



Machine Learning project: Breast Cancer Detection

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Table of contents

1

Introduction

2

Problem Statement

3

Our Goals

4

CRISP-DM
Methodology

5

Why our project?

6

Perspectives

7

Conclusion





Introduction





Problem Statement



Our Goals





**Save Lives Through
Early Detection**



**Protect At-Risk Patients
Before It's Too Late**



**Reduce Healthcare
Costs and Patient
Stress**



Business Understanding

Business Understanding

07

Breast cancer is one of the most life-threatening diseases among women worldwide.

Early detection is essential to improve survival and reduce costs.

Traditional diagnosis relies on manual interpretation—slow and error-prone.

This project uses machine learning to support healthcare professionals in detection, diagnosis, and prevention.





- 01 Confirm the presence of a breast tumor
- 02 Characterize the tumor to guide clinical decisions
- 03 Detect early risk factors in healthy patients and recommend appropriate preventive actions



Data Understanding



DSO	DSO1:Classify tumor type	DSO2:Analyze Histopathology Images	DSO3:Identify risk factors
Dataset	Wisconsin Diagnostic Breast Cancer Dataset	IDC Detection from Tissue Images (277,524 patches)	Clinical & Biochemical Data Analysis
Characteristics	Moderate class imbalance, no missing values, few outliers concave point features most correlated with diagnosis	Significant class imbalance, all filenames valid, patient-level data split to prevent leakage, visual patterns distinguish IDC from non-IDC tissue.	Moderate class imbalance, no missing values, few outliers
Goal	Classify tumors as benign or malignant	Detect Invasive Ductal Carcinoma (IDC) in breast tissue images	Identify early risk factors to support prevention



Data Preparation

Transforming Raw Data into Model-Ready Features



DSO1: Classify tumor type

- Clean: Encode M→1/B→0, remove empty columns & ID
- Split: 70/30 stratified (398 train, 171 test)
- Scale: Z-score normalization (fit on train only)

DSO2: Analyze Histopathology Images

- Preprocess: Resize 50×50, normalize [0,1], augment
- Split: Patient-wise 70/10/20 (prevent leakage)
- Pipeline: TF.data (parallel, batch 64, prefetch)

DSO3: Identify risk factors

- Feature Engineering: 4 composite features (BMI×Glucose, etc.)
- Balance: SMOTETomek (synthetic + denoise)
- Scale: StandardScaler on all features



Modeling

*From Algorithms to Clinical Decision
Support*

DSO1: Classify tumor type

14

Model 1: Linear Regression :

Hyperparameters: Batch=128, LR=0.001, Epochs=3000,
Loss=MSE, Optimizer=SGD

Why? Simple baseline, high interpretability

*Model 2: k-Nearest
Neighbors (k=1):*

Distance Metrics: Manhattan (L1) & Euclidean (L2)

Why? Non-parametric, no training required, geometric approach

*Model 3: Softmax
Regression:*

Hyperparameters: Batch=128, LR=0.001, Epochs=3000,
Loss=Cross-entropy, Optimizer=SGD

Why? Outputs probability distribution, multi-class ready, convex optimization (guaranteed convergence)



*Model 4: Support Vector
Machine (SVM):*

Hyperparameters: C=5, Norm=L2, LR=0.001, Batch=128,
Epochs=3000, Optimizer=Adam

Why? Optimal decision boundary, robust to outliers, effective in high dimensions

*Model 5: Multilayer
Perceptron (MLP)*

Architecture: 3 hidden layers of 500 neurons each, ReLU
Hyperparameters: Batch=128, LR=0.01, Epochs=3000,
Loss=Cross-entropy, Optimizer=SGD
**Why? Learns complex non-linear patterns, hierarchical
feature extraction**

Model 6: GRU-SVM Hybrid

Architecture: GRU(128 cells) → Dropout(0.5) → SVM layer
Hyperparameters: C=5, LR=0.001, Batch=128,
Epochs=3000, Optimizer=Adam
**Why? GRU learns hierarchical representations, SVM
provides optimal classification boundary**



Model 1: Custom CNN

Architecture: 3 Conv layers (32→64→128) + Dense(128) + Dropout(0.4) + Sigmoid

Parameters: 683,329 trainable

Training: 10 epochs, Adam optimizer

Why? Progressive feature extraction (edges→textures→structures), lightweight, tailored for 50×50 images

Model 2: ResNet50 Transfer Learning

Base: ResNet50 pre-trained on ImageNet (frozen)

Custom Head: Dense(128) + Dropout(0.4) + Sigmoid

Parameters: 23.8M total (262K trainable)

