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A Novel Approach for Identification and Monitoring of Critical Cancer Cases Using a Multi-Agent System

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Abstract

Recent research in cancer detection and monitoring is based on the development of multi-agent systems. They are used for multidimensional multimodal health data integration, medical data augmentation, knowledge representation, predictive diagnosis, and personalized treatment schemes. This paper addresses the last two challenges by introducing intelligent agents to build clustering, classification, and treatment-recommendation models, while also improving overall process time through feature selection and the identification of critical malignant cases. In the first stage, the Wrapper Selection Agent based on Random Forests generated an optimized model with a 98.68% accuracy. Then, the Outlier-based Clustering and Critical Malignant Cases Agents detected the critical malignant cases with a 0.84 Silhouette Score. In the next step, Treatment Clustering and Decision Rules Agents built a perfect model that proposes a personalized treatment for the patients identified by the previous agents. The entire process is automated and provides treatment recommendations in 32.85 seconds.

Keywords: multi-agent system; random forests classifier; wrapper feature selection; k-means clustering; recommendation-based decision rules system; critical cases monitoring; cancer data

1. Introduction

Recent developments in healthcare technologies include different architectures for medical health monitoring and personalized treatment based on multi-agent systems and machine learning for both anticancer research [1–7], and chronic diseases [8–10].

The work [11] proposes a multi-agent framework for healthcare monitoring chronic and aged patients using wearable devices. The framework is composed of agents simulating doctors outside the hospital and, in the hospital, agents for pharmacy, nursing, and specialists. The purpose is to reduce doctors' workload, provide remote recommendations via 5G technology, and offer emergency healthcare services.

State-of-the-art model-based agents [12] are used to automate appointment scheduling and triage classification in healthcare settings, enhancing operational efficiency.

A multi-agent architecture for complex clinical scenarios is also proposed in [13], where AI-driven support adapts to longitudinal patient data and local clinical constraints to improve decision-making.

A solution for appointment scheduling, document interpretation, and clinical question answering is proposed in [14] using a multi-agent system. The LLM-powered architecture handles patients' tasks through a messaging-based interface.

However, these approaches use standard models without recording the system execution time. Our multi-agent system aims to automate tasks in healthcare settings while also improving model performance and execution time. The proposed recommendation model is retrieved directly from the collected data for the most critical malignant cases.

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The work [15] proposes a hierarchy of agents for different disease groups, using reinforcement learning techniques, and reports improvements in the learning process of the patients' symptoms. However, the proposed system does not compute the patients' diagnosis.

Recent works focus on breast cancer detection using machine learning techniques [16–22]. However, the proposed methods are not integrated into multi-agent clinical systems to provide personalized treatment and improved response time.

2. Proposed Methodology

This paper proposes an optimized solution based on a multi-agent system for real-time notification of critical cases of malignant cancer. The proposed system consists of six agents, namely: Wrapper Selection Agent, Outlier-based Clustering Agent, Critical Malignant Cases Agent, Treatment Clustering Agent, Decision Rules Agent, and Recommendation Agent. The system architecture is described in Figure 1.

