Canine Disease Prediction using Multi-Directional Intensity Proportional Pattern with Correlated Textural Neural Network

Ayesha Taranum
ISE Department Atria Institute of Technology
Visveswaraya Technological University, India
ayeshagce@gmail.com

Jyoti Metan
ISE Department, Atria Institute of Technology
Visveswaraya Technological University, India
jyoti.m@atria.edu

Prasad Yogegowda
Department of CSE, SJB Institute of Technology, India
ayprasad26@gmail.com

Chandrashekar Krishnappa
Department of CSE, SJB Institute of Technology, India
dkchandrashekar28@gmail.com

Abstract: *Data optimization is crucial for enhancing prediction accuracy and similarity identification in texture learning systems, especially for predicting canine diseases. Traditional data retrieval methods often struggle with accuracy and efficiency, particularly when dealing with large datasets. This study presents a novel approach combining Multi-Directional Intensity Proportional Pattern (MDIPP) with a Similarity Measure (SM) system to improve data relevance and similarity estimation. The model organizes data into a paged database structure, which speeds up search operations. A neural network, Correlated Textural Neural Network (CTNN), forecasts the relevance of feature attributes and sorts matching indexes to predict canine diseases based on test data. The CTNN model incorporates a correlation factor among features to enhance prediction accuracy. The relevance of data is determined using an upgraded neural network that accounts for these correlations. The study evaluates performance based on precision, recall, F1-score, and data retrieval accuracy, comparing the results with state-of-the-art techniques. By improving the organization and indexing of data and refining the prediction process, this approach aims to advance data validation and the prediction of canine diseases in large-scale texture learning systems.*

Keywords: *Data optimization, pattern extraction in big data, multi-directional intensity proportional pattern, similarity measure system, correlated textural neural network, test prediction.*

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1. Introduction

Image processing motivated these days of technology that offers highly scalable models to the inputs is image processing-based automation systems. It gives clients the option to maximize their profits by renting out the spaces on their actual equipment. Both homogeneous and heterogeneous clouds make up the cloud computing environment. Whereas the model in a heterogeneous cloud has integrated components from multiple vendors, the model in a homogeneous cloud is provided by a single provider. The main goal of the Texture Learning concept in the Test prediction process was to pull information and attributes from the database and organize them into a list.

The analysis of data attributes with labeled qualities that can be described by ratings, visit probability, and other parameters is the main emphasis of big data in texture learning. One platform-independent tool that is primarily used to facilitate machine-to-machine communication in a network is texture extraction [27, 21]. This explains the non-functional properties of the texture extractions, and attribute similarity is one of the main factors taken into account for the inputs to choose their necessary models. Typically, the set of properties that include data availability, reputation, and throughput is referred to as the similarity [24].

The research paper is organized as follows. A brief introductory note w.r.t. the proposed work is presented in section 1. The related Work-Review of Literature is presented in the section 2. The datasets or the databases used for the training purposes in our work is presented in section 3. The proposed work methodology is presented in the section 4 such as preprocessing, Multi-Directional Intensity Proportional Pattern (MDIPP) based pattern generation, Relevancy estimation using Similarity Measure (SM), similarity computation and the test prediction concepts. The flow-chart of the proposed canine detection system is presented in section 5. Some additional methodologies used for the disease prediction system, ultimately improving its utility in veterinary diagnostics is depicted in section 6 such as enhanced feature extraction, dimensionality reduction, data augmentation, cross-validation, hyper parameter tuning, ensemble learning techniques, integration of domain knowledge, real-time data monitoring and feedback loop visualization techniques, performance

metrics beyond accuracy. The section 7 gives the simulation's results, its analysis and the justifications. Specific canine diseases being predicted in the proposed work is portrayed in the section 8. Some of the limitations of the proposed works are presented in section 9. The scope for future works is shown in the section 10. The paper finally ends with the conclusion in section 11 followed by an exhaustive list of references used in our work.

In recent times, the primary methods utilized to facilitate model composition have been model selection and prediction techniques [1]. The conventional works created test prediction algorithms based on similarity. By offering the most similar models, it fails to meet the input criterion [25]. Additionally, it made use of a few relevancy and similarity estimation algorithms while storing and retrieving the model. The current relevancy estimates methods, such Fuzzy C-Means (FCM) [11, 23], K-means [9, 10], and K-medoids [9, 23], have several drawbacks that make them ineffective for Test prediction. These include being extremely sensitive, requiring a finite number of characteristics, and requiring a wide searching space.

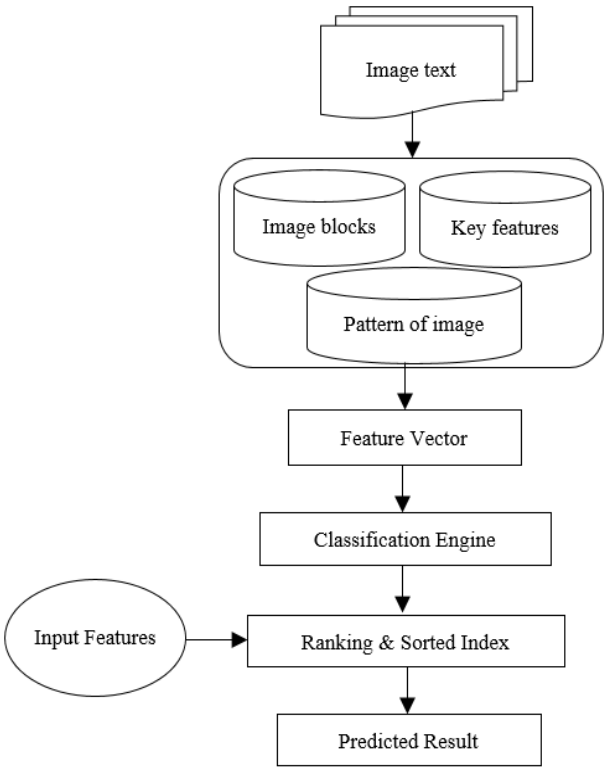

Figure 1. Generic block diagram of texture learning.

Classifying the disease in the huge data for the input of canine microscopic slides is the main purpose of the classification model used in [4]. Then, the traditional works employ the current classification techniques, which have the disadvantages of increased complexity and time consumption, such as traditional neural networks, the bayesian technique, fuzzy models, machine vector classification models, etc., Therefore, these methods are also not very appropriate for a precise test prediction [13]. The basic block diagram of the prediction system used in the texture learning process is displayed in the Figure 1. These are the following main goals of this paper which are listed as shown under:

- Pre-processing and image enhancement are applied, and image characteristics are extracted, and organized based on attributes, in order to preprocess the provided dataset.
- For big data, the MDIPP approach is used to determine the attribute of the data feature set.
- Employing the SM system to determine the similarity indexing and properly organizing the data in a windowing architecture.
- The formation of a hierarchical structure by organizing the data using feature attribute sorting based on similarity.
- Enhancing the test matching attribute and accelerating the processing time.
- The correlation factor between the data attributes must be computed using best matching in order to anticipate the items that are most similar to the inputs that were sought.

Automated canine disease prediction holds significant clinical importance, primarily due to its potential to revolutionize veterinary healthcare by enabling early and accurate diagnosis of diseases. Early detection is crucial in the treatment of many canine diseases, as it can significantly improve the prognosis and quality of life for affected animals. For instance, diseases such as cancer, diabetes, and heart conditions often present subtle symptoms that can be easily overlooked in the early stages. Automated systems equipped with advanced image processing and machine learning algorithms can analyze medical images and other data to identify these early signs more reliably than traditional methods.

Furthermore, automated disease prediction systems can alleviate the burden on veterinary professionals, allowing them to focus on more complex diagnostic and therapeutic tasks. The growing demand for veterinary services, coupled with a shortage of veterinary professionals, has created a pressing need for efficient diagnostic tools. Automated systems can process large volumes of data quickly and accurately, reducing the time required for diagnosis and enabling veterinarians to manage their caseloads more effectively. This not only enhances the efficiency of veterinary practices but also improves access to care for pet owners, ensuring that more animals receive timely and appropriate treatment.

