# LDT: LOG DECISION TREE TO CLINICAL DATA CLASSIFICATION

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## ABSTRACT

The massive recording of the continuous data in the real-time imposes huge burden in analyzing the medical data as it takes huge time for execution and may cause errors due to the data uncertainty and the inability to interpret the highly significant features. As a result, the data is classified according to the rules and the efficiency of the data classification relies on the data feature selection. To address this issue, the paper introduces a new algorithm for the optimal selection of the features that uses a novel parameter for optimally determining the features. The proposed Log Decision Tree (LDT) uses the novel parameter termed as the Log-entropy to retrieve the mutually significant feature from the data such that the future data classification depends on the LDT classification model for determining the disease/condition of the patients, which leads to the easy diagnosis. The Log-entropy function uses the entropy and the weights of the features for computing the importance of the features and based on the selected features, the LDT model is developed. The experimentation proves that the proposed LDT attained a greater value of accuracy, specificity, and sensitivity of 83.7386%, 77.6160%, and 86.4407% respectively.

**Keywords:** *Log-entropy, decision tree, medical data classification, Entropy, feature selection.*

## 1. INTRODUCTION

Clinical data mining is an interesting research area that is a process of extracting the substantial and indispensable information from the comprehensive collection of the medical data, which infers the future patterns and possibilities through facilitating the users to enable the knowledge-driven and knowledgeable decisions [12]. The Electronic Health Records (EHRs) hold a tremendous record of the hidden information that is to be explored for enabling the better health care of the patients through uncompromising decisions [14]. The knowledge extraction from the medical records performs the excellent task of establishing disease-specific concept dictionaries that are utilized for the multiple applications mainly, in the recognition of the disease cohorts and in the establishment of the diagnostic models [13] [2]. The diagnostic models enable the physician to determine the root cause of the symptoms through the knowledge and experience acquired by them and hence, enables the effective diagnosis of the disease [15]. However, manual decision is time-consuming and expensive as the root cause of a problem is framed as rules for which an expert is required to interpret the rules in order to identify the root issue [6]. Thus, the need for an automatic classification method exists to classify the data records based on the feature attributes and provide a better solution for the fast clinical decisions [4].

Classification of the medical data offers an environment for medical data analysis and designs the classification models using the training data with the purpose of inferring the future data classes [17].The classification technique enables the physicians to diagnose the disease of the patient based on the similar symptoms [4]. The main intention of the medical data classification is to analyze the data and present the data as normal or abnormal such that the physicians can spend very less on a patient for analyzing the health conditions of the person. Moreover, the classification of the clinical data smoothens the diagnosing process thus, leads to the effective health-care solution [8]. Moreover, the interpretation of the rules is easy and physicians can even verify the outcome of the classification using the rules so that the misclassification problem is reduced or may be eradicated [7]. However, these rule-based classifiers employed for classification of the medical data could manage only the categorical data and they cannot be used for classifying the continuous data conveying that the traditional methods of data classification are not applicable on real-time classification [13].

In the existing literature, there are a number of the classification strategies, namely the decision tree classifiers [18], Bayesian classifiers [17], neural networks [19], and case-based reasoning [20]. Among all the available classification methods, the decision trees are used as an effective method of classification in the data mining and the machine learning approaches because of their simplicity, interpretation, computational efficiency, and their tendency to generate understandable classification rules [21] [16]. The decision trees represent the rules underlying data wherein the nodes denote the test on the individual feature and the branch indicate the result of the test with each node denoting the class label leading to easy human interpretation and facilitates the effective knowledgeable decisions [5]. Due to their explicit nature, they enable the better understanding about the model and the decision trees presented in the traditional methods are ID3 [24], C4.5 [25], QUEST [22], and GATree [23] that concentrated on the maximization of the classification accuracy and reducing the classification error but the cost of constructing the trees stood a hectic challenge of the tradition decision tree methods [16].

The paper proposes a new algorithm for performing data classification mainly, with the aim of reducing the burden of handling the complex data with a tremendous amount of the valuable information. The importance of the knowledge discovery is to extract the highly important and essential data from the data mass such the extracted knowledge enables the physician to take effective decision in diagnosing the disease through the classified results of the data. The main role is that the physician matches the data of the patient with the already available results to determine the root cause of the problem. The proposed method uses the log-entropy function to determine the best feature and the classification is performed based on the log-entropy function. The proposed LDT is based on the log-entropy calculation of the features for the selection of the features that it enables the optimal selection and optimal splitting precedes the optimal selection of the best feature so as to develop the decision tree.

