Data Visualization Pitch

Student Individual Assignment

Predicting Breast Tumor Malignancy Using Machine Learning Models

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Research questions

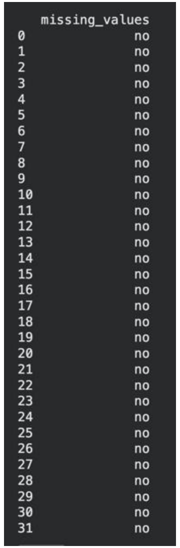
Can machine learning models accurately predict whether a breast tumor is benign or malignant using numeric features ?

- Which classification model works best for this task (Random Forest, XGBoost, SVM, KNN, Decision Tree), and how large is the performance gap between them?
- Does applying PCA (Principal Component Analysis) improve or harm predictive performance compared to using all 30 original features?
- How does balancing the dataset (via oversampling) affect model performance?
- How do different classification thresholds change the trade-off between false negatives (missing a cancer) and false positives (flagging healthy tissue as malignant)?

About Data

- **Dataset**: Breast Cancer Wisconsin (Diagnostic), downloaded from Kaggle (“Breast Cancer Wisconsin (Diagnostic) Data Set”).
- **Original source**: UCI Machine Learning Repository (Wolberg et al., 1993).
- **Target**: Diagnosis label — M = malignant, B = benign.
- **Features**: 30 numeric measurements from FNA images describing cell nuclei (shape, size, texture, etc.).
- **Data quality**: no missing values; all features numeric; moderate class imbalance (more benign).
- **Limitations**: The dataset is moderately imbalanced in the original form (more benign than malignant samples)
- **Preprocessing**: drop ID, encode M→1 / B→0, standardize features, oversample to balance classes.
- **Licence**: Kaggle copy under CC BY-NC-SA 4.0 (non-commercial use, attribution, share alike); original UCI dataset under CC BY 4.0.

Missing Values



```
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2              no
3              no
4              no
5              no
6              no
7              no
8              no
9              no
10             no
11             no
12             no
13             no
14             no
15             no
16             no
17             no
18             no
19             no
20             no
21             no
22             no
23             no
24             no
25             no
26             no
27             no
28             no
29             no
30             no
31             no
```
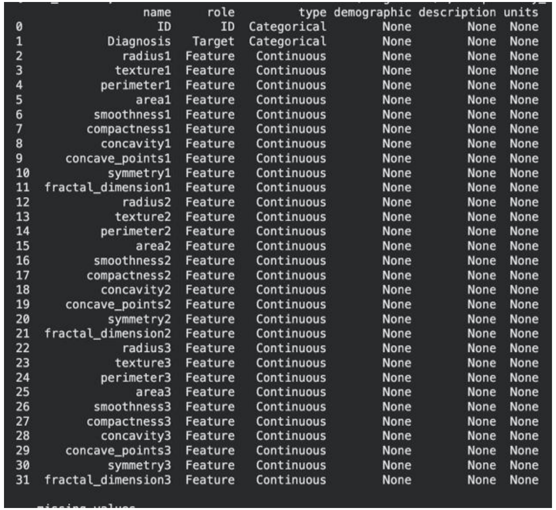

