Final Project Report

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2024-12-07

Abstract:

Introduction:

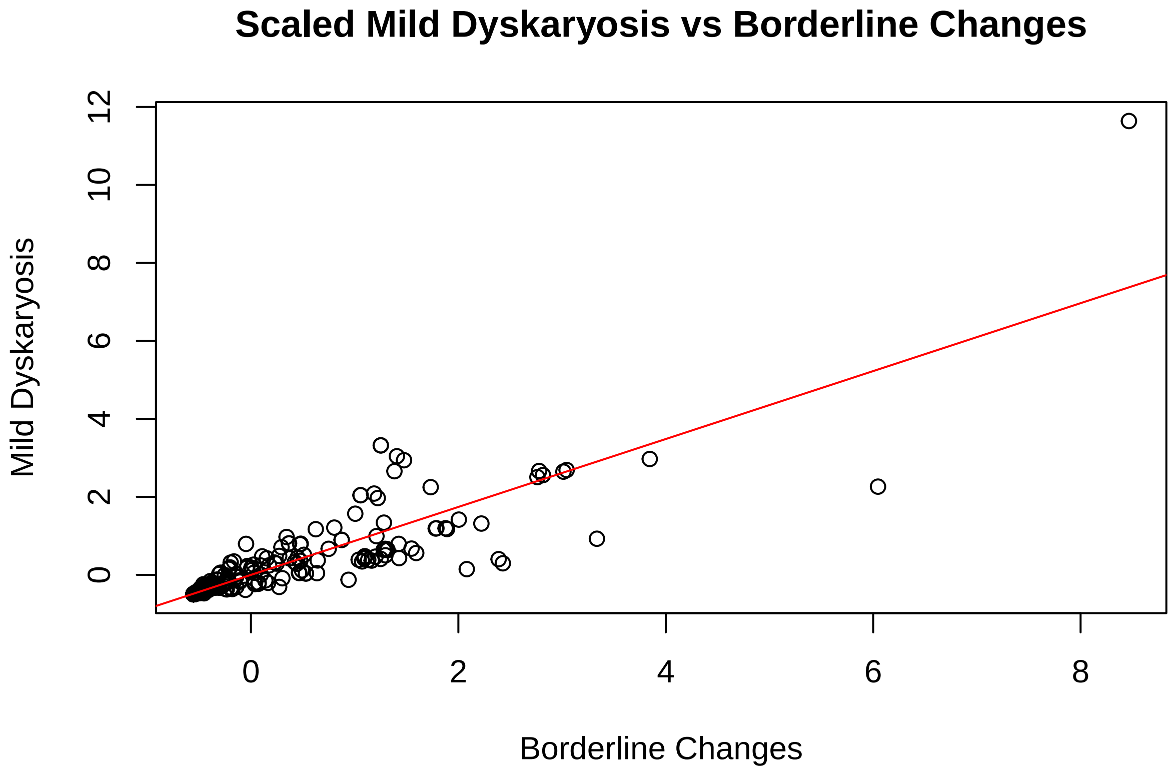
Cervical cancer is a type of cancer that occurs in the cervix, specifically the cells lining the cervix wall. It is the fourth most common cancer in women globally with around 660,000 new cases and 350,000 deaths in 2022, according to the WHO. Our project contains data on patients that have cervical cancer, taken from the NHS England. There were many datasets, but the one that we focused on was titled k61_sample_result_age_source. In this dataset, there are 330 observations, with 5 variables of focus. We chose on this one because it contained data on cervical cancer changes based on age and screening. The relevant variables we are looking at are mild, moderate, and severe dyskaryosis, age, and borderline changes. These terms are broad and hard to understand, so defining them is useful. Dyskaryosis is the change in appearance of cells that line the cervix. Mild, moderate, and severe are the classifications that this dataset uses. Mild is little change, moderate is moderate change, and severe is severe change. These changes are defined based on a 3-year screening. Borderline changes are abnormal changes in the cervix that are often pre-cancerous. These could indicate cervical cancer.

Data Cleaning:

Exploratory Data Analysis:

