**Breast Cancer Detection using Machine Learning & Deep Learning**

**Abstract :**

Information science is just posing the right inquiries, picturing the outcomes, and searching for the best methodology. Through prescient examination, it responds to the inquiry, "What is probably going to occur?" This is the investigation of PC calculations that work on themselves consequently after some time. A lot of significant worth is added to the organization in an assortment of ways. Determining is the method involved with assessing what was in store in light of at various times data.This project includes an assortment of datasets utilizing Wisconsin Breast Cancer Dataset and Breast Histopathology Dataset from there on cleaning of this dataset. Further with the assistance of different investigation algorithms,machine learning(SVM and KNN) and profound learning models(Custom CNN model,Resnet50 andVGG16) were contrasted agreeing with precision metric.

**Introduction:**

Bosom malignant growth is the world's subsequent driving reason for disease demise. It starts when cells in the bosom start to wildly multiply. The vital test to location is deciding if growths are dangerous (destructive) or harmless (non-cancerous).In clinical applications for recognizing threatening cancers from histopathological pictures, programmed and accuracy arrangement for bosom disease histological pictures are basic.

In this work, we propose an exact and comprehensive computational bosom malignant growth determination by contrasting the correctnesses of various AI and profound learning models on organized information and histopathological microscopy pictures separately. The AI models like KNN and SVM accomplish a precision of 96.27% and 93.7% separately on the Breast Cancer Wisconsin dataset. Moreover, three profound learning models are proposed and examined. The reenactment results showed that our most memorable exceptionally based CNN model accomplishes similarly lesser precision (almost 70%). The other two models utilize move learning strategies of the strong ResNet-50 and VGG-16 Convolutional Neural Networks, pre-prepared on ImageNet to prepare and order the BreakHis dataset(Histopathological Image Dataset) into harmless or threatening. The resultant correctnesses were gotten to be 92.17% and 97.96% separately.

The exploration would help us in deciding the ideal model for this kind of order. Further examination may be led in light of this correlation, and in the end, a completely utilitarian Breast malignant growth recognition framework could be worked for use in the clinical business.

**Diagram:**

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| **Figure 1 : Unified Modelling Language Diagram**  *\*Flow chart drawn using draw.io [https://app.diagrams.net/]* |

**Contribution:**

The use of different AI and profound learning models to group input information into harmless (non-carcinogenic) and threatening (malignant) classes given specific information (organized information input/Histopathological Image of Breast Tissue) and further, usage of measures like exactness, Confusion Matrix, and others to assess the presentation of the applied models and, as a reaction, perceptions to recognize the ideal model is what we intend to accomplish through this Research.

This grouping done in the wake of preprocessing the picture dataset, and testing on different AI and profound learning models will help the evaluators onto the best approach to be embraced for the recognition of bosom disease.

**II. Related Work / Literature Review :**

**Saad Awadh Alanazii et al.2021 [2]-** For the automatic identification of breast cancer, the study developed a CNN approach that evaluates the IDC tissue areas in WSIs. In this study, three distinct CNN architectures were described, along with a proper comparison. The proposed approach, which employed CNN Model 3, achieved an accuracy of 87 per cent. Model 3's five-layer CNN was best suited for this task, despite the fact that it was deeper than Models 1 and 2. A large collection of roughly 275,000 50 50-pixel RGB picture patches guided all structures. On comparing the suggested model to the machine learning (ML) algorithm, it was found that the proposed model outperformed the algorithm by 8%. The proposed model was proven to produce accurate findings, which could eliminate human error in the diagnosis process and lower the cost of a cancer diagnosis. The use of a secondary database like Kaggle is the study's biggest weakness, and future studies should be based on primary data for more accurate breast cancer detection outcomes.

**Mehedi Masud et al.2020 [1]-** This work used transfer learning to observe the classification performance of breast cancer from ultrasound pictures using eight pre-trained CNN models with fine-tuning. The photos were integrated from two separate datasets, and the Adam, RMSprop, and SGDM optimizers were used to evaluate the fine-tuned pre-trained models. The ResNet50 with Adam optimizer had the highest accuracy of 92.4 per cent, and VGG16 had the highest AUC 0.97 score. It also suggested a shallow custom model because the pre-trained models had not produced the expected results, and all of the pre-trained models had many convolutional layers and required a long training period. As feature extractors, the proposed custom model used only one convolutional layer. The custom model was 100 per cent accurate and had an AUC value of 1.0. In terms of training time, the custom model outperformed all other models and necessitated a small number of trainable parameters. The model was to be validated with other datasets, including new ultrasound pictures, in the future.