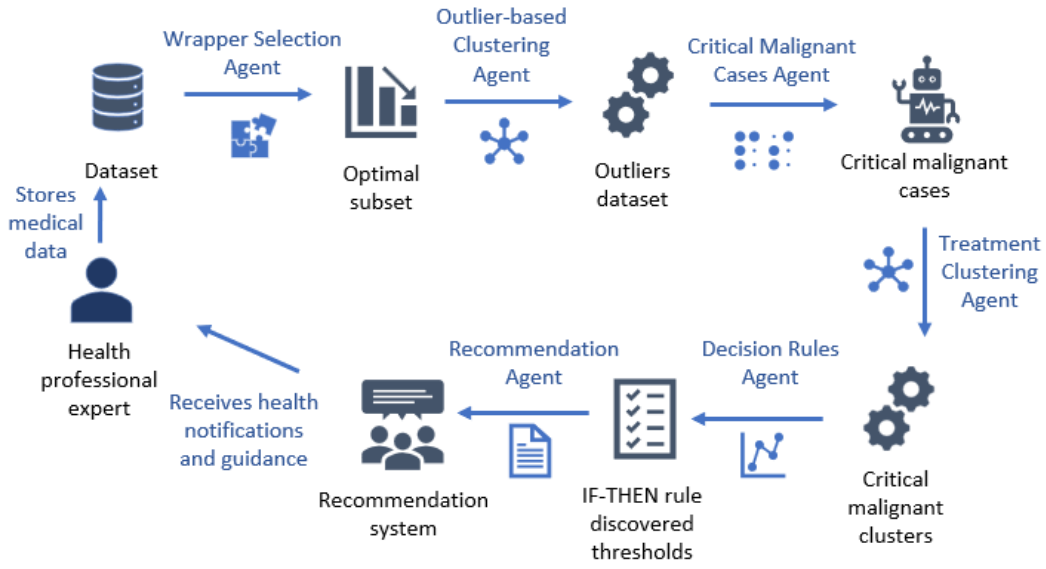

Figure 1. The concept and steps of the proposed methodology.

In the following subsections, we describe the behaviors of each agent in the proposed system, as well as the tasks and features of the health professional expert.

2.1. Health Professional Expert

The role of the health professional expert is to collect a sample of cells, tissue, or fluid from suspicious cancer areas, process it using digital imaging and specialized software analysis, and store it in a database. If the newly inserted record is a critical case, the proposed multi-agent system will notify the expert and provide guidance for immediate care or treatment. The expert can access any intermediate step in the process and visualize the preprocessed or learned data, as the system saves both the models and the data at all stages.

2.2. Wrapper Selection Agent

To optimize the entire process, we propose selecting the most relevant features using the Wrapper Feature Selection method [23] using a Forward Selection strategy. The discovered feature subsets are evaluated for classification performance using an embedded classifier.

The behavior of the Initial Wrapper Selection Agent is given below:

record the current system time and store it as start_time
set classifier to RandomForestClassifier

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set selected to empty list //selected feature set
set remaining to {f_0,f_1,…,f_{n-1}} //remaining feature set
set best_score to 0 //best global score
while len(selected) < max_features and remaining do
set scores to empty list //best current score
for each feature f in remaining
set test to selected + [f]
set score to the result returned by cross_val_score(classifier, dataset, cv=8)
compute the average of the 8 scores
pair the feature f with its corresponding score
add this pair to the scores list to keep track of results for each item in scores
set current_value to item[index 1]
if current_value > max_value_found_so_far then
set max_value_found_so_far to current_value
set best_item to item
set f to best_item[index 0]
set score to best_item[index 1]
if score > best_score then
add the feature f to the list of selected features
delete the feature f from the list of remaining features set best_score to score
else
break
return selected as the final feature subset
record the current system time and store it as end_time
compute time as end_time-start_time

To ensure the reliability of the discovered optimal subset, 8-fold cross-validation was used.

2.4. Outlier-Based Clustering Agent

For the optimally discovered subset of instances, we used K-means clustering [23] and Euclidean distance to determine the best cluster centroids for the K disease categories (for the considered case study: malignant and benign data clusters). The normal values and outliers for both data categories were graphically represented using Principal Component Analysis.

Given the optimal centroids, we computed the outlier threshold and selected the instances above it. The threshold was computed as the sum of the average of all calculated distances and their standard deviation.

The Outlier Agent behavior is described below:

record the current system time and store it as start_time
cluster the dataset into K groups using K-Means
store the cluster assignment (labels) for each data point
identify the center point (centroid) of each cluster
for each data point
find its assigned cluster center
calculate the distance between the point and the center
store the distance
compute the average of all the calculated distances
compute the standard deviation of those distances
add the average and the standard deviation together
store the sum as the threshold
outliers = distances > threshold

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apply Principal Component Analysis for data visualization
return outliers
record the current system time and store it as end_time
compute time as end_time-start_time

2.5. Critical Malignant Cases Agent

In the next step, we selected the outliers corresponding to the malignant cluster:
set critical to empty list
set index to 0
for each pred in predictions do
if pred is 1 and outliers[index] is true then
Append an index to critical
return critical

2.7. Treatment Clustering Agent

In the next step, the K-means method was applied to discover a number of clusters corresponding to the number of treatments for the critical malignant cases dataset:

record the current system time and store it as start_time
cluster the dataset into K groups using K-Means
store the cluster assignment (treatments) for each data point
record the current system time and store it as end_time
compute time as end_time-start_time

This clustering stage is a preprocessing step for the Decision Rules builder, in which the classifier requires the instances' labels to build the model during training.

