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Generalized deep learning model for Classification of Gastric, Colon and Renal Cancer

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Abstract - *Routine pathology workflows often involve a difference of opinion among pathologists and uncertainty of diagnosis. Deep learning should be used in these situations for enhancing the decision consistency and efficiency. Colon, Stomach and Kidney cancer are among the highest death rates nowadays. In this study, we propose a method to train a deep learning model to classify all gastric, colon and renal cancer using a single model. The Whole Slide Images are fed to the Efficient-Net model which is pre-trained on the ImageNet dataset. The model is trained using a transfer learning method with partial transfusion. There have been various methods suggested to accurately classify these pathology images individually using partial transfusion. This work will demonstrate generalization ability of partial transfusion in classifying pathology images.*

Key Words: **deep learning, pathology, image classification, transfer learning**

1. INTRODUCTION

Global cancer statistics from the year 2022 [1] digestive system sites stand as the second most frequent with 343,040 estimated cases right after genital system with 395,600 estimated cases. Colon alone accounts for 106,180 estimated new cases in the digestive system. Colon cancer is also one of the main causes of death in the modern world with a projection of 52,580 deaths in 2022. Stomach cancer accounts for 26,380 estimated cases and 11,090 deaths. Kidney cancer in the urinary system accounts for 79,000 estimated new cases and 13,920 deaths.

Whole slide images (WSIs), which are acquired by scanning glass slides with specialized equipment, are comparable to microscopy for primary diagnosis and provide benefits of remote consultation. [2] There have been many applications proposed in computational pathology since the debut of deep learning. These techniques had successful results in applications like segmentation of tissues, classification, cell detection and many more [3,4]. These promising results show the power of deep learning in pathology, and how it can avoid human error and ease the clinical workflow.

There have been many attempts at classifying the WSI images for individual tissue [8, 9, 10]. We propose to create a generalized model that can work for many tissues, and for this study we considered gastric, colon and renal tissues. Baqui, M. N et al. [5] carried out a study at one of the most reputed histopathology centres in Bangladesh. They found that site of origin of tissue was absent in 71.83% of the container samples. The tissue name was also absent in 7.7% of the requisition papers. This information is critical for diagnosis and our model can be put into use in such situations.

One of the major challenges when using different datasets is the varying image sizes. So, we would first need to perform appropriate data pre-processing to scale the images to the same size. And since the WSI images are very large, we will divide the images into many tiles using fixed strides and train the model using the individual tiles. We will use the partial transfer learning method [6] to finetune a pretrained model. Our work will demonstrate whether pre-trained deep learning models can be used with partial transfusion for generalizing pathology classification from any site of origin.

2. RELATED WORK

Iizuka et al. [7] have classified gastric and colonic epithelial tumors using a weekly supervised multiple instance learning technique. After extracting many tiles from each WSIs, they trained CNN from scratch using inception-v3 as the base architecture, reducing the number of weight parameters. They made use of sliding window technique with stride 256 on input tiles of 512x512 pixels, since all the tiles must be classified to obtain the slide label. The models were evaluated using max pooling and RNN (with two LSTM layers) aggregation methods. Although there were almost no statistical differences with the methods used for aggregation, if there was a difference RNN performed better. Adenocarcinoma classification got an AUC of 0.924 for stomach and 0.982 for colon. The limitation of this study is that we need a huge dataset for following this method and it takes a long time for training a model from scratch. And it is not worth the time when fine-tuned models also achieve similar accuracy scores [6].

Tsuneki et al. [8] used a partial transfer learning method to finetune the pre-trained model. They have attempted to classify the rare poorly differentiated colorectal adenocarcinoma using their model. Their approach merely entails modifying the only certain parameters of the batch normalization layers of the pre-trained model and not all. They used the EfficientNetB1 model which was trained on the ImageNet dataset. The model was able to achieve ROC AUC of 0.94.

Byeon et al., [10] have used digital photographs of pathology slides rather than using WSIs to classify colorectal lesions into six classes. They achieved a mean accuracy of 97.3% using DenseNet-161 and 95.9% using EfficientNet-B7. Gradient-weighted class activation mapping was utilized in building a saliency map that shows the area that served as the basis for the decision. An expert human pathologist assessed the Grad-CAM pictures of the test dataset and the deep learning model's region of interest as a color map. The limitation of this study was the fact that digital photographs were used instead of the WSI images, since digital photographs are not an accepted standard for primary diagnosis.

Binglu Huang et al., [11] developed deep learning models that can predict the diagnosis and can also find the overall survival of Gastric Cancer patients using pathological images. They developed two models using AI which are called GastroMIL and MIL-GC. GastroMIL model is for diagnosing Gastric Cancer and MIL-GC for predicting outcome of Gastric Cancer. They achieved an accuracy of 92.0% that is greater than junior pathologist and also that is equal to senior pathologist. For developing these models, they included clear pathological images, images of patients with Gastric Cancer and images of patients above 18 years. In the working model each image is divided into tiles with some size, then probability of these tiles that are being diseased is produced as output. After that K most suspicious tiles are selected and final prediction of the image is generated using RNN. They also developed a working website for these models. The main limitation of this model is survival rate of GC patients is different with respect to different datasets due to progress of treatment.