**Ahmad LG et al. (2013) [3] -** There were 1189 records in the dataset, 22 predictor variables, and one outcome variable. To create the predictive models, the researchers used machine learning approaches such as Decision Tree (C4.5), Support Vector Machine (SVM), and Artificial Neural Network (ANN). The major purpose of this work was to examine the sensitivity, specificity, and accuracy of these three well-known algorithms on the data. The accuracy of the DT, ANN, and SVM was 0.936, 0.947, and 0.957, respectively, according to the analysis. With the lowest error rate and maximum accuracy, the SVM classification model predicted breast cancer recurrence. The DT model's anticipated accuracy was the lowest of all. The results were obtained by utilising 10-fold cross-validation to assess each model's unbiased prediction accuracy.

**Min et al. ( 2017) [4] -** The goal of this study was to evaluate the efficacy of SVM and SVM ensembles in predicting breast cancer outcomes on small and big size datasets. Training SVM and SVM ensembles were compared in terms of classification accuracy, ROC, F-measure, and computational durations. The experimental results demonstrated that for a small-scale dataset, linear kernel-based SVM ensembles based on the bagging method and RBF kernel-based SVM ensembles using the boosting method were preferable alternatives, and feature selection must be done during the data pre-processing step. RBF kernel-based SVM ensembles based on boosting outperformed the other classifiers on a large-scale dataset.

**Assegie et al. (2021) [19] -**The k-Nearest Neighbours algorithm (k-NN) was used to classify breast cancer illness in this investigation. Furthermore, k-NN was implemented for various k values, and the resulting classification accuracies were compared. Breast cancer disease was successfully classified using k-NN, according to the study's findings. To evaluate the success of k-NN, the classification accuracies and error values were obtained. The acquired classification accuracy of k-NN was roughly 97 percent, according to the test findings. Furthermore, the findings of the study suggest that k-NN is a good classifier for classifying breast cancer disease.

**Sunil Kumar et al. (2020) [5] -** On the standard benchmark, the Wisconsin Diagnostic Breast Cancer (WDBC) database retrieved from the UCI Machine Learning Repository, the performance of the proposed SVM technique had been validated. The WDBC dataset contains 569 records (one record for each patient), 357 of which are classified as benign breast cancer patients and the rest as malignant breast cancer patients. Prior to feature selection, data pre-processing in the form of data normalisation was undertaken in this investigation. 10-fold cross-validation was used to produce accurate and impartial classification findings. The dataset was divided into 10 equal sections in a 10-fold CV. The SVM classifier was trained using nine parts (train set) in each fold, and the classification accuracy for the tenth part was calculated (test set). This procedure was performed ten times, with each portion being classed as a test set. The SVM classifier utilised in this study was a two-class classifier, which classified the selected subset of characteristics as benign or malignant breast cancer tumours. A confusion matrix containing information about the classification system's actual and expected classifications was then constructed. Using 10-fold cross-validation, the proposed method reduced the feature dimensionality from 30 to just six, resulting in a classification accuracy of 98.24 per cent.

**Subham Sadhukhan et al.(2019) [7] -** The research described a computerised system for detecting cancer in its early stages in a short amount of time. The researchers used machine learning to train a model based on the predicted features of cell nuclei.. The accuracy of each classifier was tested in a comparison study of two separate methods, KNN and SVM. Following that, image processing was used to analyse a digital image of a fine needle aspirate (FNA) of breast tissue in order to determine the nuclei of the cells. The trained model's feature values were then used to determine whether the tumour produced was benign or malignant.

**Kaiming He Xiangyu Zhang Shaoqing Ren Jian Sun et al.(2015) [10]** - The paper presented a residual learning framework for making it easier to train networks that are significantly deeper than those previously used. Instead of learning unreferenced functions, the layers were explicitly created as learning residual functions with reference to the layer inputs. The empirical evidence showed that residual networks were easier to optimise and could benefit from significantly increased depth. On the ImageNet dataset, residual nets with up to 152 layers—8 are deeper than VGG nets but have lower complexity. On the ImageNet test set, an ensemble of these residual nets achieves a 3.57 per cent error. This result took first place in the classification task at the ILSVRC 2015.