The contribution of the paper is presented below:

**LDT algorithm:** The main contribution of the paper is the LDT algorithm that is the newly designed algorithm for developing the decision tree. The parameter used for developing the tree is the Log-entropy that selects the best feature based on the highest value of the log-entropy and the split value based on the log information gain. The optimum split value is essential for developing the perfect decision tree.

The paper is organized as: Section 1 discusses the background and gives a brief introduction to the paper, section 2 presents a motivation of the paper presenting the existing methods of big data classification along with their drawbacks. In section 3, the proposed method of the clinical data classification using the LDT is presented with the algorithmic steps and section 4 presents the results and discussion of the proposed method that highlights the superior performance of the proposed method. Finally, section 5 concludes the paper.

## 2. MOTIVATION

In this section, let us see the motivation behind the work through the overview of the existing data classification methods that highlights the detailed challenges of the work.

### 2.1 Related Works

The existing methods of the medical data classification are detailed in the related work section for organizing the various recent approaches and strategies and for detailing their impacts. Narander Kumarn and Sabita Khatri [1] proposed a J48 classifier based on the decision tree for classifying the clinical data for which the specific data attributes are generated. The data attributes are the result of the genetic programming. The data attributes generated using the genetic programming increases the classification accuracy of the method and reduced the error of the classification. The main advantage is that this method reduces the data space and increases the chance of the future predictions. The shortcoming is that the method reduces the power of the performance as the attribute selection is based on the original data. Liqin Wang *et al.* [2] proposed a machine-learning-based classification for the isolation of the signal from the noise for enabling the feasibility of the approach in order to generate and retain the disease-specific vocabularies. The main advantage of the method is that the relevant medications are identified for the treatment of a disease whereas the other methods depend on some score value. However, the relevant medications are not determined automatically and the error exists. Thus, the automatic methods of the clinical data classification were presented by Marian B.

Gorzałczany and Filip Rudzi´nski [3]. The automatic classification system was inspired by the fuzzy rule based classification systems (FRBCSs) and the multi-objective evolutionary optimization algorithms (MOEOAs) that possessed the tendency to generate the number of solutions in a single iteration, which is based on various accuracy levels. Moreover, a complexity-related interpretability measure was employed that solved the semantics-related interpretability issue through the effective fuzzy partitions of attribute domains. The method was advantageous as they offer improved readability, modularity, and it is easy-to-grasp. However, this method cannot be applied for the interpretable medical decision support systems. Ximeng Liu *et al.* [4] proposed an alternate classification method based on Naive Bayes that was mainly developed for preserving the privacy of the patient-centric clinical decision support system and the major role of the method is regarding the secure diagnosis. The method held the tendency to handle the big medical data to train the classifier based on the naive bayes and the classifier provided the classified results for the disease diagnosis with data security as the system is fully encrypted. The shortcoming is regarding the user-friendly environment as it is service provider's asset. Marcin Czajkowski *et al.* [5] proposed a method called the multi-test decision tree (MTDT) for investigating the medical data and to enable the better understanding of the inferring models and decisions. The method enhanced the stability of the classification but the complexity exists in the classification method. Moreover, the incorrect size of the split subsets prevailed that tend to increase the height of the tree. Manjeevan Seera and Chee Peng Lim [6] proposed a intelligent classification system that employed the hybrid model comprising of the Fuzzy Min-Max neural network, the Classification and Regression Tree, and the Random Forest model. The FMM-CART-RF model possessed the ability to learn incrementally from data samples and provide the classification with good accuracy. The main advantage was that the knowledge gained in the previous instances are stored and ensured the stable knowledge while solved the complex learning tasks but the robustness of the method was really poor. Ahmad Taher Azar and Shereen M. El-Metwally [7] presented a decision support tool using the single decision tree (SDT), boosted decision tree (BDT) and decision tree forest (DTF) that serve as an effective method for categorizing the data. Moreover, the earlier discovery of the breast cancer was done enabling the survival period of the patient but the overall accuracy is found to be less. Chin-Yuan Fan *et al.* [8] developed a hybrid classification model using the case-based data clustering method and a fuzzy decision tree that enabled the detection of the root cause of the disease. The method improved the decision-making process of the doctors but the number of fuzzy terms of the individual feature degrades the generated rules. Vitaly Schetinin *et al.* [9] used the Bayesian decision trees for the classification of the clinical data, which enabled the easy interpretation of the ensemble model and the major advantage is that the method extracted new knowledge of the predictor but they are insensible to the interpretability of deciding the optimal processes.

