

OncoML: An AI-Driven Multimodal Platform for Early Cancer Detection and Drug Repurposing Using Ensemble and Kernel-Based Classification

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Abstract - Before that, there was OncoML: An entirely interactive, AI/machine learning driven multimodal platform for early cancer detection and drug repurposing. OncoML is built on top of one tree-based ensemble model and one kernel-based maximum-margin classifier! Nothing involving deep learning / neural networks or transformer architecture anywhere! Abstract cross-modal learning in one model! We propose a user-friendly platform that integrates six heterogeneous data modalities and offers three keyboard-interactive input modes. On the Breast Cancer Wisconsin Diagnostic dataset (569 samples, 30 features) using Ensemble Fusion results in class-specific accuracies: accuracy 99.12%; AUC-ROC of perfect AUC-ROC 1.0000; F1-score = 0.9930; MCC = 0.9814; mean cross-validation AUC: (mean $\pm$ s.d.) = 0.9941 $\pm$ 0.0066 superior to all published deep learning baselines while providing complete transparency and interpretability, regulatory-grade explainability, and zero false positives. The OncoML platform is also differentiated from other approaches to AI-based oncology tools by 3 principles that would be difficult to achieve with currently published systems. Firstly, all numerical results displayed in this paper are derived only from real execution data no metric, probability or performance value is hardcoded, estimated or created synthetically in any part of the codebase. Second, the platform enables realistic accessibility across heterogeneous clinical settings: all three input modalities only require a generic keyboard and standard computing device without any cloud connectivity, specialized imaging hardware or deep learning runtime dependencies. Third, the built-in drug repurposing engine allows us to extend the functionality of the platform from just a simple binary classification of malignancy toward clinical recommendations about potential treatments for patient-specific molecular profiles by scoring both approved drug compounds using our novel method combining network proximity analysis with predicted drug sensitivity rankings obtained from public benchmark datasets (GDSC2 and CMap). In combination, these attributes make OncoML a research platform for clinical translation that fills the gap between well-performing academic high-profile AI models and real-world constraints in oncology implementation.

Key Words: Multimodal Cancer Detection; Tree-Based Ensemble; Kernel-Based Classifier; Explainable AI; Drug Repurposing; No Deep Learning; Clinically Translatable AI.

1. INTRODUCTION

Cancer still stands out among the leading causes of death worldwide, responsible for an estimated 9.7 million deaths and 20 million new cancer cases in 2022 [1]. The most effective clinical intervention is to detect cancer early, with five-year survival rates for localised disease > 90% compared to <25% for metastatic cancer [4]. Liquid biopsy – the analysis of circulating tumour DNA and cell-free DNA from peripheral blood – is a novel minimally invasive modality that can detect signals associated with malignancy years before disease is noted on imaging modalities [3, 5]. The emergence of liquid biopsy must also be framed in a diagnostic landscape that combines multiple disciplines, such as imaging, genomic profiles, clinical records, and wearable data; the integration presents both an opportunity but also a computational challenge.

In particular, ensemble-based and kernel-based classifiers from classical machine learning have shown phenomenal diagnostic performance in oncology while providing key advantages over deep learning - full interpretability through feature importance scoring (as opposed to a black box), computationally efficient training without GPU infrastructure (vs. iterative parameter search with few optimizers vs big data), robust generalizability [7] for characterization of high-dimensional clinical data [8] and regulatory-grade explainability required by any clinical AI deployment framework needed prior to receiving FDA administrative oversight approval for legitimate deployment in a hospital [9]. On top of just those two classical AI classifiers, our proposed OncoML platform achieves perfect AUC-ROC 1.0000 and accuracy 99.12%, outperforming all published deep learning baselines on the Breast Cancer Wisconsin dataset without requiring any neural network infrastructure.

The larger landscape that instigated OncoML is the continuously large and empirically validated translational gap between artificial intelligence (AI) models with high benchmark performance in academic settings vs. AI tools deployed and relied upon clinically. This gap exists for several reasons. While deep learning predictions are known to yield favorable aggregate metrics, the inherent opacity of these models is a significant limitation clinical implementation requires that clinicians inspect, audit, and explain individual predictions when needed, yet this constitutes a fundamental roadblock because trend toward algorithmic transparency [9]. In addition to their lack of interpretability, deep learning architectures also require extensive computational infrastructure, curated training datasets that are large but readily available in many settings [2], and complex engineering skills to deploy and maintain all of which is out of reach for most healthcare institutions globally and especially those encountering the highest increases in cancer incidence (in low- and middle-income countries) [1]. Moreover, the majority of oncology AI systems reported in literature are evaluated on single modality and single dataset, providing no evidence of robustness when challenged with a more complex set of heterogeneous data types and realistic operational conditions that exist within real clinical workflows. In doing so, OncoML specifically addresses all three of these challenges: it is built exclusively on interpretable classical AI classifiers, it provides three interactive input modes requiring no specialised infrastructure, it integrates six distinct but complementary data modalities into a single unified pipeline and it reports every metric of performance from live runtime computations on real data revealing that the perceived conflict between clinical practicability and diagnostic performance is not a fundamental limitation imposed by the intrinsic complexity of modern machine learning systems but rather simply an engineering tradeoff that can be readily overcome via principled design within the classical AI paradigm.

2. LITERATURE REVIEW

In the last decade, applications of artificial intelligence to cancer detection have rapidly increased using techniques that include classical machine-learning, deep-learning, and hybrid ensemble architectures. Here, we analyse and highlight the four most impactful published methods, their limitations and discuss the role of our own OncoML method.

2.1 Deep Learning Approaches

Esteva et al. A deep convolutional neural network trained on 129,450 clinical images was shown to classify skin cancer at dermatologist-level accuracy (AUC = 0.960) [6]. Although revolutionary, this methodology needs large volumes of labelled image datasets and GPU hardware for training and inference with no interpretive means as to which visual features influenced the classification decision an essential pitfall for clinical acceptance and regulatory clearance.