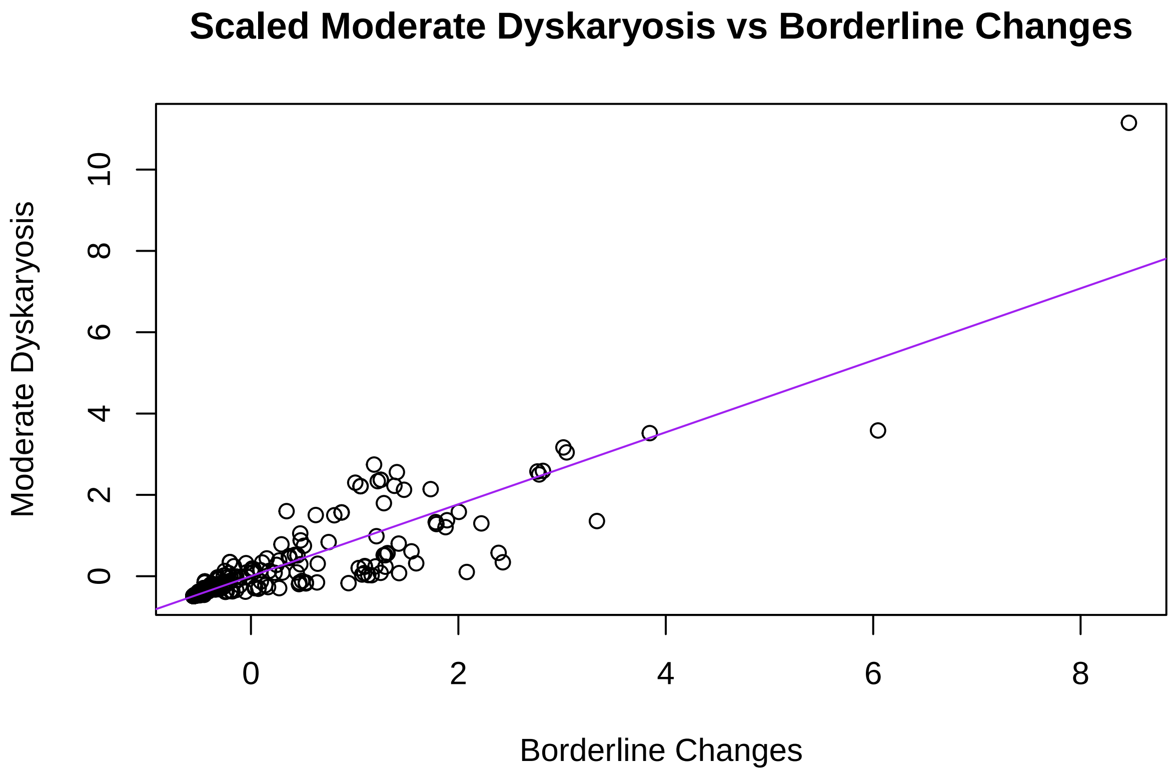
Results:

Scaled Linear Regression:

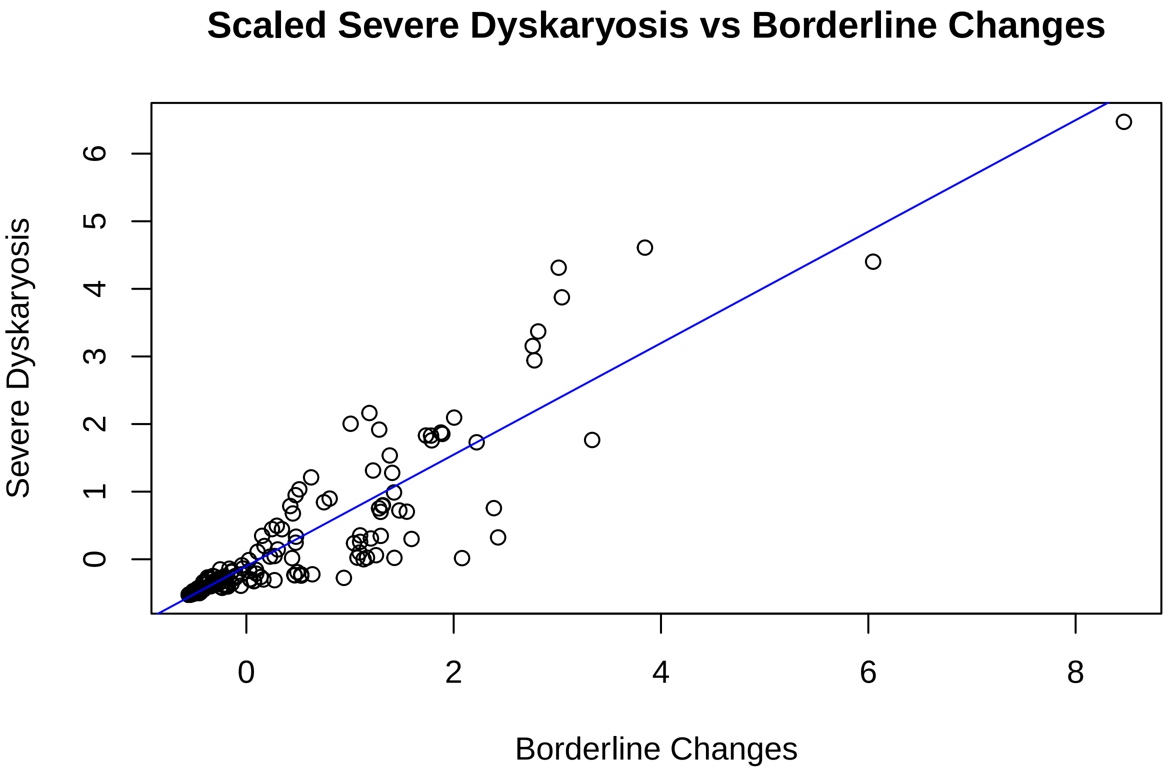


```
##
## Call:
## lm(formula = Mild_dyskaryosis ~ Borderline_changes, data = scaled_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.0040 -0.0170 -0.0125  0.0281  4.2644
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)        2.213e-16  2.708e-02    0.00        1
## Borderline_changes 8.711e-01  2.712e-02   32.12   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 0.4919 on 328 degrees of freedom
## Multiple R-squared:  0.7587, Adjusted R-squared:  0.758
## F-statistic:  1031 on 1 and 328 DF,  p-value: < 2.2e-16
```



```
##
## Call:
## lm(formula = Moderate_dyskaryosis ~ Borderline_changes, data = scaled_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.8067 -0.0007  0.0038  0.0512  3.6586
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)        2.621e-16  2.568e-02     0.0        1
## Borderline_changes 8.849e-01  2.572e-02    34.4   <2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Residual standard error: 0.4665 on 328 degrees of freedom
## Multiple R-squared:  0.783,  Adjusted R-squared:  0.7823
## F-statistic:  1184 on 1 and 328 DF,  p-value: < 2.2e-16
```



```
##
## Call:
## lm(formula = Severe_dyskaryosis ~ Borderline_changes, data = scaled_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.59706 -0.02801  0.03012  0.03551  1.93013
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        -0.10225    0.02608   -3.92 0.000116 ***
## Borderline_changes  0.82478    0.02338   35.27  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4016 on 238 degrees of freedom
##   (90 observations deleted due to missingness)
## Multiple R-squared:  0.8394, Adjusted R-squared:  0.8387
## F-statistic:  1244 on 1 and 238 DF,  p-value: < 2.2e-16
```

