Inclusive Exposure on Detection of Pancreatic Cancer – A Review

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Abstract

Cancer is usually characterized as a heterogeneous disease with different types and subtypes. Cancer is not a single disease, but rather many related diseases that involve uncontrolled cellular growth and reproduction. It is one of the leading causes of death in the developed world and second in the developing world, almost a million people around the globe are losing the fight against cancer every year. The early diagnosis and prognosis of a cancer type have become inexorable in cancer research, as it can facilitate the quality of life of patients. Pancreas cancer is one of the most common malignant tumors with the highest morbidity and mortality, which is a considerable threat to people's health and life. Advanced Pancreas cancer is likely to metastasize, which lead to corresponding symptoms in patients with great pain, and are even life-threatening. This phenomenon is referred to as the distant metastasis of this cancer, which is represented by the M staging in the TNM staging system. Computed Tomography (CT) imaging is a widely used method for the evaluation of tumor prognosis. Pancreas tumor images are segmented with high rate of accuracy and then tumors are classified whether it is malignant or benign. Because of the complexity and change in the characteristics of tumor like its shape and size. Hence the work elaborates the numerous researches for tumor recognition, segmentation and classification of previously proposed methods highlighting its strength and limitations. There are no proper research made to recognize tumor and good image quality. Till now no research has provided critical evaluation of the survey which inhibits new research. In this literature I am going to discuss about the different approaches available for segmentation and classification of pancreas tumor.

Keywords:-Pancreas Tumor, CT Imaging, Feature extraction, Segmentation, Classification.

I. INTRODUCTION

Content based image retrieval is being used in feature extraction of medical image. It is a systematic procedure and analysis of image processing. The lack of knowledge in the medical image processing causes pancreatic cancer to be the leading causes for death around the world. The majority of pancreatic cancer presents in late stages at the time of diagnosis, which explains the poor associated prognosis. Although this disease has suboptimal survival rates, it is clearly more favorable with a five-year survival rate of 85.8% for stage 0, 68.7% for stage IA and 59.7% for stage IB. So there is an urgent need of a method that will help radiologists in diagnosis of pancreatic cancer tumor at an early stage. Digital image feature extraction using statistical design and content based image retrieval (CBIR) have been employed in medical imaging science.

Although many different techniques are adapted for medical image retrieval, CBIR is considered the most. However, still a lacuna exists in general application of picture recapturing system and programming tools. CBIR has been proved worthy as it is mainly based on image feature extraction, feature storage; future comparison and query interface. Existing image processing tools (khoros / Cantata / Visi Quest 1), insights toolkits (ITK), visualization tool kit (VTK) or image 14 are available for feature extraction and comparison, but do not have a supporting system for generation of data bank. Therefore, processing tool that is not coupled with storage system may do complications and deprives with new information. Further, end user (clinician) may find difficulty for easy operations of retrieval algorithms. However there is not much work done on pancreatic tumor detection. It is found that pancreatic tumor detection is done by symptoms of the disease and by taking patients history but not using image processing.

This study presents the study of many algorithms that have been implemented successfully for detecting tumors enhancement, segmentation and classification techniques.

II. Materials and Methods

Tommaso Mazza et al [2013] made a study on functional impact of autophagy related genes on the homeostasis and dynamics of pancreatic cancer cell lines. Pancreatic cancer is a highly aggressive and chemotherapy-resistant malignant neoplasm. In basal condition, it is characterized by elevated autophagy activity, which is required for tumor growth and that correlates with treatment failure. They analyzed the expression of autophagy related genes in different cell lines. A correlation-based network analysis evidenced the sociality and topological roles of the autophagy-related genes after serum starvation. Structural and functional tests identified a core set of autophagy related genes, suggesting different scenarios of autophagic responses to starvation, which may be responsible for the clinical variations associated with pancreatic cancer pathogenesis.

Marek Ogiela et al [2000] presented new algorithm used for the recognition of morphologic lesions of selected abdominal organs shown in X-ray images. These methods are aimed to facilitate diagnosis of pancreatic cancer (PC) and chronic pancreatitis (CP), based on the analysis of X-ray images acquired by endoscopic retrograde cholangiopancreatography. This method uses catherization of the major duodenal (Vater's) papilla combined with oral administration of a contrast medium to obtain roentgenograms of the pancreatic and biliary ducts. This method is commonly found to be most suitable for morphologic examination of the pancreas as it provides high diagnostic efficacy, enabling recognition of PC as well as CP. The purpose of this work is detection of the most specific pathological changes, characterizing ducts affected by PC, including the occurrence of local dilations, stenoses and side branches in the pancreatic duct as well as cysts or cavernous bulges. For CP, in most cases, the ducts are characterized by abnormal lateral branching's of first, second, or third order and as in the case of PC, by local enlargements or constriction narrowing's. They used attribute context-free grammars, which enable quick detection of pathological changes in shape, to recognize these signs.