2.8. Decision Rules Agent

For the previously labeled dataset, we built a rule-based system to provide recommendations to patients with critical health situations. This is an important step toward automating the entire process, since the most important features and their thresholds are discovered by learning models rather than established by a human expert.

The behavior of the proposed agent is given below:

record the current system time and store it as start_time
set classifier to DecisionTreeRegressor
train and test the model
export the best discovered decision rule-set
record the current system time and store it as end_time
compute time as end_time-start_time

2.9. Recommendation Agent

The Recommendation Agent receives the if-then rules discovered by the Decision Rules Agent, uses the tests on the decision tree model's nodes as thresholds, and provides personalized treatment recommendations. The recommendations, together with the patients' lists, are sent to the health professional expert.

3. Experimental Results

3.1. Dataset Description

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The dataset used to validate the proposed architecture is a benchmark dataset, available at [24]. It contains 10 features that describe the characteristics of the cell nuclei from an image of a fine needle aspirate of a breast mass (radius, texture, perimeter, area, smoothness, compactness, concavity, concave points, symmetry, fractal dimension), plus 20 features describing the mean, standard error, and "worst" or largest (mean of the three largest values) of these features. The dataset also includes the patient ID and diagnosis (malignant – M or benign – B). The class distribution is shown in Figure 2 (357 benign and 212 malignant instances).

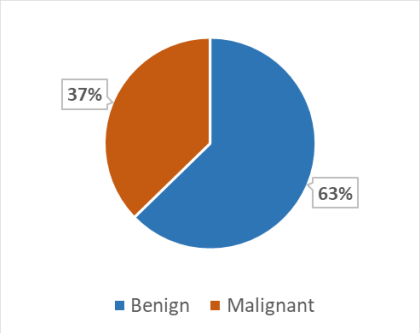

Figure 2. The dataset class distribution.

Models were trained and tested on 569 instances using a workstation with an Intel i7-1165G7 CPU and 8 GB of RAM.

3.2. First Wrapper Selection Step

3.2.1. Choosing the Best Classifier

The first step was to choose the best classifier for the dataset. We tested several models for accuracy, time to build, and precision, recall, and F1-measure for both benign and malignant classes. The results show that RandomForests achieved the best accuracy (0.9868) and a very good time (0.13 seconds) among the tested methods, including MLPClassifier, LogisticRegression, kNN, GaussianNB, GradientBoosting, and LinearSVC [23], as shown in Table 1, Figure 3, Figure 4, and Figure 5. The validation method used in the experiments was 40% split-percentage.

Table 1. Classifiers' performance.

Classifier	Accuracy	Time (sec.)	Precision B	Precision M	Recall B	Recall M	F1-score B	F1-score M
MLPClassifier	0.9649	0.76	0.96	0.98	0.99	0.93	0.97	0.95
LogisticRegression	0.9649	0.04	0.96	0.98	0.99	0.93	0.97	0.95
RandomForests	0.9868	0.13	0.99	0.98	0.99	0.99	0.99	0.98
kNN	0.9474	0.04	0.95	0.95	0.97	0.91	0.96	0.93
GaussianNB	0.9561	0.03	0.95	0.97	0.99	0.91	0.97	0.94
GradientBoosting	0.9825	0.17	0.97	1	1	0.95	0.99	0.98
LinearSVC	0.9649	0.05	0.96	0.98	0.99	0.93	0.97	0.95

