A Review on Advanced Methodologies to Identify the Breast Cancer Classification Using the Deep Learning Techniques

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Abstract

Breast cancer is among the cancers that may be healed as the disease diagnosed at early times before it is distributed through all the areas of the body. The Automatic Analysis of Diagnostic Tests (AAT) is an automated assistance for physicians that can deliver reliable findings to analyze the critically endangered diseases. Deep learning, a family of machine learning methods, has grown at an astonishing pace in recent years. It is used to search and render diagnoses in fields from banking to medicine to machine learning. We attempt to create a deep learning algorithm that can reliably diagnose the breast cancer in the mammogram. We want the algorithm to identify it as cancer, or this image is not cancer, allowing use of a full testing dataset of either strong clinical annotations in training data or the cancer status only, in which a few images of either cancers or non-cancer were annotated. Even with this technique, the photographs would be annotated with the condition; an optional portion of the annotated image will then act as the mark. The final stage of the suggested system doesn't need any based labels to be accessible during model training. Furthermore, the results of the review process suggest that deep learning approaches have surpassed the extent of the level of state-of-of-the-the-the-art in tumor identification, feature extraction, and classification. in these three ways, the paper explains why learning algorithms were applied: train the network from scratch, transplanting certain deep learning concepts and constraints into a network, and (another way) reducing the amount of parameters in the trained nets, are two functions that help expand the scope of the networks. Researchers in economically developing countries have applied deep learning imaging devices to cancer detection; on the other hand, cancer chances have gone through the roof in Africa. Convolutional Neural Network (CNN) is a sort of deep learning that can aid you with a variety of other activities, such as speech recognition, image recognition, and classification. To accomplish this goal in this article, we will use CNN to categorize and identify breast cancer photographs from the available databases from the US Centers for Disease Control and Prevention.

Keywords: Convolutional Neural Network, Deep Learning, Mammogram, Prediction, Automatic Analysis of Diagnostic Tests.

1. Introduction

With the rise of the development of the computer imaging technology during the last few decades, three distinct techniques have been used to handle medical photographs. As for annual check-ups, the first step in increasing neighborhood understanding of screening and improving screening rates is increasing the general public's awareness. For the past few decades, we've been utilizing imaging tools to further see at the human body to see if they are ill. Nonetheless, image perception benefits rely on the expertise of experts and radiologists, particularly in the field of the efficacy of medical imaging. This CAD methodology gave a positive outcome as well, since it used machine learning methods to determine the expression of genetic biomarkers through X-ray imagery. Machine learning has undergone a steady evolution during the last few years to tackle challenging issues. when DCNN's design consists of convolutional layers, pooling layers, and a set of completely linked layers, performing feature extraction, and then feature down sampling.

In 2012, there were over 1.7 million female patients affected by breast cancer. The problem of breast cancer is increasing day by day, which is because in modern years health providers are not willing to provide all the knowledge to the sufferers to eliminate any potential complications from occurring. Digital mammography is a very important screening tool used in the world, especially for breast cancer diagnosis. As a result, the diagnoses of breast cancer have been very significant. While the detection of breast cancers has been conducted for more than 35 years using X-ray, Magnetic Resonance Imaging, and ultrasound etc. biopsy procedures are still the key approaches relied on to detect breast cancer correctly. Popular biopsy tips include using fine-point needles to aspirate body fluid, vacuum-assisted biopsies, and extraction by surgical incisions. By using an in situ method, we are able to collect samples of cells or tissues, fix them onto a microscope slide, and then stain them for inspection. If the researcher has studied the microscopic images, he will then interpret and make the diagnosis made by the pathologist. Computer Aided Detection Systems (CAD Systems) are designed in a way that have encouraging outcomes and perfect judgments on Patient's symptoms that enable medical and healing professionals to identify and manage disease.