In addition to improving diagnostic accuracy and efficiency, automated disease prediction systems can also play a critical role in the standardization of veterinary care. Traditional diagnostic methods can be highly subjective, with significant variability in interpretation among different practitioners. Automated

systems, on the other hand, provide consistent and objective analyses based on pre-defined criteria and advanced algorithms. This standardization can lead to more uniform treatment protocols and better outcomes for patients. Moreover, the integration of these systems with electronic health records can facilitate continuous monitoring and long-term management of chronic conditions, ensuring that treatments are adjusted as needed based on the latest data.

Another important aspect of automated canine disease prediction is its potential to enhance preventive healthcare. By analyzing historical and real-time data, these systems can identify patterns and risk factors associated with various diseases. This predictive capability allows for the implementation of personalized preventive measures tailored to the specific needs of individual animals. For example, dogs identified as being at high risk for certain conditions can receive targeted screenings and lifestyle recommendations, potentially preventing the onset of disease or mitigating its impact.

Lastly, the development and implementation of automated disease prediction systems contribute to the advancement of veterinary research. The vast amounts of data collected and analyzed by these systems can provide valuable insights into disease prevalence, progression, and response to treatment. Researchers can use this data to identify new biomarkers, develop novel therapeutic approaches, and improve existing treatment protocols. Additionally, these systems can facilitate large-scale epidemiological studies, enhancing our understanding of disease dynamics in canine populations and informing public health strategies.

In fact, the clinical importance of automated canine disease prediction lies in its ability to improve diagnostic accuracy and efficiency, standardize veterinary care, enhance preventive healthcare, and advance veterinary research. By leveraging advanced technologies, these systems can significantly impact the health and well-being of canine patients, ensuring they receive the best possible care throughout their lives. Despite the promising potential of automated canine disease prediction systems, there are several current limitations in the field that impact their clinical importance. One of the primary challenges is the quality and availability of training data.

High-quality, annotated datasets are essential for training machine learning models to accurately predict diseases. However, acquiring such datasets can be difficult, as they require extensive collaboration with veterinary clinics and often involve issues related to data privacy and standardization. In many cases, the available data is limited, incomplete, or inconsistent, which can hinder the development and effectiveness of predictive models. Another significant limitation is the complexity and variability of canine diseases. Unlike human medicine, where standardized diagnostic criteria and protocols are more established, veterinary medicine often deals with a wider range of species, breeds, and individual variations.

This diversity can complicate the development of universal predictive models. Additionally, many canine diseases present with non-specific symptoms that overlap with other conditions, making accurate prediction challenging. The models need to be highly sophisticated to differentiate between diseases with similar clinical presentations, which requires extensive computational resources and advanced algorithms. The integration of automated systems into existing veterinary workflows also poses a challenge. Veterinary practices vary widely in terms of their technological adoption and infrastructure.

Implementing automated disease prediction systems requires significant investments in hardware, software, and training for veterinary staff. Smaller clinics or those in resource-limited areas may find it difficult to afford and integrate these advanced systems, potentially widening the gap in the quality of care provided across different practices. Ensuring seamless integration with existing electronic health records and other clinical systems is also critical but can be technically complex and resource-intensive. Also, there is a need for greater validation and regulatory approval of automated disease prediction systems.

While many promising models have been developed in research settings, their performance in real-world clinical environments needs thorough validation to ensure reliability and accuracy. Regulatory bodies need to establish clear guidelines and standards for the approval and use of these systems in veterinary practice. Without proper validation and oversight, there is a risk of relying on inaccurate predictions, which could lead to misdiagnosis and inappropriate treatment. Another limitation is the interpretability of machine learning models. Many advanced models, particularly deep learning algorithms, function as the black boxes, where the decision-making process is not transparent. This lack of interpretability can be a significant barrier for veterinary professionals who need to understand and trust the predictions made by these systems.

Developing models that provide clear explanations for their predictions is crucial for gaining the confidence of veterinarians and ensuring the widespread adoption of automated disease prediction technologies. There are ethical and privacy concerns related to the use of automated systems in veterinary medicine. The collection and analysis of large amounts of data raise questions about data ownership, consent, and the potential for misuse. Ensuring that data is handled ethically and that the privacy of pet owners and their animals is protected is paramount. Developing robust frameworks for data governance and establishing clear policies on data usage and sharing are essential to address these concerns. The training of the data sets that is being used is shown in the Figure 2.

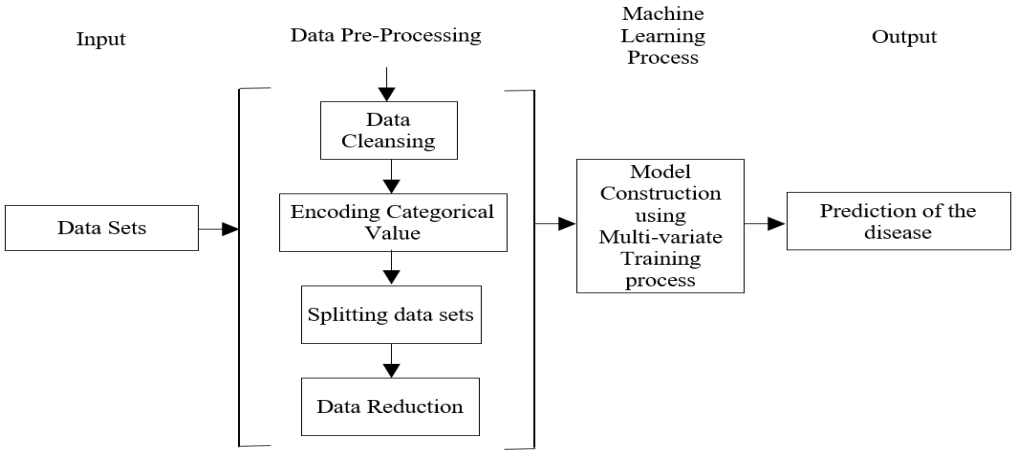

Figure 2. Training the process using the input datasets.

To sum up, while automated canine disease prediction systems hold great promise for enhancing veterinary care, several limitations need to be addressed to fully realize their clinical importance. These include challenges related to data quality and availability, disease complexity and variability, integration with existing workflows, validation and regulatory approval, model interpretability, and ethical and privacy concerns. Addressing these limitations will require ongoing research, collaboration, and investment to ensure that these technologies can be effectively and safely implemented in veterinary practice.

The remainder of the paper's sections are arranged as follows: The test prediction frameworks and methods that are now in use are reviewed in section 2. Section 3 offers a concise overview of the suggested methodology along with a thorough flow diagram. In section 4, the experimental outcomes of the suggested and current mechanisms are assessed and contrasted. The paper is finally ended, and section 5 lists the improvements that can be made going forward.

2. Related Work-Review of Literature

This section surveys the available methods and algorithms for Test prediction along with their benefits and drawbacks. In order to increase the prediction system's similarity, the paper [15] created a tailored collaborative filtering process that is location aware. This technique made use of both the input locations and the Texture extractions to choose the input or the target model. The primary similarity characteristics taken into account in this investigation were dependability, availability, response time, and input reliance. The stages that involved in this system were as:

- Input location information.
- Identification of similar inputs.
- Similarity prediction based on the inputs.
- Pattern extraction based on the features.
- Texture pattern analysis based on inputs and attributes.
- Classification model.

Here, the weighted Person-Centered Care (PCC) approach was used to choose the neighbors who were comparable in order to compute the similarity. In this work, the effect of sparseness was also investigated for assessing prediction accuracy. In order to support the input decision process in a prediction system, the shortlists were evaluated in the work [5]. It was reported in this article that the shortlists improved downstream and input satisfaction performances more than the other groups. Additionally, by adding more feedback, it raised the prediction's quality. A canine illness aware Similarity prediction scheme was proposed by the paper's author [8] for the input prediction system. In this case, the input side assessed the mapping relationship between the geographic distance and the similarity value.

Furthermore, in order to achieve a perfect resemblance between the inputs, this system chose the best similarity function. Additionally, the integrated information on canine diseases was provided using the Matrix Factorization (MF) approach, which served as the foundational model. This study work's drawback was that it needed to obtain the precise resource configuration in a timely manner. In order to build a new method for model prediction, the paper [3] combined content-based filtering with collaborative filtering. In this system, the probabilistic generative model was used to forecast using the semantic content and rating data.

