NOVEL HEURISTIC HYBRID MODEL TO HANDLE AUTOMATIC PREDICTION OF CANCER DISEASE CLASSIFICATION OVER CANCER DRUG DATA SETS

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Abstract

Drug identification is an issue with real-time population growth.To improve drug detection in real-time bio-technical applications.In many nations,agriculture is the single most important factor in increasing the supply of anti-cancer drugs.Cancer-related illnesses are effective in lowering production quality and volume while also costing computer vision applications money.While many writers have utilized machine learning and other forms of soft computing to develop methods for automatically predicting disease, the complexity of identifying cancer has made it a particularly vigorous field of study.This article proposes a Novel Heuristic Hybrid Model (NHHM) that combines SOM and CNN to automatically identify cancer diseases.Feature extraction is key to identifying cancer diseases,therefore dimensionality reduction is done in SOM to filter noise from Cancersubcancer medication data sets and distinguish disease-affected patches.CNN is used to explore color histogram-based linguistic features existing in Cancer and predict which patch is related to disease in Cancers.It is an effective option to predict accurate detection of diseases where Cancersubcancer drugdata set is matched with virus/bacteria-affected patch in Cancers.The proposed hybrid model was tested using publicly available Cancers cancer drug data sets (which are available in the UCI repository) to obtain subCancerdrug data sets from peach Cancers.This approach is used to identify the disease present in Cancers based on the subCancer drug data sets.The proposed hybrid model also requires less training to investigate disease from subCancer drug data sets, and it performs with an accuracy of almost 99.93% on various testing Cancersubcancer drug data sets. When compared to several state-of-the-art methodologies, this reduces the major running time and performs effectively in various disease detection characteristics like precision, recall, sensitivity, and specificity.

Key words: Feature extraction, histogram, convolution neural network, self-organizing map, deep learning, fruit diseases, and sub disease detection.

1. Introduction

Cancer infections are viewed as one of the principal factors impacting cancer drug creation, being liable for the huge decrease of the physical or financial efficiency of the harvests and, in certain examples, perhaps a hindrance to this action. As per [1], to limit creation misfortunes and keep up with crop maintainability, it is fundamental that infection the executives and control allots be conveyed properly, featuring the consistent observing of the crop, joined with the quick and precise determination of the illnesses. These practices are the most suggested by psychopathologists [1].The significant test for horticulture is the right ID of the side effects of significant sicknesses that influence crops [2].Manual and motorized rehearses in conventional establishing processes can't cover enormous areas of estate and give fundamental early data to dynamic cycles, as per [3]. Hence, it is important to create automated arrangements,

are pragmatic, solid, and financially ready to screen the wellbeing of Cancers giving significant data to the dynamic interaction, for instance, the application and right measurements of pesticides in explicit treatment of certain illnesses [4].Different Cancersubcancer drug data sets described in Figure 1.

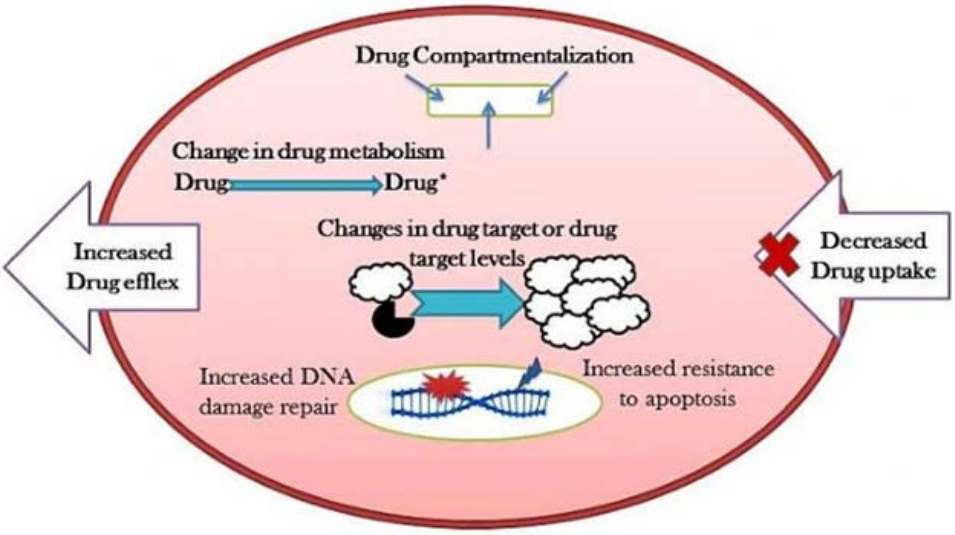

Fig.1. Different cancer drug data sets

Computer Vision, alongside Artificial Intelligence (AI), has been creating strategies and techniques for perceiving also, characterizing objects with huge advances [5]. These frameworks use Convolution Neural Networks (CNNs) [6],what's more, their outcomes in certain examinations are as of now better than people in enormous scope observation assignments. The works of [7] and [8] feature the utilization of pictures as one of the most developed techniques for the identification and acknowledgment of Cancerillnesses.J. S. Bunny et. al. [4] another procedure has been created to catch content-based Cancersubcancer drug data set information and perceive Cancersubcancer drug data sets protests that have been loudly debased and changed over through the symbolism framework. They additionally utilized a space vector model to productively list any Cancersubcancer drug data set. From that point forward, a two-venture rating system is utilized to work out the right Cancersubcancer drug data set. The calculation is especially resistant from varieties in inquiries and Cancersubcancer drug data sets from the cancer drug data set. Scale Invariant Feature Transform (SIFT) Descriptor13 is utilized in execution of this method. The photos are remade into a vector based on the frequencies of "visual" terms in the Cancersubcancer drug data set. 850 Cancersubcancer drug data sets from Nat Cancersubcancer drug data set assortments are utilized in informational indexes. There were 850 Cancersubcancer drug data sets from the public historical center's photograph assortments. 200 arbitrarily picked Cancersubcancer drug data sets were utilized to confirm the computer.

C. Szegedy et. al. [7] Tried to separate articles precisely by utilizing the strength of the DNNs. They additionally planned a strategy for building a double veil of the jumping object. DNN-subject to relapse. You exhibit that the DNN relapse can learn order highlights and assemble mathematical information. In the wake of eliminating covers from various things in a single set with DNN relapse, a little gathering of immense sub windows would be fitted with a DNN tracker. It utilizes one organization to conjecture four portions of the case in the item box veil and four organizations. The strategy has been approved with 5000 Cancersubcancer drug data sets in 20 classes in the Pascal Visual Object challenge (VOC) 2007 dataset. Test-and appraisal framework c of VOC2012

X. F. Hermidaet. al. [8] Many techniques for Cancersubcancer drug data set handling, including versatile edge discovery and point identification were utilized in the proposed Braille text acknowledgment framework utilizing Optical Character Recognizing Philosophy (OCR). The regions with two versatile edges have been changed by a strategy in high contrast districts. To work out the limits, the luminance histogram was utilized. The machine likewise noticed adulterated scores and lost focuses.