In addition, the detection of breast cancer and its prognosis, in large part, depends on the computer-aided study of histopathological images. These problems include the difficulties of analyzing the quantity of water vapour particles and the rate of ionization of water vapour particles in the atmosphere. The first step in analyzing a cancer specimen is to get transparent and accurate microscopic photographs like three-dimensional images, and then, determine the fine-grained structure of the samples. Classification can be challenging due to heterogeneity within a class and continuity across classes, especially when working with many classes. To make E-learning more successful, The first issue is that feature extraction approaches for histopathology pictures of breast cancer have limitations Scale-invariant feature transform (SIFT) (Lowe, 1999) and grey level co-occurrence matrix(GLCM) are examples of traditional picture feature extraction approaches, all depend on supervised knowledge. Furthermore, to get facts about the data, you need to be aware of the data. This makes simplifying the data very complicated, which results in a very high computing load. In the end, only the lab extracted characteristics from histopathological images are just certain low level and unrepresentative structures. The final model's system for classification is vulnerable to distortion, making a poor final classification.

Deep learning algorithms can extract attributes from data automatically, retrieve information from it, and develop sophisticated abstract representations of it. Such tools have the potential to change life as we know it. They render feature extraction easier, have been successfully extended to machine vision, and can be used to solve conventional offline tasks. These problems include the difficulties of analyzing the quantity of water vapour particles and the rate of ionisation of water vapour particles in the atmosphere. The first step in analyzing a cancer specimen is to get transparent and accurate microscopic photographs like three-dimensional images, and then, determine the fine-grained structure of the samples. When working with several classes under a classification system, we should assume that classification accuracy can differ significantly from person to person and from class to class. To make E-learning more successful, the first issue is that feature extraction approaches for histopathological picture of breast cancer have limitations.
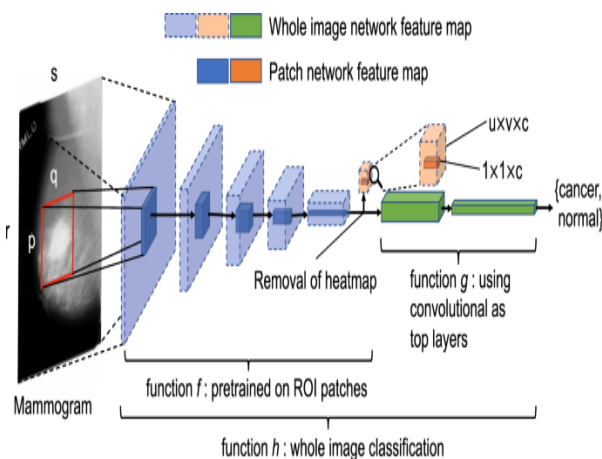

Fig.1 Image Classification

We briefly cover breast cancer and related screening approaches in this survey report. Finally, we looked at the several sorts of deep learning applications for breast cancer, such as feature extraction, detection, segmentation, prediction, and classification. The decision to focus on breast cancer for the survey was influenced by cancer statistics published by the World Health Organization in 2018, as seen in Table 1.

Table 1. World Health Organization 2018 statistical report through the global cancer observatory.

Cancer Type	New Cases (%)	Death Rate (%)
Breast Cancer	11.6	6.6
Colon Cancer	10.2	9.2
Brain Tumor	3.5	2.8
Cervical Cancer	3.2	2.5
Stomach Cancer	5.7	8.2
Liver Cancer	4.7	8.2
Lung Cancer	11.6	18.4

2. RELATED WORK

Breast Cancer
A specific form of this type of cancer in which there is an increase in the number of cells in the breast Cervical cancer is the most commonly diagnosed cancer in women and also the first type of cancer identified in the population of Ethiopia. There are four types of breast cancer: mass, malformation, spheroid, pericholigeroid, and two patterns: architectural distortion on one side or bilateral.

Screening Methods
This study by DeBecker et al.[11] begins with a general discussion about the possible benefits of screening for breast cancer, but does go on to explain the details of the procedure and anatomy necessary for breast diagnosis. film mammography (SFM), digital mammography (DM), ultrasound (MRI), and digital mammography, tomosynthesis (DBT) all provide for more accurate and thorough imaging of the breast in the chest than conventional screening.