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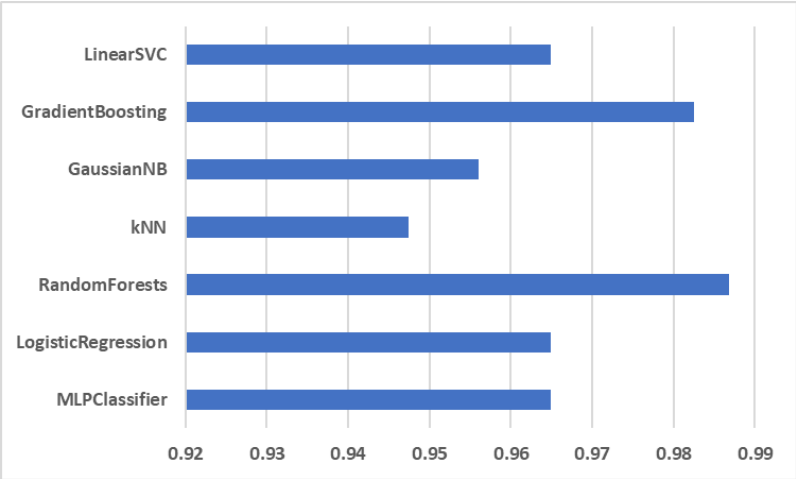

Figure 3. Classification accuracy.

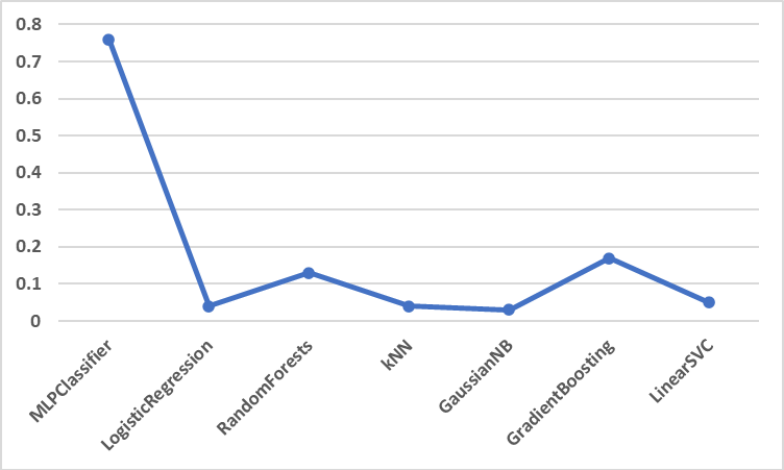

Figure 4. Time taken to build models.

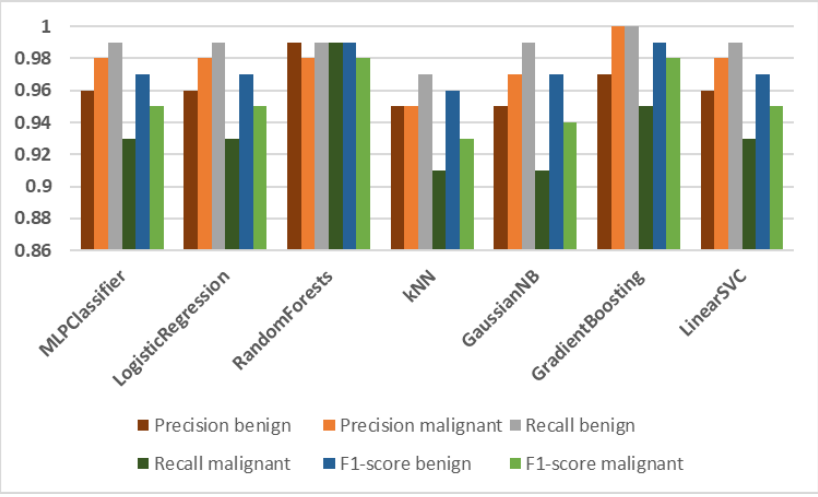

Figure 5. Precision, Recall, and F1-score for benign and malignant classes.

The Confusion Matrix for the RandomForests model shows good results for both the malignant class (for which 1 malignant instance out of 80 was incorrectly classified as benign) and the benign class (for which 2 instances out of 148 were incorrectly assigned to the malignant class), as presented in Figure 6.

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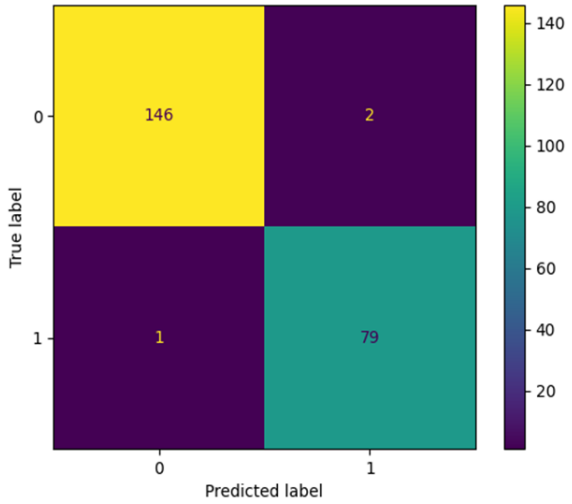

Figure 6. Confusion Matrix for the RandomForests identification model.