## 2.2 Challenges

The challenges of the work are depicted in this section:

- Most of the classification methods consumes more time for classification, which is not applicable for the real-world prediction that should be completed in the short period. Moreover, identification of the misclassified results and the cost of the classification is the major drawback of the exiting classification methods as addressed in [16].
- The constraint used for improving the performance of the classifiers is regarding the simplicity of the decision trees but the trees become complex and impossible to interpret as the trees do not satisfy the constraint [5].
- The stored medical data consumed more space and the important data is hidden within them and without an effective classification method, the data seems to be meaningless and hence, a classification method for transforming the stored data into the most meaningful data is required [4].
- The manual process of classifying the medical data is time-consuming and may cause human errors [15].
- The presence of the medical data is described as inherent heterogeneity, incompleteness, unbalanced and high dimensional nature [14] that most of the existing methods failed to address.
- The classifiers other than the decision trees failed to provide the interpretable nature, which is capable of providing the most significant data to the experts for improving the reliability of the classification [9].

- Fuzzy-based decision trees suffer from the problem that when the number of fuzzy terms of the individual feature is greater, it degrades the generated number of rules [8].

## 3. A NOVEL LDT ALGORITHM BASED ON THE LOG-ENTROPY

Data classification is the need of the current information era mainly, in the field of the medical data mining as most of the existing methods relied on performing the classification with good accuracy and free from errors. The existing methods requires human expert for interpreting the classification rules and therefore, it required much time and lead to misclassification. Due to the misclassification, it is required by the physician to verify the classification results. Due to all these reasons, the paper proposes a new classification strategy based on the feature attributes. The effective classification is enabled based on the selection of the feature attributes and in this paper, the feature selection is carried out using the entropy and the correlation factor. The log-entropy of the attributes is calculated and the decision tree is constructed such that the node represents the test attribute and the branches are the results of the classification. The proposed classification method LDT performs the classification for which initially, the log-entropy of the features are determined for the selection of the best feature and the feature attribute with the maximum value of the log-entropy symbolizes the best feature. Then, the split criterion is performed through the optimal split selection using the log information gain and the tree structure is developed for the entire medical data.

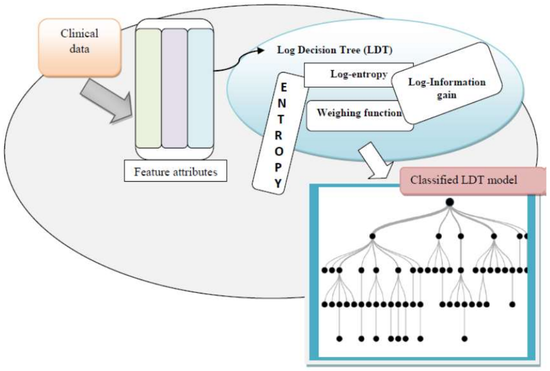


*Figure 1. Block diagram of the proposed LDT algorithm for the classification of the medical data*

### 3.1 Imputing the Input Medical Data

The input to the LDT is the medical data that enables the simpler analysis and the efficient knowledge discovery. The medical data is split into subsets as the process of analyzing the medical record as it appears may leads to complexity. In other words, the root node is selected that signifies the highly important feature and the selection is managed by the Log-entropy function. Once the root node is selected, the sub-nodes or the leaf nodes are presented based on the optimal split point selection. Let us consider the medical data, which is represented as, $D_k$ .

$$D_k = \{D_1, D_2, ..., D_g\} \tag{1}$$

where, $g$ is the total number of records present in the medical data. The dimension of the medical data is represented as $(p \times q)$. The medical data is presented to the LDT model for generating the appropriate classification through the sufficient data feature selection. The features present on the medical data are given by,

$$f_M = \{f_1, f_2, ..., f_h, ... f_x\} \tag{2}$$

where, $f_M$ is the data attributes of the medical data and $x$ is the total number of attributes present in the medical data. The attributes may be of type numeric and text including the age, height, and so on. The model generated using the LDT is mainly used for the future reference in classifying the fore-coming data that eases the classification and reduces the time.

### 3.2 New Definitions

In this section, the newly devised terms are introduced with the brief explanation and presents their importance in performing the classification.

### 3.2.1 Log Entropy

The log entropy is computed using the logarithmic value of the entropy function [10], which is the product of the entropy of the features and the weights of the feature attributes. The log-entropy of the feature is computed using the following formula,

$$L(f_n) = w \times \varepsilon(f_h) \tag{3}$$

$$\text{where, } w = 2 \times \left( \frac{1}{1 + \log\left(\varepsilon(f_h)\right)} \right) \tag{4}$$

$$\varepsilon(f_h) = -\sum_{T=1}^{U(f_h)} P_T \cdot \log P_T \tag{5}$$

where, $f_h$ is the feature vector, $U(f_h)$ is the number of unique features in the feature $f_h$ . $L$ is the log-entropy, $L(f_h)$ refers to the log-entropy of the feature $f_h$ , $U(f_h)$ is the unique values of the feature, $P_T$ is the probability distribution function of the features. The weighing function is denoted as $w$ and $\varepsilon(f_h)$ is the entropy of the feature attribute.

