Assessing Risk Factors for Sleep Disorders Through Multivariate Analysis

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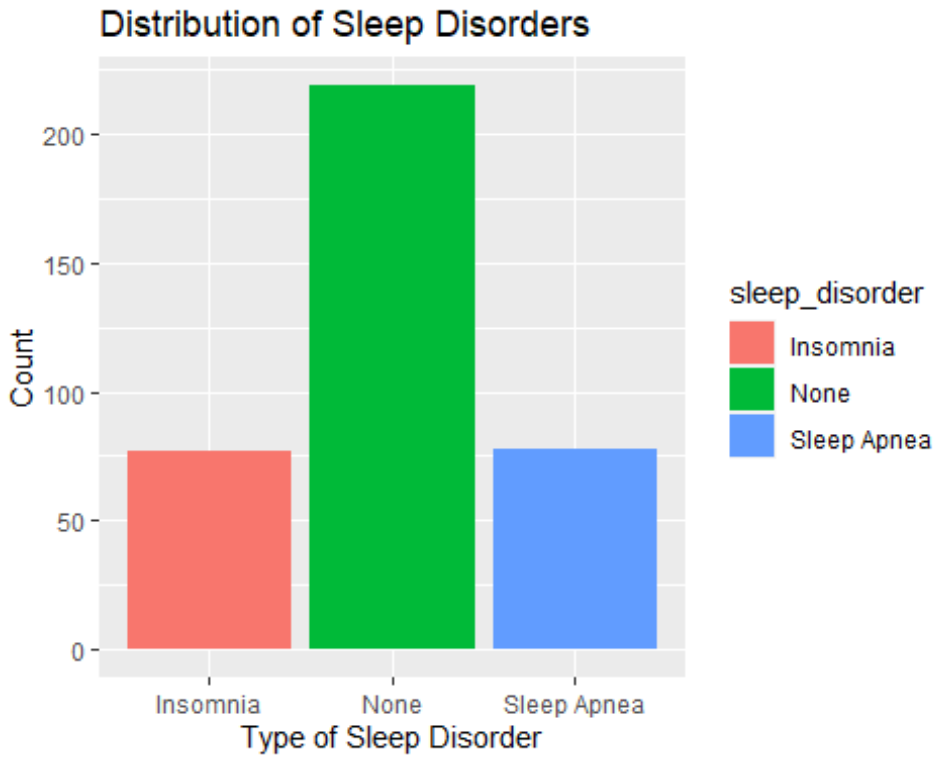
Introduction

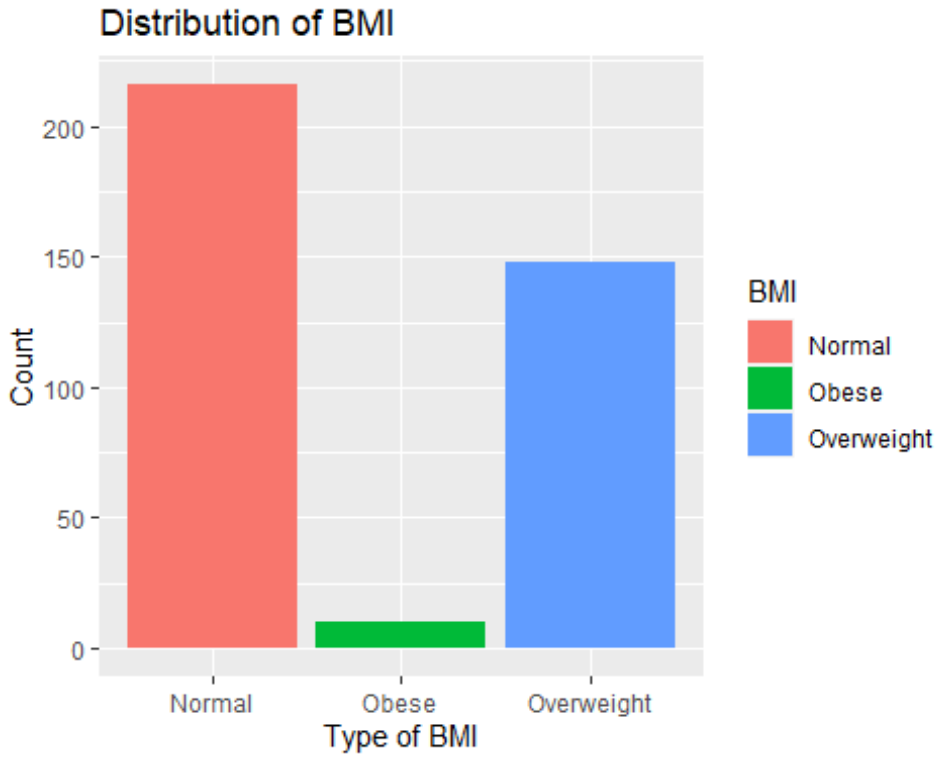
Many people develop a certain type of disorder in their life-time which can be attributed to behavioral risk factors that act as a precursor to having insomnia, sleep apnea, etc. This novel analysis is to view the group combinations of behavior risk to score the potential high risk that lead to a certain sleep disorder. The data gathered for insights in this approach involves data from the Center for Disease Control which contains answers to individual survey questions that is related to behavior and lifestyle components. The data has 374 observations with 11 variables that includes gender, age, occupation, sleep duration, sleep quality, physical activity level, stress level, BMI, heart rate, daily steps, and sleep disorder. From these variables, interaction columns are created to measure the value of risk between two variable on how it affects the response.

