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BRECNET: Breast Cancer Network for Histopathology Images Classification using Convolution Neural Network

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Abstract
Breast cancer is the leading cause of common cancer among women. Automated screening approaches may save time and minimize errorsin detecting and categorizing breast cancer subtypes, a crucial clinical activity. Breast cancer is diagnosed using the biopsy technique, which involves examining tissue samples under a microscope. Senior pathologists should analyze breast cell morphologies in histopathology images to determine this type of cancer. The world's population of pathologists is insufficient, and human error in diagnosing procedures is possible. Analysis of histopathology images using deep learning algorithms can aid pathologists in identifying cancer subtypes and making a better treatment plan. As a result, this research presents BRECNET (Breast Cancer Network), a dedicated architecture that employs a parallel convolution filter for screening breast cancer from histopathology images. In addition, to avoid overfitting and create high levels of reliability, a variety of augmentation procedures were implemented to improve the number of histopathological images. Based on histopathological image analysis, the proposed system was assessed and shown to have an accuracy of 87.25%and a kappa score of 85.40% in classifying eight subtypes of cancer with different magnification levels. The results show that the BRECNET model is much more successful and efficient, making them more acceptable for breast cancer screening.

Keywords: Breast Cancer, Histopathology Image, Deep Learning, Medical Imaging, Diagnostic Screening

Introduction

Cancer is a disease that affects the body's cells and progresses out of control. Breast cancer is a pervasive cancer kind. Breast cancer is one of the most frequent and life-threatening tumours in women, impacting 2.1 million people each year, according to the World Health

Organization. In 2018, this illness claimed the lives of over 627,000 women, accounting for roughly 15% of all cancer deaths among women. In 2030, more than 28 million women will be diagnosed with breast cancer (Bolhasani,2020). IDC is most widely seen in the milk ducts and fibrous tissue.Non-invasive procedures such as mammography, MRI, and ultrasound are used to identify breast cancer. A histopathological analysis is another standard approach for identifying breast cancer (Zeiser *et al.,*2020). This procedure examines the suspicious tissue under a microscope on glass slides stained with hematoxylin and eosin. Histologic grade is a prognostic marker and a predictor of cancer response. The images obtained from tissue slides are stored due to advancements in digital pathology. As a result, breast cancer diagnostic automation algorithms can minimize pathologists' workload. In addition, computer-aided diagnostic systems (CAD) play an essential role in breast cancer early detection (George *et al.,*2020)

The variety of tumours tissue is the most difficult part in computational pathology. In this circumstance, using deep learning (DL) algorithms with vast images to differentiate color features can significantly improve computational approaches in a short amount of time (Khosravi *et al.,*2017*)*. DL algorithms are becoming more popular in medical imaging, perform well on tasks such as segmentation and classification. DL based algorithms are currently employed for cancer screening because of their automated feature extraction and architecture necessitates the use of a GPU as well as additional RAM (Murugan *et al.,*2021).

On the other hand, deep learning approaches need to be backed up by an extensive database 7e, especially in favorable circumstances. Many transfer learning and ensemble learning techniques have been explored in the past work to address this issue. In an effective computer-aided diagnostic (CAD) system for urban healthcare in smart cities, the convolution neural network (CNN) is employed to recognize MI signals (Valério *et al.,*2019).

Related Work

Breast cancer diagnosis relies heavily on conventional feature engineering or deep learning utilizing CNN. Shape, size, and color are the primary indications of morphological aspects of nuclei, and nuclei are an essential critical feature in breast cancer detection. Image processing techniques such as thresholding, active contour, Hough transform, watershed transform, region are expanding, and others are employed (George *et al.,* 2020). They suggested a nucleus guided transfer learning method for breast cancer categorization. The nucleus features are retrieved using a Pretrained model, and the data is taken from the BreaKHis dataset, which is openly available. The proposed model has a 96.91 % average accuracy, a 97.24 % sensitivity, and a 96.18 % specificity. Recent computer vision breakthroughs show that deep network-based feature learning techniques can outperform handcrafted features. Histopathology has benefited from such techniques as well. (Cruz-Roa *et al.,*2017) Color, texture, and graph-based characteristics employing an RF classifier were exceeded by a three-layer convolutional neural network (CNN) operating on 100 X 100 pixel patches at 2.5 magnification in differentiating IDC.