### 3.2.2 Log Information Gain

The log information gain is essential to determine the information gain of the unique features using the log-entropy and the conditional log-entropy. The log-entropy and the conditional log-entropy are obtained by the integration of the logarithmic term instead of the exponential term, which is the modification of the holo-entropy and the conditional holo-entropy [10]. The importance of the information gain is about the optimal selection of the splitting criterion that picks the optimal splits points from the unique features. Let us consider the information gain is denoted as $LIG(f_h , f_j)$ and the log-entropy and the conditional log-entropy are denoted as , $CL(f_h , f_j)$. The log information gain of the feature is determined based on the following formula.

$$LIG(f_h , f_j) = L(f_h) - CL(f_h , f_j) \tag{6}$$

where, $L(f_h)$ denotes the log-entropy of the $h^{th}$ feature and $CL(f_h , f_j)$ refers to the conditional log-entropy of the features for which the unique value of the features are interpreted. The probability of the $h^{th}$ feature present in the medical data is denoted as, $P_h$.

$$CL(f_h , f_j) = \sum_{h=0}^{U(f_h)} P_h \cdot L(f_h, f_j) \tag{7}$$

$$L(f_h, f_j) = W_l . \varepsilon(f_h, f_j) \tag{8}$$

$$W_l = 2 \times \left( \frac{1}{1 + \log\left(\varepsilon(f_h)\right)} \right) \tag{9}$$

$$\varepsilon(f_h, f_j) = \sum_{h=1}^{U(f_h)} P(f_h = h, f_j = h) . \log(f_h = h, f_j = h) \tag{10}$$

$W_l$ denotes the weights of the features based on the log-entropy and $\varepsilon(f_h, f_j)$ denotes the entropy of the unique value of the best features. $L(f_h, f_j)$ denotes the log-entropy of the unique values of the features and the log-entropy of the unique feature depends on the weights of the feature and the entropy of the features.

### 3.3 The novel LDT algorithm for the clinical data classification

In this section, the discussion of the steps involved in classifying the data using the LDT model is presented. The proposed LDT is the modification of the HDT presented in [10]. The decision trees are the effective tool in classifying the big data sets because of their simplest computation methods. The classification is carried out using the simple rules that does not need any computation. In general, there are four steps involved in the classification process that includes the feature selection, splitting criterion, stopping criterion, and labeling. The term LDT refers to the Log decision tree that uses the combination of the entropy and the total correlation along with the weight of the features for the selection of the best feature. The total correlation factor determines the relationship between the features of the data and the global disorders of the data, which is determined using the entropy function. Additionally, in order to differentiate the data depending on the label, the probability distribution of the individual feature is determined that is essential for evaluating the log-entropy. At first, the root node is determined and the attributes are arranged based on the log-entropy that forms the branches. Once the best feature is identified, the split criterion is applied, which stands as an optimal split and the optimal split are based on the log entropy information gain.

### 3.3.1 Steps of the proposed LDT algorithm

The procedural steps of the proposed LDT are presented below:

*Step 1: Feature selection:* The feature selection is the basic step engaged in developing the LDT and the feature selection is carried out using the log-entropy. The log-entropy of all the features is determined and the feature that possesses the higher value of the log-entropy is selected as the best feature. The concept of log-entropy is applied to all the feature attributes in the data and the best feature is selected based on the highest value of the log-entropy. The log entropy of the features is determined based on equation (4).

*Step 2: Optimal split point obtained using the splitting rule:* The splitting criterion computes the best split point for splitting the data for which the log-entropy information gain is employed. The unique value of the features that is determined while selecting the best feature is employed as the split point. The information gain is determined from the unique values of the feature, which in turn, uses the log-entropy and the conditional log-entropy of the feature in determining the information gain of the feature. The log information gain of the unique features is computed using the equation (7). Once the node of the tree is fixed, the data that enters the branch is applied for feature selection followed with the application of the splitting rule. The process is repeated until the stopping criterion is reached in building the branches of the decision tree.

*Step 3: Stopping criterion:* The leaf node determines the stopping criterion and when all the data is distributed in the nodes that denotes the termination of the data classification.

