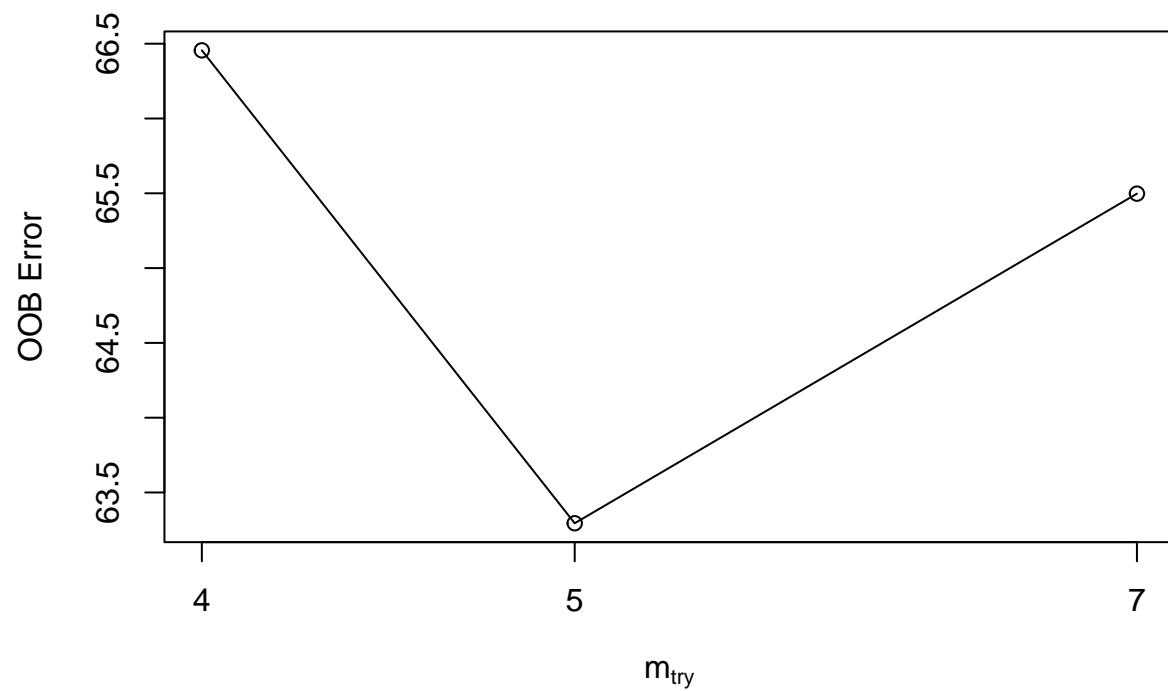
Section 3: Train-Test Split

```
set.seed(123)
train_index <- createDataPartition(nhl_data_filtered$PTS, p = 0.8, list = FALSE)
train_data <- nhl_data_filtered[train_index, ]
test_data <- nhl_data_filtered[-train_index, ]
```

Section 4: Random Forest Model

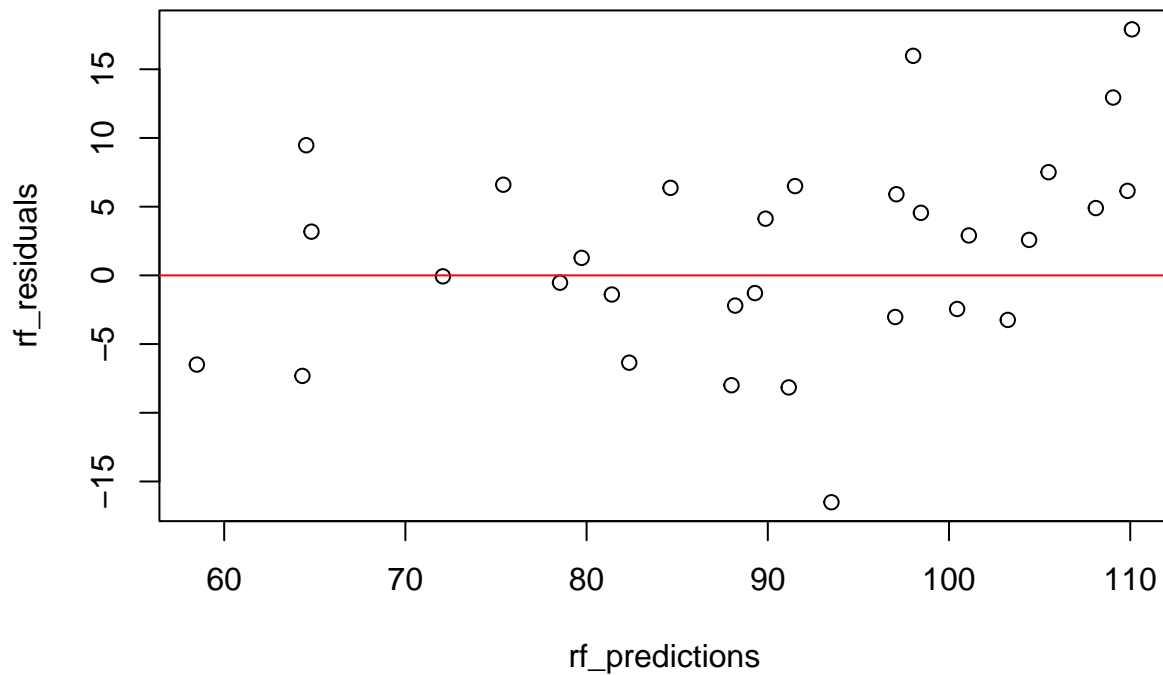
```
tune_rf <- tuneRF(train_data[, -which(names(train_data) == "PTS")], train_data$PTS, stepFactor = 1.5, i
```

```
## mtry = 5   OOB error = 63.29442
## Searching left ...
## mtry = 4   OOB error = 66.45564
## -0.04994471 0.01
## Searching right ...
## mtry = 7   OOB error = 65.49779
## -0.03481151 0.01
```



```
#300 trees to reduce overfitting (small dataset)
set.seed(123)
rf_model <- randomForest(PTS ~ ., data = train_data, mtry = 7, ntree = 300, importance = TRUE)
rf_predictions <- predict(rf_model, newdata = test_data)

rf_residuals <- test_data$PTS - rf_predictions
plot(rf_predictions, rf_residuals)
abline(h = 0, col = "red")
```



```
# Evaluate RF Model
rmse_rf <- rmse(test_data$PTS, rf_predictions)
rsq_rf <- cor(test_data$PTS, rf_predictions)^2
cat("Random Forest - RMSE:", rmse_rf, "R-squared:", rsq_rf, "\n")
```

```
## Random Forest - RMSE: 7.514855 R-squared: 0.8568228
```

```
# Cross-validation for Random Forest
set.seed(123)
rf_cv <- train(PTS ~ ., data = train_data,
