Extraction of Cancer Cell Regions and Image Post Processing

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Abstract

The study has confirmed the feasibility of using ultraviolet (UV) excitation to visualize and quantify desmoplasia in fresh tumor tissue of pancreatic adenocarcinoma (PDAC) in an orthotopic xenograft mouse model, which provides a useful imaging platform to evaluate acute therapeutic responses. Stromal network of collagen prominent in PDAC tumors is examined by imaging fresh tissue samples stained with histological dyes. Fluorescence signals are color-transferred to mimic Masson's trichrome staining. Fluorescence imaging using UV excitation is capable of visualizing collagen deposition in PDAC tumors. Both fluorescence and histology data showed collagen content of up to 30%. The collagen modulation effect due to photodynamic priming treatment was observed showing 13% of collagen reduction. Necrosis area is visible and perfusion imaging using Texas Red dextran is feasible.

Keyword: *Post Processing Image, Cancer cell, Image Classification.*

1. INTRODUCTION

CANCER is one of the most serious health problems in the world field. The mortality rate of lung cancer is the highest among all other types of cancer. Lung cancer is one of the most serious cancers in the world, with the smallest survival rate after the diagnosis, with a gradual increase in the number of deaths every year. Survival from lung cancer is directly related to its growth at its detection time. The earlier the detection is, the higher the chances of successful treatment are. An estimated 85% of lung Cancer cases in males and 75% in females are caused by cigarette smoking. Cancer causes changes in tissue at the sub-cellular scale. Pathologists examine a tissue specimen under a powerful microscope to look for abnormalities which indicate cancer. This manual process has traditionally been the de facto standard for diagnosis and grading of cancer tumors. While it continues to be widely applied in clinical settings, manual examination of tissue is a subjective, qualitative analysis and is not scalable to translational and clinical research studies involving hundreds or thousands of tissue specimens. A quantitative analysis of normal and tumor tissue, on the other hand, can provide novel insights into observed and latent sub-cellular tissue characteristics and can lead to a better understanding of mechanisms underlying cancer onset and progression

2. LITERATURE REVIEW

Dmitry Kaplun et.al (2021) With the evolution of modern digital pathology, examining cancer cell tissues has paved the way to quantify subtle symptoms, for example, by means of image staining procedures using Eosin and Hematoxylin. Cancer tissues in the case of breast and lung cancer are quite challenging to examine by manual expert analysis of patients suffering from cancer. Merely relying on the observable characteristics by histopathologists for cell profiling may under-constrain the scale and diagnostic quality due to tedious repetition with constant concentration. Thus, automatic analysis of cancer cells has been proposed with algorithmic and soft-computing techniques to leverage speed and reliability. The paper's novelty lies in the utility of Zernike image moments to extract complex features from cancer cell images and using simple neural networks for classification, followed by explain ability on the test results using the Local Interpretable Model-Agnostic Explanations (LIME) technique and Explainable Artificial Intelligence (XAI). The general workflow of the proposed high throughput strategy involves acquiring the Break His public dataset, which consists of microscopic images, followed by the application of image processing and machine learning techniques. The recommended technique has been mathematically substantiated and compared with the state-of-theart to justify the

empirical basis in the pursuit of our algorithmic discovery. The proposed system is able to classify malignant and benign cancer cell images of 40× resolution with 100% recognition rate. XAI interprets and reasons the test results obtained from the machine learning model, making it reliable and transparent for analysis and parameter tuning.

T. Jeya Priya et.al (2020) In recent years the image processing mechanisms are widely used in several medical areas for improving earlier detection and treatment stages particularly in various types of cancer. Image processing is a method to perform some operations on an image in order to get an enhanced image or to extract some useful information from it. Cancer is a most dreadful disease in this era. Time is a major factor in cancer treatment because the mortality rate and spreading of cancer is high compared to other diseases. So more focus must be given on this area. The intention of this bibliographic review is to provide researchers deciding to work and easily understand the situation to find out better approach among them.