Many methodologies as of now utilize famous designs like LeNet[9], AlexNet[10], VGGNet[11],GoogLeNet[12], InceptionV3[13], ResNet[14] and DenseNet[15], significantly expanding the exactness in the distinguishing proofof Cancer infections. In any case, various difficulties actually block the right grouping of physiopathology, for example, the hereditary and phenotypic variety of yields, the wide assortment of vermin, and infections. As well as the qualities

of the informational collections, the sorts, and characteristics of organization designs and models convolution brain and the intricacy engaged with the outcomes streamlining methods.

Deep Learning methods are propelled by the engineering of neurons present in the human mind (Haykin, 1998). These strategies use Artificial Neural Networks (ANNs), and its different variations, for example, Convolution Neural Networks (CNNs) and Recurrent Neural Networks(RNNs) to recognize the secret constructions in information. There are two conspicuous benefits of Deep Learning methods over the Machine Learning methods. In the first place, they naturally remove different highlights from crude information, and consequently there is no requirement for an additional an element extract on module. Second, Deep Learning methods diminish how much time expected to handle huge datasets of high aspects. Subsequently, the Deep Learning procedures are utilized to fabricate the proposed hybrid model. Convolution Neural Networks (CNNs) and Self Organizing Map (SOM) are two Deep Learning strategies utilized in large number computer vision applications because of their viability on Cancersubcancer drug data set information. Both these procedures use convolution activity to extricate different spatial also, transient highlights from Cancersubcancer drug data set information. CNN's are utilized to characterize input Cancersubcancer drug data sets to their separate classes, while SOMs are utilized to diminish the dimensionality of a Cancersubcancer drug data set proficiently.

So that this paper propose a Novel Heuristic Hybrid Model for the identification of automatic Cancer disease based on SOM and CNN with less training classes present in Cancersubcancer drug data set with comparison to different state-of-the-art methods. SOM is used for reduction of dimensionality with noise removal to reduce the training samples in processing of Cancersubcancer drug data sets and used CNN for the identification of automatic disease detection from CancersubCancer drug data sets.

Contribution of proposed approach is described as follows:

- Based on cancer drug data sets, proposed hybrid disease prediction framework, proposed framework identifies Cancer drug disease classification using CNN and SOM.
- Cancersubcancer drug data set-level and disease-level-based feature extraction approaches are used to obtain robust guava disease recognition.
- The proposed framework is evaluated on a high-resolution Cancersubcancer drug data set.
- Proposed approach gives better quality of service when compared to state of the art methodologies.

2. Background Methods

This section discuss about background concepts used in identification of disease from Cancer related subcancer drug data sets. To reduction of dimensionality of selected subcancer drug data set using SOM and for the prediction of diseases from subcancer drug data sets use CNN. Discuss about SOM and CNN procedures in this section.

2.1 Extensive Self-Organizing-Map Calculation

Extensive self-organizing map (ESOM) is an unsupervised learning calculation methodology which is proposed by Kohenen et.al, this approach relates to artificial neural networks domain. ESOM is an expressive excellent tool to perform extraction of patterns which are relevant to disease. ESOM consists n relevant attribute located in m*n dimensional Cancersubcancer drug data sets. For each attribute present in 2-dimensional color weight factor $w_{i1}, w_{i2}, ..., w_{in}$ where i=1.2……n which consists equal dimensions of subcancer drug data sets.

Extensive SOM consists following definitions

Define weight vector $w_t^{'}$ which consists n*m dimensions of subcancer drug data setattributes

Probably identify weight vector a(t) to dimensions present in Cancersubcancer drug data set, find the n*m dimensionality reduction attribute in subcancer drug data sets is described as

$$w = \arg\left(\max_{1\le i\le n}\left\{\| w_i(t) - a(t) \|\right\}\right) \quad \text{…… (1)}$$

||.|| Represents distance measure relates to Euclidean, a(t) and w(t) are input and out weight vector with respect to attribute reading iterations respectably. After performing update weight attribute from subcancer drug data sets from eq (1) is described as

$$w_i(t+1) = w_i(t) + h_{c,i}(t)[a(t) + w_i(t)] \quad \text{…….. (2)}$$

$h_{c,i}(t)$ be the hue interactive neighborhood attribute identification from Euclidian distance between weight vector eq (2) is described as

$$h_{c,i}(t) = \alpha(t).\exp\left(-\frac{\| r_c - r_i \|^2}{2\sigma^2(t)}\right) \quad \ldots\ldots\ldots\ldots\ldots\ldots (3)$$

Here r be the associative attribute identification of map $\alpha(t)$ and $2\sigma^2$ be the weight function from eq (3), and it is reduction of dimensionality from Cancer related subcancer drug data sets.

2.2 Convolution Neural Network Prediction

Convolution Neural Network (CNN) is a Deep Learning strategy thatutilizes convolution activity rather than straightforward network increase. Ascontrasted with other Deep Learning methods, CNN manages picturesmost productively. It extricates different spatial and transient elements from input pictures, which assume a critical part in picture characterizationalso, other Computer vision undertakings.

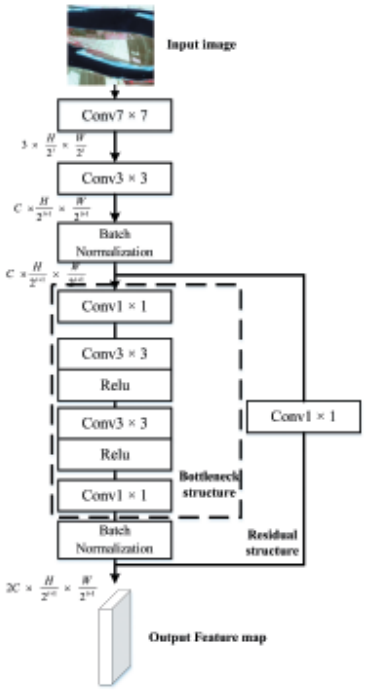

Fig.2. Layer by layer subcancer drug data set reading with associative attributes in CNN.

Convolution matrix functions are evaluated is described as

$$g(a) * f(a) = \int g(a).f(a-l) \quad \ldots\ldots\ldots\ldots\ldots (4)$$

$$g(a) * f(a) = \sum_{l=1,2,\ldots,\alpha}^{\alpha} g(a).f(a-l) \quad \ldots\ldots\ldots\ldots (5)$$

Fig. 2 portrays the engineering of a commonCNN that contains one Input layer, one Output layer, a group ofConvolution layers (each with an enactment work), Pooling layers,furthermore, Fully Connected layers (each with an actuation work).The Convolution layer present in the CNN plays out the convolutionactivity. The underlying Convolution layers of a CNN extricate the straightforwardlower-level highlights of a picture, and the Convolution layerspresent toward the finish of the organization separate the complex more significant level highlightsof a picture. The convolution activity is characterized as a double activity(addressed by cancer drug data set '$*$') between two genuine esteemed capacities (say g(a) and f(a) from eq (4) & (5)).

In CNN, g(a) and f(a) from eq (4) & (5)is named, as information and channel/piece, individually,also, the result of the convolution activity is known as the element map. The info, part/channel, and element map are put away as multi-faceted clusters. From the meaning of convolution activity, it tends to be seen that assuming the size of the information framework is m × m and the size of the channel is l × l (where l ≤m), then, at that point, the size of the result highlightmap ism−l+1×m−l+1. In this manner, it tends to be reasoned that after each convolution activity, the size of the result highlight map is diminished. In different words, the size of the info picture lessens after every convolution activity and becomes zero after certain convolutions. Henceforth, it limitsCNN's profundity by putting an upper bound on the number of Convolution layers present in a CNN. Further, the components present on the edges andcorners are utilized not exactly the components present in the focal point of theinput framework. To handle these two issues, cushioning is utilized in theConvolution layers present in the CNN.