Borderline changes are defined by visual changes in the borders of the cancer neoplasm. In this dataset, the number of people who have presented with an abnormally shaped neoplasm are counted based on clinic site and age range and recorded in borderline changes. Dyskaryosis by definition is the abnormal appearance of a cell which is due to having an abnormal nucleus. The nucleus of the cell is where all the DNA is stored, so irregularities seen in the nucleus imply that there are issues with the DNA as well. DNA structural issues and chromosomal issues imply cancer, which is why dyskaryosis is tested for using pap smears and liquid cytology tests. In this dataset, the counts of mild, moderate, and severe dyskaryosis were all measured by clinic site and age range.

For the first linear regression model of Mild Dyskaryosis vs Borderline Changes, the coefficient of the slope of the line was significant with an alpha level of <0.001. The intercept of the line was not significant at any level. The adjusted R-squared value is 0.758, indicating that 75.8% of the variance in the data can be explained by the model. The F statistic is large with a p-value < 0.05, indicating that this regression is significant.

For the second linear regression model of Moderate Dyskaryosis vs Borderline Changes, the coefficient of the slope of the line was significant with an alpha level of <0.001. The intercept of the line was not significant at any level. The adjusted R-squared value is 0.7823, indicating that 78.23% of the variance in the data can be explained by the model. The F statistic is large with a p-value < 0.05, indicating that this regression is significant.

For the third linear regression model of Severe Dyskaryosis vs Borderline Changes, the coefficient of the slope of the line was significant with an alpha level of <0.001. The intercept of the line was not significant at any level. The adjusted R-squared value is 0.8387, indicating that 83.87% of the variance in the data can be explained by the model. The F statistic is large with a p-value of < 0.05, indicating that this regression is significant.

The regression model of Severe Dyskaryosis vs Borderline Changes appears to be the best at predicting incidence of severe dyskaryosis from borderline changes due to it having the largest F-statistic value (1244) as well as the largest adjusted R-squared value (0.8387). This could be because borderline changes in a neoplasma will typically be larger and more easily detectable in later stage cancers, meaning that large borderline changes would have a higher correlation with severe dyskaryosis. Therefore, it is reasonable to assume a relationship between a higher number of patients presenting with borderline changes as well as a larger number of patients presenting with severe dyskaryosis.

BIC MIC Model Comparison:

```
## 
## Call:
## lm(formula = Severe_dyskaryosis ~ ., data = train_frame)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -1583.04   -69.40    66.49    94.30  1515.34 
## 
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)    
## (Intercept)          -92.17422   41.51175  -2.220   0.0278 *  
## Borderline_changes     0.09507    0.01087   8.748 2.77e-15 ***
## Mild_dyskaryosis      -0.14662    0.02321  -6.317 2.49e-09 ***
## Moderate_dyskaryosis   1.45536    0.09598  15.163  < 2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
## 
## Residual standard error: 398.2 on 161 degrees of freedom
## Multiple R-squared:  0.9516, Adjusted R-squared:  0.9507 
## F-statistic:  1055 on 3 and 161 DF,  p-value: < 2.2e-16
```

```
## 
## Call:
```

```
## lm(formula = Severe_dyskaryosis ~ Borderline_changes + Mild_dyskaryosis +
##     Moderate_dyskaryosis, data = train_frame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1583.04   -69.40    66.49    94.30  1515.34
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)          -92.17422   41.51175  -2.220   0.0278 *
## Borderline_changes     0.09507    0.01087   8.748 2.77e-15 ***
## Mild_dyskaryosis      -0.14662    0.02321  -6.317 2.49e-09 ***
## Moderate_dyskaryosis   1.45536    0.09598  15.163  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 398.2 on 161 degrees of freedom
## Multiple R-squared:  0.9516, Adjusted R-squared:  0.9507
## F-statistic:  1055 on 3 and 161 DF,  p-value: < 2.2e-16
```

```
##
## Call:
## lm(formula = Severe_dyskaryosis ~ Moderate_dyskaryosis, data = train_frame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2625.70   -49.93    56.48    68.43  1635.61
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)          -61.79307   48.85798  -1.265    0.208
## Moderate_dyskaryosis   1.17963    0.02726  43.274   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 508.9 on 163 degrees of freedom
## Multiple R-squared:  0.9199, Adjusted R-squared:  0.9194
## F-statistic:  1873 on 1 and 163 DF,  p-value: < 2.2e-16
```

The BIC model chooses all variables: borderline changes, mild dyskaryosis, and moderate dyskaryosis, with about equal levels of significance. However, we can see that the moderate dyskaryosis t-value is higher, at 15.163. For our BIC model, 95.16% of the variance can be explained by our model. The MIC model only chooses the moderate dyskaryosis variable, at an alpha level of <.001, with a much higher t-value than the BIC model. However, the variance that can be explained by the model goes down with a value of 91.99%.