               method = "rf",
               trControl = trainControl(method = "cv", number = 10),
               tuneGrid = expand.grid(mtry = 7),
               ntree = 300)

rf_predictions_cv <- predict(rf_cv, newdata = test_data)

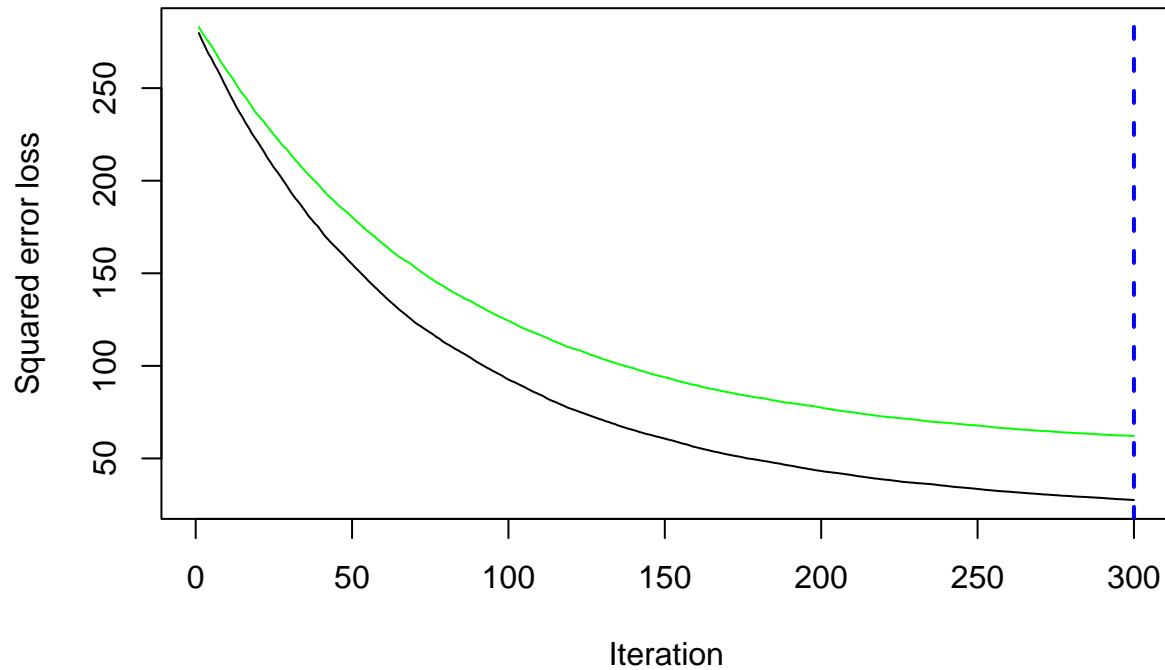
# Evaluate Random Forest model
rmse_rf_cv <- rmse(test_data$PTS, rf_predictions_cv)
rsq_rf_cv <- cor(test_data$PTS, rf_predictions_cv)^2
cat("Random Forest - RMSE:", rmse_rf_cv, "R-squared:", rsq_rf_cv, "\n")
```

```
## Random Forest - RMSE: 7.602834 R-squared: 0.8545144
```

```

# Section 5: GBM Model
set.seed(123)
gbm_model <- gbm(PTS ~ ., data = train_data, distribution = "gaussian",
                 n.trees = 300, interaction.depth = 5, shrinkage = 0.01, cv.folds = 5)
best_trees <- gbm.perf(gbm_model, method = "cv")

```

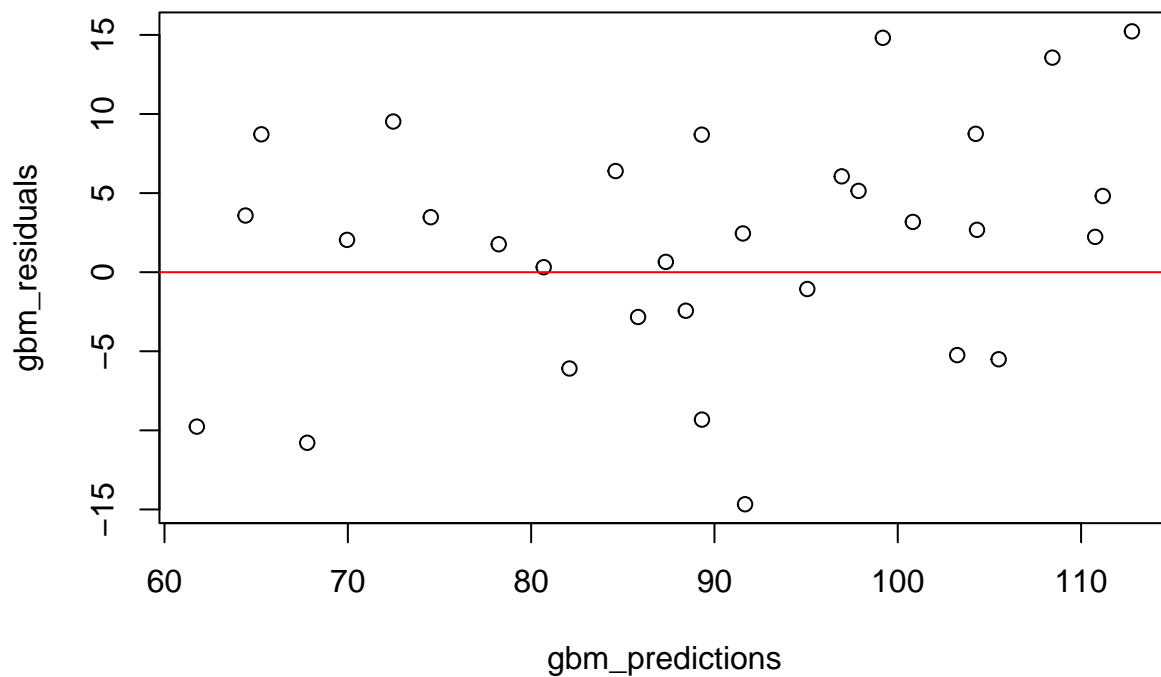


```

gbm_predictions <- predict(gbm_model, test_data, n.trees = best_trees)

gbm_residuals <- test_data$PTS - gbm_predictions
plot(gbm_predictions, gbm_residuals)
abline(h = 0, col = "red")

```



```
# Evaluate GBM Model
rmse_gbm <- rmse(test_data$PTS, gbm_predictions)
rsq_gbm <- cor(test_data$PTS, gbm_predictions)^2
cat("GBM - RMSE:", rmse_gbm, "R-squared:", rsq_gbm, "\n")
```

```
## GBM - RMSE: 7.547409 R-squared: 0.8520441
```

```