*Step 4: Leaf node labels based on the class of the data:* The label to the node is made based on the class of the maximum number of data. The class of the data is selected based on the class that is common for maximum number of the data present in the classification process.

```
LDT: Log-entropy enabled decision tree.
Input: Features of the data.
Output: Decision tree- LDT.
Start
  Fix the root node.
    If (number of samples<1)
      {
        Stop branching.
      }
    Else
      {
        For individual attribute $f_h$ .
        Compute $L(f_h)$.
      }
          Determine the unique values for the best feature.
          Form the subsets of data according to the class.
          Compute $LIG(f_h, f_j)$.
          End $j$ .
Select the best feature and the corresponding split value.
Build the new node and perform the classification.
Continue until the stopping criterion is reached.
End.
```

*Figure 2: Pseudo code of the novel LDT algorithm.*

Figure 2 shows the pseudo code for the proposed LDT algorithm that aims at the optimal classification of the medical data based on the features. The medical data classification is based on the log-entropy of the attributes present in the data that aligns the root nodes based on their log-entropies. The data classification model developed is used for the future reference model for classifying the medical data that reduces the time and provides perfect diagnosis to the patient based on the symptoms.

## 4. RESULTS AND DISCUSSION

In this section, the results and discussion is presented to prove the importance of the proposed LDT when compared with the existing methods and the superiority is proved based on the performance metrics, namely sensitivity, specificity, and accuracy.

### 4.1 Experimental setup

The experimentation is carried out using three medical datasets such as, Cleveland, Switzerland and Breast Cancer data available in the UCI machine learning repository [11]. The experimentation is performed in Windows 8, 4GB RAM and the implementation is carried out in JAVA programming with map reduce libraries.

### 4.2 Evaluation metrics

The performance of the proposed LDT classifier will be analyzed using sensitivity, specificity and accuracy.

#### 4.2.1 Sensitivity

Sensitivity is the proportionality existing between the false negative and the true positive.

$$Sensitivity = \frac{1}{1+\frac{FN}{TP}}$$

#### 4.2.2 Specificity

Specificity denotes the proportionality between the false positive and the true negative.

$$Sensitivity = \frac{1}{1+\frac{FP}{TN}}$$

#### 4.2.3 Accuracy

Accuracy shows the proportionality between the false positives and the true positives.

$$Accuracy = \frac{1}{1+\frac{FP}{TP}}$$

### 4.3 Methods taken for comparison

The proposed LDT classifier will be compared with the existing algorithms to prove the performance improvement of the proposed algorithm. The methods taken for comparison include: DT, HDT, ANN, and the proposed LDT

### 4.4 Comparative Analysis

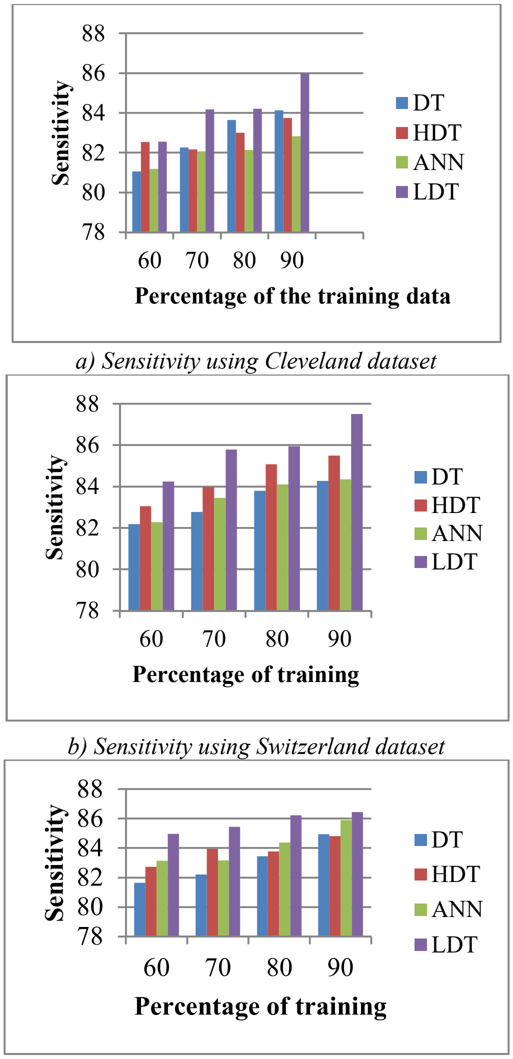
This section displays a deep insight over the comparative analysis of the proposed LDT with the existing algorithms in order to prove the superiority of the proposed method.