Model	R^2	RMSE	MAE
MIC	.997	1128.59	248.29
BIC	.996	806.2	194.54

The BIC model has a lower Rˆ2 value (.996), but the RMSE and MAE values are lower (806.2, 194.54). The MIC model has a higher Rˆ2 value (.997), but the RMSE and MAE values are higher (1128.59, 248.29). Both models have a high RMSE value but low MAE value, which indicate that there are a few cases where the models performs poorly, such as when outliers are present in the data, inflating the RMSE value.

Overall, the BIC model seems to be a candidate for a good model, however, because it selects all 3 variables, this model might not have reasonable clinical application in predicting severe dyskaryosis levels in cervical cancer.

Lasso Model:

```
## 8 x 1 sparse Matrix of class "dgCMatrix"
##                                  s1
## (Intercept)             43.856266409
## Inadequate               0.010508865
## Negative                -0.002947647
## Borderline_changes       0.141868446
## Mild_dyskaryosis         .
## Moderate_dyskaryosis     0.545530007
## Severe_dyskaryosis_Inv   1.861428691
## Glandular_neoplasia      5.102203558
```

```
##                  [,1]
## lambda.1se 0.9540652
```

```
## [1] 243.8997
```

```
## [1] 154.4453
```

For the lasso model, the independent variables acting as name tags for the data were removed so the model could be simplified and fitted to the best predictors. The goal of this model is to see if any variables within this data would be a good predictor of a severe dyskaryosis diagnosis. Looking at the R-squared of the lasso model, we see that the model explains 95.18% of the variability within the data which means the model is fitted very well to the data. However, looking at the RMSE and MAE, we see that the model is very lacking in its predictions. This can be because of the odd way the data is organized and collected.

Some data within this dataset is taken across multiple year frames, while others are taken within the same year. The data also varies widely between the number of observations that are taken at each “location”. The largely variability and inconsistency of the data could contribute to a high RMSE and MAE seen within the lasso model.

Because of the data, a portion of the data is singled out to be evaluated again. The data taken from 2012-2023 in England for all ages were subsetted into a new data frame, and the lasso model was ran again under these restrictions.

```
## 8 x 1 sparse Matrix of class "dgCMatrix"
##                               s1
## (Intercept)             3.3837175
## Inadequate              .
## Negative                .
## Borderline_changes      0.0363594
## Mild_dyskaryosis        .
## Moderate_dyskaryosis    0.4306823
## Severe_dyskaryosis_Inv .
## Glandular_neoplasia     2.7541747
```

```
##                  [,1]
## lambda.1se 0.9902593
## [1] 45.23053
```

```
## [1] 24.63821
```

The R-squared, RMSE, and MAE have all improved from the previous model. However, since the data does have the quality of time attached to it, it may still be an issue in terms of predictions. This may explain the large RMSE and MAE values.

Chosen Model:

Lasso Model, but linear regression and BIC shows strong correlation between severe dyskaryosis and borderline changes.

Appendix:

Data Cleaning:

```
source <-
  read.csv("cervical-programme-annual-2022-23-csvs/kc61_sample_result_age_source.csv")

dim(source)
```

```
## [1] 330  17
```

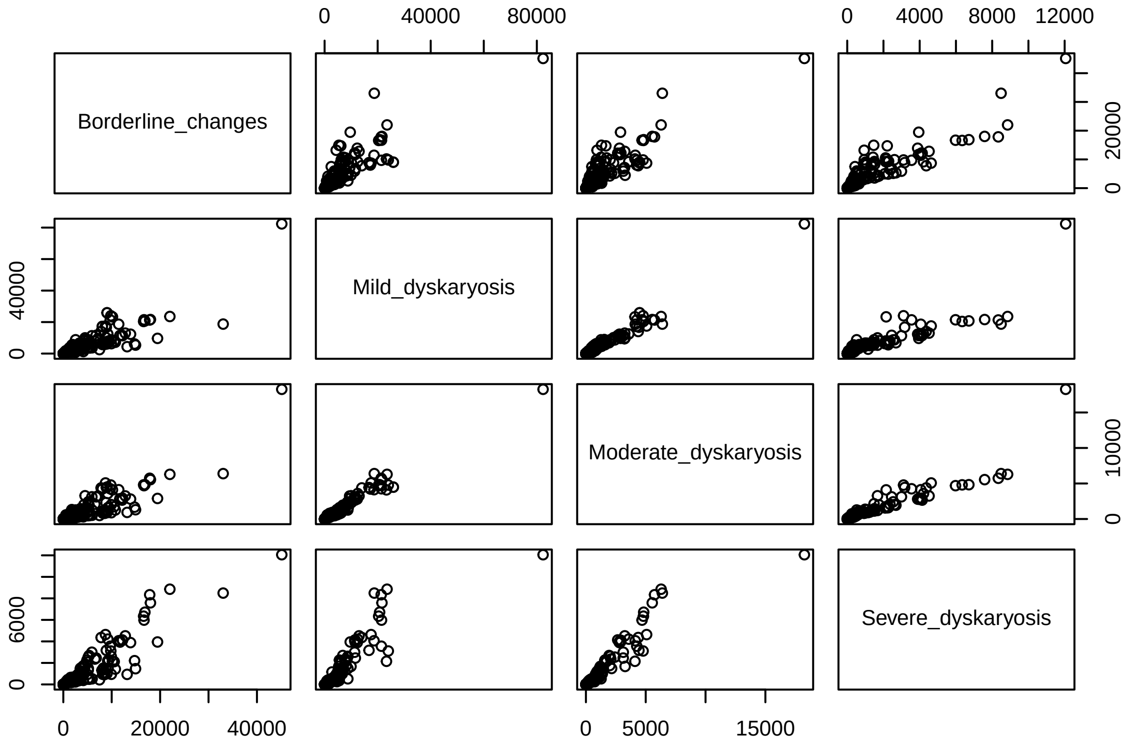
```
#columns of interest: Indicator (age), Borderline changes, mild, moderate,
#and severe dyskaryosis

#only column that has NA's is severe dyskaryosis; sub in values for NA to clean
source$Severe_dyskaryosis <- gsub("not included", NA, source$Severe_dyskaryosis)
sum(is.na(source$Severe_dyskaryosis) == TRUE)
```

```
## [1] 90
```

```
uniq_ind <- unique(source$Indicator)
for (i in 1:length(uniq_ind)){
  source$Indicator <- gsub(uniq_ind[i], i, source$Indicator)
}
source$Indicator <- as.numeric(source$Indicator)
#changing each age group to correspond with a number from 1-19. for example, <20 is 1

#removing NAs and converting to numeric values
severe_NA <- source[is.na(source$Severe_dyskaryosis) == FALSE, ]
severe_NA$Severe_dyskaryosis <- as.numeric(severe_NA$Severe_dyskaryosis)

comparison_data <- source[,c("Borderline_changes", "Mild_dyskaryosis", "Moderate_dyskaryosis","Severe_dy
comparison_data$Severe_dyskaryosis <- as.numeric(comparison_data$Severe_dyskaryosis)
```