Kishor Kumar Reddy C et al [2015] proposed a method for identifying the cancer affected part. Initially, the images are collected and then converted into RGB as the original image is in greyscale format. *K*-means clustering technique is adopted so as to segment the images in order to capture the region of interest. This diagnostic application makes use of MATLAB software for processing of the image, by making use of Haar wavelet transform and

clustering techniques. The whole analysis is done based on the threshold values and the images are justifying by checking if the threshold falls within the same range estimated for each image. The result obtained found to be a pragmatic approach for the early and accurate detection of cancer cells.

Jan Egger et al [2018] studied the in-depth assessment of an interactive graph-based approach for the segmentation for pancreatic metastasis in US images of the liver with two specialists in Internal Medicine. This approach evaluates the method with over one hundred different acquisitions of metastases. The two physicians or the algorithm had never assessed the acquisitions before the evaluation. In summary, the physicians first performed a pure manual outlining followed by an algorithmic segmentation over one month later. As a result, the experts satisfied in up to ninety percent of algorithmic segmentation results. Furthermore, the algorithmic segmentation was much faster than manual outlining and achieved a median Dice Similarity Coefficient (DSC) of over eighty percent. Ultimately, the algorithm enables a fast and accurate segmentation of liver metastasis in clinical US images, which can support the manual outlining in daily practice.

Yang Ning et al [2018] proposed a new automated pancreas segmentation framework Recurrent Adversarial Learning based on Generative Adversarial Network (Pancreas-GAN) to tackle the challenge of very high anatomical variability. Pancreas-GAN consists of three novel modules: 1) a dilated convolutions auto encoder module (DCAE) not only explicitly maintains global resolution of CT images but also enlarges the receptive field of filters to effectively incorporate larger context without increasing the computation complexity; 2) a local long short-term memory module (Local-LSTM) can capture the contextual segmentation correlation across neighboring image patches for boosting precise boundary segmentation; and 3) an adversarial module can constrain the spatial smoothness consistency among successive image slices based on the global distribution constraints, which further boosts the performance of Pancreas-GAN. Experiments are conducted on the CT scans of 80 patients using 4-fold cross-validation and have demonstrated that Pancreas-GAN outperforms the state-of-the-art methods in terms of both the Dice similarity coefficient (DSC) of 88.72%±3.23 and the pixel wise accuracy of 95.34%±3.05. This reveals the effectiveness and the potential of our method in the clinical setting.

Fuyong Xing et al [2010] propose a learning-based framework for accurate and automatic nucleus segmentation with shape preservation. Given a nucleus image, it begins with a deep convolutional neural network (CNN) model to generate a probability map, to which an iterative region merging approach is performed for shape initializations. Next, a novel segmentation algorithm is exploited to separate individual nuclei combining a robust selection-based sparse shape model and a local repulsive deformable model. One of the significant benefits of the proposed framework is that it is applicable to different staining histopathology images. Due to the feature learning characteristic of the deep CNN and the high level shape prior modeling, the proposed method is general enough to perform well across multiple scenarios. I tested the proposed algorithm on three large-scale pathology image datasets using a range of different tissue and stain preparations, and the comparative experiments with recent state of the arts demonstrate the superior performance of the proposed algorithm.

Johannes Schwaiger et al [2012] proposed patient-specific models of organs to improve the planning of surgical resections and the intra operative approach. Pancreatic cancer surgery can benefit from a manufactured, patient-specific model. Therewith, the complex anatomical

structures of and around the pancreas, especially the vessels, can be visualized. Several CT data sets showing the pancreas / pancreatic cancer were segmented. A special software system was used which allows segmentation of different tissues and export of three dimensional model data. A patient-specific model containing the pancreas, pancreatic cancer, arteries and veins was created for each case using rapid prototyping technologies. Different prototyping techniques were applied to show details and anatomical structures within the pancreas. The patient-specific models of the pancreas / pancreatic cancer allowed better visualization of the three-dimensional anatomical structure as well as the perception of size and relations of dimensions and volume. Additionally, the vessels and the cancer within the pancreas were highlighted. The described procedure of creating patient specific models of the pancreas promises advantages for pre and intra operative planning of pancreatic cancer surgery.