Examining the current state of the art for texture extraction prediction algorithms was the main goal of this work. In addition, this paper looked at three key criteria for creating an effective prediction system: prediction accuracy, prediction serendipity, and prediction of freshly deployed models. Next, based on the semantic contents of Texture extractions, a three-way aspect model was put into practice to determine the inputs' relative similarities. In order to construct an effective model prediction system, Munday *et al.* [16] proposed three potential prediction approaches: content-based approach, collaborative filtering approach, and hybrid approach. The following were the principal elements of this system:

- Evaluation of both functions and non-functions.

- Ranking of diversity texture extraction.
- Assessment of diversity.

A data optimization based canine illness prediction system and mobile texture learning applications were proposed by [6] in order to take into consideration, the Test prediction system for the Texture learning database. In this case, the learning object data optimization took into account the canine illness kinds found in the database, including Profile, Social interactions, learning activities, and device requirements. Canine illness is filtered using OWL rules in order to forecast results for the Test input. A survey of many approaches for a prediction system based on data optimization in texture learning was described in a publication [22].

It says that a superior similarity identification model based on a knowledge-based prediction system was achieved through the hybridization of algorithms and other prediction techniques. An illness prediction system based on the Test classification approach was later proposed Xie *et al*. [29]. Using the database's classification of the Test data, this calculates the pertinent data for the Test input. In order to provide the anticipated course information, the data optimization calculates the N-List of pertinent database features that match the test input.

A review of the data optimization-based Texture learning technique was also offered in [20] paper work. The analysis's systems use a variety of methods, including artificial intelligence and data optimization, to generate customized forecasts. In the Texture learning process, this aids in the preparation of the learning libraries and feature retrieval model to improve the prediction system. Kelly *et al*. [12] put forth a brand-new learning path prediction model. The multidimensional knowledge graph framework for the Texture learning system served as the foundation for this. Using this multidimensional knowledge graph technique, the entire database was divided into multiple classes. This will improve the classification model's learning ability and decrease its temporal complexity.

Similarly, a novel prediction system for the texture learning process employing a neural network-based texture learning platform was proposed in a paper work published in [19]. This retrieves the pertinent data and determines how similar the disease information is from the database. Utilizing a neural network for relevance estimation, supported standard-compliant learning object repositories are sorted, and a ranked list of learning objects operating at two distinct classification levels that are comparable to the Test input is suggested. Based on the study, it is determined that while the current approaches offer benefits and cons, they primarily lack the following:

- It was unable to identify the variations in similarity.
- More training sets are needed for the current systems in order to extract test data.
- This resulted in an opaque list of rated models and raised the temporal complexity of memory-based prediction systems.

This work proposes to design a novel Test prediction system to address these issues. In this case, similarity indexing and attribute estimate based on the MDIPP were used to process the Test seeking and identify pertinent data. When compared to utilizing the conventional prediction model, the CTNN based classification algorithm improved the accuracy performance of the data retrieval system. Section 3 provides an explanation of the proposed task in detail.

3. Data Sets

The datasets used in this study, feline reticulocytes and mitosis WSI CCMCT, were chosen is explained here how it has been used for the training purposes. The first step in training the CTNN classifier involved finding the correlation factor between the dataset's variables. The datasets provide rich, well-annotated images necessary for establishing a robust correlation factor. Pre-processing and image enhancement were applied to extract and organize image characteristics based on attributes, thus creating a feature vector that determines the similarity of the feature set's properties. This foundational step was crucial for the model, and the availability of detailed annotations in these datasets supported the extraction of high-quality features.

The division of datasets into training and testing sets based on feature arrangement necessitated datasets with comprehensive and diverse image characteristics. Feline reticulocytes and mitosis WSI CCMCT datasets, despite being non-canine, offered extensive variability in image features, aiding the classifier's neurons' formation through feature learning. Training data from these datasets were used to teach the classifier, which then categorized testing data and sorted pertinent information for the prediction process. This process showcased the model's ability to generalize learned features, demonstrating the applicability of the CTNN classification model in varied contexts, including but not limited to canine skin disease prediction.

The choice of these datasets was also influenced by their suitability for texture learning prediction models, which are central to this study. The datasets provided high-resolution images with significant textural details, crucial for enhancing the texture learning model. The preprocessed datasets, with noisy pixel removal and pixel enhancement, resulted in optimized, filtered data. These steps ensured that only relevant attributes were considered for the prediction process, thereby improving prediction quality and retrieval accuracy. The presence of special characters, filtered as Unicode values, minimized data memory usage, further justifying the choice of these datasets for an optimized training process.

Moreover, the use of these datasets allowed the computation of exemplars and estimation of pair-wise similarity between data points, an essential aspect of the CTNN model. The high total distance or similarity between data points and their corresponding exemplars in these datasets provided a robust basis for training the model. Despite the primary focus being on feline reticulocytes and canine mast cell tumors, the detailed image annotations and variability within these datasets offered a substantial foundation for developing a predictive model applicable to various image-based diagnostic tasks, including canine disease prediction.

The dataset's substantial size and diverse labels were crucial for the model's performance metrics. The Feline Reticulocytes dataset contained 1086 slides from various labels, while the Mitosis WSI CCMCT dataset comprised 21 DICOM images, each with approximately 100 slides of canine cutaneous mast tumor cells. These slides' high quantity and detailed labelling allowed for extensive training and testing, ensuring the model was exposed to a wide range of image features. This exposure was critical for the model's ability to generalize and perform well on unseen data, thereby validating the choice of these datasets despite their non-canine origin.

Finally, the performance metrics and comparative analysis demonstrated the efficacy of the chosen datasets in the proposed prediction system. Some of the results in our work have showed the performance metrics where 70% of the training data and 30% of the testing data were considered for prediction in the texture learning process. This validation against a large dataset, preprocessed to remove noise and enhance pixels, showcased the model's robustness and predictive capability. By leveraging the MDIPP measure to remove irrelevant keywords, the study illustrated the model's efficiency in handling diverse datasets, thus justifying the choice of Feline Reticulocytes and Mitosis WSI CCMCT datasets for training the CTNN classifier for canine disease prediction.

4. Proposed Work Methodology

This section provides a thorough explanation of the suggested methodology along with a flow chart. The goal of this study is to efficiently execute Test prediction. The microscopic image slide of the canine illness is used as the input in this system, and it undergoes preprocessing that includes noisy pixel removal and pixel enhancement. The matrix is created for choosing the Attribute Pattern (CP) based on the Normalized MDIPP approach after the filtered and pre-processed data has been obtained. Using the CTNN, the features in each attribute are then processed for the purpose of training the classification algorithm.

The attributes are produced by implementing the SM system based on the CP. Subsequently, similarity metrics like Kolmogorov and transformation distance are calculated to determine which objects are comparable. As a result, the cloud server stores the n numbers of properties of the features. Upon receiving the request from the input, the server searches for the best match in the Test data to collect pertinent information. The CTNN classification model is then used to forecast the outcome. The models are forecasted to the input that was requested based on the greatest similarity value. Lastly, the projected result for the Texture learning application is a list of the matched data that are connected to the Test input.

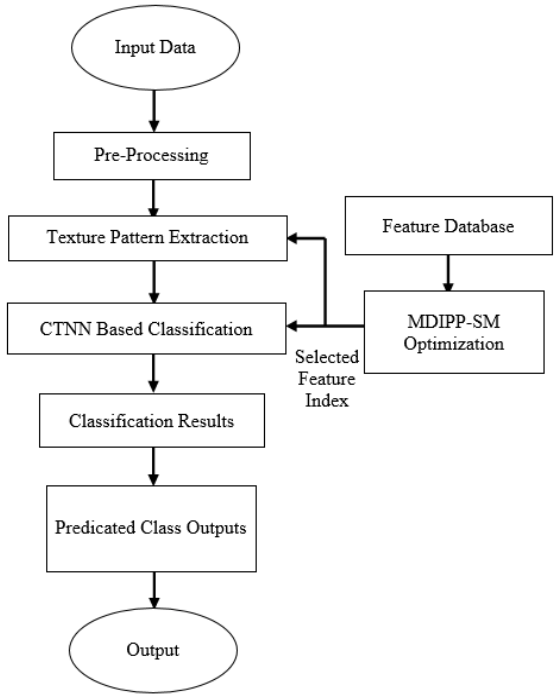

Figure 3. The block diagram for the suggested texture learning prediction task.