Datasets
There are various imaging modalities for which medical research may be done, each of which might have a different dataset. Mammograms and histopathology databases are the most frequently found and most frequently used dataset for breast cancer research. In the table below, several of the more commonly encountered datasets are mentioned.

Table 2. Image datasets for breast cancer image analysis.

Dataset	Size	#Classes/Targets	Format	Type	Author/Repository, Year
MIAS	322	2	Pgm	Mammography	Suckling, J. et al. [14]

DDSM InBreast	55,890	410	npy XML	Mammography Mammography	Scuccimarra [15] Moreira et al. [16]
Breast Cancer Wisconsin	568	3	Csv	Mammography	Dua, D. and Graff, C. [17]
BreakHis	7909	2	Png	Histology	Bukun [18]
BACH/ICIAR2018	400	4	Tiff	Histology	G.Aresta [19]

The utility of deep learning for detecting breast cancer by means of diagnostic imaging techniques Two researchers Li Shen et al. [2] introduced a deep learning-based breast cancer detection algorithm, a technique for machine learning, that examines every mammogram from the Digital Screening Mammography (DDSM) and INBre databases from start to finish to detect the entire models. A model from the research team of ResNet-50 and a more complex model from VGG-16 were proposed in their article. It was analyzed in terms of AUC on the single-level and Averaging four (using ResNet and VGG, with the ResNet-based model, using VGG and the VNet, and both, VNet and ResNet) In this particular, the best single model in the DDSM dataset obtained a value of 0.88, while still becoming useful on individual images, and that gave rise to four models that increased to an even higher value of 0.91 with respect to sensitivity of 80.1 percent and accuracy of 80.1 percent. For INbre database, the best mean model per-imaging accuracy of 0.95 provided a sensitivity of 86.7% although an addition of two additional models improved accuracy to the other's, bringing it to a value of 0.98% of the target and the original

Wuṗ, et al. [20] designed a DCNN around four-based model to deal with breast cancer screening image classifications (i.e.p. AssRes22) Wu, et al. [20] suggested a four-column version of the DCNN, which was based on the MRI ResNet, for detecting breast cancer (iMRI) classifications There were more than two million examples for the current new DCNN model, which encompassed more than a thousand photographs to use in training and evaluate. Their success has a performance has an AUC of 0.95, which classifies the likelihood of breast cancer as applied to the screening community has a cutoff value of 0.895, which classifies that as equal to the performance of 14 radiologists, as radiologist, meaning that they all classify screening findings as accurate.

A 74-layer expansion of the Alzub learning strategy in order to expand the CNN made by Al Zubair et al. their model was trained on the same dataset prior to using the same domain representation (Images of peripheral blood smears samples taken from patients with Sickle Cell Disease can be found in the erythrocytesIDB collection.). Each part of the original image was then separated into 12 sections and majority vote labels were used to form a new images, where the most common section of the class is assigned to the identity of the image. Additionally, the model reached a degree of precision of 90.5% and a precision of 97.4% while considering the models' images. A way to resolve this will be to extend the scheme's categorization system to cover more than cells which normally include regular constituents and cancerous cells so that it can render a valid categorization seems doubtful.

The two neural network models [Zhu et al., 22] suggested two neural methods to quantify the risk of an infectious cancer on magnetic resonance images. The first strategy was a technique called transfer learning in which a GoogleNet's pre-trained model was used to evaluate whether cancer was present. Finally, the scientists obtained features from nature and then used a support vector machine to identify whether or not the sample photos were showing invasive disease. in terms of AUC, the generalization performance of the most beneficial for transfer learning, it was estimated to be around 0.53, and the best benefit for selected features to be 0.7.

Tucked within convolutional Cal breast Tom Li et al. [23] tested the capabilities of deep neural networks (DNN) and field of view digital mammography (FFDM) for mass classification with or the use of the whole breast imaged with training lacking. Additionally, they tried to discover a suitable strategy for classification by way of using a hybrid of dynamometry and fatigometry, or fatigometry. Instead of the the number of convolutional layers (like normalizing with VNC-12) they instead apply a 16-layer VGG network (a VGG-16) and a DCNN normalization procedure (ExtendedVDST) to photos in 2D and apply the DCNN to 3D imagery gold standard problems of the Concorde, Terra sigraph [average classifier output with best split- DC PCR applied on Terra sigraph's (3 classification problems:)], whereas the ADMM solution obtained a somewhat better overall on these problems, albeit with a lower precision and percentage of the true positives (better specificity but worse precision at 72 percent) and sensitivity (benign, malignant, normal).