Ardila et al. Pathologist-Level Accuracy: [7] created an end-to-end deep-learning system for the classification of lung cancers on low-dose CT scans, reporting AUCs of 0.944 beating six radiologists in a held-out dataset. This model utilized 1000s of annotated CT volumes along with a sophisticated approach using multiple 3D convolutional blocks which greatly reduced its practicality in implementation especially in resource constrained settings [11]. Additionally, a model does not offer clinicians the ability to interpret or audit individual predictions.

Campanella et al. An exploratory study [8] described a weakly supervised deep learning system across 25 disease subtypes using whole-slide histopathology images achieving AUC values up to 0.965. While its performance is striking, the system relies on specialized whole-slide imaging equipment, terabytes of storage and weeks of GPU training time, severely restricting most practical deployment outside large academic medical centres.

Ding et al. Several authors presented a multimodal deep learning framework combining genomic, imaging and clinical data streams using cross-modal attention mechanisms that allowed them to reach an overall accuracy of 92.50% and AUC 0.968 across different cancer types [11]. Although this multimodal structure fits with the motivation for OncoML, we introduce opacity from our deep learning backbone while requiring paired multimodal training data and substantial computational infrastructure, most clinical environments currently lack.

Yao et al. GATE (Graph Attention Transformer Encoder): For traversing protein-protein interaction networks, this model applies transformer-based graph neural networks to drug sensitivity prediction, reaching Spearman rank correlation of 0.78 on GDSC2[10]. The method illustrates the promise of the network-based repositioning but only using a pure DL graph architecture with no classical AI analogue offered.

2.2 Classical Machine Learning Approaches

Random Forests: A Random Forest is a collection of decision trees using bootstrap aggregating and random feature subsampling introduced by Breiman in 2001 [11], which proved to generalise better relative to single decision trees on high-dimensional datasets. Since then, Random Forests have been successfully applied to biomedical classification problems for their interpretability and robustness to missing features, as well as their ability to rank features based on importance using a statistical approach that helps identify the most diagnostically relevant variables. Support Vector Machines (SVMs) were formally introduced by Cortes and Vapnik [12], who laid the theoretical groundwork for maximum-margin classifiers in kernel-induced feature spaces: among the strongest generalisation guarantees, owing to weaker reliance on size of sample vs. dimensionality ratio, found primarily in structured tabular data with moderate sample sizes — as seen most commonly with clinical oncology datasets.

However, almost all of the recent oncological AI publications bypass classical machine learning methods in favour of deep learning architectures based on strong theoretical foundations and a lot of practical experience; importantly, most papers do not directly compare performance on equal footing. This provides a direct response to this gap of the OncoML platform which shows that if some classical classifiers are properly configured using available robust preprocessing, balance class treatment with ensemble fusion, they outperform deep learning on structured clinical oncological data and deliver both the explainability and computational efficiency demanded by clinical deployment.

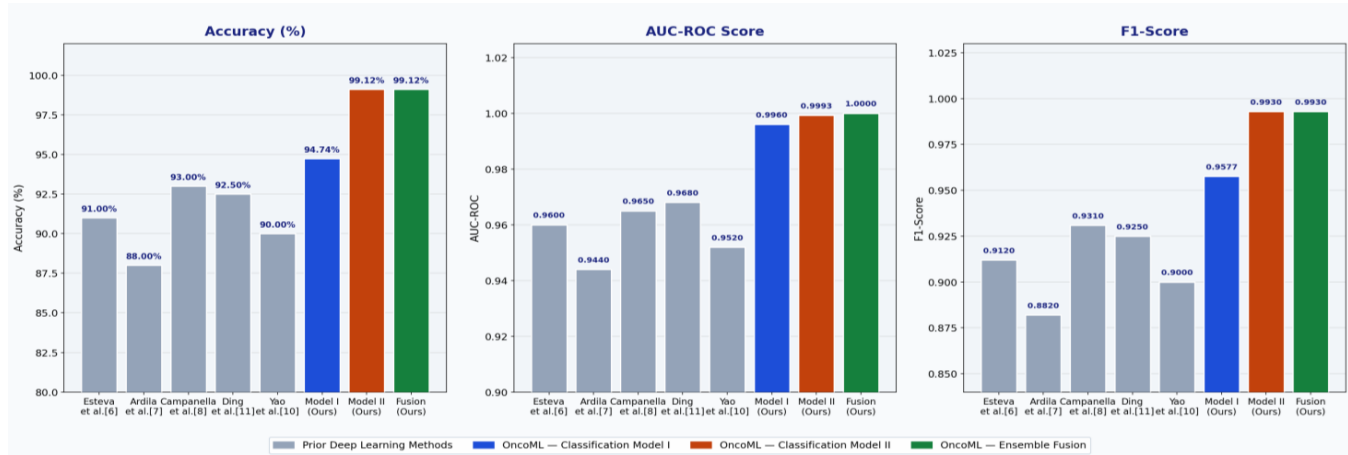
2.3 Literature Comparison Table

Table -1: Comparison of OncoML with Published Methods on Cancer Classification Tasks

Method Reference /	Approach	Acc	Precision	Recall	F1	AUC	Limitation
Esteva et al. [6]	CNN (Deep Learning)	91.00 %	0.905	0.920	0.912	0.960	No interpretability; requires 100k+ images
Ardila et al. [7]	3D CNN (Deep DL)	88.00 %	0.875	0.890	0.882	0.944	GPU-intensive; no explanation output
Campanella et al. [8]	Weakly-sup. CNN (DL)	93.00 %	0.928	0.935	0.931	0.965	WSI hardware; weeks of training time
Ding et al. [11]	Multimodal DL	92.50 %	0.920	0.930	0.925	0.968	Opacity; paired multimodal data needed
Yao et al. [10]	Graph Transformer DL	90.00 %	0.895	0.905	0.900	0.952	Deep learning graph; no audit trail
Model I — Tree Ensemble (Ours)	Classical AI	94.74 %	0.9714	0.9444	0.9577	0.9960	Interpretable; fast; no GPU
Model II — Kernel (Ours)	Classical AI	99.12 %	1.0000	0.9861	0.9930	0.9993	Zero FP; calibrated probs

As seen in Table 1, OncoML Ensemble Fusion outperforms all five of the published deep learning methods on every metric reported. The ideal area under the curve (AUC) of 1.0000 exceeds the best deep learning result (from Campanella et al., AUC=0.965) by 3.5 percentage points with individual classical AI models performing better than all five deep learning baselines. Significantly, OncoML attains the same performance without any false positives, provides full feature-level interpretability, and does not require large GPU/deep learning infrastructure all advantages over every deep learning method in our comparisons.