(Litjens *et al.,*2016) employed a deep network for with 128x128-pixel patches at five magnifications for prostate cancer delineation. (Janowczyk *et al.,*2016) have deep learning to perform various tasks, including IDC identification employing 32 x32 pixel patches at 2.5 magnification. (Lu *et al*.,2021) proposed a brcaseg model to classify breast cancer and achieved 91.02% overall accuracy of 91.02% using histopathology images. (Barsha *et.al,*2021) proposed the architecture by ensemble the different pre-trained model like DenseNet-121, DenseNet-201, ResNet-101v2, and ResNet-50. The ensemble method achieves the Accuracy of 69.31%, 75.07%, 61.85%, and 60.50% on patch level classification. CNN-based cell characteristics were expected to enhance histopathology image analysis and classification graph coding accuracy(Shi *et al.,* 2020). To improve classification accuracy, a stacked ensemble deep learning model was introduced(Abhishek *et.al.,*2021*)*. The first level's base classifiers are three CNN. The Empirical Wavelet Transform and Variational Mode Decomposition methods were used to deconstruct the dataset, allowing the models to be trained at the molecular level, making our approach more resilient than current methods. This paper suggests employing an incremental boosting convolution network to detect breast cancer, with the network identifying the 4 balanced classes using a histopathological image. The main advantage of this system is that it extracts visual characteristics from multiscale images using ensemble DCNN and then improves classification using a boosting framework(Vo *et.al.,* 2019).For pixel-level labelling and categorization of slide-level visuals, saliency and classification maps are integrated. The experiments were conducted on 240 full-size slide images, indicating that saliency detector and classifier networks outperformed competing approaches(Gecer *et. al.,* 2018).The authors proposed a 3 tier CNN model to classify the benign and malignant classes from histopathology images by achieving the overall accuracy of 98.35%. (Jabeen *et.al.,* 2022) proposed a CNN models with probability based optimal feature fusion techniques by using used an ultrasound images to classify normal, benign and malignant and achieved the accuracy of 99.1%. (Takahashi *et.al*,2022) proposed the DL models using the xception model to classify the CT images with 4 different degrees and achieves the area under the curve of 93.6% in distinguishing breast cancer.This work aims to develop a supervised model for detecting mitotic signals in WSI images of breast histopathology. Deep learning architecture and handmade features were used to create the model. Morphological, textural, and intensity aspects are the most common handcrafted characteristics. The suggested design enhanced Accuracy by 92 %, recall by 88 % and F-score by 90 %(Saha *et. al.,*2017)

In this study, an automated method for detecting mitosis is proposed. Mitotic detection is treated as a semantic segmentation problem, and it is tackled with a CNN. The training label of mitosis data is usually in the format of centroid pixel, rather than all the pixels relating to mitosis, and had an F-score of 0.669, in contrast to conventional training data used in semantic segmentation systems(Li *et.al.,*2019).A unique reliability-based training data selection technique has been developed to overcome mismatch problems in shape. The training data's reliability is measured and assessed using unsupervised expectation

maximization (EM)with soft probabilistic output. The training data selection strategy outperforms traditional methods(Chavez *et.al.,* 2021).

Table 1.Breast Cancer sub classes of Benign and Malignant

Benign	**Malignant**
carcinoma (DC)	Adenosis (A)
lobular carcinoma (LC)	Fibroadenoma (F)
mucinous carcinoma (MC)	Phyllodes Tumor (PT)
papillary carcinoma (PC)	Tubular Adenomas (TA)

This study used CNN to analyze breast cancer histopathology images obtained using surgical open biopsy (SOB). Unlike earlier methods, we perform image-based classification of eight medically relevant classifications provided in Table 1.

The following are the contribution of this research:

1. The BRECNET model was created from the bottom up to classify the eight types of breast cancer based on histopathological pictures using parallel convolution block.
2. Histopathological images show the severity and course of illnesses. As a result, DL algorithm utilized to automatically interpret cancer screenings.
3. Using assessment measures like as accuracy and kappa score is measured to test the efficacy of the proposed systems.
4. To improve the proposed method's generalization efficacy and avoid overfitting, a novel training strategy was used, helped by different combinations of training parameters.

Proposed Methodology

Dataset Description

The Breast Cancer Histopathological Image dataset includes 9,109 microscopic photos of breast tumours tissue acquired from 82 people and magnified at different magnifications (40X, 100X, 200X, and 400X)(Spanhol *et.al.,*2016). Partial mastectomy or excisional biopsy are used to acquire the data. The photos are 700x460 pixels in size, RGB, and each channel has an 8-bit depth. Furthermore, the dataset is separated into benign and malignant subclasses. A, F, PT, and TA are the subclasses of benign tumours, while DC, LC, MC, and PC are the subclasses of malignant tumours. Table 2 shows the dataset distribution at various magnification levels. The breast cancer detection system's is shown in Figure 1, which comprises BRECNET model to learn discriminative and effective feature representations

from preprocessed images in the image datastore. Figure 2 shows representative image from the dataset for each subclass and 400X under benign and malignant