Features



```
                  name     role         type demographic description units
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1            Diagnosis   Target  Categorical        None        None  None
2              radius1  Feature   Continuous        None        None  None
3             texture1  Feature   Continuous        None        None  None
4           perimeter1  Feature   Continuous        None        None  None
5                area1  Feature   Continuous        None        None  None
6         smoothness1  Feature   Continuous        None        None  None
7         compactness1  Feature   Continuous        None        None  None
8           concavity1  Feature   Continuous        None        None  None
9      concave_points1  Feature   Continuous        None        None  None
10           symmetry1  Feature   Continuous        None        None  None
11  fractal_dimension1  Feature   Continuous        None        None  None
12             radius2  Feature   Continuous        None        None  None
13            texture2  Feature   Continuous        None        None  None
14          perimeter2  Feature   Continuous        None        None  None
15               area2  Feature   Continuous        None        None  None
16         smoothness2  Feature   Continuous        None        None  None
17        compactness2  Feature   Continuous        None        None  None
18          concavity2  Feature   Continuous        None        None  None
19     concave_points2  Feature   Continuous        None        None  None
20           symmetry2  Feature   Continuous        None        None  None
21  fractal_dimension2  Feature   Continuous        None        None  None
22             radius3  Feature   Continuous        None        None  None
23            texture3  Feature   Continuous        None        None  None
24          perimeter3  Feature   Continuous        None        None  None
25               area3  Feature   Continuous        None        None  None
26         smoothness3  Feature   Continuous        None        None  None
27        compactness3  Feature   Continuous        None        None  None
28          concavity3  Feature   Continuous        None        None  None
29     concave_points3  Feature   Continuous        None        None  None
30           symmetry3  Feature   Continuous        None        None  None
31  fractal_dimension3  Feature   Continuous        None        None  None
```
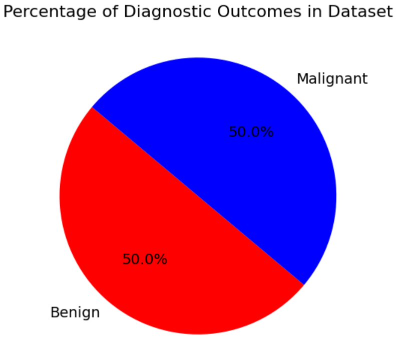
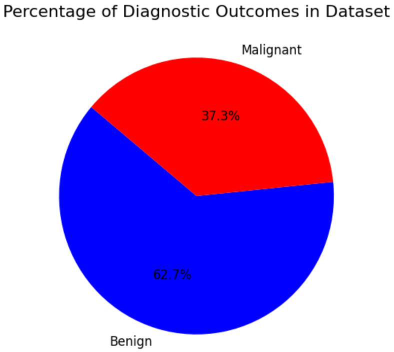



After oversampling



Before oversampling

Methodology

Data collection:

- Breast Cancer Wisconsin (Diagnostic) dataset downloaded from Kaggle.

Tools:

- Python (Jupyter) with: pandas, numpy, scikit-learn, xgboost, imblearn, matplotlib, seaborn.

Pre-processing & transformation:

- Dropped ID column; encoded diagnosis (M → 1, B → 0).
- Standardized all numeric features (StandardScaler).
- Balanced classes with RandomOverSampler (~50% benign / 50% malignant).
- Tested models with and without PCA on the standardized features.
- Stratified train/test split.

Modeling:

- Tried: Random Forest, XGBoost, SVM, KNN, Decision Tree (basic + regularized).
- Used K-fold cross-validation and GridSearchCV to tune XGBoost and SVM.

Evaluation

- Metrics: accuracy, precision, recall, F1-score, confusion matrix, precision–recall curve.
- Best model: tuned XGBoost without PCA (≈98.6% accuracy, precision and recall).

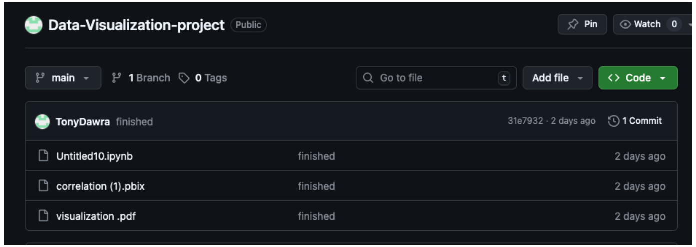
Use of AI tools

- Used ChatGPT to clarify functions, comment code, and prepare presentation text.

Source code:
https://github.com/TonyDawra/Data-Visualization-project

Content :

- Pdf
- Power bi correlation
- Notebook



Data-Visualization-project

TonyDawra finished 31e7932 · 2 days ago 1 Commit

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correlation (1).pbix	finished	2 days ago
visualization .pdf	finished	2 days ago