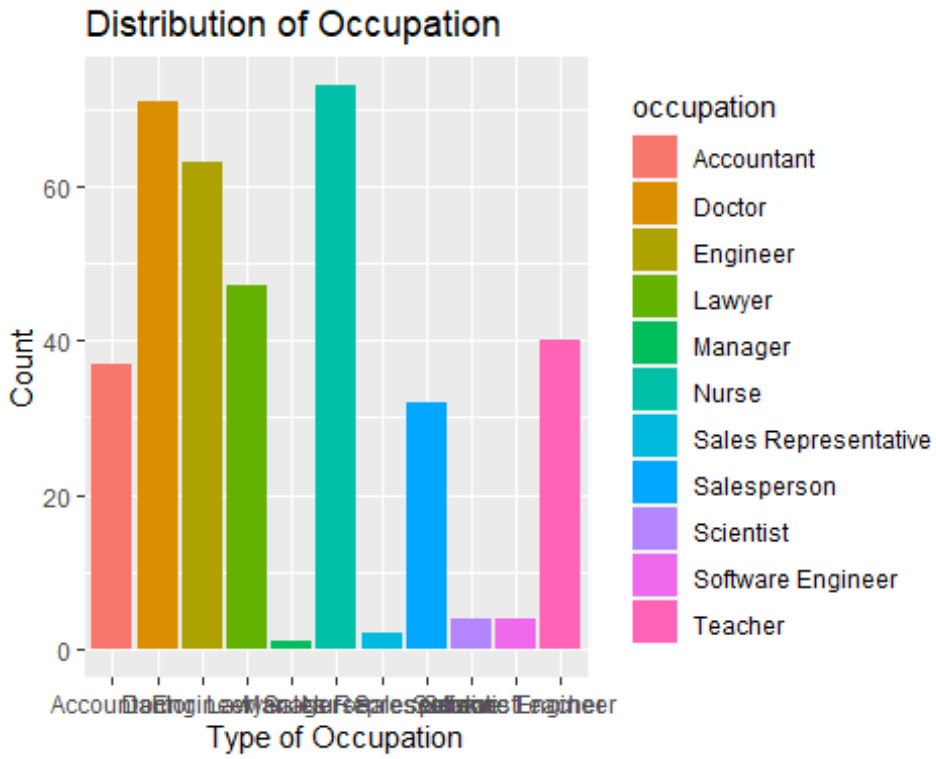
Pre-Processing

Feature Building - Creating Risk Severity Indicators

To start, a few columns and variables need to be created and changed to measure the direct interactions that may affect the type of sleep disorder. The modification of the BMI category from “Normal Weight” to “Normal” helps maintain consistency across data values. Several columns (sleep_disorder, BMI, occupation) are converted to factors, this is needed to quantify categorical variables that will be needed in the model. To first view the data, a couple of numerical plots are created. These plots illustrate the distribution of sleep disorders, BMI, and occupation which are the three variables that are categorical.


