# MATH 9102 - Probability and Statistical Inference Assignment Final Assignment

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## Contents



## Abstract

Breast cancer is the most common cancer in women in developed countries, and 12% of breast cancer occurs in women 20-34 yearscite(Hickey et al. 2009).

Advancements in prediction and diagnosis are crucial for maintaining a healthy life. Accurate cancer prediction mechanisms are vital for improving patient treatment and survival rates. Predictive techniques play a significant role in the early diagnosis of breast cancer, allowing for timely intervention and better management of the disease. In this study, we focus on enhancing the accuracy of breast cancer predictions by employing advanced data analysis techniques. Specifically, we utilized Principal Component Analysis (PCA) to reduce the dataset's dimensionality. This step is essential as it helps to simplify the dataset, making the predictive model more efficient and effective. By reducing the number of variables, we can focus on the most significant features that contribute to accurate predictions, thus improving the model's overall performance.

Additionally, we applied Logistic Regression to perform the prediction of the binary outcome (presence or absence of breast cancer). Logistic Regression is well-suited for this task as it provides a clear probabilistic framework for binary classification problems. The dataset used for this analysis is the Breast Cancer Wisconsin (Diagnostic) datasetparencite(Repository 1995), a well-known dataset in the field of medical diagnostics. We conducted our analysis and reporting using *R Studio, specifically version 4.3.2, released on October 31, 2023.*

# Introduction

Advances in predictive analytics and diagnostic technologies are crucial for improving public health. Early detection and accurate diagnosis of diseases like cancer significantly improve treatment outcomes and survival rates. Since breast cancer is one of the most common cancers affecting women worldwide, developing reliable prediction methods is essential. This study aims to explore advanced data analysis techniques to improve the accuracy of breast cancer diagnosis.

Predicting breast cancer involves analyzing various physiological and pathological features that indicate malignant tumors. Traditional methods often rely on clinical exams and imaging techniques, which, while effective, can be enhanced by computational methods.

Principal Component Analysis (PCA) is a useful tool for reducing the number of variables in a dataset. By simplifying the data without losing important information, PCA improves the performance of predictive models. In this study, we use PCA on the Breast Cancer Wisconsin (Diagnostic) dataset to streamline the features and improve the prediction model's efficiency. This step is essential for handling high-dimensional data in medical diagnostics and ensures that the model is robust and easy to interpret.

Logistic Regression, a common method for binary classification, is used to predict whether a tumor is malignant or benign. This technique is well-suited for medical diagnostics because it provides probabilities and can handle various predictor variables. By applying Logistic Regression to the PCA-transformed dataset, we aim to achieve high accuracy in predicting breast cancer. Combining PCA and Logistic Regression offers a comprehensive approach to addressing the complexity of breast cancer prediction.

The dataset used in this study is the Breast Cancer Wisconsin (Diagnostic) dataset, a well-known resource in medical research. This dataset includes various features extracted from digitized images of fine needle aspirate (FNA) of breast masses(Repository 1995), making it ideal for predictive analysis. We conducted the analysis and reporting using *R Studio (version 4.3.2, released on October 31, 2023)*, which provides a robust environment for statistical computing and graphics. Through this study, we aim to enhance breast cancer detection and improve patient outcomes, supporting the broader goal of advancing healthcare through data-driven methods.

# Method

## Participants

The Breast Cancer Wisconsin (Diagnostic) dataset includes data from patients who underwent fine needle aspirate (FNA) of breast masses.

The dataset consists of 569 instances with data collected from real women.

The dataset does not provide personal demographic information such as age, ethnicity, or geographic location, focusing instead on the clinical and pathological features of the breast masses.

For each participant, 30 features were extracted from the FNA samples. These features describe the characteristics of the cell nuclei present in the samples. The features include measurements such as radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, and fractal dimension. These features were recorded for both the mean, standard error, and "worst" or largest values across the samples.

Each sample is labeled with a diagnosis indicating whether the breast mass is benign (B) or malignant (M). This binary outcome is used to train and test predictive models aimed at diagnosing breast cancer.

## Procedure

### Dataset Exploration & Analysis

The dataset includes the following features (variables): We do not have any variables related to the individual, except for the ID. There is a categorical variable indicating whether the tumor is benign or malignant. All other variables are numerical, and for each, the mean, standard error, and worst value were measured during the exam.

| Variable | Type | Description |
|---|---|---|
| id | Ordinal | Number of the patient |
| diagnosis | Categorical | M = malignant, B = benign |
| radius | Continuous | Mean of distances from center to points on the perimeter |
| texture | Continuous | Standard deviation of gray-scale values |
| perimeter | Continuous | |
| area | Continuous | |
| smoothness | Continuous | Local variation in radius lenghts |
| compactness | Continuous | (perimeter ^ 2 / area - 1) |
| concavity | Continuous | Severity of concave portions of the contour |
| symmetry | Continuous | |
| fractal_dimension | Continuous | "Coastline approximation" - 1 |

```
data <- read.csv("data.csv")
desc_data <- data %>% select(-X, -id)
desc_data <- suppressWarnings(describe(desc_data))
desc_data <- desc_data %>% mutate(across(where(is.numeric), round, 2))
kable(desc_data, format = "latex",
      caption = "Descriptive Analysis of the dataset") %>%
  kable_styling(latex_options = c("striped", "scale_down"))
```

The descriptive analysis shown in Table 2 reveals the following observations:

- Most features exhibit some degree of right skewness, indicating that extreme values on the higher side are common;