Using the U-Net model, researchers sought to investigate the effects of data augmentation for classifying masses in 3D imaging on the volume analysis of breast tomoscopy images, with and without it were found to have different results. The U-Net model was more successful than the others, scoring 92.32% in sensitivity, 80.47% in precision, and 85.95% in accuracy for an AUC of 86.40.

The four different Deep Learning models which are derived from ResNetV were utilized for this project, along with two deep feature classes in a 2DnnIn feature engineering to create four different model classes, with ResNet as the dominant component and a patch for each This classifier had an AUC of 0.91 for determining benign and malignant masses, with a possible falsely classifying a massing 8.2 percent of the samples (sensitivity of 86.1%, and the corresponding possible miss rate for possibly benign masses was 8.2%) on the DDSM (data-set for).

Usage of U-net construction was used for the segmentation and feature extraction of fat tissue from the bone within the breast, with respect to non-fibrog legs and other organs outside the breast, as well as FGT with regards to other tissue of the whole legs. It was achieved for breast volume DSC of 0.95 and for FGT's measurement; and mean BSC was 0.97 and the coefficient of error was 0.95 for FGT's measurements.

Zhou et al. used 3D deep convolutional net (37-layer) with a CNN to localize lesionized images with a 3D DenseNet [Z-3D(DNN)] weakly supervised environment to apply extra details to current (DENSE) Deep Learning (DLS) at an image's dynamic contrast-enhanced MRI in a dataset [the 'local lesions diagnosed with dynamic contrast enhanced 3D-Modified Jacobi algorithm was 86.67 percent sensitivity, 68.3 percent precision, 0.5 percent negative predictive value, and 0.501 The algorithm's proposed

efficiency was found to be 86.7%/sensitivity 68.3%/specificity, 0.59%/specificity, and 0.503.5% distance.

Most large numbers of rules are calculated computationally more by complicated algorithms, contributing to both computational cost and the development of additional rules that could be superfluous. that uses a new association rule mining mechanism focused on Animal Migration as an association algorithm developed on Animal Migration suggested new rule mining system that integrates an association process that uses (AMO). the behavior-based Animal movement has served as a critical model for (and tool) for exploration of how much of the best algorithms in the process, rules which have a low overall support and those rules which are totally unrelated to the query will be omitted Only the rules that are likely to be seen frequently are recorded and shown. In order to have a greater number of rules created from the expanding fundamental laws, all of these properties are incorporated into the fitness function of the AMO. In comparison to the existing algorithm, ARM-PS, the new ARM-AM algorithm reduces the number of rules by a large amount while having a significant impact on overall system performance and memory usage. Led by three researchers to the task of classifying histopathological images, with several image input scales and feature spaces being employed in a CNN, had the result of producing the network analysis shown they concatenate four exponential magnitudes ($1 \times$, $0.5 \times$, $0.33 \times$, and $0.25 \times$) as well as the cell-variant scale (zero-to-to-one) normal and cell-fixed (one-to-one) exponential (this image's normal) values and use them as the network input This dataset was used as a training and validation set for the model proposed in ICIAR2018 and BreakH. The IC2018 dataset was successful in training a model with a model with a mean accuracy of 0.83, and the BreakHis data, yielding a greater accuracy of 0.98. While the overall ICI2018 model's accuracy was 60% on the ICIAR dataset, the only breakdown they could use was between 1, 2 class, which they called 'red undistributed accuracy.'