Table 2.Dataset Distribution

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Magnification Level	A	F	PT	TA	DC	LC	MC	PC	Total
400X	106	237	115	130	788	137	169	138	1820
200X	111	264	108	140	896	163	196	135	2013
100X	113	260	121	150	903	170	222	142	2081
40X	114	253	109	149	864	156	205	145	1995
Total	444	1014	453	569	3451	626	792	560	7909

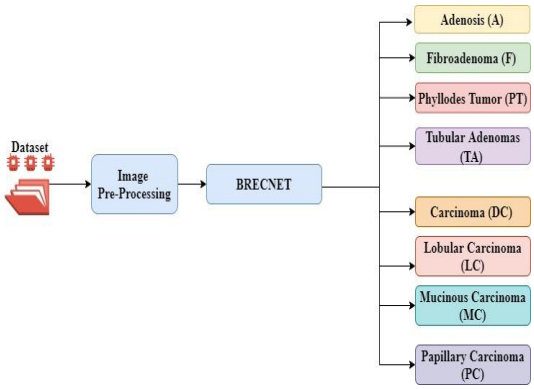


Fig. 1: Methodology of proposed system

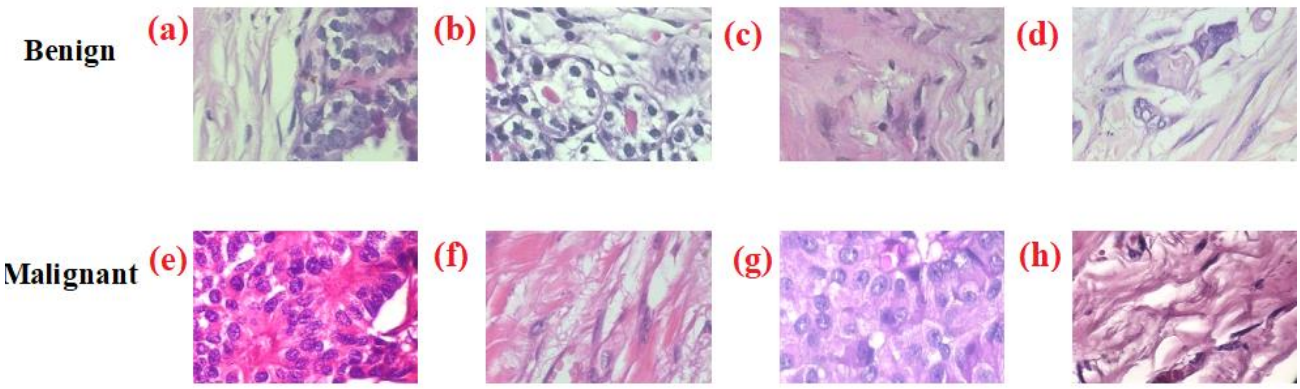


Fig. 2. Sample images (a) A (b) (c) PT (d) TA (e) DC (f) LC (g) MC (h) PC

Image Pre-processing

Deep learning methods rely primarily on the amount of training data available, with higher-complexity models requiring more data to generalize successfully and prevent overfitting the training samples. A lack of sufficient data is a significant problem in the medical field(Vo et.al., 2019). The breast histology images in the data collection are huge, measuring 700x460 pixels in size. The data set is transformed rigorously to increase the number of training examples to address the issues of limited images. The images in the dataset are resized to 64x64 pixels to fit the model. We rotated, blurred, cropped, brightened, contrasted, and flipped the images to different extents to improve the training set. Because pathologists do not use a fixed orientation

when reviewing histology slides/images, this data augmentation technique closely resembles a real-world scenario. A similar classification problem was previously addressed using a dataset augmentation strategy(Yari *et.al.,*2020). Table 3 lists the parameters that were employed in the augmentation strategies.

BRECNET Architecture

The proposed BRECNET model consists of three key elements: feature extraction, detection, and classification. First, we use parallel layers of convolution, activation, and max-pooling in our model.

Then, at the function level, we join parallel layers. The flattened features are then fed into the dropout layer to avoid overfitting. The final layer performed the classification process, which included the SoftMax layer. These layers generate class activation maps as well. Class activation maps are used as a classification translator in conjunction with the final convolution layer.

Table 3. Augmentation parameters

Augmentation Techniques	**Parameters**
Flip Horizontally	True
Flip Vertically	True
Width Shift range	0.2
Height Shift range	0.2
Rotation	45
Brightness limit	Range= (0.5,1.0)
Sheer range	0.2

The input images are fed into the four consecutive convolution filters with stacked layers of convolution layer, batch normalization and max-pooling layers. Then the extracted features from the four layers are concatenated and fed into the two convolution layers. The BRECNET architecture is designed in a way 4:2:1 convolution layer at each stage. The neurons at each layer is determined using the Keras tuner library to fine-tune the model hyperparameters. Using several hyperparameter tuning approaches, the model is constructed to avoid overfitting and underfitting(Venkatesan *et.al.,*2022).