Table 2: Descriptive Analysis of the dataset

| | vars | n | mean | sd | median | trimmed | mad | min | max | range | skew | kurtosis | se |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| diagnosis* | 1 | 569 | 1.37 | 0.48 | 1.00 | 1.34 | 0.00 | 1.00 | 2.00 | 1.00 | 0.53 | -1.73 | 0.02 |
| radius_mean | 2 | 569 | 14.13 | 3.52 | 13.37 | 13.82 | 2.82 | 6.98 | 28.11 | 21.13 | 0.94 | 0.81 | 0.15 |
| texture_mean | 3 | 569 | 19.29 | 4.30 | 18.84 | 19.04 | 4.17 | 9.71 | 39.28 | 29.57 | 0.65 | 0.73 | 0.18 |
| perimeter_mean | 4 | 569 | 91.97 | 24.30 | 86.24 | 89.74 | 18.84 | 43.79 | 188.50 | 144.71 | 0.99 | 0.94 | 1.02 |
| area_mean | 5 | 569 | 654.89 | 351.91 | 551.10 | 606.13 | 227.28 | 143.50 | 2501.00 | 2357.50 | 1.64 | 3.59 | 14.75 |
| smoothness_mean | 6 | 569 | 0.10 | 0.01 | 0.10 | 0.10 | 0.01 | 0.05 | 0.16 | 0.11 | 0.45 | 0.82 | 0.00 |
| compactness_mean | 7 | 569 | 0.10 | 0.05 | 0.09 | 0.10 | 0.05 | 0.02 | 0.35 | 0.33 | 1.18 | 1.61 | 0.00 |
| concavity_mean | 8 | 569 | 0.09 | 0.08 | 0.06 | 0.08 | 0.06 | 0.00 | 0.43 | 0.43 | 1.39 | 1.95 | 0.00 |
| concave.points_mean | 9 | 569 | 0.05 | 0.04 | 0.03 | 0.04 | 0.03 | 0.00 | 0.20 | 0.20 | 1.17 | 1.03 | 0.00 |
| symmetry_mean | 10 | 569 | 0.18 | 0.03 | 0.18 | 0.18 | 0.03 | 0.11 | 0.30 | 0.20 | 0.72 | 1.25 | 0.00 |
| fractal_dimension_mean | 11 | 569 | 0.06 | 0.01 | 0.06 | 0.06 | 0.01 | 0.05 | 0.10 | 0.05 | 1.30 | 2.95 | 0.00 |
| radius_se | 12 | 569 | 0.41 | 0.28 | 0.32 | 0.36 | 0.16 | 0.11 | 2.87 | 2.76 | 3.07 | 17.45 | 0.01 |
| texture_se | 13 | 569 | 1.22 | 0.55 | 1.11 | 1.16 | 0.47 | 0.36 | 4.88 | 4.52 | 1.64 | 5.26 | 0.02 |
| perimeter_se | 14 | 569 | 2.87 | 2.02 | 2.29 | 2.51 | 1.14 | 0.76 | 21.98 | 21.22 | 3.43 | 21.12 | 0.08 |
| area_se | 15 | 569 | 40.34 | 45.49 | 24.53 | 31.69 | 13.63 | 6.80 | 542.20 | 535.40 | 5.42 | 48.59 | 1.91 |
| smoothness_se | 16 | 569 | 0.01 | 0.00 | 0.01 | 0.01 | 0.00 | 0.00 | 0.03 | 0.03 | 2.30 | 10.32 | 0.00 |
| compactness_se | 17 | 569 | 0.03 | 0.02 | 0.02 | 0.02 | 0.01 | 0.00 | 0.14 | 0.13 | 1.89 | 5.02 | 0.00 |
| concavity_se | 18 | 569 | 0.03 | 0.03 | 0.03 | 0.03 | 0.02 | 0.00 | 0.40 | 0.40 | 5.08 | 48.24 | 0.00 |
| concave.points_se | 19 | 569 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.00 | 0.05 | 0.05 | 1.44 | 5.04 | 0.00 |
| symmetry_se | 20 | 569 | 0.02 | 0.01 | 0.02 | 0.02 | 0.01 | 0.01 | 0.08 | 0.07 | 2.18 | 7.78 | 0.00 |
| fractal_dimension_se | 21 | 569 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.03 | 0.03 | 3.90 | 25.94 | 0.00 |
| radius_worst | 22 | 569 | 16.27 | 4.83 | 14.97 | 15.73 | 3.65 | 7.93 | 36.04 | 28.11 | 1.10 | 0.91 | 0.20 |
| texture_worst | 23 | 569 | 25.68 | 6.15 | 25.41 | 25.39 | 6.42 | 12.02 | 49.54 | 37.52 | 0.50 | 0.20 | 0.26 |
| perimeter_worst | 24 | 569 | 107.26 | 33.60 | 97.66 | 103.42 | 25.01 | 50.41 | 251.20 | 200.79 | 1.12 | 1.04 | 1.41 |
| area_worst | 25 | 569 | 880.58 | 569.36 | 686.50 | 788.02 | 319.65 | 185.20 | 4254.00 | 4068.80 | 1.85 | 4.32 | 23.87 |
| smoothness_worst | 26 | 569 | 0.13 | 0.02 | 0.13 | 0.13 | 0.02 | 0.07 | 0.22 | 0.15 | 0.41 | 0.49 | 0.00 |
| compactness_worst | 27 | 569 | 0.25 | 0.16 | 0.21 | 0.23 | 0.13 | 0.03 | 1.06 | 1.03 | 1.47 | 2.98 | 0.01 |
| concavity_worst | 28 | 569 | 0.27 | 0.21 | 0.23 | 0.25 | 0.20 | 0.00 | 1.25 | 1.25 | 1.14 | 1.57 | 0.01 |
| concave.points_worst | 29 | 569 | 0.11 | 0.07 | 0.10 | 0.11 | 0.07 | 0.00 | 0.29 | 0.29 | 0.49 | -0.55 | 0.00 |
| symmetry_worst | 30 | 569 | 0.29 | 0.06 | 0.28 | 0.28 | 0.05 | 0.16 | 0.66 | 0.51 | 1.43 | 4.37 | 0.00 |
| fractal_dimension_worst | 31 | 569 | 0.08 | 0.02 | 0.08 | 0.08 | 0.01 | 0.06 | 0.21 | 0.15 | 1.65 | 5.16 | 0.00 |

Table 3: Tumors dataset classification

| Classification | Frequency |
|---|---|
| Benign | 357 |
| Malignant | 212 |

- The standard errors are relatively low compared to the mean values, suggesting that the measurements are fairly consistent;
- `area` and `radius` show high variability, which may be significant in distinguishing between benign and malignant tumors.

The next tables summarizes the counts of benign and malignant cases in the dataset:

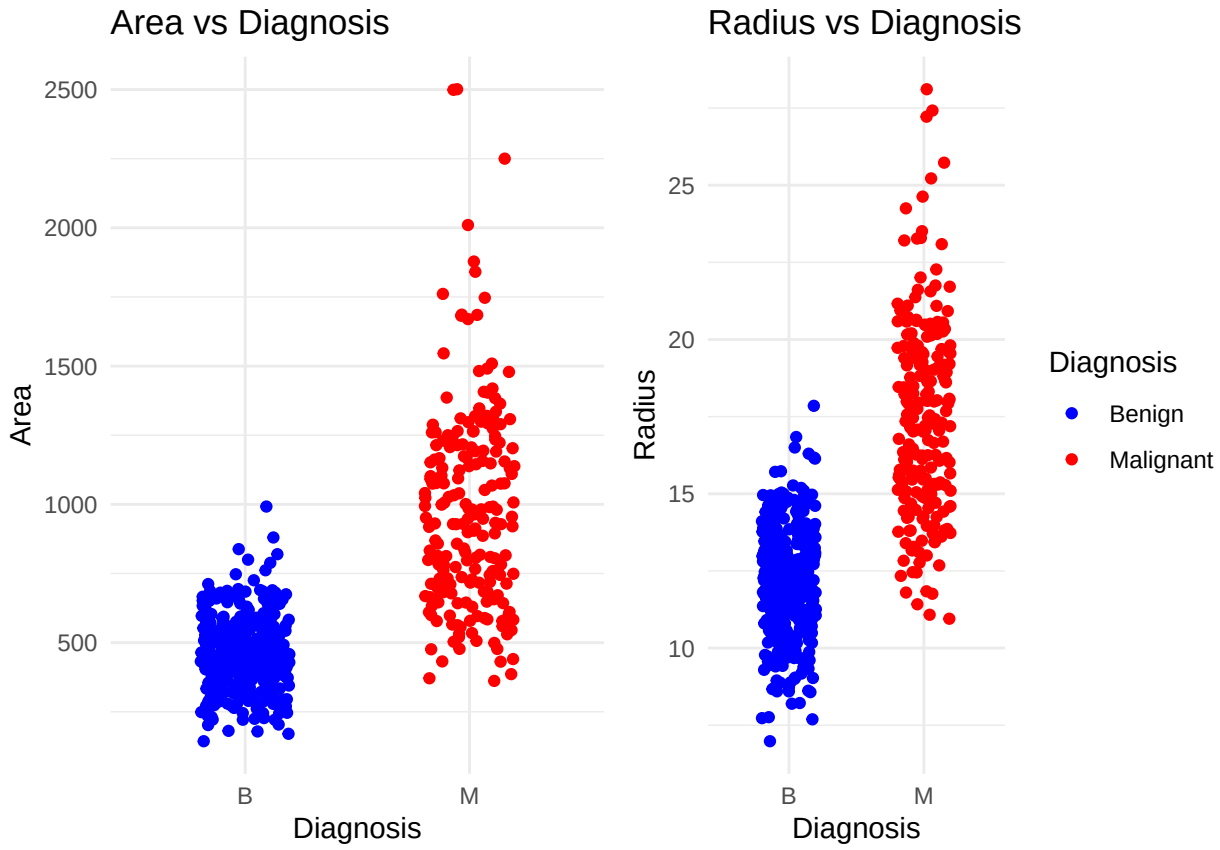
- Benign: There are 357 cases where the tumor is classified as benign;
- Malignant: There are 212 cases where the tumor is classified as malignant.