3.2.2. Finding the Optimum Feature Subset

Using the best discovered model, we applied a Forward Selection strategy with a Wrapper Selection method, and we discovered that the optimum feature subset was composed of 5 out of 31 features, namely: perimeter_worst, smoothness_worst, texture_worst, area_worst, concavity_mean.

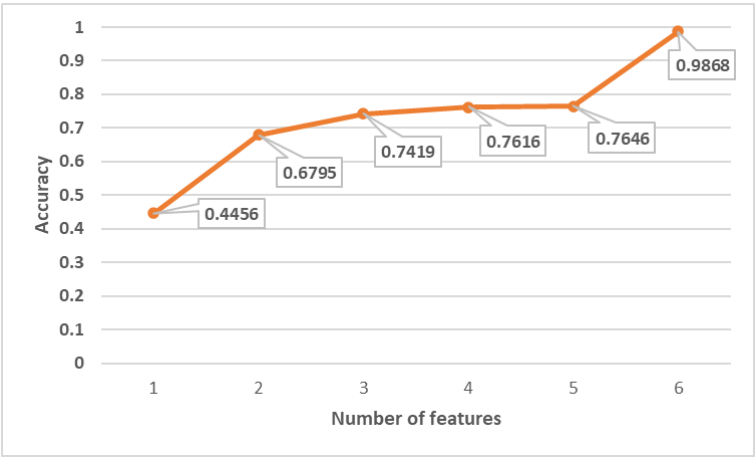

Figure 7. Classification accuracy in relation to the number of selected features.

The feature selection step took 6.76 seconds, and we used this preprocessing stage to improve the time and accuracy for building the models in the next stages of the process.

We used visualization techniques to analyze the model built so far (Figure 8), to observe the generated thresholds for each considered node in the tree, and to compare them with the threshold from the final model of the proposed system. The model generated at this stage includes tests for both classes of the dataset, and the aim is to generate a model next for the critical malignant cases.

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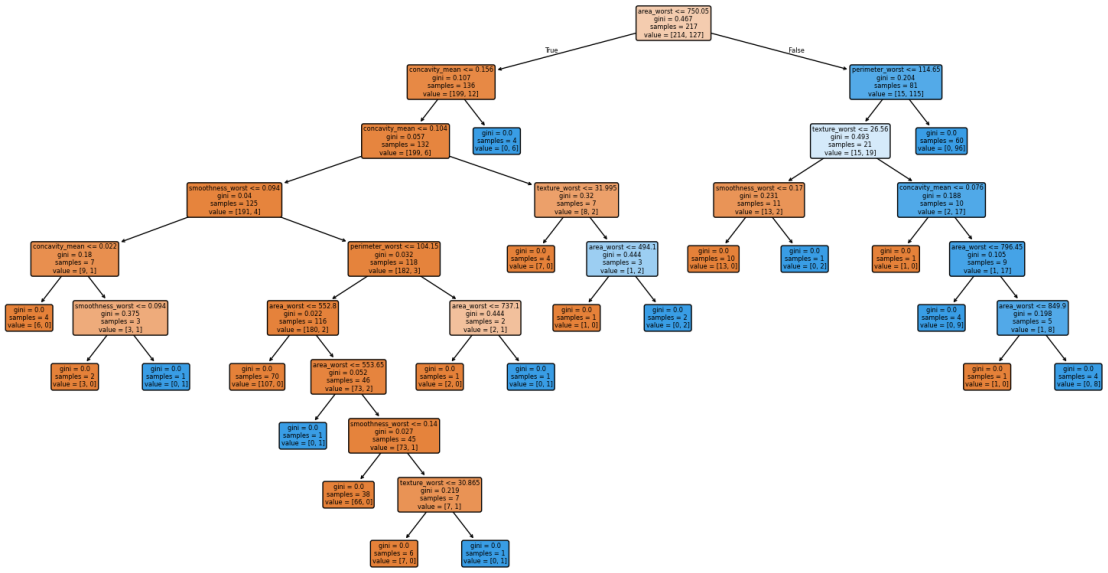

Figure 8. RandomForests identification model built with the optimal feature subset.

