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REVOLUTIONIZING EARLY BREAST CANCER DETECTION:A COMPREHENSIVE ANALYSIS OF AI APPLICATIONS

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ABSTRACT:

An algorithm framework based on CycleGAN and an upgraded dual-path network (DPN) is suggested to address the difficulties of uneven staining in pathological pictures and difficulty of discriminating benign from malignant cells. CycleGAN is used for color normalization in pathological pictures to tackle the problem of uneven staining. However, the resultant detection model is ineffective. By overlapping the images, the DPN uses the addition of small convolution, deconvolution, and attention mechanisms to enhance the model's ability to classify the texture features of pathological images on the BreaKHis dataset. The parameters that are taken into consideration for measuring the accuracy of the proposed model are false-positive rate, false-negative rate, recall, precision, and F1 score. Several experiments are carried out over the selected parameters, such as making comparisons between benign and malignant classification accuracy under different normalization methods, comparison of accuracy of image level and patient level using different CNN models, correlating the correctness of DPN68-A network with different deep learning models and other classification algorithms at all magnifications. The results thus obtained have proved that the proposed model DPN68-A network can effectively classify the benign and malignant breast cancer pathological images at various magnifications. The proposed model also is able to better assist the pathologists in diagnosing the patients by synthesizing the images of different magnifications in the clinical stage.

INTRODUCTION

The most definitive criterion for detecting breast disorders is a histological examination of breast tissue [1]. To aid pathologists in diagnosis, the traditional auxiliary diagnostics employ

edge detection to segment cell nuclei [2]. Support vector machines [3], random forest [4], and other machine learning-based approaches employ artificially derived features for modelling and classification [5, 6]. The classification

accuracy is low because pathological pictures typically have considerable differences [7], feature extraction relies on high professional expertise, and comprehensive feature extraction is challenging. Deep learning can overcome the limits of manual feature extraction and extract complicated nonlinear characteristics automatically, which has become increasingly popular in the categorization of diseased pictures [8]. In literature [9] on the BreakHis dataset, the classification accuracy of the patient-level and image-level classifications was 90 percent and 85.6 percent, respectively, based on the AlexNet model paired with the maximum fusion approach for classification. Literature [10] used a single-task CNN model to train two CNN (convolutional neural network). Breast cancer can occur in two different categories [22–24], namely, benign [25] and malignant [26], and is a difficult task for pathologists to identify the type of cancer.

LITERATURE SURVEY
Report From National Cancer
Registry Programme, India. In JCO
Global Oncology. American Society of
Clinical Oncology
AUTHOR Mathur P., Sathishkumar
K., Chaturvedi

ABSTRACT: The systematic collection of data on cancer is being performed by various population-based cancer registries (PBCRs) and hospital-based cancer registries (HBCRs) across India under the National Cancer Registry Programme–National Centre for Disease Informatics and Research of Indian Council of Medical Research since 1982
Of fine needle biopsy material from the breast cancer.

AUTHORS:

Marciniak A., Obuchowicz A.,
Monczak A., Kołodziński M.
Cytomorphometry

ABSTRACT: During a fine needle aspiration (FNA), a small amount of breast tissue or fluid is removed from a suspicious area with a thin, hollow needle and checked for cancer cells. This type of biopsy is sometimes an option if other tests show you might have breast cancer (although a core needle biopsy is often preferred). It might also be used in other situations.

EXISTING SYSTEM:

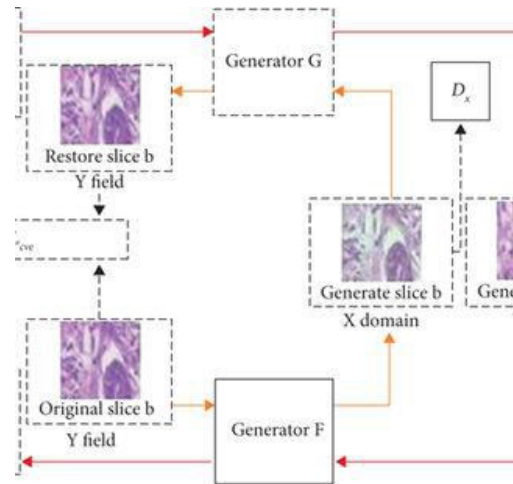
in image generation, the generative adversarial network (GAN) [15] is commonly utilized. A generator and a discriminator form the foundation of the system. The loss function is continuously optimized to generate actual data, which is extremely close to pseudodata, through the game between

the generator and the discriminator. The CycleGAN presented in literature [16] is a ring network structure based on GAN that can realize style transfer between unpaired images and ensure that the generated image's color changes while remaining consistent with the source image. The specifics have not changed.