This imbalance could affect the performance of predicting model, making it biased towards the more frequent class.

```
diagnosis_table <- table(data$diagnosis)
names(diagnosis_table) <- c("Benign", "Malignant")
kable(diagnosis_table, format = "latex",
      caption = "Tumors dataset classification",
      col.names=c("Classification", "Frequency"))
```

```
data$diagnosis <- as.factor(data$diagnosis)
```

```r
plot_area <- ggplot(data, aes(x = diagnosis, y = area_mean, color = diagnosis)) +
  geom_jitter(width = 0.2) +
  theme_minimal() +
  labs(title = "Area vs Diagnosis",
       x = "Diagnosis",
       y = "Area") +
  scale_color_manual(values = c("B" = "blue", "M" = "red"), name = "Diagnosis") +
  theme(legend.position="none")

plot_radius <- ggplot(data, aes(x = diagnosis, y = radius_mean, color = diagnosis)) +
  geom_jitter(width = 0.2) +
  theme_minimal() +
  labs(title = "Radius vs Diagnosis",
       x = "Diagnosis",
       y = "Radius") +
  scale_color_manual(values = c("B" = "blue", "M" = "red"),
                     name = "Diagnosis",
                     labels = c("Benign", "Malignant"))

grid.arrange(plot_area, plot_radius, ncol = 2)
```




Both area and radius are useful features for distinguishing between benign and malignant tumors. The scatterplots show that malignant tumors tend to have higher values for these features compared to benign tumors.

In terms of data cleaning, there is no need to impute data as there are no missing values. Additionally, we do not need to address outliers because they are related to the diagnosis, and excluding them could negatively

Table 4: Correlation Matrix for Selected Features

| | radius | texture | perimeter | area | smoothness | compactness | concavity | concave.points | symmetry | fractal.dimension |
|---|---|---|---|---|---|---|---|---|---|---|
| radius | **1** | 0.32 | **1** | **0.99** | 0.17 | 0.51 | 0.68 | **0.82** | 0.15 | -0.31 |
| texture | 0.32 | **1** | 0.33 | 0.32 | -0.02 | 0.24 | 0.3 | 0.29 | 0.07 | -0.08 |
| perimeter | **1** | 0.33 | **1** | **0.99** | 0.21 | 0.56 | 0.72 | **0.85** | 0.18 | -0.26 |
| area | **0.99** | 0.32 | **0.99** | **1** | 0.18 | 0.5 | 0.69 | **0.82** | 0.15 | -0.28 |
| smoothness | 0.17 | -0.02 | 0.21 | 0.18 | **1** | 0.66 | 0.52 | 0.55 | 0.56 | 0.58 |
| compactness | 0.51 | 0.24 | 0.56 | 0.5 | 0.66 | **1** | **0.88** | **0.83** | 0.6 | 0.57 |
| concavity | 0.68 | 0.3 | 0.72 | 0.69 | 0.52 | **0.88** | **1** | **0.92** | 0.5 | 0.34 |
| concave.points | **0.82** | 0.29 | **0.85** | **0.82** | 0.55 | **0.83** | **0.92** | **1** | 0.46 | 0.17 |
| symmetry | 0.15 | 0.07 | 0.18 | 0.15 | 0.56 | 0.6 | 0.5 | 0.46 | **1** | 0.48 |
| fractal.dimension | -0.31 | -0.08 | -0.26 | -0.28 | 0.58 | 0.57 | 0.34 | 0.17 | 0.48 | **1** |

impact our analysis.

### Feature Selection

Based on dataset we will select only the following variables.

We will exclude all variables ending with `_se` and `_worst`. These variables are highly correlated with their corresponding `_mean` values, reducing their significance.

For example:

- `area_worst` represents the *worst* value for the area;
- `area_se` represents the *standard error* for the area;
- `area_mean` represents the *mean* for the area.

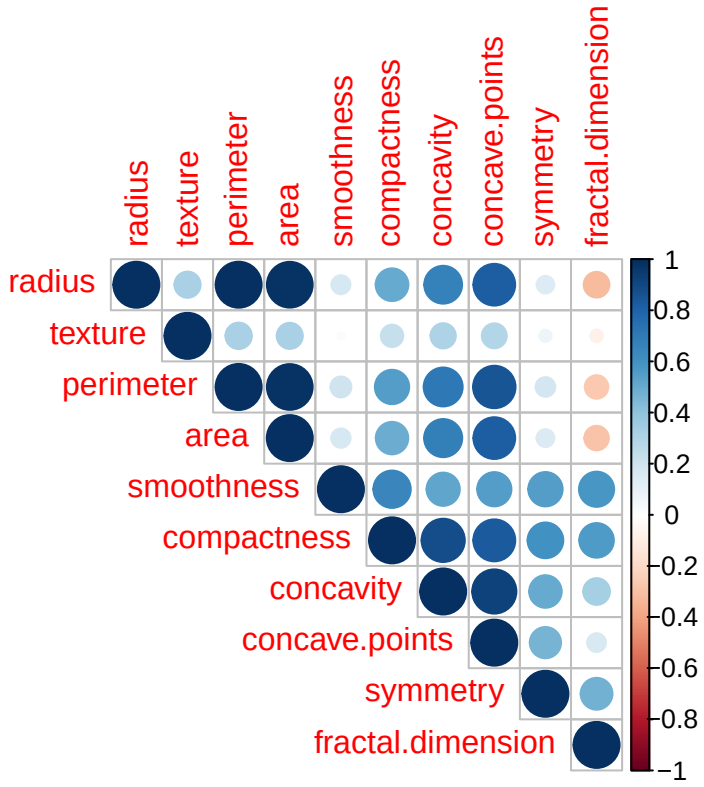
So we believe that the `area_mean` is the most representative feature for the area.

`diagnosis` will be our *dependent variable*.

```
selected_features <- data %>%
  select(contains("_mean"))  %>%
  rename_with(~ sub("_mean$", "", .))  %>%
  rename_with(~ gsub("_", ".", .))

corr_mt <- cor(selected_features)

corr_mt_formatted <- as.data.frame(corr_mt) %>%
  mutate(across(where(is.numeric), function(x){
    n <- round(x, 2)
    highly_correlated <- abs(x) > 0.9
    high_correlated <- abs(x) > 0.8
    cell_spec(n,
                format = "latex",
                color = ifelse(highly_correlated, "red",
                               ifelse(high_correlated, "blue", "black")),
                bold = ifelse(highly_correlated | high_correlated, T, F))
  }))

kable(corr_mt_formatted, format = "latex", escape = FALSE,
      caption = "Correlation Matrix for Selected Features") %>%
  kable_styling(latex_options = c("striped", "scale_down"))
```

```
corrplot(corr_mt, type = "upper",
         title = "Correlation Matrix of Selected Features",
         mar = c(0, 0, 2, 0))
```

## Correlation Matrix of Selected Features




By the correlation matrix and plot we can conclude:

- There is a *Very High Correlation* (0.9+) between `area`, `perimeter` and `radius`;
- There is also a *Very High Correlation* (0.9+) between `concavity` and `concave.points`;
- There is *High Correlation* (0.8+) between `concavity`, `concave.points`, `compactness`, `area`, `perimeter` and `radius`.

Based on the previous correlation matrix we will discard all the features with correlation bigger than 0.9 between them. So we will:

- Keep the feature `area` and discard `perimeter` and `radius`;
- Keep the feature `concavity` and discard `concave.points`.

Our final selected features are:

- diagnosis (target/dependent variable);
- area;
- texture;
- smoothness;
- compactness;
- concavity;
- symmetry;
- fractal.dimension.