Use this method in our proposed approach to predict automatic identification of disease from subcancer drug data sets.

2.3 Multi CancerLabeled Generative Functional Approach

To evaluate labeled Cancerdrug data set analysis using supervised learning procedure as follows, let us consider Cancerdrug data setsets as

$$\gamma = \sum_{(a,b)\in K_l} \zeta(a,b) + \sum_{a\in K_u} v(a) + \alpha \mathrm{E}_{(a,b)\in K_t}[-\log p_\phi(b \mid a)] \quad \text{…….. (6)}$$

K_t,K_u multi labeled setcancer drug data sets from eq (6), α is labeled additional classification hyper-parameter, $p_\phi(b \mid a)$ be the distribution function for multi labeled Cancerdrug data set, $\zeta(a,b)$ & $v(a)$ are the single to multi labeledCancerdrug data set point from uncertain cancer drug data set exploration. $\zeta(a,b)$ is described as follows:

$$\zeta(a,b) = \mathrm{H}_{CL}(p_\phi(z(a,b)) \,||\, q(z)) - \log p_\phi(b) - \mathrm{E}_{p_\phi((z(a,b))}[\log q\theta(a \mid b,z) \quad \text{…….. (7)}$$

Here first term is described as Leibler\Kullbackdivergentcancer drug data set exploration from eq (7) between prior distribution function q(z) & $p_\phi(z(a,b)$ is the posterior function and last term described as conditional expectation of latent variable like hood function, $v(a)$ should be described as

$$v(a) = \sum_b p_\phi(b \mid a)\zeta(a,b) - \mathrm{T}(p_\phi(b \mid a)) \quad \text{……. (8)}$$

$\mathrm{T}(p_\phi(b \mid a))$ be the classifier entropy of input data $(p_\phi(b \mid a))$, from loss of noise in input Cancercancer drug data set from eq (8), multi labeled distribution functions are performed $p_\phi(b \mid a), p_\phi(z(a,b) \& q\theta(a \mid b,z)$ are generative functions to generate multi labeled Cancer drug data set.

2.4 Recurrent Neural Networks (RNN)

RNN is the most efficient advanced approach used in deep learning for learning of different features in sequential manner, and it is time series generative function and it is used solves many scientific problems with high accuracy and prediction ofCancer detection parameters.RNN have different type of applications in sharing of Cancer drug data setwith prediction of Cancer diseases on many more applications. Basic architectural design of RNN is described in figure 1.

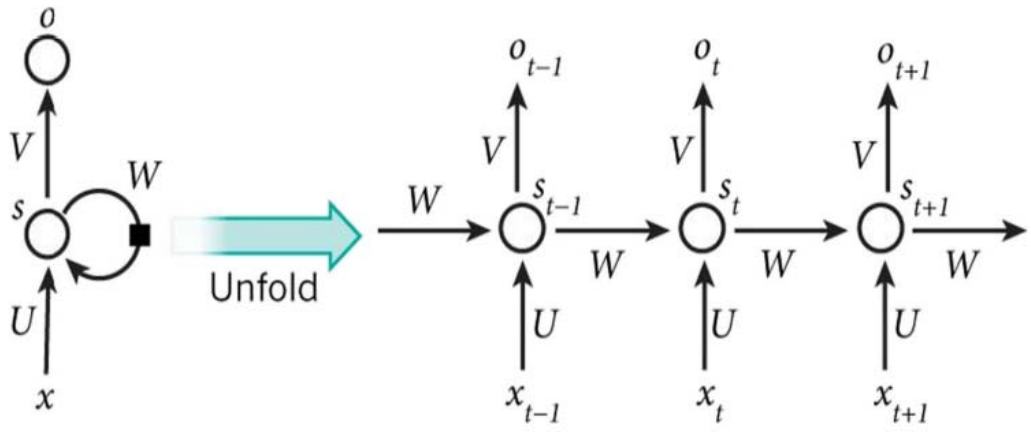

Fig.3. Semantic representation of recurrent neural network to predict diseases.

As shown in figure 3, output of the each time step is calculated and hidden state prediction is successor on figure 2, where x, s, 0 are the output, input and hidden nodes representation. W,V,U are the weights of shared matrices input to hidden and hidden to output and output to hidden and hidden to input and perform inside hidden processing on all series of time stamps. Three different types of models are presented in real time processing of plat cancer drug data setdata i.e. simple model, LSTM model and gated recurrent unit (GRU) model. To classify multi-labeled data we use GRU model in out implemented approach to reduce the tensor operations i.e. update, reset which are employed with replacement of LSTM model. Characteristics and tensor cell operations are described in following manner:
More cell equations are represented with GRU which consist update (z_t), reset (r_t) and state of hidden (h_t) are

$$r_t = \sigma(W_r * [a_t, h_{t-1}] + y_r)$$
$$z_t = \sigma(W_r * [a_t, h_{t-1}] + y_z)$$
$$\hat{h}_t = \tanh(r_t * [a_t, h_{t-1}] + y_h))$$
$$h_t = z_t * \hat{h}_t + (1 - z_t) * h_{t-1} \quad \ldots\ldots\ldots\ldots\ldots\ldots (9)$$

As discussed above based on dependencies distribution of input and output across over different time stamps. This is the procedure we used in our implementation to measure multi label inputs and provide multi label outputs with processing of different Cancerdrug data set data.

3. Proposed Methodology

In this section, we present the process of proposed hybrid heuristic model for the detection of Cancer disease based on color space scale invariant transform performed on selected subCancersubcancer drug data sets. First dimensionality reduction based color space on subCancerdrug data sets are discussed with SOM and then perform disease detector using CNN for the reliable prediction of scale invariant feature with disease patch identification.Basic procedure of implemented hybrid model shown in following figure 3. Proposed hybrid model consists different modules for the identification of disease from CancersubCancersubcancer drug data sets using the procedures discussed in section 3.