PROPOSED SYSTEM :

Due to the different doses of different doctors when dyeing pathological images, it is easy to cause different shades of stained pathological images, especially pathological images of different periods, which are very different, such as original slice a and original slice b in Figure 5. The training and modeling of pathological images with different staining will lead to a decrease in the accuracy of the model, so it is necessary to perform color normalization on pathological images. The red arrows in Figure 5 indicate cycle loss, yellow arrows indicate GAN loss, and dotted arrows indicate L_{cyc} .

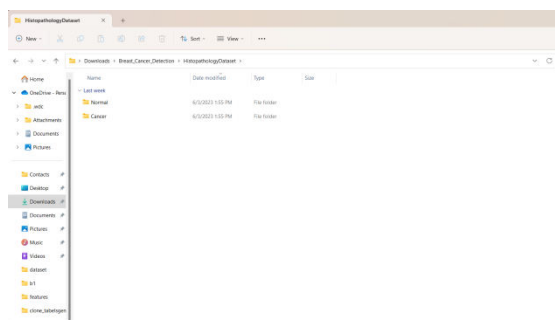
SYSTEM ARCHITECTURE :



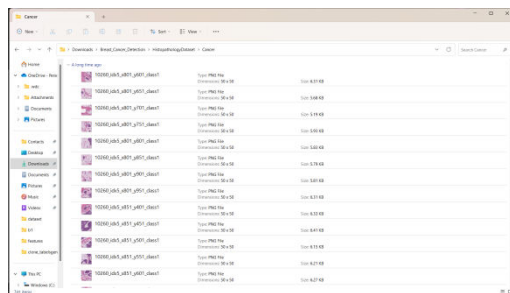
WORKING METHODOLOGY

Several machine learning (ML), artificial intelligence (AI), and neural network technologies have recently been investigated for image processing. The CAD system have created an authentic and trustworthy system which can reduce experimental errors and can perform benign and malignant lesions differentiation with increased accuracy. With these systems image quality can be improved for human judgement and automate the image readability process for perception and interpretation. Recently, a number of papers applying machine learning and artificial intelligence algorithms for breast cancer detection, segmentation, and classification were published. Deep learning models have recently made significant progress in computer vision, particularly in biomedical image processing, due to its ability to automatically learn complicated and

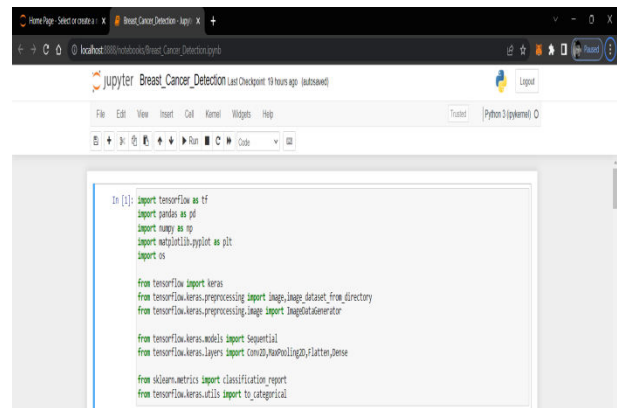
advanced features from images. This has prompted a number of researchers to use these models to classify breast cancer histopathology images. Because of its ability to effectively communicate parameters across several layers within a deep learning model, convolutional neural networks (CNNs) are commonly utilised in image-related tasks.



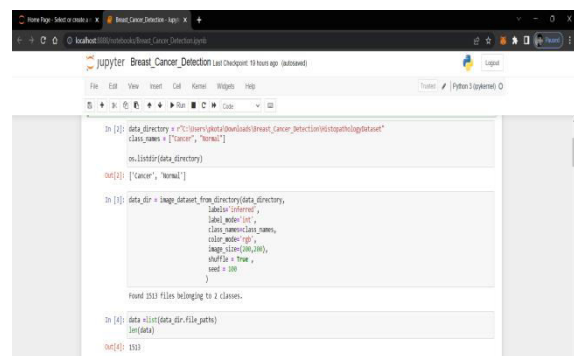
In above screen we can see dataset contains 2 folders called Normal and Cancer and just go inside any folder to view images



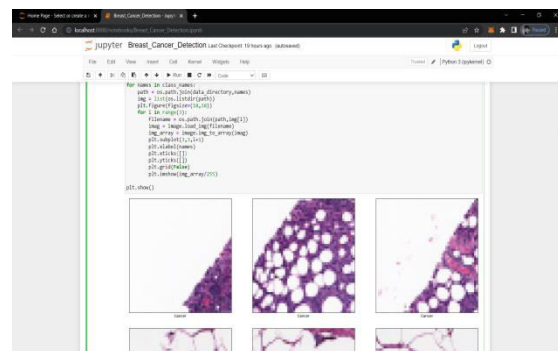
So by using above images we are training all the algorithms and to train this algorithms we have used JUPYTER notebook and below screen showing code and output details. Each block in JUPYTER designed for specific purpose and you can read blue colour comments to know about the purpose