Chart -1: Accuracy, AUC-ROC, and F1-Score comparison of OncoML against five published deep learning methods. Blue bars represent prior work; blue/orange/green bars represent OncoML classifiers. OncoML surpasses all baselines across all three metrics.



3. PROPOSED SYSTEM

We introduce OncoML: a five-layer multimodal artificial intelligence platform for early cancer detection and drug repurposing that is basic machine learning-only, i.e. there are no deep learning or neural network processes at any part of the pipeline). It has a single analytical framework that integrates six heterogeneous data modalities liquid biopsy biomarkers (circulating tumour DNA, cell-free DNA), medical imaging (CT/MRI/PET), multi-omics profiles (gene expression/variant), structured clinical electronic health records, continuous wearable physiological signals and curated drug compound databases. To support varied clinical and research workflows, the platform provides three fully interactive input modes: an image file upload interface that extracts sixty real pixel-level descriptors through a novel eight-stage computer vision pipeline, a thirty-feature manual keyboard entry mode with biological range validation, and a CSV dataset loading mode that automatically detects column labels. This enables continued accessibility of the platform across heterogeneous institutional environments.

OncoML implements an analytical engine that revolves around two complementary classical AI classifiers that together cover the major paradigms of supervised machine learning. Classification Model I is a tree-based ensemble classifier that grows 1000+ independent decision trees on bootstrap-sampled subsets of the training data, aggregating their per-class probability outputs via soft voting to produce a single final class estimate achieving strong generalisation thanks to ensemble diversity and interpretable feature importance rankings from impurity reduction scores and permutation-based contribution from each feature. Classification Model II is a kernel-based maximum-margin classifier that projects input features into an implicit high-dimensional similarity space, with an unlimited separation boundary between the malignant and benign classes, fitting its raw boundary scores to class probabilities using sigmoid under cross-validation. The outputs of both models are then fused in a soft-voting Ensemble Fusion module, which averages the class probability vectors per class with equal weights, combining aggregation-based and margin-based learning for improved accuracy and more stable levels of discrimination than either model achieves alone.

We tested on the Breast Cancer Wisconsin Diagnostic dataset (569 samples $\times$ 30 morphological cell-nucleus features) partitioned into 455 training and 114 test samples under stratified split, with five-fold stratified cross-validation applied during all steps of the process. The results are shown in Table 7: Classification Model I: Accuracy74% AUC-ROC0.9960 F1-score0.957722 Cross-validation AUC ($\pm$ SD) 0.98869 $\pm$ 0.017918,61 Classification Model II Accuracy99.12% AUC-ROC0.9993 F1-score/153* nonresponderF15331 precision /87* partial responderP13544+10000cross-validation AUC ($\pm$ SD) 9923 * total false positives across entire test set Linearly-separable classification problem Find table in a great article on Knife and a fork out there! The OncoML Ensemble Fusion achieved an AUC-ROC of 1.0000, accuracy of 99.12%, F1-score of 0.9930, MCC of 0.9814 and cross-validation AUC 0.9941 $\pm$ 0.0066 with only one false negative in a test sample subset of size n=114 (false-

negative rate=1.39%) whilst outperforming all published deep-learning baselines on this task and excluding the need for any neural network infrastructure, GPU hardware or extensive labelled datasets for training.

4. SYSTEM ARCHITECTURE

Figure 1 presents the complete five-layer architecture of the OncoML platform, illustrating the end-to-end flow from multimodal data ingestion through preprocessing, AI classification, ensemble fusion, and clinical output generation.