Md Shahariar Alam et.al (2019) In recent decades, human brain tumor detection has become one of the most challenging issues in medical science. In this paper, we propose a model that includes the template-based K means and improved fuzzy C means (TKFCM) algorithm for detecting human brain tumors in a magnetic resonance imaging (MRI) image. In this proposed algorithm, firstly, the template-based K-means algorithm is used to initialize segmentation significantly through the perfect selection of a template, based on gray-level intensity of image; secondly, the updated membership is determined by the distances from cluster centroid to cluster data points using the fuzzy C-means (FCM) algorithm while it contacts its best result, and finally, the improved FCM clustering algorithm is used for detecting tumor position by updating membership function that is obtained based on the different features of tumor image including Contrast, Energy, Dissimilarity, Homogeneity, Entropy, and Correlation. Simulation results show that the proposed algorithm achieves better detection of abnormal and normal tissues in the human brain under small detachment of gray-level intensity. In addition, this algorithm detects human brain tumors within a very short time—in seconds compared to minutes with other algorithms.

Yousef Al-Kofah et.al (2018) Automatic and reliable characterization of cells in cell cultures is key to several applications such as cancer research and drug discovery. Given the recent advances in light microscopy and the need for accurate and high-throughput analysis of cells, automated algorithms have been developed for segmenting and analyzing the cells in microscopy images. Nevertheless, accurate, generic and robust whole-cell segmentation is still a persisting need to precisely quantify its morphological properties, phenotypes and sub-cellular dynamics. We present a single-channel whole cell segmentation algorithm. We use markers that stain the whole cell, but with less staining in the nucleus, and without using a separate nuclear stain. We show the utility of our approach in microscopy images of cell cultures in a wide variety of conditions. Our algorithm uses a deep learning approach to learn and predict locations of the cells and their nuclei, and combines that with thresholding and watershed-based segmentation. We trained and validated our approach using different sets of images, containing cells stained with various markers and imaged at different magnifications. Our approach achieved a 86% similarity to ground truth segmentation when identifying and separating cells. The proposed algorithm is able to automatically segment cells from single channel images using a variety of markers and magnifications.

Yuting Xie et.al (2017) Human visual mechanisms (HVMs) can quickly localize the most salient object in natural images, but it is ineffective at localizing tumors in ultrasound breast images. In this paper, we research the characteristics of tumors, develop a classic HVM and propose a novel auto-localization method. Comparing to surrounding areas, tumors have higher global and local contrast. In this method, intensity, blackness ratio and superpixel contrast features are combined to compute a saliency map, in which a Winner Take All algorithm is used to localize the most salient region, which is represented by a circle. The results show that the proposed method can successfully avoid the interference caused by background areas of low echo and high intensity. The method has been tested on 400 ultrasound breast images, among which 376 images succeed in localization. This means this method has a high accuracy of 94.00%, indicating its good performance in real-life applications.

3. METHODOLOGY

Manual Segmentation Methods

Manual segmentation requires the radiologist to use the multi-modality information presented by the MRI images along with anatomical and physiological knowledge gained through training and experience. Procedure involves the radiologist going through multiple slices of images slice by slice, diagnosing the tumor and manually drawing the tumor regions carefully. Apart from being a time consuming task, manual segmentation is also radiologist dependent and segmentation results are subject to large intra and inter rater variability. However, manual segmentations are widely used to evaluate the results of semi-automatic and fully automatic methods.

Semi-Automatic Segmentation Methods

Semi-automatic methods require interaction of the user for three main purposes; initialization, intervention or feedback response and evaluation. Initialization is generally performed by defining a region of interest (ROI), containing the approximate tumor region, for the automatic algorithm to process. Parameters of pre-processing methods can also be adjusted to suit the input images. In addition to initialization, automated algorithms can be steered towards a desired result during the process by receiving feedbacks and providing adjustments in response. Furthermore, user can evaluate the results and modify or repeat the process if not satisfied.