Training: 5 epochs, Adam optimizer

Why? Leverage pre-trained features from 14M images, less data needed, proven architecture



DSO3: Identify risk factors in healthy patients

17

Model 1: Random Forest

Hyperparameters: n_estimators: 100 ,class_weight: balanced, max_depth: unconstrained , random_state: 42
Why? Handles non-linearity, feature importance for clinical interpretation, robust to noise

Model 2: Support Vector Machine (SVM)

Hyperparameters: kernel: RBF (Radial Basis Function), class_weight: balanced, probability: enabled
Why? Captures complex relationships, flexible decision boundaries, maps to infinite dimensions

Model 3: Gradient Boosting

Hyperparameters: n_estimators: 100 ,learning_rate: default
max_depth: default
Why? Corrects mistakes iteratively, high accuracy on tabular data, handles complex interactions

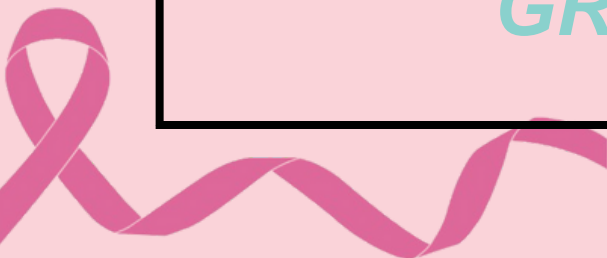
Model 4: XGBoost

Hyperparameters: n_estimators: 100 ,learning_rate: 0.1 ,
eval_metric: log-loss ,random_state: 42
Why? State-of-the-art for tabular data, fast training, built-in regularization, industry standard



Evaluation

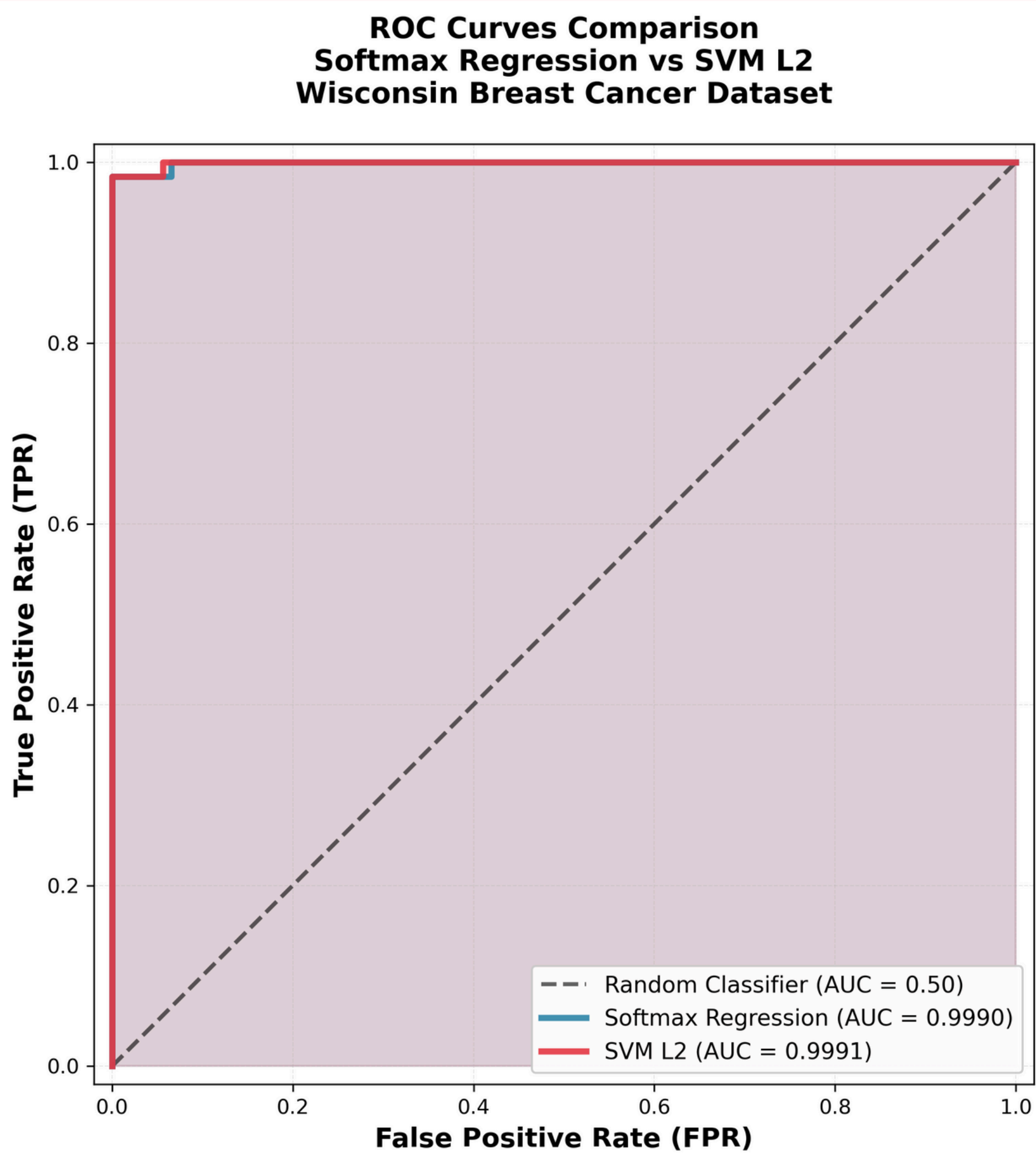
Algorithm	Accuracy	TPR	TNR	Article Comparison
Linear Regression	96.49%	90.62%	100.00%	+0.40%
Nearest Neighbor (L1)	95.91%	93.75%	97.20%	+2.34%
Nearest Neighbor (L2)	94.15%	90.62%	96.26%	-0.58%
Softmax Regression	98.83%	96.87%	100.00%	+1.17%
SVM (L2)	98.25%	95.31%	100.00%	+2.15%
MLP	96.49%	92.19%	99.07%	-2.55%
GRU-SVM	96.49%	90.62%	100.00%	+2.74%