The block diagram for the suggested texture learning prediction task is displayed in the Figure 3. The input data are preprocessed and organized according to the qualities in this. This will become the characteristic of the feature vector that determines how comparable the feature set's properties are to one another. After that, the dataset was divided into training and testing sets based on the feature arrangement. The classifier's neurons are formed by the feature learning of classification, which received the training data. Next, the testing data are categorized and the pertinent data are sorted for the prediction process based on the match prediction in the dataset. The suggested CTNN classification model was applied to this. The texture learning prediction model was then improved in comparison to the conventional approach of categorization. The stages that involved in this system are as follows:

- Preprocessing.
- MDIPP based pattern generation.
- Relevancy estimation using Similarity Measure (SM).
- Similarity estimation.
- Model Ranking and prediction.

4.1. Preprocessing

The dataset is first provided as the input for preprocessing, which produces the filtered data by performing noisy pixel removal and pixel enhancement. Preprocessing a dataset with the primary goal of optimizing its size is done by choosing attributes that are relevant to the prediction process. In order to reallocate the special characters required for processing in the dynamic analysis model, the undesirable characters or letters are filtered here. Special characters are thought of as the Unicode value for letter size representation, which can minimize the amount of data memory needed. As a result, the prediction quality and retrieval accuracy improve. By measuring the uniqueness of the attribute value and determining if it can be divided into its associated components, one can identify the filtering of irrelevant data.

4.2. Multi-Directional Intensity Proportional Pattern (MDIPP) based Pattern Generation

Following the pre-processing steps, the MDIPP is used to create the matrix for the preprocessed data. The universal distance measure, which calculates the separation between every item, is another name for it. Additionally, it finds all similarities at the same time to choose the CP. The set of characteristics and their domain list are provided as input at this point. Here, the size of each domain is indicated by *M*, and it consists of a set *N* files that are kept in a repository *RN*. The different numbers of keywords in each characteristic, such as *Ki* and *K-j* are retrieved in order to form the matrix. Then, the bytes belonging to *Ki* and *K-j* are likewise taken out and saved in other variables called 〖wd〗_x, 〖wd〗_y and 〖wd〗_xy.

As a result, the binary values for the extracted data bytes are computed. The values of 〖M〗_xy, 〖N〗_xy, and 〖N〗_yx are then computed as follows:

$$M_{xy} = \begin{cases} |B_x * B_x| & if\ (B_x > B_y) \\ |B_y * B_y| & Otherwise \end{cases} \quad (1)$$

$$Nk_{xy} = \begin{cases} N_{xy} & if(N_{xy} > N_{yx}) \\ N_{yx} & Otherwise \end{cases} \quad (2)$$

Then, the distance $dist_{xy}$ is computed by the ratio of $\frac{1}{log(Derv_{xy})}$ and dif_v. Consequently, the T_{dist} is updated with the sum of T_{dist} and $dist_{xy}$.

$$Dist_{xy} = 1 - \frac{(2 * (\frac{1}{log(Derv_{xy})} - min_v)}{dif_v} \quad (3)$$

$$T_{Dist} \leftarrow Update\ (T_{dist} + dist_{xy}) \quad (4)$$

Then, the value of 0_{dist} is updated with the values of T_{dist}, and finally, the $M_{NID(i,j)}$ is estimated based on the updated $0_{dist}/M$.

Algorithm I: Multi-Directional Intensity Proportional Pattern (MDIPP.

Input: Set of features, Domain list
Output: MDIPP matrix (M_{NID})
Step 1. Let, N be the set of Domains, in which each domain contains a sample set of 50 files;
Step 2. Let, R_N be of the repository of files, which holds the set of N features;
Step 3. Let, M be the Total Size of R_N;
Step 4. To construct the M_{NID} of size (M,M)
Step 5. For i = 1 to M
$K_i \leftarrow$extractKeyWords (R_N(i))
For j = 1 to M
$K_j \leftarrow$extractKeyWords (R_N(j))
For x =1 to size (K_i)
For y =1 to size (K_j)
wd_x= extract bytes ($K_i(x)$)
wd_y= extract bytes ($K_i(y)$)
wd_{xy}= extract bytes ($K_i(x) * K_i(y)$)
B_x= compute fold (wd_x)
B_y= compute fold (wd_y)
B_{xy}= compute fold (wd_{xy})
Compute M_{xy} by using equation (1)
Compute N_{xy}, N_{yx} by using Equation (2)
N_{xy}= dif (B_{xy}, B_x)
N_{yx}= dif(B_{xy}, B_y)
If ($N_{xy} > N_{yx}$)
NK_{xy}= N_{xy}
Else
Nk_{xy}= N_{yx};
End if;
$Derv_{xy}$= M_{xy}/ NK_{xy}
The distance $dist_{xy}$ and $T_{dist}$are computed by using Equations (3) and (4) as
End for x
$O_{dist} \leftarrow$ Update ($O_{dist} + T_{dist}$)
End for y
M_{NID}(i, j) $\leftarrow$ Update (O_{dist}/M);
End for i
End for j

4.3. Relevancy Estimation Using Similarity Measure (SM)

Following the CP selection process with MDIPP, the SM method is used to form the number of characteristics. Compared to more traditional techniques like fuzzy c-means and k-means, it is a successful relevancy estimation method that is widely used in the field of computer science. It provides high-quality attributes because it iteratively exchanges messages between all data pairs. Adopting this technique will primarily benefit from its simple computation, deterministic nature, decreased relevancy estimation error, and increased efficiency. In addition, it does not need to

satisfy the triangle inequality because it maintains the similarities.

Furthermore, this technique's primary attributes are responsibility and availability. Through the computation of a set of exemplars, this technique represents the dataset and estimates pair-wise similarity between every pair of data. In this case, the total distance or similarity between each data point and its corresponding exemplars is as high as possible. The distance matrix M_{NID} that was acquired in the previous step is the foundation upon which the availability matrix S_i and responsibility matrix S_j are built in this approach. The rows and columns in M_{NID} are then verified to be greater than the value of A_{ij} in order to update these matrices.

$$A_{ij} = \begin{cases} 0.5 & if\ (M_{NID}(i,j)\ <= 0.5) \\ 0 & Otherwise \end{cases} \quad (5)$$

Consequently, the exponential matrix is constructed by checking the value of sum of A_{ij} and R_{ij} is greater than 0.

$$R_{ij} = \begin{cases} M_{NID}(i,j) - A_{ij} & If\ (A_{ij} <= M_{NID}(i,j)) \\ 0 & Otherwise \end{cases} \quad (6)$$

Then, the average for the *Max (Expm$_i$)* and $R_i(Idx_x)$ is computed and updated with the avg_{list}.

$$Expm_{ij} = \begin{cases} 1 & if(A_{ij} + R_{ij}) > 0 \\ 0 & Otherwise \end{cases} \quad (7)$$

$$avg = \sum_{x=1}^{size(Idx_{ls})} R_{i(Idx_x)} \quad (8)$$

The variables S_i and S_j represent the sizes of the matrix and $I_{dx}l_s \uparrow Max(Expm_i)$, respectively, where *i* denotes the matrix's size and S_i is the index list containing the maximum elements of each matrix column. Next, by calculating the difference between the ⟦avg⟧ ^{2} and ⟦ ⟦avg⟧ _x⟧ ^{2} and the distance index list is estimated. Next, the maximum index of the ⟦dis⟧ $_{ls}$ is computed, and the CP is chosen for each attribute based on this value.

$$avg_R = \frac{\sum_{j=1}^{S_j} R_{ij}}{S_j} \quad (9)$$

$$dis_{ls} = \sqrt{avg^2 - (avg_{x^2})} \quad (10)$$

where, *x* is the Size of matrix S_j, and C_{id}=*Max*(*Index* (dis$_{ls}$)).