Insights from the Data

Key quantitative insights

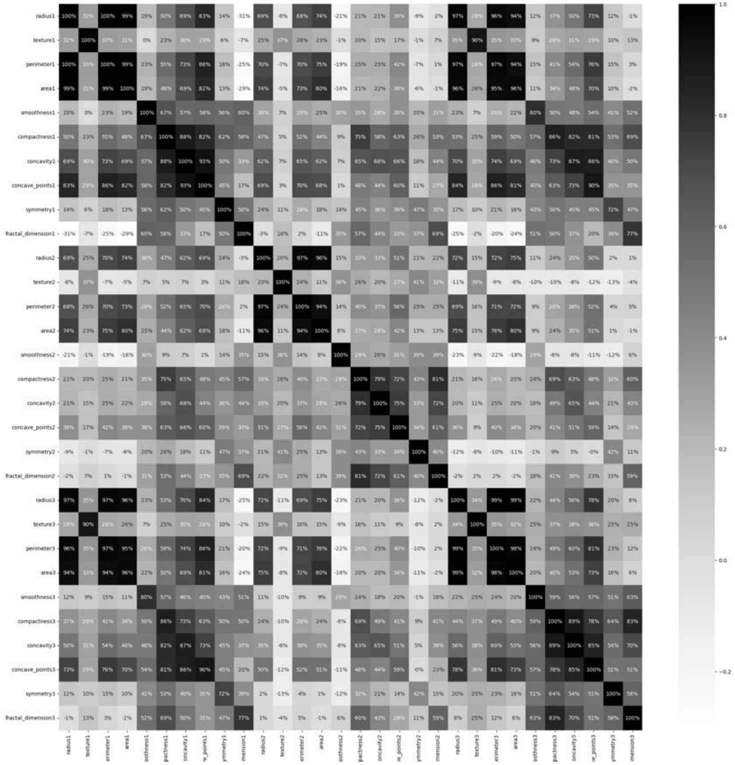
- After oversampling, the dataset is balanced (50% benign / 50% malignant).
- All models perform well; tuned XGBoost without PCA is best (≈98.6% accuracy, high and balanced precision/recall).
- Regularized SVM is close but slightly worse.
- PCA does not improve results; best performance is with the 30 scaled original features.
- Confusion matrix for XGBoost shows very few false negatives and a small, acceptable number of false positives.

Analysis performed

- Descriptive analysis of class distribution and feature correlations.
- Comparative analysis of 8 models, with vs without PCA, and with/without regularization.
- Error analysis using confusion matrix and TN/FP/FN/TP bar chart.
- Threshold analysis using precision–recall curve to study precision vs recall trade-off.

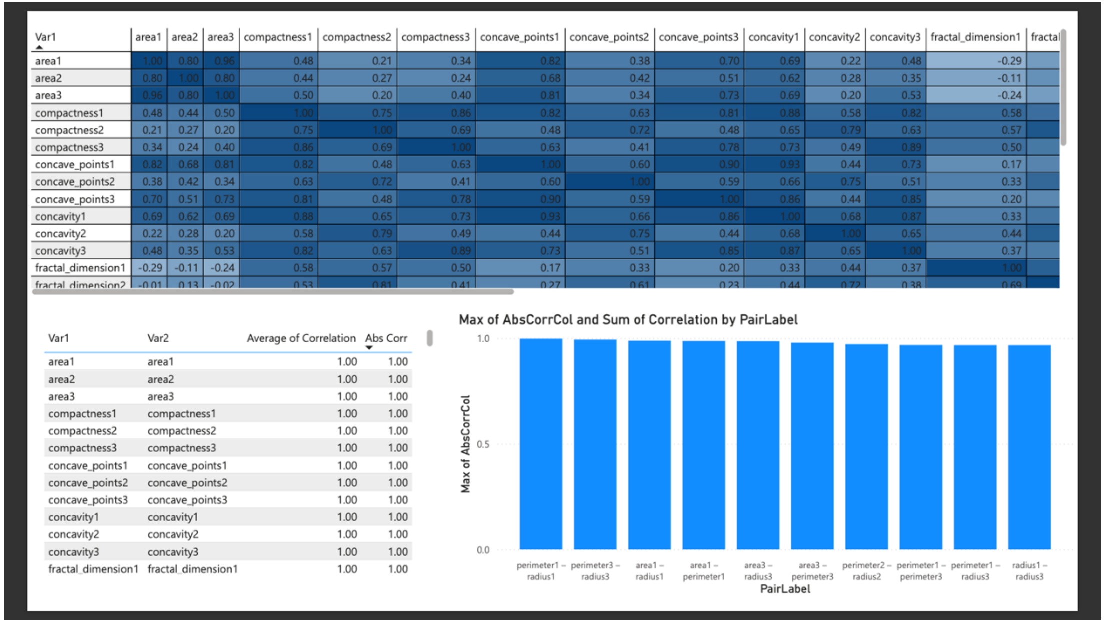
Main story

- Identify the best model (XGBoost).
- Show how its predictions relate to clinical trade-offs between false positives and false negatives.



Feature Correlation and Redundancy

- Several feature groups are strongly correlated (e.g., radius–perimeter–area), meaning they carry similar information.
- This confirms the dataset has redundant measurements, which is useful for interpretation and for considering dimensionality reduction (e.g., PCA).