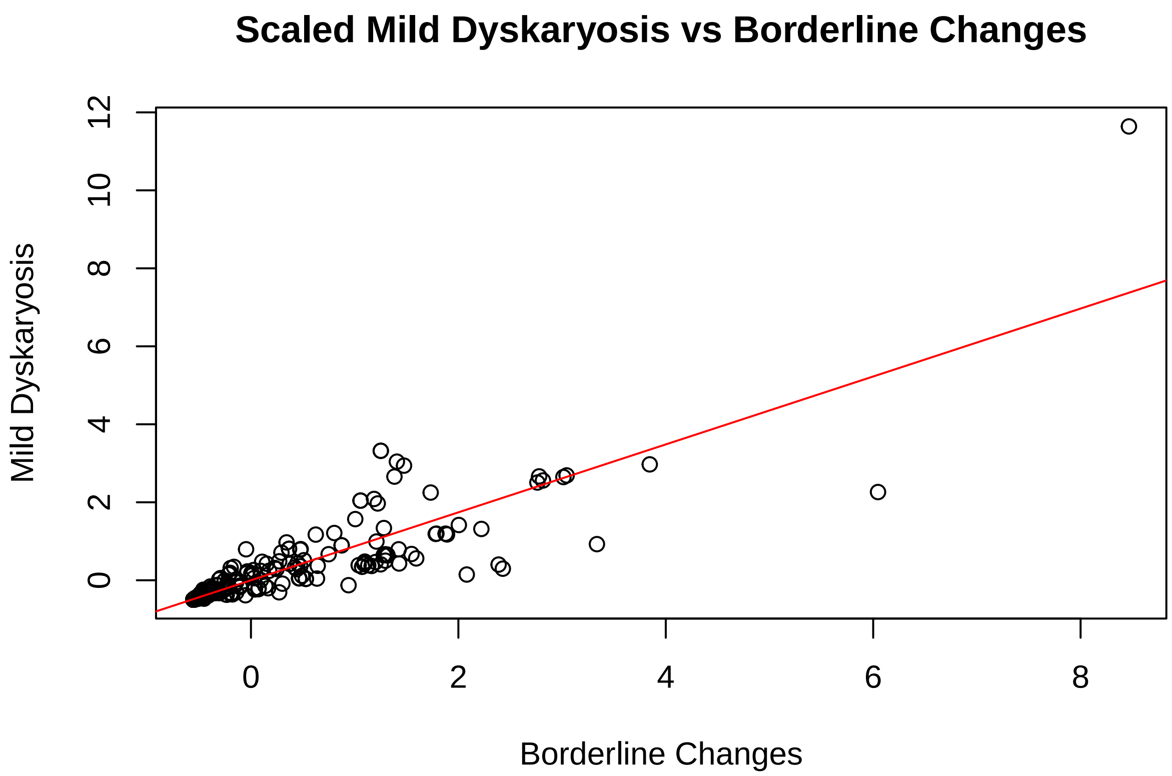
Subsetting Source Data:

```
## Subset source data for only borderline changes and mild, moderate, severe dyskaryosis

comparison_data <- source[,c("Borderline_changes", "Mild_dyskaryosis", "Moderate_dyskaryosis","Severe_dy
comparison_data$Severe_dyskaryosis <- as.numeric(comparison_data$Severe_dyskaryosis)

pairs(comparison_data)
```



Scaled Linear Regression:

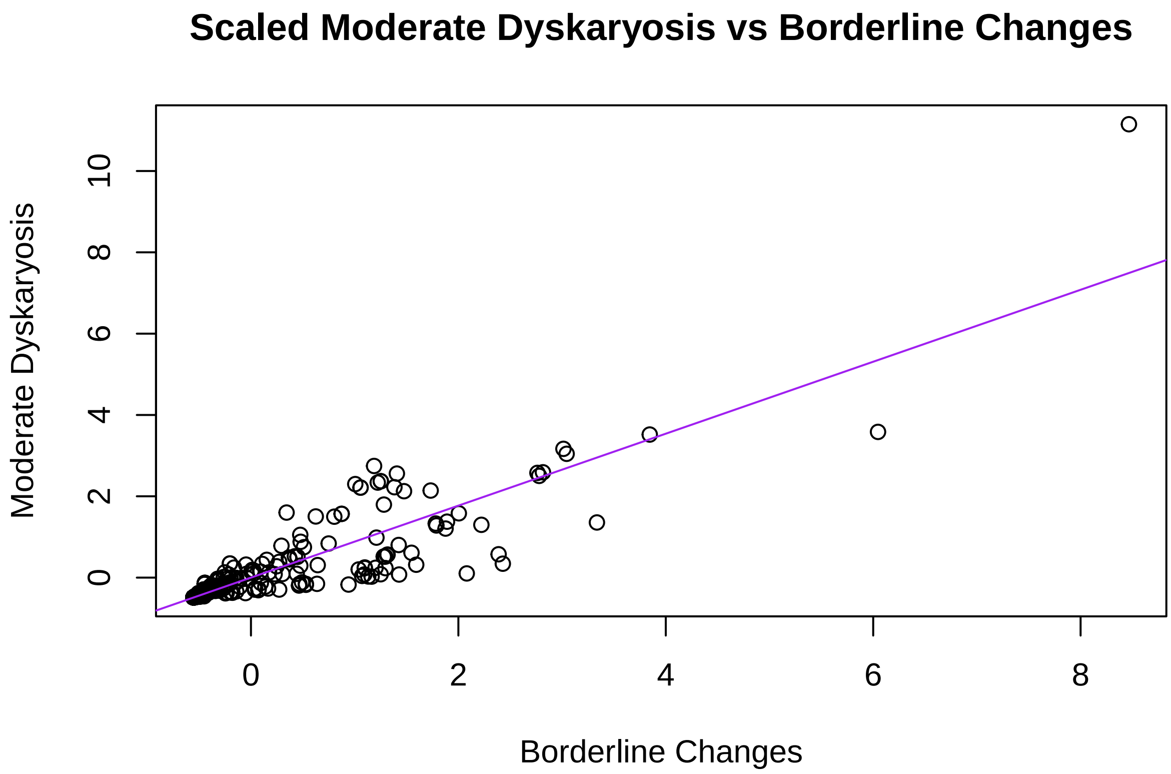
```
scaled_data <- as.data.frame(scale(comparison_data))

# mild dyskaryosis scaled
scaled_mild_model <- lm(Mild_dyskaryosis ~ Borderline_changes, data = scaled_data)
plot(scaled_data$Borderline_changes, scaled_data$Mild_dyskaryosis,
     main = "Scaled Mild Dyskaryosis vs Borderline Changes",
     xlab = "Borderline Changes",
     ylab = "Mild Dyskaryosis")
abline(scaled_mild_model, col = 'red')
```



```
summary(scaled_mild_model)
```

```
##
## Call:
## lm(formula = Mild_dyskaryosis ~ Borderline_changes, data = scaled_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.0040 -0.0170 -0.0125  0.0281  4.2644
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)        2.213e-16  2.708e-02    0.00        1
## Borderline_changes 8.711e-01  2.712e-02   32.12   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4919 on 328 degrees of freedom
## Multiple R-squared:  0.7587, Adjusted R-squared:  0.758
## F-statistic:  1031 on 1 and 328 DF,  p-value: < 2.2e-16
```

