PANCREAS DISEASE DETECTION AND SEGMENTATION USING ABDOMINAL CT SCAN

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Abstract

CT scans may now examine regional morphological and textural defects in the pancreas thanks to accurate sub-regional segmentation of the pancreatic head, body, and tail. Manual sub-region mapping of the pancreas requires a lot of time and effort and might lead to mistakes. Current methods for zonal segmentation of various anatomical features make use of many deep learning networks. As a result, the current algorithms can only make limited use of the contextual data since the three sub areas are rarely visible together on the two-dimensional CT abdominal slices. Using computed tomography (CT) images of the pancreas, we offer a multi-stage approach for precise and automated 3D segmentation. The U-Net model is then used to perform the optimum sub-regional segmentation by computing the joint probability of the two maps. A healthy pancreas from the public NIH dataset and the datasets D1 and D2 of contrast-enhanced abdominal CT images were used to assess the model's accuracy.

Keywords— pancreas, segmentation, CT scan

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INTRODUCTION

In 2020, an estimated 48,220 people will lose their lives to pancreatic cancer in the United States, with an additional 60,430 cases being diagnosed. After colon and lung cancers, pancreatic cancer is the fourth most lethal form of the disease. It is anticipated that the member states of the European Union (EU28) willhave 111,500 deaths due to pancreatic cancer by the year 2025. There were 458 918 new instances of pancreatic cancer diagnosed in 2018, with 432 242 people losing their lives to the illness. That is to say, roughly 94.2% of all cases were fatal. Pancreatic cancer ranks sixth among all cancer types in terms of prevalence. World Cancer Statistics estimated that in 2020 there will be 495,773 new instances of pancreatic cancer and 466,003 deaths related to the disease. During the year 2000, the number of new cases of pancreatic cancer has increased by 1% year. Authors Hu and others (2012).

Furthermore, the pancreas's asymmetrical shape, individual anatomical variations (body weight, height, fat ratio, etc.), gender, age, and the proximity of other organs make it challenging to detect its borders on CT scans. Despite this, CT imaging techniques, when used properly, are a crucial tool for identifying the early diagnosis of pancreatic cancer.

Pancreatic disease detection is a laborious process for doctors. Algorithms for picture segmentation, object detection, and classification have been developed as a result using artificial intelligence (AI). In addition, the margin for mistake in healthcare should be small.

Consequently, highly sensitive techniques are required for use in medical image prediction. The use of pixel-based categorization methods is required for this purpose. Since this is the case, segmentation algorithms see heavy use in medical picture analysis.
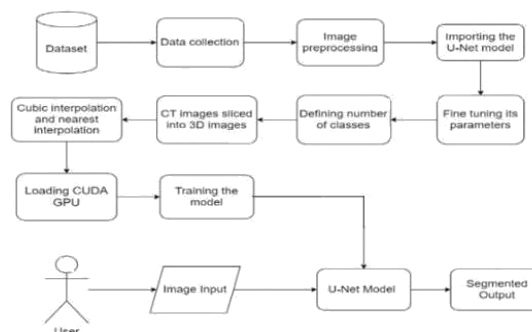

Fig. 1 . Flow Diagram

It is possible that these AI-supported algorithms may help doctors make more precise diagnoses and initiate treatment for patients sooner. This study focuses on how the pancreas, an organ located in the digestive system, gets divided up. Hence, the research employed a number of different segmentation models, such as the U-Net, Attention U-Net, Residual U-Net, Attention Residual U-Net, and Residual UNet++. Models were trained and evaluated with data taken from CT scans. Residual U-Net++ segmentation model performed best in head-to-head competition.

RELATED WORK

[1] There are a variety of therapeutic applications that rely on accurate and automated pancreas segmentation, such as computer-aided diagnostics and radiotherapy for pancreatic cancer, however this is a challenging task (CAD). In addition to low contrast and blurriness of the pancreatic border, patient-to-patient heterogeneity in body shape presents a significant obstacle to precise CT pancreas segmentation. In this study, we present a two-stage, ensemble-based fully convolutional neural network to solve the pancreatic segmentation problem in CT scans (FCN). The first step in creating candidate areas is classifying patches as superpixels. Five FCNs built on top of the U-Net are also taught to accomplish different tasks. Instead of feeding each network the computationally intensive 3D convolutions, we feed each network 2.5D

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slices to offer more data for the 3D image. Finally, the five final segmentation output segmentation maps are integrated using an ensemble model. Knowing how likely a patient is to die is a crucial yet challenging task in the ICU. Finding the predicted components that will aid doctors in acting quickly to prevent mortality is not always easy due to the complexity of the temporal data collected. These are some of the issues that arise from the need for precision and interpretation. Recently, Subgraph Augmented Nonnegative Matrix Factorization (SANMF) has been successfully applied to time series data, addressing a gap in the interpretability of existing methods by providing a way to appropriately interpret the features.