Var1	area1	area2	area3	compactness1	compactness2	compactness3	concave_points1	concave_points2	concave_points3	concavity1	concavity2	concavity3	fractal_dimension1	fractal
area1	1.00	0.80	0.96	0.48	0.21	0.34	0.82	0.38	0.70	0.69	0.22	0.48	-0.29	
area2	0.80	1.00	0.80	0.44	0.27	0.24	0.68	0.42	0.51	0.62	0.28	0.35	-0.11	
area3	0.96	0.80	1.00	0.50	0.20	0.40	0.81	0.34	0.73	0.69	0.20	0.53	-0.24	
compactness1	0.48	0.44	0.50	1.00	0.75	0.86	0.82	0.63	0.81	0.88	0.58	0.82	0.58	
compactness2	0.21	0.27	0.20	0.75	1.00	0.69	0.48	0.72	0.48	0.65	0.79	0.63	0.57	
compactness3	0.34	0.24	0.40	0.86	0.69	1.00	0.63	0.41	0.78	0.73	0.49	0.89	0.50	
concave_points1	0.82	0.68	0.81	0.82	0.48	0.63	1.00	0.60	0.90	0.93	0.44	0.73	0.17	
concave_points2	0.38	0.42	0.34	0.63	0.72	0.41	0.60	1.00	0.59	0.66	0.75	0.51	0.33	
concave_points3	0.70	0.51	0.73	0.81	0.48	0.78	0.90	0.59	1.00	0.86	0.44	0.85	0.20	
concavity1	0.69	0.62	0.69	0.88	0.65	0.73	0.93	0.66	0.86	1.00	0.68	0.87	0.33	
concavity2	0.22	0.28	0.20	0.58	0.79	0.49	0.44	0.75	0.44	0.68	1.00	0.65	0.44	
concavity3	0.48	0.35	0.53	0.82	0.63	0.89	0.73	0.51	0.85	0.87	0.65	1.00	0.37	
fractal_dimension1	-0.29	-0.11	-0.24	0.58	0.57	0.50	0.17	0.33	0.20	0.33	0.44	0.37	1.00	
fractal_dimension2	-0.01	0.13	-0.02	0.53	0.81	0.41	0.27	0.61	0.23	0.44	0.72	0.38	0.69	

Var1	Var2	Average of Correlation	Abs Corr
area1	area1	1.00	1.00
area2	area2	1.00	1.00
area3	area3	1.00	1.00
compactness1	compactness1	1.00	1.00
compactness2	compactness2	1.00	1.00
compactness3	compactness3	1.00	1.00
concave_points1	concave_points1	1.00	1.00
concave_points2	concave_points2	1.00	1.00
concave_points3	concave_points3	1.00	1.00
concavity1	concavity1	1.00	1.00
concavity2	concavity2	1.00	1.00
concavity3	concavity3	1.00	1.00
fractal_dimension1	fractal_dimension1	1.00	1.00

Max of AbsCorrCol and Sum of Correlation by PairLabel

The first graph is a heatmap that shows the correlation between all features.

The bar chart shows the top 10 different feature pairs (not the same feature) with the highest correlation.

The table on the left lists those self-correlations (all equal to 1, which is correct).

PCA: Variance & Class Separation

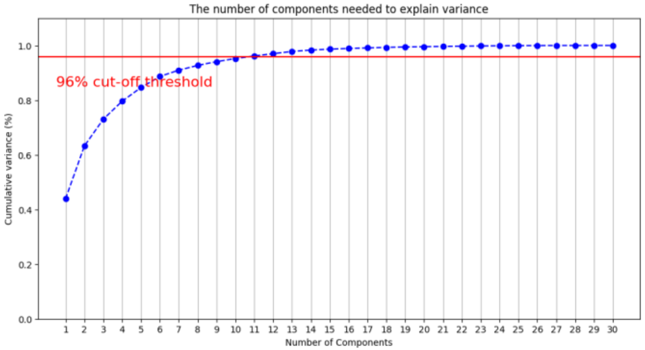
The top plot shows the cumulative explained variance of the PCA components. The first few components already capture most of the information in the data: roughly 90% of the total variance is explained by about the first 7 components (instead of the original 30 features).