**III. Dataset Description:**

**Date Set Used in the Minor Project**

The following two datasets have been used in the project**:**

* **Wisconsin Breast Cancer Dataset**

**[**[**https://www.kaggle.com/datasets/uciml/breast-cancer-wisconsin-data**](https://www.kaggle.com/datasets/uciml/breast-cancer-wisconsin-data)**]**

* **Breast Histopathology Dataset**

**[**[**https://www.kaggle.com/datasets/paultimothymooney/breast-histopathology-images**](https://www.kaggle.com/datasets/paultimothymooney/breast-histopathology-images)**]**

**3.2 Date Set Features**

**Types of Data Set**

Two kinds of datasets were utilized for the proposed correlation model, one of them incorporated the organized .csv information and the other incorporated the histopathological pictures of the bosom tissue. The dataset was then isolated into Training and testing areas for the important approval. Further definite depiction of the dataset for the twofold characterization has been given above also.

Number of Attributes, fields, portrayal of the informational collection

The quantity of classes in this dataset are 2, for the presence of dangerous and non-harmful tissue in the bosom. Dangerous or carcinoma and harmless or non destructive. The significant two sorts of bosom malignant growths :

Ductal or lobular carcinoma is a sort of malignant growth that influences the digestive organs.

Most of bosom diseases are carcinomas, which are growths that start in the epithelial cells that line the organs and tissues in the body. Adenocarcinoma, which starts in cells in the conduits (milk channels) or the lobules, is the most widely recognized kind of carcinoma that structures in the bosom (organs in the bosom that make milk).

In situ versus intrusive bosom malignant growths : The kind of bosom disease can likewise allude to regardless of whether the malignant growth has spread. In situ bosom malignant growth (ductal carcinoma in situ or DCIS) is a pre-disease that beginnings in a milk pipe and has not developed into the remainder of the bosom tissue. The term obtrusive (or penetrating) bosom disease is utilized to portray any kind of bosom malignant growth that has spread (attacked) into the encompassing bosom tissue.

**Wisconsin Breast Cancer Dataset Description**

A digitized picture of a fine needle suction (FNA) of a bosom mass is utilized to process highlights. They portray the properties of the cell cores that show up in the photo.

The 3-layered space is depicted in: [K. P. Bennett and O. L. Mangasarian: "Powerful Linear Programming Discrimination of Two Linearly Inseparable Sets", Optimization Methods and Software 1, 1992, 23-34].

Property Information:

1) ID number

2) Diagnosis (M = dangerous, B = harmless)

3) Ten genuine esteemed highlights are processed for every cell core:

a) span (mean of good ways from focus to focuses on the edge)

b) surface (standard deviation of dim scale values)

c) edge

d) region

e) perfection (neighborhood variety in range lengths)

f) smallness (perimeter^2/region - 1.0)

g) concavity (seriousness of curved segments of the shape)

h) sunken focuses (number of curved bits of the form)

I) balance

j) fractal aspect ("shoreline estimate" - 1)

For each picture, the mean, standard blunder, and "most obviously awful" or most horrendously terrible (mean of the three biggest qualities) highlights were figured, yielding 30 elements.

For instance, field 3 addresses Mean Radius, field 13 addresses Radius SE, and field 23 addresses Worst Radius.

With four huge digits, all element values are caught.

Property estimations that are absent: none

357 harmless growths, 212 dangerous cancers

**Histopathology Dataset Description**

162 entire mount slide pictures of Breast Cancer (BCa) examples were filtered at 40x in the first dataset.

277,524 50 x 50 patches were recovered from that (198,738 IDC negative and 78,786 IDC positive).

The pictures were in png design.

model uxXyYclassC.png uxXyYclassC.png

where u is the patient ID (10253idx5), X is the x-direction of where this fix was trimmed from, Y is the y-direction of where this fix was edited from, and C is the class, with 0 being non-IDC and 1 addressing IDC.

The picture exhibit of the Histopathological dataset has 2 classes : Benign(0) and Malignant(1).

The shape of the given image was found out to be of the dimension 50X50 with 3 channels indicating the RGB coloured image.

Since the Image dimensions were large and would hence result in less training rate of the model, I standardised the image using the pixel range. The pixel range ranges from 0 - 255.

Therefore , we normalised our data in the range of 0 - 1 by dividing the obtained pixel dimension of the image with maximum pixel range i.e 255.  
The obtained Min and Max Normalised pixel range obtained was 0.188 and 0.957.  
Next I converted the RGB coloured image to the grayscale since it is easier to process the grayscale images.

The images were standardised to obtain the bell shaped Gaussian Curve with mean = 0 and Standard Deviation = 1.

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| **Figure 2: Breast Histopathological Images** |

**IV. Techniques Used:**

**KNN(K- Nearest Neighbour)**

It is an AI calculation that is administered. The calculation can tackle grouping and relapse issue explanations. The image 'K' addresses the quantity of closest neighbors to another obscure variable that should be anticipated or arranged. A similar rule is utilized by the KNN calculation. Its will likely find all of the closest neighbors to another obscure piece of information to figure out what class it has a place with. It's a technique in view of distance.

**SVM(Support Vector Machine)**

Support Vector Machine, or SVM, is a well known Supervised Learning calculation that is utilized for both grouping and relapse issues. In any case, it is essentially utilized in Machine Learning for Classification issues. The SVM's calculation will probably track down the best line or choice limit for arranging n-layered space so we can undoubtedly put new pieces of information in the right classification later on. A hyperplane is the best choice boundary.SVM chooses the outrageous focuses/vectors that guide in the making of the hyperplane. These outrageous cases are alluded to as help vectors, and the calculation is known as the Support Vector Machine.

**CNN (Convolutional Neural Networks)**

A convolutional brain organization (CNN) is a type of counterfeit brain network that is explicitly expected to handle pixel input and is utilized in picture acknowledgment and handling.

CNNs are picture handling, computerized reasoning (AI) frameworks that utilize profound figuring out how to do both generative and distinct assignments, frequently including machine vision, which incorporates picture and video acknowledgment, as well as recommender frameworks and normal language handling (NLP).

A CNN utilizes an innovation like a multi-facet perceptron that is streamlined for low handling prerequisites. An information layer, a result layer, and a secret layer with a few convolutional layers, pooling layers, completely associated layers, and normalizing layers make up CNN's layers. The evacuation of requirements and upgrades in picture handling productivity bring about a framework that is fundamentally more viable and simpler to prepare for picture handling and normal language handling.

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| **Figure 3: General Working Of CNN in Image Classification**  **Image Source:** [**http://surl.li/bxlgd**](http://surl.li/bxlgd) |

A convolution is portrayed in the picture above. To get the convolved include, we apply a channel/kernel(3 network) to the information picture. The following layer gets this convolved include. A convolution is portrayed in the picture above. To get the convolved highlight, we apply a channel/kernel(3 network) to the info picture. The following layer gets this convolved include.

**RESNET50**

In the ResNet50 engineering, a mix of convolution channels of different sizes is utilized to address the crumbling issue of CNN models and diminish the preparation time brought about by the profound design. ResNet50 is made out of 48 convolutional layers, as well as a maxpool layer and a typical pool layer. There are more than 23 million teachable boundaries in this engineering.

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| **Figure 5(b) : ResNet-50 Architecture** |

**VGG16:**

VGG16 is a convolution brain net (CNN) design that won the 2014 ILSVR (Image net) contest. It is viewed as one of the most incredible vision model designs to date. The most distinctive element of VGG16 is that rather than an enormous number of hyper-boundaries, they zeroed in on having convolution layers of 3x3 channel with step 1 and generally utilized a similar cushioning and maxpool layer of 2x2 channel with step 2. All through the engineering, this course of action of convolution and max pool layers is steady. At long last, it has two FC (completely associated layers) and a softmax for yield. The 16 in VGG16 alludes to the way that it has 16 weighted layers. This organization is very enormous in size.

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| **Figure 5(a): VGG-16 Architecture** |

**The above architectures depict that:**

The VGG engineering is partitioned into blocks, every one of which is comprised of 2D Convolution and Max Pooling layers.

ResNet or Residual Network utilizes Skip Connections which permit the evaporating slope issue to be survived.

**V. Architecture / proposed work**

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| **Figure 3 : Design of Problem Statement**  *\*Flow chart drawn using draw.io [https://app.diagrams.net/]* |

The proposed study's major objective is to:

* classify input data (structured data and histopathological breast tumour image data) into benign (non-cancerous) and malignant (cancerous) categories.
* Application of Various Machine Learning & Deep Learning Models for the classification.
* Use of metrics such as accuracy, Confusion Matrix, and others to assess the performance of the applied models.
* Identification of the best model through visualisation.

**VI. Metrics used**

**a. Accuracy:**

Arrangement precision, which is characterized as the quantity of right forecasts partitioned by the all out number of expectations increased by 100, is maybe the most straightforward measurement to utilize and carry out. We can do this by looking at the valid and anticipated values in a circle, or we can basically utilize the scikit-learn module.

**b. Precision:**

It is characterized as the extent of genuine up-sides of absolute up-sides anticipated. An accuracy score of 1 demonstrates that your model missed no obvious up-sides and can recognize accurately from erroneously named places. A low accuracy score (<0.5) shows that your classifier has countless misleading up-sides, which can be brought about by an imbalanced class or inappropriately tuned model hyperparameters.

**c. Recall:**

A review is the proportion of genuine encouraging points to all up-sides in the ground truth. Review towards 1 shows that your model missed no evident up-sides and can recognize accurately and mistakenly named focuses. A low review score (<0.5) shows that your classifier has countless misleading negatives, which can be brought about by an imbalanced class or inappropriately tuned model hyperparameters.

**d. F1-score:**

Accuracy and review are utilized in the F1-score metric. The F1 score is, as a matter of fact, the consonant mean of the two. A high F1 score signifies both high accuracy and high review. It has a decent equilibrium between accuracy and review and performs well on imbalanced grouping issues.

A low F1 score tells you barely anything — it just enlightens you regarding execution at a specific level. Low accuracy implies that we didn't accurately recognize a considerable lot of the cases we distinguished as certain.

**e. Confusion matrix**

The Confusion Matrix is a plain portrayal of ground-truth names versus model forecasts. The occasions in an anticipated class are addressed by each line of the disarray network, while the examples in a genuine class are addressed by every section. Disarray Matrix isn't by and large a presentation metric, however it fills in as an establishment for different measurements to assess the outcomes. In the disarray network, every cell addresses an assessment factor:

True Positive (TP) signifies the number of positive class tests your model accurately anticipated.

True Negative (TN) signifies the number of negative class tests your model accurately anticipated.

The quantity of False Positives (FP) addresses the number of negative class tests your model anticipated inaccurately.

False Negative (FN) addresses the quantity of positive class tests that your model anticipated inaccurately.

**VII. RESULTS AND OBSERVATIONS**

Analysis of results:

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| **Figure 5 (a)-5(b) Accuracy Vs Loss curve for Custom CNN model** | |

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| **Figure 6(a)-6(b) Accuracy Vs Loss curve for Resnet50 CNN model** | |

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| **Figure 7: Training and validation Accuracy and Loss curve for Resnet50 CNN model** | |

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| **Figure 8: Accuracy and Loss curve for VGG-16 CNN model** |

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| **Figure 9: Training and Testing Accuracy & Loss for VGG-16 CNN model** |

The plots for precision measurements contrasting the exhibition of preparing exactness and approval exactness got during the preparation interaction are given in above figures. Both exactness bends are consistently expanding as indicated by the plot, with a quicker roof level acquired for preparing precision. Furthermore, it shows plots for the misfortune work looking at the way of behaving of preparing misfortune and testing misfortune got during the preparation cycle. The two misfortunes are efficiently diminishing.

| **Model** | **Dataset** | **Accuracy Obtained** |
| --- | --- | --- |
| KNN | Wisconsin Dataset | 96.27% |
| SVM | Wisconsin Dataset | 93.7% |
| Custom CNN Model | Histopathological Image Dataset | 69.71% |
| ResNest-15 Pre-Trained Model | Histopathological Image Dataset | 92.17% |
| VGG-16 Pre-Trained Model | Histopathological Image Dataset | 97.96% |

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| **Figure 10: Accuracy Plot for the different Models** |

In ML, KNN performs better compared to SVM on the Wisconsin Dataset.

While in profound learning models, the precision metric shows that VGG16 outflanked Custom CNN model and Resnet 50 model. The preparation and approval exactness were most extreme for the VGG16 .The conceivable justification for its precision could be the bigger number of the boundaries that makes it powerful to overfit to the dataset quicker. In the long run, we additionally experienced early halting which was countered by the callback function..More boundaries makes it a superior element extractor. These outcomes plainly show VGG16's order abilities and its strong presentation on our dataset.

**VIII. Conclusion**

Based on the above observations and metrics performed on various machine learning and deep learning models on both structured and image datasets, we finally concluded that our datasets (Wisconsin dataset & Histopathological Image dataset) performed well on KNN and VGG16 pre-trained model techniques respectively.

To prove our validation for the same, two methods could be adopted :

**MANUAL VALIDATION :**

In this, we could provide our predicted results to the domain expert mainly from the healthcare domain to validate the actual and predicted output results.

**MACHINE ORIENTED PREDICTION :**

In this, we can provide the predicted results to the machine, which would further predict the actual and predicted results based on the performance metrics , for instance, confusion matrix or accuracy to get the authentication on the achieved results.  
  
Based on these observations, we can then provide a better solution to the healthcare department to get a reliable solution in detecting breast cancer.

**References:**

[1] Masud, M., Eldin Rashed, A. E., & Hossain, M. S. (2020). Convolutional neural network-based models for diagnosis of breast cancer. Neural Computing and Applications. doi:10.1007/s00521-020-05394-5.

[2] Alanazi, S. A., Kamruzzaman, M. M., Islam Sarker, M. N., Alruwaili, M., Alhwaiti, Y., Alshammari, N., & Siddiqi, M. H. (2021). Boosting breast cancer detection using convolutional neural network. Journal of Healthcare Engineering, 2021.

[3] Ahmad, L. G., Eshlaghy, A. T., Poorebrahimi, A., Ebrahimi, M., & Razavi, A. R. (2013). Using three machine learning techniques for predicting breast cancer recurrence. J Health Med Inform, 4(124), 3.

[4] Huang, M. W., Chen, C. W., Lin, W. C., Ke, S. W., & Tsai, C. F. (2017). SVM and SVM ensembles in breast cancer prediction. PloS one, 12(1), e0161501.

[5] Agarap, A. F. M. (2018, February). On breast cancer detection: an application of machine learning algorithms on the wisconsin diagnostic dataset. In Proceedings of the 2nd international conference on machine learning and soft computing (pp. 5-9).

[6] Dey, S. CNN application on structured data-Automated Feature Extraction. URL: https://towardsdatascience. com/cnn application-on-structured-data-automated-feature extraction-8f2cd28d9a7e.(accessed: 20.05. 2019).

[7] Huang, G., Liu, Z., Van Der Maaten, L., & Weinberger, K. Q. (2017). Densely connected convolutional networks. In Proceedings of the IEEE conference on computer vision and pattern recognition (pp. 4700-4708).

[8] Yamashita, R., Nishio, M., Do, R. K. G., & Togashi, K. (2018). Convolutional neural networks: an overview and application in radiology. Insights into imaging, 9(4), 611-629.

[9] Gandhi, R. (2018). Support vector machine—introduction to machine learning algorithms. Towards Data Science, 7.

[10] Kaiming He, Xiangyu Zhang, Shaoqing Ren, Jian Sun(2015)-Deep Residual Learning for Image Recognition.

[11] Frid-Adar, M., Diamant, I., Klang, E., Amitai, M., Goldberger, J., & Greenspan, H. (2018). GAN-based synthetic medical image augmentation for increased CNN performance in liver lesion classification. Neurocomputing, 321, 321-331.

[12] Dabiri, S., & Heaslip, K. (2018). Inferring transportation modes from GPS trajectories using a convolutional neural network. Transportation research part C: emerging technologies, 86, 360-371.

[13] Russakovsky, O., Deng, J., Su, H., Krause, J., Satheesh, S., Ma, S., ... & Fei-Fei, L. (2015). Imagenet large scale visual recognition challenge. International journal of computer vision, 115(3), 211-252.

[14] Krizhevsky, A., Sutskever, I., & Hinton, G. E. (2012). Imagenet classification with deep convolutional neural networks. Advances in neural information processing systems, 25.

[15] Gulshan, V., Peng, L., Coram, M., Stumpe, M. C., Wu, D., Narayanaswamy, A., ... & Webster, D. R. (2016). Development and validation of a deep learning algorithm for detection of diabetic retinopathy in retinal fundus photographs. Jama, 316(22), 2402-2410.

[16] Bejnordi, B. E., Veta, M., Van Diest, P. J., Van Ginneken, B., Karssemeijer, N., Litjens, G., ... & CAMELYON16 Consortium. (2017). Diagnostic assessment of deep learning algorithms for detection of lymph node metastases in women with breast cancer. Jama, 318(22), 2199-2210.

[17] Christ, P. F., Elshaer, M. E. A., Ettlinger, F., Tatavarty, S., Bickel, M., Bilic, P., ... & Menze, B. H. (2016, October). Automatic liver and lesion segmentation in CT using cascaded fully convolutional neural networks and 3D conditional random fields. In International conference on medical image computing and computer-assisted intervention (pp. 415-423). Springer, Cham.

[18] Hubel, D. H., & Wiesel, T. N. (1968). Receptive fields and functional architecture of monkey striate cortex. The Journal of physiology, 195(1), 215-243.

[19] Assegie, T. A. (2021). An optimized K-Nearest Neighbor based breast cancer detection. Journal of Robotics and Control (JRC), 2(3), 115-118.