## HIDDEN MARKOV MODEL CLASSIFICATION SCHEME FOR CANCER DETECTION IN IMAGE PROCESSING

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# ABSTRACT

The development of detection systems using artificial intelligence techniques has been very helpful in medical computing. The employment of machine learning algorithms has improved the medical health sector drastically. This research work has employed the Hidden Markov Model classification scheme for the detection of breast cancer. During the classification analysis some miss fit were discovered which were discussed in this work with recommendations given. The R statistical programming language has been used in the analysis of this system. The HMM was able to classify completely the non-cancerous (Benign) data with an accuracy of 100% but, fail to completely classify the cancerous data giving an accuracy of 97.1% with a misclassification of 0.028%. The model, generally, did not perform well as it produces a performance accuracy of 37.2% when it was summarized to check for the states correctness. However, the performance accuracy was not a thing to worry about as the HMM documentation has clearly stated that the "Viterbi" function can be unstable or unreliable.

**KEYWORDS:** Image Processing, Hmm, Artificial Intelligence, R Programming Language, Cancer Detection.

# I. INTRODUCTION

Cancer is a major public health challenge globally and its epidemic nature in recent times is becoming alarming and something to worry about. It is an uncontrollable abnormal growth caused by some cells and can appear in any part of the body. According to Carbone (2020) as at 2018, cancer cases grew globally to an estimated verified case of 18.1 million and recorded mortality of about 9.6 million and its mortality rate is expected to increase to 16.3 million (Nath et al., 2019) with about 29 million registered cases by 2040. In Nigeria, as at 2020, the total estimated number of cancer cases as recorded in a report by Globocan to world health organization (WHO) is 124,815 with the total number of deaths at 78,899 Sung et al. (2021). Detecting or predictive system via artificial intelligence would be a major breakthrough in reducing the mortality rate of cancer patients.

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Predictive and detection models for cancer can help with the design and organization of clinical trials, as well as the evaluation of therapies and preventive actions (Nath et al., 2019). Early detection and diagnosis are significant aspect in determining a patient's prognosis in cancer and to tell if patient is going to survive; it also reduces the mortality rate (Elgamal, 2013; Hoshyar et al., 2014; Dildar et al., 2021). The biopsy procedure is commonly used by doctors to identify skin cancer. A sample of a suspicious skin lesion is removed for medical testing to determine if it is malignant or not. This is a painful, slow, and time-consuming process. The use of computer technology allows for a more comfortable, less expensive, and quicker diagnosis of cancer symptoms (Dildar et al., 2021). The process followed to achieve this prediction or detections is an artificial intelligent method that has to do with image processing.

In image processing, when it comes to cancer detection, image processing is crucial. It has a wide range of applications in modern science and technology, and it will continue to do so in the future. It is an approach for implementing various operations on photos in order to obtain a more useful image in early identification and detection of disease like cancer (Paliwal, 2016). Image processing increases the visual information on images and this information are based on surface characteristics which involves the transformation of raster data into a finite collection of classes that represent different surface types in photographs (Anand, 2017). The artificial intelligence or machine learning model used for this purpose is the hidden Markov model.

The name, Hidden Markoz Model was derived from the fact that its process cannot be observed but the labelled balls sequence. The Hidden Markov Model (HMM) is a statistical model which analyses the pattern of a succession of seen symbols to interpret the (non-observable) process. A doubly stochastic process is used in a Hidden Markov Model, in which the underlying (or hidden) stochastic process can be inferred indirectly by studying the sequence of observed symbols of another set of stochastic processes (Awad & Khanna, 2015). Blasiak & Rangwala (2011) has opined that the success of HMMs is due to the ease with which they simplify assumptions. This artificial intelligence technique and its classification scheme is being employed in the detection of cancer.

The increasing mortality rate of cancer patients is disturbing and a cause for concern and as opined by Elgamal (2013) that early detection will reduce drastically the mortality rate of cancer patients globally. The problem statement of this research work is the continuous increase in the mortality rate of cancer patients globally. The rate at which these patients die of this disease is still a thing to look into especially in the developing countries where the AI technology has not been taking full advantage of. Therefore, reducing the mortality rate through early detection of cancer in image processing while exploring the HMM classification scheme to achieve the research goal. The aim of this research work is the development of Hidden Markov Model classification scheme for early detection of cancer in image processing. This can be achieved through the following objectives: (1) To carry out a detailed study of the Hidden Markov Classification Scheme that will be used for detection of the cancer, (2) To acquire the cancerous image dataset for the proposed system analysis and HMM classification. (3) To carryout preprocessing and segmentation of the acquired cancer image dataset of the proposed system. (4) To extract the desired and salient features from the image dataset for the proposed system. (5) To detect and classify the various images from the dataset using R programming language.