#### 4.4.1 Comparison using sensitivity

Figure 3 shows the comparative analysis of sensitivity based on the three datasets, such as Cleveland dataset, Switzerland dataset, and Breast Cancer dataset. Figure 3 a) shows the analysis of the sensitivity using the Cleveland dataset that provides the clear view of the sensitivity for all the comparative method including the proposed LDT. The sensitivity is analyzed for the various percentages of the training data. When the training percentage is 60, the percentage of sensitivity obtained using the methods DT, HDT, ANN, and LDT are 81.0514, 82.5269, 81.1808, and 82.5432 respectively. Similarly, when the training percentage is 80, the sensitivity obtained is 83.64%, 83.006%, 82.1262%, and 84.2071 respectively for the methods DT, HDT, ANN, and LDT proving that the sensitivity of the proposed LDT method is superior over the other methods.

Figure 3 b) shows the analysis of the sensitivity using the Switzerland dataset that provides the clear view of the sensitivity for all the comparative method including the proposed LDT. The sensitivity is analyzed for the various percentages of the training data. When the training percentage is 60, the percentage of sensitivity obtained using the methods DT, HDT, ANN, and LDT are 82.1831, 83.0521, 82.2881, and 84.2432 respectively. Similarly, when the training percentage is 90, the sensitivity obtained is 84.2781%, 85.5025%, 84.3542%, and 87.5149% respectively for the methods DT, HDT, ANN, and LDT proving that the sensitivity of the proposed LDT method is superior over the other methods.

Figure 3 c) shows the analysis of the sensitivity using the Breast cancer dataset that provides the clear view of the sensitivity for all the comparative method including the proposed LDT. The sensitivity is analyzed for the various percentages of the training data. When the training percentage is 70, the percentage of sensitivity obtained using the methods DT, HDT, ANN, and LDT are 83.1996, 83.9377, 83.1596, and 85.4474 respectively. Similarly, when the training percentage is 90, the sensitivity obtained is 84.9361%, 84.8221%, 85.8965%, and 86.4407% respectively for the methods DT, HDT, ANN, and LDT proving that the sensitivity of the proposed LDT method is superior over the other methods.



*a) Sensitivity using Cleveland dataset*

*b) Sensitivity using Switzerland dataset*

*c) Accuracy using Cleveland dataset*

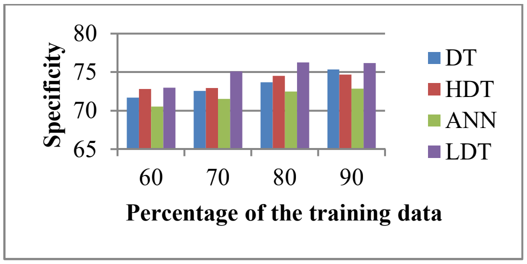
*Figure 3. Analysis of Sensitivity using the Cleveland, Switzerland, and Breast Cancer dataset*

### 4.4.2 Comparison using Specificity

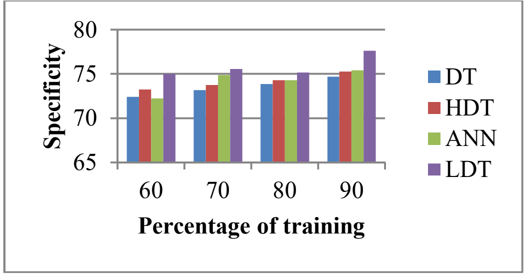
Figure 4 shows the comparative analysis of specificity based on the three datasets, such as Cleveland dataset, Switzerland dataset, and Breast Cancer dataset. Figure 4 a) shows the analysis of the specificity using the Cleveland dataset that provides the clear view of the specificity for all the comparative method including the proposed LDT. The specificity is analyzed for the various percentages of the training data. When the training percentage is 60, the percentage of specificity obtained using the methods DT, HDT, ANN, and LDT are 71.7003, 72.8024, 70.5165, and 72.9647 respectively. Similarly, when the training percentage is 90, the specificity obtained is 75.3563%, 74.6806%, 72.8435%, and 76.1681 respectively for the methods DT, HDT, ANN, and LDT proving that the specificity of the proposed LDT method is superior over the other methods.

Figure 4 b) shows the analysis of the specificity using the Switzerland dataset that provides the clear view of the specificity for all the comparative method including the proposed LDT. The specificity is analyzed for the various percentages of the training data. When the training percentage is 60, the percentage of specificity obtained using the methods DT, HDT, ANN, and LDT are 72.4040, 73.2521, 72.2102, and 75.0223 respectively. Similarly, when the training percentage is 90, the specificity obtained is 74.7041%, 75.2635%, 75.4182%, and 77.6160% respectively for the methods DT, HDT, ANN, and LDT proving that the specificity of the proposed LDT method is superior over the other methods.

