

GENETIC ALGORITHM BASED ATTENTION UNET OPTIMIZATION FOR BREAST TUMOR SEGMENTATION

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As one of the main causes of cancer-related mortality among women worldwide, breast cancer requires better diagnostic techniques that can provide non-invasive, fast, and accurate detection. The World Health Organization (WHO) has a dedicated cancer agency called the International Agency for Research on Cancer (IARC), whose mission is to undertake and coordinate research on cancer causes. Mammography is one of many imaging modalities that is frequently used to find abnormalities. Although automated breast mass segmentation in mammography is vital, the uniform sizes and shapes of tumors make it a difficult process. UNet models have shown a significant segmentation in the medical images. In this study, we propose a prominent genetic algorithm (GA) for the generation of UNet models by selecting the optimal parameters. The experiments involved manually generated architectures, basic UNet model and an attention based UNet, AUNet model with different filter sizes. As a result of the manual approach, the AUNet outperformed the base model and hence the AUNet is considered as the base model for the GA process. The experiments show that the models evolved using GA are simple and are of small architecture. The model yielded a better segmentation of the images and outperformed the manually created UNet models, with dice scores and Intersection over Union (IoU) scores of 91.6% and 89.2%, respectively.

Keywords Convolution Neural Network, Breast cancer, Segmentation, UNet, Genetic Algorithm

INTRODUCTION

Breast cancer is one of the most prevalent cancers that affect women globally, and its incidence rates are rising in a number of demographics. Developing a treatment plan effectively

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and improving patient outcomes are dependent on early and precise detection of breast cancers. The Indian Council for Medical Research (ICMR) reports that this disease has a high death rate in India and that, among urban and rural areas, the incidence is higher in the former due to a delayed diagnosis as discussed in UTHAYAN *et al.* (2019). Physical examinations, non-invasive imaging methods including mammography, ultrasound, followed by a histological investigation after invasive biopsy extraction of the tissue are the key components of the diagnosis process for breast cancer. Although it takes a great deal of experience to interpret, ultrasound is a supplemental technique that can help distinguish solid tumors from fluid-filled cysts. Although expensive and not always available, magnetic resonance imaging (MRI) provides comprehensive insights. The final diagnosis is made by a biopsy and histological investigation, which are invasive procedures that depend on the availability of qualified pathologists.

Recent technological developments have had a profound impact on the field of breast tumor diagnostics. Artificial intelligence (AI) and machine learning algorithms have an important role in the interpretation of complicated diagnostic data. With the use of these technologies, it may be possible to minimize invasive procedures, speed up diagnosis times, and improve accuracy. Large volumes of data are analyzed, and they discover patterns that may be too subtle or intricate for human vision, thereby leading to the earlier detection of cancer than would be possible with conventional techniques. However, even with the sophisticated approaches, there are still a lot of challenges such as false negatives and positives. Segmenting breast tumor images effectively is a critical component of diagnosing and treating breast cancer. In the paper LECUN *et al.* (2015), the authors have discussed Convolutional Neural Networks (CNNs) for image classification tasks. CNNs are becoming a very useful tool in medical imaging, especially when it comes to diagnosing breast tumors. This use of CNNs takes advantage of their capacity to extract information efficiently and automatically from images, which is essential for recognizing and categorizing cancers in mammograms. Segmentation of the Region of Interests includes both traditional and deep models. The traditional approach includes several disadvantages tabulated in table 1. Some encoder decoder-based models are widely used in segmentation tasks. However, choosing and fine-tuning machine learning models for tasks like image recognition and segmentation involves a series of critical decisions and challenges.

Table 1. Disadvantages of traditional segmentation approaches

Traditional approaches	Demerits
Edge detection	Produce poor results for irregular and smooth edges.
Region seeding	Choice of the seed values and each seed value produce unique results.
Thresholding	Not suitable for medical images due to its complex underlying pattern.

The selection of appropriate hyperparameters can be optimized using evolutionary algorithms. Natural selection serves as the inspiration for one particular kind of evolutionary algorithm

called a genetic algorithm (GA). These algorithms are especially well-suited for hyperparameter tweaking in machine learning models because they can be very successful at optimizing complicated issues with expansive and diverse search areas. GA is particularly effective in navigating large and complex hyperparameter spaces where the parameters interact in non-linear ways that affect the performance of the model. In this work, we propose to utilize genetic algorithms for the selection of best choices for the hyperparameter tuning and model construction.

MATERIALS AND METHODS

Literature Survey

YOUSEFIKAMAL (2019) proposed an efficient CAD system for segmenting the RoIs of the breast tumor images. The given dataset is distinguished into benign and malignant followed by RoI segmentation. Image enhancement is achieved by reducing the artifacts and noises using block matching and filtering techniques. Further, the pectoral muscles are suppressed, and the tags are removed. CNN is used for understanding the underlying patterns and for feature extraction. The localization of the tumor is marked with a clustering technique, spatial fuzzy clustering. It is considered to be an efficient approach as it focuses on learning spatial and local intensity information.

DONG *et al.* (2017), devised a fully convolution UNet for identifying tumors in the brain. The dataset is augmented using color transformations, geometrical based deformation, and other distortion-oriented transformations. In this work, the authors utilized soft dice-based loss to handle unbalanced samples. HUANG *et al.* (2020) proposed a U-Net to validate on liver datasets for segmentation tasks. Remodeled full scale skip connections are utilized, which assists to create precise RoIs with fewer parameter extraction. The proposed approach includes deep supervision and classification, where the patterns are extracted from the hierarchical feature maps with a novel loss function. Classification guided module adds more generalization to the extraction of the RoIs. From the results it substantiates that the proposed model outperformed other models on the given dataset.

SATHYAN *et al.* (2020) localized lesions and the calcifications in the mammogram images using UNet architectures. The authors proposed two models, where the first model is validated on CBIS-DDSM dataset to identify and segment the masses whereas the other model is validated on INBreast dataset. However, the model is likely to produce false negatives and positives. SUN *et al.* (2020) proposed an attention based Unet model for a better segmentation of the RoIs. This work targets to reduce the loss of information during the decoder phase by including an attention guided approach which extracted both the high- and low-level features for segmentation. CBIS-DDSM and INbreast dataset are used to validate the attention-based model with a dice coefficient of 81.8% for CBIS-DDSM and 79.1% for INbreast.

There are several other imaging datasets are available where the authors of LAI *et al.* (2020) experimented on proposed a UNet architecture Digital breast tomosynthesis (DBT) images. The images are preprocessed using enhancement and transformation, where certain filters are applied to smooth the edges. Furthermore, the dataset is augmented and an accuracy of 0.871 is achieved. On the contrary PI *et al.* (2021) designed a feature-oriented model which enables a

higher level of feature extraction. The vital features are extracted using parallel dilated convolutions and also include a loss function which assists to yield a better accuracy. CAO *et al.* (2021) utilized a cascaded unet where six of the Unets are connected to yield a better segmentation which is validated on CBIS-DDSM and INBreast dataset.

Several variations in the UNet and the corresponding skip connections are utilized to segment the RoIs from the medical images. In this research we will consider a base UNet and add attention component to them for a better understanding of the features and localization of the tumors in the mammograms.

Breast Tumor Segmentation

Figure 1 illustrates the proposed model for breast tumor diagnosis. The images are preprocessed and enhanced for a better segmentation of the images. A genetic based algorithm is infused in the model in order to identify the best model that contributes towards the segmentation of the tumors in the mammogram images.

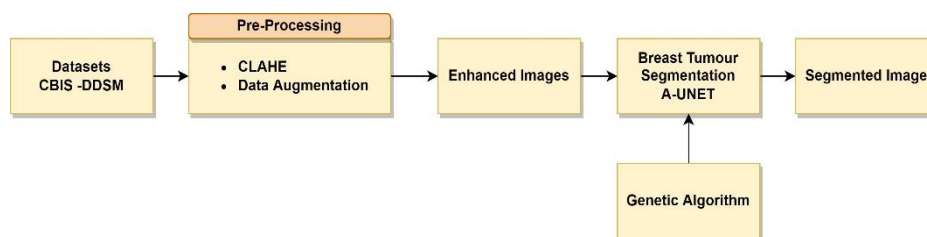


Figure 1. Block diagram of the breast tumor segmentation

Table 2. Geometric transformations used in the proposed model

Methods	Description
Flipping	Horizontal and vertical flip
Rotation	Image rotation is done with chosen angles.
Scaling	Resizing of images
Translation	Shifting the image vertically or horizontally

Data augmentation

Data augmentation is a crucial method with respect to medical images as it involves ethical and privacy concerns, especially when training deep learning models. Class imbalance or skewed data leads to overfitting and decreases the performance of the model. Data augmentation makes training datasets larger and more diverse artificially, which aids in the learning of more generalizable characteristics and improved performance on unseen data. Several techniques discussed in table 2 are the traditional methods to augment images. The values must be chosen in such a way that the underlying information is not compensated. In research contributions by DHIVYA *et al.* (2020B) includes the data augmentation techniques which involve both the traditional and deep model approaches to augment the datasets. In this research, we consider

only traditional geometrical transformation to scale up the dataset which has made the corpus five times larger than the original dataset.

Encoder Decoder Architecture

The encoder decoder-based architecture is basically a deep CNN for segmentation of the images. The structure includes an encoder network pixel-based segmentation. The objective of the encoder is to extract the low-level features whereas the aim of the decoder is to map the output of the encoder layer features to obtain a better resolution of the images.

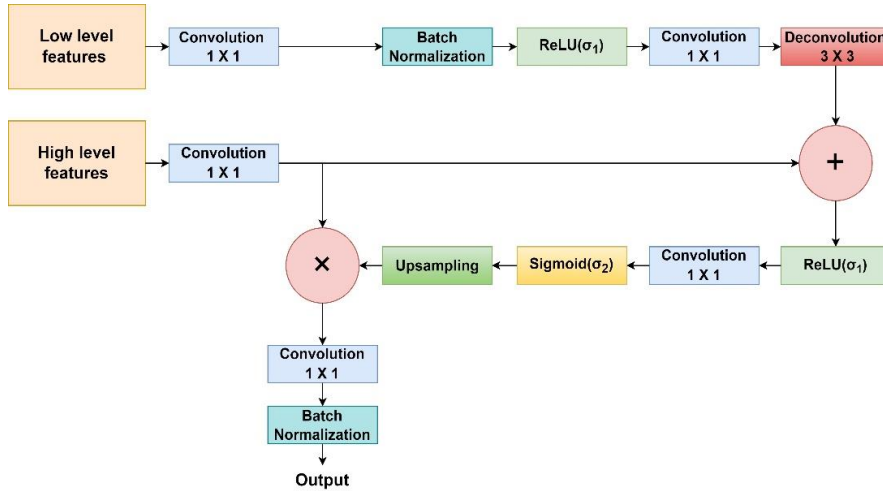


Figure 2. Attention Mechanism

Attention Mechanism

The attention mechanism in Attention U-Net is specifically implemented at each stage of the expanding path where features from the contracting path are concatenated. These are called Attention Gates (AG). The attention gates automatically learn to focus on target structures of varying shapes and sizes. They filter the feature response propagated through the skip connections by explicitly modeling inter-spatial relationships (dependencies) between them. This results in the gating mechanism only highlighting salient features useful for specific tasks. The architecture of the attention mechanism in AUNet is given in Figure 2.

U-Net

U-Net is a highly efficient convolutional neural network (CNN) originally designed for biomedical image segmentation tasks. Its architecture is uniquely suited for medical image processing, featuring a symmetric structure that consists of a contracting path to capture detailed contextual information and an expansive path that aids in precise localization of structures within the image. The key innovation of U-Net lies in its use of skip connections that bridge the contracting and expansive paths, allowing the network to propagate context information directly

across the network for more precise segmentation. This capability makes U-Net particularly effective at delineating complex biological structures, which is often required in medical imaging tasks such as tumor segmentation or organ delineation. The network's ability to operate efficiently with relatively few training images and its adaptability to different tasks without substantial modifications also contribute to its popularity in medical image segmentation.

The attention techniques integrated into the Attention U-Net architecture focus the computing resources of the model on significant portions of the input data, thereby improving upon the conventional U-Net framework. In order to filter and improve the feature maps prior to concatenating them with the upsampled outputs, this version of the U-Net integrates attention gates into its skip connections. Using input from the contracting and expanding routes, the attention gates conduct changes via convolution layers before employing sigmoid activation to produce attention coefficients. The architecture of the model is illustrated in the below Figure 3.

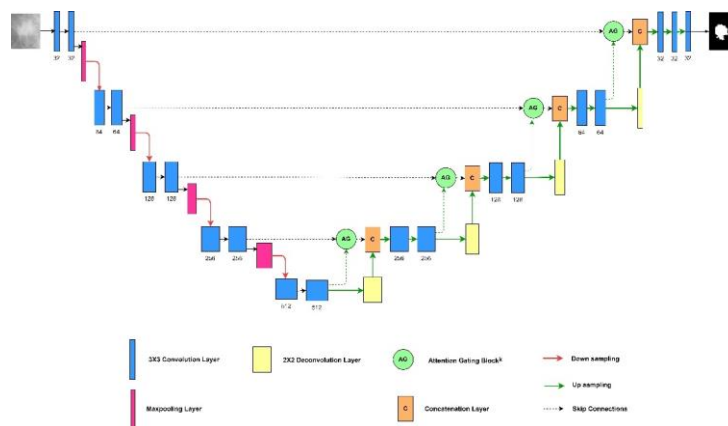


Figure 3. Architecture of Attention UNet

Genetic Algorithm

The idea of evolution by natural selection served as the foundation for the Genetic Algorithm (GA). GAs chooses the most fit people, which is similar to how natural selection works, and reproduction to create the future generation's children (UTHAYAN, 2021). In order to incorporate GA, the encoding of a typical solution from a particular problem is created. The processes associated with biological evolution are used where the individuals I , represent answers to a particular problem. The I , involves three elements in general: Phenotype, genotype and score. The characteristics of the individuals are observed as the phenotype Ph and with respect to this problem, the U-Net architecture is denoted as Ph . There are certain parameters to be optimized namely $(ph_1, ph_2, ph_3, ph_4, ph_5)$ called Ph as a whole. Thus, with this Ph , a set of solutions are obtained and further the quality is evaluated, which is referred to as a fitness function. This function designates a fitness score to Ph called as S . As to obtain more new solutions, a part of the solutions namely Q obtained from I are merged. This process is quite similar to the DNA

encoding of living organisms. Nonetheless, there are several approaches to calculate and often used approach is using bitstring. The encoding of P using the bits is termed as genotype G , which includes an output of encoded information represented as $(g_1, g_2, g_3, g_4, g_5)$. The length of G and Ph are of same, however each g includes an array of bits represented as $(b_1, b_2 \dots b_n)$, where n is the maximum number of bits used for encoding. GA always considers individuals with high probability from Q with a higher score S which is used to further crossover to obtain more optimal solutions. The process ends once it reaches the given criterion to halt. This process is explained in Algorithm 1. Thus, this evolution assists in producing more solutions and the process ends as the optimal solution is obtained.

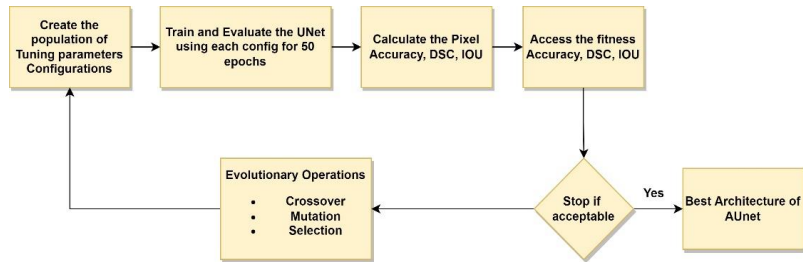


Figure 4. Genetic algorithm for the selection of best UNet architecture

Algorithm 1: Genetic Algorithm

1. create an m -chromosome population of random type, $f(y)$.
 2. Fitness: Estimate the population-wide fitness of each chromosome y .
 3. New population: Iterate through the following steps to obtain a new population.
 - (a) Selection: Choose the couple of chromosomes of parent from the population based on fitness score S
 - (b) Crossover: Apply cross over to obtain a new offspring. If no crossover, traits from parents are obtained.
 - (c) Mutation: Create new offspring with a mutation at each locus using a mutation probability.
 - (d) Acceptance: Add a fresh generation to a recent population
 4. Use the newly created population in a subsequent algorithm run.
 5. If the final criterion is met, finish the procedure, and return the optimal option from the current population.
 6. Go to step 2
-

Table 3. Dataset Description

Dataset	Benign	Malignant	Total
CBIS-DDSM	849	743	1592

RESULTS AND DISCUSSIONS

Dataset

Derived from the broader and extensively cited DDSM (Digital Database for Screening Mammography), the CBIS-DDSM (Curated Breast Imaging Subset of Digital Database for Screening Mammography) is a well-structured dataset. The CBIS-DDSM has been selected to support computer-aided diagnostic and machine learning research in mammography. It has thousands of mammography images with professional annotations and labeling identifying benign and malignant tumors. This dataset is especially useful for creating and evaluating algorithms intended to automate the use of mammography in the identification and diagnosis of breast cancer. The CBIS-DDSM is a comprehensive resource for training and validating diagnostic models since it includes detailed metadata for each image, such as lesion kind, pathology diagnosis, and lesion outlines. Table 3 represents the description and distribution of the dataset.

Performance Metrics

In this research to evaluate the models and the role of genetic algorithm, the performance metrics that are considered are the dice score and the intersection over union (iou). The appropriate true positives (tp), true negatives (tn), false positives (fp), false negatives (fn) are derived for the calculation of pixel accuracy.

Pixel Accuracy: The percentage of the image pixels that are correctly categorized is known as the pixel accuracy illustrated in equation 1. Pixel accuracy is assessed using binary masks for segmentation tasks; successfully identified pixels are labeled as true positives, whereas pixels that do not belong to the class are labeled as true negatives. However, pixel accuracy is not an appropriate choice of metric for precise segmentation.

$$\text{Pixel accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (1)$$

Dice coefficient: Dice coefficient also referred to as dice score, is a statistical tool used to gauge the similarity between two images. The coefficient calculates the overlap between the predicted segmentation from an algorithm and the ground truth. The dice score is calculated as

$$Dice\ score = \frac{2|A \cap B|}{|A| + |B|} \quad (2)$$

A is the predicted set of pixels and B is the actual mask. The result is a score ranging from 0 to 1, where 0 indicates no overlap and 1 represents perfect agreement between the predicted and actual segmentations. This makes the Dice score extremely useful for evaluating how effectively a segmentation model can replicate expert-level annotations, providing a quantitative measure to refine and optimize computational approaches in automated medical image analysis.

Intersection over Union: Intersection over Union (IoU), also known as the Jaccard Index, is a widely used performance metric in the fields of computer vision and image segmentation, particularly for evaluating object detection and segmentation models. IoU measures the overlap between two sets of data: the predicted area and the ground truth, quantifying the accuracy of a model. It is calculated by dividing the area of overlap between the predicted segmentation and the ground truth by the area of their union. The value of IoU ranges from 0 to 1, where 0 indicates no overlap and 1 signifies perfect overlap, or exact correspondence between the predicted and actual segments.

$$I(A, B) = \frac{A \cap B}{A \cup B} \quad (3)$$

Table 4. Representation of manual UNet Models

Models	Depth	Pooling	Kernel Size	Optimizer
UNet	4	MaxPooling	3×3	SGD
Model 2	2	MaxPooling	3×3	Adam
Model 3	4	MaxPooling	3×3	Adam
Model 4	2	MaxPooling	3×3	Adam

Table 5. Filter parameters of the UNet models

Models	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12	F13	F14	F15	F16	F17
Model 1																	
1	32	64	64	128	128	256	256	256	512	256	128	256	128	64	128	64	64
Model 2																	
2	64	64	128	128	256	256	512	512	1024	512	512	256	256	128	128	64	64
Model 3																	
3	32	32	64	64	128	128	256	256	512	256	256	128	128	64	64	32	32
Model 4																	
4	64	64	128	128	-	-	-	-	-	-	512	256	256	128	128	64	64

Ablation of U-Nets

In our proposed work the benchmark breast cancer dataset images are used, and segmentation of the mass lesions is achieved using an Attention based UNet. However, we

compare the Attention based UNet with the traditional baseline model proposed by olaf Ronnenberger. The baseline architecture is considered as Model 1, where the parameters set for the UNet includes a kernel of 3×3 , MaxPooling as its pooling type and the optimizer is set as stochastic gradient descent. The Model 2 includes the attention based UNet, with Adam as the optimizer and maxpooling as the pooling type. The number of iterations is given as 150 for training the images. The parameters are further exploited in Model 3 by reducing the number of filters, the parameters obtained for the learning process are completely reduced to halve rate and the depth of the models are also reduced. All the models have similar configurations as illustrated in Table 4. However, the filter sizes for these models have changed but the number of filters remains the same for all the models. In Model 4 the last two layers are removed, thereby this model involves two layers with ten filters.

Genetic Algorithms for Automated UNets

The GA algorithm is incorporated in order to automatically create models with the parameters illustrated in Table 7 and 8. The hyperparameters are optimized with two different iteration values for the training phase. With the given parameters, each model is trained for 50 epochs, and the optimal solutions obtained with the GA, that is the best UNet is selected, and further the model is trained for 150 iterations, thereby achieving an optimized segmentation of the images. The list of the parameters considered for optimization is articulated in Table 6.

Table 6. Representation of GA Parameters

Parameter	Runs	Total Generations	Population size	Crossover rate	Mutation Rate	Initial Epochs	Best model_ Epochs
Value	1 for each experiment	20	10	0.7	0.1	50	150

Table 7. Representation of genome composition for the parameters and genes

Parameter	Genes	Choices	Bit-string	Bits	Qty	Size
Depth	D	{1,2,3,4}	(b1,b2)	2	1	2
Filter Size	{F1...F17}	{16,32,64,128,256,512,1024}	(b3,b4,b5)...(b39,b40,b41)	3	13	39
Pooling Type	P1,P2,P3,P4	{MaxPooling, AveragePooling}	(b42)(b45)	1	4	4
Filter Type	K1,K2,K3,K4	{(3,3),(5,5),(7,7),(9,9)}	(b46,b47)...(b52,b53)	2	4	8
Optimizer	O	{sgd, adam}	(b54,b55)	2	1	2

Table 7 represents the genome composition along the parameters chosen to optimize the UNet architectures. The genotype represented as g includes a group of genes such as (D, F, P, K,O) where 2,3,1,2 and 2 are the bits assigned respectively. Thus, the size of the genome is composed of 55 bits. The important parameter that determines the architecture of the UNets is the depth parameter. Thus, parameter D has four options between 1 to 4 and requires two bits for encoding. All parameters are taken into consideration if the depth of the architecture is 4. some

of the other parameters are neglected if the depth is chosen less than 4. For instance, if D is 2, then the pooling and kernel parameters are chosen for the first two layers. The depth reduction curtails the number of filters chosen. In this scenario, there are ten filters involved in two layers of the UNet. The other parameters involved are encoded with the corresponding bits illustrated in Table 7.

Table 8. GA based selected U-Net architectures and parameters

Models	Depth	P1	P2	P3	P4	K1	K2	K3	K4	Optimizer
Model 5	4	Average	Average	Average	Average	(3,3)	(5,5)	(7,7)	(9,9)	Adam
		Pooling	Pooling	Pooling	Pooling					
Model 6	2	Max Pooling	Max	Average	Max	(9,9)	(9,9)	(9,9)	(9,9)	Adam
			Pooling	Pooling	Pooling					
Model 7	4	Max Pooling	Max	Max	Max	(9,9)	(9,9)	(3,3)	(3,3)	Adam
			Pooling	Pooling	Pooling					
Model 8	2	Max Pooling	Average	Max	Average	(9,9)	(9,9)	(5,5)	(7,7)	Adam
			Pooling	Pooling	Pooling					

Table 9. GA based selected filters for the U-Net architectures

Models	F																
	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12	F13	F14	F15	F16	F17
Model 5	32	32	64	256	512	-	-	-	-	-	512	1024	512	64	128	32	32
Model 6	32	16	32	8	16	-	-	-	-	-	16	32	16	32	128	32	16
Model 7	64	128	16	32	256	-	-	-	-	-	32	64	256	128	128	64	64
Model 8	32	64	128	256	-	-	-	-	-	-	32	64	32	16	32	16	16

Table 8 represents four models and their parameters selected by the GA algorithm. From Table 8, it can be inferred that the GA prefers UNet architectures with large kernel sizes, Adam as the optimizer in all the models and Maxpooling as the pooling type in several layers. It is observed that the GA selects the maximum kernel size of (9,9) often.

All the models involve 2 as its depth, hence the filters are bound to 10 which are illustrated in Table 9. The model 6 considers the least values as filters in the encoder path whereas the model 8 takes the least values in its decoder path. Model 5 encompasses the largest filter values amongst all the four models. Figure 5 consolidates all the information of both manual and GA automated models.

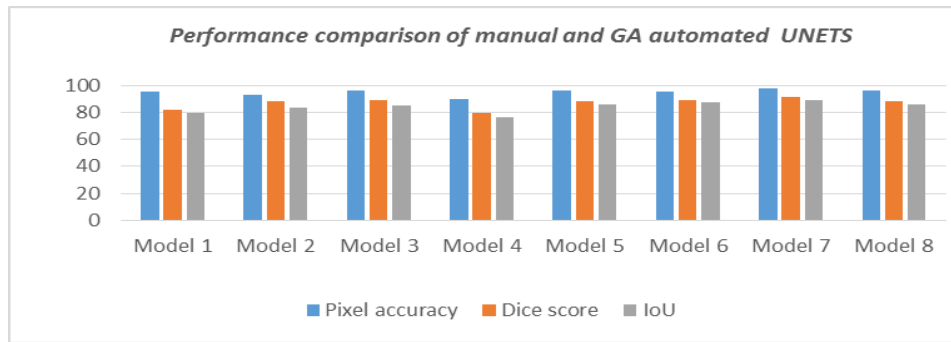


Figure 5. Performance comparison of manual and GA automated UNETS

Table 10. Comparison of the performance metrics of manual and GA automated UNets

Models	Pixel accuracy	Dice score	IoU	Training Time (in hrs)	Testing Time (in minutes)
Model 1	95.6	82.3	79.9	10	8
Model 2	93.5	88.4	83.5	6	5
Model 3	96.1	89.3	85.7	8	6
Model 4	90.3	79.6	76.3	4	4
Model 5	96.3	88.7	86	13	5
Model 6	95.9	89.1	88.1	14	5
Model 7	97.8	91.6	89.2	16	6
Model 8	96.1	88.2	86.5	15	5

Table 10 includes the overall performance shown by both manual and GA generated UNet architectures. The GA algorithm is executed for one experimental run with the settings illustrated in Table 6. The dice score and the IoU for manually set models, model 1 to model 4 are illustrated in Table 10. The GA section represents the optimal UNet architectures resulted using the GA approach. The selection is based mainly on the depth, optimizer and the pooling type. The performance during the training phase is measured with metrics such as pixel accuracy and the pixel accuracy is considered to be the fitness score to choose the best UNet architectures. In manual models, Model 3 achieved a better pixel accuracy and their corresponding dice score and the IoU score as calculated using Equation (2) and (3). This is due to the involvement of the attention-based approach, hence the base architecture for the GA approach included the AUNet. With respect to the GA approach, the Model 7 showed a better pixel accuracy score with a bigger kernel size of (9,9) and Adam as optimizer. The other parameters are tabulated in Table 8 and 9. From Table 10, it is shown that the Model 3 has a better dice and IoU score compared to other models in the manual approach with 91.6 and 89.2 respectively. From Table 10, it can be inferred that the Model 7 has outperformed the other GA generated models and also the manual models. With respect to time taken for the training and testing, the GA based AUNet approaches have taken double the time for the training phase. Model 1 and Model 2 architectures are large

compared to the Model 3 and 4. The architectures generated by GA are in general smaller than the architectures of the manual approach. However, the reduction in the architecture has an impact in the training process making it computationally intensive.

Table 11. Comparison of the proposed model with existing systems

Model	Method	Dice Score	IOU Score
RAVITHA et al. (2021)	DS-Unet	81.8	Nil
SATHYAN et al. (2020)	Unet-mass	67.3	Nil
SUN et al. (2021)	ASU-Net	91.41	Nil
ABDELHAFIZ et al. (2019)	R-Unet	90.5	89.1
SOULAMI et al. (2021)	Unet128Adam	Nil	89.1
Proposed	GA-UNet	91.6	89.8

CONCLUSION

In this research, we aim to segment the mammogram images using the benchmark dataset CBIS-DDSM. The traditional approaches majorly involve deep networks, which leads to complexity as it goes deeper. The manual designing of architectures is quite tedious as it involves a lot of parameters switching. Thus, a two set of approaches, manual and GA based architecture tuning has been proposed. The manually designed UNets include the traditional UNet architecture, and an attention based UNet, AUnet. Among them, the AUNets outperformed the traditional model. Hence the AUnet is considered as the base model for the GA approaches. A prominent GA approach is used to exploit the UNet architectures. The experiments and their respective results emphasize that GA can build networks with minimal parameters which outperformed the traditional models. Thus, the GA evolved architecture was able to achieve 91.6% of dice score and 89.2% of IoU score. For future work, a finetuned GA with an increased size of population and generations can be implemented thereby improving the performance of the segmentation.

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REFERENCES

- ABDELHAFIZ, D., S., NABAVI, R., AMMAR, C., YANG, J., BI (2019): Residual deep learning system for mass segmentation and classification in mammography. In Proceedings of the 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics, 475-484.
- CHOUGRAD, H., H., ZOUAKI, O., ALHEYANE (2018): Deep convolutional neural networks for breast cancer screening, Computer methods and programs in biomedicine, 157: 19-30.
- DHIVYA, S., S., MOHANAVALI, S., KARTHIKA, S., SHIVANI, R., MAGESWARI (2020A): GAN based data augmentation for enhanced tumor classification. 2020 4th International Conference on Computer, Communication and Signal Processing (ICCCSP) special focus on data visualization, 1-5. IEEE.
- DHIVYA, S., R.J., ANJALI, S., MOHANAVALI, N., SRIPRIYA, K., SRINIVASAN (2020B): Investigations of Shallow and Deep Learning Algorithms for Tumor Detection, International conference on engineering in the 4th industrial revolution, IEEE-HYDCON Sep 11-12, 1-5. IEEE.

- DHIVYA, S., S., MOHANAVALLI, S., KAVITHA (2023): Automated carcinoma classification using efficient nuclei-based patch selection and deep learning techniques. *Journal of Intelligent & Fuzzy Systems*, 45(1):521-535.
- DONG H., G., YANG, F., LIU, Y., MO, Y., GUO (2017): Automatic Brain Tumor Detection and Segmentation Using U-Net Based Fully Convolutional Networks. *Medical Image Understanding and Analysis (MIUA)*. arXiv:1705.03820
- HUANG, H., L., LIN, R., TONG (2020): UNet 3+: A Full-Scale Connected UNet for Medical Image Segmentation. *ICASSP 2020 - 2020 IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP)*, Barcelona, Spain, 1055-1059.
- LECUN, Y., Y., BENGIO, G., HINTON (2015): Deep learning. *Nature*, 521(7553): 436-444.
- LEE, R. S., F., GIMENEZ, A., HOOGI, K. K., MIYAKE, M., GOROVOY, D.L., RUBIN (2017): A curated mammography data set for use in computer-aided detection and diagnosis research. *Scientific data*, 4(1):1-9.
- PI, J., Y., QI, M., LOU, X., LI, Y., WANG, C., XU, Y., MA (2021): FS-UNet: Mass segmentation in mammograms using an encoder-decoder architecture with feature strengthening. *Computers in Biology and Medicine*, 137:104800.
- PONRAJ, D.N., M.E., JENIFER, P., POONGODI, J.S., MANOHARAN (2011): A survey on the preprocessing techniques of mammogram for the detection of breast cancer, *Journal of emerging trends in computing and information sciences*, 2(12):656-664.
- RAJALAKSHMI, N., R., VIDHYAPRIYA, N., ELANGO, N., RAMESH (2021): Deeply supervised u-net for mass segmentation in digital mammograms. *International Journal of Imaging Systems and Technology*, 31(1): 59-71.
- SATHYAN, A., M., DINO, K., COHEN (2020): Mass and Calcification Detection from Digital Mammograms Using UNets, *7th International Conference on Soft Computing & Machine Intelligence (ISCMI)*, 229-232.
- SOULAMI, K. B., N., KAABOUCH, M.N., SAIDI, A., TAMTAOUI (2021): Breast cancer: one-stage automated detection, segmentation, and classification of digital mammograms using UNet model based-semantic segmentation. *Biomedical Signal Processing and Control*, 66: 102481.
- SUN, H., C., LI, B., LIU, Z., LIU, M., WANG, H., ZHENG, S., WANG (2020): AUNet: attention-guided dense-upsampling networks for breast mass segmentation in whole mammograms. *Physics in Medicine & Biology*, 65(5): 055005.
- SUN, K., Y., XIN, Y., MA, M., LOU, Y., QI, J., ZHU (2021): ASU-Net: U-shape adaptive scale network for mass segmentation in mammograms. *Journal of Intelligent & Fuzzy*, 42(4):4205-4220.
- UTHAYAN, K.R. (2019): A novel microarray gene selection and classification using intelligent dynamic grey wolf optimization. *Genetika-Belgrade*, 51(3):805-828.
- UTHAYAN, K. R., S., MOHANAVALLI, B., NIVETHA, S., DHIVYA (2021): Optimised feature selection for early cancer detection. *Genetika*, 53(3):1297-1309.
- YOUSEFIKAMAL, P. (2019): Breast Tumor Classification and Segmentation using Convolutional Neural Networks. arXiv preprint arXiv:1905.04247.

OPTIMIZACIJA UNET MODELA ZA SEGMENTACIJU TUMORA DOJKE ZASNOVANOG NA GENETIČKOM ALGORITAMU

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IZVOD

Kao jedan od glavnih uzroka smrtnosti od raka kod žena širom sveta, rak dojke zahteva bolje dijagnostičke tehnike koje mogu da obezbede neinvazivno, brzo i tačno otkrivanje. Svetska zdravstvena organizacija (SZO) ima namensku agenciju za rak pod nazivom Međunarodna agencija za istraživanje raka (IARC), čija je misija da preduzima i koordinira istraživanje o uzrocima raka. Mamografija je jedan od mnogih modaliteta snimanja koji se često koristi za otkrivanje abnormalnosti. Iako je automatska segmentacija mase dojke u mamografiji od vitalnog značaja, ujednačene veličine i oblici tumora čine to teškim procesom. UNet modeli su pokazali značajnu segmentaciju na medicinskim slikama. U ovoj studiji predlažemo istaknuti genetski algoritam (GA) za generisanje UNet modela izborom optimalnih parametara. Eksperimenti su uključivali ručno generisane arhitekture, osnovni UNet model i UNet, AUNet model zasnovan na različitim veličinama filtera. Kao rezultat ručnog pristupa, AUNet je nadmašio osnovni model i stoga se AUNet smatra osnovnim modelom za GA proces. Eksperimenti pokazuju da su modeli razvijeni korišćenjem GA jednostavniji i male arhitekture. Model je dao bolju segmentaciju slika i nadmašio je ručno kreirane UNet modele, sa rezultatima kockice i Intersection over Union (IoU) rezultatima od 91,6% i 89,2%, respektivno.

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