#### II. Related Literature

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In 2009, Lau & Al-Jumaily presented an automatically skin cancer classification system is developed and the relationship of skin cancer image across different type of neural network are studied with different types of pre-processing. Babu et al. (2018) has presented an overview on image classification methods in image processing. Classification is based on the description, texture or similarity of items or things. Image classification considers two approaches - supervised classification and unsupervised classification. Tanimu et al. (2021) presented a contemporary machine Learning Method for accurate prediction of cervical cancer. With the advent of new technologies in the medical field, huge amounts of cancerous data have been collected and are readily accessible to the medical research community. Liu (2005) looked into supervised classification and unsupervised classification. His project uses migrating means clustering (MMC) unsupervised classification, maximum likelihood classification (MLC) trained by picked training samples and trained by the results of unsupervised classification (Hybrid Classification) to classify 512 pixels by 512 lines NOAA-14 AVHRR Local Area Coverage (LAC) image.

In 2014, Keroglou & Hadjicostis performed Hidden Markov Model classification based on empirical frequencies of observed symbols. Given a sequence of observations, classification among two known hidden Markov models (HMMs) can be accomplished with a classifier that minimizes the probability of error (i.e., the probability of misclassification) by enforcing the maximum a posteriori probability (MAP) rule. Blasiak & Rangwala (2011) applied HMM variant for sequence classification. Sequence classification is central to many practical problems within machine learning. Distances metrics between arbitrary pairs of sequences can be hard to define because sequences can vary in length and the information contained in the order of sequence elements is lost when standard metrics such as Euclidean distance are applied. Akshay et al. (2019) in his paper; classification among HMM has opined that, an important task in AI is one of classifying an observation as belonging to one class among several (e.g. image classification).

Benyacoub et al. (2014) opined that classification and statistical learning by Hidden Markov Model has achieved remarkable progress in the past decade. They have been applied in many areas like speech recognition and handwriting recognition. Esmael et al. (2012) has used HMM to improve time series classification. Time series data are ubiquitous and being generated at an unprecedented speed and volume in many fields including finance, medicine, oil and gas industry and other business domains. Stoner & Economou (2020) applied an advanced HMM for hourly rainfall time series data prediction. The hidden Markov framework is adapted to construct a compelling model for simulation of sub-daily rainfall, capable of capturing important characteristics of sub-daily rainfall well, including: long dry periods or droughts; seasonal and temporal variation in occurrence and intensity; and propensity for extreme values.

# III. Analysis of the Proposed System

The proposed cancer detection system in image processing using the Hidden Markov Model (HMM) classification scheme is a machine learning technique that explores the availability of historical image data to classify the presence of cancer in a patient. This technology (i.e. AI) reduces the waiting time dramatically in cancer diagnosis by capturing image from a tissue sample in minutes. It bypasses the protocols of preparation, staining or modification and encourages reuse. The HMM classification scheme explores the properties of the image pixel

through scanning, segmentation and classification to detect and extract portions of the cancerous boundaries.

The proposed scheme follows the detection system algorithms which are from the image capture to the classification to tell that the issue the patient is suffering is cancerous. The classification scheme is shown in the structural illustration given in figure 3.1. It diagrammatically explains the HMM classification scheme to the cancer detection in image processing.



Figure 3.1: Architectural Design of the Proposed Hidden Markov Model Classification Scheme for Cancer Detection in Image Processing.

Figure 3.1 is the architectural design of the proposed cancer detection system in image processing. It involves four distinct steps to the cancer detection, they include: image data acquisition, pre-processing, HMM classification scheme, detection result display. Each of these stages has its importance to the general output of the system. To detect the cancer, we need to acquire some images, prepare them to be used by the classifier and the result is displayed. Figure 3.1 is further explained in details thus:

### A. Image Data Acquisition

The proposed system is a cancer detection system in image processing using the HMM classification scheme. The system looks into the detection of breast cancer and dataset made available by Merish Nasuwal in Kaggle website; a machine learning and data science community was collected. This dataset includes 569 observations with 6 variables. These attributes are namely: mean radius, mean texture, mean perimeter, mean area and mean smoothness. The dataset was acquired for the use of this research work.