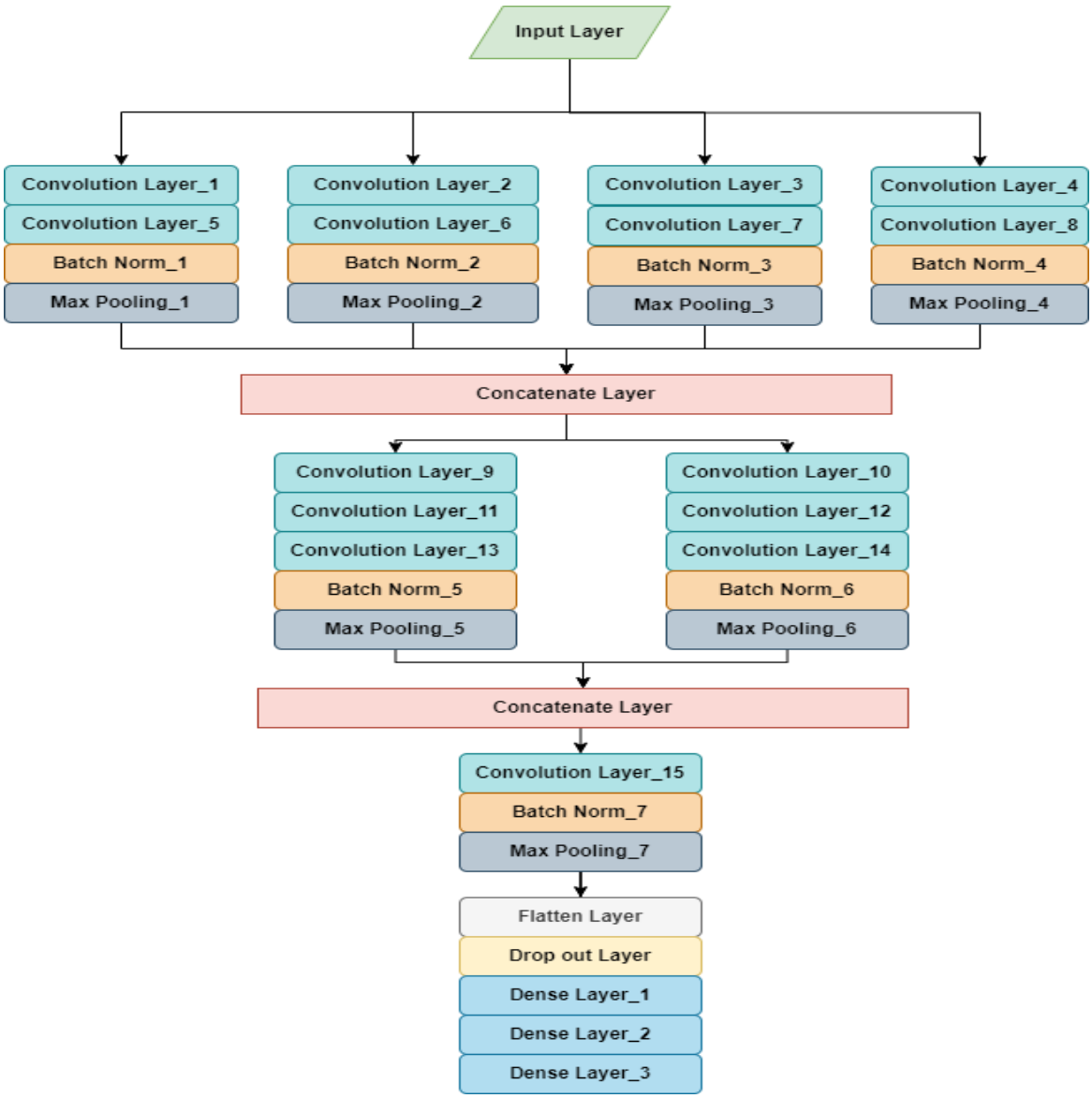


Fig.3. BRECNET Model architecture for breast cancer screening

The SoftMax layer probability is used to classify the output classes. The advantage of using the parallel architecture of the convolution layer is to extract a variety of features which will be helpful in discriminating the output classes. Table 4 provides the layer by layer calculation of parameters in the BRECNET model.The proposed model consists of 19,68,056 are trainable and 544 are non-trainable parameters.