Rather than the in [as opposed to] the addition of the 4th pooling layers of Densen, they modified the Dense-121 and the Squeeze-excitation (SEN) modules by removing the pooling process of squeezing and pooling of feature maps and feeding the resultant images to the Squee-extracted breast histopaths directly to the integration (DET) system. expanding their sensory net, they activate their SEN in a channel-centric way after compiling each sentence as a SENet, they constructed a full-connected layer to use as a classifier They used a previously learned architecture, as a pre-training data for their architecture utilizing the transfer-learning technique. as a statistic shows shows the public dataset used in BreakHer so they achieved an accuracy of 88% with regards to different levels of magnification. This procedure relies on an LSTM model of Yan et al. used to classify histopathology images into 4 types of natural, intrusive, and in situ: picture Google's Inception-v3 model was used for classification of images in their classification pipeline, as part of an approach that utilizes an LSTM system to classify histopathological images. The Inception-3 model was tuned to boost the functionality. The model was moderately successful, achieving an average accuracy of around 91% on the ICIAR dataset.

Sharma et al. (a team of researchers) studied pre-trained feature extractors from cancer pathology images to see if they could identify patterns that were related to breast cancer.[32] They implemented transference learning over the pre-existing convolutional convolutiona networks (VGG16, VG-19, and ResNet50) by using these as feature extractors. SVM was applied to the extracted features and classified them based on its result Three models emerged that had an accuracy (measured by percentage of the total number of correct predictions) of 93.97%, 92.92%, 91.23% and 91.79% respectively for the expansion of the VGG16 network, each increasing the network's scale by 40 times, but at different factors.

This method calls for a combination of classifier and reinforcement learning in normal, benign, and in situ classes to be more complex because of the introduction of ensemble and refined ensembles, which lead to highly nuanced results: (plethora of) classifications (intentions). A majority voting ensemble system was applied, followed by gradient boosting (GBM) machine learning (ML) and logistic regression to predict the image level. offered both of these patients showed no response to one class of painkillers and one class of painkillers failed to produce an effect on them (benign and normal). As feature extractor results were added to the other models, the normal and benign prediction methods were fine-tuned to take advantage of the dual path resolution, the resulting models were both had increased in sensitivity In addition, the collected features were transferred to the next level of ensemble prediction fusion using GBM, logistic regression, and support vector machine (S) for model development. This was quantified based on measurement and the results obtained were graded as being correct with a grade of 87.5 percent.

3. RESEARCH OBJECTIVE

This paper presents an overview of different deep learning based approaches used for mammography and breast histology and proposes a bridge between these two fields employing deep learning concepts. We have focused on mammography, since this is the most common modality used in breast screening, and H&E stained histology, since it is considered as the gold standard for final decision making.

The main objectives of this paper are:

To develop a deep learning based model that can be introduced and their fundamental structures could be summarized. To create a model that can recognize histopathological images of breast cancer that are fine-grained, high-resolution images with complex geometric shapes and textures. The next challenge is to reduce the limitations of feature extraction methods for histopathological images of breast cancer and improve the accuracy in deriving the features. To extract prior data knowledge in order to select useful features with high feature extraction efficiency and low computational load. Finally, the retrieved features are simply a few low-level and non-representative aspects of histopathology pictures. Finally, a good classification results to be obtained for stating the accuracy of the breast cancer.

4. RESEARCH SCOPE

Also, we would try to deploy the combining deep learning with clustering and utilizing the dimension-reduction functionality of the auto-encoder network, by proposing a new auto-encoder network structure to apply non-linear transformations to features in histopathological images of breast

cancer extracted from the dataset. This effectively maps the extracted features to a lower dimensional space. The newly obtained features are then used as input for the classical clustering algorithm known as K-means to perform clustering analysis on histopathological images of breast cancer. Also, we would like to design a number of comparable experiments to verify the validity of our proposed method of histopathological image analysis of breast cancer images based on deep learning techniques. With the support of deep learning techniques, computer systems have improved their abilities to automatically extract features, collect information from big data automatically and learn the sophisticated abstract representations of data. With their low-noise characteristics and compact footprint, features derived from EOAS glasses can assist in the assessment of image sequences and patterns. A early understanding of the issue tackled through the use of tiny datasets for images, as well as machine-learning algorithms, which are more reliable than others but are comparatively low-performing. Much like deep learning can deal with massive volumes of data (huge amounts of data: huge data), it can generate even more complex features from data automatically, too.