# Cross-validation for GBM
set.seed(123)

# Define tuning grid with correct parameters for GBM
gbm_grid <- expand.grid(
  n.trees = c(100, 200, 300),
  interaction.depth = c(3, 5, 7),
  shrinkage = c(0.01, 0.1),
  n.minobsinnode = c(10, 20)
)

# Train the GBM model using caret with 10-fold cross-validation
gbm_cv <- train(
  PTS ~ .,
  data = train_data,
  method = "gbm",
  trControl = trainControl(method = "cv", number = 10),
  tuneGrid = gbm_grid,
```

```

    verbose = FALSE
  )

  # Get the best model and make predictions
  gbm_predictions_cv <- predict(gbm_cv, newdata = test_data)

  # Evaluate the GBM model
  rmse_gbm_cv <- rmse(test_data$PTS, gbm_predictions_cv)
  rsq_gbm_cv <- cor(test_data$PTS, gbm_predictions_cv)^2
  cat("GBM - RMSE:", rmse_gbm_cv, "R-squared:", rsq_gbm_cv, "\n")

```

```
## GBM - RMSE: 7.324712 R-squared: 0.8574602
```

```

# Section 6: Bagging
set.seed(123)
bagging_model <- randomForest(PTS ~ ., data = train_data, mtry = ncol(train_data) - 1,
                             importance = TRUE, ntree = 200)
importance(bagging_model)

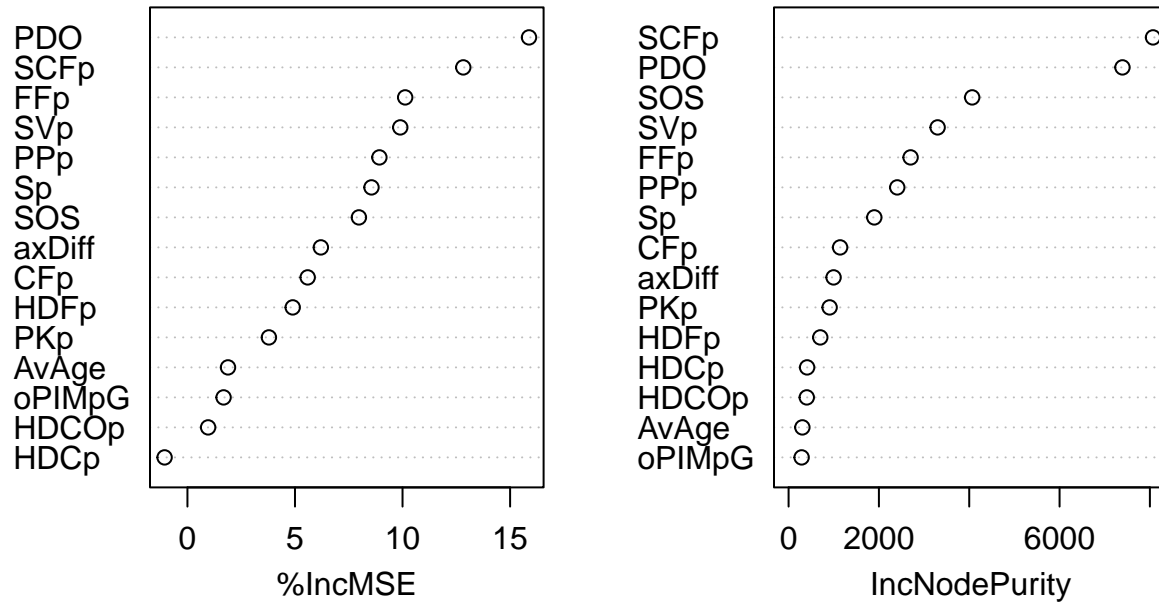
```

```
##           %IncMSE IncNodePurity
## AvAge      1.8857131      305.3603
## SOS        7.9708661     4065.2239
## PPp        8.9236187     2405.9426
## PKp        3.7873342      909.1050
## oPIMpG     1.6795372      