

# VGGIN-Net: Deep Transfer Network for Imbalanced Breast Cancer Dataset

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**Abstract—** In this paper, we have presented a novel deep neural network architecture involving transfer learning approach, formed by freezing and concatenating all the layers till block4 pool layer of VGG16 pre-trained model (at the lower level) with the layers of a randomly initialized naïve Inception block module (at the higher level). Further, we have added the batch normalization, flatten, dropout and dense layers in the proposed architecture. Our transfer network, called VGGIN-Net, facilitates the transfer of domain knowledge from the larger ImageNet object dataset to the smaller imbalanced breast cancer dataset. To improve the performance of the proposed model, regularization was used in the form of dropout and data augmentation. A detailed block-wise fine tuning has been conducted on the proposed deep transfer network for images of different magnification factors. The results of extensive experiments indicate a significant improvement of classification performance after the application of fine-tuning. The proposed deep learning architecture with transfer learning and fine-tuning yields the highest accuracies in comparison to other state-of-the-art approaches for the classification of BreakHis breast cancer dataset. The articulated architecture is designed in a way that it can be effectively transfer learned on other breast cancer datasets.

**Index Terms**—VGG16, pre-trained model, Inception module, transfer learning, deep learning, convolutional neural networks, fine tuning.

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## 1 INTRODUCTION

Cancer is a grievous health problem that affects both developed and developing countries [1]. Breast cancer is one of the most commonly found cancer in women. There are certain challenges faced while diagnosing cancer manually from the Histopathological biomedical images due to a high probability of inaccurate detection that might occur due to human error. In order to avoid the manual time consuming task for diagnosis of cancer, a computer-aided diagnosis system is required which automates the process efficiently. Various automated processes are already available to distinguish the Malignant and Benign cancer images [2]. Deep learning has further improved the performance of the automated process for the diagnosis of cancer at the early stage. The role of deep learning in various applications has increased tremendously with the recent advancements in computational hardware accelerators and parallel processing. Health care and biomedical are popular fields where deep learning has shown remarkable improvements [3].

The core of the deep learning architecture is the convolutional neural network (CNN) [4]. Basic CNN architecture consists of various convolutional building blocks stacked together for automating the process of feature extraction and classification, unlike machine learning where both the steps are performed separately. Broadly CNN networks are categorized into (i) networks

which are trained from scratch, and (ii) the pre-trained networks [5] which are trained beforehand on a large dataset facilitating the transfer of knowledge from one domain into another.

A common problem associated with real-world datasets is the class imbalance problem. It is a challenging task to tackle the imbalanced dataset due to the disproportionate distribution of samples of different classes. The BreakHis breast cancer dataset is an instance of an imbalanced dataset with the Malignant samples outnumbering the Benign samples. The imbalanced nature of this dataset [6] brings in several challenges as the class imbalance problem causes several incorrect predictions. So there is a need to have a model which can handle the class imbalance situation effectively and will be able to correctly detect cancerous patterns from bio-medical data. In order to tackle this problem, we have proposed a novel deep learning based architecture incorporating transfer learning in this paper. The transfer learning approach using pre-trained networks has the advantage of transferring the learned weights from an architecture which is trained on another domain to the biomedical domain, which will ultimately reduce the training time and computational cost required to train the model from scratch. The contribution of the paper can be summarized as: (a) Successful design of novel deep network architecture using transfer learning approach to solve

class imbalance problem in breast cancer datasets. The proposed architecture is created by combining the relevant layers from VGG16 pre-trained network (layers till block4 pool layer) along with the naïve Inception module in combination with flatten, batch normalization and dense layers. Also, certain regularization techniques have been infused in the proposed model such as data augmentation and dropout which overall helps to reduce the overfitting to a great extent. (b) The proposed network has been successfully tried and tested on images of different magnification factors: 40X, 100X, 200X and 400X, establishing the network's invariance to size and scale of the image. The results indicate an overall improvement in the classification performance in comparison to other state-of-the-art approaches. (c) We have analyzed the effect and significance of block wise fine-tuning on the proposed deep transfer neural network architecture which has substantial impact on the classification performance. (d) The proposed 24 layer network architecture has been articulated by integrating the right combination of layers in well-ordered way to reduce the computational complexity involved. The formulated network architecture is designed in the way that it can be successfully transfer learned on other breast cancer datasets.

The various sections of the paper are summarized as follows. Section 2 describes the state of the art in the fields of machine learning and deep learning for breast cancer diagnosis. In section 3, the architecture and learning methodology used in the proposed work are discussed in detail. Further, in Section 4, a discussion regarding the datasets used in the experimental task along with the implementation details have been presented. In section 5, the final analysis and discussion on results related to the classification task performed and comparison with other state-of-the-art networks is presented. The final conclusion is given in the last section of the research paper.

## 2 RELATED WORK

Various machine learning and deep learning based networks have been proposed for detecting cancerous patterns from cell images [7]. In [46], authors had proposed an appropriate feature-classifier combination for multi-class imbalanced datasets by extracting the deep features using visual codebook generation along with the non-linear Chi2 SVM classifier. A number of studies have been reported in the literature using CNN for classification of medical images. Spanhol et al. (2016) used patches, extracted by applying the sliding window mechanism in order to efficiently train CNNs [8]. Feng et al (2018) had also focused on the patch based learning from images so in order to emphasize on the reduction of complexity of the network by reducing the number of parameters [9]. Bayramoglu et al. (2016) proposed single-task and multi-task CNN models for the classification of BreakHis Histopathological dataset [10]. Bardou et al. (2018) had compared various configuration combinations of CNN with other traditional approaches. They have also emphasized the role of data augmentation operations on the performance of the model. From the

results analysis, it was validated that the deep features extracted using CNN outperforms the handcrafted features [11].

