



COS40007

Studio 1 - 3

Duc Thuan Tran|104330455

Portfolio Assessment 1

# **Overview**

This project examines the prediction of breast cancer diagnosis using the Wisconsin Diagnostic dataset, which contains 30 features characterizing cell nuclei from fine needle aspirate (FNA) images. By organizing features into mean, standard error, and worst measurement groups, the exploratory data analysis revealed strong correlations between size-related measurements and boundary irregularity features with diagnosis outcomes. After transforming the binary classification into a balanced 5-class risk assessment model, various feature engineering and selection approaches were implemented. Decision tree models trained on five different feature sets demonstrated that strategic feature selection significantly outperforms using all available features. The Representative Features set achieved 95.91% accuracy with only 7 carefully selected features, matching the performance of the 10-feature Worst Features set while using fewer variables. This work demonstrates the importance of effective feature selection in medical diagnostics, showing that model simplicity and performance can be simultaneously optimized through data-driven feature engineering.

# **Dataset Selection**

## 2.1 Selected Dataset: Breast Cancer Dianosis

## 2.2 Chosing Reason: I chose the Breast Cancer Diagnosis dataset because, as an Artificial Intelligence major, I am interested in how AI can benefit in biomedical engineering field. AI can improve Early Detection & Diagnosis, Treatment Planning, and Prediction Disease Outbreak, making it a powerful tool for healthcare. This dataset allows me to explore how AI can assist in diagnosing medical conditions, particularly breast cancer, and understand its potential to improve patient outcomes through early and accurate detection.

# **Summary of Exploratory Data Analysis**

## Variable Identification

**Target variables:** diagnosis

**Predictors:**

**+** radius1, texture1, perimeter1, area1, smoothness1, compactness1, concavity1, concave\_points1, symmetry1, fractal\_dimension1

**+** radius2, texture2, perimeter2, area2, smoothness2, compactness2, concavity2, concave\_points2, symmetry2, fractal\_dimension2.

**+**  radius3, texture3, perimeter3, area3, smoothness3, compactness3, concavity3, concave\_points3, symmetry3, fractal\_dimension3