Experimental Results

On the histopathology dataset, many sufficiently large experiments were done to demonstrate the efficacy of the recommended methods and compare their results to those of existing state-of-the-art methodologies. NVIDIA Quadro RTX 6000 24GB graphics card is used to train the model developed using TensorFlowframework. All experiments were carried out

Layer (type)	Output Shape	Param #
input_1	None, 64, 64, 3	0
conv2d	None, 64, 64, 32	896
conv2d_2	None, 64, 64, 24	1824
conv2d_4	None, 64, 64, 16	2368
conv2d_6	None, 64, 64, 8	224
conv2d_1	None, 64, 64, 32	9248
conv2d_3	None, 64, 64, 24	14424
conv2d_5	None, 64, 64, 16	12560
conv2d_7	None, 64, 64, 8	584
batch norm	None, 64, 64, 32	128
batch_norm_1	None, 64, 64, 24	96
batch_norm_2	None, 64, 64, 16	64
batch_norm_3	None, 64, 64, 8	32
max_pooling2d	None, 32, 32, 32	0
max_pooling2d_1	None, 32, 32, 24	0
max_pooling2d_2	None, 32, 32, 16	0
max_pooling2d_3	None, 32, 32, 8	0
concatenate	None, 32, 32, 80	0
conv2d_8	None, 32, 32, 64	46144
conv2d_11	None, 32, 32, 32	64032
conv2d_9	None, 32, 32, 64	369828
conv2d_12	None, 32, 32, 32	25632
conv2d_10	None, 32, 32, 64	36928
conv2d_13	None, 32, 32, 32	25632
batch_norm_4	None, 32, 32, 64	256
batch_norm_5	None, 32, 32, 32	128
max_pooling2d_4	None, 16, 16, 64	0
max_pooling2d_5	None, 16, 16, 32	0
concatenate_1	None, 16, 16, 96	0
conv2d_14	None, 16, 16, 96	83040
batch_norm_6	None, 16, 16, 96	384
max_pooling2d_6	None, 8, 8, 96	0
Flatten	None, 6144	0
Dropout	None, 6144	0
Dense	None, 256	1573120
dense_1	None, 128	32896
dense_2	None, 8	1032

Table 4. BRECNET Model parameters

by utilising an 80% of training dataset for the proposed DL systems. During the training phase, 10% of the data used as a validation set to assess model performance and store the weight combinations.The BRECNET model is trained using Adam optimizers with a learning rate strategy that slows down when it becomes validation patience(Suriya et.all., 2019)]. In the Adam optimizers for training, the following hyperparameters were used:

The learning rate is 0.5e-4, the number of epochs is 70, the batch size is 8 to 32, and the move is twice the initial
value; patience is 6; and momentum is 0.95. Finally, class weights are generated for each class so that the model can pay more attention to underrepresented groups. The distribution of class weights in each category is shown in Table 5. The class weights are useful when the dataset is class imbalanced and also improve the single label classification. By providing the class weights the model bias is reduced, which is more prone to the model when dataset are class

imbalance(De Angeli *et.al.*,2022). The BRECNET make uses a bunch of batch normalization layer and dropout layer to prevent the model from overfitting.

Table 5. Weights distribution among each class label in training data

Label	**Class Weights**
A	17.80
F	7.79
PT	17.45
TA	13.88
DC	2.29
LC	12.62
MC	9.98
PC	14.12

The performance of our proposed system is compared to that of existing systems using the following performance indicators:

i) Model Accuracy $= \frac{T_P + T_N}{T_P + F_P + T_N + F_N}$

ii) Kappa Score $= \frac{\text{Observed agreement} - \text{expected agreement}}{1 - \text{expected agreement}}$

We present the outcomes of the proposed systems' various trials utilizing the breast cancer histopathology dataset with an 80–20 % train-test split in this part to ensure that execution durations were not expensive; that split was chosen.The proposed method can classify the eight classes by extracting discriminate features using the parallel convolution blocks.

Fig. 4 depicts the BRECNET model's training and validation accuracy, demonstrating that the model is converging without many oscillations. To achieve the model convergence with small number of oscillations the epoch and learning are fine-tuned manually to find optimal values. BRECNET model's training and validation losses are shown in Figure 5. Table 6 compares the BRECNET model's performance to that of otherbreast cancer classification models. BRECNET compares various art screening strategies for breast cancer detection. The results proves BRECNET is capable of classifying 8different subtypes of cancer and non-cancerbreast images. The overall an accuracy of 87.25% and a kappa score of 85.40% is achieved by BRECNET. But when compared to other models results provided in the table, BRECNET achieves comparatively good results. The model achieved the better performance metric eventhough it is classifying the eight class consists of sub types of classes and also with different magnifying values. The most challenging task for the proposed model is classifying the subtype classes where the patterns looks very similar. By making use of different training strategies and parallel convolution block architecture, the BRECNET model extracts the discriminate features to classify the subtype

classes. The kappa score is computed to measure the degree of agreement between the true values and predicted values.