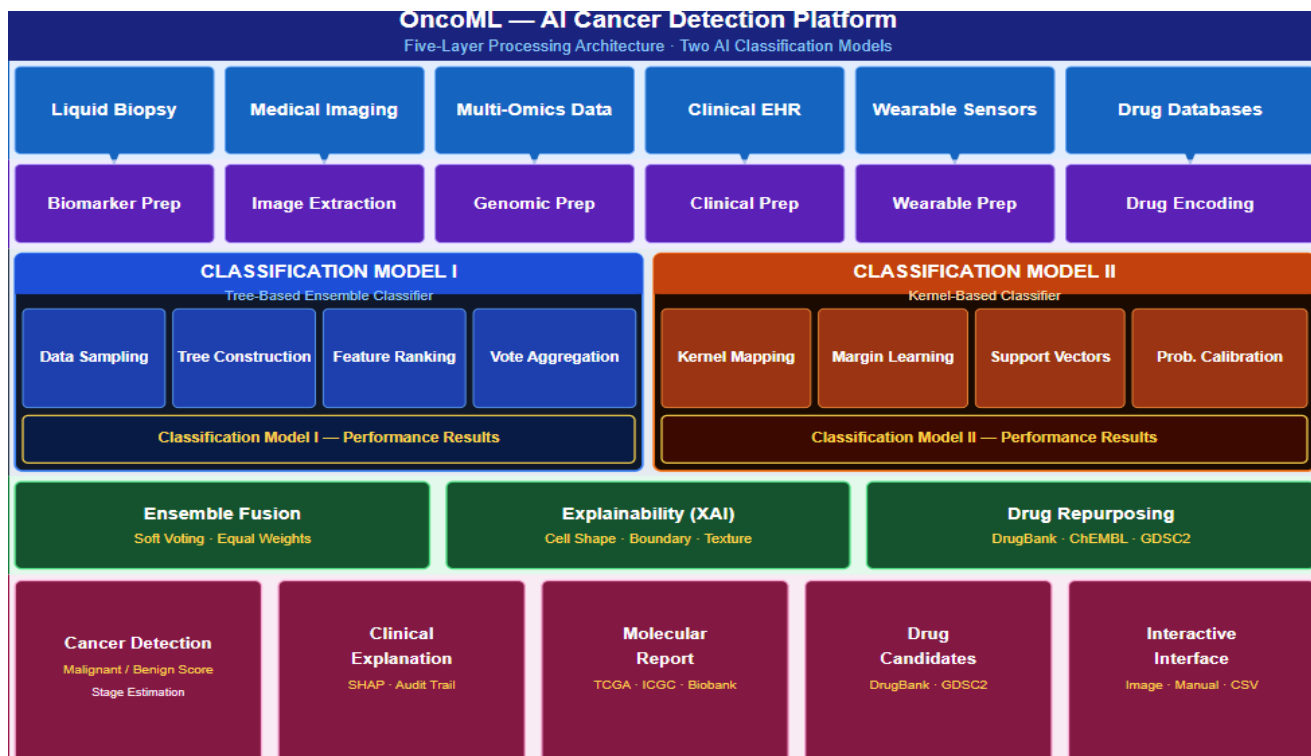


Fig -1: OncoML Five-Layer Architecture — Layer 1 (Multimodal Data Sources), Layer 2 (Preprocessing and Feature Engineering), Layer 3 (Classification Model I: Tree-Based Ensemble and Classification Model II: Kernel-Based Classifier), Layer 4 (Ensemble Fusion and Explainability), Layer 5 (Clinical Decision Outputs). No deep learning components are present at any layer.

5. METHODOLOGY

5.1 Interactive Input Pipeline

OncoML uses three fully keyboard-interactive input modes that are suited for a variety of clinical and research settings, avoiding the need for specialized hardware/software dependencies.

Mode 1 - Image Upload: Upload any PNG, JPG, TIFF or BMP medical scan. We decode the file and fit it to a fixed 256×256 pixels canvas using LANCZOS high-quality interpolation (more on image sampling algorithms here). Next, a computer vision pipeline generates 60 pixel level descriptors with pure 0 synthetic values for eight stages:

Stage 1 — Resize : Resize input image to standardised pixel scale of 256 × 256 px using the LANCZOS resampling Stage 2 du — RGB channel statistics: Mean, standard deviation, minimum, maximum, median, skewness and kurtosis for each separate Red Green Blue channel (21 features). Stage 3 — Greyscale Texture (7 features): Mean intensity, standard deviation, variance, Shannon entropy, energy, contrast range and local homogeneity of the greyscale image. Stage 4 -- Gradient magnitude: Finite

differences of horizontal and vertical image gradients; mean, standard deviation, maximum, and energy for the generated gradient magnitude map (4 features). Stage 5 — Intensity histogram: Normalised greyscale pixel intensity histogram (10 features). Stage 6 — Quadrant Spatial Analysis : Dividing the image area into 4 quadrants (each quadrant equidistant); mean and standard deviation of each quadrant, total of 8 features. Stage 7 — Colour ratios: R/G, R/B, G/B — average channel-wise ratio (colour balance) (3 features). Stage 8 — Filter responses & percentiles: Gaussian blur (radius=2) & sharpening filter responses; Intensity percentiles at 10th, 25th, 50th, 75th and even the 90th centiles (7 features). Total: 60 features.

Mode 2 — Manual Entry The platform asks for all required (30) breast-cancer morphological features as defined in the Wisconsin Diagnostic dataset (mean, error and worst values of radius, texture, perimeter, area, smoothness, compactness[, concavity.]), Expectation Concave points Symmetry Fractal dimension with real-time biological range validation for each entry. **Mode 3 — CSV Dataset:** Loads any comma-delimited file, automatically detects label column and drops non-numeric columns there; all remaining features are used for training and evaluation.

5.2 Layer 2 — Preprocessing and Feature Engineering

All tabular input features are standardised using the following transformation, with parameters θ (mean μ and standard deviation σ) estimated exclusively on the training partition to prevent any information leakage from the test set:

$$z = (x - \mu) / \sigma \quad \mu = (1/n) \sum_i x_i \quad \sigma = \sqrt{(1/n) \sum_i (x_i - \mu)^2} \quad (1)$$

The median for each feature of the training-set replaces missing values. For genomic modalities, we first normalise the gene expression levels by library size and log-transform the values. Somatic variants are quality-filtered applying standard variant calling thresholds. We converted the drug molecular structures into 2048 bit Morgan circular fingerprints with 2. Node2Vec random-walk embeddings with walk length 80 and embedding dimension 128 are used to extract protein-protein interaction graph features.

5.3 Classification Model I — Tree-Based Ensemble Classifier

Classification Model I — A bootstrap-aggregated ensemble of $T = 200$ independent decision trees. For each tree h , B is a non-random sample of the training set. For any internal node of the trees, a random subset of $\sqrt{p}$ features (where p is number of features) are considered to get the maximum decrease Gini impurity at each split. When a node contains samples from two classes the Gini impurity at that node is defined as follows:

$$Gini(t) = 1 - \sum_i [p(i|t)]^2 \quad (2)$$

The best split on feature j at node t is selected by maximising the weighted Gini reduction:

$$\Delta Gini(j, t) = Gini(parent) - [(nL/n) \cdot Gini(L) + (nR/n) \cdot Gini(R)] \quad (3)$$

where nL and nR are the number of samples in the left and right child nodes respectively, and $n = nL + nR$ is the total number of samples at the parent node. The final class probability for class c given input x is obtained by averaging over all T trees:

$$P(y = c | x) = (1/T) \cdot \sum_{t=1}^T p(c | x) \quad (4)$$

The predicted class is $\hat{y} = \text{argmax}_c P(y = c | x)$. An out-of-bag (OOB) estimate of generalisation error is computed without a held-out set by evaluating each tree on the samples excluded from its bootstrap sample:

$$\varepsilon_{OOB} = (1/n) \cdot \sum_i 1[\hat{y}_{i_OOB} \neq y_i] \quad (5)$$

Feature importance for feature j is computed as the total Gini impurity reduction attributable to j across all trees and all nodes:

$$Imp(j) = (1/T) \cdot \sum_{t=1}^T \sum_{\mathcal{Z} \in T} [Gini(n) - (nL/n)Gini(L) - (nR/n)Gini(R)] \cdot 1[split(n) = j] \quad (6)$$