## Univariate Analysis

**Continuous variable:**

**radius1** - Moderately right-skewed distribution -- radius1 is skewed to higher values.

**texture1** - Approximately normal distribution -- texture1 is symmetrically distributed around the mean.

**perimeter1** - Right-skewed distribution -- perimeter1 is skewed to higher values.

**area1** - Strongly right-skewed distribution -- area1 is highly skewed to higher values.

**smoothness1** - Approximately normal distribution -- smoothness1 is symmetrically distributed.

**compactness1** - Right-skewed distribution -- compactness1 is skewed to higher values.

**concavity1** - Right-skewed distribution -- concavity1 is skewed to higher values.

**concave\_points1** - Right-skewed distribution -- concave\_points1 is skewed to higher values.

**symmetry1** - Right-skewed distribution -- symmetry1 is skewed to higher values.

**fractal\_dimension1** – Right-skewed distribution – fractal\_dimension1 is skewed to higher values.

**radius2** - Moderately right-skewed distribution – radius2 is skewed to higher values.

**texture2** - Moderately right-skewed distribution – texture2 is skewed to higher values.

**perimeter2** - Right-skewed distribution – perimeter2 is skewed to higher values.

**area2** - Strongly right-skewed distribution – area2 is highly skewed to higher values.

**smoothness2** - Moderately right-skewed distribution – smoothness2 is highly skewed to higher values.

**compactness2** - Right-skewed distribution – compactness2 is skewed to higher values.

**concavity2** – Moderately right-skewed distribution – concavity2 is skewed to higher values.

**concave\_points2** - Moderately right-skewed distribution -- concave\_points2 is skewed to higher values.

**symmetry2** - Moderately right-skewed distribution – symmetry2 is skewed to higher values.

**fractal\_dimension2** – Moderately right-skewed distribution – fractal\_dimension2 is skewed to higher values.

**radius3** - Right-skewed distribution – radius3 is skewed to higher values.

**texture3** – Approximately normal distribution – texture3 is symmetrically distributed around the mean.

**perimeter3** - Right-skewed distribution – perimeter3 is skewed to higher values.

**area3** - Strongly right-skewed distribution – area3 is highly skewed to higher values.

**smoothness3** - Approximately normal distribution – smoothness3 is symmetrically distributed around the mean.

**compactness3** - Right-skewed distribution – compactness3 is skewed to higher values.

**concavity3** – Right-skewed distribution – concavity2 is skewed to higher values.

**concave\_points3** - Right-skewed distribution -- concave\_points3 is skewed to higher values.

**symmetry3** - Moderately right-skewed distribution – symmetry3 is skewed to higher values.

**fractal\_dimension3** – Right-skewed distribution – fractal\_dimension3 is skewed to higher values.

**Categorical Variable**

Diagnosis with two classes: Benign (B) and Malignant (M). The distribution shows: 62.7% Benign (B) and 37.3% Malignant (M)

Benign cases are more frequent, but malignant cases still make up a significant portion, ensuring a balanced analysis.

## Study Summary Statistics

**Sample size**: 569 observations for all features

**Size measurements**:

Areas (area1, area2, area3) have the largest values, with area3 having the highest mean (880.58) and maximum (4254.0).

Perimeters (perimeter1, perimeter2, perimeter3) are also substantial, with means ranging from about 2.87 to 107.26.

Radius (radius1, radius2, radius3) show interesting differences, with radius1 and radius3 having similar magnitudes (means of 14.12 and 16.27), but radius2 is much smaller (mean of 0.41).

**Shape descriptors**:

Texture features (texture1, texture2, texture3) show significant variation between groups.

Smoothness, compactness, concavity, and concave\_points generally have small values below 1.0.

The "2" features (smoothness2, compactness2, etc.) generally have smaller values than their "1" and "3" counterparts.

Symmetry and fractal\_dimension features are relatively small across all three sets.

**Variability**:

Area measurements show high standard deviations, indicating wide dispersion.

Several concavity features have minimum values of 0, suggesting some observations lack concavity entirely.

**Distribution characteristics**:

For most features, the median (50%) is closer to the 25% quartile than the 75% quartile, suggesting right-skewed distributions.

The maximum values are often substantially higher than the 75% quartiles, indicating potential outliers.

## Multivariate Analysis

## Introduction and Feature Organization

The Breast Cancer Wisconsin Diagnostic dataset contains 30 distinct features derived from digitized images of fine needle aspirate (FNA) of breast masses. These features represent various cellular characteristics that can help differentiate between malignant and benign tumors. Due to the large number of features, this analysis organizes them into three meaningful groups:

1. **Mean Features**(suffix "1"):Average values of cell nucleus characteristics
2. **Standard Error Features**(suffix "2"): Standard error of measurements
3. **Worst Features**(suffix "3"): The "worst" or most extreme values observed

This grouping strategy allows for more effective visualization and interpretation of relationships between features and their diagnostic value. The following analysis examines each feature group separately, identifying patterns that can inform feature selection and engineering for breast cancer diagnosis.

## Diagonal Analysis

The KDE diagonal plots across all three feature types (mean, standard error, worst) show consistent bimodal distributions in most features, particularly pronounced in the "worst" features.

The separation between malignant (blue) and benign (green) classes is most distinct in size-related measures (radius, perimeter, area) and boundary irregularity features (concavity, concave\_points) across all three measurement types.

The "worst" features show the clearest separation between diagnostic classes, followed by mean features, while standard error features generally show more overlap between classes.

Features like smoothness, symmetry, and fractal\_dimension demonstrate less distinct separation between diagnostic classes in their diagonal distributions.