Distribution of Sleep Disorders
Count
200
150
100
50
0
Insomnia
None
Sleep Apnea
Type of Sleep Disorder
sleep_disorder
Insomnia
None
Sleep Apnea


Distribution of BMI
Count
200
150
100
50
0
Normal
Obese
Overweight
Type of BMI
BMI
Normal
Obese
Overweight



These distributions are essential to view which multinomial values more significant than others. For distribution of sleep disorders, the none value is more prevalent than other in context of this survey. Normal weight seems to be the mode of this distribution while overweight being close second. Finally, the typical occupations include nurse, doctor, and engineer roles.

10k-fold Cross Validation on Random Forest for Multiclass Classification

```
## Random Forest
##
## 301 samples
##  14 predictor
##   3 classes: 'Insomnia', 'None', 'Sleep Apnea'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 270, 271, 270, 272, 271, 271, ...
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##    2    0.9169744  0.8545745
##   13    0.9071895  0.8379661
##   24    0.9072970  0.8378567
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 2.
```

The Random Forest model was trained using the train function from the caret package, which simplifies the process of creating predictive models and their evaluation.A 10-fold cross-validation method was used, which is effective for estimating the model's performance reliably. The results show that the model achieved the highest accuracy of approximately 91.70% when mtry was set to 2. This indicates that using a smaller subset of predictors at each split is preferable in this context, likely because it helps in reducing the model variance without significantly increasing the bias.

The chosen mtry value of 2, based on the highest accuracy, signifies that the model's random feature selection helped in mitigating over fitting while still capturing the patterns necessary for predicting sleep disorders. Basically, finding the optimal mtry value is needed to achieve a balanced model between accuracy and generalization.

Random Forest Feature Selction by Grid Search & Model Evaluations

```
## Mean Accuracy: 0.910487

## Standard Deviation of Accuracy: 0.005618558

## Random Forest
##
## 301 samples
##  14 predictor
##   3 classes: 'Insomnia', 'None', 'Sleep Apnea'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 270, 271, 271, 271, 270, 272, ...
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##   2     0.9175269  0.8553384
##   3     0.9175269  0.8553384
##   5     0.9141935  0.8490884
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 2.

## Confusion Matrix and Statistics
##
##              Reference
## Prediction    Insomnia None Sleep Apnea
##   Insomnia          14    3           3
##   None               1   39           2
##   Sleep Apnea        0    1          10
##
## Overall Statistics
##
##                Accuracy : 0.863
##                  95% CI : (0.7625, 0.9323)
##     No Information Rate : 0.589
```

```
##     P-Value [Acc > NIR] : 3.604e-07
##
##                   Kappa : 0.7613
##
##  Mcnemar's Test P-Value : 0.2276
##
## Statistics by Class:
##
##                      Class: Insomnia Class: None Class: Sleep Apnea
## Sensitivity                   0.9333      0.9070             0.6667
## Specificity                   0.8966      0.9000             0.9828
## Pos Pred Value                0.7000      0.9286             0.9091
## Neg Pred Value                0.9811      0.8710             0.9194
## Prevalence                    0.2055      0.5890             0.2055
## Detection Rate                0.1918      0.5342             0.1370
## Detection Prevalence          0.2740      0.5753             0.1507
## Balanced Accuracy             0.9149      0.9035             0.8247

## Confusion Matrix and Statistics
##
##              Reference
## Prediction    Insomnia None Sleep Apnea
##   Insomnia          14    2           3
##   None               1   40           2
##   Sleep Apnea        0    1          10
##
## Overall Statistics
##
##                Accuracy : 0.8767
##                  95% CI : (0.7788, 0.942)
##     No Information Rate : 0.589
##     P-Value [Acc > NIR] : 7.828e-08
##
##                   Kappa : 0.7832
##
##  Mcnemar's Test P-Value : 0.2998
##
## Statistics by Class:
##
##                      Class: Insomnia Class: None Class: Sleep Apnea
## Sensitivity                   0.9333      0.9302             0.6667
## Specificity                   0.9138      0.9000             0.9828
## Pos Pred Value                0.7368      0.9302             0.9091
## Neg Pred Value                0.9815      0.9000             0.9194
## Prevalence                    0.2055      0.5890             0.2055
## Detection Rate                0.1918      0.5479             0.1370
## Detection Prevalence          0.2603      0.5890             0.1507
## Balanced Accuracy             0.9236      0.9151             0.8247
```

```
## rf variable importance
##
##   only 20 most important variables shown (out of 24)
##
##                           Overall
## risk.BMI                  100.000
## BMI_duration.interaction   94.937
## BMIOverweight              83.233
## age                        82.109
## duration                   76.536
## occupationNurse            62.148
## heart_rate                 59.506
## daily_steps                58.696
## physical_activity_level    58.435
## stress_level               48.938
## sleep_quality              38.700
## sleep.quality_stress       30.750
## risk.duration              30.631
## occupationSalesperson      22.497
## genderMale                 16.197
## occupationDoctor           16.115
## occupationTeacher          12.697
## occupationEngineer          9.530
## BMIObese                    6.717
## occupationLawyer            2.919
```