289.1515
## Sp         8.5562809     1897.8392
## SVp        9.8943423     3300.1974
## PDO       15.8799504     7392.7431
## CFp        5.5904913     1141.0801
## FFp       10.1227632     2701.4835
## axDiff     6.2022986      996.1368
## SCFp      12.8233852     8069.3328
## HDFp       4.8950224      701.9289
## HDCp      -1.0627580      410.4966
## HDCOp      0.9619299      402.9820

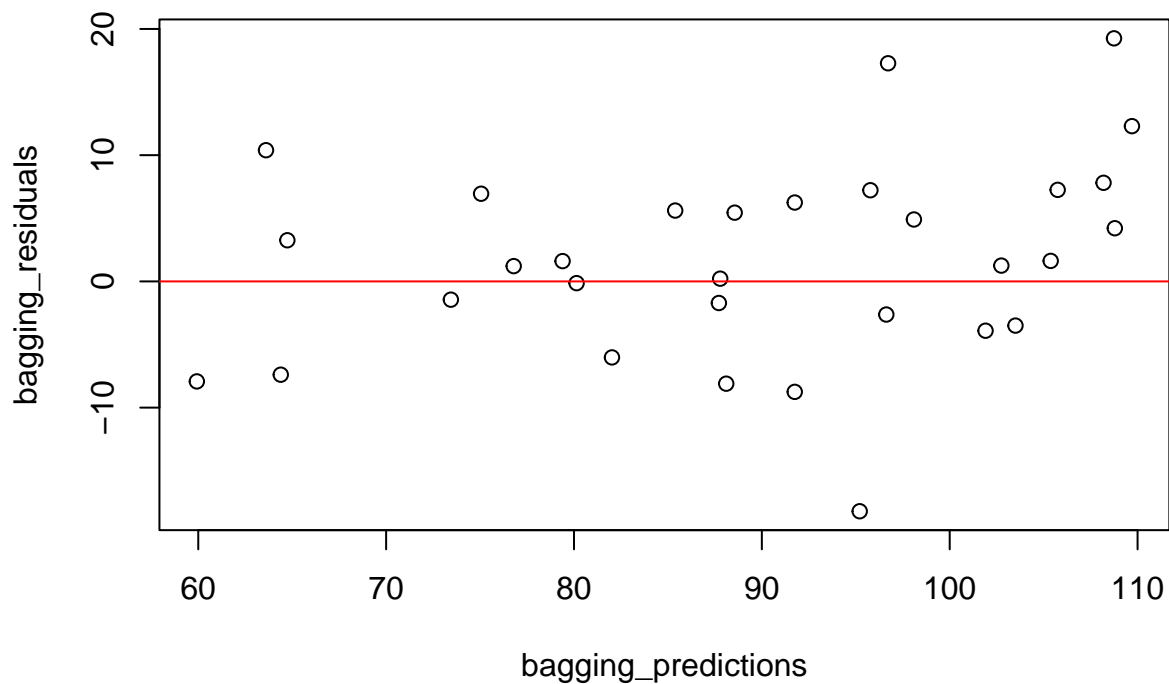
```

```
varImpPlot(bagging_model)
```

bagging_model



```
bagging_predictions <- predict(bagging_model, test_data)
bagging_residuals <- test_data$PTS - bagging_predictions
plot(bagging_predictions, bagging_residuals)
abline(h = 0, col = "red")
```



```
#Evaluate Bagging Model
```

```
rmse_bagging <- rmse(test_data$PTS, bagging_predictions)
rsq_bagging <- cor(test_data$PTS, bagging_predictions)^2
cat("Bagging - RMSE:", rmse_bagging, "R-squared:", rsq_bagging, "\n")
```

```
## Bagging - RMSE: 7.972839 R-squared: 0.8327265
```

```
# Cross-validation for Bagging (Random Forest)
```

```
set.seed(123) # Set seed for reproducibility
bagging_cv <- train(PTS ~ ., data = train_data,
  method = "rf",
  trControl = trainControl(method = "cv", number = 10),
  tuneGrid = expand.grid(mtry = ncol(train_data) - 1),
  ntree = 200) # Set number of trees
```

```