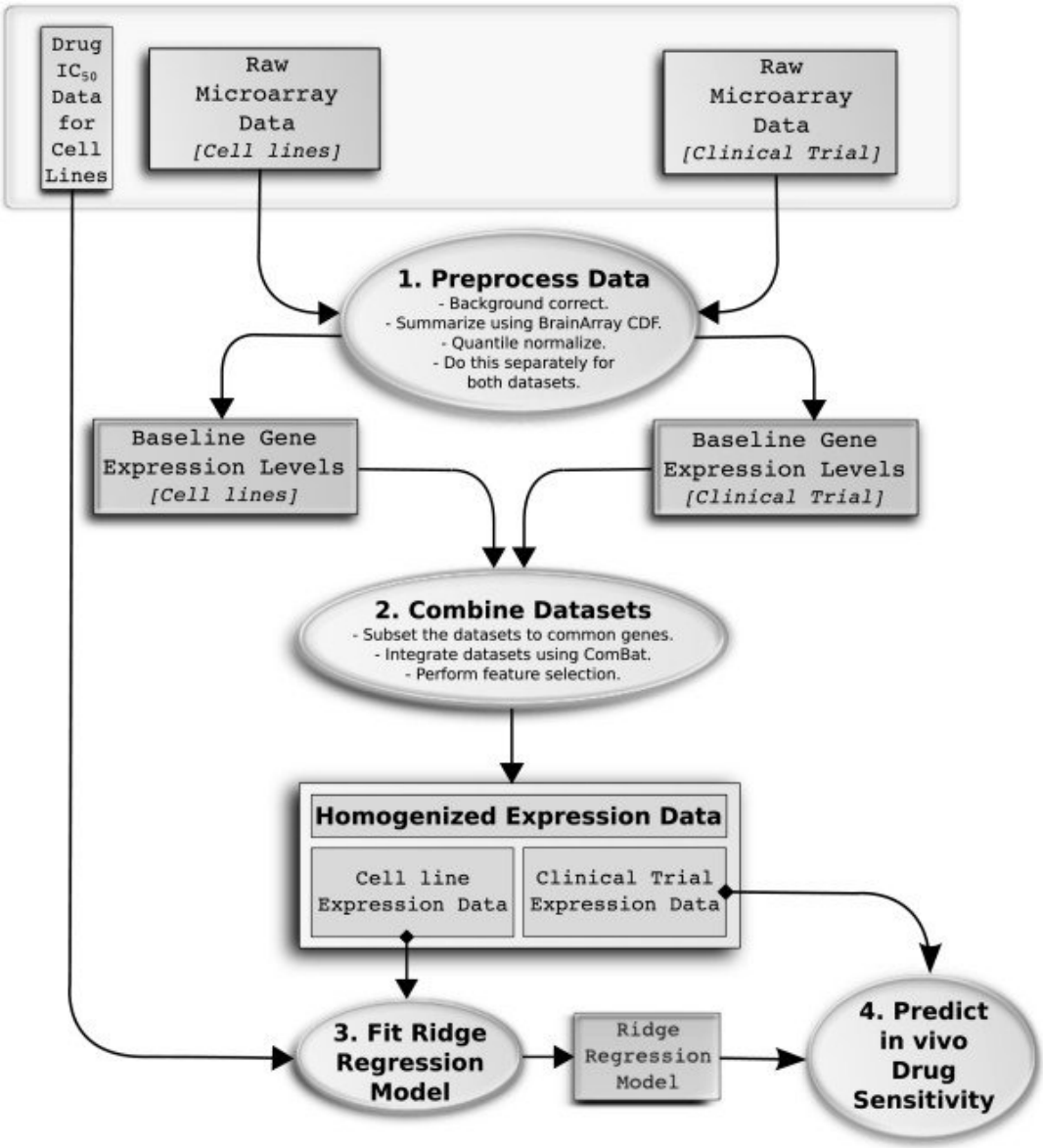

Fig.4.Proposed methodology to predict Cancersub disease detection

4. Generating Color Spaces

Mainly Cancersubcancer drug data set photographic effects like shading, texture, and shadowing, geometric dimensionality are modulated with reflection appropriate methodology from [18]. Invariant quasi color space feature model is used in proposed hybrid model which is derived from [15] for RCB based orthogonal transformation from Cancersubcancer drug data sets which is discussed in SOM. This transformation is used and performs chromatically rotated and transformation at different axis then color scale invariant is described as

$$CSF = \begin{pmatrix} 0_1 \\ 0_2 \\ 0_3 \end{pmatrix} = \begin{pmatrix} \frac{R-G}{\sqrt{2}} \\ \frac{R+G-2B}{\sqrt{6}} \\ \frac{R+G+B}{\sqrt{3}} \end{pmatrix} \quad \ldots\ldots\ldots\ldots (10)$$

Based on RGB with private visual processing opponent colors like blue, red/yellow and Green represented at end points o1 and o2 of color space from eq 9 & 10. As seen above equation combination of red and green or bluish yellow then it is represented with co-occurrence of colors with opponent colors. Then transmission of polarity between endpoints with color space intensity is described as

$$CHI = \begin{pmatrix} \phi_1 \\ \phi_2 \\ \phi_3 \end{pmatrix} = \begin{pmatrix} \tan^{-1}(\frac{o1}{o2}) \\ \sqrt{o_1^2 + o_2^2} \\ o_3 \\ \end{pmatrix} \quad \ldots\ldots\ldots\ldots (11)$$

ϕ_1 be the hue component function on both invariant color space effects on shading of Cancersubcancer drug data set at secular direction. ϕ_1, ϕ_2, ϕ_3 are the hue component, saturation component and intensity component on invariant color space based on color huge intensity from eq (11). Based on this equation evaluate saliency function with respect to magnitudes of gradient, color saliency function is necessary because of different opponent co-occurrence probabilities between color vectors, it is color boosting function which are having equal maintenance of saliency colors then saliency function (sf) at attribute position (a) is described as

$$sf_a = H_\sigma(f(g_a), f(g_b)) \quad \ldots\ldots\ldots\ldots (12)$$

H_σ be the hue saliency function on scale σ and g_a & g_b are the functions relates to gradient at b,a color vectors at attribute location (a) from eq (12), then it is transformed into estimation of gradient saliency function such that

$$q(g_{1,a}) = q(g_{2,a}) \leftrightarrow \| f(g_{1,a}) \| = \| f(g_{2,a}) \| \quad \ldots\ldots\ldots\ldots (13)$$

$g_{1,a}$, $g_{2,a}$ are the gradient functions at direction of color vectors of CancersubCancersubcancer drug data sets based on eq (13), this estimation transformation function is derived from distribution between colors which can be represented as ellipsoid on 3-dimensional color ellipsoid function is described as

$$\left(\alpha v_a^1\right)^2 + \left(\beta v_a^2\right)^2 + \left(\gamma v_a^3\right)^2 = R^2 \quad \ldots\ldots\ldots\ldots (14)$$

V be the vector and its transmission functions like $v_a^{1,\ldots n}$, on different gradient functions with associated color space from equation (14), this color association gives transmission of saliency color space aligns at attributes in subCancersubcancer drug data set. This is used for disease identification over gradient color vectors.

Input: Input subCancersubcancer drug data set from different Cancers.
Output: Cancer disease detection Cancersubcancer drug data set with scalar functions
S1: Based on above procedure, evaluate dimensionality reduction with
S2: Evaluate the features of explored subCancersubcancer drug data set based on scale invariant feature transform from selected region is explored as

$$R = \left\{ h \mid \left(\hat{a}(h) > \hat{a}(h-1) \right) \& \left(\hat{a}(h) > \hat{a}(h+1) \right) \right\}$$

Where R be the Region of all the attributes present in Cancer disease detection

S3: Identify the threshold of all Cancersubcancer drug data sets with attribute locations from classified region is

$$K = \left\{ h \,|\, \left(\widehat{a}(h) > \widehat{a}(h-1) \right) \&\& \left(\widehat{a}(h) > \widehat{a}(h+1) \right) \right\}$$

Where K be the all the attribute threshold of Cancersubcancer drug data set based on height and weight ofCancersubCancersubcancer drug data set

S4: Remove all the background attributes

$$\widehat{a}(h+1) \neq \widehat{a}(h-1)$$

S5: Check each foreground and background attributes values

If (h is high) &

Where R=R-h;

$$\widehat{a}(h+1) \neq \widehat{a}(h-1)$$

If (h is low)& then K=K-;

S6: Based on interaction values of all the attributes in Cancersubcancer drug data set evaluated and represented as

$$\{[1, i_1], [2, i_2], [3, i_3], ..., [n, i_n]\};$$

S7: Prediction of Cancer disease from subCancersubcancer drug data sets $P_1, P_2, P_3, ..., P_{|n|}$

Table 1.Algorithm 1 Procedure to predict Cancer disease from sub-Cancersubcancer drug data sets.