[2] The k-nearest neighbour approach makes predictions for a given instance by looking at other nearby examples. It is a dependable supervised method of categorization that is simple to apply. Nevertheless, this usually causes some vital regional data to be lost. The traditional k-nearest neighbour method relies on a simple majority to determine which category a given object belongs to. In this study, we propose a way to improve the k-nearest neighbour algorithm by heuristically reorganising the properties of the local distribution to yield more informative results for classification.

[3] In order to use Bayesian classification effectively, it is necessary to develop a model for the distribution of probabilities, such as a Gaussian distribution for each class. The majority of the aforementioned methods assumed a normal distribution over all possible samples. In reality, however, events are sometimes too complex to describe using the complete sample space; hence, simplifying the global model necessitates making certain essential assumptions, such as the class conditional independence assumption for naive Bayesian classification. The key idea of this research is that simplifying the essential assumptions that may not be valid over the

full sample space, a local probabilistic model designed for a limited area is projected to be substantially more easy.

[4] Many IoT human-centered applications require action recognition technology (IoT). Action recognition is particularly useful in the IoMT for surgical assistance, patient monitoring,and other similar purposes. Action detection using a skeleton's three-dimensional sequence has received a lot of interest lately. An efficient model of interframe temporal dynamics and intraframe skeletal representations is necessary to achieve this challenging task.

[5] Rapid advances in wearable technology have made it feasible to continuously capture a single lead ECG wave in a practical and inconspicuous manner. This suggests that atrial fibrillation (AF) detection by data mining of single lead ECG waves is gaining popularity. In this study, we introduce a dual-channel neural network to detect AF from a standard electrocardiogram (ECG) (ECG). Preprocessing the data and using a neural network with two inputs are the two most crucial steps.

[6]Many people's lives are negatively impacted by diseases of the thorax. It is impossible to overstate the value of the chest X-ray in modern medicine as one of the most widely used diagnostic methods for thoracic illnesses. Expert radiologists still have a hard time figuring out what's going on in a patient's chest X-rays. As deep learning's reputation grew in the field of computer vision, several researchers began applying it to the classification of chest X-ray images.

[7] When it comes to computers and vision, representing images is ground zero. In contrast, most current methods of image representation treat each input image in isolation from the others. Relationships between images can intuitively aid in understanding the images and keeping the

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model consistent across related images, which in turn improves explainability.

[8] Noise in medical images was reduced using a median and mean filtering technique. This method was fundamental to their overall plan. It has been suggested that a unique approach be used, one that makes use of both linear and nonlinear filters. To achieve a more accurate reading from each pixel in such a noisy picture,

the average and mode filter settings are applied.

[9] Numerical measurements such as Recognition rate, SNR, and RMSE were used to compare the recommended technique with filtering based upon that mean, the average, and the halfway point. The outcomes of this research were contrasted with the typical sound pattern.

EXISTING SYSTEM

Accurate pancreatic segmentation is required for the generation of annotated data sets used in the education of artificial intelligence and computer-assisted interventional guidance. Automated deep learning segmentation does badly in pancreatic CT imaging due to the complexity of the anatomy and the absence of grey value contrast.

More recently, an interactive deep learning architecture for CT scans of the brain seemed like a reasonable option. With this framework's help, initial automated segmentation was much enhanced with minimal user involvement. The subpar performance seen when applying this technique to pancreatic CT may have resulted from a less-than-ideal neural network construction.

PROPSED SYSTEM

In this study, we demonstrate a completely automated approach to 3D pancreatic

subregion segmentation using CT image outline data. We propose a multi-stage anatomy-guided framework that first generates a probability map for subregional segmentation using the Nave Bayes model, which leverages the length and volumetric proportions of subregions, based on their adjacency arrangement, and then incorporates the probability map into the conventional 3D U- Net segmentation model [22] to perform improved segmentation.