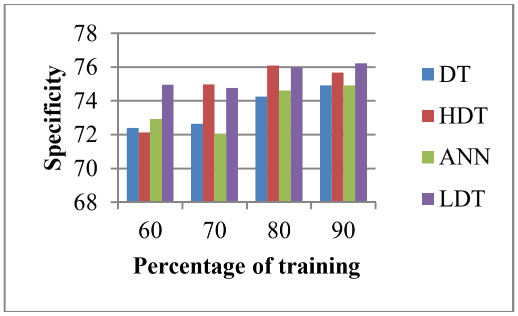
Figure 4 c) shows the analysis of the specificity using the Breast cancer dataset that provides the clear view of the specificity for all the comparative method including the proposed LDT. The specificity is analyzed for the various percentages of the training data. When the training percentage is 70, the percentage of specificity obtained using the methods DT, HDT, ANN, and LDT are 72.6484, 74.9732, 72.0358, and 74.7642 respectively. Similarly, when the training percentage is 90, the specificity obtained is 74.9145%, 75.6826%, 74.9238%, and 76.2249% respectively for the methods DT, HDT, ANN, and LDT proving that the specificity of the proposed LDT method is superior over the other methods.



*a) Specificity using Cleveland dataset*



*b) Specificity using Switzerland dataset*



*c) Specificity using Breast cancer dataset*

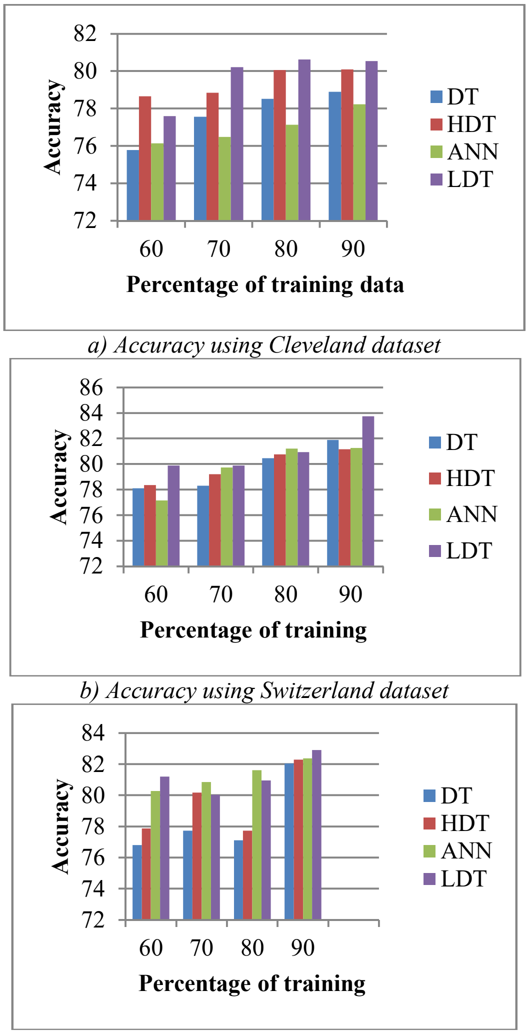
*Figure 4. Analysis of Specificity using the Cleveland, Switzerland, and Breast Cancer dataset*

### 4.4.3 Comparison using Accuracy

Figure 5 shows the comparative analysis of accuracy based on the three datasets, such as Cleveland dataset, Switzerland dataset, and Breast Cancer dataset. Figure 4 a) shows the analysis of the accuracy using the Cleveland dataset that provides the clear view of the accuracy for all the comparative method including the proposed LDT. The accuracy is analyzed for the various percentages of the training data. When the training percentage is 60, the percentage of accuracy obtained using the methods DT, HDT, ANN, and LDT are 75.7748, 78.6552, 76.1325, and 77.5907 respectively. Similarly, when the training percentage is 90, the accuracy obtained is 78.8941%, 80.1012%, 78.2337%, and 80.5467% respectively for the methods DT, HDT, ANN, and LDT proving that the accuracy of the proposed LDT method is superior over the other methods.

Figure 5 b) shows the analysis of the accuracy using the Switzerland dataset that provides the clear view of the accuracy for all the comparative method including the proposed LDT. The accuracy is analyzed for the various percentages of the training data. When the training percentage is 60, the percentage of accuracy obtained using the methods DT, HDT, ANN, and LDT are 78.0957, 78.3422, 77.1498, and 79.8781 respectively. Similarly, when the training percentage is 90, the accuracy obtained is 81.8758%, 81.1618%, 81.2522%, and 83.7386% respectively for the methods DT, HDT, ANN, and LDT proving that the accuracy of the proposed LDT method is superior over the other methods.