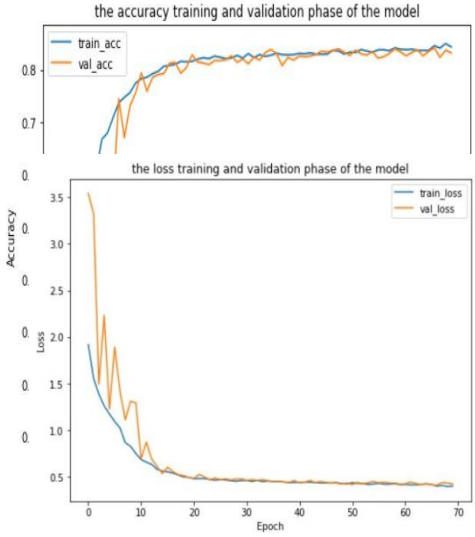


Fig.4. BRECNET model Training and Validation accuracy

Fig.5. BRECNET model Training and Validation loss

To better understand the model interpretability in classifying the subtypes by computing precision and recall of each class. The figure 6 present each class precision and recall value of BRECNET model on classifying benign and malignant subtypes of breast screening. From the figure 6 we can understand that the BRECNET model achieves the minimum precision of 83.5% for class F and 82.5% for class LC.The model achieves minimum recall value is achieved by class DC with 79.54% and class F with 84.77%. It is clearly showing that the model is underperforming for minority classes and also classes with similar features. But model performing well with good precision and recall value for the classes A, PT, TA, DC, MC and PC. Hence the proposed method can have capability to classifying the sub types of breast cancer classification.

Table 6. Performance Analysis of BRECNET with other models

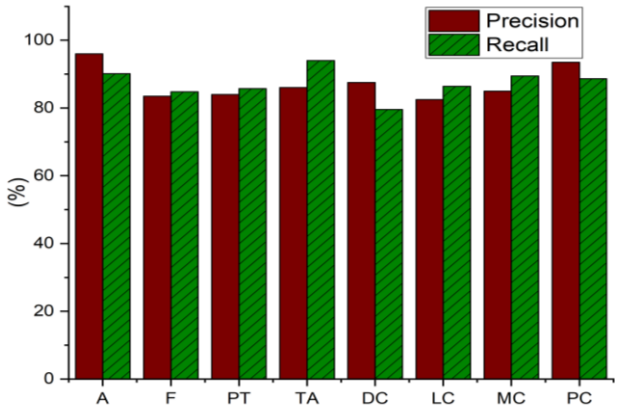
Recent Works	**Dataset**	**Class Mode**	**Accuracy (%)**	**Kappa Score (%)**
BRECNET	Breakhis	Eight-Class	87.25	85.40
Zhang et.al .,2021	FFDM	Two-Class	96.40	Not Provided
Knan et.al., 2021	Breakhis	Two-Class	76.00	45.00
Das et.al.,2021	IDC	Two-Class	75.64	Not Provided
Model Fusion	Breakhis	Two-Class	95.52	Not Provided
Shi et.al.,2020	-	Two-Class	86.50	Not Provided

Fig. 6: Precision and Recall values for each class

Conclusion and Future scope

The BRECNET model is proposed for breast cancer detection uses histopathology images to distinguish between 8 classes in Break his dataset. The model designed in such way to handle different magnification levels of 40x, 100x, 200x, and 400x. BRECNET employs image preprocessing techniques to boost the intensity of the histopathology image and minimize noise. Due to the chain of parallel block of convolution layers, the BRECNET extracts the useful features to provide consistent results. The initial weight declaration for each reduces the model bias and faster convergence. BRECNET model was trained with preprocessed images to prevent overfitting and enhance model performance. The proposed technique classified the breast cancer categories with an overall accuracy of 87.25 % and a Kappa score of 85.40 %.

In the future, more datasets will be collected in order to improve the model's performance in breast cancer screening. Other priorities include the creation of new classification optimization algorithms and the evaluation of performance using different methods.



Data Availability: The data used to support the findings of this study are included in the article.

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References

[1] H. Bolhasani, E. Amjadi, M. Tabatabaeian, and S. J. Jassbi, 2020 “A histopathological image dataset for grading breast invasive ductal carcinomas,” Informatics Med. Unlocked, vol. 19, no. December, p. 100341, 2020, doi: 10.1016/j.imu.2020.100341.