### PCA

Before applying PCA, it is essential to select the predictor variables and scale them. This step is important because PCA assumes that the data is normally distributed and is sensitive to the variance of the variables. Standardizing the data ensures that each variable contributes equally to the analysis and that the results

Table 5: PCA Summary

| | PC1 | PC2 | PC3 | PC4 | PC5 | PC6 | PC7 |
|---|---|---|---|---|---|---|---|
| Standard deviation | 1.870985 | 1.292742 | 0.8870152 | 0.7041895 | 0.6096074 | 0.3120227 | 0.2767252 |
| Proportion of Variance | 0.500080 | 0.238740 | 0.1124000 | 0.0708400 | 0.0530900 | 0.0139100 | 0.0109400 |
| Cumulative Proportion | 0.500080 | 0.738820 | 0.8512200 | 0.9220600 | 0.9751500 | 0.9890600 | 1.0000000 |

Table 6: Eigenvalues and variance

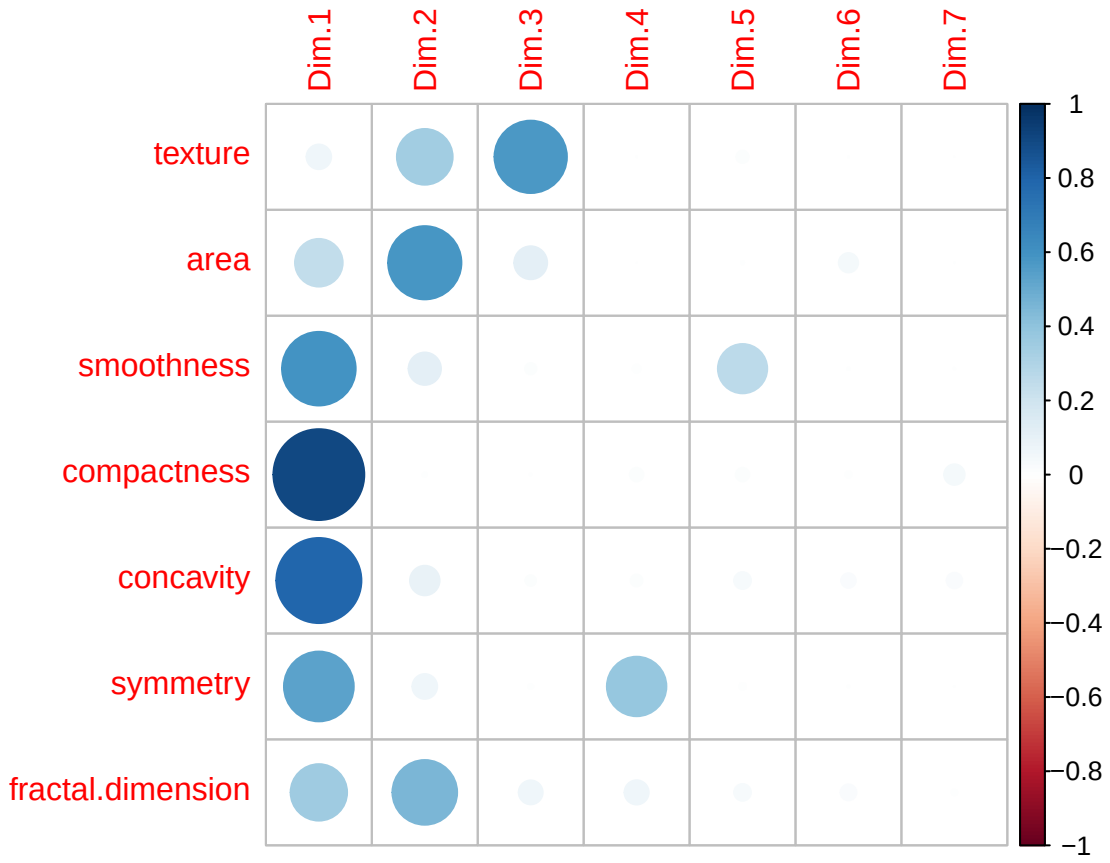
| | eigenvalue | variance.percent | cumulative.variance.percent |
|---|---|---|---|
| Dim.1 | 3.5005842 | 50.008346 | 50.00835 |
| Dim.2 | 1.6711809 | 23.874013 | 73.88236 |
| Dim.3 | 0.7867959 | 11.239941 | 85.12230 |
| Dim.4 | 0.4958828 | 7.084040 | 92.20634 |
| Dim.5 | 0.3716212 | 5.308874 | 97.51521 |
| Dim.6 | 0.0973581 | 1.390831 | 98.90605 |
| Dim.7 | 0.0765768 | 1.093954 | 100.00000 |

are not dominated by variables with higher variance. Luckily we can do it using the `center` and `scale.` parameter from the `prcomp` (Principal Components Analysis) function.

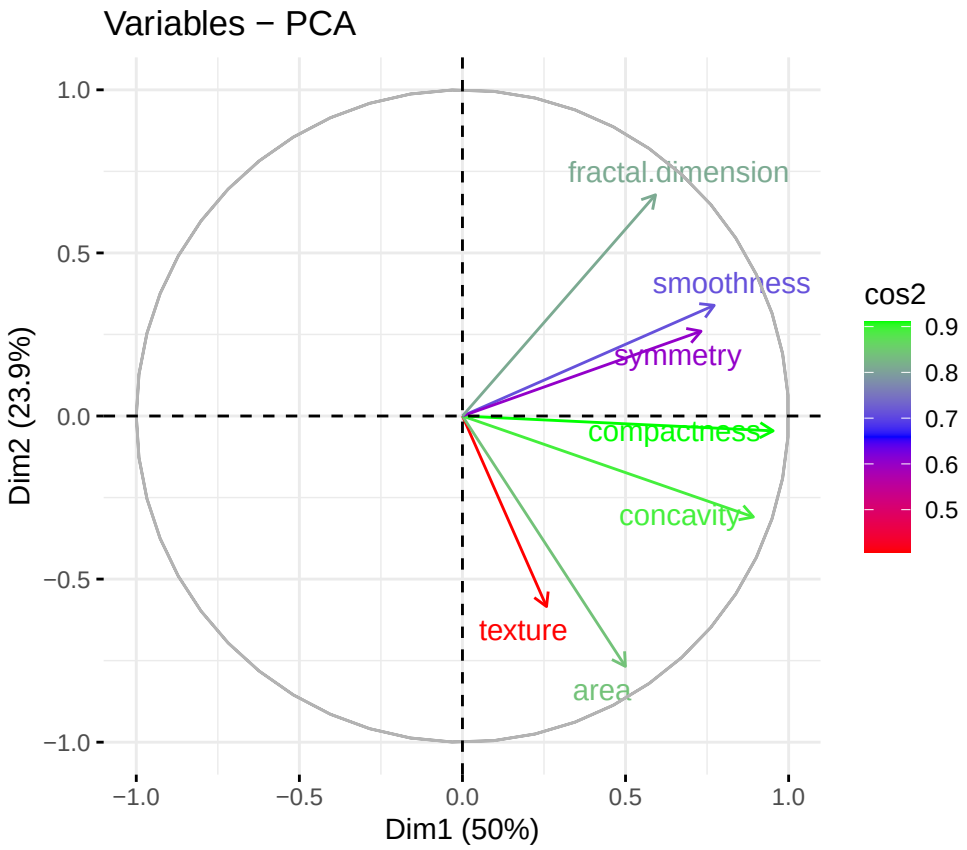
```
pca_selected <-  data %>%
  select(contains("_mean")) %>%
  rename_with(~ sub("_mean$", "", .))  %>%
  rename_with(~ gsub("_", ".", .)) %>%
  select(-c("perimeter", "radius", "concave.points"))

pca <- prcomp(pca_selected, center = TRUE, scale. = TRUE)

pca_summary <- summary(pca)

kable(pca_summary$importance, format = "latex", escape = FALSE,
      caption = "PCA Summary") %>%
  kable_styling(latex_options = c("striped", "scale_down"))
```

```
eig.val <- get_eigenvalue(pca)
kable(eig.val, format = "latex", escape = FALSE,
      caption = "Eigenvalues and variance") %>%
  kable_styling(latex_options = c("striped", "scale_down"))
```