ROC CURVE



‘Softmax Regression was chosen for production’

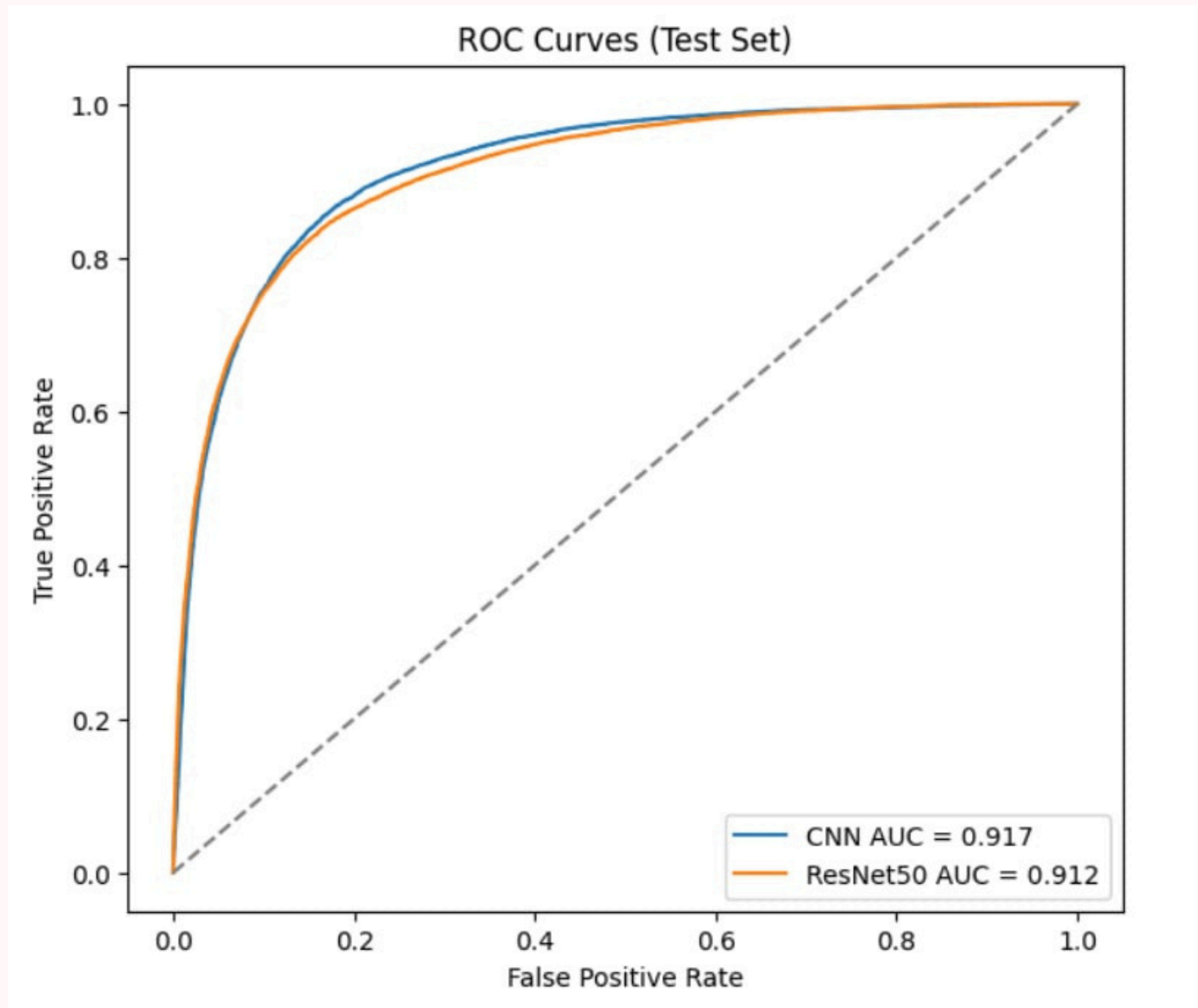


Algorithm	Accuracy	Loss	Training Time
CNN	85.69%	0.3918	500 seconds per epoch
ResNet50	85.78%	0.3516	700 seconds per