In order to tackle the class-imbalance problem which occurs due to an unequal distribution of samples in the dataset, several methods have been suggested in data mining such as undersampling, oversampling and hybrid sampling strategies [12],[13]. Data augmentation operations can be applied on minority class and majority class, or it can be applied separately on the minority class [14] [43] in order to make the samples of the minority class equivalent to the majority class. In [43], the authors had increased the number of samples in the minority class using the Deep Convolutional Generative Adversarial Network (DCGAN) by synthetically generating the fake samples, and the augmented dataset was learned using a modified VGG16 based architecture. In previous work, comparison of BOVW, deep neural networks and data augmentation for the imbalanced computer vision dataset was presented in [15]. It was observed from the study that the deep neural network mitigates the effect of class imbalance in the most effective manner. Traditionally, the methods that are used to tackle the class-imbalance problem modify the data distribution, which can be challenging for medical datasets as it may cause loss of relevant information. Ding et al. (2017) demonstrates that the use of very deep networks (models with more than 10 layers) improves the network training process and achieves better rate of convergence for imbalanced datasets [45]. The authors experimentally validate the claim by using deep network architectures which are trained for 100 epochs in comparison to shallower networks. There are other relevant approaches also proposed by researchers to deal with the imbalance situation such as Abbas et al [44] had proposed a Decompose, transfer and compose (DeTraC) model using the concept of class decomposition within CNN approach, which helps to learn the class boundaries effectively. The classification task is performed after ensuing the error correction criteria applied to the softmax layers of the network which indeed had improved the classification performance.

Different pre-trained networks have been used before by many researchers to detect cancer patterns. Rakhlin et al. (2018) had worked upon the ICIAR 2018 Grand Challenge on Breast Cancer Histology Images by extracting deep features from the pre-trained networks, that were trained using the gradient boosted trees classifier [16]. Deniz et al. (2018) concatenated the features extracted from various layers of AlexNet and VGG16 pre-trained models. The deep features extracted from these layers were used in conjunction with support vector machine classifier for the classification of Benign and Malignant cancer images [17]. Gupta and Bhavsar (2018) had proposed a sequential framework which consists of deep multi-layer features extracted from fine-tuned DenseNet on BreakHis dataset. The deep features extracted from multiple layers were given to XGBoost classifier [18]. In our proposed transfer learning approach, we have created a new deep architecture by concatenating pre-trained layers at lower level with trainable layers at

higher level. The higher layer features are learned specific to the breast cancer dataset. This makes our approach distinctive from previous works since we focus on transferring general features from the lower layers of pre-trained large convolutional models while the higher-level features are learned specifically from the cancer dataset.

### 3 PROPOSED DEEP TRANSFER NETWORK: VGGIN-NET

A novel deep neural network architecture is proposed by concatenating the VGG16 architecture layers [19] with a single naïve Inception block [20], as shown in Figure 1. Inception block is a module which is popularly used in Inception architecture (a.k.a. GoogLeNet) [20]. We have presented a transfer learning approach involving the novel deep neural network architecture, that we have named as VGGIN-Net, which is formed by freezing and concatenating all the layers till block4 pool layer of the VGG16 pre-trained model (at the lower level) with the layers of a randomly initialized (using Glorot uniform distribution) naïve Inception module (at the higher level). Further, several randomly initialized higher layers are added such as the dense layer along with batch normalization, flatten, and dropout layers. The proposed architecture is created by concatenating the layers as shown in Figure 2. The new deep network is now trained on the breast cancer dataset.

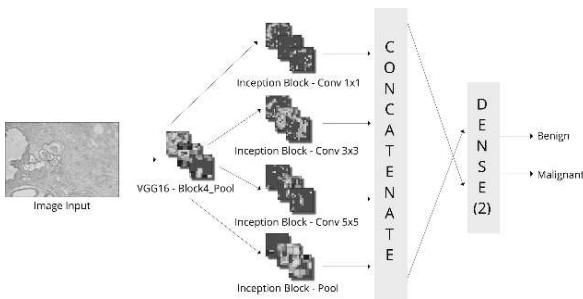


Figure 1. Proposed deep network architecture VGGIN-Net showing the lower layers till block4 pool layer of VGG16 pre-trained network and the higher layers comprising of naïve Inception module and the dense layers.

The 24-layer architecture is constructed as shown in Figure 2 by first stacking the VGG16 layers, starting from the VGG16 pre-process layer till the block4 pool layers. The  $224 \times 224 \times 3$  image is given to the VGG16 pre-trained network as input. The reason for considering the features till block4 pool layers from the VGG16 pre-trained model is to extract the most relevant bottleneck features. Also, the consideration of features beyond the block4 pool layer would only increase the computational difficulties with improvement in the performance of the model, as validated by our experimental results. Further, the obtained relevant bottleneck features till block4 pool layer of VGG16 pre-trained network are concatenated with the layers of naïve Inception block. The naïve Inception block consists of convolutional layers having filters of sizes of  $1 \times 1$ ,  $5 \times 5$  and  $3 \times 3$ , with each layer having stride of size  $3 \times 3$  and ReLU (Rectified linear unit) activation function [21], with addition of max pooling 2D layer.

In this paper, we have considered the goodness of both the pre-trained models (VGG16 and Inception) to create a more robust architecture which effectively resolves the class imbalance problem. The use of VGG16 pre-trained layers in the initial stage of our network was motivated by the fact that VGG16 architecture achieves good accuracy for most of the image classification problems and this network is efficient in dealing with images of different scales and magnification factors. This is particularly useful for our study as one of the target datasets that we experiment with, is the BreakHis dataset which consists of images of varying magnification factors. Throughout our study, we do not introduce skip connections or depth separable convolutions as they are well beyond our scope of this study. The idea is to improvise the goodness of popularly used existing architectures through a sequentially stacked layer model and use of multi-level features that adapt better to histopathological datasets.