bagging_predictions_cv <- predict(bagging_cv, newdata = test_data)
```

```
# Evaluate Bagging model
```

```
rmse_bagging_cv <- rmse(test_data$PTS, bagging_predictions_cv)
rsq_bagging_cv <- cor(test_data$PTS, bagging_predictions_cv)^2
cat("Bagging - RMSE:", rmse_bagging_cv, "R-squared:", rsq_bagging_cv, "\n")
```

```
## Bagging - RMSE: 7.845305 R-squared: 0.8403278
```

```
# Section 7: Model Comparison
```

```
# Create a data frame with predictions from the original models
```

```
predictions <- data.frame(  
  Actual = test_data$PTS,  
  RF = round(rf_predictions, 2),  
  GBM = round(gbm_predictions, 2),  
  Bagging = round(bagging_predictions, 2),  
  RF_CV = round(rf_predictions_cv, 2),  
  GBM_CV = round(gbm_predictions_cv, 2),  
  Bagging_CV = round(bagging_predictions_cv, 2)  
)
```

```
# Print the predictions for comparison
```

```
print(predictions)
```

	##	Actual	RF	GBM	Bagging	RF_CV	GBM_CV	Bagging_CV
## 1	114	98.02	99.18	96.72	98.21	106.82	98.11	
## 2	113	108.10	110.77	108.79	107.97	114.25	108.07	
## 3	107	104.42	104.32	105.38	104.02	102.36	104.96	
## 4	91	84.63	84.61	85.39	84.68	81.85	83.39	
## 5	88	89.29	87.35	87.78	89.89	85.78	89.32	
## 6	78	78.53	74.52	76.79	78.69	75.77	80.00	
## 7	77	93.51	91.67	95.21	93.61	88.62	94.12	
## 8	52	58.49	61.76	59.92	58.89	58.38	58.59	
## 9	103	97.10	97.86	95.78	96.77	98.34	96.37	