Hamamci et al. proposed the "Tumor Cut" method. This semi-automatic segmentation method requires the user to draw the maximum diameter of the tumor on input MRI images. After initialization a cellular automata (CA) based seeded tumor segmentation method run twice, once for tumor seeds provided by the user and once for the background seeds to obtain a tumor probability map. This approach includes separately applying the algorithm to each MRI modality (e.g. T1, T2, T1-Gd and FLAIR), then combining the results to obtain the final tumor volume.

A recent semi-automatic method employed a novel classification approach. In this approach segmentation problem was transformed into a classification problem and a brain tumor is segmented by training and classifying within that same brain only. Generally, machine learning classification methods, for brain tumor segmentation, requires large amounts of brain MRI scans (with known ground truth) from different cases to train on. This results in a need to deal with intensity bias correction and other noises. However in this method, user initializes the process by selecting a subset of voxels belonging to each tissue type, from a single case. For these subsets of voxels, algorithm extracts the intensity values along with spatial coordinates as features and train a support vector machine (SVM) that is used to classify all the voxels of the same image to their corresponding tissue type.

Despite semi-automatic brain tumor segmentation methods are less time consuming than manual methods and can obtain efficient results, they are still prone to intra and inter rater/user variability. Thus, current brain tumor segmentation research is mainly focused on fully automatic methods.

Fully Automatic Segmentation Methods

In fully automatic brain tumor segmentation methods no user interaction is required. Mainly, artificial intelligence and prior knowledge are combined to solve the segmentation problem.

Post processing

The post processing means filling and thinning. The series of operations evolved in enhancement after segmentation are Morphological opening, Morphological closing, Morphological thinning, Morphological filling is applied on threshold image for the enhancement. Morphological opening eliminates the small objects inside and outside the lungs. Morphological closing is then applied on the image. It enhances borders and fills the gaps in the border. After Morphological operations boundary of the enhanced image is detected. Morphological thinning is then applied on the boundary extracted image. After the thinning process Morphological filling is applied on the image to get the final post-processed image. Thinning brings down the width of the line. While Filling gets rid of small breaks and holes in the contour, remove extra part from image and make image more clear for nodule detection.

4. ANALYSIS

Recent performances of deep learning methods, specifically Convolutional Neural Networks (CNNs), in several object recognition and biological image segmentation challenges increased their popularity among researches. In contrast to traditional classification methods, where hand crafted features are fed into, CNNs automatically learn representative complex features directly from the data itself. Due to this property, research on CNN based brain tumor segmentation mainly focuses on network architecture design rather than image processing to extract features. CNNs take patches extracted from the images as inputs and use trainable convolutional filters and local subsampling to extract a hierarchy of increasingly complex features. Although currently very few in number compared to other traditional brain tumor segmentation methods, due to state-of-the-art results obtained by CNN based brain tumor segmentation methods, we will focus the review on these methods in this section. Comparison of the reviewed deep learning and traditional glioma segmentation methods is presented in Table 1.

Table 1. Comparison of the reviewed brain tumor segmentation methods (results are obtained using challenge dataset of BRATS 2013 benchmark[5] . Note that, we only considered dice scores as the performance measure. Refer to the benchmark for further evaluation metrics)