There are certain crucial deployment challenges faced in the VGG based architecture which motivated us to modify the VGG16 architecture. As inspired from the previous works [22],[23],[24],[25] we have modified the VGG16 architecture so as to overcome the deployment challenges that comes with VGG-Nets. Such computational challenges are prevalent even on powerful single-GPU systems (Graphical Processing Units) due to its large memory footprint. The sequential ConvNet, VGG16 bears a large number of parameters (140 million) due the presence of multiple convolutional layers of varying receptive fields, hence, it can become inefficient for inference at test time. Due to the large number of parameters, VGG16 network is also prone to vanishing gradient problem. The presence of three fully connected layers in the original VGG16 architecture is primarily responsible for the major bulkiness of the model. So we have extracted the relevant deep features upto block4 of the pre-trained model and removed all the layers after that which added extra complexity and computation in the proposed architecture. Further, to address the shortcomings seen in the VGG16 architecture, we have added the naïve Inception block as an additional block in the proposed architecture. The GoogLeNet incarnation of the Inception architecture uses multiple auxiliary classifiers connected to intermediate layers to tackle the vanishing gradient problem. In our case, any auxiliary loss has not been used to train the inception block because of the presence of lesser number of images in the currently used dataset in comparison to the large-scale ImageNet. The reason for the addition of a single Inception block in the higher layers of the proposed architecture is that it would not require auxiliary classifiers and the model can converge by itself using a single loss only. Also, it would be less computationally expensive to add a single Inception module instead of addition of multiple similar modules. The main idea behind adding the naïve Inception module in the higher end of our network is to cover a larger region of a convoluted image yet preserving the finer details. The naïve inception block is specifically engineered to convolve in parallel such that accurate detailing is

possible through  $1 \times 1$ ,  $3 \times 3$ ,  $5 \times 5$  convolutions (64, 128, 32 filters were used respectively). The goal of adding the naïve module is to increase the CNN's learning ability and abstraction of complex filters which was also found to be a drawback in VGG-based architectures. Moreover, the advantage of the Inception architecture is that it is able to perform well even with a single fully connected layer [20].

Our consideration of the naïve Inception block as a suitable choice along with a single dense layer makes the architecture less computationally expensive. A single dense (fully connected) layer with softmax activation function is present at the output to learn the proposed network architecture to deal with the higher end linear features and to find the probability of occurrence of the image belonging to each class for the two class classification problem (i.e. Benign and Malignant). Further, batch normalization, flatten, and dropout layers are added to enhance the network performance. We refrain from using multiple batch normalization layers

(one batch normalization per convolutional layer) as per inspiration from [26] as a single batch normalization should suffice when layers are being concatenated as in case of the Inception module. Flatten layer is added after batch normalization to reduce the features into one dimension of size 144256. Dropout regularization [27] with a rate of 0.4 is added after the flatten layer which in turn helps to avoid overfitting problems.

Our transfer network thus, facilitates the transfer of domain knowledge from the larger ImageNet object dataset [28] to the smaller breast cancer dataset in the lower layers itself, and learns the higher layer features specific to cancer images. In doing so, we follow the guidelines of Yosinski et al. (2014) [29] who propounded the theory that when the base and target datasets are dissimilar, the use of pre-trained weights alone may degrade the performance. It is essential that the higher level features should be specific to the target dataset instead of the base dataset. Another regularization technique involved in the proposed architecture,

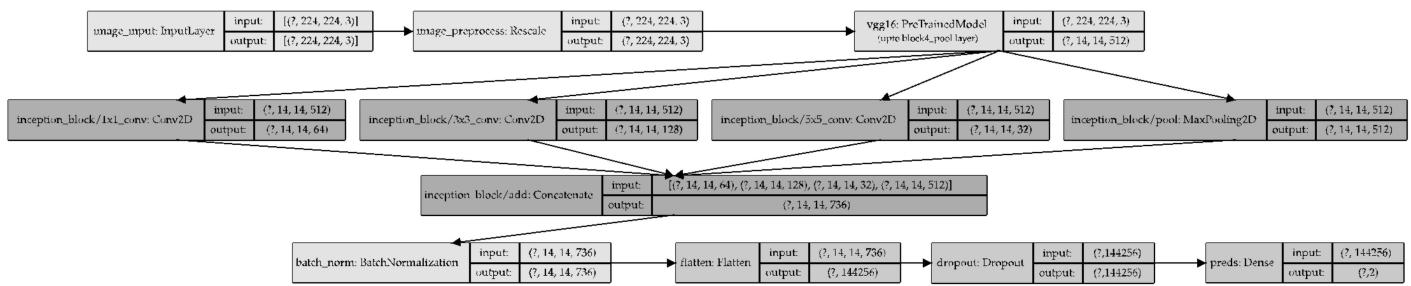


Figure 2. Proposed model architecture VGGIN-Net formed by concatenating VGG16 layers upto block4 layer with the naive Inception module along with dense layer used for the classification

specifically at data-level, is data augmentation which is applied on the training dataset in order to synthetically increase the number of samples and also to improve the overall performance of the network by reducing the fitting problem [30]. The typical CNN training process employing data augmentation would include on the fly generation of random image samples across training mini-batches by use of affine transformations. In the proposed network, we have applied certain data augmentation operations as inspired from [31] on both the classes (Benign and Malignant). Figure 3 displays some randomly generated samples after applying data augmentation operations. The data augmentation operations applied on images include: (a) random rotation within range of 20 degrees, (b) random width and height shift operation with range 0.2 i.e. translation of the images both horizontally as well as vertically by number of pixels less than or equal to 20% of the actual image dimensions, (c) random horizontal and vertical flip, combined with (d) random shear and random zoom operations with the same range as that of translation. These values were determined after lots of experimental trials in order to maximize performance. To improve the regularization of our network further we make use of random crops [31] which helps the network to learn even better due to the translation invariance property of convolutional networks. The image patches are resized to  $224 \times 340$  using bilinear resizing and then randomly

cropped into patches of  $224 \times 224$ . At inference (test) time, central crop was used.

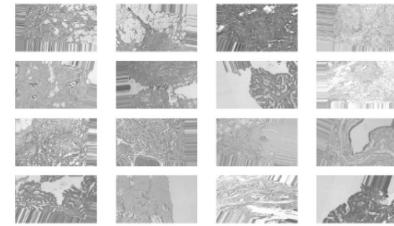


Figure 3. Illustration of various data augmentation operations applied on the BreakHis dataset

Fine tuning approach has further been adapted on the proposed deep transfer learning architecture, inspired from several works in literature. In the case of the DeTrac approach, Abbas et al [43] had focused on the relevance of applying fine-tuning on different architectural blocks of pre-trained CNN. Similarly, Sharma and Mehra (2018) had emphasized the role of transfer learning, full training, and fine-tuning of several pre-trained networks for the medical image dataset [32]. From the analysis it was found that VGG16 pre-trained network features with logistic regression as classifier gives best performance amongst other combinations of VGG19 and ResNet-50 pre-trained network with regression. The same authors

had further extended their work in [33] and elaborated on the role of layer wise fine-tuning and had presented the in-depth study of layer wise fine-tuning on AlexNet for the BreakHis dataset. From the study they had depicted that different magnification factors had influence in selecting the appropriate layers to be fine-tuned in the network architecture. Kandel and Castelle (2020) [34] had also conducted an extensive comparative analysis of block wise and complete fine-tuning of various pre-trained networks. The pre-trained networks used were: VGG16, VGG19 and Inception on histopathological image dataset. From the analysis it was found that fine-tuning of complete pre-trained network might not be the ideal choice in all the situations while considering different magnification factor images. All these previous works motivated us to apply block-wise fine tuning approach on the proposed network.