## 10	98	100.45	103.24	101.91	101.43	101.06	102.17	
## 11	86	88.20	88.44	87.71	88.69	89.45	88.42	
## 12	81	79.73	80.69	79.39	80.78	75.24	78.96	
## 13	122	109.06	108.43	109.70	108.63	109.05	109.18	
## 14	116	109.85	111.18	108.19	110.06	115.45	108.64	
## 15	113	105.49	104.25	105.75	105.10	106.99	105.74	
## 16	94	97.03	95.06	96.63	95.95	98.64	96.46	
## 17	76	82.35	82.09	82.02	81.73	85.25	83.26	
## 18	74	64.53	65.28	63.61	64.85	59.72	64.55	
## 19	68	64.82	64.42	64.74	64.86	58.05	65.62	
## 20	57	64.32	67.78	64.39	63.93	62.39	64.49	
## 21	128	110.10	112.78	108.75	109.77	116.38	109.45	
## 22	104	101.09	100.82	102.75	101.40	101.59	103.11	
## 23	103	98.45	96.94	98.09	97.67	96.50	96.53	
## 24	100	103.24	105.50	103.50	103.03	102.20	103.00	
## 25	82	75.40	72.48	75.06	75.25	68.66	76.15	
## 26	80	81.39	78.23	80.14	81.01	80.98	80.14	
## 27	72	72.07	69.96	73.45	72.27	67.90	73.06	
## 28	98	91.50	89.31	91.75	90.24	85.56	91.99	
## 29	94	89.87	91.55	88.55	90.05	89.88	86.69	
## 30	83	91.16	85.83	91.75	91.88	85.77	93.05	
## 31	80	88.00	89.32	88.10	87.11	86.09	87.26	

```
# Save the rounded predictions to a CSV file
```

```
write.csv(predictions, "predictions.csv", row.names = FALSE)
```

```

# Separate the predictions into two datasets: Tuned Models and Cross-Validated Models
predictions_long <- predictions %>%