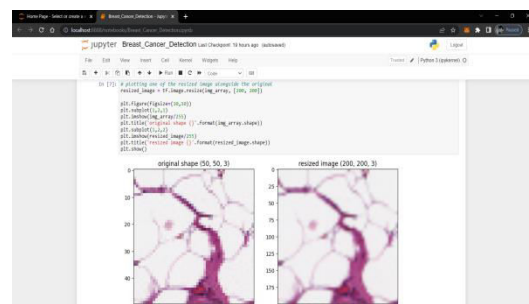
In above screen we are loading require python packages



In above screen we are displaying assigned dataset and the length of the dataset.



In above screen we are exploring 3 files from each class (Normal and Cancer)



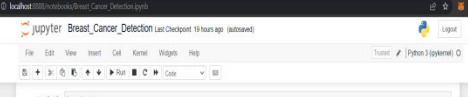
[illegible]

The screenshot shows a Jupyter Notebook titled "Breast_Cancer_Detection" with a code cell containing the following Python code:

```
def fit_validation_data(
    batch_size = 32,
    epochs=10,
    validation_data=validation_data):
    for epoch in range(1, epochs+1):
        # Fit the model
        model = fit_model(validation_data, batch_size=batch_size, epochs=epoch)
        # Evaluate the model
        accuracy, val_size, val_accuracy = evaluate_model(validation_data, model)
        print(f'Epoch {epoch} - size: {val_size} - accuracy: {accuracy} - val_size: {val_size} - val_accuracy: {val_accuracy}')
    return accuracy, val_size, val_accuracy
```

The output of the code cell shows the results of the fit_validation_data function for 10 epochs. The output is a table with 6 columns: epoch, size, accuracy, val_size, val_accuracy, and a final accuracy column. The data is as follows:

epoch	size	accuracy	val_size	val_accuracy	accuracy
1/10	32	0.8589	0.3889	0.8011	0.8589
2/10	32	0.8672	0.3889	0.8011	0.8672
3/10	32	0.8712	0.3889	0.8011	0.8712
4/10	32	0.8712	0.3889	0.8011	0.8712
5/10	32	0.8712	0.3889	0.8011	0.8712
6/10	32	0.8712	0.3889	0.8011	0.8712
7/10	32	0.8712	0.3889	0.8011	0.8712
8/10	32	0.8712	0.3889	0.8011	0.8712
9/10	32	0.8712	0.3889	0.8011	0.8712
10/10	32	0.8712	0.3889	0.8011	0.8712

[illegible]

The screenshot shows a Jupyter Notebook titled "Breast_Cancer_Detection" with a Python kernel. The code in the notebook is as follows:

```
def predict(file_path):
    img = image.load_img(file_path)
    img_array = image.img_to_array(img)
    resized_img = image.resize(img_array, [224, 224])
    x = resized_img/255.0
    x = np.expand_dims(x,1)
    y = model.predict(x)
    predict = np.argmax(y)
    img = cv.imread(file_path)
    img = cv.cvtColor(img, CV_RGB2BGR)

if predict == 0:
    cv.putText(img, 'Cancer Detected', (10, 40), cv.FONT_HERSHEY_SIMPLEX, 1.4, (255, 0, 0), 4)
else:
    cv.putText(img, 'Normal Detected', (10, 40), cv.FONT_HERSHEY_SIMPLEX, 1.4, (255, 0, 0), 4)

plt.imshow(img)
```

The screenshot shows a Jupyter Notebook window titled 'Untitled - Last checkpoint 3 hours ago - untitled'. The notebook contains a single cell with the following code and output:

```
def spy_path(y):
    Model: "sequential_34"
    Layer (type)                Original Shape      Param #
    =====
    resnet181 (ResNet)           (None, 1, 1, 64)    4203576
    max_pooling_40 (MaxPooling)  (None, 1, 1, 32)    0
    max_pooling_41 (MaxPooling)  (None, 1, 1, 32)    0
    conv1d_317 (Conv1D)          (None, 1, 1, 32)    0
    conv1d_318 (Conv1D)          (None, 1, 1, 32)    0
    max_pooling_42 (MaxPooling)  (None, 1, 1, 32)    0
    Flatten_34 (Flatten)         (None, 288)         0
    dense_32 (Dense)             (None, 288)         79884
    dense_33 (Dense)             (None, 1)           114
    Total params: 46,796,288
    Trainable params: 845,122
    Non-trainable params: 46,701,179
    None
```

Below the code cell, the output is displayed in a scrollable area:

```
In [34]: description on test data only: resnet181
          predict = resnet181.predict_proba(test)
          predict = np.argmax(predict, axis=-1)
          print('Accuracy: %f' % np.mean(predict == test_labels))
```

The bottom of the image shows the Windows taskbar with the Start button, a search bar, and several open application icons including File Explorer, Edge, and Jupyter Notebook.