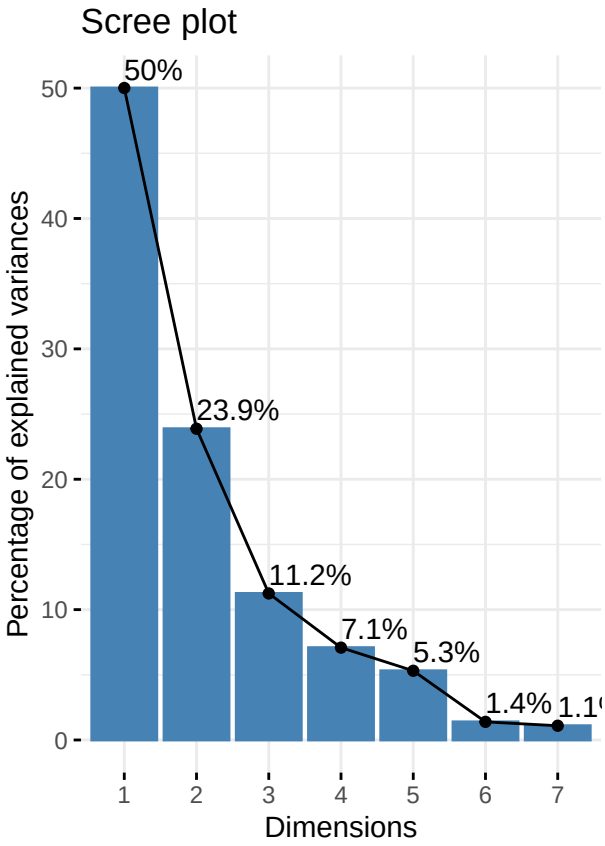
```
screeplot <- fviz_eig(pca, addlabels = TRUE)

vars = get_pca_var(pca)
corrplot(vars$cos2)
```

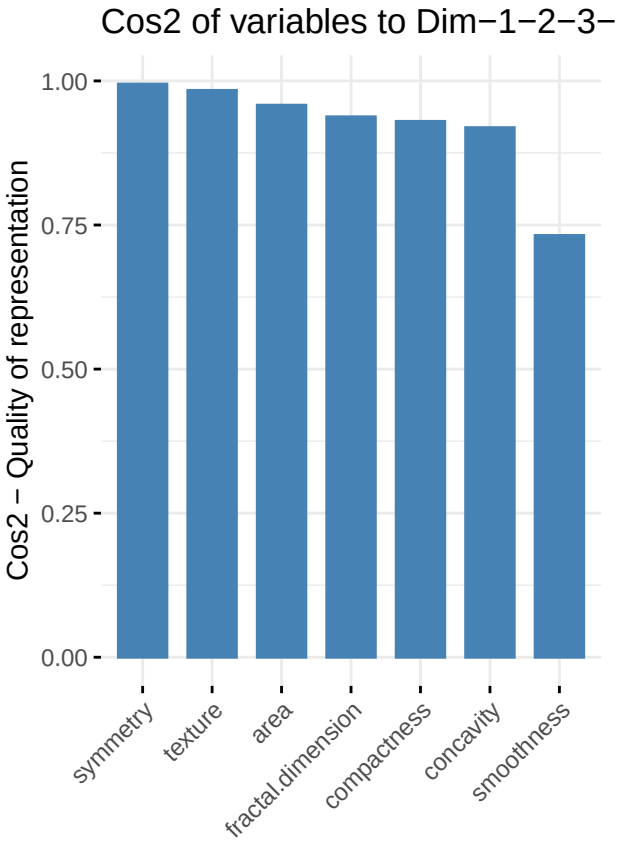



```
top_feature_contributors <- fviz_cos2(pca, choice = "var", axes=1:4)

eigenvectors <- fviz_pca_var(pca, col.var = "cos2",
             gradient.cols = c("red", "blue", "green"),
             repel = TRUE)

eigenvectors
```




```
plot_grid(screeplot, top_feature_contributors)
```




As we can see by the PCA Summary Table we saw that the first four components represents $\sim 92.2\%$ of the variance. is It a quite high value and we reduce from 7 to 4 variables to use in our model later it's a $\sim 43\%$ reduction of our initial features.

The first four principal components together explain about 92.2% of the total variance. This high percentage indicates that these components effectively summarize the majority of the variability in the dataset.

Initially, we have 7 features. By using PCA, we reduce this number to 4 principal components representing about 43% decrease in the number of dimensions (features)

$$Reduction\ Percentage = \frac{7-4}{7} = 0.4285714286 \approx 43.86\%$$

Using fewer features (4 instead of 7) simplifies the model, making it easier to interpret and faster to compute retaining an high explanatory power.

The eigenvectors and feature contributions plots reveal the following insights:

- All features are positively correlated;
- The most significant features for the first principal component are compactness, concavity, symmetry, and smoothness.
- The second principal component is primarily influenced by area and fractal.dimension;
- The third principal component is dominated by texture;
- Beyond the third dimension, the contributions of the features diminish. This reduction is expected since the first three principal components account for 85.12% of the total variance.

**Prepare the selected data for the model**

As mentioned earlier, our goal is to predict whether a patient has cancer based on data obtained from a fine needle aspirate (FNA) of a breast mass exam.

Table 7: Model data first rows

| PC1 | PC2 | PC3 | PC4 | diagnosis |
|---|---|---|---|---|
| 5.1370976 | 1.641103 | -2.0036533 | 0.1801931 | 1 |
| -0.4135265 | -1.621847 | -1.1658057 | -0.5143533 | 1 |
| 2.2934161 | -1.266826 | -0.5936102 | -0.4227546 | 1 |
| 6.5007434 | 3.772279 | 1.3135824 | 0.6362549 | 1 |
| 1.1901024 | -1.133655 | -2.0739767 | 0.1966861 | 1 |
| 2.7082503 | 2.205598 | -0.3591657 | 0.4687445 | 1 |

We will utilize the first four principal components from the PCA, given their high explanatory power and the reduced set of features they represent.

Given that our *dependent variable is binary* (indicating whether a patient has cancer or not) and we have multiple predictors (the first four principal components from PCA), the most appropriate method for analysis is *multivariate logistic regression*.

This model will predict the probability of having cancer (the probability of diagnosis is malignant or value M).

So our model will be the following one (Assumming the probability of a malignant cancer is $Y = 1$):

$$logit(P(Y = 1)) = \beta_0 + \beta_1 PC1 + \beta_2 PC2 + \beta_3 PC3 + \beta_4 PC4$$

The hypotheses that we want to test with this model is if our model significant predict the cancer diagnosis:

$$\begin{cases} H_0 : \beta_1 = \beta_2 = \beta_3 = \beta_4 = 0 \\ H_1 : \exists i \in \{1, 2, 3, 4\} : \beta_i \neq 0 \end{cases}$$

- The null hypothesis states that the first four principal components do not significantly predict cancer diagnosis.
- The alternative hypothesis states that the first four principal components do significantly predict cancer diagnosis.