For the multinomial logistic regression, I needed to extract the most important features from the random forest model. I introduced a grid search for random forest to optimally select the best variables to predict the potential risk from a group of behavioral risk factors. Based on the summary of results, The model achieved an accuracy of approximately 89.04%, which is quite high. This metric indicates the proportion of total correct predictions out of all predictions made. The confidence interval (95% CI: 0.7954, 0.9515) suggests that the accuracy is consistently high across different samplings of the data, showing model stability.

The Cohen's Kappa value is 0.8073, which is very good. Kappa is a measure of how much better the classifier is performing over the performance of a classifier that simply guesses at random according to the frequency of each class. The no information rate is 0.589, indicating that if one always predicted the most frequent class, they would be correct about 58.9% of the time.

High sensitivity for 'Insomnia' (93.33%) and 'None' (93.02%), but slightly lower for 'Sleep Apnea' (73.33%). This indicates the model's effectiveness in identifying true positive cases for each disorder, with a need for improvement in detecting 'Sleep Apnea'. Excellent specificity across all classes, with the highest being for 'Sleep Apnea' (98.28%).The prevalence reflects how common each class is in the dataset. Most of the data points belong to the 'None' category (58.90%), which could influence the model's learning and predictive behavior. The Random Forest model performs exceptionally well in predicting whether a

person has ‘Insomnia’, ‘None’, or ‘Sleep Apnea’, with robust statistical support for its predictions.

Multinomial Logistic Regression

```
## # weights:  78 (50 variable)
## initial  value 330.682299
## iter  10 value 152.812250
## iter  20 value 98.425286
## iter  30 value 87.688004
## iter  40 value 84.868101
## iter  50 value 82.371511
## iter  60 value 80.050943
## iter  70 value 79.263192
## iter  80 value 79.078752
## iter  90 value 78.996771
## iter 100 value 78.950836
## final  value 78.950289
## converged

## Call:
## multinom(formula = sleep_disorder ~ ., data = trainData, maxit = 200)
##
## Coefficients:
##             (Intercept) genderMale        age occupationDoctor
## None          -41.41992  -1.164026 -0.3487808         3.254916
## Sleep Apnea  -117.18542   3.408437 -0.2203255         9.815470
##             occupationEngineer occupationLawyer occupationManager
## None                  1.125168         1.759851          43.10965
## Sleep Apnea          15.941502        16.423098          -1.67578
##             occupationNurse occupationSales Representative
## None                1.47592                      0.2298486
## Sleep Apnea        23.18768                     41.8633922
##             occupationSalesperson occupationScientist
## None                    0.4235574            24.17786
## Sleep Apnea            20.8238097            50.40563
##             occupationSoftware Engineer occupationTeacher  duration
## None                          16.20310        -0.0460934 0.7391728
## Sleep Apnea                  -39.11998        24.8324892 2.7215403
##             sleep_quality physical_activity_level stress_level  BMIObese
## None             6.899109              0.01747136     5.316575  -53.8257
## Sleep Apnea     16.127295             -0.08440396    16.199865 -131.0003
##             BMIOverweight  heart_rate  daily_steps risk.duration
risk.BMI
## None            -15.65547 0.008155149 0.0003924048      21.87045  -
0.9528941
## Sleep Apnea     -62.40270 0.405848497 0.0014664493      41.73053 -
27.1529109
##             BMI_duration.interaction sleep.quality_stress
## None                       -7.798776           -0.6643233
## Sleep Apnea               -15.114384           -1.6377745
```

```
##
## Std. Errors:
##              (Intercept)  genderMale        age occupationDoctor
## None        0.0009870527 0.007920414 0.04646870      0.005465872
## Sleep Apnea 0.0018480783 0.019697292 0.06210097      0.001930098
##             occupationEngineer occupationLawyer occupationManager
## None                0.01161161      0.006833025      1.410750e-16
## Sleep Apnea         0.01193823      0.011034775      1.495885e-35
##             occupationNurse occupationSales Representative
## None             0.00800550                   4.028496e-17
## Sleep Apnea      0.01933944                   1.136650e-06
##             occupationSalesperson occupationScientist
## None                  0.004252824        0.0004002719
## Sleep Apnea           0.003693790        0.0004002719
##             occupationSoftware Engineer occupationTeacher   duration
## None                       1.545305e-05       0.014583469 0.02356627
## Sleep Apnea                1.675093e-32       0.001585121 0.03821753
##             sleep_quality physical_activity_level stress_level
BMIObese
## None           0.03358878              0.02907650   0.01914688
0.0000181457
## Sleep Apnea    0.06365779              0.03965966   0.04050990
0.0011996591
##             BMIOverweight heart_rate  daily_steps risk.duration   risk.BMI
## None           0.02191585 0.04312802 0.0004150379    0.01779294 0.02252746
## Sleep Apnea    0.01688805 0.05782132 0.0004927759    0.02545712 0.02457053
##             BMI_duration.interaction sleep.quality_stress
## None                       0.0975663           0.05559496
## Sleep Apnea                0.1150985           0.08931367
##
## Residual Deviance: 157.9006
## AIC: 253.9006

##              Actual
## Predicted     Insomnia None Sleep Apnea
##   Insomnia          14    3           2
##   None               1   39           2
##   Sleep Apnea        0    1          11
```