Contrast-enhanced abdomen CT scans were used to evaluate the models, together with the NIH's public dataset [23] of healthy pancreatic images and two in-house datasets (one for each of the pre-cancerous and cancerous pancreas).
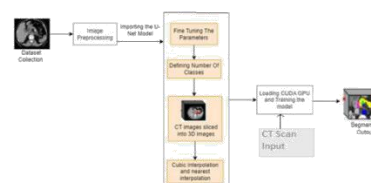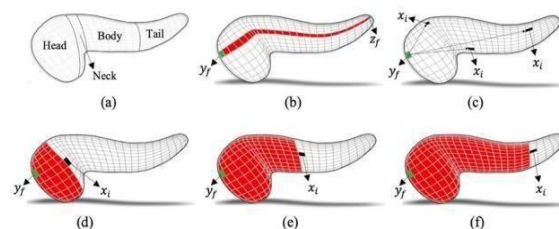

Fig 2:Architecture diagram

Fig 3: Pancreas structure

Data Acquisition

The term "data collection" is used to describe the steps used to amass data for use in training deep neural networks. Information should be stored in a format suitable for its intended usage. Kaggle will be mined for information. The resolution of these photos is 512 pixels on a side. There are 18,942 pictures in all.

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Data Preprocessing

In data mining, preprocessing is a procedure that transforms raw data into a more usable and efficient format. When data is preprocessed, it is transformed into a form that is more conducive to data mining, machine learning, and other data science operations. The methods are often implemented at the outset of the machine learning and AI development pipeline to guarantee accurate results. Because to the nature of picture segmentation, we won't be performing any preprocessing on the 2D photos. Instead, we'll be performing preprocessing on the 3D images, which involves slicing them up into many 2D images.

To store and display pictures, we utilise numpy arrays. Often referred to as "grayscale," a single-channel picture is a 2-dimensional matrix of pixel intensities (row, column). The volumetric nature of 3D pictures is achieved by first assembling a set of 2D slices (plane, row, column).

Multichannel information has a further channel dimension, this one denoting the hues and tones of the data at rest. Certain 3D visuals, such a computer-generated depiction of a sphere, are made with the same amount of detail in each dimension. Most experimental data, for instance, pictures thin layers to represent a three-dimensional structure as a stack of two-dimensional images, with the resolution of one dimension being lower than that of the other two. The spacing, or distance between pixels in each dimension, can be utilised as a parameter by several skimage methods to alter the filter's contribution. A tuple stores the value of the spacing.

Data Augmentation

Data augmentation refers to the process of increasing the data set's size and diversity. Instead than collecting new data, we refine what already exists. Data augmentation is essential to the deep learning process since it is not always feasible to gather hundreds of thousands or millions of pictures for training purposes.

In machine learning, "generalisation" describes how well a model performs on data it has never seen before relative to how well it performed on training data. U-invariance net's property allows it to assign labels to objects that may be observed in a wide range of scales, perspectives, and illuminations.

The imgaug library will be used to explore different data augmentation techniques. Besides bounding boxes, segmentation maps, heat maps, critical areas, and landmarks, Imgaug offers an image enhancement library. As this is the case, we run pip install imgaug to get the library set up. We'll flip an image as a first step in modifying it using basic data augmentation.

Changing the image's orientation to either the vertical or horizontal planes is possible. Images may be flipped horizontally with Fliplr. Here is the correct syntax:

#flipping image horizontally

flip_hr=iaa.Fliplr(p=1.0)

flip_hr_image=

flip_hr.augment_image(image)

ia.imshow(flip_hr_image)

Similarly, we can flip the image vertically using flipup function. Here is the syntax for the same:

flip_vr=iaa.Flipup(p=1.0)

flip_vr_image=

flip_vr.augment_image(image)

ia.imshow(flip_vr_image)

Model Creation

Segmentation, in its simplest form, is the process of dividing a picture into smaller

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parts. It's a kind of image processing that helps us identify and isolate certain features, like faces and buildings, from their background. In remote sensing and cancer diagnosis, for example, segmentation is the method of choice.

When it comes to architecture and convolutional neural network layer-based picture segmentation, U-Net outperforms more traditional models. You can still get good results with smaller datasets of photos.