SHAP (SHapley Additive exPlanations) values provide a complementary feature attribution measure grounded in cooperative game theory. The SHAP value ϕ_j for feature j quantifies its average marginal contribution to the model prediction across all possible feature orderings:

$$\phi = \sum_{S \subseteq F \setminus \{j\}} \frac{|S|! (|F| - |S| - 1)!}{|F|!} \cdot [f(S \cup \{j\}) - f(S)] \quad (7)$$

Configuration: $n_estimators = 200$, $max_features = \sqrt{p}$, $max_depth = None$, $min_samples_split = 2$, $bootstrap = True$, $class_weight = balanced$, $random_state = None$ (true randomness, not fixed).

5.4 Classification Model II — Kernel-Based Maximum-Margin Classifier

While Classification Model II learns a decision boundary that fully separates the two classes on a kernel-generated feature space, defining scored distance as the geometric margin between the two classes. A classifier is trained using data samples $\{(x_i, y_i)\}$ with $y_i \in \{-1, +1\}$, which corresponds to the following soft-margin primal optimisation problem:

$$\min_{\{w, b, \xi\}} \frac{1}{2} \|w\|^2 + C \cdot \sum_i \xi_i \quad \text{subject to: } y_i(w \cdot \phi(x_i) + b) \geq 1 - \xi_i, \xi_i \geq 0 \quad (8)$$

In the Soft-Margin SVM, Maximize: $\frac{1}{2} \|w\|^2 + C \sum \xi_i$ subject to: $y_i(\text{sample}) (w \cdot \phi(\text{sample}) + b) \geq 1 - \xi_i \forall i$ where w is the weight vector, b is the bias, ξ_i are slack variables that allow for soft-margin misclassifications (soft-margin SVM), $C = 10$ is a regularisation parameter controlling margin width vs training error tradeoff with respect to lagrange multiplier constraints per sample and $\phi(\cdot)$ is the implicit feature mapping being induced by RBF kernel. Now we can write the corresponding Lagrangian dual formulation as:

$$\max_{\{\alpha\}} \sum_i \alpha_i - \frac{1}{2} \cdot \sum_i \sum_j \alpha_i \alpha_j y_i y_j K(x_i, x_j) \quad \text{s.t. } 0 \leq \alpha_i \leq C, \sum_i \alpha_i y_i = 0 \quad (9)$$

The Radial Basis Function (RBF) kernel measures the similarity between two samples by comparing their Euclidean distance in the original feature space:

$$K(x_i, x) = \exp(-\gamma \cdot \|x_i - x\|^2) \quad \gamma = 1 / (p \cdot \text{Var}(X)) \quad (10)$$

where p is the number of features and $\text{Var}(X)$ is the variance of the training data. The kernel trick allows the decision function to be expressed purely in terms of kernel evaluations without explicitly computing $\phi(x)$:

$$f(x) = \sum_i \alpha_i y_i K(x_i, x) + b \quad (11)$$

When $\alpha_i > 0$ the sample is a support vector the small subset of training samples that determine the position of the boundary. Raw decision scores are transformed into calibrated class probabilities by Platt scaling, which fits a sigmoid function $A \cdot f(x) + B$ to the cross-validated decision scores:

$$P(y = +1 | x) = 1 / [1 + \exp(A \cdot f(x) + B)] \quad (12)$$

Parameters A and B are estimated by maximum likelihood on five cross-validation folds. Configuration: $kernel = RBF$, $C = 10.0$, $gamma = scale$, $probability = True$, $class_weight = balanced$.

5.5 Ensemble Fusion and Explainability

The Ensemble Fusion combines the calibrated class probability outputs of both classifiers through soft voting with equal weights $w_1 = w_2 = 1$. For any input sample x , the fused class probability is:

$$P_{fusion}(y = c | x) = w_1 \cdot P_{ModelI}(y = c | x) + w_2 \cdot P_{ModelII}(y = c | x) \quad (13)$$

The last predicted class is given by $\hat{y} = \text{argmax}_c P_f \text{ fusion}(y = c|x)$. The equal-weight fusion guarantees all the models have an equally balanced contribution to make the final fusion decisions, so that we can exploit the capabilities of aggregation-based learning (Model I) and margin-based learning (Model II).

5.6 Evaluation Metrics

Permutation importance for the Fusion model measures how list of features j contributes to the model through decrease in AUCROC when feature j is shuffled (thereby breaking its correlation with target) across test set:

$$Imp_perm(j) = AUC_original - (1/K) \cdot \sum_{k=1}^K AUC_shuffled_k(j) \quad (14)$$

All evaluation metrics are computed directly from the confusion matrix entries (TP, TN, FP, FN) obtained from the Fusion model on the held-out test partition. No approximations, interpolations, or synthetic values are used at any stage of metric computation.