The results shown above is from conducting a multinomial logistic regression analysis. Each coefficients here represents the change in the log odds of being in a particular category of sleep disorder for a one-unit change in the predictor, holding all other predictors constant. The model includes various occupation dummies (Doctor, Engineer, Salesperson, etc.). The coefficients for these variables show how the likelihood of each sleep disorder changes for individuals in these occupations compared to the baseline occupation. BMI_duration_interaction, which captures how the combined effect of BMI and the duration of the condition influences the likelihood of a sleep disorder. A significant coefficient here suggests that the impact of BMI on sleep disorder likelihood changes with the duration.

Listed below the coefficients, these provide a measure of the statistical significance and the precision of the coefficient estimates, respectively. A small p-value (typically <0.05) indicates that the effect is statistically significant, meaning there is a strong likelihood that the effect observed is not due to random chance.

Multinomial Logistic Regression Model Evalulation

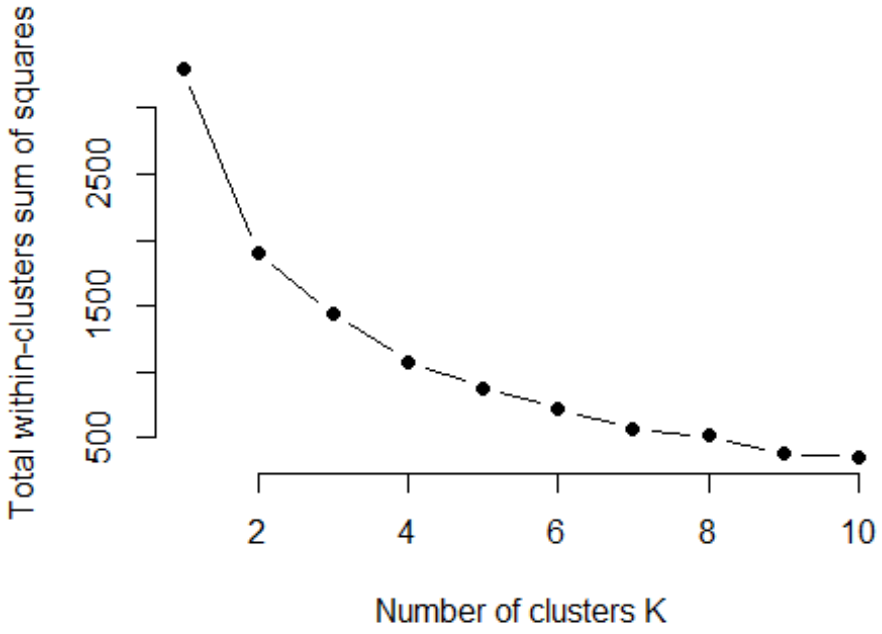
```
## [1] "Accuracy:  0.876712328767123"

## Confusion Matrix and Statistics
##
##              Reference
## Prediction    Insomnia None Sleep Apnea
##   Insomnia          14    3           2
##   None               1   39           2
##   Sleep Apnea        0    1          11
##
## Overall Statistics
##
##                Accuracy : 0.8767
##                  95% CI : (0.7788, 0.942)
##     No Information Rate : 0.589
##     P-Value [Acc > NIR] : 7.828e-08
##
##                   Kappa : 0.7852
##
##  Mcnemar's Test P-Value : 0.343
##
## Statistics by Class:
##
##                      Class: Insomnia Class: None Class: Sleep Apnea
## Sensitivity                   0.9333      0.9070             0.7333
## Specificity                   0.9138      0.9000             0.9828
## Pos Pred Value                0.7368      0.9286             0.9167
## Neg Pred Value                0.9815      0.8710             0.9344
## Prevalence                    0.2055      0.5890             0.2055
## Detection Rate                0.1918      0.5342             0.1507
## Detection Prevalence          0.2603      0.5753             0.1644
## Balanced Accuracy             0.9236      0.9035             0.8580
```