Shuhao Sun et al [2014] presented a new approach using non constant mutation rate and hence reveal several important biological parameters of cancer progression, such as initial mutation rate as well as doubling time (or selective advantage coefficients) in different stages, and eventually present a better time scheme. Under more realistic assumptions regarding gene mutation and a more reasonable mutation rate, the averaged values of doubling time and selective advantage coefficient generated by our model are consistent with the predictions made by the published models.

Derya Arslan et al [2017] used microarray gene expression profile to estimate the persons affected with pancreatic cancer. In accordance with this purpose, Anova method was used to reduce the size of high-dimensional pancreatic cancer gene expression profile and eliminate redundant features. Reduced size pancreas cancer gene expression profiles were classified by k-nearest neighbor (k-NN) and artificial neural network (ANN) algorithms. The classification accuracy is %82.7 and 84.6% with k-NN, ANN respectively. The promising results indicate that pancreatic cancer can be diagnosed with high accuracy.

Gleb R. Haynatzki et al [2007] compared nonparametric and semi parametric statistical tests for paired data. This comparison was illustrated on an example of familial pancreatic cancer where study subjects were taken from the Pancreatic Cancer Collaborative Registry (PCCR). The nonparametric test performed on our example better than the two semi parametric tests, and was more efficient in detecting risk differences at earlier ages. After adjusting for follow up time, all methods detected genetic anticipation.

Xiaoying Shan et al [2017] proposed a segmentation pipeline for pancreas using Dixon water magnetic resonance image (MRI) data from five healthy volunteers. The threshold method was used to obtain the approximate outline of the pancreas and the Morphological method was used to separate the pancreas from the surrounding tissues. The segmentation results were compared with manual contours using Dice Index (DI) and they achieved DI: 0.80 ± 0.08 which was better than the level Set Methods (LSMs) DI: 0.64 ± 0.08. The proposed method was simple and easy to integrate with the Medical Imaging Interaction Toolkit (MITK) workbench, so it provided an efficient and simple segmentation method for processing large clinical datasets.

Young Hwan Chang et al [2017] proposed a Deep learning based Nucleus Classification (DeepNC) approach using paired histopathology and immune fluorescence images (for label), and demonstrate its classification prediction power. This method can solve current issue on discrepancy between genomic- or transcriptomic-based and pathology-based tumor purity

estimates by improving histological evaluation. They also explain challenges in training a deep learning model for huge dataset.

S.No	Title	Year	Algorithm Used	Sample Images Taken	Drawbacks / Results / Accuracy
1.	K.Sujatha, et al.,	2019	Recurrent Neural Networks (RNNs)	99	89%
2.	B.Aruna Devi,et al.,	2019	Least square support vector machine(LSSVM),Gray-level coocurrence matrix (GLCM)	168	96%
3.	Jithendra Reddy Dandu, et al.,	2018	DBCWMF, CAT swarm optimization based SIFT (CSO-SIFT) and BPNN classifier	100	90.2%
4.	Ayushi Shukla, et al.,	2018	OTSU thresholding, watershed,SVM	-	90%
5.	Jan Egger, Dieter Schmalstieg, et al.,	2018	Intelligent graph based Segmentation method	-	90%
6.	R. Balakrishna,R. Anandan,	2018	SFTA and SVM based soft computing technique	-	83 %
7.	Fengying Xie, et al.,	2016	SGNN,Features extraction,Classification	240	97.46%
8.	Kishore kumar Reddy, et al.,	2015	K-means clustering & haar wavelet	400	-
9.	Hong Chen, Gary Y. Hou, Yang Han,et al.,	2015	Harmonic motion based Imaging Technique	-	57%
10.	Bhagyashri G.Patil, et al.,	2014	Thresholding & Marker –Controlled watershed segmentation	10	85.27%
11.	Jeenal Shah, Sunil Surve,et al.,	2011	Minimum distance Classifier	-	65.26%
12.	Marek Ogiela, et al.,	2000	ERCP based Image recognition method.	-	85%

III. Conclusion

In this work a moderate survey of numerous techniques for the segmentation and classification of pancreatic cancer image. Evaluation of traditional techniques is neatly explained for detection of tumor and their results are also discussed. By utilizing modified algorithms for detection of pancreatic tumor more effective results can be provided than the existing methods. For comparison of the techniques computational time is the major criterion. As detection of pancreatic tumor is the challenging task, sensitivity, accuracy and reliability have gained major significant. So detailed techniques which highlight the important criteria for the enhancement of image segmentation methodology is much needed.

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