## Off Diagonal Analysis: Relationships between Independent Features

### Mean Features

Strong positive linear relationships exist between radius1, perimeter1, and area1 (r-value near 1), indicating high redundancy among these size measurements.

Concavity1 and concave\_points1 show strong correlation with each other and moderate correlation with size features.

Texture1, smoothness1, symmetry1, and fractal\_dimension1 display weaker correlations with other features, suggesting they capture different cell characteristics.

### Standard Error Features

Strong correlations exist between radius2, perimeter2, and area2, indicating measurement redundancy.

The standard error features generally show more spread and less clear separation between diagnostic classes compared to mean and worst features.

The relationships between different standard error measurements appear more scattered, suggesting higher variability in these measurements.

### Worst Features

The strongest correlations again appear among radius3, perimeter3, and area3, with near-perfect linear relationships.

Compactness3, concavity3, and concave\_points3 show moderate to strong correlations with each other.

The worst features demonstrate the most pronounced separation between malignant and benign cases, particularly for concave\_points3, concavity3, and the size-related measures.

Even texture3 shows better separation between classes than its mean and standard error counterparts.

## Diagnosis Relationship: Patterns across Feature Types

### Mean Features vs Diagnosis

Concave\_points1, concavity1, radius1, perimeter1, and area1 show the strongest separation between malignant and benign cases.

Smoothness1 and fractal\_dimension1 show the least separation among mean features.

### Standard Error Features vs Diagnosis

Standard error features generally show less clear separation between diagnostic classes.

Radius2, area2, and concave\_points2 offer the best, though modest, separation among standard error features.

### Worst Features vs Diagnosis

The worst features provide the clearest distinction between malignant and benign cases.

Concave\_points3, concavity3, perimeter3, area3, and radius3 show excellent separation between classes.

Even features like compactness3 and texture3 demonstrate better diagnostic value compared to their counterparts in mean and standard error measurements.

## Cross-Feature Type Observations

For each characteristic (e.g., radius, texture), the "worst" measurement consistently provides better diagnostic separation than mean or standard error, making worst features the strongest predictors of diagnosis.

Standard error measurements generally provide the least distinct separation between diagnostic classes and are therefore less reliable predictors.

The correlation patterns between features remain consistent across the three feature types, with similar relationships observed in mean, standard error, and worst measurements.

Among all measurements, the best predictors of diagnosis include from the worst features group - concave\_points3, concavity3, radius3, perimeter3, and area3; from the mean features group - concave\_points1, concavity1, radius1, perimeter1, and area1; and from the standard error group - radius2, area2, and concave\_points2, though these are less effective than their counterparts in the other groups.

## Correlation

**Overall Correlation Heatmap:**

Strong positive correlations (dark red) exist between size-related measurements across all three feature types (radius, perimeter, area)

Concavity and concave\_points show strong positive correlations with each other across all feature types

Features within the same measurement type (mean, SE, worst) tend to correlate more strongly with each other than with features from other types

**Mean Features Correlations:**

Radius1, perimeter1, and area1 have extremely high positive correlations (0.99-1.00) with each other, indicating redundancy

Concavity1 and concave\_points1 show very strong positive correlation (0.92), suggesting they measure similar aspects of cell nuclei

Compactness1 shows strong positive correlation with concavity1 (0.88) and concave\_points1 (0.83)

Fractal\_dimension1 has moderate negative correlation with radius1 (-0.31), perimeter1 (-0.26), and area1 (-0.28)

Texture1 shows relatively weak correlations with other features, suggesting it captures unique information

**Standard Error Features Correlations:**

Radius2, perimeter2, and area2 show very strong positive correlations (0.94-0.97) with each other

Compactness2 has strong positive correlations with concavity2 (0.80) and fractal\_dimension2 (0.80)

Concavity2 and concave\_points2 show strong positive correlation (0.77)