5. Color based Disease Point Extraction

Neighbor attribute position identification based on color gradient distribution of subCancersubcancer drug data set in matrix formation based oneq (14) is described as

$$m(a, \sigma_i, \sigma_d) = \left\{ \sigma_d^i, F(\sigma_i) \otimes \begin{bmatrix} K_a^2(\sigma_d) & K_a K_b(\sigma_d) \\ K_a K_b(\sigma_d) & K_b^2(\sigma_d) \end{bmatrix} \right\}(a) \quad \ldots\ldots\ldots\ldots\ldots\ldots (15)$$

$\otimes$ describes the convolution function, $F(\sigma_i)$ be the kernel size σ_i of gradient function, $K_a(\sigma_d)$ =i+ $F(\sigma_i)$ convolution derivative of region layers $K_a K_b$, K_a^2, K_b^2 are the multiplying matrix functions described in (15) . Elements present in matrix function is described as

$$K_a^2(\sigma_d) = \sum_{i=1}^{n} c_{i,a}^2 \sigma_d$$

$$K_a K_a(\sigma_d) = \sum_{i=1}^{n} c_{i,a}^2 (\sigma_d), c_{i,b}^2 (\sigma_d)$$

$$K_b^2(\sigma_d) = \sum_{i=1}^{n} c_{i,b}^2 \sigma_d \quad \ldots\ldots\ldots\ldots\ldots\ldots (16)$$

$c_{i,a}^2$, $c_{i,b}^2$ are the transformed color gradient channel on scale σ_d which represents a,battribute direction over subCancersubcancer drug data set from eq 15. Eigen vector representation of augmented matrix is represented as

$$e(a, \sigma_i, \sigma_d) = \det\left(m(a, \sigma_i, \sigma_d) \right) - \kappa . trace^2 \left(m(a, \sigma_i, \sigma_d) \right) \quad \ldots\ldots\ldots\ldots\ldots\ldots (17)$$

κ be the constant function at slope of subCancersubcancer drug data set zero value i.e. correlation between edge and corner of subCancersubcancer drug data set based on Eigen vector configuration described in 17. This function describes stable values are represented as noise and scale invariant function at random color. Based on this procedure next section describe the identification of disease from subCancersubcancer drug data sets based on scale invariant color transform functions.

6. Detection of Disease based on Scale Invariant Points

Based on above procedure, implemented scale invariant feature transform is carried out based on single saliency subCancersubcancer drug data set(I) function. Based on Eigen vector function, proposed approach takes no training Cancersubcancer drug data set templates but its self color channel generates the color distribution for gradient function. Then proposed algorithm process is described as, let us consider I be the subCancersubcancer drug data set and D be the color space consists color vectors i.e. $I_D = \{g_1, g_2, ..., g_m\}$ and for ever gi consists m components of color i.e. $g_i = [d_1, d_2, ..., d_m]$ which are represented with normalization of zero value of input Cancersubcancer drug data set from augmented matrix equation described in (eq.18). Then evaluate the Eigen value hue color vector g_i is represented as

$$g_i = g_i.e_1 \quad \text{..... (18)}$$

Then evaluate attribute feature variable for Cancersubcancer drug data set structure with removal of noise filtering function from eq (19) is defined as

$$\wedge_{a,\sigma} = \left[\left(\frac{\partial^2 \hat{I}}{\partial^2 \hat{I}} + \frac{\partial^2 \hat{I}}{\partial^2 \hat{I}} \right) \otimes F_{\sigma_d} \otimes \Gamma_{\sigma_d} \right](a) \quad \text{..... (19)}$$

Γ_{σ_d} be the symmetric circulated function which represented at each attributefromeq (10) of explored subCancercancer drug data set (a_e,b_e)

$$\Gamma_{\sigma_d} = \frac{1 + \left(\cos\left(\frac{\pi}{\sigma_d} \sqrt{a_e^2 - b_e^2} \right) \right)}{3} \quad \text{..... (20)}$$

Convolution of each patch Cancersubcancer drug data set layer gives based on Gaussian scale invariant decision with computational efficiency at different class label of Cancersubcancer drug data setattribute described from eq 20 at mathematical values are preferred as

$$\wedge_{a,\sigma_d} = \left\{ \left[\sigma_d^2 \mid K_a^2(a,\sigma_d) + K_b^2(a,\sigma_d) \mid \right] \otimes \Gamma_{\sigma_d} \right\}(a) \quad \text{..... (21)}$$

It is the well known corner attribute locations based on scale invariant feature transform at each subCancersubcancer drug data setattribute from eq 21. Scale feature functions are evaluated with processing time of Cancersubcancer drug data set which increases the size of kernel functions. Disease detection patch is explored based on scale variant extreme functions

$$\nabla \Lambda_{a,\sigma_d} = \nabla \Xi_{H,\sigma_d,a,\sigma_d} = o \quad \text{..... (22)}$$

The above equation shows different attribute locations in region extraction with their scale variant features which are explored from subCancersubcancer drug data set from eq (22). $\nabla \Lambda_{a,\sigma_d}$ be the largest Cancersubcancer drug data set structure which is explored from subCancersubcancer drug data set with processing time. This expression gives the exact disease point extraction from subCancersubcancer drug data set relates to different Cancers.

7. Experimental Evaluation

Out proposed approach is implemented using advanced deep learning framework with Java programming based on system configurations; we crop the original data into sub divided patch Cancersubcancer drug data sets which contain semantic dimensions with 256*256 attributes notations. Comparatively, we check our proposed approach with generalized learning abilities and we apply random left to right and top-bottom flipping in selection of transformation gradient factors.

7.1 Cancersubcancer drug data set Repository:

To evaluate the performance of proposed method is with carried experiments from Cancersubcancer drug data set repository. All the regional Cancersubcancer drug data sets are captured from different countries like China, India, and Province 2018-2021. Data Cancersubcancer drug data set repository consists 1500-2000 training and testing Cancersubdrug data sets, each Cancersubdrug data setattribute region is 4950*4950. All the Cancersubcancer drug

data sets are captured by using Cancersubcancer drug data sets repository compared to Arial Cancersubdrug data sets which are shown in Figure 5.