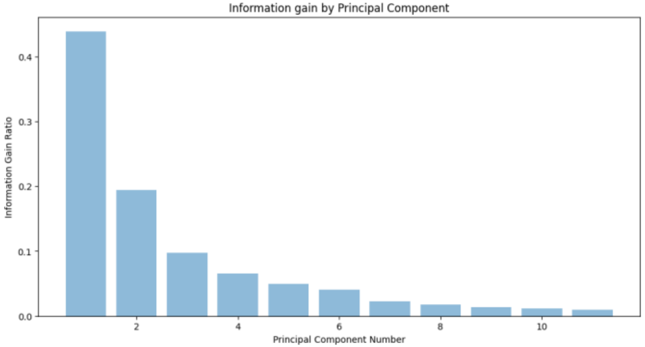
The bar chart in the middle shows the variance explained by each single component.

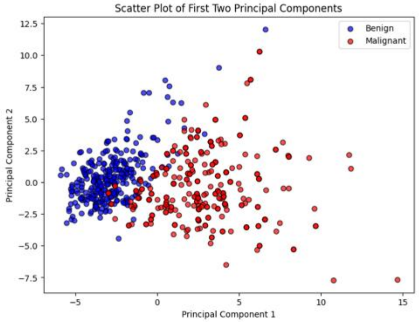
- PC1 explains the largest share of variance,
- the following components contribute less and less,
  which illustrates the diminishing returns of adding more components.

The scatter plot of PC1 vs PC2 (bottom) shows that benign and malignant tumors are partially separated in the PCA space, although there is still some overlap. This means PCA is useful to visualize the structure of the data and reduce dimensionality with limited information loss.

However, when I later compared models with and without PCA, the best performance was obtained without PCA, so PCA is mainly used here for exploration and visualization, not for the final classifier.







Model Accuracy Comparison

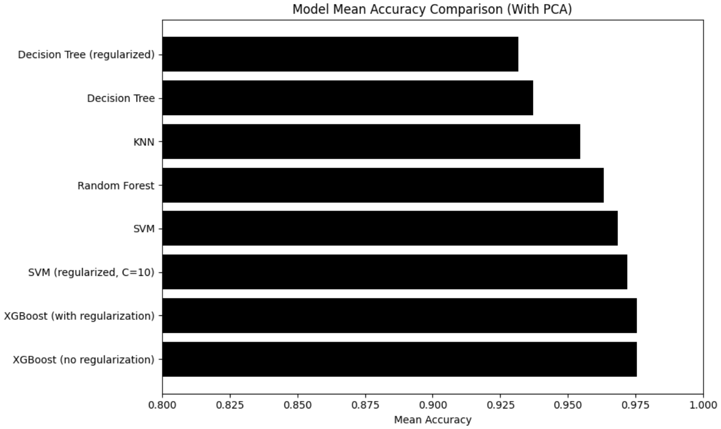
This chart compares the mean cross-validated accuracy of eight different models, evaluated both with and without PCA.

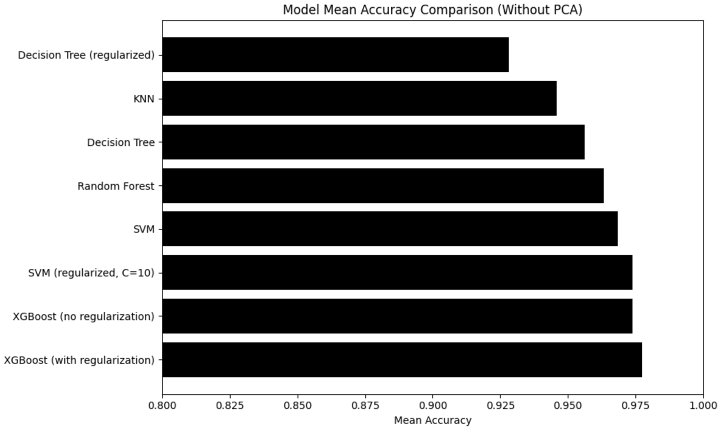
Two main patterns emerge:

- **XGBoost (with regularization, without PCA)** is the clear winner, achieving the highest mean accuracy across all configurations.
- **PCA does not systematically improve performance**; in many cases, the models without PCA perform slightly better.

This suggests that, after proper scaling, the original 30 features already provide a good representation of the data. Tree-based models like XGBoost can naturally handle correlations between features and do not require dimensionality reduction to perform well.

Based on this comparison, I selected **XGBoost without PCA** as my final model for further analysis and deployment on the external competition data.