3.3. Outlier-Based Clustering Results

At this stage, we identified outliers in both the benign and malignant classes using K-Means clustering and instances with distances significantly larger than the typical average distance. The outlier distance was automatically discovered by computing the sum of the average of all the calculated distances and the standard deviation of those distances. The identified outliers in the considered dataset are shown in Figure 9.

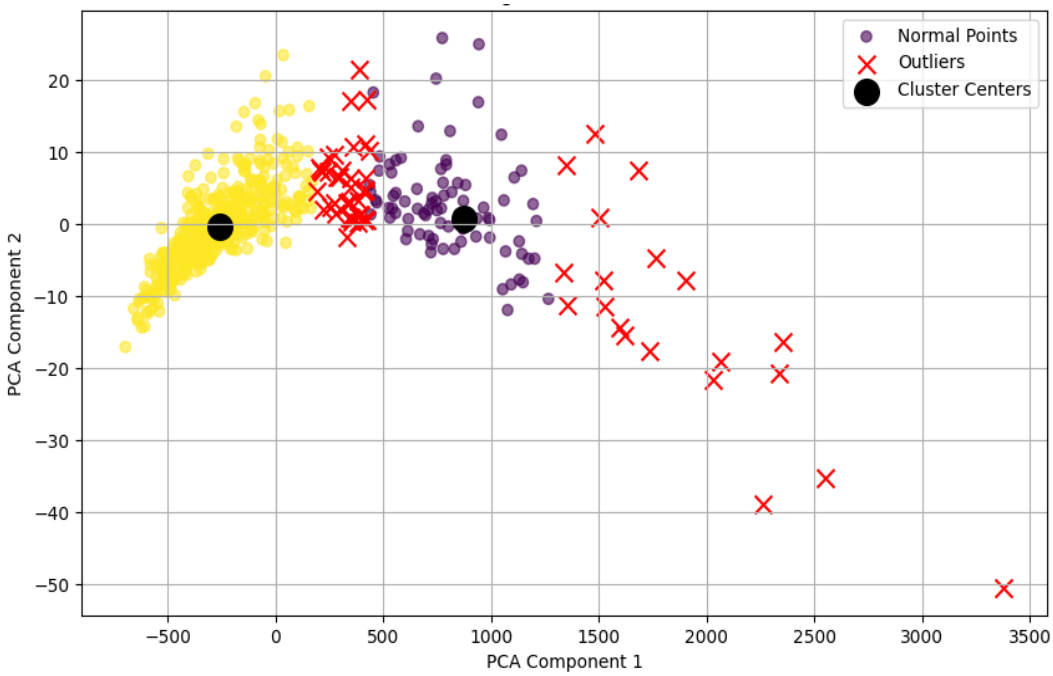

Figure 9. K-Means clustering with outliers (reduced with Principal Component Analysis).

The k-means performance metrics used were: the Sum of Squared Errors (54808390.092), the Silhouette Score (0.711), and the Calinski-Harabasz Index (1344.675).

3.4. Clustering Critical Malignant Patients for Treatment Decision

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In this stage, we considered only malignant outliers and applied K-Means again to group them for personalized treatment. We received two groups for the two considered treatments, as follows:

- Selected patients (IDs) for treatment1: 18, 23, 24, 82, 108, 162, 164, 180, 212, 219, 236, 265, 272, 339, 352, 368, 369, 461, 503, 521
- Selected patients (IDs) for treatment2: 10, 11, 16, 28, 29, 34, 35, 75, 83, 117, 118, 119, 131, 132, 141, 156, 167, 172, 182, 197, 201, 203, 207, 223, 230, 253, 258, 261, 262, 277, 328, 330, 370, 389, 400, 441, 444, 489, 566

The treatment clustering model was generated in 0.03 seconds, and the performance metrics were: Sum of Squared Errors equal to 5161166.695, Silhouette Score equal to 0.842, and Calinski-Harabasz Index equal to 344.256.