Texture2 generally shows weak correlations with other standard error features

Overall, the standard error features show more moderate correlations than mean or worst features

**Worst Features Correlations:**

Radius3, perimeter3, and area3 show extremely high positive correlations (0.98-0.99) with each other

Concavity3 and concave\_points3 show strong positive correlation (0.86)

Compactness3 shows strong positive correlations with concavity3 (0.89), concave\_points3 (0.80), and fractal\_dimension3 (0.81)

Concave\_points3 has strong positive correlations with radius3 (0.79) and perimeter3 (0.82)

Fractal\_dimension3 shows very low correlation with size measurements (radius3, perimeter3, area3)

**Key Insights from Correlation Analysis:**

The size measurements (radius, perimeter, area) are highly redundant across all feature types and could be reduced to a single representative feature

Boundary irregularity features (compactness, concavity, concave\_points) form another highly correlated group

Texture features generally have weaker correlations with other features, suggesting they provide complementary information

Fractal dimension shows negative correlation with size measurements but positive correlation with boundary irregularities

# **Class Labeling For Target Variable / Developing Ground True Data**

## Approach to Multi-class Classification

For the Breast Cancer Wisconsin Diagnostic dataset, the original target variable is binary, classifying tumors as either malignant (M) or benign (B). To develop a more nuanced classification system, I transformed this binary classification into a 5-class risk assessment scale using a composite score approach based on key predictive features identified in the EDA.

The composite score method used the following steps:

1. Selected the most discriminative features based on correlation analysis and multivariate visualization:
   * concave\_points3
   * concavity3
   * radius3
   * perimeter3
   * area3
2. Normalized these features using MinMaxScaler to ensure equal contribution to the composite score
3. Created a composite risk score by calculating the mean of these normalized features
4. Divided the population into quintiles based on this composite score
5. Assigned risk categories to each quintile:
   * Very Low Risk
   * Low Risk
   * Moderate Risk
   * High Risk
   * Very High Risk

## Results of Class Labeling

The implementation resulted in a nearly perfect balance among the five classes:

|  |  |
| --- | --- |
| Risk Class | Sample Count |
| Very High Risk | 114 |
| High Risk | 114 |
| Low Risk | 114 |
| Very Low Risk | 114 |
| Moderate Risk | 113 |

## Correlation with Original Diagnosis

# Note: Results might vary slightly between runs due to normalization processes and percentile-based division methods.

The newly created risk classes show strong alignment with the original diagnosis, with a clear progression of malignancy rates:

|  |  |  |
| --- | --- | --- |
| Risk Class | Malignant % | Benign% |
| Very High Risk | 100.00% | 0.00% |
| High Risk | 78.07% | 21.93% |
| Moderate Risk | 6.19% | 93.81% |
| Low Risk | 1.75% | 98.25% |
| Very Low Risk | 0.00% | 100.00% |

This distribution demonstrates that the risk classification effectively captures the underlying diagnostic information while providing a more graduated assessment scale.

# **Feature Engineering and Feature Selection**

## Feature Engineering

Several new features were engineered based on insights from exploratory data analysis:

1. **Ratio features**: Created ratios of worst to mean measurements (e.g., radius3/radius1) to quantify the degree of cellular abnormality by measuring how extreme the worst measurements are compared to average values.
2. **Difference features**: Calculated the absolute difference between worst and mean measurements to capture the range of variation in cell characteristics.
3. **Composite scores**: Combined related features into meaningful group scores:
   * Irregularity scores: Combined concavity, concave points, and compactness measures
   * Size scores: Integrated radius, perimeter, and area measurements

This engineering process created 26 new features that potentially capture important patterns in the data that individual features might miss.