Author	Method	Level of user interaction	Performance (Dice Scores)		
			Whole Tumor	Core Tumor	Active Tumor
Human Rater[5]	Medical training and experience	Manual	0.88	0.93	0.74
Pereira et al.[31]	CNN with small (3x3) filters for deeper architecture	Fully automatic	0.88	0.83	0.77
Kwon et al.[15]	Generative model that performs joint segmentation and registration	Semi-automatic	0.88	0.83	0.72
Havaei et al.[29]	Cascaded Two-pathway CNNs for simultaneous local and global processing	Fully automatic	0.88	0.79	0.73
Tustison et al.[19]	Concatenated RFs, trained using asymmetry and first order statistical features	Fully automatic	0.87	0.78	0.74
Urban et al.[27]	3D CNN architecture using 3D convolutional filters	Fully automatic	0.87	0.77	0.73
Havaei et al.[10]	Uses SVM; training and segmentation implemented within the same brain	Semi-automatic	0.86	0.77	0.73
Dvorak and Menze[32]	Local structured prediction with CNN and k-means	Fully automatic	0.83	0.75	0.77
Davy et al.[30]	Two-pathway CNN for simultaneous local and global processing	Fully automatic	0.85	0.74	0.68
Zikic et al.[28]	3D input patches are interpreted into 2D input patches to train a CNN	Fully automatic	0.837	0.736	0.69
Hamamci et al.[9]	Generative model, uses cellular automata to obtain tumor probability map	Semi-automatic	0.72	0.57	0.59
Rao et al.[33]	Four CNNs, one for each modality, with their outputs concatenated as an input into a RF	Fully automatic	Not reported	Not reported	Not reported

The Performance Metrics for the test data are shown in Table2. The formulations are shown in percentage, each column indicates the neural networks Classifier used and the rows indicate the Metric value respectively.

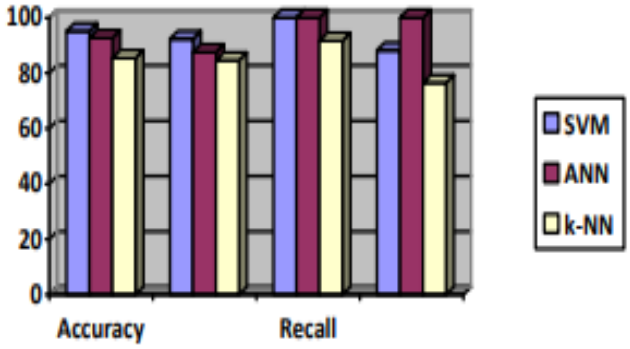

Fig-2: Performance metrics of Classifiers

From table 1 it is shown that accuracy of SVM is 95.12% which is better that ANN classifier (92.68%) and k-NN classifier (85.37%). The graph of the Table 1 is given in Figure 2.

These results shown in figure 2 with 24 images of stage I and 17 images of stage II is used as test dataset. Value of accuracy, precision, recall and specificity is in percentage (%).

Table-2: Performance Metrics In Percentage For Test Data

		Classifier		
		SVM	ANN	KNN
Metrics	Accuracy(%)	95.12	92.68	85.37
	Precision(%)	92.31	87.50	84.62
	Recall(%)	100.00	100.00	91.67
	Specificity(%)	88.24	100.00	76.47

For experimentation of the technique, the CT images are obtained from a NIH/NCI Lung Image Database Consortium (LIDC) dataset. This data consists of 1000 lung images. Those images are progressed to this system. The diagnosis rules are then produced from those images and these rules are progressed to the classifier for the learning process. After learning, a lung image is progressed to the proposed system. Then the proposed system will execute its processing and finally it will detect whether the input image is having cancer or not. The proposed CAD system is capable of detecting lung nodules with diameter $\geq$ 2.5 mm, which means that the system is capable of detecting lung nodules when they are in their early stages. Thus facilitating early diagnosis will improve the patients' survival rate.

5. CONCLUSION

The team successfully created an automated microscope with an artificial intelligence post-processing that is able to detect cell clusters. Furthermore, the team went beyond the standard requirements by giving the device the capabilities to send the results wirelessly to other devices. This project acts as a

proof-of-concept and stepping stone for automation in the field of pathology. Though the current design only detects cell clusters, with time the system can be adapted to do more significant things like diagnose cancer without a pathologist or even count cell clusters and diagnose cancer on unstained samples. This advancement has the potential to save many lives by getting the patients their treatment faster, and the team is very proud to have a part in this design.

6. REFERENCE

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