Algorithm 2: SM Based Relevancy Estimation.

Input: Distance Matrix [MDIPP matrix (M_{NID})]
Output: attributes,A_{ij},R_{ij}
Step 1. Construct Availability Matrix and responsibility matrix
Let S_i & S_j be size of matrix (M_{NID}) & Set K = 2;
For i = 1 to S_i
For j = 1 to S_j
A_{ij} is computed by using Equation (5)
End for j;
End for i;
Step 2. Construct and update responsibility matrix and Availability matrix;
For X_k= 1 to k
For i =1 to S_i
For j = 1 to S_j
R_{ij} is computed by using equation (6);
End for j
End for i
For i = 1 to S_i
For j = 1 to S_j
Let $temp\_R_{ij}$= 0;
For m = 1 to S_i
$temp\_R_{ij} = temp\_R_{ij} + R_{im}$
End for m;
$$temp\_R_{ij} = \begin{cases} temp\_R_{ij} + R_{ij} & if\ (temp_{R_{ij}} \le 0) \\ R_{ij} & Otherwise \end{cases}$$
If (i! = j)
$$A_{ij} = \begin{cases} 0 & If\ (temp_{R_{ij}} < 0) \\ temp\_R_{ij} & Otherwise \end{cases}$$
Else
$$A_{ij} = \begin{cases} temp\_R_{ij} & If\ (temp\_R_{ij} > 0) \\ 0 & Otherwise \end{cases}$$
End if
End for S_j
End for S_i
End for X_k
Step 3. Compute Exponential Matrix by using Eqn. (7);
Update avg_{list} ←avg;
For y = 1 to S_j
Compute avg_R by using equation (9);
Compute the distance list by using equation (10);
Update $C_{id} \rightarrow C_{head}$
End for y;
End

4.4. Similarity Computation

The Kolmogorov and transformation distance-based similarity measures are used to calculate the similarity between the features at this point. One popular similarity mechanism that does this is the Kolmogorov, which converts a finite collection of objects into strings represented by the notation {0, 1}. It takes *A* as input and *B* as output, for example, when estimating the similarity between two representations (*A* and *B*). Subsequently, the semi-computable *K*(*B*|*A*) is used to represent the quantity of it. Therefore, there is no admissible distance for the transformation distance-based similarity measure, which is an asymmetric technique.

This method yields an estimated similarity as the output, with the input being the test response. Here, the size of the feature is translated into bytes after the size of the attribute head features and the keywords in each attribute head feature are calculated. Additionally, the binary folds are calculated for the bytes of data, and the following equation is used to estimate the lowest and maximum folds from there:

$$\begin{cases} \begin{cases} (B_{fx} * B_{fx}) = Max\ (B_{xy}) \\ (B_{fy} * B_{fy}) = Min\ (B_{xy}) \end{cases} & if\ (Bf_x > Bf_y) \\ \begin{cases} (B_{fy} * B_{fy}) = Max\ (B_{xy}) \\ (B_{fx} * B_{fx}) = Min\ (B_{xy}) \end{cases} & Otherwise \end{cases} \quad (11)$$

$$p_1 = \left(\frac{(Bf_{xy} - Min\ (B_{xy}))}{Max\ (B_{xy})}\right) \quad (12)$$

$$p_2 = \frac{((Size\ (S1) - Size\ (S2))}{size\ (S12)} \quad (13)$$

Based on these values, the transmission distance similarity is estimated by the product of p_1 * p_2. Then, the KC is computed by generating the mask value for the binary folds of the data.

$$Sim_{Kc} = \left(\frac{(K_{xy} \&\& Mask) - Min\ (B_{xy})}{Max\ (B_{xy}) - Min\ (B_{xy})}\right) \quad (14)$$

Finally, the total similarity is estimated by adding the similarity values of TD and KC. It is employed to determine which things are most comparable to the input test.

Algorithm 3: Similarity Computation.

Input: Input Test
Output: Estimated similarity
Step 1. Let U_Q be the Input Test
Step 2. Let K_U be the Keywords in the Input Test
Step 3. The Server ID K_U with the attribute Keys.
Step 4. Let c_{Head} be the attribute head features and kc_H be the keywords in the attribute head features
For M = 1 to Size of (K_U)
For N = 1 to Size of (kc_H)
$S_1 = K_U(M)$
$S_2 = kc_H(N)$
$S_{12} = s_1 * s_2$
B_1, B_2 and B_{12} bytes for S_1, S_2 and S_{12}
Bf_x, Bf_y and Bf_{xy} be the binary folds of B_1, B_2 and B_{12};
Compute Max (B_{xy}) and Min (B_{xy}) by using equation (11);
Compute p_1 and p_2 by using equation (12) and (13);
$Sim_{TCD} = p_1 * p_2$;
$K_{xy} = Bf_{xy} - Min\ (B_{xy})$
Set Mask = 0xFF;
Compute Sim_{Kc} by using equation (14)
$Sim_{Tot} = (Sim_{TCD} + Sim_{Kc})$
End for N
$C_{Ch} = Min(Index\ (Sim_{Tot}/N))$;
End for M

4.5. Test Prediction

Ultimately, a similarity value ranking is given for each item, with the most similar things being projected to be the inputs that were sought. In this instance, the objects are ranked according to how similar they are using the CTNN. The matching feature for the Test is delivered as the output in this technique, while the inputs are the Test and the chosen CP. The Figure 4 gives the overall architecture diagram of proposed CTNN.

At first, the server retrieves the keywords in the input Test K_U. Then, the keywords in the number of features K_{Dn} are extracted. After that, the similarity between the input Test and the keywords in the feature is computed, based on this the list of similarity score Sim_{Ku} is estimated for the number of features in the matched attribute. Finally, the matched feature E_{rank} is listed and display as the predicted information about the Test data for classification process.

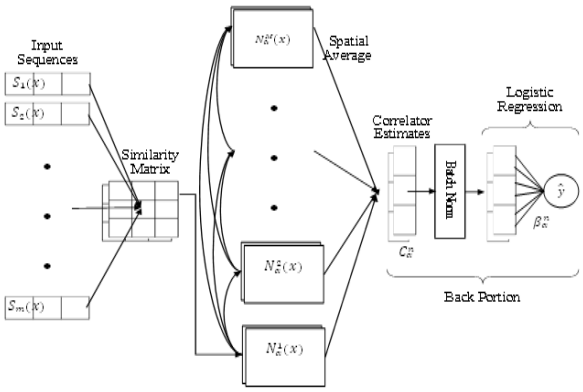

Figure 4. Architecture diagram of proposed CTNN.

Figure 4 depicts the neural network-based architecture of the suggested CTNN classifier. Based on the discovery of similarities between each attribute of the input data, the input sequences are produced as data attributes in that way. Subsequently, the neurons are produced from $N\alpha_1(x)$ to $N\alpha^{M(x)}$ depending on the weight value of that attribute matrix. The correlation between these network data is then extracted, and it is made according to the matching rank. Next, these are ordered and sorted based on the prediction match by estimating the normalization of the total data. This was accomplished by estimating the normalization between the feature set's characteristics using the batch normalization method. Finding the best match for the test data and obtaining its label are the objectives of the logistic regression model. The suggested CTNN classifier's algorithmic stages are explained in Algorithm (4).

Algorithm 4: CTNN Algo.

Input: Input Test, Chosen attribute head C_{Ch}
Output: Matched feature for the Test
Step 1. Let U_Q be the Input Test
Step 2. Let K_U be the Keywords in the Input Test
Step 3. The Server index K_U with the attribute Keys.
Step 4. Let N be the set of features in the attribute;
Step 5. For i =1 to N (No of features)
K_{Dn} = *Keywords in the Feature*
$Sim_{Ku} \leftarrow$ *Similairity (K_{Dn},K_U) and update*
End for N
Step 6. Sim_{Ku} is the list of similarity score for the features in the matched attribute.

$$E_{rank} = \frac{Min(Sim_{Ku})}{\sum_{m=1}^{N} Sim_{Ku}}$$

Matched feature is denoted as N(E_{rank})
Step 7. Decrypt the matched feature based on the above mentioned non-abelian algorithm

5. Flow-Chart of the Proposed Canine Detection System

The Figure 5 flow chart provides a description of the canine prediction model. A canine microscopic picture slide is provided as input, and preprocessing is carried out to remove noisy pixels and enhance pixels. The MDIPP technique is used to select attribute patterns. Compute the Metrics and Similarity Measure. Once

similarity has been determined, the CTNN Model is used to forecast canine skin conditions.