Our research work proposes a novel approach by combining modified VGG16 architecture with naïve Inception block to tackle imbalanced problem in breast cancer classification. The same has been empirically validated by conducting extensive experimentation along with ablation study to prove the veracity of our claim that our proposed architectural combination is able to solve the breast cancer classification task effectively by proposing the explainable and less computationally costly architecture. By adjusting the sequence and right combination of appropriate layers in the proposed architecture we are able to obtain the competent architecture to enhance the performance of the classifier that can be utilized for transfer learning on any other breast cancer dataset. The modified VGG16 architecture is chosen in such a way to resolve the deployment issues associated with original VGG-Nets by reducing the number of dense layer to one and extracting the appropriate features from suitable layers. In addition, we have introduced the naive Inception block with the batch normalization layer to address the vanishing gradient problem, and data augmentation, regularization and fine-tuning techniques have been used for improving the prediction performance.

#### 4. EXPERIMENTAL SETUP

##### 4.1 Datasets

Two different datasets are considered in the experimental task: BreakHis and Breast-Histopathological-Images dataset. BreakHis dataset is used to train the proposed network. The trained network also supports transfer learning as validated by the classification task performed on the Breast-Histopathological-Images dataset.

###### 4.1.1 BreakHis Histopathological dataset

BreakHis dataset [35] used for current study is a publicly available dataset consisting of 7909 high resolution breast cancer images belonging to two different classes. i.e. Benign and Malignant, and composed of different magnification factors, 40X, 100X, 200X and 400X as illustrated in Table 1. The dataset also contains labels comprising of eight sub types belonging to four benign tumor types: adenosis (A), fibroadenoma (F), phyllodes tumor (PT), and tubular adenoma (TA); and four

malignant tumor types: carcinoma (DC), lobular carcinoma (LC), mucinous carcinoma (MC) and papillary carcinoma (PC). Skewed classes are observed in scenarios where the number of observations belonging to one class is significantly lower than other class. This is usually referred to as the class imbalance problem; this problem is prevalent in the BreakHis dataset as evident from Table 1 where the number of Malignant samples is far more than the number of Benign samples. For conducting the experimental task, 70:30 split is selected. 60% samples are selected for the training, 10% samples are kept for validation and remaining 30% samples are for testing purpose. The original size of images present in the BreakHis dataset is 700 x 460.

TABLE 1  
SAMPLE DISTRIBUTION OF BENIGN AND MALIGNANT IMAGES IN THE BREAKHIS DATASET WITH RESPECT TO THE DIFFERENT MAGNIFICATION FACTORS

Class	Magnification Factor			
	40X	100X	200X	400X
Benign	625	644	623	588
Malignant	1,37	1,43	1,39	1,23
Total No of Images (7909)	0	7	0	2
	1,99	2,08	2,01	1,82
	5	1	3	0

###### 4.1.2 Breast-Histopathological-Images dataset

We have also validated our deep transfer network on another breast cancer dataset. For another set of experiments we have considered the Breast-Histopathological-Images dataset [36]. The Breast-Histopathological-Images dataset comprises of 277524 image samples having microscopic views of breast cell specimens at 40X magnification factor. Each image patch extracted from whole slides is of size 50 x 50 and all experiments are evaluated using a similar stratified split such that 30% of the total samples are kept for testing purpose and remaining 60% for training and 10% for validation. The dataset tries to address growing challenges in detecting invasive ductal carcinoma (IDC), which is the most common type of breast cancer. A highly imbalanced class distribution is observed in this dataset with 198738 IDC -ve images and 78786 IDC +ve images. It is interesting to note in this particular dataset, images from the IDC -ve class are in majority in comparison to the number of images present in the IDC +ve classes.

##### 4.2 Experimental setup

All the experiments were conducted on Google Cloud Platform using a single Compute Engine VM instance with dual-core Intel Xeon CPU (2.00 GHz) and 8GBRAM, and a NVIDIA Tesla T4 GPU accelerator with 16 GB memory. For performing all our experiments, we used the TensorFlow v2.3.0 framework with the help of Keras API [37] using Python v3.8.9. The source code containing the code for our implementations is available in our GitHub

repository.<sup>1</sup> The different hyperparameters were selected so as to maximize the performance. (i) Adam optimizer, used with learning rate initially assigned as 0.001; the Adaptive Momentum optimization automatically adjusts the learning rate for further training. (ii) The loss function used was categorical cross entropy. (iii) The training batch size was set to 128 with a net budget of 100 epochs. The proposed architecture is fine-tuned for four different magnification factors. While fine tuning the network, the learning rate is significantly reduced so as to make sure that any large gradient updates would not cause the network to abruptly change any of the pre-trained weights. The training process is conducted with the help of a simple learning rate schedule where we exponentially decay the learning rate after 15 starting warmup epochs. During the fine tuning process the network is trained for a total of 50 sweeps (epochs). The warmup steps linearly increase the learning rate from 1e-5 to 5e-5 which is further exponentially decayed by a factor of 0.8.

In order to verify our claim that the proposed network architecture can further support transfer learning based tasks on other target histopathological images dataset, we use the weights of our VGGIN-Net trained on BreakHis 40X dataset with some amount of fine tuning to classify IDC +ve and -ve images from Breast-Histopathology-Images dataset. The weights chosen were from the 40X magnification factor as the target dataset also consists of images scanned at 40X zoom factor. The hyperparameters for training the terminal dense layer for the new classification is similar to our other experiments except that we use the Adam optimizer with a learning rate of 0.001 as any learning rate higher than that would affect the performance of the classifier.