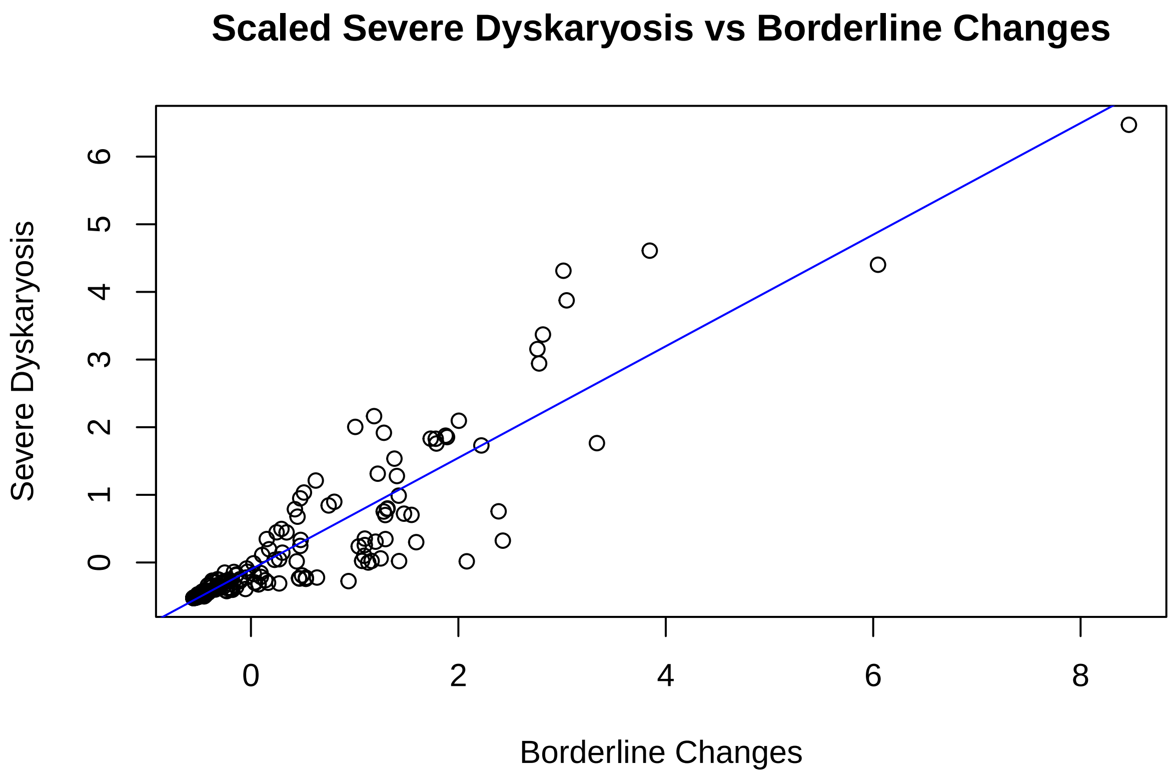
```
# moderate dyskaryosis scaled
scaled_mod_model <- lm(Moderate_dyskaryosis ~ Borderline_changes, data = scaled_data)
plot(scaled_data$Borderline_changes, scaled_data$Moderate_dyskaryosis,
     main = "Scaled Moderate Dyskaryosis vs Borderline Changes",
     xlab = "Borderline Changes",
     ylab = "Moderate Dyskaryosis")
abline(scaled_mod_model, col = 'purple')
```



```
summary(scaled_mod_model)
```

```
##
## Call:
## lm(formula = Moderate_dyskaryosis ~ Borderline_changes, data = scaled_data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.8067 -0.0007  0.0038  0.0512  3.6586
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)        2.621e-16  2.568e-02     0.0        1
## Borderline_changes 8.849e-01  2.572e-02    34.4   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4665 on 328 degrees of freedom
## Multiple R-squared:  0.783,  Adjusted R-squared:  0.7823
## F-statistic:  1184 on 1 and 328 DF,  p-value: < 2.2e-16
```

```
# severe dyskaryosis scaled
scaled_severe_model <- lm(Severe_dyskaryosis ~ Borderline_changes, data = scaled_data)
plot(scaled_data$Borderline_changes, scaled_data$Severe_dyskaryosis,
     main = "Scaled Severe Dyskaryosis vs Borderline Changes",
     xlab = "Borderline Changes",
     ylab = "Severe Dyskaryosis")
abline(scaled_severe_model, col = 'blue')
```



```
summary(scaled_severe_model)
```

```
##
## Call:
## lm(formula = Severe_dyskaryosis ~ Borderline_changes, data = scaled_data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.59706 -0.02801  0.03012  0.03551  1.93013
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        -0.10225    0.02608   -3.92 0.000116 ***
## Borderline_changes  0.82478    0.02338   35.27  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 0.4016 on 238 degrees of freedom
##   (90 observations deleted due to missingness)
## Multiple R-squared:  0.8394, Adjusted R-squared:  0.8387
## F-statistic:  1244 on 1 and 238 DF,  p-value: < 2.2e-16
```

BIC MIC Model Comparison:

```
#splitting data into test and train
train_index <- 1:165
test_index <- 166:nrow(comparison_data)

train_frame <- comparison_data[train_index,]
test_frame <- comparison_data[test_index,]


train_model <- lm(Severe_dyskaryosis ~ ., data = train_frame)
summary(train_model)
```

```
##
## Call:
## lm(formula = Severe_dyskaryosis ~ ., data = train_frame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1583.04   -69.40    66.49    94.30  1515.34
##
## Coefficients:
##                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)          -92.17422   41.51175  -2.220   0.0278 *
## Borderline_changes     0.09507    0.01087   8.748 2.77e-15 ***
## Mild_dyskaryosis      -0.14662    0.02321  -6.317 2.49e-09 ***
## Moderate_dyskaryosis   1.45536    0.09598  15.163  < 2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Residual standard error: 398.2 on 161 degrees of freedom
## Multiple R-squared:  0.9516, Adjusted R-squared:  0.9507
## F-statistic:  1055 on 3 and 161 DF,  p-value: < 2.2e-16
```

```
back_BIC <- step(train_model, direction = "backward",
                 k = log(nrow(train_frame)), trace = 0)
summary(back_BIC)
```

```
##
## Call:
## lm(formula = Severe_dyskaryosis ~ Borderline_changes + Mild_dyskaryosis +
##     Moderate_dyskaryosis, data = train_frame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1583.04   -69.40    66.49    94.30  1515.34
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)          -92.17422   41.51175  -2.220   0.0278 *
## Borderline_changes     0.09507    0.01087   8.748 2.77e-15 ***
## Mild_dyskaryosis      -0.14662    0.02321  -6.317 2.49e-09 ***
## Moderate_dyskaryosis   1.45536    0.09598  15.163  < 2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Residual standard error: 398.2 on 161 degrees of freedom
## Multiple R-squared:  0.9516, Adjusted R-squared:  0.9507
## F-statistic:  1055 on 3 and 161 DF,  p-value: < 2.2e-16
```

```
back_MIC <- step(train_model, direction = "backward",
                 k = nrow(train_frame), trace = 0)
summary(back_MIC)
```

```
##
## Call:
## lm(formula = Severe_dyskaryosis ~ Moderate_dyskaryosis, data = train_frame)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2625.70   -49.93    56.48    68.43  1635.61
##
## Coefficients:
##                       Estimate Std. Error t value Pr(>|t|)
## (Intercept)          -61.79307   48.85798  -1.265    0.208
## Moderate_dyskaryosis   1.17963    0.02726  43.274   <2e-16 ***
## ---
## Signif. codes:  0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1 ’ ’ 1
##
## Residual standard error: 508.9 on 163 degrees of freedom
## Multiple R-squared:  0.9199, Adjusted R-squared:  0.9194
## F-statistic:  1873 on 1 and 163 DF,  p-value: < 2.2e-16
```

```
test_MIC <- predict(back_MIC, test_frame)
test_BIC <- predict(back_BIC, test_frame)

cor(test_MIC, test_frame$Severe_dyskaryosis, use = "complete.obs")^2 #r-squared for back_MIC model
```

```
## [1] 0.9966765
```

```
cor(test_BIC, test_frame$Severe_dyskaryosis, use = "complete.obs")^2 #r-squared for back_BIC model
```

```
## [1] 0.9958021
```

```
errors_MIC <- test_frame$Severe_dyskaryosis - test_MIC
errors_BIC <- test_frame$Severe_dyskaryosis - test_BIC

sqrt(mean(errors_MIC^2, na.rm = TRUE)) #RMSE for back_MIC
```

```
## [1] 1128.586
```

```
sqrt(mean(errors_BIC^2, na.rm = TRUE)) #RMSE for back_BIC
```

```
## [1] 806.2014
```

```
mean(abs(errors_MIC), na.rm = TRUE) #MAE for back_MIC
```

```
## [1] 248.288
```

```
mean(abs(errors_BIC), na.rm = TRUE) #MAE for back_BIC
```

```
## [1] 194.5406
```