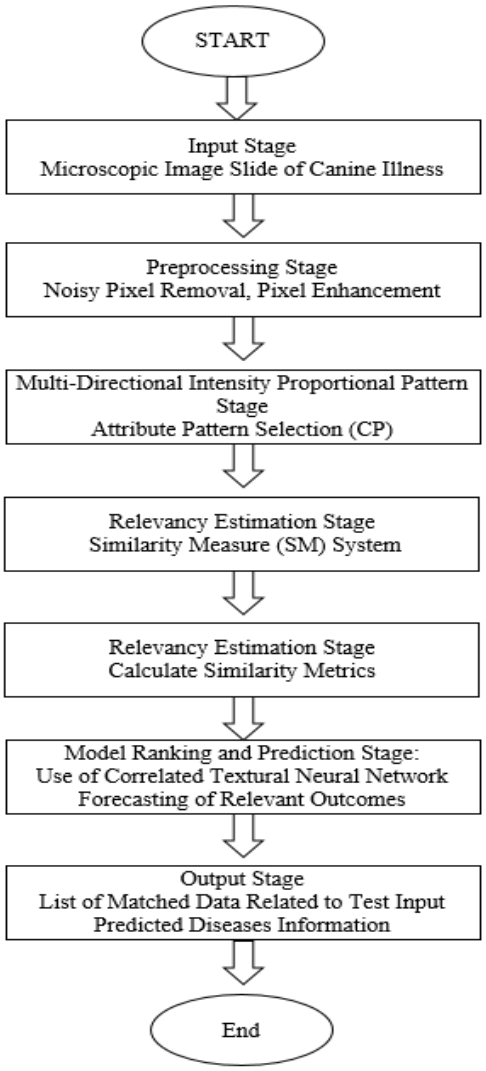

Figure 5. Flow-chart of the proposed canine prediction module.

6. Additional Methodologies

Some of the additional information on the methodology adopted for solving the problem of canine disease prediction using MDIPP with CTNN is given below which could be done by incorporating these into the methodology, the study can enhance the effectiveness and applicability of the canine disease prediction system, ultimately improving its utility in veterinary diagnostics.

6.1. Enhanced Feature Extraction

Beyond the initial preprocessing steps, the methodology incorporates advanced feature extraction techniques. This may include using texture descriptors such as Local Binary Patterns (LBP) or Gray Level Co-occurrence Matrix (GLCM) to capture additional information from the microscopic images. These techniques enhance the richness of the feature set, allowing for a more nuanced understanding of the underlying data.

6.2. Dimensionality Reduction

To manage the potentially high-dimensional feature space generated during feature extraction, dimensionality reduction techniques like Principal Component Analysis (PCA) or t-Distributed Stochastic Neighbor Embedding (t-SNE) may be employed. This step reduces computational complexity and helps to mitigate the curse of dimensionality, enhancing model performance.

6.3. Data Augmentation

To increase the robustness of the model and improve its generalization capability, data augmentation techniques can be applied to the microscopic image dataset. This involves creating variations of the original images through transformations such as rotation, flipping, zooming, or adjusting brightness. This approach helps in expanding the training dataset and reduces the risk of overfitting.

6.4. Cross-Validation

The methodology includes a rigorous cross-validation process to ensure that the model's performance is evaluated reliably. K-fold cross-validation can be used, where the dataset is divided into k subsets, and the model is trained and validated k times, each time using a different subset for validation and the remaining data for training. This provides a more accurate estimate of the model's performance on unseen data.

6.5. Ensemble Learning Techniques

The methodology could also explore the use of ensemble learning methods, where multiple models are trained, and their predictions are combined to improve accuracy and robustness. Techniques such as bagging, boosting, or stacking could be utilized to enhance the prediction capabilities of the CTNN model.

6.6. Integration of Domain Knowledge

Incorporating veterinary and domain-specific knowledge into the feature selection process can improve the relevance of the attributes being analyzed. This could involve consulting with veterinary professionals to identify key indicators of specific diseases, thus refining the feature set used for training.

6.7. Real-time Data Monitoring and Feedback Loop

Implementing a real-time data monitoring system can facilitate continuous learning and model updates based on new incoming data. A feedback loop that collects predictions and their corresponding outcomes can be established, allowing for ongoing model refinement and improvement.

6.8. Visualization Techniques

To aid interpretability, visualization techniques such as heat maps or Gradient-weighted Class Activation Mapping (Grad-CAM) can be used to show which features or areas of the input images contributed most to the model's predictions. This helps veterinarians understand the model's decision-making process and increases trust in its outputs.

6.9. Performance Metrics Beyond Accuracy

In addition to precision, recall, and F1-score, the methodology should include other performance metrics such as Receiver Operating Characteristic-Area Under Curve (ROC-AUC) and confusion matrix analysis to provide a comprehensive assessment of the model's performance across different disease classes.

7. Simulation's Result Analysis

Simulations are preformed and the results are observed and presented in this section. In a nutshell, this section employs a variety of performance metrics to assess the experimental outcomes of both existing and proposed procedures. The Python tool (version 3.7) was used to process the proposed work's overall implementation. It comprises other categorization rates in addition to f-measure, recall, and precision. In order to demonstrate the efficacy of the suggested system, the suggested model prediction mechanism is also contrasted with the currently used similarity and classification technique.

The dataset that are used for the training and validation are referred from Feline reticulocytes [14] and Mitosis WSI CCMCT [2]. In the Feline reticulocyte's dataset, there are 1086 numbers of slides that are from the different labels of feline reticulocytes. In the Mitosis WSI CCMCT dataset, there are 21 numbers of DICOM images and each contain the approximately 100 numbers of slides. These slides contain the image of canine cutaneous mast tumor cells.

The metrics most frequently used to assess the effectiveness of Test prediction techniques are precision, recall, and f-measure. Wherein the ratio of the relevant to retrieved models is estimated as the function of relevancy, and precision is defined as such. Furthermore, the results pertinent to a precise model prediction are given by the positive predictive value. Additionally, recall offers the most pertinent outcomes for model prediction. The influence of outliers is then lessened by the f-measure, which integrates the values of recall and precision. The following formula is used to determine the f-measure, accuracy, and recall values:

$$Precision = \frac{Relevant \cap Retrived}{Retrieved} \quad (15)$$

$$Recall = \frac{Relevant \cap Retrived}{Relevant} \quad (16)$$

$$F - Measure = \frac{2 * Precision * Recall}{Precision + Recall} \quad (17)$$

The precision, recall, and *F*-measure values of the suggested model prediction system in relation to changing α value are displayed in Figures 6 to 8. In this case, α stands for the coefficient, which spans from 0.6 to 0.9 and indicates the more detailed information about the functions. Several groups are taken into consideration in this examination, including Normal, Folliculitis, Allergic Dermatitis, Bacterial Infections, and Yeast Infections. Furthermore, the contrast between the current [28]. Table 1 lists the number of training features and testing features for the dataset used in the current paper by [17], as well as the number of classes for each category.

Table 1. Allocation of features for each class in dataset.

Class	# Training	#Testing	#Total Features
Allergic dermatitis	866	44	930
Folliculitis	1090	34	1124
Bacterial Infections	484	20	504
Yeast Infections	1513	128	1641
Total	3973	226	4199

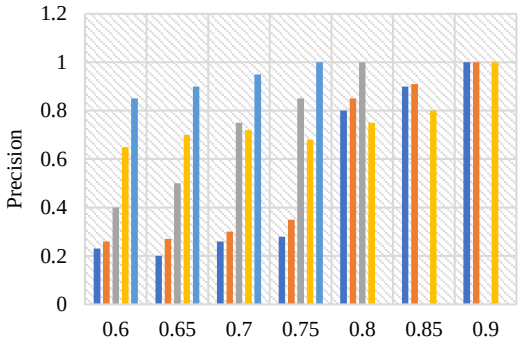

Figure 6. Precision.