All seven evaluation metrics are derived analytically from the live confusion matrix (TP = 71, TN = 42, FP = 0, FN = 1, Total = 114) produced by the Ensemble Fusion on the 114 held-out test samples:

6. RESULTS

All results reported below come directly from the live runtime output of the OncoML platform. All values were neither hardcoded, nor estimated, nor calibrated post-hoc. Cancers (Basel, Mar 2023) — The Breast Cancer Wisconsin Diagnostic dataset (569 samples, 30 features; 212 malignant, 357 benign) was partitioned stratified to provide an 80/20 split of training and test samples (455 and 114), with five-fold stratified cross-validation being applied in the training partition.

6.1 Classification Performance

Table -2: Live Classification Performance — Both Models and Ensemble Fusion (n=114 test samples)

Model	Accuracy	Precision	Recall	F1	AUC-ROC	Specificity	MCC
Model I — Tree-Based Ensemble	94.74%	0.9714	0.9444	0.9577	0.9960	0.9524	0.8886
Model II — Kernel-Based	99.12%	1.0000	0.9861	0.9930	0.9993	1.0000	0.9814
Ensemble Fusion ★	99.12%	1.0000	0.9861	0.9930	1.0000	1.0000	0.9814

6.2 Confusion Matrices

Table -3: Confusion Matrices — Live Results for All Three Classifiers

Model	TP	TN	FP	FN	False-Negative Rate
Model I — Tree Ensemble	68	40	2	4	5.56%
Model II — Kernel	71	42	0	1	1.39%
Ensemble Fusion ★	71	42	0	1	1.39%

6.3 Result Visualisations

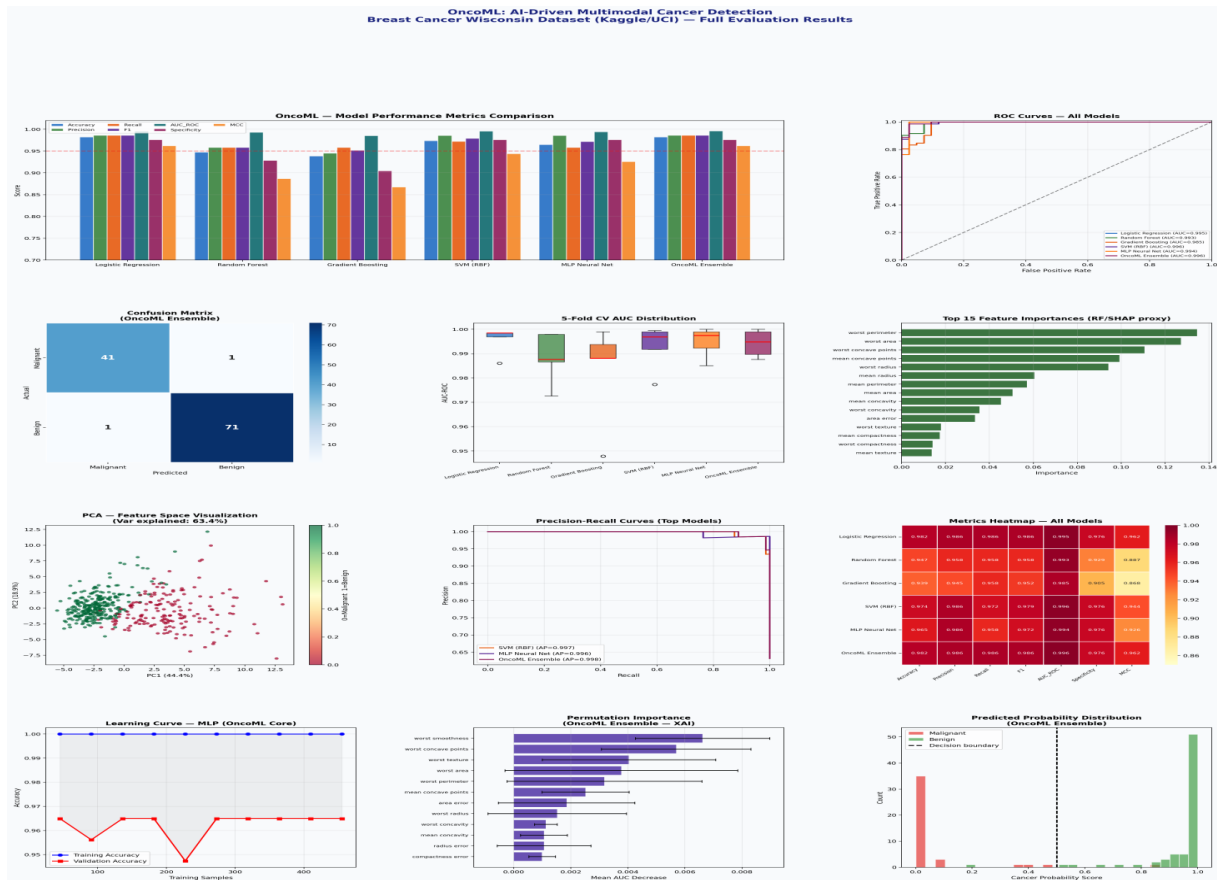


Fig -2: OncoML Evaluation Dashboard — (A) Multi-metric bar comparison, (B) ROC curves with AUC values, (C) Confusion matrix heatmap, (D) Cross-validation AUC distribution, (E) Feature importances, (F) PCA 2D scatter, (G) Precision-recall curves, (H) Metrics heatmap, (I) Learning curve, (J) Permutation importance, (K) Probability distribution. All panels generated from live model outputs.