## 5 RESULTS AND DISCUSSION

### 5.1 Performance Analysis

In our study, we have done the comparative analysis of the proposed architecture with few state-of-the-art deep learning approaches as well as popularly used CNN architectures. For this curated set of architectures we primarily apply a transfer learning approach based on weights pre-trained on the ImageNet dataset. This is due to the fact that our target imbalanced classification dataset contains much less samples in comparison to large scale datasets (a few million images) which is almost always required to effectively train a large ConvNet from scratch. Initially, we experiment with VGG architecture using the well-known VGG16 network proposed by Zisserman et al. [19] (2015). We also used the GoogLeNet incarnation of the Inception architecture (as per work done in [20] by Szegedy et al. (2015)) as well as deep residual network ResNet-50 [26] proposed by He et al (2018) to classify histopathological images from the imbalanced BreakHis dataset. These methods when applied using transfer learning serve as effective baseline methods. So we have evaluated the performance of popular deep learning

approaches i.e., VGG16, GoogLeNet and ResNet-50 in Table 2. We have also done the comparative analysis between these methods and our proposed deep transfer network, named VGGIN-Net, obtained after considering the features extracted till block4 pool layer of VGG16 with a single dense layer, and also with the addition of an Inception block and a single dense layer which is the proposed architecture. The VGG16 architecture had been modified with a single dense layer but after the addition of a naïve Inception block, the same network architecture had shown tremendous improvement in the results. From the results tabulated in Tables 2 to 9, it is observed that VGGIN-Net shows remarkable improvement in terms of accuracy, F1 score, IBA and GMean. ROC curve analysis with its AUC is also shown in Figure 5 to validate the proposed approach.

In Table 3, comparative analysis with state-of-the-art methods is shown for the BreakHis dataset using accuracy as the evaluation parameter with scores reported across several runs. Hence, it is evident that our proposed network with and even without fine tuning shows remarkable improvement in results.

To emphasize the veracity of our claim that the proposed network architecture helps to tackle the class imbalance problem, certain experiments were conducted. A comparative analysis illustrates the use of various well known approaches that deems to solve the class imbalance problem i.e., with undersampling and oversampling techniques. We observe from the comparisons to sampling experiments in Table 4 that the proposed architecture itself is able to tackle the class imbalance problem by itself without requirement of any sampling technique.

Extensive experiments were conducted related to the block-wise fine-tuning technique applied on the proposed network. It is observed from the analysis that the block-wise fine tuning operations have shown significant improvement in the performance as depicted in Table 5. It is evident that different fine tuning combinations are found suitable for different magnification factors. For 40X, fine tuning of block3, block4 and Inception block seems to be an ideal choice, whereas in case of 400X, fine tuning of block4 and Inception block was only found to be the perfect fit. Fine tuning of the complete network was found to be ideal in case of 100X and 200X magnification factor images. It can be inferred from the results that complete fine-tuning of the network is not always the perfect choice for different magnification factor images as different block wise fine tuning combinations also be deemed to be suitable in certain scenarios. Figure 4 depicts the validation accuracy and loss corresponding to the four magnification factors. It is clearly visible that with the help of suitable block-wise fine tuning, the network training improves its anytime performance, and learning curves get more and more stable. The proposed approach along with fine tuning has shown significant improvements in the classification performance. For 40X, 100X, 200X and 400X magnification factors of the BreakHis dataset, the best obtained accuracies are 98.51%, 97.53%, 96.688% and 95.528% respectively. So in a nutshell, it is notable to mention that our work

<sup>1</sup> <https://github.com/SainiManisha/VGGIN-Net>

demonstrates that single branch models can converge quite well and our work is not intended to deal with training of increasingly complex residual models. Rather, we are aimed at building a simple model with reasonable depth and favorable accuracy that can be simply implemented using basic architecture blocks (like convolution, ReLU, max pooling, etc.) on a single branch while tackling imbalanced biomedical datasets.

To validate that our design of the proposed deep transfer architecture supports further transfer learning on any other breast cancer biomedical dataset we performed experiments as illustrated in Table 6 using Breast-Histopathological-Images dataset. From the analysis it was validated that the VGGIN-Net architecture also supports transfer learning concept when tested on other breast cancer datasets.

## 5.2 Ablation Study

Ablation study has been conducted for the proposed VGGIN-Net architecture. In Table 7, we show experimental results on the 40X magnification factor to compare and contrast the use of block 3, 4 and 5 as the backbone features for our network. We inferred that feature extraction till block4 pool layer is an ideal combination. Another set of experiments were conducted to demonstrate the selection of naïve Inception block in the proposed architecture. Comparison with another variant of the Inception block as tabulated in Table 8 proves that the naïve Inception block is apt for our model. Although, the dimensionality reduction block variant of the Inception module is less computationally expensive in

comparison to the naïve inception block, the attained model performance obtained after combining the dimensionality reduction block to the proposed architecture is less in comparison to the naïve Inception block as validated by the experimental results illustrated in Table 8. The naïve Inception block was initially used with 64, 128, 32 filters for 1x1, 3x3, 5x5 conv layers respectively. In Table 9, we show experiments on using diverse widening factors (K) where each value of K indicates the multiple factor by which the filters are increased. It was found that K value as 1 is the ideal choice instead of K values of 2, 3, 5 and 10 in the naïve Inception block. Also, it helps to validate our choice of the number of filters besides keeping the computational complexity optimum since K=1 is the lowest possible considered value. More results in the supplementary file highlight the significance of data augmentation for enhancing the performance of the various deep networks including VGGIN-Net. Table 10 illustrates the experiments related to the proposed VGGIN-Net with and without data augmentation for different magnification factors for the BreakHis dataset. Experiments show that VGGIN-Net with data augmentation works significantly better in comparison to VGGIN-Net without Data Augmentation. The incorporation of data augmentation in the training pipeline helps reduce over-fitting by imparting the necessary regularization, allowing the models to learn continually across several epochs. For our case, we have applied all random transformations including random cropping of samples to a fixed crop size.