## Feature Selection

Five distinct feature sets were created for model comparison:

1. **Feature Set 1**: All 30 original features (normalized) - provides a baseline using the complete feature set
2. **Feature Set 2**: 10 worst features only (those ending with '3') - focuses on the measurement type that showed best class separation
3. **Feature Set 3**: 10 top correlated features with diagnosis - includes the most predictive features identified through correlation analysis
4. **Feature Set 4**: 7 representative features from different correlation groups - maintains diversity while minimizing redundancy:
   * radius3 (representing size measures)
   * texture3
   * concave\_points3 (representing boundary irregularity)
   * symmetry3
   * fractal\_dimension3
   * radius1 (mean size representation)
   * concave\_points1 (mean boundary irregularity)
5. **Feature Set 5**: 26 engineered features only - tests whether derived features outperform original measurements

# **Training And Decision Tree Model Development**

## Model Training Process

The model training process followed a structured approach to evaluate how different feature engineering and selection strategies affected breast cancer diagnostic performance:

**Data Preparation**: First, the code cleaned all feature sets using a custom function that replaced infinity values with NaN and then filled these with column means to ensure model stability.

**Dataset Organization**: Five distinct feature sets were prepared:

1. All Original Features (feature set 1)
2. Worst Features Only (feature set 2)
3. Top Correlated Features (feature set 3)
4. Representative Features (feature set 4)
5. Engineered Features (feature set 5)

**Train-Test Split**: For each feature set, the data was split into training (70%) and testing (30%) sets using train\_test\_split with stratification to maintain the same class distribution in both sets.

**Model Initialization**: A DecisionTreeClassifier was initialized with a fixed random\_state=42 to ensure reproducibility across all experiments.

**Model Training**: The classifier was fitted to the training data using the fit () method with the feature set and corresponding target labels.

**Prediction**: The trained model generated predictions on the test set using the predict () method.

## Evaluation Process

After training each model, a comprehensive evaluation was performed:

**Metric Calculation**: Four key performance metrics were calculated for each model: Accuracy, Precision, Recall and F1-score

**Results Storage**: All metrics along with feature counts and confusion matrices were stored in a dictionary for each feature set.

**Classification Reports**: Detailed classification reports were generated showing class-specific performance metrics (precision, recall, F1-score) for both benign and malignant classes, as well as macro and weighted averages.

# **Comparison Table**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Accuracy | Precision | Recall | F1 score |
| Worst Features Only | 0.959064 | 0.959287 | 0.959064 | 0.958856 |
| Representative Features | 0.959064 | 0.960135 | 9.959064 | 0.958700 |
| Top Correlated Features | 0.918129 | 0.917855 | 0.918129 | 0.917858 |
| Engineered Features | 0.906433 | 0.906201 | 0.906433 | 0.905782 |
| All Original Features | 0.900585 | 0.900166 | 0.900585 | 0.900079 |

# Note: Results might vary slightly between runs due to normalization processes and percentile-based division methods.

## Key Observations

* + "Worst Features Only” and "Representative Features" both achieved the highest accuracy of 95.91%, demonstrating that carefully selected features outperform using all original features.
  + The "Representative Features" set achieved top performance with only 7 features, showing that a small set of well-chosen features can be just as effective as larger feature sets. This set also achieved the highest precision (0.960135).
  + Despite having all 30 original features, the "All Original Features" set performed worst with just 90.06% accuracy, confirming that more features don't necessarily lead to better performance.
  + The "Engineered Features" set performed only slightly better than using all original features, suggesting that the specific engineering approach used may not have captured additional discriminative information.
  + The "Top Correlated Features" set performed well with 91.81% accuracy, but not as well as the worst or representative feature sets.

# **Appendix: Source Code Repository**

The source code is in my GitHub, here is the link access to it:

# **References**

<https://www.kaggle.com/code/vinayakshanawad/random-forest-with-bootstrap-sampling-for-beginner>

<https://archive.ics.uci.edu/dataset/17/breast%2Bcancer%2Bwisconsin%2Bdiagnostic>

<https://www.geeksforgeeks.org/decision-tree-implementation-python/>