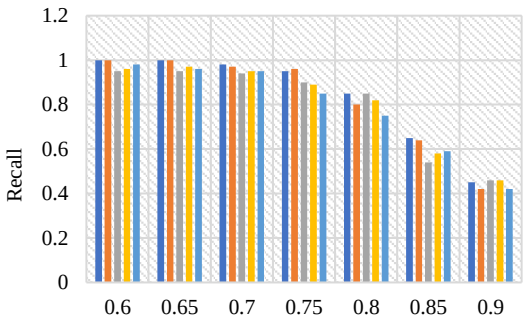

Figure 7. Recall.

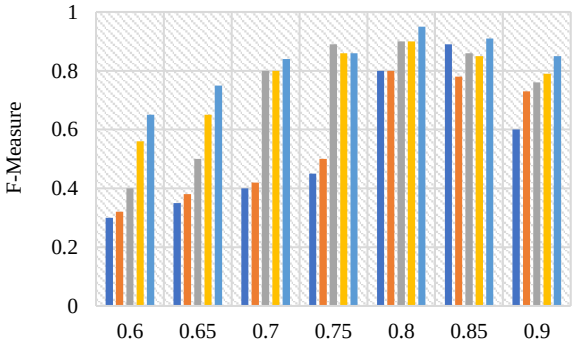

Figure 8. F-Measure.

The contrast between the suggested Test prediction and the current systems is displayed in the Fig. 9. This

is an example of how well the suggested prediction system performed using the Texture Learning - Web KB dataset. According to the investigation, the suggested model prediction process yields better results by giving the inputs high-ranking models. Additionally, a comparison of the accuracy and error rate of the suggested data optimization-based Texture learning procedure was prepared in Figure 10.

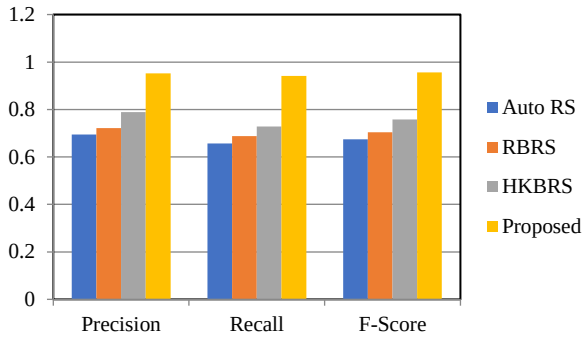

Figure 9. Overall comparison chart.

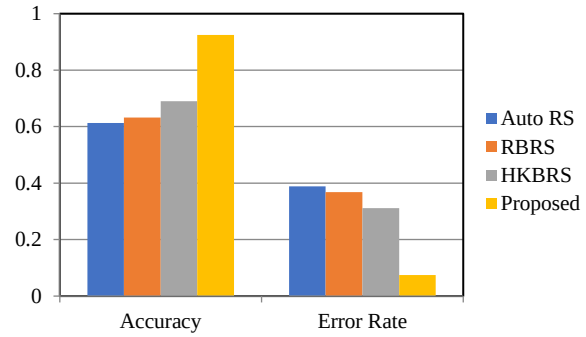

Figure 10. Comparison chart of accuracy and error rate.

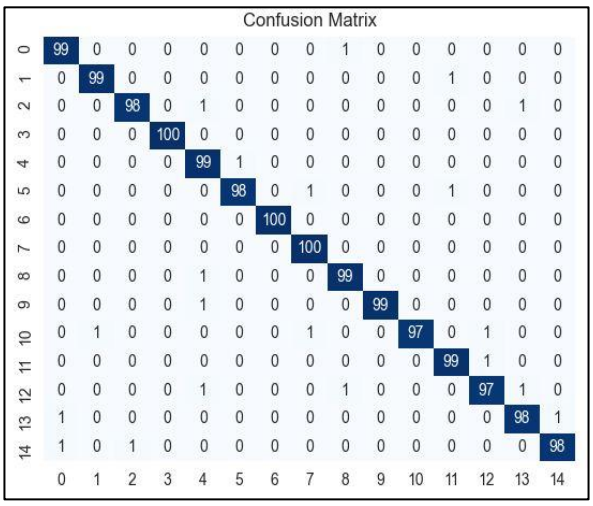

Figure 11. Confusion matrix of proposed work result.

An analysis of the confusion matrix of the prediction result can be used to explain the experimental result for the suggested work of the texture learning system. The Table 2 displays the confusion matrix. By evaluating the parameters of accuracy result, which are referred to as sensitivity, specificity, precision, recall, F_1 Score, and other parameter result, the performance of the suggested work can be evaluated using this confusion matrix. All of them are shown in the bar chart diagram as the classifier's output compared to the dataset's ground truth, which is stored in the database. In light of this, Figures 11 and 12 show the performance metrics of the suggested work for the dataset, where 70% of the training data and 30% of the testing data are taken into account while testing the entire dataset for prediction in the texture learning process.

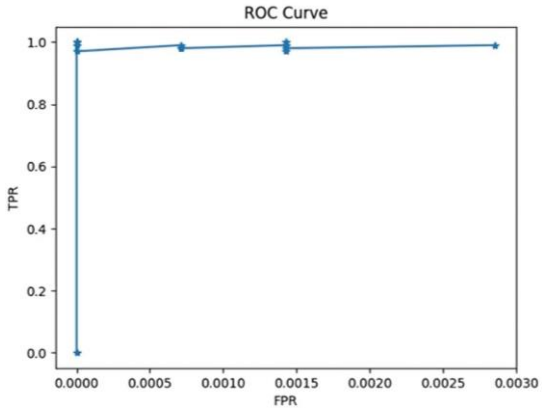

Figure 12. ROC curve of proposed work result.

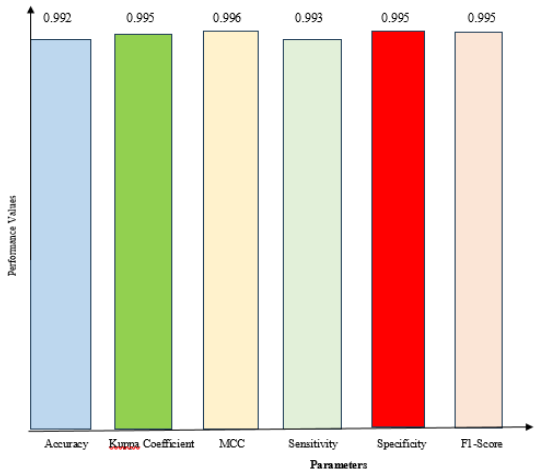

Figure13. Performance measures of proposed work result.

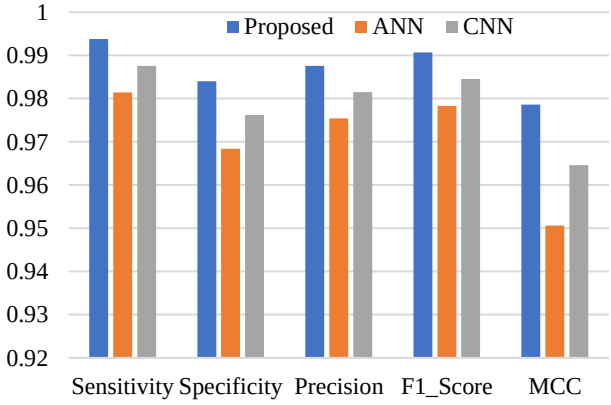

Figure 14. Comparison chart of accuracy and error rate.

By assessing the performance measures of the final labeled output in comparison to the Artificial Neural Network (ANN) and Convolutional Neural Network (CNN) model of [17, 28] based neural network development, one can describe the comparison result for

the texture learning and prediction system. This can be seen in Figures 14 and 15 respectively.