We will also attempt to deploy the mixing deep learning with clustering and using the dimension-reduction capabilities of the auto-encoder network, by proposing a new auto-encoder network structure that would apply non-linear transformations to features of histopathological images of breast cancer derived from the dataset. This effectively decreases the retrieved features' dimensions to a lower-dimensional space. The features obtained from the 10K images are then interpreted by the next step called K-Means applied in the commonly used "Image for Sarcoma Location tool" to do some clustering analysis of such images. As well, We'd like to create an equal number of related tests to confirm the feasibility of our proposed deep learning-based method for histological image interpretation of breast cancer images.

5. METHODOLOGY

The System is developed using the classification and clustering schemas using the Convolution Neural Networks methodology.

5.1 Classification Analysis:

This segment will address our studies of classifying histopathological photographs of breast cancer using the deep learning models of Inception_V3 and Inception_ResNet_V2 as well as the analyses of our experimental findings.

5.2 Network Structures for Classification:

We used the Inception ResNet V2 (16 ResNets) along with an Inception V3 (V3 ResNet) along with a Seated 5 ResNet_V1 (5 ResNets) in the Inception_V2, and Seated 1 ResNet_V1 (1 ResNet) along with an Inception_ResNet_V2 (V3 ResNet) in the Inception V3. It has been shown in the ILSVRC rivalry with big data that Inception_V3 ResNet_V2 will beat the Inception V3 network when added to big data. Unlike the previous algorithm, ResNet-101 is loaded with redundant connections. These unwanted connections can be eliminated to be more like a supervised neural network. In this research, these two networks are used to classify histological images of breast cancer in order to see if the experimental findings from Inception ResNet V2 are

superior to those from Inception V3 on small datasets.The network architecture as seen in the following Figure 2.

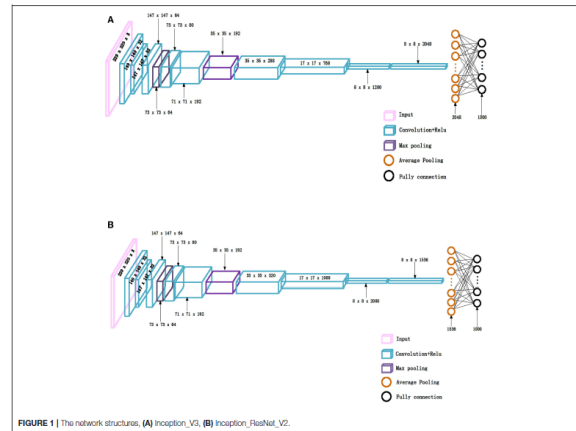FIGURE 1 | The network structures, (A) Inception_V3, (B) Inception_ResNet_V2.

Fig 2: Network structure

This could be shown from Figure 2, which is seen in the next image, that the configurations of the two networks are very close. The first few layers are typical transformations through convolutional and pooling layers, and the middle section is made up of several Inception modules stacked together. The Soft max function was applied once the fully-connected layer was trained, and the output was revealed. The varied structure of the Inception _V3 (Inception V3) and Inception ResNet (Inception ResNet) networks is one of the fundamental differences between the two networks. Inception modules. The Inception V3 network is comprised of numerous subsets of the traditional Inception network: 1×1, 1×3, 3×1. A miniature and reduced variant of the normal 3×3 convolver will be created to allow the network to learn in a wider range of data sets. In the Inception Resnet V2 network and its several layers, as the network gets more and more layers, the likelihood of two neurons in the same community converging to the same performance decreases, as the shift in metrics, such as surprise, are kept constant. To compensate for this, a residual module is often introduced after each layer for each Inception network using various types of filters.