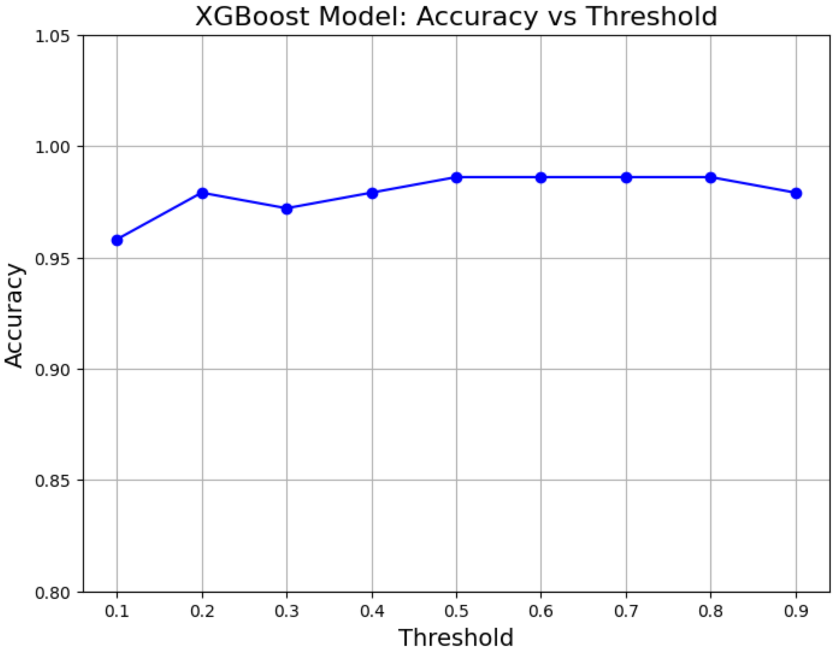




XGBoost Decision Threshold Tuning

- XGBoost outputs a probability of “malignant” (class = 1).
- The threshold is the cutoff: predict malignant if probability ≥ threshold.
- Changing the threshold shifts the trade-off between:

  -False Negatives (missing malignant cases) vs
  False Positives (flagging benign as malignant).
- Accuracy stays high across thresholds, so the best threshold should be chosen based on the clinical cost of errors, not accuracy alone.



Error Analysis

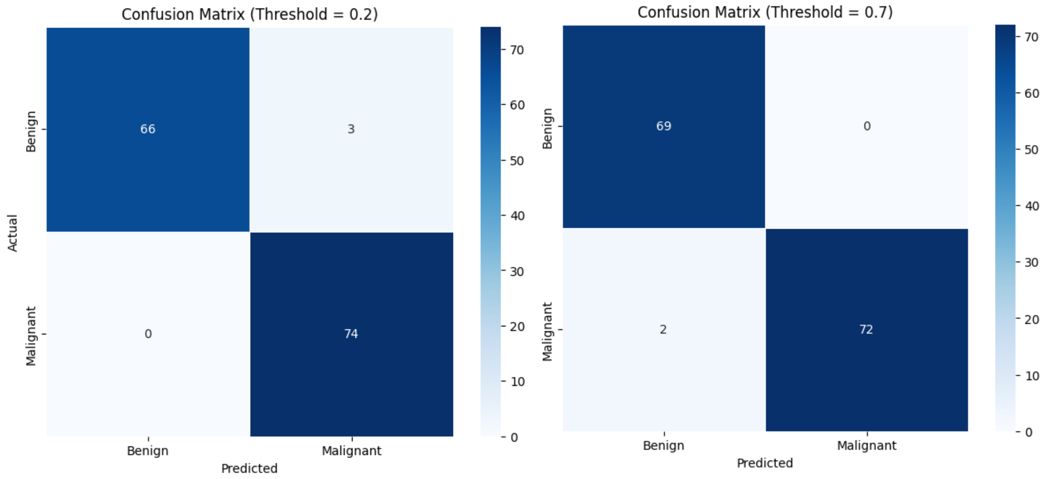
This visualization focuses on the error structure of the final XGBoost model rather than just its accuracy.