### Data preparation

```
model_data <- as.data.frame(pca$x[, 1:4])
model_data$diagnosis <- ifelse(data$diagnosis == "M", 1, 0)

kable(head(model_data), format = "latex",
      caption = "Model data first rows") %>%
  kable_styling(latex_options = c("striped", "scale_down"))
```

```
str(model_data)
```

```
## 'data.frame':    569 obs. of  5 variables:
##  $ PC1      : num  5.137 -0.414 2.293 6.501 1.19 ...
##  $ PC2      : num  1.64 -1.62 -1.27 3.77 -1.13 ...
##  $ PC3      : num  -2.004 -1.166 -0.594 1.314 -2.074 ...
##  $ PC4      : num  0.18 -0.514 -0.423 0.636 0.197 ...
##  $ diagnosis: num  1 1 1 1 1 1 1 1 1 1 ...
```

```
levels(model_data$diagnosis)
```

```
## NULL
```

### Model

```
model <- glm(diagnosis ~ ., data = model_data, family = binomial)
summary(model)
```

```
##
## Call:
## glm(formula = diagnosis ~ ., family = binomial, data = model_data)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.5064     0.1994  -2.539 0.011110 *
## PC1           2.5606     0.2710   9.449  < 2e-16 ***
## PC2          -3.2317     0.3708  -8.716  < 2e-16 ***
## PC3          -0.7794     0.2333  -3.341 0.000834 ***
## PC4          -0.2983     0.2913  -1.024 0.305947
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 751.44  on 568  degrees of freedom
## Residual deviance: 180.19  on 564  degrees of freedom
## AIC: 190.19
##
## Number of Fisher Scoring iterations: 8
```

```
suppressWarnings(stargazer(model, type="text"))
```

```
##
## ===============================================
##                         Dependent variable:
##                     ---------------------------
##                              diagnosis
## -----------------------------------------------
## PC1                          2.561***
##                               (0.271)
##
## PC2                          -3.232***
##                               (0.371)
##
## PC3                          -0.779***
##                               (0.233)
##
## PC4                           -0.298
##                               (0.291)
##
## Constant                     -0.506**
##                               (0.199)
##
## -----------------------------------------------
## Observations                    569
## Log Likelihood                -90.094
## Akaike Inf. Crit.             190.189
## ===============================================
```

```
## Note:                *p<0.1; **p<0.05; ***p<0.01
```

By the model analysis we can conclude:

- The first three principal components (PC1, PC2, PC3) are significant predictors of cancer diagnosis and should be considered important in the model;
- The fourth principal component (PC4) does not significantly contribute to the prediction and might be excluded in a simplified model.

We can disregard the fourth component as it only accounts for 7% of the total variance. By using the first three components, we can still explain 85% of the variance, which is acceptable.

Restating the the model hypothesis we have:

Model:

$$logit(P(Y = 1)) = \beta_0 + \beta_1 PC1 + \beta_2 PC2 + \beta_3 PC3$$

The hypothesis:

$$\begin{cases} H_0 : \beta_1 = \beta_2 = \beta_3 = 0 \\ H_1 : \exists i \in \{1, 2, 3\} : \beta_i \neq 0 \end{cases}$$

The new model is the following:

```r
model_data_reduced <- as.data.frame(pca$x[, 1:3])
model_data_reduced$diagnosis <- ifelse(data$diagnosis == "M", 1, 0)
model_reduced <- glm(diagnosis ~ ., data = model_data_reduced, family = binomial)
suppressWarnings(stargazer(model_reduced, type="text"))
```

```
##
## ===============================================
##                         Dependent variable:
##                     ---------------------------
##                               diagnosis
## -----------------------------------------------
## PC1                           2.550***
##                                (0.269)
##
## PC2                           -3.223***
##                                (0.367)
##
## PC3                           -0.782***
##                                (0.233)
##
## Constant                      -0.502**
##                                (0.198)
##
## -----------------------------------------------
## Observations                    569
## Log Likelihood                -90.612
## Akaike Inf. Crit.             189.223
## ===============================================
## Note:                *p<0.1; **p<0.05; ***p<0.01
```

Our final model is (Log-Odds Equation):

$$logit(P(diagnosis = 1)) = -0.502 + 2.550 \times PC1 - 3.223 \times PC2 - 0.782 \times PC3$$

The results and performance of the model will be discussed in the next section.

# Results

After applying the Logistic Regression algorithm and PCA for feature reduction, we will discuss the model's performance and accuracy. The key metrics we will analyze include the null hypothesis vs. alternative hypothesis deviance, log-likelihood, Akaike Information Criterion (AIC), confusion matrix, and ROC curves.

Comparing Null Deviance vs. Residual Deviance we assess how much the inclusion of predictors improves the model's fit. A significant reduction in deviance suggests that the predictors significantly contribute to explaining the variability in the data.

The log-likelihood helps us understand how well the model explains the observed data. Higher log-likelihood values indicate a better fit of the model to the data.

AIC combines the log-likelihood of the model with a penalty for the number of parameters used. It helps in model selection by balancing model fit and complexity. Lower AIC values indicate a better model, considering both goodness of fit and model simplicity. AIC helps to avoid overfitting by penalizing models with too many predictors.

The confusion matrix provides insights into the model's accuracy, precision, recall, and overall effectiveness in classifying instances correctly. It is essential for understanding the types of errors the model is making.

ROC Curve. It plots the true positive rate (sensitivity) against the false positive rate (1 - specificity).

We will review the PCA process to understand how it reduces the dataset's dimensionality by transforming original features into principal components. Additionally, we will identify and discuss the features that have the highest contributions to the principal components, providing insights into the variables that most significantly influence the data's structure.

## Model Performance

```
summary(model_reduced)
```

```
##
## Call:
## glm(formula = diagnosis ~ ., family = binomial, data = model_data_reduced)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -0.5021     0.1981  -2.534  0.01128 *
## PC1           2.5499     0.2693   9.467  < 2e-16 ***
## PC2          -3.2232     0.3675  -8.771  < 2e-16 ***
## PC3          -0.7823     0.2328  -3.360  0.00078 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 751.44  on 568  degrees of freedom
## Residual deviance: 181.22  on 565  degrees of freedom
## AIC: 189.22
##
## Number of Fisher Scoring iterations: 8
```

Conclusions:

- The intercept represents the log-odds of a malignant diagnosis when all principal components are zero.
- PC1: Has a significant positive effect on the likelihood of a malignant diagnosis;
- PC2: Has a significant negative effect on the likelihood of a malignant diagnosis;

- PC3: Also has a significant negative effect on the likelihood of a malignant diagnosis.
- The intercept has significance of 0.01128 and the Principal Components lower than 0.001 indicating that all components are strong predictors of cancer diagnosis.

### Null deviance vs Residual Deviance

The significant reduction in deviance from the null model to the full model indicates that the predictors greatly improve the model's fit to the data.

## AIC

When we compare the AIC of the model using the three principal components to the model using all four, we observe a slight decrease in AIC from 190.19 to 189.22. This indicates that removing the statistically insignificant component slightly improves the model's performance.

## Likelihood ratio test

```
lrtest(model_reduced)
```

```
## Likelihood ratio test
##
## Model 1: diagnosis ~ PC1 + PC2 + PC3
## Model 2: diagnosis ~ 1
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   4  -90.61
## 2   1 -375.72 -3 570.22  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The Likelihood ratio test compare the current model against the null model. The $\chi^2$ test has a value of 570.22 suggesting that our model (Model 1) explains the variability much better than the null model (Model 2). It also has a The p-value less than 2.2e-16 indicating that our model is statistically significant. The reduction in log-likelihood from -375.72 in the null model to -90.61 in the our model indicates that the inclusion of PC1, PC2, and PC3 substantially improves the model's fit.

## Confusion Matrix

```
predicted_probs <- predict(model_reduced, type = "response")
predicted_classes <- ifelse(predicted_probs > 0.5, 1, 0)
actual_classes <- ifelse(data$diagnosis == "M", 1, 0)

confusion_matrix <- suppressWarnings(caret::confusionMatrix(factor(predicted_classes),
                                                            factor(actual_classes),
                                                            positive = "1"))
print(confusion_matrix)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction   0   1
##          0 342  25
##          1  15 187
##
##                Accuracy : 0.9297
##                  95% CI : (0.9055, 0.9493)
```