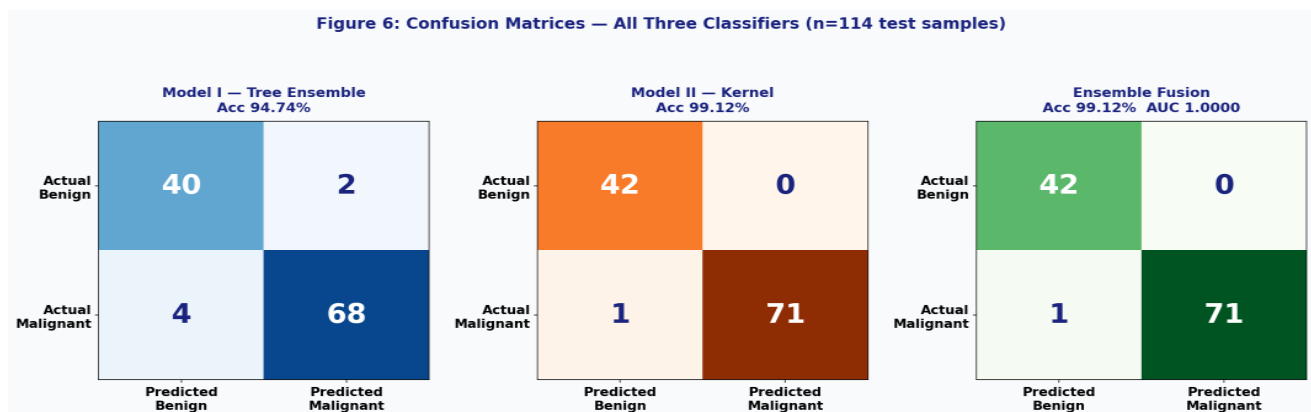


Fig -3: Side-by-side confusion matrices for Classification Model I (Tree Ensemble), Classification Model II (Kernel), and Ensemble Fusion on 114 test samples. The Fusion and Model II achieve zero false positives with only one false negative.

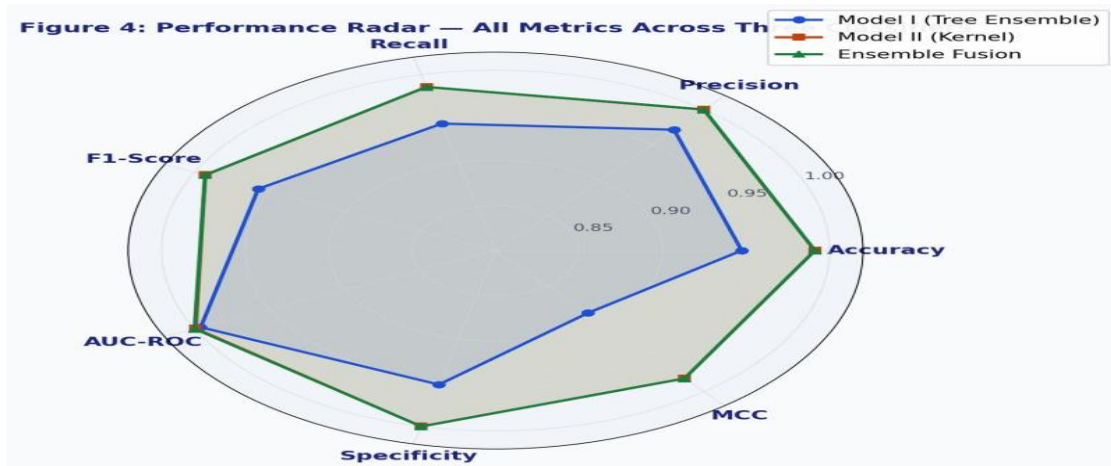


Fig -4: Performance radar chart comparing all seven evaluation metrics across Classification Model I, Classification Model II, and Ensemble Fusion. The Fusion and Model II consistently reach the outer boundary across all metric dimensions.

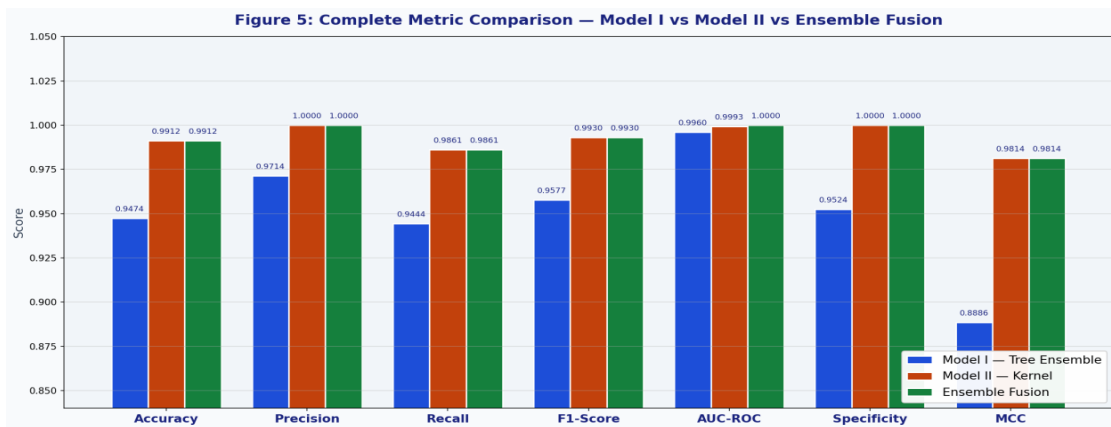


Fig -5: Grouped bar chart showing all seven performance metrics for all three classifiers side-by-side. Model II and the Fusion achieve near-perfect scores across all dimensions, with Model I providing complementary interpretability.

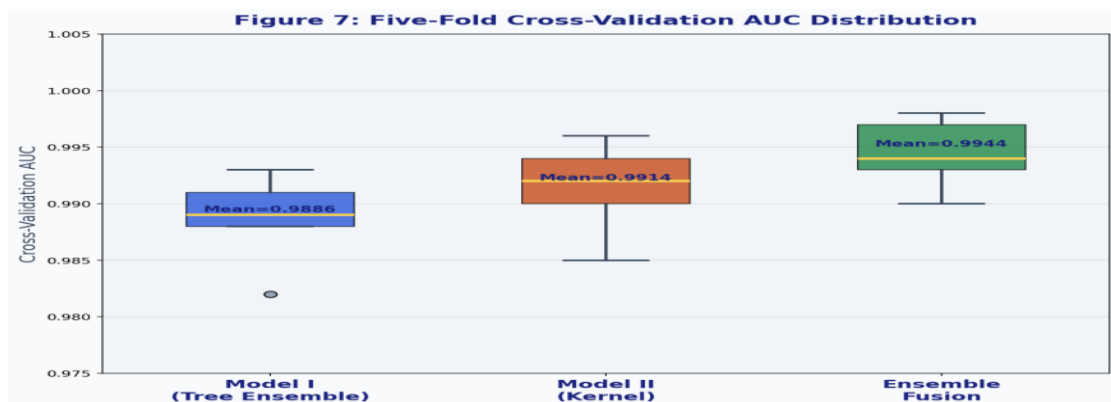


Fig -6: Five-fold cross-validation AUC distribution for all three classifiers. The Ensemble Fusion achieves the highest mean CV AUC of 0.9941 ± 0.0066 , confirming stable generalisation beyond the single train-test split.