[2] F. A. Zeiser, C. A. da Costa, G. de O. Ramos, H. C. Bohn, I. Santos, and A. V. Roehe,2021, “DeepBatch: A hybrid deep learning model for interpretable diagnosis of breast cancer in whole-slide images,” Expert Syst. Appl., vol. 185, no. October 2020, 2021, doi:

10.1016/j.eswa.2021.115586.
[3] K. George, P. Sankaran, and P. J. K,2020, “Computer assisted recognition of breast cancer in biopsy images via fusion of nucleus-guided deep convolutional features,” Comput. Methods Programs Biomed., vol. 194, p. 105531, 2020, doi: 10.1016/j.cmpb.2020.105531.
[4] P. Khosravi, E. Kazemi, M. Imielinski, O. Elemento, and I. Hajirasouliha, 2018,“Deep Convolutional Neural Networks Enable Discrimination of Heterogeneous Digital Pathology Images,” EBioMedicine, vol. 27, pp. 317–328.DOI: 10.1016/j.ebiom.2017.12.026.
[5] Murugan, S., Venkatesan, C., Sumithra, M. G., Gao, X. Z., Elakkiya, B., Akila, M., & Manoharan, S. 2021, DEMNET: a deep learning model for early diagnosis of Alzheimer diseases and dementia from MR images. IEEE Access, 9, 90319-90329.
[6] M. T. Valério, S. Gomes, M. Salgado, H. P. Oliveira, and A. Cunha,2019, “Lesions Multiclass Classification in Endoscopic Capsule Frames,” Procedia Comput. Sci., vol. 164, pp. 637–645. doi: 10.1016/j.procs.2019.12.230.
[7] K. George, S. Faziludeen, P. Sankaran, and P. Joseph K, 2020,“Breast cancer detection from biopsy images using nucleus guided transfer learning and belief based fusion,” Comput. Biol. Med., vol. 124, no. July, p. 103954.DOI: 10.1016/j.compbiomed.2020.103954.
[8] Cruz-Roa, Cruz-Roa, A., Gilmore, H., Basavanhally, A., Feldman, M., Ganesan, S., Shih, N.N., Tomaszewski, J., González, F.A. and Madabhushi, A., 2017. Accurate and reproducible invasive breast cancer detection in whole-slide images: a deep learning approach for quantifying tumor extent. Scientific reports, 7(1), pp.1-14.
[9] G. Litjens Litjens, G., Sánchez, C.I., Timofeeva, N., Hermsen, M., Nagtegaal, I., Kovacs, I., Hulsbergen-Van De Kaa, C., Bult, P., Van Ginneken, B. and Van Der Laak, J., 2016. Deep learning as a tool for increased accuracy and efficiency of histopathological diagnosis. Scientific reports, 6(1), pp.1-11.
[10] Janowczyk, A. and Madabhushi, A., 2016. Deep learning for digital pathology image analysis: A comprehensive tutorial with selected use cases. Journal of pathology informatics, 7.
[11] Lu, Z., Zhan, X., Wu, Y., Cheng, J., Shao, W., Ni, D., Han, Z., Zhang, J., Feng, Q. and Huang, K., 2021. BrcaSeg: a deep learning approach for tissue quantification and genomic correlations of histopathological images. Genomics, proteomics & bioinformatics.
[12] Barsha, N.A., Rahman, A. and Mahdy, M.R.C., 2021. Automated detection and grading of Invasive Ductal Carcinoma breast cancer using ensemble of deep learning models. Computers in Biology and Medicine, 139, p.104931..
[13] Shi, X., Su, H., Xing, F., Liang, Y., Qu, G. and Yang, L., 2020. Graph temporal ensembling based semi-supervised convolutional neural network with noisy labels for histopathology image analysis. Medical image analysis, 60, p.101624.
[14] Das, A., Mohanty, M.N., Mallick, P.K., Tiwari, P., Muhammad, K. and Zhu, H., 2021. Breast cancer detection using an ensemble deep learning method. Biomedical Signal Processing and Control, 70, p.103009.
[15] D. M. Vo, N. Q. Nguyen, and S. W. Lee,2019, “Classification of breast cancer histology images

using incremental boosting convolution networks," Inf. Sci. (Ny)., vol. 482, pp. 123–138, 2019, doi: 10.1016/j.ins.2018.12.089.

[16] B. Gecer, S. Aksoy, E. Mercan, L. G. Shapiro, D. L. Weaver, and J. G. Elmore, 2018,"Detection and classification of cancer in whole slide breast histopathology images using deep convolutional networks," Pattern Recognit., vol. 84, pp. 345–356, DOI: 10.1016/j.patcog.2018.07.022.