Biomedical image analysis was initially used to materialise the display of this design. It is well-known that the dimension increase in the second half of the model is the result of the dimension reduction in the height and breadth that we apply throughout the convolutional neural network, namely in the pooling layer.

The two primary components of the U-Net architecture are the encoder and the decoder. The encoder is built up of convolutional and pooling layers that stretch the number of feature channels while decreasing the spatial dimensions of the input picture. Then, the decoder takes this encoded representation and upsamples it to the input image's original spatial dimensions.

As the encoder and decoder are separated by a series of skip connections, the U-Net is so named for its design. With these skip

connections, the decoder can recycle data that the encoder has learnt at various resolutions and help to preserve fine-grained details in the segmentation.

Define the input shape of your images and the number of output classes for segmentation. Create the encoder portion of the model using a series of convolutional and pooling layers.

Each convolutional layer should be followed by a ReLU activation function and possibly batch normalization. The pooling layers can either be max pooling or average pooling.

Save the output of each convolutional block in the encoder portion of the model using skip connections.

Create the decoder portion of the model using a series of upsampling and convolutional layers. Each upsampling layer should be followed by a convolutional layer and a ReLU activation function. Optionally, you can also add batch normalization after each convolutional layer.

Concatenate the skip connections from the encoder portion of the model with the output of each corresponding decoder block to allow the decoder to access the feature maps at different resolutions.

Add a final convolutional layer with a softmax activation function to generate the segmentation map with the same spatial dimensions as the input image.

Representation: Max and Avg. Pooling

The pooling layer decreases height and breadth information while maintaining the same number of input matrix channels. In order to simplify things, a computation is performed (Each element of the image matrix is called a pixel). The pooling layer is a pixel that stands in for many other pixels.

It is important to remember that alternative methods, such as the maximum, average, or median layers, can be used with pooling layers.

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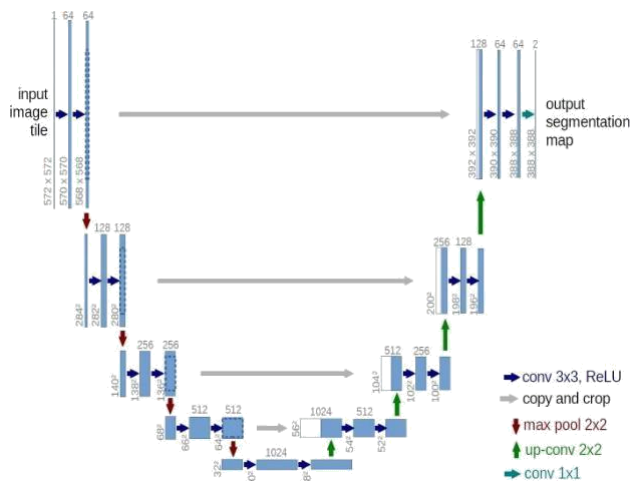
The purpose of these extra layers is to boost output quality. Sampled data is merged with model-wide high-resolution characteristics to aid with localisation. Then, a sequential convolution layer uses this data to hopefully provide more accurate results.

Taking a quick glance at the shown design, we can see why it is most likely called U-Net architecture. This type of building gets its name from its distinctive 'U' shape, which is used as a metaphor in the following phrase. Looking at the architecture and the many parts used to create it, we can see that the network constructed is a fully convolutional network. They haven't tried any alternative layers like thick or flatten. In the illustration, a narrowing route is shown to be followed by a wider one.

The model's architecture reveals that an input picture is processed by a few convolutional layers using the ReLU activation function. We can see that the resolution is decreasing from 572x572 to 570x570 to 568x568. They used

unpadded convolutions (designated the convolutions as "valid"), which led to a decrease in the total number of dimensions.

By the use of the max-pooling layers in strides 2, the encoder block is able to maintain a steadily decreasing picture size. In the encoder, we use a similar pattern of repeated convolutional layers with a growing number of filters. Once reaching the decoder stage, it becomes apparent that the number of filters in the convolutional layers begins to decrease, followed by a steady upsampling in the next layers that continues all the way to the top. In the decoder blocks, we also see skip connections that link up the previous outputs to the layers.