```
##     No Information Rate : 0.6274
##     P-Value [Acc > NIR] : <2e-16
##
##                   Kappa : 0.8482
##
##  Mcnemar's Test P-Value : 0.1547
##
##             Sensitivity : 0.8821
##             Specificity : 0.9580
##          Pos Pred Value : 0.9257
##          Neg Pred Value : 0.9319
##              Prevalence : 0.3726
##          Detection Rate : 0.3286
##    Detection Prevalence : 0.3550
##       Balanced Accuracy : 0.9200
##
##        'Positive' Class : 1
##
```

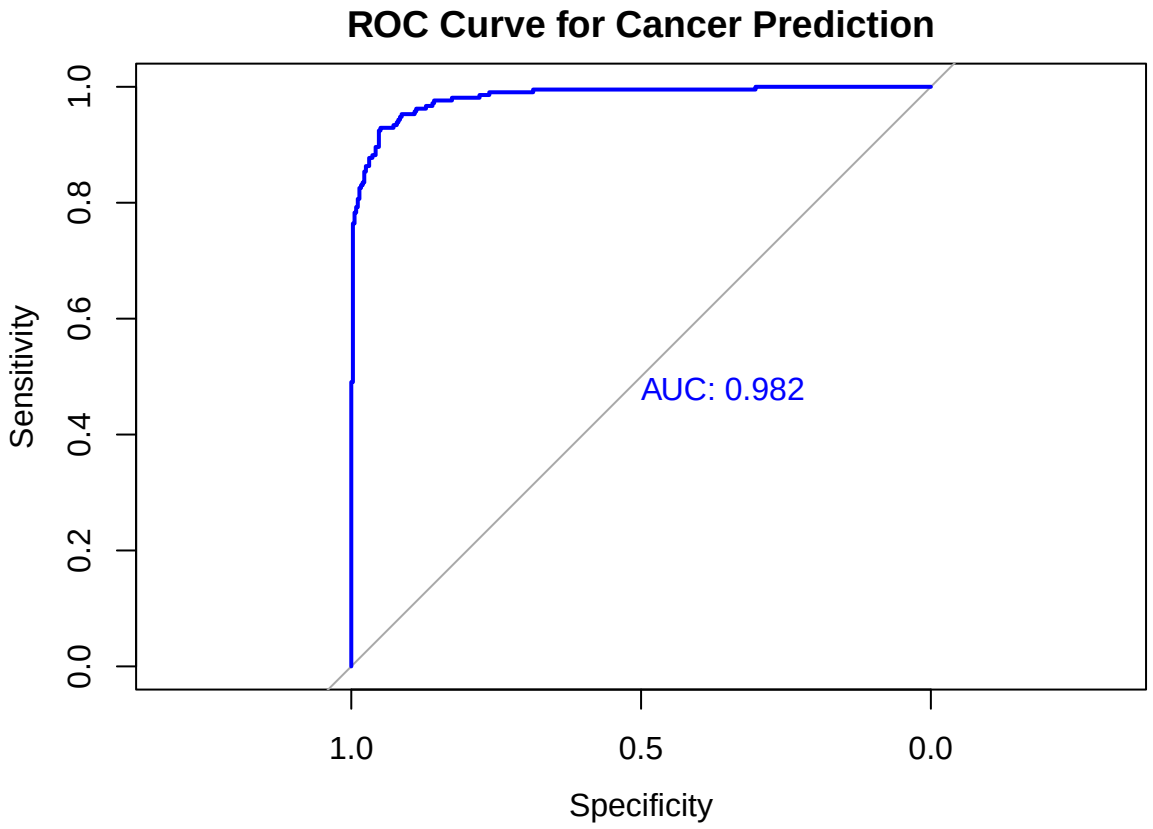
The confusion matrix has the following format:

| | |
|---|---|
| True Negatives (342) | False Negatives (25) |
| False Positives (15) | True Positives (187) |

Our model achieves an accuracy of 92.97%, demonstrating that the logistic regression model, which utilizes the first three principal components, is highly effective in predicting cancer diagnosis.

## ROC Curve and AUC

```
roc_curve <- roc(actual_classes, fitted(model_reduced))
roc_obj <- plot(roc_curve, main="ROC Curve for Cancer Prediction", col="blue",
     print.auc = T, control = 0, case = 1, direction = "<")
```