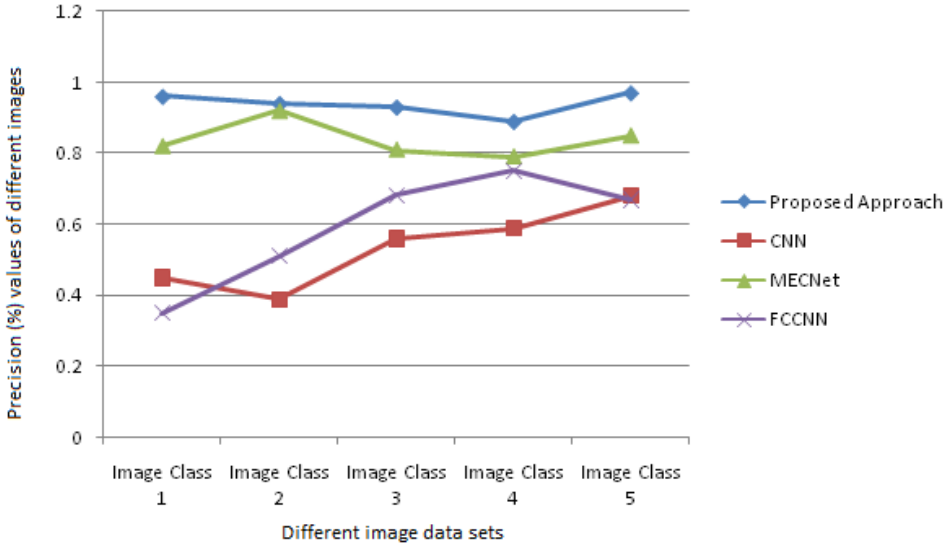

Fig.5. Performance of precision with different Cancersubcancer drug data set classes

7.2 Results of Cancer Disease Prediction

We compare our proposed approachNovel Heuristic Hybrid Model (NHHM) with different state-of-the-art methods like CNN, MECNet, Fully convolution connected neural network (FCCNN), and all these models are compared in terms of accuracy and other visual metric parameters from real time Cancer sub drug data sets. Table 1 shows the different precision values to evaluate the Cancer sub cancer drug data sets for prediction from different Cancer sub cancer drug data set cancer drug data sets.

Precision				
cancer drug data set datasets	Proposed Approach	CNN	MECNet	FCCNN
Cancer drug data set 1	0.96	0.45	0.82	0.35
Cancer drug data set 2	0.94	0.39	0.92	0.51
Cancer drug data set 3	0.93	0.56	0.81	0.68
Cancer drug data set 4	0.89	0.59	0.79	0.75
Cancer drug data set 5	0.97	0.68	0.85	0.67

Table 2. Different Precision values.

As shown in Figure 5, it shows the performance of precision of proposed approach with comparison to traditional approaches, we performed different Cancer sub cancer drug data sets and compare different approaches. When increase different Cancer sub cancer drug data set classes then proposed approach gives almost 97-99% precision which means exact matched layout contains disease where as other approaches gives less performance in matching of water prediction of satellite Cancer sub cancer drug data sets.

Recall				
Cancer drug data setCancer drug data sets	Proposed Approach	CNN	MECNet	FCCNN
Cancer drug data set 1	0.96	0.52	0.81	0.51
Cancer drug data set 2	0.97	0.46	0.86	0.46
Cancer drug data set 3	0.98	0.61	0.86	0.56
Cancer drug data set 4	0.92	0.65	0.74	0.54
Cancer drug data set 5	0.99	0.59	0.96	0.46

Table 3. Different recall values.

Table 2 and figure 6 gives the recall performance of proposed approach with traditional approaches with comparison to different Cancersubcancer drug data setcancer drug data sets. Whenever improve Cancersubcancer drug data set class cancer drug data sets proposed approach gives 99% from average Cancersubcancer drug data sets.

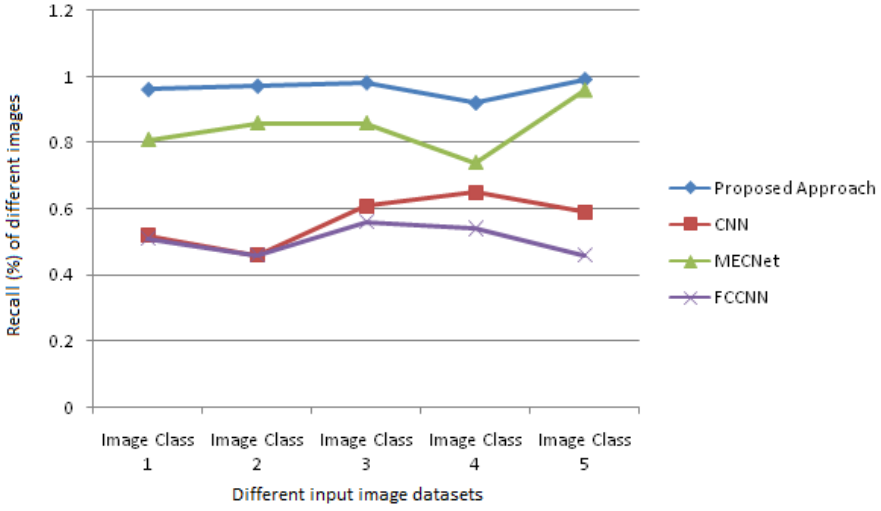

Fig.6. Performance of recall with different Cancer sub cancer drug data sets

Whereas other methods give fluctuations in getting efficient recall from different satellite Cancersubcancer drug data sets. Table 3 describes the values related to f-measure with Cancersubcancer drug data set classes relates toCancersubcancer drug data sets.

	F-measure			
Cancersubcancer drug data set datasets	Proposed Approach	CNN	MECNet	FCCNN
Cancer drug data set 1	0.96	0.72	0.91	0.84
Cancer drug data set 2	0.97	0.64	0.96	0.76
Cancer drug data set 3	0.97	0.81	0.89	0.79
Cancer drug data set 4	0.98	0.86	0.95	0.81
Cancer drug data set 5	0.99	0.79	0.91	0.78

Table 4. F-measure values

As shown in figure 7, it shows the performance of proposed approach with traditional approaches, whenever we give no. of Cancersubcancer drug data sets then NHHM gives better performance compare to CNN, FCCNN and MECNet.

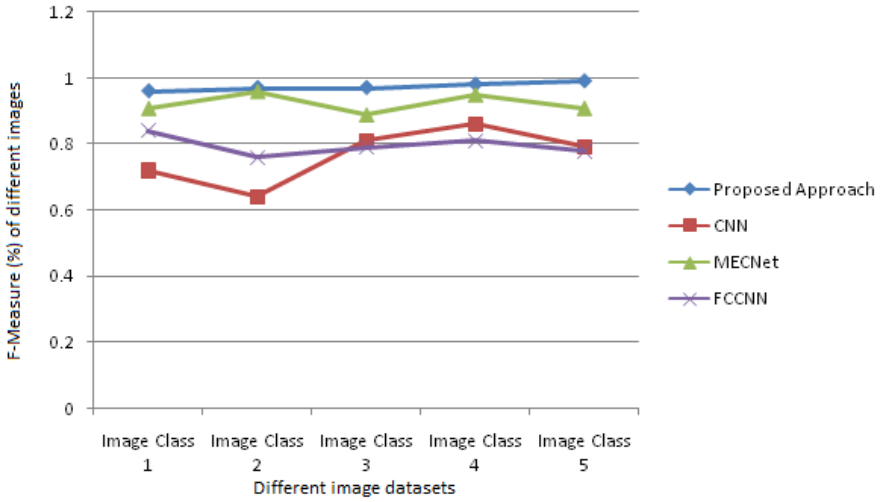

Fig.7. Performance of f-measure in processing of different Cancer sub cancer drug data sets

Cancersubcancer drug data sets are increased then processing of matched content is high in NHHM i.e. it near to 100 % compares to state-of-the art methods. It mainly depends on precision and recall, if these parameters are increase then automatically f-measure increased in proposed approach and all approaches. Table 4 shows the values related to time duration to process overall execution and prediction of Cancer disease from subcancer drug data sets.