3.5. The Recommender System Model for Critical Malignant Cases

Using the personalized treatment groups, we built a recommender model based on a DecisionRules classifier. The best discovered recommender model was composed of the following rules:

IF area_worst <= 1764.00 THEN class=treatment2
IF area_worst > 1764.00 THEN class=treatment1

As shown, the final model considered only the area_worst attribute, and the discovered threshold was set to the critical malignant cases (1764.00), compared to the threshold in the general model (750.05), which included both benign and malignant instances (Figure 10).

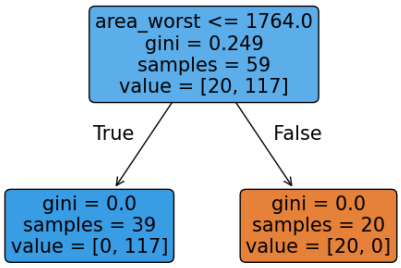

Figure 10. The Decision Trees recommender model.

The Confusion Matrix shows a perfect model, with patients assigned to the correct treatments (Figure 11). The time taken to build the recommender model was 0.01 seconds.

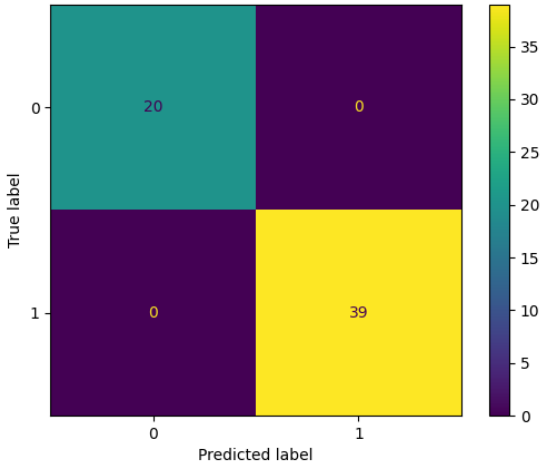

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Figure 10. Confusion Matrix for the Decision Trees recommender model.

4. Discussion

The execution time of the entire multi-agent system was 32.85 seconds, indicating a performant system in terms of response time. Other multi-agent systems that include consulting multi-modal clinical data [25] reported an overall time of 10.6 minutes.

Regarding the RandomForests identification model's performance (0.9868), it was comparable to, or even better than, other accuracies reported for breast cancer classification. The work [26] reported accuracy values of 0.878, 0.836, and 0.882 for breast cancer diagnosis. The CNN classifier achieved perfect accuracy for depth and health status, and 0.9286 for diameter, in work [27]. Long Short-Term Memory was used for breast cancer detection in [28], achieving a performance of 0.94. For other cancer types, the RandomForests classifier returned 0.963 accuracy and 0.965 precision, as presented in [29].

The recommender model based on DecisionRules reached 100% accuracy due to the feature selection and instances' selection in the previous steps. The system generated the simplest and most performant model for the data at hand, assisting the specialist in determining personalized treatment for critical malignant cases.

5. Conclusions

The paper proposes a novel architecture for a multi-agent system that is able to identify with high accuracy the malignant breast cancer patients and assist the health professional in providing specialized treatment for critical malignant cases. The proposed system can be applied to any dataset, as all steps and models are automatically generated from the data.

The feature selection and critical outlier identification steps result in an overall system time of 32.85 seconds, demonstrating a performant system across the response time, identification (98.68%), and recommendation (100%) models.

Author Contributions: Conceptualization, M.V.M.; methodology, M.V.M.; software, M.V.M., and U.K.I.; validation, M.V.M., D.M.C., and U.K.I.; formal analysis, M.V.M., D.M.C., and U.K.I.; investigation, M.V.M., D.M.C., and U.K.I.; resources, M.V.M., and D.M.C.; data curation, M.V.M., D.M.C., and U.K.I.; writing—original draft preparation, M.V.M.; writing—review and editing, M.V.M.; visualization, M.V.M. and U.K.I.; supervision, M.V.M.; project administration, M.V.M.; funding acquisition, M.V.M. All authors have read and agreed to the published version of the manuscript.

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Conflicts of Interest: The authors declare no conflict of interest.

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