```
roc_obj
```

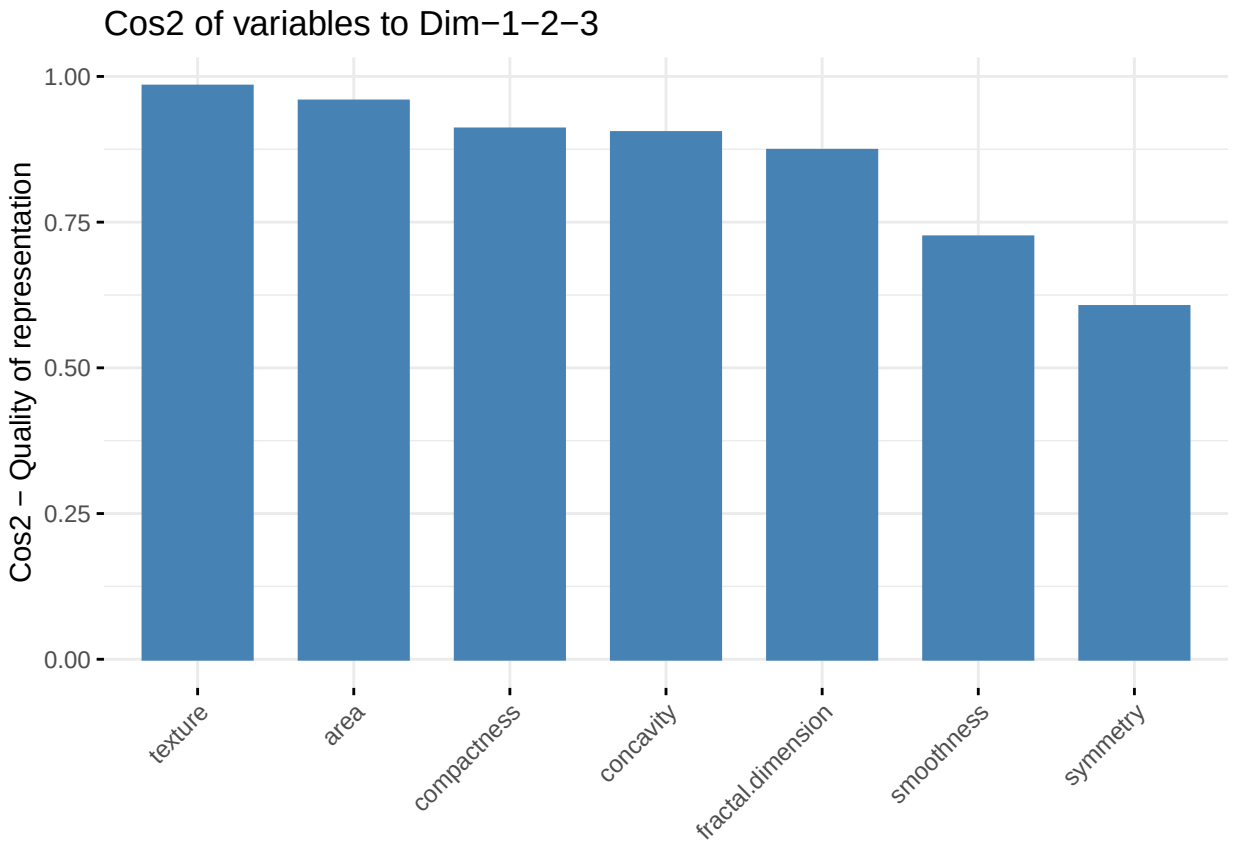
```
##
## Call:
## roc.default(response = actual_classes, predictor = fitted(model_reduced))
##
## Data: fitted(model_reduced) in 357 controls (actual_classes 0) < 212 cases (actual_classes 1).
## Area under the curve: 0.9824
```

The curve is close to the top-left corner, which indicates high sensitivity and specificity, meaning the model performs very well in distinguishing between malignant and benign cases.

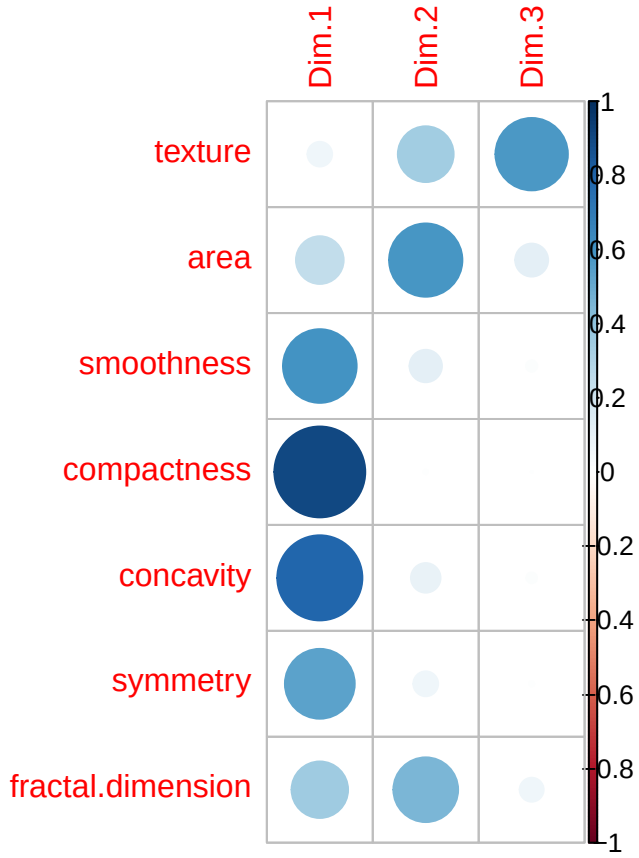
The AUC of 0.982 (closer to 1) indicates that the model has a high ability to distinguish between malignant and benign diagnoses. This means that the model is highly effective at correctly classifying patients with and without cancer.

### Principal variables in PCA

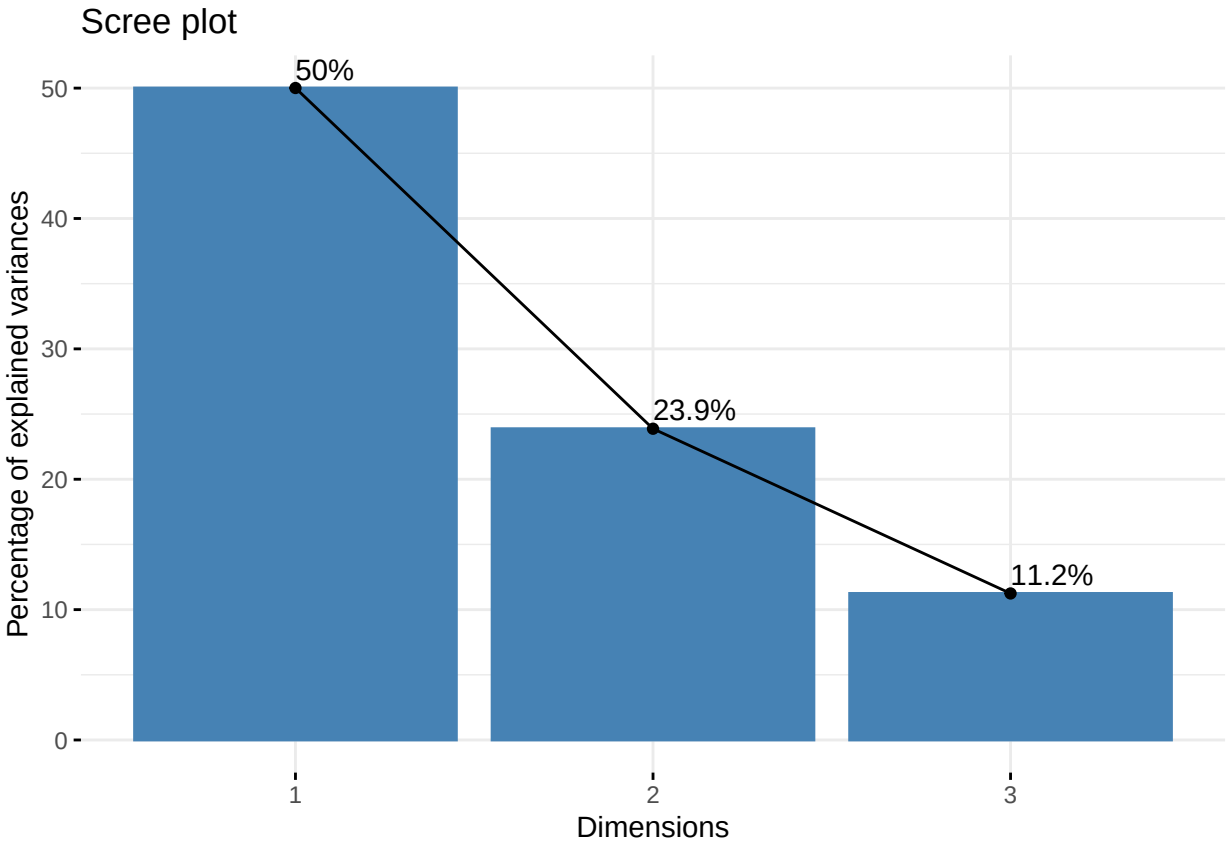
```
fviz_cos2(pca, choice = "var", axes=1:3)
```




```
vars = get_pca_var(pca)
corrplot(vars$cos2[, 1:3])
```




```
fviz_eig(pca, addlabels = TRUE, ncp = 3)
```




We have three plots. The first plot shows the overall contribution of the features to the three principal components combined. The second plot displays the contribution of each feature to each individual principal component. The last shows the explained variance per dimension.

- For the PC1 the most important features were compactness, concavity and smoothness;
- PC2 area and fractal dimension;
- PC3 texture.

In terms of total of importance across all the components we have:

- texture;
- area;
- compactness;
- concavity.

Variance explained per component

- PC1: 50%;
- PC2: 23.9%;
- PC3: 11.2%

# Discussion

In this study, we aimed to predict cancer diagnosis using a logistic regression model enhanced by Principal Component Analysis (PCA) to reduce dimensionality. The key findings revealed that our model, utilizing the first three principal components, achieved an impressive accuracy rate of 92.97%. This high accuracy indicates that the model is highly effective in distinguishing between malignant and benign cases.

One concerning factor is that our model produced 25 false negatives. In our dataset, this represents approximately 4.39% of the cases ($\frac{25}{569} * 100 \approx 4.39\%$). We can potentially reduce the number of false negatives by increasing the size of the dataset or incorporating additional variables into the model. Despite reducing the number of predictors from 32 to 3, the model maintained its accuracy, which is a significant improvement.

The model's performance was further validated by a significant reduction in the Akaike Information Criterion (AIC) from 190.19 to 189.22, demonstrating that eliminating the statistically insignificant fourth component improved the model's performance.

The ROC curve, with an Area Under the Curve (AUC) value of 0.982, underscores the model's excellent ability to discriminate between cancerous and non-cancerous diagnoses.

These results support our original hypothesis that the first three principal components can significantly predict cancer diagnosis.

Relating these findings back to our original predictions, the results affirm the hypothesis that PCA can effectively reduce dimensionality without sacrificing predictive accuracy.

Our study has certain limitations. One potential weakness is that the dataset used might not represent the full spectrum of patient variability seen in broader populations.

In conclusion, this study demonstrates that integrating PCA with logistic regression is a highly effective method for predicting cancer diagnosis. The model not only achieved high accuracy and excellent discriminative power but also provided valuable insights into the significance of various features. These findings underscore the potential of data-driven methodologies to enhance diagnostic accuracy and patient outcomes in medical practice. Future research building on these results can further advance the field of predictive analytics in healthcare, ultimately contributing to better health outcomes and more personalized treatment plans.

# References

Hickey, M, M Peat, C Saunders, and M Friedlander. 2009. "Breast Cancer in Young Women and Its Impact on Reproductive Function." *Human Reproduction Update* 15 (3): 323–39.

Repository, UCI Machine Learning. 1995. "Breast Cancer Wisconsin (Diagnostic)." 1995. https://archive.ics.uci.edu/dataset/17/breast+cancer+wisconsin+diagnostic.