[17] V. Kate and P. Shukla,2021, "A 3 Tier CNN model with deep discriminative feature extraction for discovering malignant growth in multi-scale histopathology images," Informatics Med. Unlocked, vol. 24, no. May, p. 100616, 2021, doi: 10.1016/j.imu.2021.100616.

[18] Jabeen, K., Khan, M.A., Alhaisoni, M., Tariq, U., Zhang, Y.D., Hamza, A., Mickus, A. and Damaševičius, R., 2022. Breast Cancer Classification from Ultrasound Images Using Probability-Based Optimal Deep Learning Feature Fusion. Sensors, 22(3), p.807.

[19] Takahashi, K., Fujioka, T., Oyama, J., Mori, M., Yamaga, E., Yashima, Y., Imokawa, T., Hayashi, A., Kujiraoka, Y., Tsuchiya, J. and Oda, G., 2022. Deep Learning Using Multiple Degrees of Maximum-Intensity Projection for PET/CT Image Classification in Breast Cancer. Tomography, 8(1), pp.131-141. doi: 10.3390/tomography8010011.

[20] M. Saha, C. Chakraborty, and D. Racoceanu,2017, "Efficient deep learning model for mitosis detection using breast histopathology images," Comput. Med. Imaging Graph., vol. 64, no. March, pp. 29–40, 2018, doi: 10.1016/j.compmedimag.2017.12.001.

[21] C. Li, X. Wang, W. Liu, L. J. Latecki, B. Wang, and J. Huang,2019, "Weakly supervised mitosis detection in breast histopathology images using concentric loss," Med. Image Anal., vol. 53, pp. 165–178, DOI: 10.1016/j.media.2019.01.013.

[22] T. Chavez, N. Vohra, K. Bailey, M. El-Shenawee, and J. Wu,2021, "Supervised Bayesian learning for breast cancer detection in terahertz imaging," Biomed. Signal Process. Control, vol. 70, no. July, p. 102949, doi: 10.1016/j.bspc.2021.102949.

[23] F. A. Spanhol, L. S. Oliveira, C. Petitjean, and L. Heutte,2016, "A Dataset for Breast Cancer Histopathological Image Classification," IEEE Trans. Biomed. Eng., vol. 63, no. 7, pp. 1455–1462,DOI: 10.1109/TBME.2015.2496264.

[24] D. M. Vo, N. Q. Nguyen, and S. W. Lee, 2019,"Classification of breast cancer histology images using incremental boosting convolution networks," Inf. Sci. (Ny)., vol. 482, pp. 123–138, 2019, doi: 10.1016/j.ins.2018.12.089.

[25] Y. Yari, T. V. Nguyen, and H. T. Nguyen, 2020, "Deep learning applied for histological diagnosis of breast cancer," IEEE Access, vol. 8, pp. 162432–162448, 2020, doi: 10.1109/ACCESS.2020.3021557.

[26] C. Venkatesan, M. G. Sumithra, and M. Murugappan, 2022, "NFU-Net: An Automated Framework for the Detection of Neurotrophic Foot Ulcer Using Deep Convolutional Neural Network," Neural Process. Lett.,doi: 10.1007/s11063-022-10782-0.

[27] M. Suriya, V. Chandran, and M. G. Sumithra,2019, "Enhanced deep convolutional neural network for malarial parasite classification," Int. J. Comput. Appl., vol. 0, no. 0, pp. 1–10,

doi: 10.1080/1206212X.2019.1672277.

[28] De Angeli, K., Gao, S., Danciu, I., Durbin, E.B., Wu, X.C., Stroup, A., Doherty, J., Schwartz, S., Wiggins, C., Damesyn, M. and Coyle, L., 2022. Class imbalance in out-of-distribution datasets: Improving the robustness of the TextCNN for the classification of rare cancer types. Journal of biomedical informatics, 125, p.103957. doi: 10.1016/j.jbi.2021.103957.

[29] Zhang, X., Liang, C., Zeng, D., Jiang, X., Zhong, R., Lan, Y., Ma, J. and Bai, L., 2021. Pattern classification for breast lesion on FFDM by integration of radiomics and deep features. Computerized Medical Imaging and Graphics, 90, p.101922. doi: 10.1016/j.compmedimag.2021.101922.

[30] Khan, S.I., Shahrior, A., Karim, R., Hasan, M. and Rahman, A., 2021. MultiNet: A deep neural network approach for detecting breast cancer through multi-scale feature fusion. Journal of King Saud University-Computer and Information Sciences.," doi: 10.1016/j.jksuci.2021.08.004.