  gather(key = "Model", value = "Prediction", -Actual)

predictions_tuned <- predictions_long %>%
  filter(Model %in% c("RF", "GBM", "Bagging"))

predictions_cv <- predictions_long %>%
  filter(Model %in% c("RF_CV", "GBM_CV", "Bagging_CV"))

# Create the plot for Tuned Models
ggplot(predictions_tuned, aes(x = Actual, y = Prediction, color = Model)) +
  geom_point(alpha = 0.7, size = 3) +
  geom_abline(slope = 1, intercept = 0, linetype = "dashed", color = "gray") +
  geom_smooth(method = "lm", se = FALSE, aes(color = Model), linetype = "solid") +
  labs(
    title = "Tuned Models: Comparison of Predicted vs Actual Values",
    subtitle = "Dashed line represents perfect predictions",
    x = "Actual Values",
    y = "Predicted Values"
  ) +
  scale_color_manual(values = c("RF" = "blue", "GBM" = "green", "Bagging" = "red")) +
  theme_minimal() +
  theme(
    plot.title = element_text(size = 14, face = "bold"),
    plot.subtitle = element_text(size = 12, face = "italic"),
    axis.text = element_text(size = 10),
    axis.title = element_text(size = 12),
    legend.title = element_text(size = 12),
    legend.text = element_text(size = 10),
    panel.grid.major = element_line(color = "gray", size = 0.5, linetype = "dotted"),
    panel.grid.minor = element_line(color = "gray", size = 0.25, linetype = "dotted")
  )

```

```