5.3 Clustering Analysis:

The previous section described a deep convolutional neural network-based categorization analysis of histopathology images of breast cancer. About how difficult and daunting it sounds, the task of classifying images into the healthy or malignant category is very straightforward and shouldn't require a doctor's expertise. It really is only a matter of looking at the images and accurately assigning them to the category. This is a difficult, time-consuming, and expensive task, especially given the increasing amount of samples in the dataset. Unsupervised learning, particularly clustering, on the other hand, does not require any marks for the samples it works with. It simply organizes the samples into clusters based on their associations, in such a way that the samples in the same cluster are identical and dissimilar to the samples from the other clusters. As a follow-up to this, we have selected clustering methods to study the histopathological images of breast cancer.

Network frameworks for cluster analysis. Because of its success in reliably handling these pictures, the Inception ResNet for V2

network is used to construct the features for rating highly the histological images of breast cancer.. while scoring using the benefit of extracting features automatically from the images. The retrieved features of the 1,536-dimension vector generated by the Inception ResNet V2 model before its last classification layer can well represent the anomaly function of each histological picture of breast cancer. In order to perform clustering analysis on the histopathological pictures of breast cancer, the obtained feature vectors are fed into a clustering algorithm.

One of the key clustering studies is to describe clustering's using one of the most basic, normal clustering algorithms, "K-means." In order to find the proper value of K for the K-means algorithm, we follow SSE (Silhouette Score) as the internal criterion, and select the K (K-means clustering) as the optimal value. The features collected by the Inception ResNet v2 network for breast cancer histological images can be considered of as a representation of the images, and the breast cancer histopathological images are clustered using the K-means clustering technique.

5.4 Transfer Learning

Deep learning is the product of computer learning or data mining. Deep learning is currently being suggested to do tasks that were historically only feasible for people, such as learning unstructured data from unstructured data sources. Furthermore, there is no preparation that can be used to build the provide a network framework for a particular mission. What we can do is leverage the model and parameters developed by other researchers through time-consuming and computationally costly training on Image-extremely Net's large image dataset as pre-training for our own model. Particular research mission. Then, we will train the deepest layers of our network using very little details, and these layers can produce a good outcome for our target mission. These layers will be the last layers of our network.
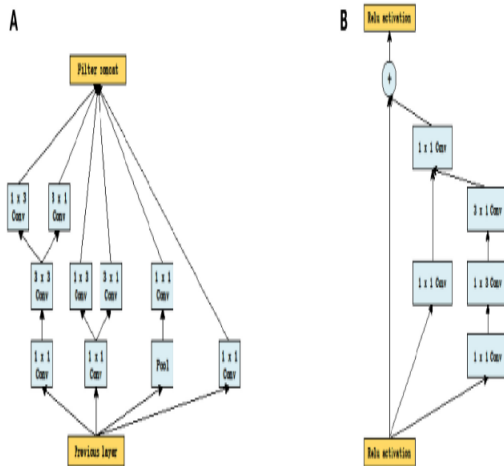
| The inception module of size 8 × 8 in two networks, (A) Inception_V3, (B) Inception_ResNet_V2.

Fig-3: Inception Model

This paper relies on earlier transfer learning research to create an implementation of the Inception V3 and Inception ResNet V2 networks for breast cancer tissue classification.

6. CONCLUSIONS AND FUTURE WORK

In this paper, state-of-the-art deep learning techniques for study of brain tumors, malignant tumors, and colon images are reviewed. Combining several technologies, the CNN solution was used to meet the current task in order to learn massive dataset requirements. Breast, cervical, and colorectal analysis, also hads have been accomplished in several of the above works through the use of normal photographs and dataset samples that cover two or more architectures. This paper would suggest the advanced approaches for the study of histopathological photographs of breast cancer. This will be achieved by using deep convolutional neural networks with 1024 and 2048 layers and equipped using transfer learning from Inception_V3, Inception_ResNet from Image Net. In the Image Net dataset, these two networks are pre-trained., which includes labeled photographs from animals, humans, and things. When this occurs, the learned configuration and parameters of the memory are frozen. Number of neurons in each of the layers of the completely connected deep learning network are set according to the problem that we want to solve, and then the layer parameters are modified. The machine learning approach can be used to perform binary or multi-class recognition of histological pictures of breast cancer in order to do this.

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