In turn, the model's features may be extracted to aid with picture recognition and categorization. On the U-net with ReLu and Dropout Rectified linear unit (ReLu) successfully propagates a gradient, thereby solving the gradient issue. If the input is

positive, the ReLuoutput will be the same, and if the input is negative, the ReLuoutput will be 0. ReLu is often employed in deep networks thanks to its notable properties. The following equation can be used to express ReLu in a mathematical notation.

$$ReLu(P) = \begin{cases} 0 \ if \ P < 0 \\ P \ if \ P >= 0 \end{cases}$$

Dropout is the process of arbitrarily disregarding some groups of neurons during training, whether they be hidden or visible units. When forward and reverse propagation are performed, the ignored units are removed from later levels. Overfitting the model due to interdependence between units is avoided by dropout.

Model Training

GPUs are well-suited to deep learning because the computations involved are similar to those that GPUs were designed to do. Images, movies, and other visuals are stored in a data structure called a matrix, and any manipulation we perform, such as a zoom effect or a camera rotation, is actually just a mathematical change of that matrix.

As a result, graphics processing units (GPUs) are superior to CPUs when it comes to handling matrix operations and a wide range of other complicated mathematical tasks.
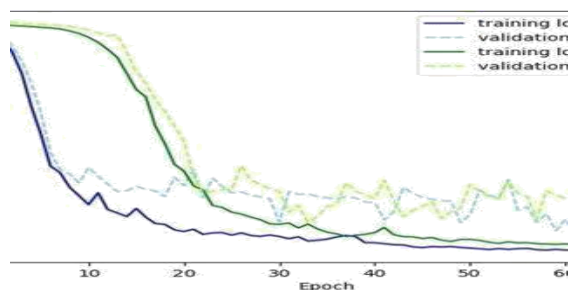
Processors (CPUs) at performing transformations. These days, a GPU can execute a deep learning algorithm multiple times faster than a CPU can. Very often, days-long learning sessions may be

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compressed into a few hours. Hence, we use the GPU to do the training for our model.

Make sure your Nvidia drivers are up to date first. You may also install cudatoolkit directly from this page. Install Anaconda next, adding it to the environment as you go. The following commands are entered into the command line after all installs have been completed:

Conda install numba&conda install cudatoolkit is the appropriate code. Then, we run the normal function on the CPU on the training dataset. Then, we make a function optimized to run on the GPU. In the end, we get the results of time with GPU and without GPU. In our model, training the model with GPU provides greater efficiency and performance and speed. We train our model on 100 epochs.

ANALYSIS:

In this research, abdominal CT images from 1006 people who had checkups were used to demonstrate an automated deep learning approach to pancreatic segmentation and volumetry. A promising DL network for pancreatic segmentation has been recently proposed by several research.

Nevertheless, to our knowledge, no study has yet been conducted to use and assess a DL method on a large abdomen CT dataset of more than 1000 patients. To a large extent, the amount of data points is critical for DL-based medical picture segmentation.

In contrast, the NIH pancreas-CT dataset (n = 82) was employed in previously disclosed DL-based pancreatic segmentation research. High performance in pancreatic segmentation was attained by the previously suggested DL networks (mean DSC of 0.86611, 0.85413, and 0.85930), however there is not enough evidence to conclude their reliability. Thus, we presented a DL-based pancreatic segmentation on a large dataset (i.e., 1,006 abdominal CT images) and performed external validation on the NIH pancreas-CT dataset using four state-of-the-art 3D segmentation networks.

We showed that residual dense u-net allows for precise pancreas segmentation and volumetry, with mean precision, recall, and DSC of 0.869, 0.842, and 0.842 for internal validation, and 0.779, 0.749, and 0.735 for external validation, respectively.

It was verified that the segmentation efficiency of the DL methods increased in direct correlation with the number of trainable parameters. On the external NIH pancreas CT dataset, segmentation performance lagged far behind that on the internal dataset. We attribute these findings to the fact that the external dataset was obtained using a thinner slice thickness (1.5–2.5 mm) for the CT images.

CONCLUSION

We have come to the conclusion that U-Net provides a better baseline for pancreatic segmentation than the present methods. Additionally, U-Net can achieve expert manual performance in the instance of pancreatic CT much more quickly than manual segmentation can. In the realm of medical imaging in general, our novel U-Net design has the potential to be a ground-breaking solution for semi-automatic picture segmentation.

Also in the future scope, multi-model algorithms can be implemented and the efficiency and architecture of the algorithm can be changed and the accuracy can also be improved. Also the precision and recall value can also be increased by trying out many epoch trainings.

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