#### **B.** Pre-processing

The pre-processing of the proposed system is done to remove missing values and to prepare the dataset to be used by the HMM classifier. The features of the images are extricated since each image data feature is uniquely identified. The shape, intensity and colour which are the features of the cancer are extracted using a feature extraction technique known as Scale Invariant Feature Transformation before employing the HMM classifier.

# C. HMM Classification Scheme

This classifier, when applied, segments the cancerous portion in the breast image via 2D segmentation (Sharma & Rattan, 2019). Since the model is unsupervised, and the weights for producing output are the likelihoods of sequence belonging to one class or the other when it comes to output produced by initial state. In HMM, the states are not directly visible, nevertheless, observations that are reliant on the states are visible with each state having a probability distribution over the likely output observation (Esmael et al.). The breast image dataset will be used to train the HM model. From the trained model, an evaluation will be carried

out to correct and confirm the classified result. This Markov process can be seen in figure 3.2 as illustrated



Figure 3.2: Hidden Mark Model Classification Process of the Proposed System

After obtaining the breast image dataset into the work environment as seen in Figure 3.2, the dataset is then trained to create the model. The created model is then evaluated with the test dataset for performance accuracy and misclassification. When the model is evaluated using the test dataset, the classified result can now be displayed from which the percentage error can be checked.

# **D.** Detection Result display

The result of the proposed cancer detection is then displayed after the HMM classifier has been used with the extracted features to differentiate cancerous from non-cancerous breast images. The result shows the accuracy and performance of the model on the breast image dataset and how minimal the error produced is from which efforts can also be put to reduce the errors until an optimal model is produced.

#### **3.2.1** Justification of the Proposed System

The proposed classification scheme shows good potentials in the improvement of strategies for breast cancer detection in image processing. With this system, reassurance can be given to patients for quick and reliable diagnosis of breast cancer. The employment of the proposed scheme describes the evolution of some observable events that rely on internal factors, which cannot be directly observed whose probability distribution of the observed detection is dependent on the fundamental state. Decoding, evaluation and learning to find the most likelihood classification; these are three (3) problems HMM provides solutions for

# 4.3 System Implementation Analysis and Results Output Analysis

#### 4.3.1 System Implementation Analysis

The proposed Hidden Markov Model classification scheme for cancer detection in image processing has been carried out in this research. A breast cancer dataset was acquired from Kaggle; A machine learning and data science community and was used to achieve the HMM classification. The dataset was read into the work environment and analysed. It was discovered that the "mean area" attribute of the breast cancer dataset can be used to achieve the model classification. The diagnosis attribute of the dataset showed that the binary '0' was classified as Benign (meaning, no cancer or non-cancerous) and Malignant (meaning, there is cancer or cancerous). Hence, the system was able to distinguish the dataset to identify the 'Benign' and 'Malignant' data. The Benign and Malignant were used as the two states of the data, which means that the breast cancer dataset can either be Benign or Malignant. The 'mean area' was chosen as the observation feature since, the architecture of the HMM does not allow more attributes to be used in the classification and both the states and the observable features must be equal. The observation class was used as the transition probability after logically separating the Benign and the Malignant.

#### 4.3.2 Result Output Analysis

After fitting the states and observation class of the model, a 2-dimension discrete Markov Chain defined by the following states: Benign and Malignant and a transition matrix (by row). The output analysis of the model is shown through the graphical illustrations shown in the Figures and Tables showing the matrix of the model.



Figure 4.1: Graphical Representation of the Benign and Malignant Data of the Proposed System

Figure 4.1 is the graphical illustration of the Benign and Malignant dataset which are the different states to be used by the model. The threshold shows that, more of the values of the Benign lies around 800 to 1200 and for the Malignant, the values lies around 750 and below, with some of the figures overlapping. Appendix A1 demonstrates the actual measurement using a bar chart to distinguish the both. Below is Figure 4.2 representing the mean area plot.