TABLE 2

PERFORMANCE EVALUATION OF VGG16, GOOGLENET, AND RESNET-50 WITH THE MODIFIED VGG16 ARCHITECTURE AND THE PROPOSED APPROACH ON BREAKHIS DATASET (I) 40x, (II) 100x, (III) 200x, (IV) 400x

Technique	40X				100X			
	Accuracy	F1	IBA	GMean	Accuracy	F1	IBA	GMean
VGG16 [19]	0.9294	0.87 / 0.95	0.79	0.89	0.9240	0.86 / 0.95	0.80	0.89
GoogLeNet [20]	0.8682	0.78 / 0.91	0.71	0.84	0.8674	0.78 / 0.91	0.72	0.85
ResNet50 [26]	0.9350	0.89 / 0.95	0.85	0.92	0.9381	0.89 / 0.96	0.86	0.93
Modified VGG16 w/ Single Dense Layer	0.9387	0.89 / 0.96	0.84	0.91	0.9522	0.92 / 0.97	0.90	0.95
Modified VGG16 w/ Inception Block w/ Single Dense Layer	<b>0.9628</b>	<b>0.93 / 0.97</b>	<b>0.93</b>	<b>0.96</b>	<b>0.9681</b>	<b>0.95 / 0.98</b>	<b>0.93</b>	<b>0.96</b>

Technique	200X				400X			
	Accuracy	F1	IBA	GMean	Accuracy	F1	IBA	GMean
VGG16 [19]	0.9119	0.86 / 0.94	0.83	0.91	0.8913	0.81 / 0.92	0.72	0.85
GoogLeNet [20]	0.8880	0.82 / 0.92	0.78	0.88	0.8668	0.77 / 0.91	0.69	0.83
ResNet50 [26]	0.9431	0.90 / 0.96	0.87	0.93	0.9221	0.87 / 0.94	0.81	0.90
Modified VGG16 w/ Single Dense Layer	0.9357	0.88 / 0.96	0.82	0.91	0.8893	0.82 / 0.92	0.77	0.88
Modified VGG16 w/ Inception Block w/ Single Dense Layer	<b>0.9651</b>	<b>0.88 / 0.96</b>	<b>0.80</b>	<b>0.89</b>	<b>0.9364</b>	<b>0.89 / 0.95</b>	<b>0.86</b>	<b>0.93</b>

TABLE 3

COMPARISON OF THE PROPOSED APPROACH WITH THE STATE-OF-THE-ART APPROACHES ON BREAKHIS DATASET BASED ON MEAN ACCURACY ACROSS DIFFERENT MAGNIFICATION FACTORS

Technique	40X	100X	200X	400X
Spanhol et al. [8]	$0.8960 \pm 0.0650$	$0.8500 \pm 0.0480$	$0.8400 \pm 0.0320$	$0.8080 \pm 0.0310$
Spanhol et al. [39]	$0.8460 \pm 0.0290$	$0.8480 \pm 0.0420$	$0.8420 \pm 0.0170$	$0.8160 \pm 0.0370$
Bayramoglu et al. [10]	$0.8300 \pm 0.0300$	$0.8310 \pm 0.0350$	$0.8460 \pm 0.0270$	$0.8210 \pm 0.0440$
Zhu et al. [40]	$0.8570 \pm 0.0190$	$0.8420 \pm 0.0320$	$0.8490 \pm 0.0220$	$0.8010 \pm 0.0440$
Gupta et al. [41]	$0.8674 \pm 0.0237$	$0.8856 \pm 0.0273$	$0.9031 \pm 0.0376$	$0.8831 \pm 0.0301$
Deniz et al. [17]	$0.9096 \pm 0.0159$	$0.9058 \pm 0.0196$	$0.9137 \pm 0.0172$	$0.9130 \pm 0.0740$
Song et al. [42]	$0.9002 \pm 0.0302$	$0.9120 \pm 0.0440$	$0.8780 \pm 0.0530$	$0.8740 \pm 0.0720$
Gupta et al. [18]	$0.9471 \pm 0.0088$	$0.9590 \pm 0.0420$	$0.9676 \pm 0.0109$	$0.8911 \pm 0.0012$
<b>Ours</b>	<b><math>0.9588 \pm 0.0033</math></b>	<b><math>0.9657 \pm 0.0087</math></b>	<b><math>0.9500 \pm 0.0122</math></b>	<b><math>0.9315 \pm 0.0034</math></b>
<b>Ours (with fine tuning)</b>	<b><math>0.9710 \pm 0.0046</math></b>	<b><math>0.9667 \pm 0.0022</math></b>	<b><math>0.9716 \pm 0.0033</math></b>	<b><math>0.9368 \pm 0.0053</math></b>

TABLE 4

PERFORMANCE EVALUATION OF THE PROPOSED APPROACH WITH UNDERSAMPLING AND OVERSAMPLING TECHNIQUES ON BREAKHIS DATASET  
(i) 40X, (ii) 100X, (iii) 200X, (iv) 400X

Sampling Technique	40X				100X			
	Accuracy	F1	IBA	GMean	Accuracy	F1	IBA	GMean
Undersampling	0.9591	0.93 / 0.97	0.89	0.94	0.9381	0.90 / 0.96	0.89	0.94
Oversampling	0.9406	0.90 / 0.96	0.89	0.94	0.9593	0.93 / 0.97	0.90	0.95
None	<b>0.9628</b>	<b>0.93 / 0.97</b>	<b>0.93</b>	<b>0.96</b>	<b>0.9681</b>	<b>0.95 / 0.98</b>	<b>0.93</b>	<b>0.96</b>

Sampling Technique	200X				400X			
	Accuracy	F1	IBA	GMean	Accuracy	F1	IBA	GMean
Undersampling	0.9540	0.91 / 0.97	0.86	0.92	0.9262	0.88 / 0.95	0.84	0.91
Oversampling	0.9669	0.94 / 0.98	0.92	0.96	0.9303	0.88 / 0.95	0.83	0.91
None	<b>0.9651</b>	<b>0.88 / 0.96</b>	<b>0.80</b>	<b>0.89</b>	<b>0.9364</b>	<b>0.89 / 0.95</b>	<b>0.86</b>	<b>0.93</b>

