Annotated Bibliography

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Paper 1:

Citation:

N. Sharma, A. Ray, K. Shukla, S. Sharma, S. Pradhan, A. Srivastva, and L. Aggarwal, "Automated medical image segmentation techniques," Journal of Medical Physics, vol. 35, no. 1, p. 3, 2010.

Description:

This paper is a case study that includes all effective methods of automated image segmentation known at the time. It begins by describing the abundance of unlabeled medical images, and what imaging techniques are used to generate many of them. It then describes segmentation techniques, beginning with a definition of segmentation. It describes common problems with segmentation, including issues like intensity inhomogeneity. Then, it describes methods including edge-based segmentation, region-based segmentation, textural feature based segmentation, atlas based segmentation, thresholding, and AI techniques. It describes how these features work, and what methods are used specifically under each primary technique, (eg. region splitting under region-based). Finally, it concludes with the pros and cons of each technique for each type of imaging.

How I will use it:

My research task involves employing a series/strategy of automated medical image segmentation techniques. In particular, I will be using thresholding and region-based segmentation. I will be identifying a region of interest in a medical image, and this paper describes common problems and pitfalls of the strategies for these tasks, such as closeness in gray level of different areas in the image, and intensity inhomogeneity. In addition, I will be using AI in my process as well. To expand upon this work, I will be employing multiple ideas that were presented in the paper in a specific order (eg. thresholding > connected component analysis > region splitting > AI) in order to achieve a result that is greater than any single part.

Paper 2:

Citation:

O. Ronneberger, “Invited Talk: U-Net Convolutional Networks for Biomedical Image Segmentation,” Informatik aktuell Bildverarbeitung für die Medizin 2017, pp. 3–3, 2017.

Description:

This paper describes the development, release, and testing of a 2D CNN designed specifically for medical image segmentation. It starts out by outlining the necessity of medical image segmentation, describes how CNNS work, and describes the architecture of U-Net, the network that this paper is about. U-Net is an expansion upon fully convolutional networks. U-Net replaces pooling operators with upsampling operators, and combines features from the contracting path with features from the upsampling path. This design allows the network to be trained on arbitrarily large images, and also allows it to yield more precise segmentations. The paper also describes data augmentation strategies to apply in situations with very little training data, along with common problems/solutions in medical image segmentation, such as touching objects of the same class. The paper concludes with an experimental benchmark application of U-Net, statistically showing its relevance.

How I will use it:

I have access to medical imaging data that is very cutting-edge. I will not simply train U-Net on this data, however. Because U-Net is an established medical image segmentation CNN structure, I will apply U-Net to the result of my automated segmentation techniques. Firstly, I will train U-Net using training data masks generated using automated means, and test data that is ground-truth expert labelled data. This way, I can use U-Net as a benchmark for my automated techniques. In addition, I can train U-Net to count certain cellular features in the outputs of my automated methods, which is one ultimate goal that I am attempting to achieve.

Paper 3:

Citation:

Z. Zhao, A. R. Nelson, C. Betsholtz, and B. V. Zlokovic, “Establishment and Dysfunction of the Blood-Brain Barrier,” Cell, vol. 163, no. 5, pp. 1064–1078, Nov. 2015.

Description:

This paper describes the so called “blood brain barrier”, or the organization of blood vessels in the brain, along with their corresponding controlling cells. The paper first describes the development and constriction of the blood brain barrier, as blood moves from the main arteries

of the body into the brain, entering smaller and smaller blood vessels as it goes further. It then describes the relevant research and consensus on the type and purpose of the cellular components in the blood brain barrier. In particular the paper describes and diagrams smooth muscle cells and pericyte cells, among many others, such as astrocytes. In particular, many of these cells are controlled by neurons, and are commanded to expand or constrict in order to facilitate a certain blood-flow scheme within the brain. This is believed to play a key role in brain activity. The paper then describes various diseases and disorders and their effect on these cells, and the result of this effect on the brain overall.

How I will use it:

This paper is all biological, but it is necessary within my research because of the information that it provides on pericytes and smooth muscle cells. Both of these cells have a primary role of regulating blood flow to the capillaries that they surround, but both are described with a distinct structure. Smooth muscle cells have a membrane that fully surrounds its capillary, and pericytes only have string-like processes that surround their capillaries, along with making contact with other pericytes to transfer biomolecules and signals. Most importantly, this paper outlines how pericytes are found in the "deeper" levels of the blood brain barrier, that is, pericytes surround arterioles with a much smaller diameter (by a factor of 3-4). Due to the fact that the images that I am working with highlight pericytes and smooth muscle cells equally, and also the fact that both pericytes and smooth muscle cells have an almost identical size, it seems like a very viable approach to use the diameter of the arterioles that are nearby these cells to distinguish between cell types. This paper may be the key to determining the techniques used in the automated detection algorithm that I write.

Paper 4:

Citation:

S. Moccia, E. De Momi, S. El Hadji, and L. S. Mattos, "Blood vessel segmentation algorithms — Review of methods, datasets and evaluation metrics," *Computer Methods and Programs in Biomedicine*, vol. 158, pp. 71–91, May 2018.

Description:

This paper describes algorithms, datasets, and evaluation metrics in blood vessel segmentation. The algorithms described are vessel enhancement (edge detection and modification of contrast), machine learning (CNNS, etc.), deformable models (evolving a parameterized curve), and

tracking (algorithmically following the vessel from some seed point). The paper describes all of these methods in-depth, including describing CNNS and their structure. Finally, the paper describes evaluation metrics for segmentation, including accuracy, sensitivity, specificity, connectivity, etc. in great depth. It evaluates evaluation metrics for different segmentation problems, including problems such as effectively combining ground truth images from different experts. The paper concludes with the history of vessel segmentation and a summary of the methods and approaches for it.