To measure the accuracy of the model, the confusion matrix shows the number of correct and incorrect predictions for each class. The model has done well in predicting 'None' and 'Sleep Apnea' but shows some confusion between 'Insomnia' and 'None'. Correct predictions for 'None' are particularly high, which could be influenced by its higher prevalence in the dataset (No Information Rate of 0.589). The overall accuracy of 0.8767 is quite good, indicating that the model correctly predicts the sleep disorder status in about 87.67% of the cases. The 95% confidence interval for accuracy (0.7788, 0.942) suggests that the model's accuracy is consistently high across different samples. A kappa value of 0.7852 shows substantial agreement beyond chance, confirming that the model is effective at distinguishing between the different classes of sleep disorders. The extremely low p-

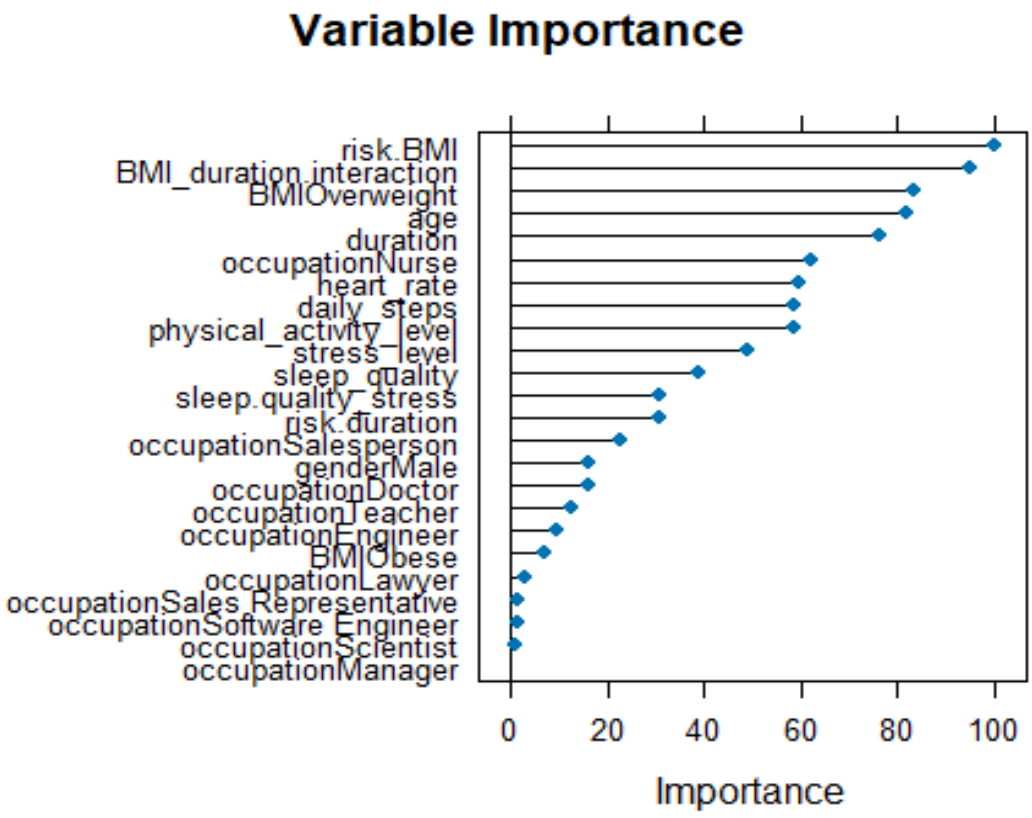
value (7.828e-08) statistically confirms that the model performs significantly better than a naive model that would always predict the most frequent class.