	Time Efficiency			
Cancersubcancer drug data set datasets	Proposed Approach	CNN	MECNet	FCCNN
Cancer drug data set 1	5.1	9.2	5.1	7.2
Cancer drug data set 2	4.6	8.6	5.6	6.2
Cancer drug data set 3	5.6	9.1	6.4	6.8
Cancer drug data set 4	5.4	7.5	7.4	5.4
Cancer drug data set 5	4.6	9.6	6.5	6.7

Table 5. Different time duration values.

Figure 8 shows the performance of proposed approach in terms of overall time duration when compare to traditional approaches.

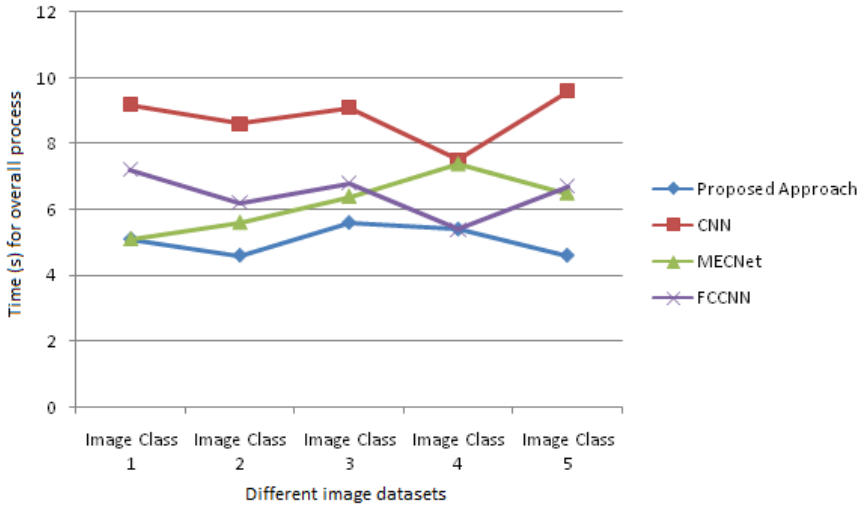

Fig.8. Performance of Time duration to process different Cancer sub cancer drug data sets.

Time duration for proposed approach is very less when compare to CNN, FCCNN. These approaches take high time because of iterations performed to evaluate prediction of water body from Cancer sub cancer drug data sets, where as MECNet gives very equal time duration to process all the Cancer sub cancer drug data sets.

Table 6 shows the IoU values in processing of different Cancer sub cancer drug data sets with extraction of total attribute from region.

Table 6 Different IoU values.

IoU				
Cancer sub cancer drug data set datasets	Proposed Approach	CNN	MECNet	FCCNN
Cancer drug data set 1	0.91	0.82	0.81	0.81
Cancer drug data set 2	0.93	0.86	0.86	0.86
Cancer drug data set 3	0.92	0.71	0.86	0.84
Cancer drug data set 4	0.89	0.75	0.85	0.79
Cancer drug data set 5	0.94	0.89	0.90	0.86

Figure 9 shows the overall performance of Union of Attributes in processing of different satellite Cancersubcancer drug data sets related to remote sensing applications.

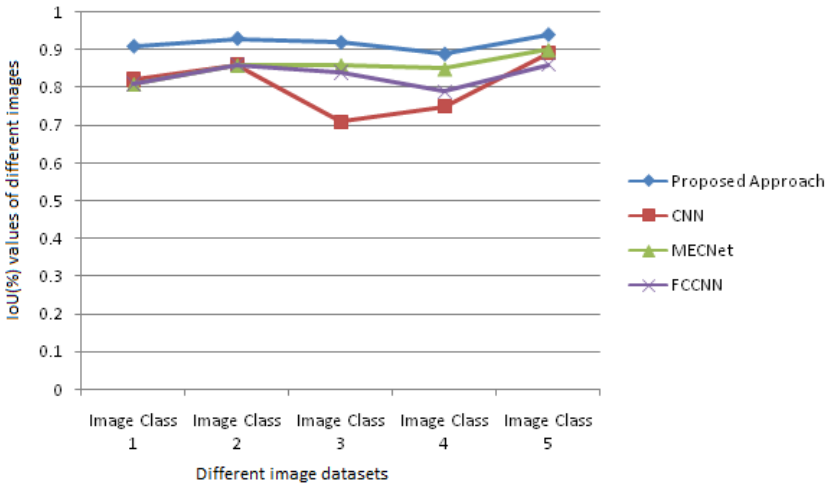

Fig.9. Performance of IoU in Prediction of satellite Cancer sub cancer drug data sets.

IoU mainly depends on precision, recall with efficient true positive and true negatives in selection of different features with processing of Cancer sub cancer drug data sets. Proposed approach gives better results when compare to CNN, FCCNN and MECNNET approaches.

Table 7 shows the values relates to overall accuracy which is related to prediction of sub disease from Cancer sub Cancer sub cancer drug data sets. It describes the efficient accuracy values when compare to traditional approaches.

Accuracy				
Cancer sub cancer drug data set datasets	Proposed Approach	CNN	MECNet	FCCNN
Cancer drug data set 1	84	71	68	69
Cancer drug data set 2	96	61	81	62
Cancer drug data set 3	92	76	76	75
Cancer drug data set 4	89	60	84	63
Cancer drug data set 5	93	67	88	71

Table 7.Final prediction accuracy values.

Overall accuracy of proposed approach gives almost 99% when compared to traditional CNN, FCCNN and MECNET; MECNET almost gives better performance with proposed approach whereas other approaches give less accuracy compare to NHHM.

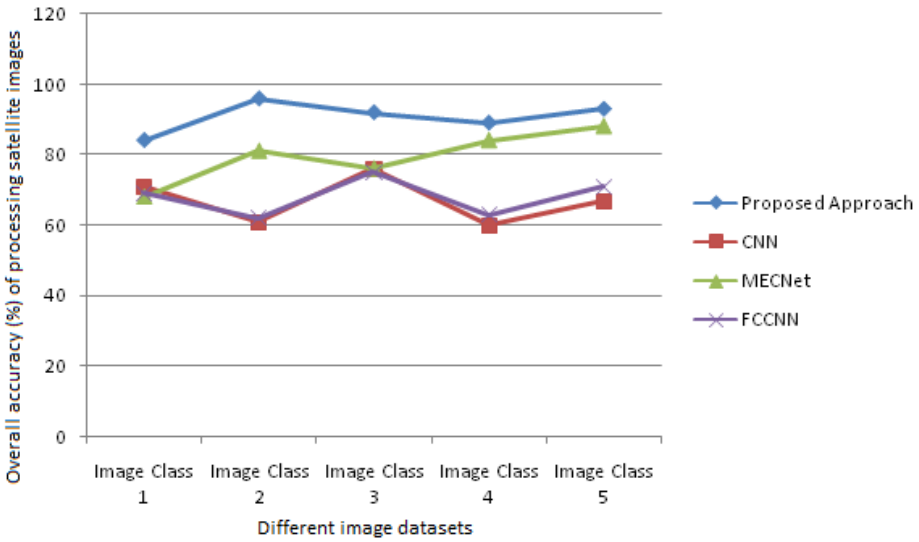

Figure 10.Performance of overall accuracy in CancersubCancersubcancer drug data sets.