Figure 5 c) shows the analysis of the accuracy using the Breast cancer dataset that provides the clear view of the accuracy for all the comparative method including the proposed LDT. The accuracy is analyzed for the various percentages of the training data. When the training percentage is 70, the percentage of accuracy obtained using the methods DT, HDT, ANN, and LDT are 77.8653, 80.1743, 77.7172, and 82.2785 respectively. Similarly, when the training percentage is 90, the accuracy obtained is 81.20004%, 80.0290%, 80.9542%, and 82.9046% respectively for the methods DT, HDT, ANN, and LDT proving that the accuracy of the proposed LDT method is superior over the other methods.



*a) Accuracy using Cleveland dataset*

*b) Accuracy using Switzerland dataset*

*c) Accuracy using Breast Cancer dataset*

*Figure 5. Analysis of Accuracy using the Cleveland, Switzerland, and Breast Cancer dataset*

### 4.5 Discussion of the comparative methods

The comparative discussion of the proposed method is provided in this section and the table shows the discussion of the performance metrics. For the analysis, three datasets are utilized and the comparative methods are compared in terms of the metrics, such as accuracy, specificity, and sensitivity. The accuracy values convey that the proposed LDT possess a greater percentage when compared with DT, HDT, and ANN. BY using the first dataset, the Cleveland dataset, the table highlights the percentages of accuracy, specificity, and sensitivity. The accuracy is 80.6286% for the proposed LDT whereas for the existing DT, HDT, and ANN, the accuracy percentages are 78.8941, 80.1012, and 77.1363 respectively. Similarly, the specificity and the sensitivity analysis are carried out that shows the better performance for the proposed LDT, which attained 76.2773% and 85.9881% respectively. The existing methods DT, HDT, and ANN attained a sensitivity of 84.1289, 83.7367, and 82.8298 percentages respectively that is very low compared with the proposed LDT. Likewise, the specificity of the existing methods DT, HDT, and ANN are 73.6708, 74.6806, and 72.8435 respectively. The comparison using the Switzerland dataset in terms of the performance metrics show the proposed LDT is superior over the other existing methods and the proposed method achieved an accuracy of 83.7386%, sensitivity of 87.5149, and specificity of 77.6160 respectively that is greater than the other existing methods. The breast cancer dataset analyzed to prove the effectiveness of the proposed method yields a greater percentage of accuracy at 82.9046, sensitivity of 86.4407, and specificity of 76.2249 respectively. Thus, the effectiveness of the proposed LDT is proved and clearly highlighted in the comparison table.

*Table 1. Comparative discussion based on the performance metrics*

| Datasets | Metrics (%) | Classification Methods | | | |
|---|---|---|---|---|---|
| | | DT | HDT | ANN | **Proposed LDT** |
| Cleveland dataset | Accuracy | 78.8941 | 80.1012 | 77.1363 | **80.6286** |
| | Sensitivity | 84.1289 | 83.7367 | 82.8298 | **85.9881** |
| | Specificity | 73.6708 | 74.6806 | 72.8435 | **76.2773** |
| Switzerland dataset | Accuracy | 81.8758 | 81.1618 | 81.2522 | **83.7386** |
| | Sensitivity | 84.2781 | 85.5025 | 84.3542 | **87.5149** |
| | Specificity | 74.7041 | 75.2635 | 75.4182 | **77.6160** |
| Breast Cancer dataset | Accuracy | 81.2004 | 80.8543 | 80.9542 | **82.9046** |
| | Sensitivity | 84.9361 | 84.8221 | 85.8965 | **86.4407** |
| | Specificity | 74.9145 | 76.0924 | 74.9238 | **76.2249** |

## 5. CONCLUSION

The paper presents the novel classification model termed as the LDT that employs the log-entropy function to select the best feature. The best feature is the highly significant feature that enables the accurate and the effective classification of the medical data facilitating the faster and efficient generation of the disease vocabulary leading to the sooner diagnosis of the patient. The proposed LDT uses the log-entropy, which is the integration of the weights of the features and the entropy of the features. The LDT develops the classification models that could be inferred for performing the data classification in future based on the disease vocabularies that carry the symptoms and the corresponding diseases. The experimentation of the proposed method is performed to prove the superiority of the proposed method when compared with the existing methods like the DT, HDT, and ANN. The proposed method LDT offers better classification accuracy when compared with the existing methods and the accuracy percentage is 83.7386, sensitivity is 86.4407%, and specificity is 77.6160% respectively. The proposed LDT is highly applicable for extracting the disease specifications from the medical data.

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