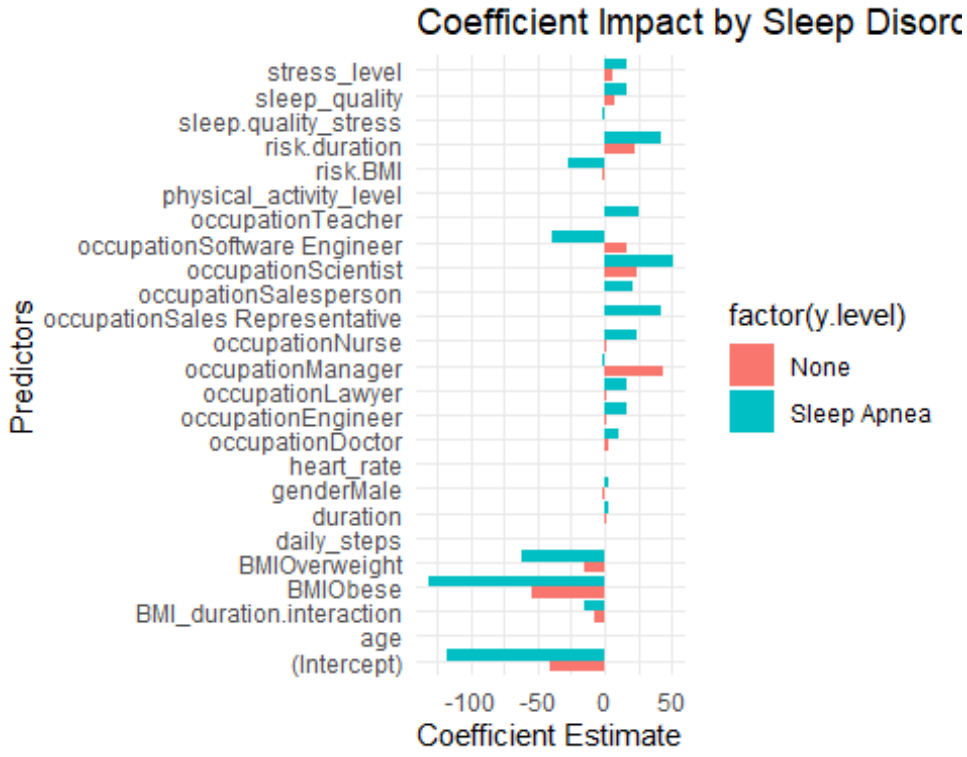
Clustering Analysis

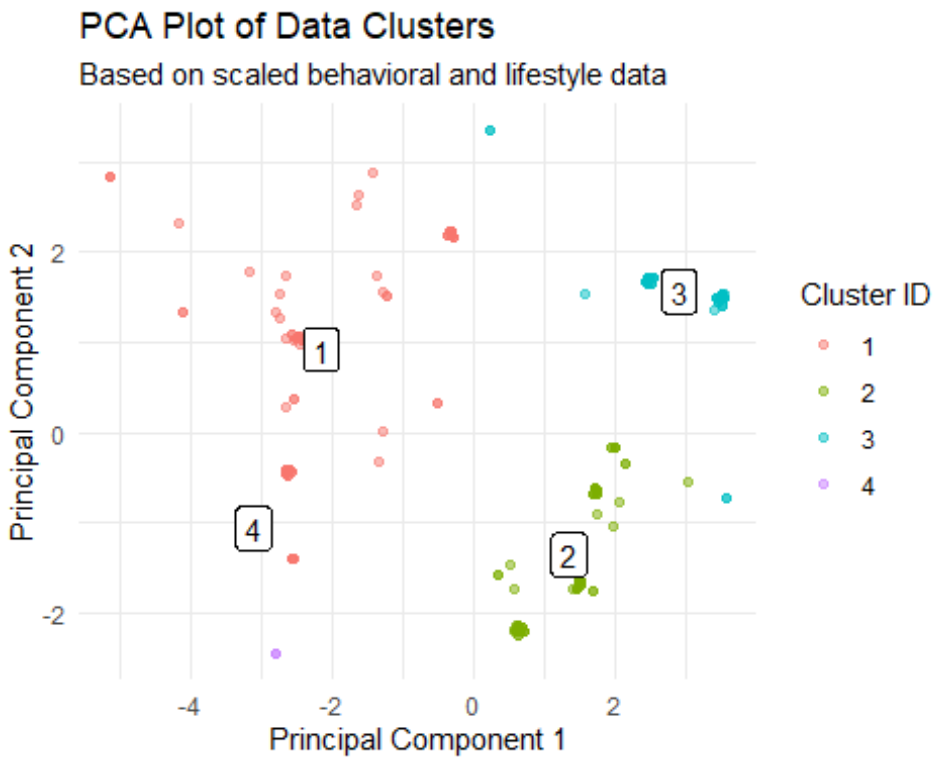
Normalizing the Clustering algorithms such as k-means are sensitive to the scale of the data, so it's crucial to standardize or normalize the data so that each feature contributes equally to the distance computations. Using Elbow Method the plot of within-cluster sum of squares (WCSS) against the number of clusters to find the "elbow" point where the WCSS starts to level off. The Silhouette Method evaluates the quality of clustering by assessing how close each point in one cluster is to points in the neighboring clusters.




```
## Warning: There was 1 warning in `summarise()`.
## i In argument: `across(where(is.numeric), mean, na.rm = TRUE)`.
## i In group 1: `cluster = 1`.
## Caused by warning:
## ! The `...` argument of `across()` is deprecated as of dplyr 1.1.0.
## Supply arguments directly to `.fns` through an anonymous function instead.
##
##   # Previously
##   across(a:b, mean, na.rm = TRUE)
##
##   # Now
##   across(a:b, \(x) mean(x, na.rm = TRUE))
```


Variable Importance
risk.BMI
BMI_duration.interaction
BMIOverweight
age
duration
occupationNurse
heart_rate
daily_steps
physical_activity_level
stress_level
sleep_quality
sleep.quality_stress
risk.duration
occupationSalesperson
genderMale
occupationDoctor
occupationTeacher
occupationEngineer
BMIObese
occupationLawyer
occupationSales Representative
occupationSoftware Engineer
occupationScientist
occupationManager
0
20
40
60
80
100
Importance


Coefficient Impact by Sleep Disorc
stress_level
sleep_quality
sleep.quality_stress
risk.duration
risk.BMI
physical_activity_level
occupationTeacher
occupationSoftware Engineer
occupationScientist
occupationSalesperson
occupationSales Representative
occupationNurse
occupationManager
occupationLawyer
occupationEngineer
occupationDoctor
heart_rate
genderMale
duration