Based on above figure 10 performance metrics with comparison to different approaches, proposed approach gives better and efficient results when compare to traditional approaches developed for prediction of disease from Cancersubcancer drug data sets.

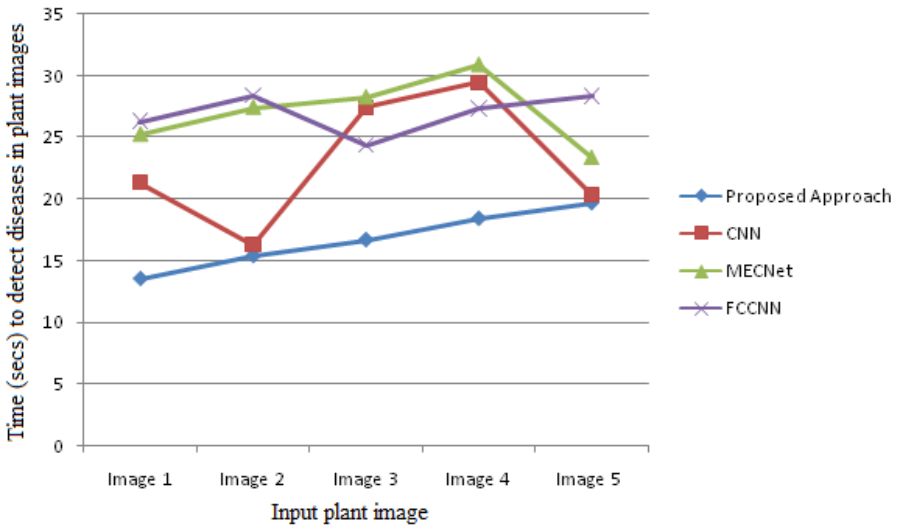

Figure 11.Performance evaluation of time with respect to Cancer disease detection.

As shown in figure 11, it describes the overall performance of time with respect to detection of Cancer disease detection while increasing the Cancersubcancer drug data sets, performance of proposed approach gives better and efficient when compare to traditional approaches. CNN, FCCN almost having high time in detection of Cancer diseases from Cancersubcancer drug data sets.

Time (Secs) Cancer Disease Detection				
Cancer drug data setCancer drug data sets	Proposed Approach	CNN	MECNet	FCCNN
Cancer drug data set1	13.56	21.32	25.24	26.32
Cancer drug data set2	15.42	16.31	27.45	28.41
Cancer drug data set3	16.72	27.39	28.28	24.38
Cancer drug data set4	18.45	29.44	30.92	27.35
Cancer drug data set5	19.72	20.33	23.35	28.35

Table 6Cancer disease detection time values

As shown table 7, it shows the time values of Cancersubcancer drug data set with respect to disease detection of different Cancersubcancer drug data sets. Table 8 shows detection of disease from Cancersubcancer drug data sets with respect to improvement of Cancersubcancer drug data sets.

Cancer disease detection ratio				
Cancer drug data setCancer drug data sets	Proposed Approach	CNN	MECNet	FCCNN
Cancer drug data set1	99.5	94.14	86.89	79.16
Cancer drug data set2	92.6	85.14	80.86	82.53
Cancer drug data set3	98.8	91.15	86.32	84.15
Cancer drug data set4	97.6	85.91	88.44	79.23
Cancer drug data set5	99.4	87.42	85.08	83.71

Table 7.Cancer disease detection ratio values**.**

Whenever, increase the Cancersubcancer drug data sets then detection ratio also increases when compare to traditional approaches.

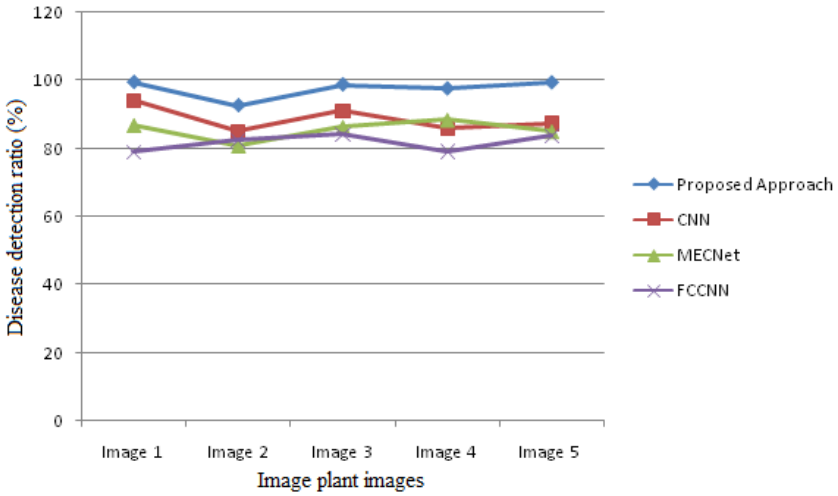

Fig.12. Performance of detection of with respect to Cancersubcancer drug data sets.

As shown in figure 12, it describes the performance of disease detection of Cancersubcancer drug data sets with respect to improvement of subcancer drug data sets. When increase the Cancersubcancer drug data sets, proposed approach gives better and efficient detection ratio when compare to traditional approaches. CNN, MECNET gives closely better detection ratio with respect to cancer drug data set dimensionality. But all approaches fails in detection because of color space dimensionality and layer extraction from patched cancer drug data sets from different Cancersubcancer drug data sets. Finally our proposed approach gives better and efficient quality in results when compare to other approaches.

8. Conclusions

Detection of disease in Cancers is aggressive challenge in scientific computer vision related application. Different computer vision related deep learning; machine learning approaches which are introduced by different researchers for the identification of disease from subCancersubcancer drug data sets. In this paper, we propose a Novel Heuristic Hybrid Model which is the combination of Self-Organizing Map (SOM) and Convolution neural networks (CNN) for automatic identification of disease in Cancers. Feature extraction is the major issue in identification of diseases in Cancers so that dimensionality reduction plays major role to filter noise from Cancersubcancer drug data set and separate the patch of Cancersubcancer drug data set which is impacted by disease is implemented in SOM. To explore color histogram based textual features present in Cancer and predict which patch is related to disease in Cancers is described using CNN. To test this approach results, proposed approach applied to identify diseases which are appear based on virus, bacteria in bio-technical applications. The proposed method gives 99.98 % accuracy in terms of prediction of Cancer disease from subCancersubcancer drug data sets compared to traditional techniques. Further improvement of our research continues to predict whether the sub consist disease or not with appropriate visual features in Cancersubcancer drug data sets.

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