TABLE 5

PERFORMANCE EVALUATION OF BLOCK WISE FINE-TUNING ON PROPOSED VGGIN-NET FOR 40x, 100x, 200x AND 400x MAGNIFICATION FACTORS ON BREAKHIS DATASET

Fine Tuning	40X				100X			
	Accuracy	F1	IBA	GMean	Accuracy	F1	IBA	GMean
Complete Network	0.9666	0.99 / 0.97	0.89	0.94	<b>0.9753</b>	<b>0.96 / 0.98</b>	<b>0.96</b>	<b>0.98</b>
Block 2, 3, 4, Inception block	0.9777	0.96 / 0.98	0.95	0.97	0.8674	0.71 / 0.91	0.56	0.74
Block 3, 4, Inception block	<b>0.9851</b>	<b>0.97 / 0.99</b>	<b>0.96</b>	<b>0.98</b>	0.9646	0.94 / 0.98	0.89	0.94
Block4, Inception	0.9610	0.93 / 0.97	0.88	0.94	0.9700	0.95 / 0.98	0.92	0.96

block No Fine Tuning	0.9628	0.93 / 0.97	0.93	0.96	0.9752	0.95 / 0.98	0.93	0.97
Fine Tuning	200X				400X			
	Accuracy	F1	IBA	GMean	Accuracy	F1	IBA	GMean
Complete Network	<b>0.9688</b>	<b>0.95 / 0.98</b>	<b>0.92</b>	<b>0.96</b>	0.9077	0.86 / 0.93	0.85	0.93
Block 2, 3, 4, Inception block	0.9467	0.91 / 0.96	0.91	0.95	0.9323	0.89 / 0.95	0.83	0.91
Block 3, 4, Inception block	0.9651	0.94 / 0.98	0.89	0.94	0.9426	0.90 / 0.96	0.85	0.92
Block 4, Inception block	0.9614	0.93 / 0.97	0.92	0.96	<b>0.9528</b>	<b>0.92 / 0.97</b>	<b>0.91</b>	<b>0.95</b>
No Fine Tuning	0.9651	0.88 / 0.96	0.80	0.89	0.9364	0.89 / 0.95	0.86	0.93

TABLE 6

TRANSFER LEARNING OF PROPOSED VGGIN-NET ON BREAST HISTOPATHOLOGICAL DATASET WITH AND WITHOUT FINE-TUNING

Transfer Learning	Accuracy	F1	IBA	GMean
VGGIN-Net as Fixed Feature Extractor	0.8470	0.89 / 0.73	0.66	0.81
Fine Tuning the VGGIN-Net Inception Block	<b>0.8678</b>	<b>0.91 / 0.75</b>	<b>0.67</b>	<b>0.82</b>

TABLE 7

ANALYSIS OF FEATURES EXTRACTED FROM DIFFERENT BLOCKS OF VGG16 ARCHITECTURE TO FIND THE APPROPRIATE FEATURES IN THE PROPOSED ARCHITECTURE FOR 40x MAGNIFICATION FACTOR ON BREAKHIS DATASET

Technique	40X			
	Accuracy	F1	IBA	GMean
Proposed Network using block3_pool	0.9536	0.92 / 0.97	0.89	0.94
Proposed Network using block4_pool	<b>0.9628</b>	<b>0.93 / 0.97</b>	<b>0.93</b>	<b>0.96</b>
Proposed Network using block5_pool	0.9536	0.92 / 0.97	0.89	0.94

TABLE 8

ANALYSIS OF PROPOSED ARCHITECTURE WITH THE INCEPTION BLOCK AND DIMENSIONALITY REDUCTION INCEPTION BLOCK FOR

40x MAGNIFICATION FACTOR ON BREAKHIS DATASET

Technique	40X			
	Accuracy	F1	IBA	GMean
Proposed Network w/ Naïve Inception Block	<b>0.9628</b>	<b>0.93 / 0.97</b>	0.93	0.96
Proposed Network w/ Dimensionality Reduction Inception Block	0.9443	0.90 / 0.96	0.82	0.90

TABLE 9

ANALYSIS OF APPROPRIATE NUMBER OF FILTERS IN INCEPTION BLOCK TO BE USED IN THE PROPOSED ARCHITECTURE FOR 40x MAGNIFICATION FACTOR ON BREAKHIS DATASET

Widening Factor	40X			
	Accuracy	F1	IBA	GMean
k=1	<b>0.9628</b>	<b>0.93 / 0.97</b>	0.93	0.96
k=2	0.9443	0.90 / 0.96	0.83	0.91
k=5	0.9684	0.95 / 0.98	0.93	0.96
k=10	0.9684	0.94 / 0.98	0.90	0.95

TABLE 10

PROPOSED VGGIN-NET WITH AND WITHOUT DATA AUGMENTATION FOR 40x, 100x, 200x AND 400x MAGNIFICATION FACTORS ON BREAKHIS DATASET

Technique	40X				100X			
	Accuracy	F1	IBA	GMean	Accuracy	F1	IBA	GMean
VGGIN-Net w/ Data Augmentation	0.9628	0.93 / 0.97	0.93	0.96	0.9681	0.95 / 0.98	0.93	0.96

VGGIN-Net w/o Data Augmentation	0.9239	0.86 / 0.95	0.80	0.89	0.9134	0.85 / 0.94	0.78	0.88
<hr/>								
<b>Fine Tuning</b>	<b>200X</b>				<b>400X</b>			
	<b>Accuracy</b>	<b>F1</b>	<b>IB A</b>	<b>GMean</b>	<b>Accuracy</b>	<b>F1</b>	<b>IB A</b>	<b>GMean</b>
VGGIN-Net w/ Data Augmentation	<b>0.9651</b>	<b>0.88 / 0.96</b>	<b>0.80</b>	<b>0.89</b>	<b>0.9364</b>	<b>0.89 / 0.95</b>	<b>0.86</b>	<b>0.93</b>
VGGIN-Net w/o Data Augmentation	0.9155	0.85 / 0.94	0.78	0.88	0.8852	0.79 / 0.92	0.68	0.82