daily_steps
BMIOverweight
BMIObese
BMI_duration.interaction
age
(Intercept)
Predictors
-100
-50
0
50
Coefficient Estimate
factor(y.level)
None
Sleep Apnea



Results

The variable importance plot ranks the predictors in terms of their importance in determining the outcome of the model. Importance might be measured in terms of mean decrease in impurity or any other metric that quantifies the increase in the model's prediction error when the data for that variable is permuted while all others are left unchanged. The variables towards the top of the plot contribute more to the prediction model. Variables like "BMI_duration_interaction" and "risk_BMI" appear to be among the most significant, suggesting that factors involving BMI and its interaction with other variables (like duration) are critical in predicting the outcome.

Based om the cluster plot of PCA, Cluster 1 (red): Concentrated around the center of PC1 and slightly negative on PC2. This cluster's central positioning along PC1 suggests average values of the underlying variables that are most strongly correlated with this component. Cluster 2 (green): Positioned towards positive values on both PC1 and PC2, indicating that individuals in this cluster score high on the variables that load positively on both these components. Cluster 3 (blue): Located further along the positive end of PC1 and around the center of PC2. This suggests that this cluster's characteristics are heavily influenced by the factors most strongly positively correlated with PC1. Cluster 4 (purple): This cluster is more spread out and mainly found in the negative territory of both PC1 and PC2, which could indicate lower scores or negative loadings on the principal components. Individuals in Cluster 2 might share certain positive health behaviors or lifestyle choices that distinguish them from those in Cluster 4, who might have less favorable scores.