## Warning: The 'size' argument of 'element_line()' is deprecated as of ggplot2 3.4.0.
## i Please use the 'linewidth' argument instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.

```

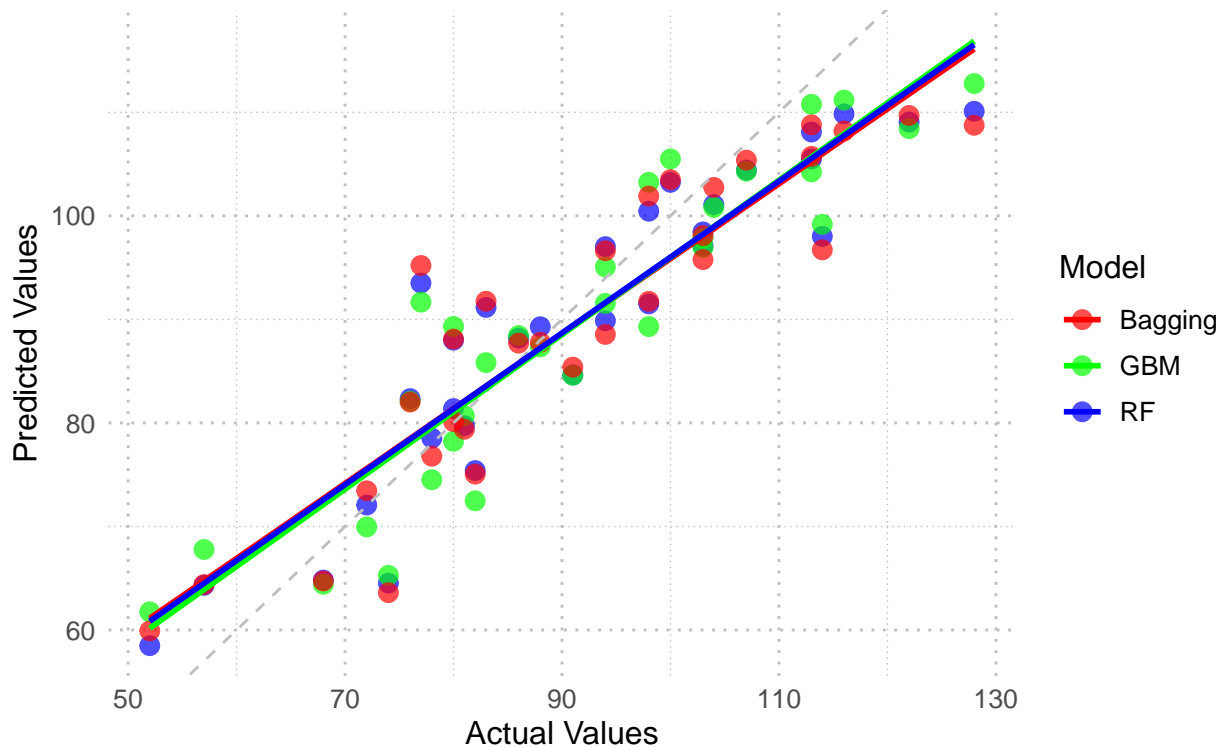
```

## 'geom_smooth()' using formula = 'y ~ x'

```

Tuned Models: Comparison of Predicted vs Actual Values

Dashed line represents perfect predictions



```
# Create the plot for Cross-Validated Models
ggplot(predictions_cv, aes(x = Actual, y = Prediction, color = Model)) +
  geom_point(alpha = 0.7, size = 3) +
  geom_abline(slope = 1, intercept = 0, linetype = "dashed", color = "gray") +
  geom_smooth(method = "lm", se = FALSE, aes(color = Model), linetype = "solid") +
  labs(
    title = "Cross-Validated Models: Comparison of Predicted vs Actual Values",
    subtitle = "Dashed line represents perfect predictions",
    x = "Actual Values",
    y = "Predicted Values"
  ) +
  scale_color_manual(values = c("RF_CV" = "purple", "GBM_CV" = "orange", "Bagging_CV" = "brown")) +
  theme_minimal() +
  theme(
    plot.title = element_text(size = 14, face = "bold"),
    plot.subtitle = element_text(size = 12, face = "italic"),
    axis.text = element_text(size = 10),
    axis.title = element_text(size = 12),
    legend.title = element_text(size = 12),
    legend.text = element_text(size = 10),
    panel.grid.major = element_line(color = "gray", size = 0.5, linetype = "dotted"),
    panel.grid.minor = element_line(color = "gray", size = 0.25, linetype = "dotted")
  )
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```

Cross-Validated Models: Comparison of Predicted vs Actual Val

Dashed line represents perfect predictions