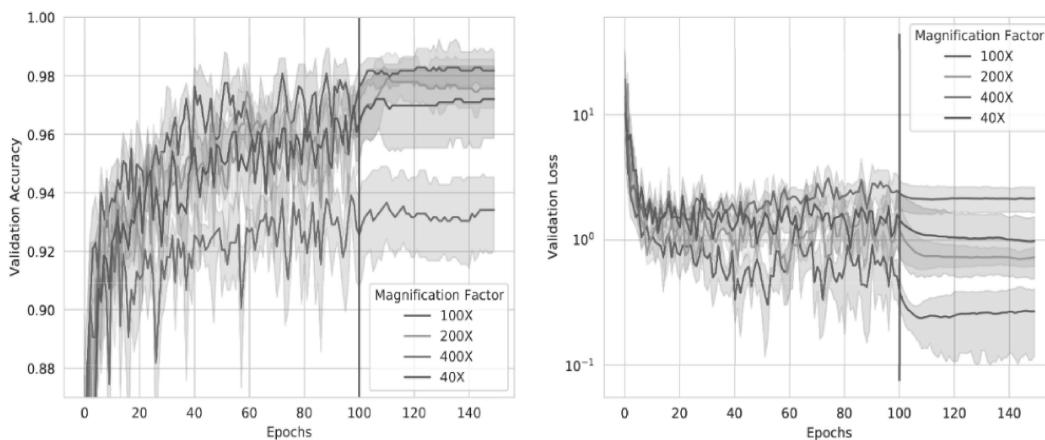


Figure 4. Validation accuracy and loss plot corresponding to the proposed architecture VGGIN-Net for different magnification factors (40X, 100X, 200X and 400X). Purple line indicate start of fine tuning.

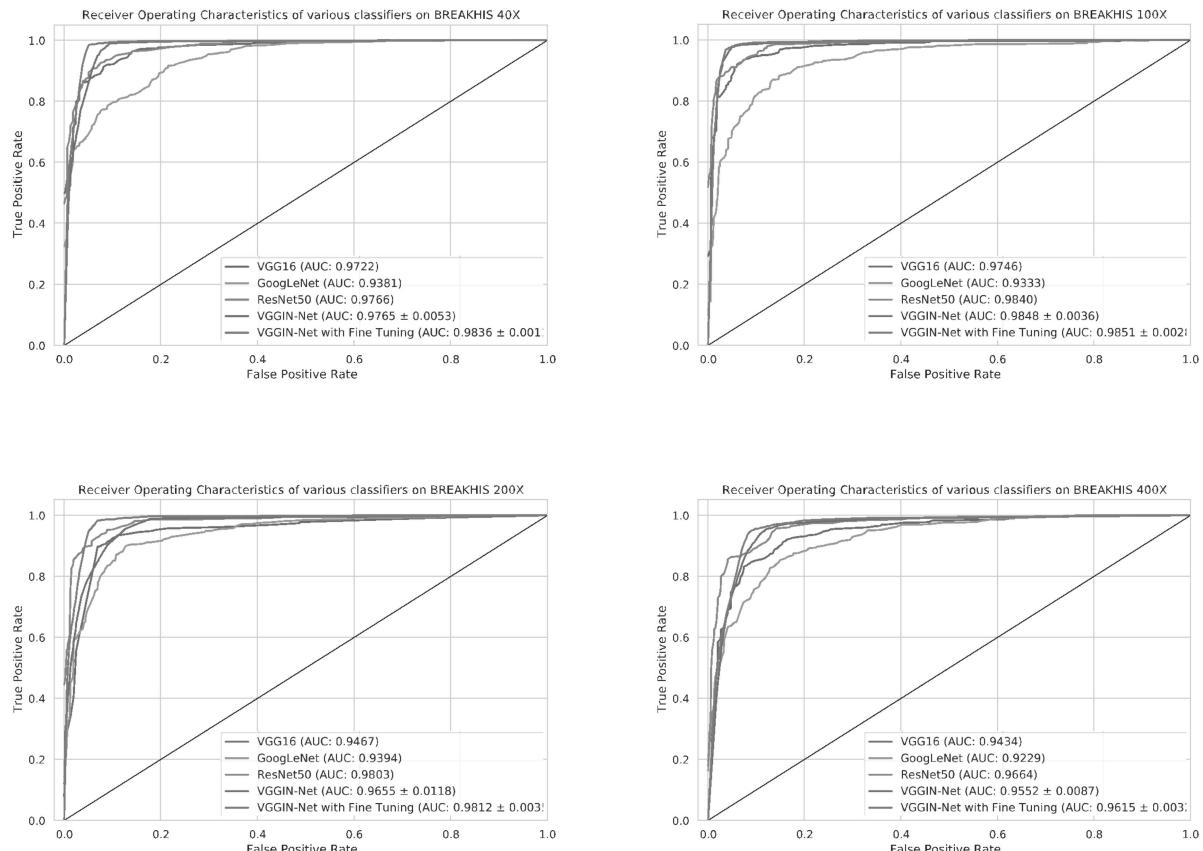


Figure 5. ROC curve comparison of proposed approach with state-of-the-art networks in case of (i) 40X, (ii) 100X, (iii) 200X and (iv) 400X

magnification factors for the BreakHis dataset

## 6 CONCLUSION AND FUTURE SCOPE

In this paper, a novel deep learning based network VGGIN-Net has been proposed using layers from the pre-trained deep network VGG-16 at lower level, and trainable

Inception module and dense layers at the higher level. The proposed transfer network has been compared with different state-of-the-art approaches on the basis of various performance evaluation metrics. It is validated from the experiments that VGGIN-Net designed to deal with the imbalanced breast cancer dataset and overall helps to improve robustness and generalizability of the approach. The proposed deep transfer network with fine tuning has achieved accuracies of 97.10%, 96.67%, 97.16% and 93.68% for the 40X, 100X, 200X and 400X magnification factors respectively, for the BreakHis dataset. The proposed network was able to classify both the minority and majority classes effectively. We also validated through experiments that the trained VGGIN-Net model supports transfer learning on other breast cancer datasets.

In future, we shall explore the use of skip connections inside deep neural nets. Also, we would look into constructing other deep network architectures for classification of multi-class imbalanced biomedical datasets. We would seek to create a hybrid approach based on techniques similar to DeTraC [43], combined with popular CNN pre-trained models to deal with multi-class imbalanced datasets.

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