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Figure 4.2: Mean Area Dataset Plot Showing the Threshold between the Benign and Malignant of the Proposed System

Figure 4.2 is the mean area dataset plot showing the threshold of the data. This plot has chosen between 500 and 1000 as the point in which both the Benign and Malignant values overlap in the mean area attribute of the dataset. After the model was fitted, Figure 4.3 was plotted.



Figure 4.3: Graphical Representation of the Developed Hidden Markov Model Classification Scheme for Breast Cancer

Figure 4.3 is the developed plot from the Hidden Markov Model Classification scheme for breast cancer. The model showing two straight plots on the graph which represents the Benign and the

Malignant. The plot shows that we have more of the Benign (0.0) over the 500 threshold or index than the malignant. The Benign falls in-line with the 0.0 while the Malignant is at the 1.0 line.

# TABLE 4.1: TRANSITION MATRIX ESTIMATION OF THE MARKOV CHAINFITTING OF THE STATES

	Benign	Malignant	Total
Benign	0.4952830	0.5047170	1
Malignant	0.2977528	0.7022472	1

Table 4.1 shows the estimation of the Markov Chain model fitting which summarizes the different states of the data produce a figure that when summed row-wise it should give a total of 1 as seen in the Table. A misclassification analysis was done on the HMM model as shown in Table 4.2.

#### TABLE 4.2: MISCLASSIFICATION OF THE MODEL OF BOTH STATES AND OBSERVATIONS

	В	Μ
Benign	212	0
Malignant	10	347

From Table 4.2, we can see that 10 rows of malignant dataset were misclassified as Benign. Though, the picture is not very clear as to if the misclassified dataset are actually Malignant. But, Table 4.3 explained it clear enough that the misclassified rows are actually Malignant.

#### TABLE 4.3: THE PROBABILITY DISTRIBUTION OF MISCLASSIFIED DATASET

	В	Μ
Benign	1.0000000	0.0000000
Malignant	0.0280112	0.9719888

Table 4.3 clearly shows that the misclassified rows were actually Malignant. Benign were classified as 100% (1.0000000) and Malignant classified as 97.1% (0.9719888). The misclassified row resulted to 0.28% (0.0280112) of the proposed model.

#### 4.4 Discussion of Result

The Hidden Markov Model classification scheme for breast cancer detection in image processing has been developed. The system has employed the use of dataset acquired from Kaggle website in the development of this scheme. The dataset contains 569 observations of 6 variable which include: Mean radius, mean texture, mean perimeter, mean area, mean smoothness and diagnosis, but, 2 of the variables (mean area and diagnosis) were used for the HMM classification scheme. Pre-processing analysis was carried out on the dataset and features were plotted on a graph.

Figure 4.1 was used to show the different states of the model in the raw form. The figure showed that there are two states 0 and 1 designated as Benign and Malignant which shows non-cancerous (as Benign) and cancerous (as Malignant) dataset. The Figure 4.2 is used to establish where the threshold lie which was shown in the figure and Figure 4.3 is the representation of the model or classification scheme. It shows the Benign at the lower part of the plot which is 0.0 and 1.0 indicate the Malignant of the plot.

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Table 4.1 is the transition matrix estimation of the Markov Chain fitting of the two states. In this table, the rows must sum up to 1 (one) to show the correctness. Table 4.2 is the misclassification table of the model. It shows where the mode misclassified the dataset which in this case, 10 rows of the dataset which are malignant was misclassified to be Benign as shown in the table. To know how true this is, the Table 4.3 which gives the probability of the model clearly shows that the Benign was correctly classified with a probability of 1 while the malignant had the probability of 0.97 and the probability of the misclassification came to 0.028.

Generally, the summary of the model when calculated has presented an accuracy of 37.2% which shows that the model did not do well enough but can be improved upon.

# CONCLUSIONS

We will therefore conclude that, Hidden Markov Model Classification scheme for cancer (Breast Cancer) detection has been developed. The research work has been able isolate the key variables that can be used with the Markov Model. From the analysis, we have been able to identify the Benign and Malignant of the dataset. The model was able to completely classify the non-cancerous data giving a percentage accuracy of 100% and failed to completely classify the cancerous data giving an accuracy of 97.1% with a misclassification of 0.028. The model's general performance was summarized to 37.2% but from the HMM documentation of the Viterbi function, we know that there could be an error in the summary given.

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