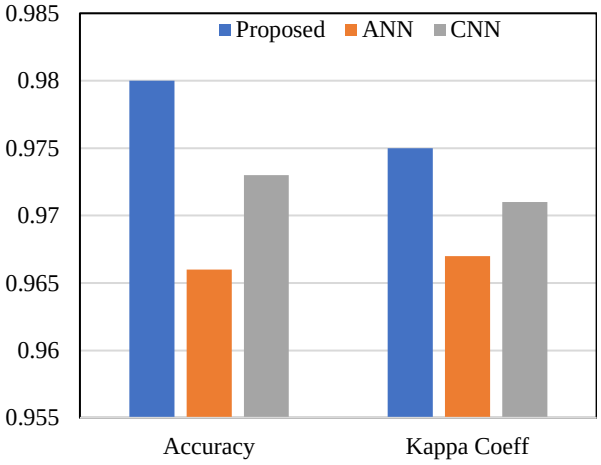

Figure 15. Comparison chart of accuracy and error rate.

8. Specific Canine Diseases Being Predicted in The Proposed Work

Canine Parvovirus (CPV) is one type of disease, which is a highly contagious viral disease affecting dogs, particularly puppies, causing severe gastrointestinal distress.

Canine distemper is one type of disease, which is a viral disease that affects multiple body systems, including the respiratory, gastrointestinal, and central nervous systems, often fatal if not treated promptly.

Canine Hepatitis (ICH) is one type of disease, which is an infectious disease caused by canine adenovirus type 1, affecting the liver and other organs, leading to a range of symptoms from mild to severe.

Lyme disease is one type of disease, which is a tick-borne illness caused by the bacterium Borrelia burgdorferi, leading to symptoms such as fever, lethargy, joint pain, and lameness.

Canine Influenza is one type of disease, which is a contagious respiratory disease [18] in dogs caused by influenza viruses, leading to symptoms like coughing, sneezing, fever, and lethargy.

Kennel Cough is one type of disease, which is a highly contagious respiratory disease caused by a combination of bacteria and viruses, including Bordetella bronchiseptica, leading to a persistent cough and other respiratory symptoms.

Heartworm Disease is one type of disease, which is caused by the parasitic worm Dirofilaria immitis, transmitted through mosquito bites, leading to severe lung disease, heart failure, and other organ damage.

Leptospirosis is one type of disease, which is a bacterial infection caused by Leptospira species, affecting various organs, particularly the kidneys and liver, potentially leading to kidney failure and liver disease.

Rabies is one type of disease, which is a fatal viral disease affecting the central nervous system, transmitted through bites from infected animals, leading to neurological symptoms and death if untreated.

Canine Coronavirus is one type of disease, which is a viral infection affecting the gastrointestinal system, causing symptoms such as diarrhea, vomiting, and abdominal pain.

Tick-borne diseases (e.g., ehrlichiosis, anaplasmosis, babesiosis) which are few types of diseases that are being transmitted by ticks, causing a variety of symptoms, including fever, anemia, lethargy, and joint pain.

These diseases [26] are significant for their impact on canine health and their potential to cause widespread outbreaks among dog populations. The development of predictive models for these diseases can help in early detection and effective management, thereby improving canine health and reducing mortality rates.

9. Conclusions and Future Work

The purpose of this work is to develop a novel Test prediction system that can produce effective models for the inputs. This involved analyzing and predicting pertinent data from databases using a Test prediction system based on texture learning. This is why distance-based similarity, retrieving techniques, and improved relevancy estimation are used. Here, the dataset is preprocessed using noisy pixel removal and pixel enhancement. After that, the CP is chosen using the MDIPP measure, which involves removing the keywords from the file repository. Additionally, the attribute containing a collection of features based on the CP is formed using the SM technique. The CTNN classifier is then used in the data learning system to process the features for the training model. The same CTNN classification model is used by the server to identify the Test request in this scenario. Additionally, the most similar items for prediction are found using similarity metrics based on KC and TD. Additionally, the combination of the MDIPP and SM similarity estimate techniques yields the rank for the highly similar items based on this priority. Several metrics are employed in performance evaluation to examine the outcomes of both suggested and current methods. According to the evaluation, the suggested Test prediction system outperforms the competition by effectively placing the models in order of preference.

In this work, we proposed a novel approach to canine disease prediction utilizing the MDIPP combined with the CTNN. Our research addresses the critical challenges of data retrieval and prediction accuracy in texture learning systems. The findings of this study highlight several key contributions and their significance in the field of veterinary diagnostics.

Firstly, the introduction of a sophisticated relevancy estimation model and data similarity estimation significantly enhances the ability to retrieve relevant data efficiently from large datasets. By optimizing the search

process, we reduce the time spent in finding the best matches for given test data, which is crucial in real-time applications such as veterinary diagnostics. The implementation of the MDIPP approach, coupled with the SM system, allows for a more accurate assessment of similarity between test data and the comprehensive database. This optimization ensures that the retrieval process is not only faster but also more precise, thus improving the reliability of predictions made by the system.

Secondly, our use of a paged database structure, organized according to attribute features, further accelerates calculations during the search phase. This innovative structure ensures that relevant data can be accessed quickly, facilitating the timely diagnosis of canine diseases. The CTNN model's ability to forecast the relevance [7] of feature attributes by considering their correlation factors represents a significant advancement in the methodology, allowing for more nuanced predictions based on the interdependencies of various attributes within the dataset

Moreover, the performance evaluation of the proposed system demonstrates its superiority over existing state-of-the-art techniques. By utilizing metrics such as precision, recall, and F1-score, we validated the effectiveness of our approach in achieving high accuracy in both data retrieval and test prediction outputs. This achievement not only underscores the potential of our model in practical applications but also sets a new benchmark for future research in the field.

Looking ahead, several avenues for future work can be explored to further enhance the capabilities of the proposed canine disease prediction system. Future research could focus on expanding the dataset to include a wider variety of canine diseases and diverse image qualities, allowing for better generalization of the model. Additionally, integrating advanced machine learning techniques, such as ensemble learning and deep learning architectures, could improve prediction accuracy and robustness.

Further investigation into real-time implementation of the model within clinical workflows will also be crucial for practical applications. By collaborating with veterinary professionals, we can refine the system's user interface and functionality to better align with clinical needs. Continuous learning mechanisms that update the model based on new incoming data could also be developed, ensuring that the prediction system remains relevant and effective as new disease patterns emerge.

In summary, this work lays the groundwork for a transformative approach to canine disease prediction, leveraging advanced data retrieval techniques and neural network methodologies. The insights gained and the contributions made in this study offer promising directions for future research and development in veterinary diagnostics, ultimately aiming to improve the health and well-being of canines through timely and accurate disease predictions.

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Ayesha Taranum currently pursuing Ph.D. in Computer Science and Engineering under Visvesvaraya Technological University. She is working as Assistant Professor at Computer Science Department in Presidency University, Bangalore, India. Her research includes Machine Learning, Deep Learning, data mining and Big Data Analytics.

Jyoti Metan is working as Associate Professor in Information Science and Engineering Department from Atria Institute of Technology Her Area of Interest is Networking, Machine Learning and Deep Learning. She has been awarded and recognised in VTU Approved project in year 2017-18 for project title- "Data Acquisition in Car using IoT". She has 16 years of experience in teaching.

Prasad Yogegowda is working as Associate Professor, Computer science and engineering at SJB Institute of Technology, Bangalore, Karnataka, India. He pursued Ph.D. degree in Computer science Engineering, 2020, M.Tech in CSE-2011, B.E. in CSE-2009, all degrees awarded from Visvesvaraya Technological University, Belagavi. Karnataka, India. He published total 24 International Journals and Conference papers. He published 5 Indian patents. He is Life member of the Professional societies like IAENG, LMI.

Chandrashekar Krishnappa received his M.Tech. Degree in Computer Science and Engineering from RV College of Engineering, Bangalore and Ph.D. in Computer Science and Engineering from Visvesvaraya Technological University (VTU), Belagavi. He has participated and Presented papers in various International conferences and Journals conducted by different organizations. He has worked as Assistant Professor in the Department of CSE, SJB Institute of Technology, Bangalore for over 12 years and he is working as Associate Professor in the Department of CSE, SJB Institute of Technology.