CONCLUSION

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on the classification of pathological images. It is proposed to use DPN to establish a detection model. A 1×1 small convolution is added to the network structure to enhance the nonlinear expression ability of the network and better capture the texture features of pathological images. By adding a deconvolution layer and an attention mechanism, the model can better allocate the intermediate features. The weight of the network improves the classification accuracy of breast pathological images. A discriminant strategy combining confidence rate and voting mechanism is proposed to improve the classification accuracy of patient-level lesions. Experiments show that the proposed DPN68-A network can classify benign and malignant breast pathological images. It has a good effect and has certain clinical application value. In the future, the segmentation network will be combined to accurately label malignant areas on the basis of correctly classifying malignant images, to achieve more accurate clinical auxiliary judgments.

REFERENCES

1. Mathur P., Sathishkumar K., Chaturvedi M., et al. Cancer Statistics, 2020: Report From National Cancer Registry Programme, India. In JCO Global Oncology. *American Society of Clinical Oncology*. 2020;(6):1063–1075. doi: 10.1200/go.20.00122. [[PMC free article](#)] [[PubMed](#)] [[CrossRef](#)] [[Google Scholar](#)]
2. Marciniak A., Obuchowicz A., Monczak A., Kołodziński M. Cytomorphometry of fine needle biopsy material from the breast cancer. In: Kurzyński M., Puchala E., Woźniak M., Żolnierek A., editors. *Advances in Soft Computing*. Berlin, Heidelberg: Springer-Verlag; pp. 603–609. [[Google Scholar](#)]
3. Pereira J., Barata R., Furtado P. Experiments on automatic classification of tissue malignancy in the field of digital pathology. *Proc. SPIE 10443, Second International Workshop on Pattern Recognition*; 2017; pp. 188–194. [[CrossRef](#)] [[Google Scholar](#)]
4. Roulliera V., Lezoraya O., Tab V.-T., Elmoataza A. Multi-resolution graph-based analysis of histopathological whole slide images: application to mitotic cell extraction and visualization. *Computerized Medical Imaging and Graphics*. 2011;35(7-8):603–615. doi: 10.1016/j.compmedimag.2011.02.005. [[PubMed](#)] [[CrossRef](#)] [[Google Scholar](#)]
5. Veta M., Pluim J. P., Van Diest P. J., Viergever M. A. Breast cancer histopathology image analysis: a review. *IEEE Transactions on Biomedical Engineering*. 2020;(6):1063–1075.

Engineering . 2014;61(5):1400–1411.
doi: 10.1109/TBME.2014.2303852.

[[PubMed](#)] [[CrossRef](#)] [[Google Scholar](#)]

6. Araújo T., Aresta G., Castro E., et al. Classification of breast cancer histology images using convolutional neural networks. *PLoS One* . 2017;12(6):p. 0177544.

doi: 10.1371/journal.pone.0177544.

[[PMC free article](#)] [[PubMed](#)] [[CrossRef](#)]

[[Google Scholar](#)]

7. Zhu C., Song F., Wang Y., Dong H., Guo Y., Liu J. Breast cancer histopathology image classification through assembling multiple compact CNNs. *BMC Medical Informatics and Decision Making* . 2019;19(1):p. 198.
doi: 10.1186/s12911-019-0913-x. [[PMC free article](#)] [[PubMed](#)] [[CrossRef](#)]

[[Google Scholar](#)]

8. Yan R., Ren F., Wang Z., et al. Breast cancer histopathological image

classification using a hybrid deep neural network. *Methods* . 2020;173:52–60.
doi: 10.1016/j.ymeth.2019.06.014.

[[PubMed](#)] [[CrossRef](#)] [[Google Scholar](#)]

9. Hafemann L. G., Oliveira L. S., Cavalin P. Forest species recognition using deep convolutional neural networks. *International Conference on Pattern Recognition*; 2014; pp. 1103–1107. [[Google Scholar](#)]

10. Cruz-Roa A., Arevalo Ovalle J., Madabhushi A., Gonzalez Osorio F. A. A deep learning architecture for image representation visual interpretability and automated basal-cell carcinoma cancer detection. *Medical Image Computing and Computer-Assisted Intervention- MICCAI 2013 ser*; 2013; Berlin Heidelberg. pp. 403–410. [[PubMed](#)] [[Google Scholar](#)]