epoch (slower due to larger architecture)



ROC CURVE

22

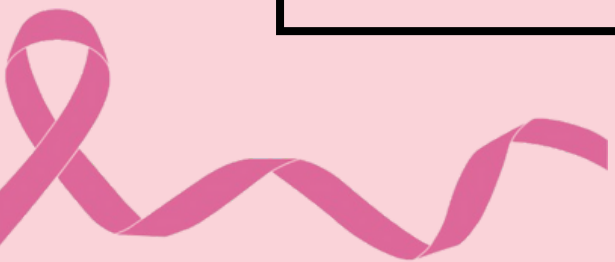


'CNN was chosen for production'

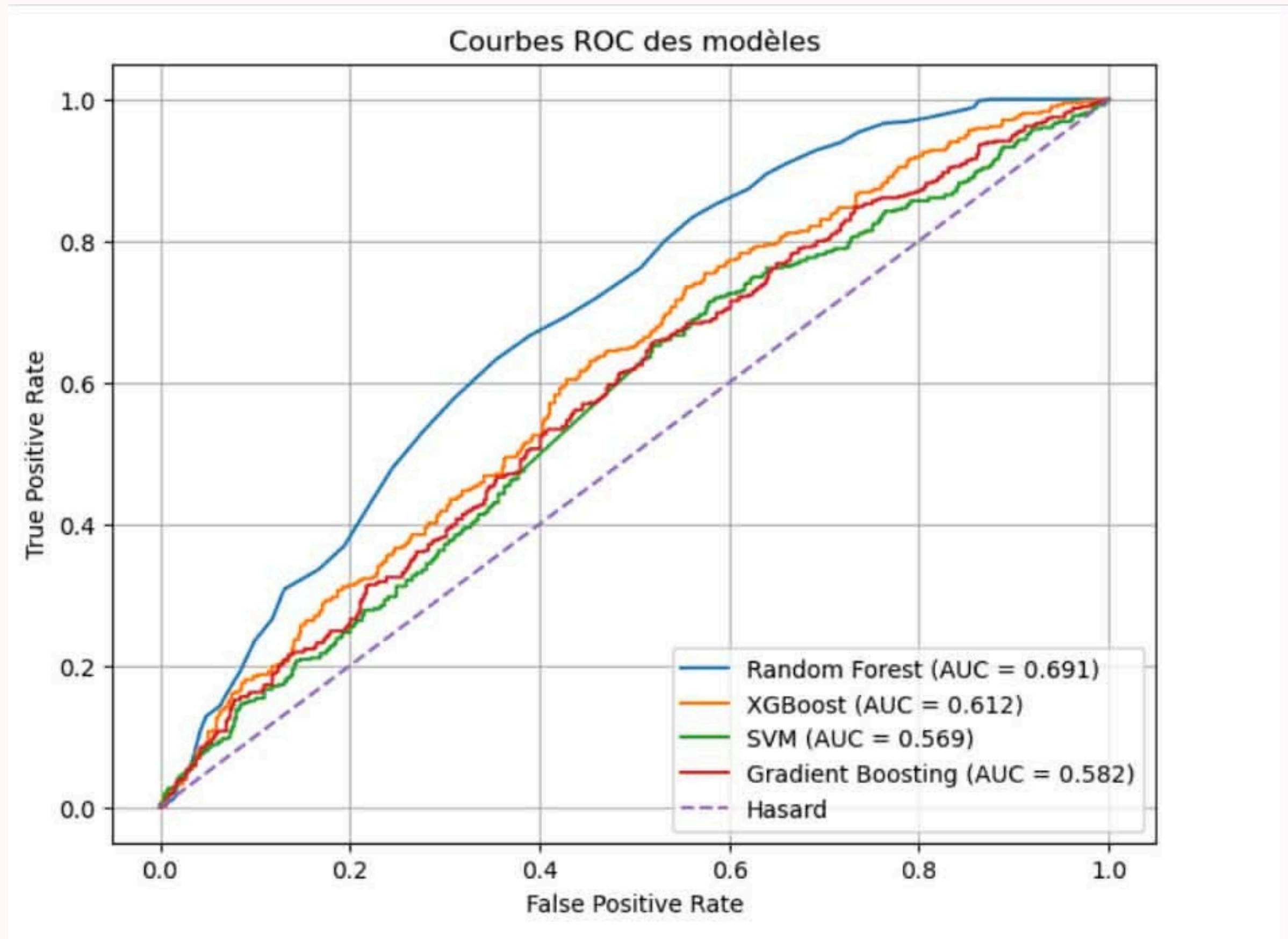
DSO3: Identify risk factors in healthy patients