Lasso Model:

```
row_select <- sample(1:nrow(severe_NA), nrow(severe_NA) / 2)
col_exclude <- c(1:8, 17)

source_train <- severe_NA[row_select, -col_exclude]
source_test <- severe_NA[-row_select, -col_exclude]

suppressMessages(library(glmnet))

cn <- colnames(source_train)
exclude <- which(cn == "Severe_dyskaryosis" | cn == "CollectionYearRange")
X <- as.matrix(source_train[ , -exclude])

suppressWarnings(source_lasso <- cv.glmnet(X, source_train$Severe_dyskaryosis))
coef(source_lasso)
```

```
## 8 x 1 sparse Matrix of class "dgCMatrix"
##                                 s1
## (Intercept)            38.19985900
## Inadequate              .
## Negative                .
## Borderline_changes      0.04934676
## Mild_dyskaryosis        .
## Moderate_dyskaryosis    0.66896110
## Severe_dyskaryosis_Inv  .
## Glandular_neoplasia     1.38850649
```

```
Y <- as.matrix(source_test[ , -exclude])
suppressWarnings(source_predict <- predict(source_lasso, newx = Y))

cor(source_predict, source_test$Severe_dyskaryosis) ^ 2
```

```
##                 [,1]
## lambda.1se 0.891256
```

```r
source_errors <- source_test$Severe_dyskaryosis - source_predict
sqrt(mean(source_errors ^ 2))
```

```
## [1] 665.3689
```

```r
mean(abs(source_errors))
```

```
## [1] 286.0864
```

```r
lasso_data <- severe_NA[severe_NA$CollectionYearRange == "2022-23" &
                          suppressWarnings(severe_NA$Indicator == c(1:13)), ]
row_select <- sample(1:nrow(lasso_data), nrow(lasso_data) / 2)
col_exclude <- c(1:8, 17)

source_train <- lasso_data[row_select, -col_exclude]
source_test <- lasso_data[-row_select, -col_exclude]

cn <- colnames(source_train)
exclude <- which(cn == "Severe_dyskaryosis")
X <- as.matrix(source_train[ , -exclude])

suppressWarnings(source_lasso <- cv.glmnet(X, source_train$Severe_dyskaryosis))
coef(source_lasso)
```

```
## 8 x 1 sparse Matrix of class "dgCMatrix"
##                                  s1
## (Intercept)             7.50440510
## Inadequate             -0.10398437
## Negative                .
## Borderline_changes      0.04303953
## Mild_dyskaryosis       -0.04369862
## Moderate_dyskaryosis    0.73520983
## Severe_dyskaryosis_Inv  .
## Glandular_neoplasia     2.22129128
```

```r
Y <- as.matrix(source_test[ , -exclude])
suppressWarnings(source_predict <- predict(source_lasso, newx = Y))

cor(source_predict, source_test$Severe_dyskaryosis) ^ 2
```

```
##                   [,1]
## lambda.1se 0.9765133
```

```r
source_errors <- source_test$Severe_dyskaryosis - source_predict
sqrt(mean(source_errors ^ 2))
```

```
## [1] 71.305
```

```r
mean(abs(source_errors))
```

```
## [1] 41.91222
```

Sources:

Acknowledgements:

Data Cleaning: Paulina Yao

Scaled Linear Regression: Anika Dachiraju

BIC MIC Model Comparison: Raynah Cheng

Lasso Model: Paulina Yao

Bibliography: