# Computational Framework of Inverted Fuzzy C-Means and Quantum Convolutional Neural Network Towards Accurate Detection of Ovarian Tumors

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## ABSTRACT

Due to the advancements in the lifestyle, stress builds enormously among individuals. A few recent studies have indicated that stress is a major contributor for infertility and subsequent ovarian cancer among women of reproductive age. In view of this, the present study proposes a two-stage computational methodology to identify and segment the ovarian tumour and classify it as benign or malignant. Using computerized tomography images, the first stage involves image segmentation using inverted fuzzy c-Means clustering, and second stage consists of deep quantum convolutional neural network in order to detect the tumours. The efficacy of the proposed method is demonstrated using in-house clinically collected dataset by comparing the results with the state-of-the-art methods. The experimental results confirm that the proposed approach outperforms the existing fuzzy C means algorithm by achieving the average Jaccard score of (0.65, 0.84, 0.79) (min, max, avg) and Dice score of (0.70, 0.83, 0.77) (min, max, avg), classification result of 78% for benign and 70.03% for malignant tumours. The classification results using the variant of convolutional neural network (CNN) model ResNet16 are compared with the quantum convolutional neural networks (QCNN) and obtained the classification performance of 87.02% for benign and 79.4% for malignant tumours and 84.4% for benign and 77.03% for malignant tumours respectively.

## KEYWORDS

Classification, Clustering, Fuzzy C-Means, Gaussian Filter, Genetic Algorithms, Ovarian Cancer Detection, Quantum CNN

## 1. INTRODUCTION

In every country of the world, Cancer ranks as one of the leading causes of death. Ovarian cancer is the third most common gynaecological cancer in Indian women. From age 35, the risk of Ovarian cancer increases and reaches a peak between 55-64 (Labidi-Galy et al., 2012). Ovarian cancer has the worst prognosis as it is diagnosed in advanced stages such as stage III or IV. Since the cause of

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ovarian cancer is unknown, effective screening strategies for it are not found. The process of ovarian cancer segmentation using MRI and CT images has received considerable amount of attention in biomedical image segmentation and classification. As per the National Cancer Institute statistics, around 19,880 people were diagnosed with ovarian cancer and approximately 12,810 deaths were due to ovarian cancer by 2022 (National Cancer Institute, 2023). Greater efforts have been made for the early detection of ovarian cancer. Computer-aided diagnosis system is less time consuming and also gives more accurate and reliable results. With the advancement in the Image Processing techniques, Machine Learning algorithms, Deep Learning models and more importantly the computational devices, it is more evident to there is tremendous developments in the CAD systems. In the literature there are many works which has focused on the development of CADs using various medical images (Alharbi & Tchier, 2017; Bron et al., 2017; Chang et al., 2017; Chen et al., 2014; de Carvalho Filho et al., 2017; Nishio & Nagashima, 2017; Wang et al., 2016; Yilmaz et al., 2017). There are CADs which are developed for diagnosing the various cancer such as liver, brain, breast etc using CT and other modalities using Image Processing techniques (Chang et al., 2017), automatic image analysis for detection of various cancers and classifying as benign and malignant using classical machine learning algorithms (Nishio & Nagashima, 2017), there are many works which are carried out for the detection of ovarian cancer with the help of Deep Convolutional Neural Networks (Alharbi & Tchier, 2017; Bron et al., 2017; Chen et al., 2014; de Carvalho Filho et al., 2017; Suzuki, 2017; Wang et al., 2016; Yilmaz et al., 2017).

The rest of the paper is organized as follows. Section 2 presents the literature survey, with the detailed methodology and the description of algorithms is presented in Section 3, with the experimental results reported in Section 3, Section 4 provides conclusion.

## 2. LITERATURE SURVEY

As per the Otsu's et al (2021), segmentation of the images is carried out based on the threshold value. In this research, thresholding was based on within class variance, between class variance and total variance of grey levels. As per research work carried by Joe et al (1999), threshold value is used to segment the images. The method proposed in this study requires to identify two initial starting points - one each on the inside and outside the tumour's enhancing border in order to select a threshold value. The method is applied on T1 MRI images. This method is faster than manual trace methods, which is advantageous. The limitation found is that it was semi-automatic. According to Heath et al (2001), proposed Fuzzy C-Means clustering with knowledge-based techniques for the delineation of non-enhancing ovarian tumour regions using T1, T2 and proton density (PD) images. Failing to identify small tumours was the limitation found. The tumour is segmented correctly if it is present in at least three consecutive slices. Liu et al (2005), proposed Fuzzy connectedness algorithm for the segmentation of tumours using T1, T1-contrast-enhanced (CE) and Fluid Attenuation Inversion Recovery (FLAIR) images. Requiring to know the location of the tumour beforehand is the limitation of this process. As per the work by He Zhang et al (2014), A skilled radiologist was consulted to perform the all kinds of lesion segmentations. MATLAB software was used to manually outline the segmentation. Filtration-histogram-based textural analysis technique is used by Teramoto et al (2017). According to Wang et al (2009), Fluid vector flow method was used on the MRI images for the segmentation of synthetic tumours. Concave shapes were extracted efficiently using this method. The limitation of this method is that it is only partially-automatic and that it was not tested on several types of tumour groups. Khotanlou et al (2009) uses Fuzzy Possibilistic C-Means (FPCM) algorithm and symmetry analysis method for the segmentation of various cerebral tumours using T1 and T1-CE images. The limitation in this method is that it was unsuccessful in the identification of symmetrical tumours positioned each side of the mid-sagittal plane. Cordier et al (2013), proposed Patch-based segmentation approach for tumour delineation. Pre-processing steps like global intensity alignment, tumour localization, learning phase are the limitations. Islam et al (2018) used Random decision forest

classifier for the classification of the abnormality into different constituents. Limitations found in this system are pre-processing phase of bias field correction, histogram matching and the necessity of a learning phase that is specific to the data. Doyle et al (2013) proposed fully automatic method based on the hidden Markov fields and the variational expectation maximization for the tumour segmentation. The limitation of this method is that Prior probabilistic maps are necessary. According to Meier et al (2013), Context-sensitive features along with a random forest and conditional random fields mechanism was used for segmentation of the tumor region. The limitation of this approach is the requirement for multispectral images and training phase. In Reza et al (2013) study, fully automatic abnormal brain tissue segmentation method was proposed using multimodal MRI. This method was based on novel texture features like piece-wise triangular prism surface area, textons and the intensity difference of the multispectral images. Limitations of this method is pre-processing phase that includes slice co-registration, skull-stripping, bias field correction and intensity inhomogeneity correction. Zhao et al (2013), used learned Markov field on super-voxel clusters with updated unary potentials and spatial decision forests. Requiring to deionize and standardise the data in the initial phases itself is the limitation of this method. Vijaykumar et al (2007), worked with self-organizing maps for the segmentation of tumours. The images employed were T2, FLAIR and apparent diffusion coefficient maps. Limitation is on limited dataset of 10 it has been demonstrated. Ashwini et al (2021) (2021) (2022) (2022) (2022) (2021) (2021), worked on the CT scanned images for segmentation of the tumors using cGAN and classified using variants of CNN. Steven et al. (2018) (2020) (2018) (2018) (2017) (2017), worked on different medical imaging modalities and used various segmentation techniques for examining the tumors for the early prediction of disease which helps the clinicians.

### Motivations and Contributions

With the literature survey, it can be concluded that genetic algorithms induced clustering are better suited for segmentation of medical images since they possess natural selection for optimization in order to provide adequate solutions to specific modalities. And when it comes to classifying the malign and benign images, state-of-the-art methods on various modalities illustrate that shape characteristics play a significant role. Hence, shape features are primarily considered in our approach as well.

This paper presents a system comprising two methods in sequel - One for segmentation of tumours and the other for classification.

1. Genetic optimization induced Inverted Fuzzy C-Means Clustering method for segmentation of tumours from Ovarian CT images. Performance of the method is tested using Jaccard and Dice co-efficient.
2. Segmented images obtained in step 1 are classified using Quantum Convolutional Neural Networks.

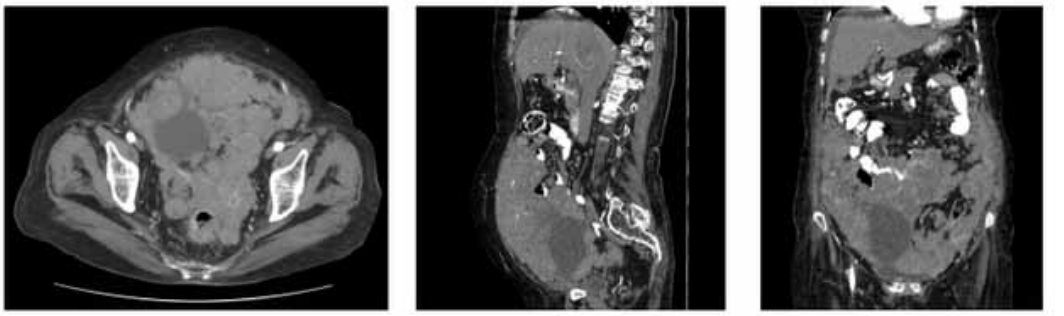
## 3. PROPOSED SYSTEM AND METHODOLOGY

### 3.1. Dataset

For the study, 78 women currently undergoing treatment at SDM Dharwad hospital were considered. A total of 5437 images, out of which 2814 were benign, and 2623 were malignant were obtained. The consent was taken from the hospital to carry out the research work. The ethical clearance is obtained from the competent authorities and consent is taken from the patients. The data collection includes the women who is currently taking treatment from SDM Dharwad hospital between the age of 30 to 55 years. Women who is pregnant and currently under any substance abuse is excluded from this study. Each image is of size 512*512. For this study all the three views of CT scanned images were considered – Axial, Coronial and Sagittal. The views of the images are shown in Figure 1.

It is important to consider all the three views of the CT scanned images in order to understand more characteristics of the tumour. Axial, Sagittal and Coronal views are 3 sides of same cube. Each

**Figure 1.**

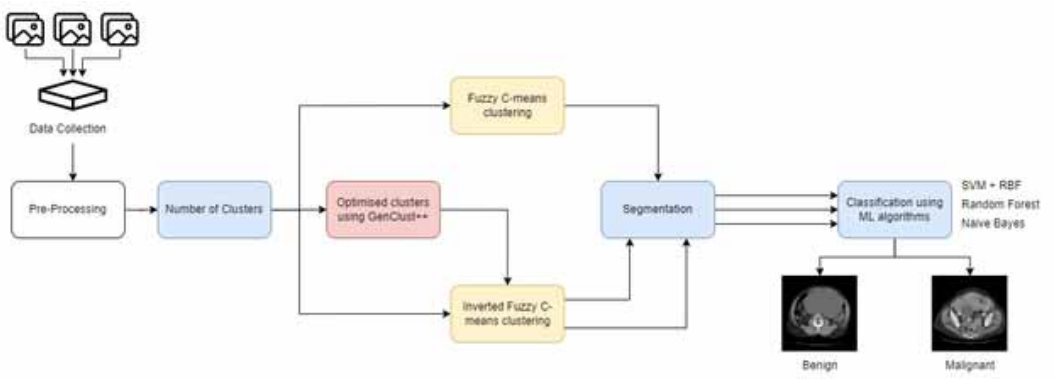


view is as important as the other in decision making. The primary images are acquired in axial view. And the reconstructed images are seen in the other two views by the radiologist to take the decision. Overall, a lesion can be visualised in multiple planes and the results are more accurate than visualising with just a single plane.

The architecture of the proposed system consisting of two phases - Segmentation and Classification and is presented in Figure 2. The data, as mentioned before, is collected from CT scans of several women patients with their approval. These images then undergo pre-processing to retain only the important parts i.e., the lower body of the patient in study. Fuzzy c-means is applied on the data by choosing a random number of clusters 'c' is to start with. A random point is chosen as a centroid for each cluster. Hence, 'c' number of points are chosen as centroids for 'c' clusters respectively. Then, the remaining points are assigned into different clusters based on their distance to the centroid. The centroid is then re-calculated multiple times and the clusters change accordingly. This is repeated till the points in the clusters do not change. Using this data, segmentation is performed on the images to segment out the cyst and it is then fed into Machine Learning algorithms like Support Vector Machines (SVM with RBF kernel is used here), Random Forest classifier and Naïve Bayes classifier for classifying the case into benign or malignant.

Parallelly, Inverted Fuzzy c-means is also applied on the pre-processed images with a random 'c' number initially. The steps of this algorithm are described in the upcoming section. The resulting number is used for segmentation process. This segmented image is again fed into the same ML classifiers to get results. Along with this, rather than using a random number, the 'c' value is chosen by "optimising the clusters" using the GenClust++ algorithm. The obtained 'c' value is used in

**Figure 2.**



Inverted Fuzzy c-means and then to segment the image into 'c' clusters. The image attained this way is also fed into the ML classifiers to gather results. These three results are then compared with each other. It is also compared with the classification results achieved using Deep Learning classifiers. The outcome of the comparisons is shown in the "Results and Discussions" section.

## 3.2. Proposed Algorithm for Segmentation

### *3.1.1. Inverted Fuzzy C-Means Clustering*

The Inverted Fuzzy c-Means algorithm is described below.

The newly proposed inverted fuzzy c-means clustering algorithm steps is given below:

**Step 1:** Start with n clusters.
**Step 2:** For (n-1) clusters, find the best two samples that can make a cluster and formulate the general sample that represent the cluster.
**Step 3:** Continue till it makes m clusters.

Once m clusters are found, the image pixels are clustered using m value.

### *3.1.2. Optimization*

The following are the steps involved to optimize the number of clusters obtained using inverted fuzzy c-means using GenClust++.

The main objective is:

**Step 1:** Select a good quality of chromosomes:

- Use hill – climber in mk means.
- Use several k values, for each k value run mk-means.
- Start with initial population on n=30.
- $P_n$ , set of initial chromosomes.
- Build the initial population.
- $P_f = P_s \times 3$
- Number of k value calculated as $(3 \times n) / 10$ .
- 9 chromosomes in 1 iteration, a total iteration of 5.
- Hence, $9 \times 5 = 45$ chromosomes during first run.
- A total of 2-stages are run, hence 45+45 = 90 chromosomes.

The ideas in GENCLUST++ (Junior et al., 2019) is to begin with a set of quality chromosomes rather than choosing them at random. This enhances the fitness of the population by a large margin. A set of quality chromosomes can be achieved using the hill-climbing method of K-means. The GENCLUST++ algorithm hence must operate under different k-values. There will be multiple instances of MK-MEANS++ (Sadati et al., 2021) running for each k value. The GENCLUST++ algorithm is composed of eight components. The algorithm uses pre-processing of dataset before initializing the population for crossover. The pre-processing involves normalizing the dataset and applying a modified k-means for clustering the data records. In the subsequent step, the algorithm initializes the population using a function to generate a set of high-quality chromosomes from which the initial sample population can be selected. That way, the probability of having a high poor fitness score will be likely reduced. The algorithm has a very low time complexity of O(n) compared to its previous version, GENCLUST (Guezouli & Abdelhamid, 2018). The algorithms retain a diversity while selecting a high-quality initial population. GENCLUST++ starts with an initial population size of n, which consist of set of chromosomes denoted as $P_n$. Each chromosome consists of k vectors

with dimensions as the set A of attributes in the original dataset. To establish an initial population, a new set $P_f$, three times the size of $P_n$ is created. The function to create this population iterates in rage starting from $\sqrt{|R|}$ to |R|, where R is the number of records in the original dataset. Thus, in the first stage to produce the initial population, a modified k-means runs on many different k values. At each run the function to produce chromosomes produces half the number of chromosomes from the given population $P_f$. At the end of this stage we have multiple clusters, each for a value of k. A fitness score is computed for each of these clusters and the clusters are arranged in descending order based on their fitness score. A probabilistic selection based directly on the fitness value is run. When a k value is selected its subsequent fitness value is calculated and the cluster is arranged in the descending order. The resulting solutions are promoted to $P_n$ (the initial population). The added ones become disqualified for the following selection. This is repeated n times and at the end of the entire stage we have a total of n chromosomes in $P_n$.

Once the initial population is ready the algorithm applies crossover. At first, the chromosomes are sorted according to their fitness value and a pair of chromosomes are selected as parents. One among them would be the chromosome at the front of the sorted list (with the high fitness score) and the other one is selected from the list created using a roulette technique. Two offspring are created using a conventional single point crossover operation. A new empty population, $P_e$ will be added with the newly created offspring. As a final step in the crossover a duplicate removal function is invoked on the population $P_e$. Elitism is the following step in the GENCLUST++ algorithm. The sole intention of this step is to re-insert the chromosome with a better fitness score in situations where iterations produce weak individuals. The stage also introduces mutation on cloned population of $P_n$ to increase the diversity. The final stage of the algorithm merges all chromosomes between the recent generation and the one produced after completing all the stages of GENCLUST++. This helps to prevent radical disruption by the genetic operators. Hence, the algorithms retain the best fitted population during its each run. Further this helps in efficient selection from the given population before running the population through further steps of the presented work.

### *3.1.3. Classification Using Deep Learning*

The segmented results are then used for the classification. Different variants of CNN algorithms are used for this purpose.

The algorithms used in this study are Resnet16, VGG16 and Inception-v4, which are all fundamentally densely-built CNNs, however each of them excel in different purposes. They are all mostly made up of several convolutional layers, fully connected layers, activation functions etc. Residual Network or ResNet for short, is a powerful CNN consisting of more than 150 layers. ResNet16 considered here contains 16 layers. As the neural network gets deeper by including more and more layers, it is common to encounter the Vanishing Gradient (VG) problem. ResNet is known to handle the VG problem due to its "Skip connection" or "Shortcut connection" feature and perform well even with 152 layers. ResNet was created a year after VGGNet and Inception, and due to its ability to achieve great accuracy, avoiding the VG problem, it made a path to build deep and complex CNNs. In our study as well, ResNet has outperformed the other two CNNs.

VGGNet on the other hand, leads in terms of time taken as its architecture was designed in such a way, using fixed size kernels, to efficiently reduce the number of features thereby reducing the training time and making it more stable to overfitting. VGG16 used in this study consists of 16 layers in total. Inception algorithms can be distinguished from VGGNet by the main feature of variable-sized kernels as opposed to fixed-size kernels as seen in VGGNet (Gull & Akbar, 2021; Majib et al., 2021). Inception incorporates different sized kernels in the same layer in order to find different sized features, during Image classification, which is the characteristic of this algorithm. Inception-v4 is a version of Inception without any residual connections. Although Inception-v3 has comparatively lesser Inception modules, Inception-v4 has a simpler architecture (Ba Alawi et al., 2021; Nazir et al., 2022).

Figure 3 illustrates the architecture diagram of the classification process used. The image dataset obtained is stored on the local system, which then undergoes pre-processing. Though the images do not contain PII or Personally Identifiable Information of the patient in order to maintain anonymity, textual information like date and time of the scan, type of scan, machine used, gender of the patient etc., are still present. To avoid noise or bias when fed into the algorithms, the images are pre-processed by cropping out these markers so as to retain only the Region of Interest (ROI) and is saved in JPG format. This processed set of images are then fetched by the script where it is first split into three for training, validation and testing in 70:10:20 ratio. The images used for training are annotated by marking the potential cyst. It is then fed into different Convolutional Neural Network-based algorithms. ResNet16, VGG16 and Inception-v4 are the algorithms chosen in this study for the classification of images into two categories namely, benign and malignant. A case is considered to be Benign is when the cysts might not be a dangerous one and Malignant, as the name says, is potentially dangerous and might be a cancer cyst. Each algorithm is trained for 200 epochs and is then checked for validation. Finally, it is tested using the 20% of the images and their performances are checked and compared using evaluation metrics such as validation accuracy, test accuracy etc.

### *3.1.4. Classification Using Quantum CNN*

The architecture of the QCNN is shown in Figure 4.

At the input layer the data that will be used is the CT scanned images. The data has only two classes (Benign and Malignant). In implementing QCNN, the large resources are required, therefore the image is resized to $8 \times 8$ pixels and removing the contradicting data. In the next step, the pixel value of 0.5 will have a value 1 and less than the pexel value 0.5 will get the value 0 which is called binning process. Since the input size is $8 \times 8$, 64 qubits which are cluster states. To transform the data into data circuits, the data having a value one will be added Pauli-x gate and the data having a value zero will be added no Pauli-x gate. The framework og QCNN is af follows: At the initial step,

**Figure 3.**

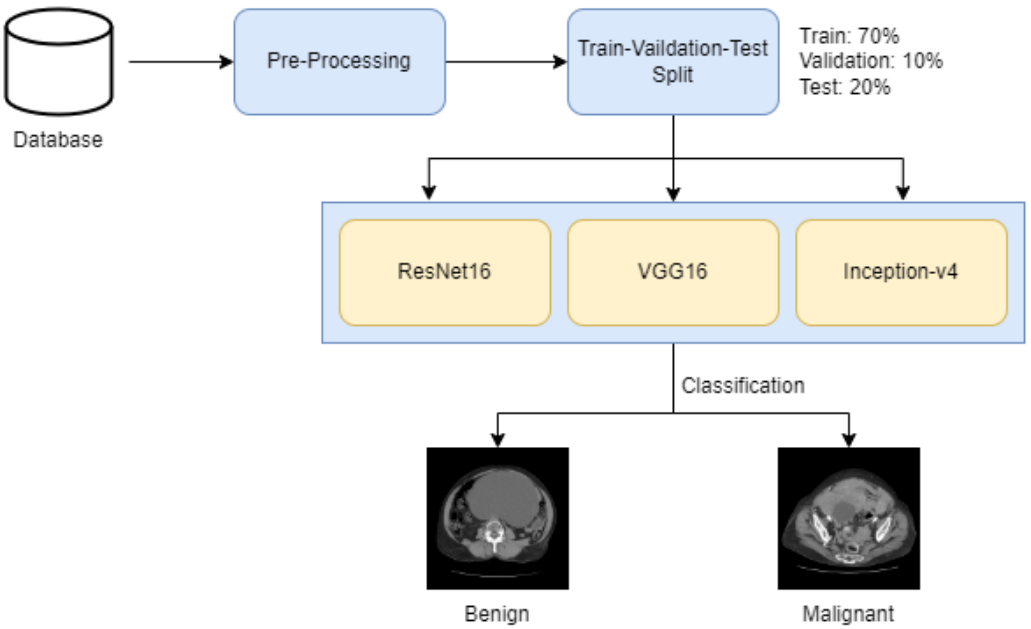
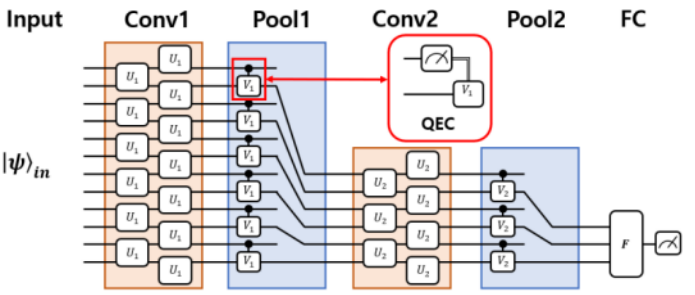


**Figure 4.**




preparation model will receive the image x and uses the binary encoding to encodes the image grid data into a quantum state. Using the quantum circuits, the model extracts features in the quantum states. At the Conv1 layer, since image information is encoded in the binary form, two-qubit unitary operation is performed. In the Pool1 layer, reduces the dimensions of the feature mapping. The process is repeated for several iterations where number of qubits will decrease. At the final Fully Connected layer (FC), the layer is used to classify the image using remaining qubits.

## 4. RESULTS AND DISCUSSIONS

### 4.1. Segmentation Results

The following are the segmentation results obtained using Inverted Fuzzy C Means algorithm and the number of clusters optimized using modified GenClust++ algorithm.

Figure 5 shows the results that are obtained by applying inverted Fuzzy c-Means algorithm. Algorithm was applied on all the different views of CT images and obtained the Jaccard and Dice score of (0.63, 0.82, 0.77) (min, max, avg) and (0.67, 0.80, 0.747) (min, max, avg) respectively. Figure 5a shows the results using clusters optimised by using GenClust++ and obtained the Jaccard and Dice score of (0.65, 0.84, 0.79) (min, max, avg) and (0.70, 0.83, 0.77) (min, max, avg) respectively.

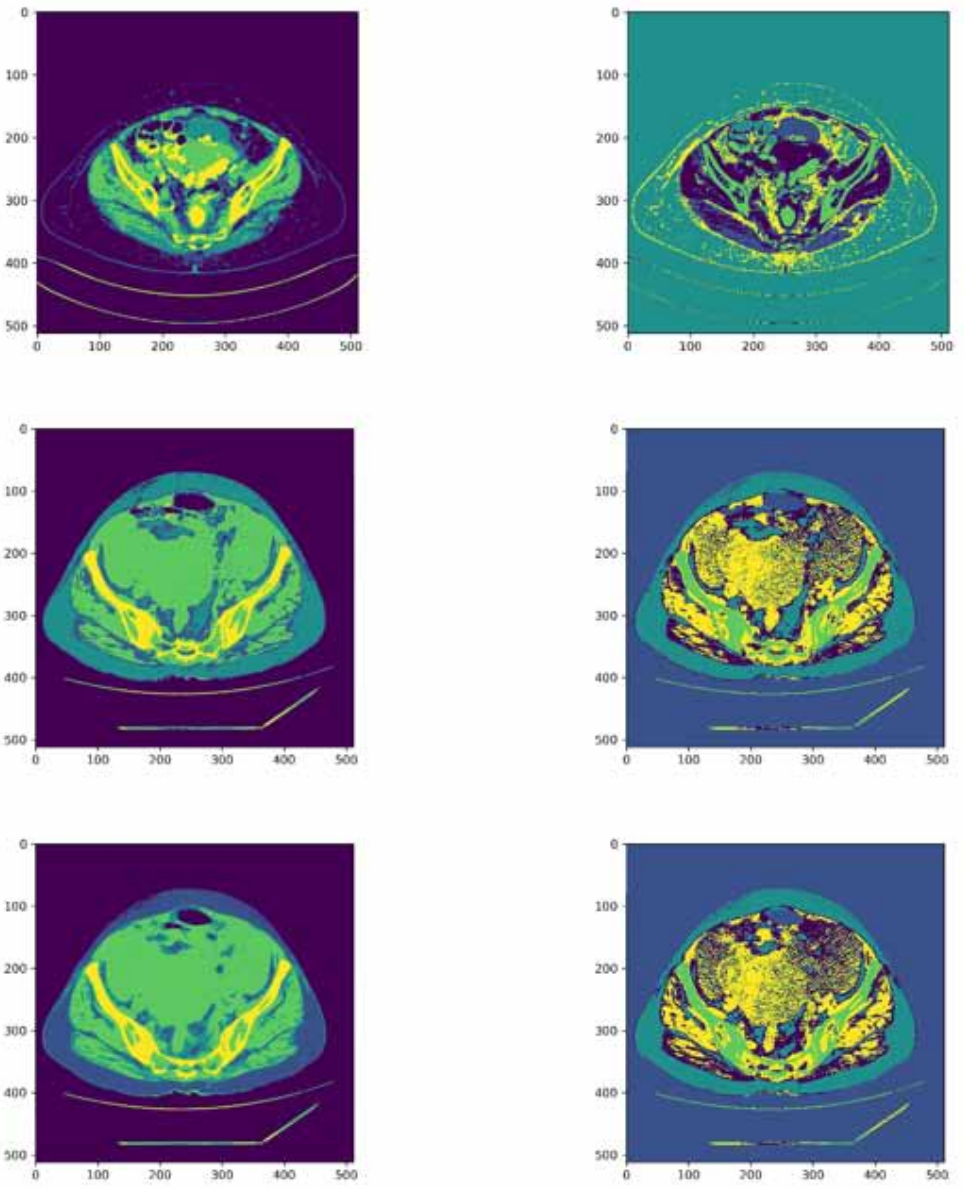
After segmentation, the segmented images are classified using classical Machine Learning Algorithms Support Vector Machine, Naïve Bayes and Random Forest algorithms. Among all the classifiers it is observed that Support Vector Machine algorithm outperformed when compared to the other classifiers with the accuracy of 78% for benign and 70.03% for malignant tumour as shown in the Figure 6. The clusters are optimized using modified GenClust++ algorithm and segmented results are then classified using SVM. There is a considerable improvement in the result with the accuracy of 78.4% for benign and 72.03% for malignant tumors with the optimized value of c using GenClust++ as shown in the Figure 7.

Results are compared with Fuzzy c-Means and it is observed that Inverted Fuzzy c Means outperformed comparing to Fuzzy C Means algorithm. The results of the study display that the proposed approach outperforms the existing Fuzzy C Means algorithm which is shown in Figure 8.

### 4.2. Deep Learning (CNN) Results

Due to the advancement of Deep Convolutional Neural Networks algorithms and the computational devices, the images are classified using variants of CNN: ResNet16, VGG16 and Inception-v4. The obtained results from the conventional machine learning algorithms are compared with the results obtained from Deep Learning Models. ResNet16 outperformed with the validation accuracy of 87.02% and test accuracy of 79.4% than VGG16 and Inceptionv4. Among VGG16 and Inceptionv4, VGG16

**Figure 5.**



obtained better result with validation accuracy of 78.7% and test accuracy of 68.6%. Inceptionv4 obtained the validation accuracy of 74.5% and test accuracy of 62.3%. From the results it is observed that ResNet16 outperformed the other CNN models and conventional machine learning algorithms.

The training and testing loss and accuracy is shown in Figure 9. The implementation code is available at https://drive.google.com/drive/folders/1cxKbW6xuU_EGEIPS4PXpjZuoBe4QZRLs?usp=sharing.

**Figure 6.**

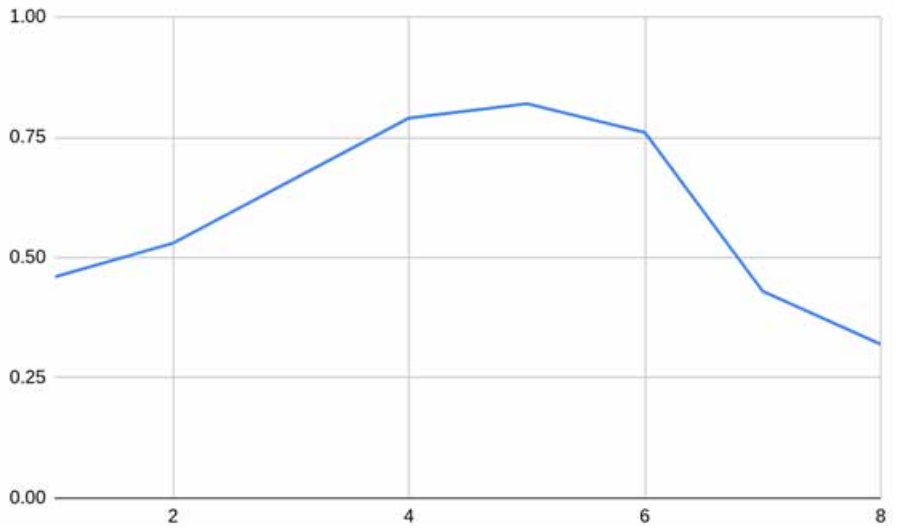
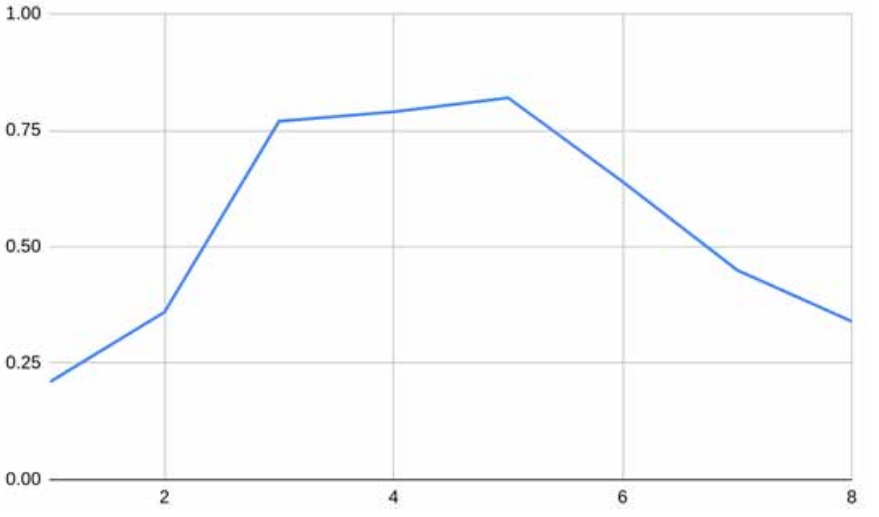



**Figure 7.**




### 4.3. Quantum Results and Comparisons

The QCNN has 16 qubits. The architecture has 2 quantum convolutional layer, 2 quantum pooling layer and 1 fully connected layer. The number of iterations I = 1000 with the batch size s=16. The entire dataset is divided into 70-30 training and testing. From the results it is observed that the test accuracy gradually improved for initial few iterations as shown in the Figure 10 and reached highest of 84.4% for benign and 77.03% for malignant.

From the experiments it is clear that as the size of the input increases the number of qubits required to classify increases.

**Figure 8.**

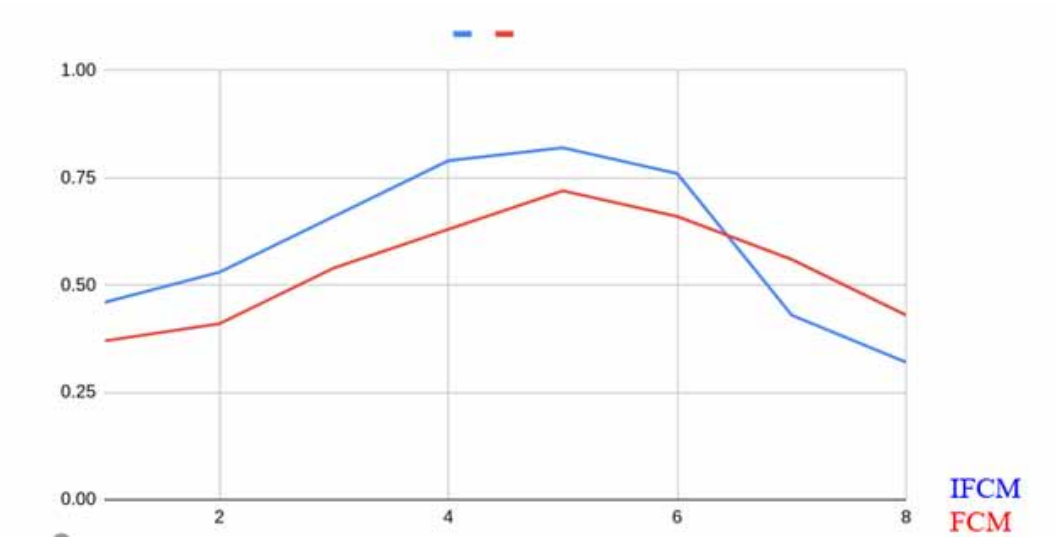
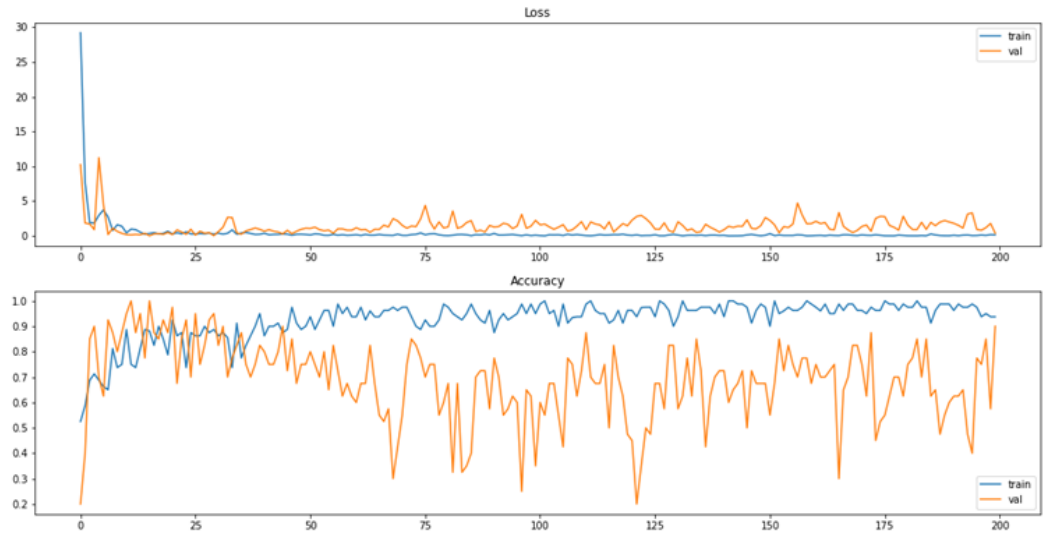


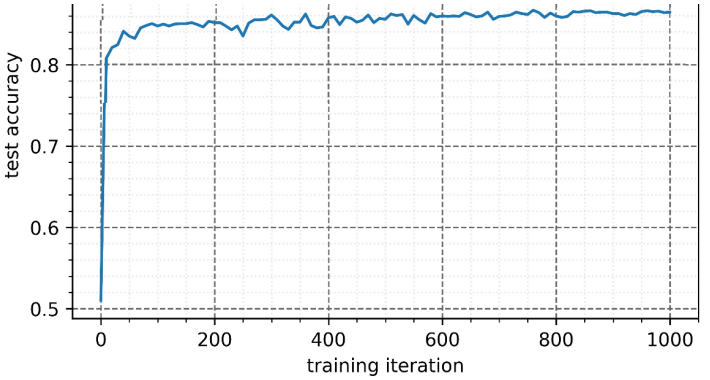

**Figure 9.**




## 5. CONCLUSION

There are extensive studies on detection of ovarian cancer/tumour using soft sets and MRI. Computed Tomography provides a clear and discriminating visualization of soft tissue which potentially can provide an improved performance. The current study proposes and demonstrates identification and classification of ovarian cancer using CT scan images integrated with inverted fuzzy c-means clustering and genetic algorithm, GenClust++ based optimization for finding an optimal number of clusters. The segmented CT images are further classified using conventional machine learning classifiers, deep convolutional neural networks and QCNN. The proposed methodology provided improved

**Figure 10.**




performance of the average Jaccard score of (0.65, 0.84, 0.79) (min, max, avg) and Dice score of (0.70, 0.83, 0.77) (min, max, avg), classification result of 78% for benign and 80.03% for malignant tumours with support vector machine. The proposed Inverted Fuzzy C Means algorithm classification results are compared with the variants of CNN model ResNet16 and Quantum Convolutional Neural Networks and obtained the classification results of 87.02% for benign and 79.4% for malignant tumours and 84.4% for benign and 77.03% for malignant respectively. From the results it can be clearly inferred that the deep CNN ResNet16 not only outperformed, but also provides an efficient and robust method with increased computational complexity followed by the quantum CNN. This methodology is applicable in the clinical and gynaecological practice and can bring new, quick diagnostics, can also help in the emerging economies and can reduce burdens on clinicians and timely, cost effective yet accurate diagnosis. Further the experiments will be carried out with more dataset and with the increased number of Quantum layers in the architecture.

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