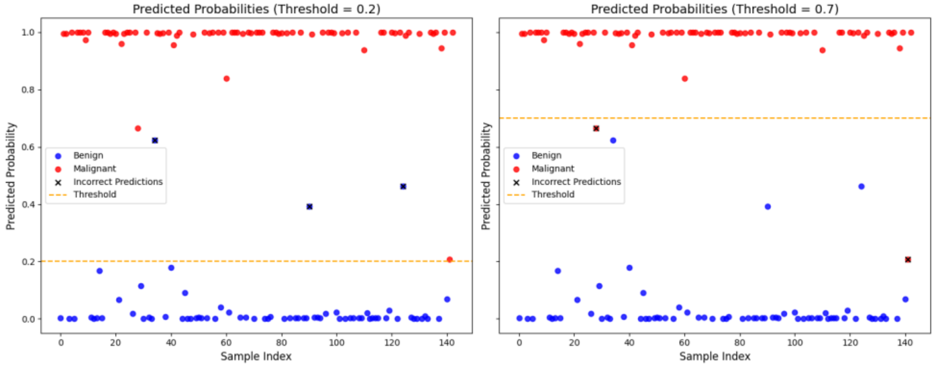
At the chosen decision threshold, the confusion-matrix-based bar chart shows:

- A high number of true positives, meaning the model correctly identifies most malignant tumors.
- Very few false negatives (malignant cases classified as benign), which is essential in a medical diagnosis context because missing a cancer case can have severe consequences.
- A small, acceptable number of false positives, i.e., benign tumors that are flagged as malignant and may receive additional diagnostic tests.

The precision–recall curve illustrates how changing the decision threshold allows us to trade off precision and recall. For early cancer detection, a high recall is usually prioritized, even if it slightly lowers precision, because it is safer to over-flag suspicious cases than to miss a malignant tumor.

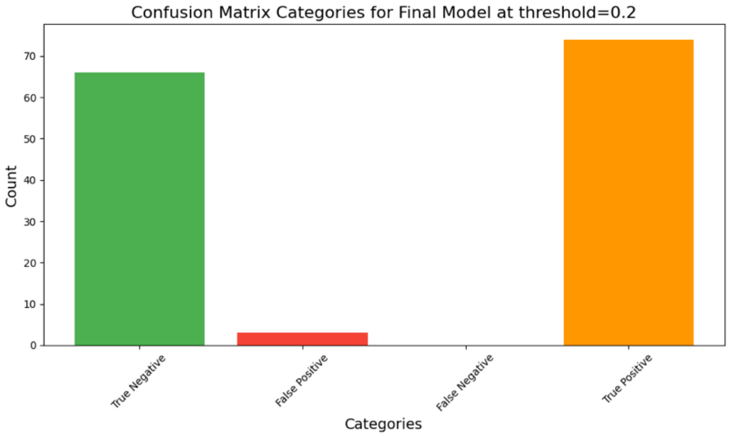
Overall, these visualizations confirm that the final XGBoost model is not only accurate but also has an error profile compatible with clinical decision support, especially when the threshold is tuned to favor recall.

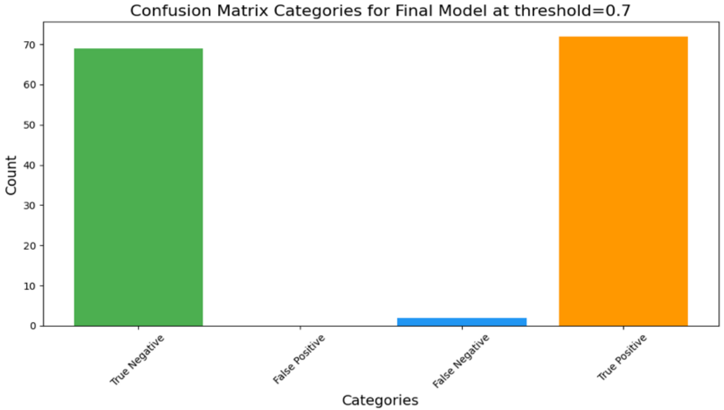




Threshold Impact on Final Model

- These charts break the confusion matrix into True Negatives, False Positives, False Negatives, and True Positives.
- At threshold = 0.2, the model is more “sensitive”: it predicts more positives, which can reduce False Negatives but may increase False Positives.
- At threshold = 0.7, the model is more “strict”: it predicts fewer positives, which can reduce False Positives but may increase False Negatives.
- Overall, both thresholds keep high True Positives and True Negatives, so the best threshold depends on what is more important:
  - Minimize False Negatives (medical screening) → prefer lower threshold
  - Minimize False Positives (avoid unnecessary alarms) → prefer higher threshold





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