23

<i>Algorithm</i>	<i>Accuracy</i>	F1-Score
<i>Random Forest</i>	63,92%	0.636
SVM	56,85%	0.569
<i>XGBoost</i>	56,43%	0.569
<i>Gradient Boosting</i>	55,8%	0.533



ROC CURVE



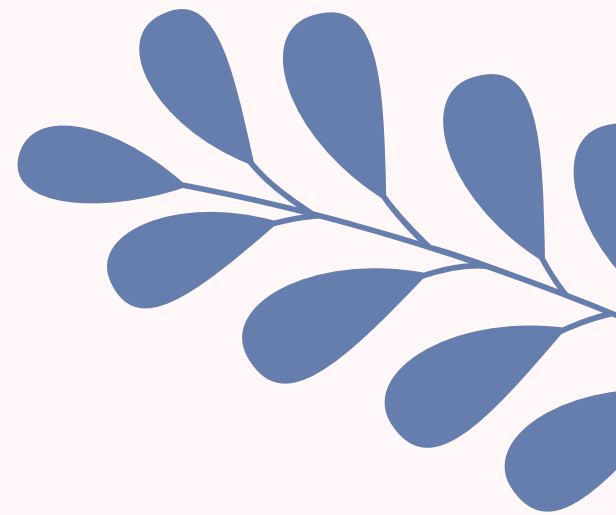
'Random Forest outperformed other models and was chosen for production'




Deployment

*a web-based
deployment was implemented*

- **Flask** framework
- **HTML, CSS, and JavaScript**





Breast Cancer Diagnostic Portal


Dashboard

Histopathology

Clinical Data


Tumor Features

Models




Breast Cancer Diagnostic Portal

Advanced AI-powered diagnostic tools for medical professionals




Model Status




Histopathology Model

Ready




Clinical Data Model

Ready




Tumor Features Model

Ready




Histopathology Analysis

Upload breast mass histopathology images for AI-powered malignancy detection.



Clinical Data Analysis

Upload patient clinical data (age, tumor size, etc.) for risk assessment.



Tumor Feature Analysis

Upload tumor feature data (radius, texture, perimeter, etc.) for comprehensive diagnosis.

to assist medical professionals in



Why Choose Our Solution?



Faster Decisions, Better Outcomes:

Deliver diagnoses in minutes, not weeks—giving patients the care they need when they need it.



Stay Ahead of the Disease:

Catch cancer risk before it becomes cancer—protecting more patients with early intervention



Reduce Costs, Increase Efficiency:

Cut down on unnecessary procedures and save valuable resources while improving accuracy





Perspectives



Expand to Other Cancers:

Apply our proven approach to lung, prostate, and colon cancer detection for broader impact



Patient Portal

Integrate a patient portal counterpart to facilitate access to diagnosis results and streamline doctor - patient communication



Real-Time Clinical Integration:

Connect directly with hospital systems and electronic health records for seamless, automated screening





Conclusion



Breast cancer doesn't wait—and neither should we.

Our project delivers faster, smarter diagnosis through machine learning that empowers doctors and saves lives. We're transforming early detection from a challenge into an opportunity.

The technology works. The need is real. The time is now. Let's catch cancer earlier and give patients the future they deserve.





**THANK
YOU**