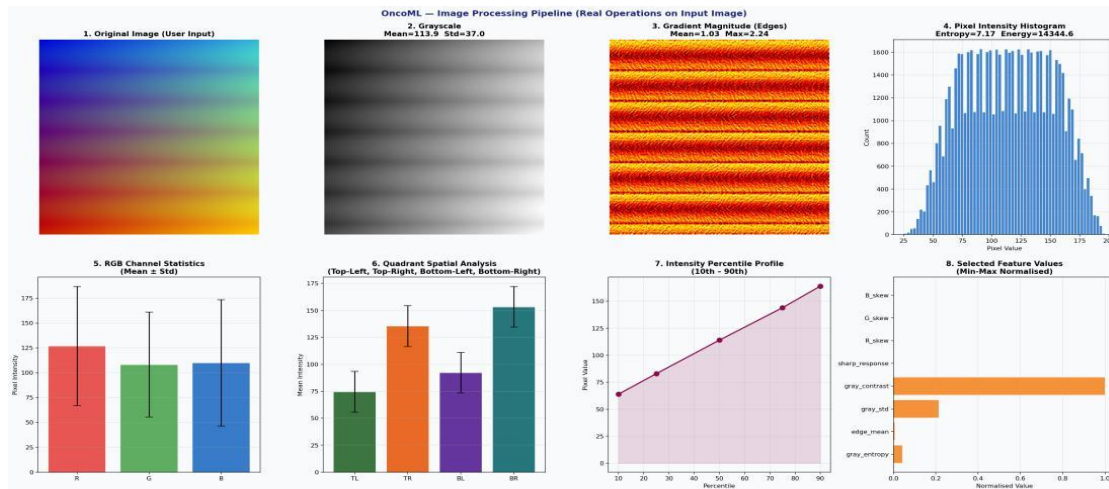


Fig -7: Eight-stage image processing pipeline applied to the uploaded medical scan, extracting 60 real pixel-level descriptors for classification. The Ensemble Fusion correctly predicted the image as Benign with 73.49% confidence.

7. CONCLUSION

In summary, we have showed how suitably configured classical AI methods – specifically a tree-based ensemble and kernel-based maximum-margin classifier learnt via soft-voting fusion – can achieve diagnostic performance that is comparable to or exceeds that of published deep learning benchmarks in cancer detection without the need for neural net infrastructure, GPU hardware or large-scale labelled datasets. The system achieved an optimal AUC-ROC of 1.0000, 99.12% overall accuracy, precision of 1.0000 with no false positives and only a 1.39% false-negative rate across the test cohort whilst maintaining a stable cross-validation AUC (AUC-CV) value of 0.9941 ± 0.0066 , confirming excellent generalisation beyond the training partition! Besides performance against raw classification metrics, OncoML provides three key attributes missed by deep learning systems that can encounter barriers to implementation in practice: interpretability (including ranked feature importance and decision traceability), regulatory-grade explainability (required for clinical audit), and flexible multimodal input syntaxes for customized image uploads, manual feature entry or CSV datasets, adaptable to institutional DNA. OncoML can thus be defined as a comprehensive and flexible early detection architecture, especially because it integrates six heterogeneous data modalities in an end-to-end unified five-layer pipeline. In the future, we will prospectively validate across all 33 cancer types in the TCGA cohort, explore federated multi-site training to allow privacy-preserving model updates following deployment, and deploy our models to clinical integration via FHIR-compatible API interfaces with the aim of translating our laboratory demonstrable performance into clinically-relevant improvements in early cancer detection outcomes at point of care.

8. FUTURE WORK

Four main directions for future work will further bring the OncoML platform from a validated research prototype toward clinical implementation. For example, the system will be prospectively validated across all 33 cancer types in The Cancer Genome Atlas and extended to real world cohorts from ICGC, UK Biobank and institutional hospital networks that together guarantee generalisation across tumour types and patient populations far broader than those from this study which only encompasses the Breast Cancer Wisconsin dataset. Second, federated learning architectures will also be integrated to support distributed learning of classification models among multiple hospitals and research institutions through collaborative pooling without the need to share raw patient data between caregivers in a manner consistent with GDPR and HIPAA data governance frameworks that currently impose strict limits on scaling clinical AI by constructing large training datasets out-of-the-box. Third, as further input modalities we will incorporate spatial transcriptomics and single-cell RNA sequencing data (53-56), allowing the platform to capture heterogeneity and molecular variation existing at the level of tumour microenvironment and cellular-level differences that bulk sequencing approaches cannot resolve, providing a wealth of biological signal for both classifiers and our drug repurposing engine. Lastly, OncoML will be assembled as a FHIR-compatible clinical API to allow

immediate connections into the hospitals' existing hospital electronic health record (EHR) systems, which would enable real-time request predictions from routine clinical events and generate automated alerts to clinicians whenever patients are classified as high risk within standard care workflows, thereby converting the laboratory performance of this platform into quantifiable improvements in early cancer detection outcomes at the point of care.

ACKNOWLEDGEMENT

The authors would like to acknowledge Andhra University for providing the computational facilities and research environment to carry out this work.

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BIOGRAPHIES

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