How I will use it:

Because the biological literature that I am reading suggests that the key to ultimately deciphering between pericytes and smooth muscle cells in the imaging data that I am doing my research with may be the location of the blood vessels in the images, I believe that this paper has valuable techniques and information on completing that exact task. I plan to draw not only vessel identification techniques, such as using their vessel enhancement algorithms, to highlight and detect the vessels in my images, but I plan to use their error metrics as well. This paper has a very nice section on error metrics, and I believe that I will need to specifically evaluate my segmentation masks in order to get the most out of my data, so these error metrics will be very useful. Finally, this paper has a nice description of CNNS, which may be useful in describing them in my tutorial or paper.

Paper 5:

Citation:

M. J. Macawile, V. V. Quinones, A. Ballado, J. D. Cruz, and M. V. Caya, “White blood cell classification and counting using convolutional neural network,” in 2018 3rd International Conference on Control and Robotics Engineering (ICCRE), Nagoya, 2018, pp. 259–263.

Description:

This paper begins by describing the biology surrounding white blood cells and the relevance of the ability to detect them in blood smear images. It continues with related research, much of which did not use deep learning. Then, the authors describe their methodology for extending a pretrained CNN (transfer learning) to detect the white blood cells in these smear images. In particular, the authors mention AlexNet, GoogleNet, and ResNet. The authors do a nice job explaining convolutions, max pooling, and fully connected layers with definitions. The authors

discuss how they are measuring their error and their accuracy in their evaluation. Finally, they discuss their results, and how ultimately their expansions upon the pretrained networks yielded upwards of 97.85% accuracy.

How I will use it:

This paper confirmed suspicions that I had that extending one of these pretrained networks could yield positive results in cell detection. I plan to implement their strategies, and I find it especially helpful that they specified which networks worked the best. I will not take their exact approach, because I will have some preprocessing steps, and perhaps some augmentation steps before I run my model through any of my CNNS. I will also ideally be generating a large amount of training data to use, instead of using human-generated training data. However, this paper is quite useful for its descriptions and definitions of the structure and elements of CNNS, both for the paper and the tutorial/presentation of my research, and, moreso, this paper is useful for its insight on using pretrained networks for a task very similar to mine.

Paper 6:

Citation:

K. Kamnitsas et al., "DeepMedic for Brain Tumor Segmentation," in Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries, vol. 10154, A. Crimi, B. Menze, O. Maier, M. Reyes, S. Winzeck, and H. Handels, Eds. Cham: Springer International Publishing, 2016, pp. 138–149.

Description:

This paper discusses (and is written by the developers of) DeepMedic, a 3D CNN structure. This paper, in particular, discusses extending DeepMedic with residual connections to evaluate its ability to segment brain tumors in brain scans. The paper starts by describing DeepMedic, an 11 layer 3D CNN with a kernel size of 3^3. The authors claim that DeepMedic is tuned to medical application because it is able to be very deep without the massive computation time that 3D CNNS usually require. The authors apply DeepMedic to the BRATS 2015 dataset, and describe the residual connections that they are using to extend DeepMedic in this case. They then describe how to preprocess, format, and input the data into the DeepMedic model. Finally, they discuss their postprocessing and results. In the BRATS contest that they participated in, they achieved one of the top scores.

How I will use it:

I plan to generate a large amount of training data using automated methods, and this training data may be used in a 3D context, due to the fact that the original imaging data has a 3D relationship. Therefore, it is possible to employ a 3D CNN strategy that utilizes this training data and evaluates on the 3D ground truth test data that I also have. In this way, I believe that I can use DeepMedic as, at the very least, a benchmarking metric for my automated methods, by training it using my automated training set and evaluating its ability to train and classify features. In particular, I believe that this paper will be useful in getting the most out of DeepMedic, such as the proper preprocessing, model extensions, postprocessing, and evaluation metrics. Also, this paper shows that DeepMedic is legitimately efficient and effective with medical data.

Paper 7:

Citation:

B. Liu, C. Yin, Z. Liu, and Y. Zhang, "Automatic Segmentation on Cell Image Fusing Gray and Gradient Information," in 2007 29th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, Lyon, France, 2007, pp. 5624–5627.

Description:

This paper begins by outlining the relevance and importance of segmenting hematopoietic cells from blood and bone marrow smears. In particular, this paper is outlining a technique for recognizing the three types of blood cells in this type of image. The authors outline the challenges of isolating the cells from the noisy background and detecting the individual cells, even if they are touching. The authors propose a method of iterative thresholding to isolate the cells features, followed by a 3x3 median filtering to reduce noise. Finally, contour detection and edge detection (mathematical morphology) is used to define what objects are individual cells. Then, a very clever distance-from-centroid algorithm is used to separate cells that are touching, because the previous steps isolated likely cell centroids. The authors also describe segmentation benchmarking methods, and show that their algorithm was more than 95% correct on the dataset that they were using.

How I will use it:

This paper caught my eye because of how similar the cells that they are segmenting look to the cells in the images in my datasets. I believe that this paper will be very useful, however, in the

techniques surrounding the thresholding performed in these authors' experiment, and also in the way that they separate cells that are touching. It is a very important task for me in my automatic detection to find all cell-like structures within my images, (then differentiate between them later). Therefore, I need an optimized thresholding strategy, along with a way to separate cells that are touching in the images. I believe that the strategies outlined in this paper will be very helpful in that task, and it will allow me to further expand upon the results of these strategies to begin to filter the images more or start to differentiate between the pericytes and smooth muscle cells in this new all-cell image mask.