Xiaodong Wang et al., [12] developed a model that can predict cancer of the stomach from a removed lymph node which contains three phases like Segmentation, Classification, T/MLN Ratio. To develop this model, they selected 120 Whole Slide Images that show metastasis from the tumor and 60 whole-slide images devoid of metastases. To isolate the area of the lymph nodes the WSI slide is given as the segmentation network's input in the working model. The classification network then classifies tissues inside a lymph node area to determine the tumor region. The ResNet-50 model is used for classification which has more accuracy and inference speed than Inception V4 and also ResNet-101. This method's main flaw is that it used a dual-center retrospective research of GC from one country for its prognostic analysis of T/MLN.

Hisham Abdeltawab et al., [13] suggested a new model for automated classification to take care of diagnostic chores using a deep learning pipeline. This approach can both identify and categorize kidney tumor- and non-tumor-bearing regions. The framework consists of three CNNs and WSI images of the kidney that are divided into groups of 3 different sizes which are considered as input. This model can provide patch wise and pixel wise classification. The suggested model has a 92.0% accuracy rate. The pyramidal deep learning model that has been presented makes use of a hierarchy of three CNNs to handle various picture sizes. In this model the image sizes are 250*250, 350*350, 450*450. The main limitation of this model is mislabeled images, folded tissues and torn tissues.

Yasmine Abu Haeyeh et al., [14] For RCC subtyping, a multiscale weakly supervised deep-learning technique was developed. The RGB-Histogram standard stain normalization is first applied to the entire slide pictures in the proposed system to reduce the impact of color fluctuations on system performance. To retain the tissue connectedness, they divided the input data into several overlapping patches using the multiple instance learning technique. To get the final classification judgment, they train three multiscale CNNs and then apply decision fusion to their anticipated outcomes. With a 97.9% accuracy rate and no need for fine-grained annotations at the patch level, this model eases the load of pathologists' annotations.

Michael Fenstermaker et al., [15] created a deep learning model to determine whether histopathological specimens include Renal Cell Carcinoma (RCC), which had a 99.1% accuracy rate. To maintain the RGB color channel information, a digitized (H&E) slide is divided into groups and represented as a 3D matrix in this approach. One pattern is sought after by a feature detector. In order to be analyzed by a neural network, the pooled 2D picture is flattened to a 1D vector. The data is flattened and sent through several layers of neurons. that are all completely connected, up until the layer that determines subclass probabilities in the final output layer. In this model, the algorithm successfully identified the related ultimate pathology in more than 97% of instances, even when just using a single 100 um2 patch of renal tissue.

Amit Kumar Chanchal et al., [16] proposed a utilizing deep learning architecture Separable Convolution Pyramid Pooling Network (SCPP) for segmentation of histopathological images. They worked on three datasets that are breast cancer, kidney, multi organ disease histopathology. Encoder-decoder architecture serves as the foundation for segmentation, SCPP more pertinent features

are being extracted at a higher level. When compared to earlier deep learning models that had less computational complexity, the suggested SCPP-Net architecture performed the best at F1 and AJI score.

Glovanna Maria Dimitri et al., [17] suggested a solid decision-making aid for the automated assessment of the Karpinski measure. This will assist medical professionals in determining whether or not the kidney is transplantable by assisting them in identifying the presence of sclerotic glomeruli. Using human kidney samples from scanned Whole Side Images, sclerotic and non-sclerotic glomeruli were identified and distinguished. The DeepLab V2 model was used to segment the pictures, and 512 × 512 patches taken from the original WSIs were encoded using a pretrained ResNet101 encoder.

Fengyi Li et al., [18] suggested a unique technique for fine-grained glomeruli categorization. Glomeruli was divided as Neg - tubule and artery, SS - an area of the glomerular tuft that has sclerosis, GS - sclerosis affecting the entire tuft in full, C - Bowman's space has more than two layers of collecting cells, usually with deposits of collagen and fibrin; NOA - none of the above. DenseNet-121 chooses the GS and Neg samples, which are then forwarded to the glomerular refinement module. A component of the adversarial correlation guided network is the feature extractor, along with a separator and an adversarial correlation loss (CGN).

S. Shubham et al., [19] locating human kidney tissues using deep learning to identify glomeruli. In order to scale several dimensions utilizing a primary technique, UNet is using EfficientNetB4 as the segmentation model, and foundation. The dataset used was Human BioMolecular Atlas Program (HuBMAP). When the area of interest (ROI) in medical imaging is ambiguous, it is feasible to overcome the constraints of UNet deep neural network by fine-tuning the model.

Fuzhe Ma et al. [20] In order to identify and segment chronic renal failure, an HMANN model (Heterogeneous Modified Artificial Neural Network) that is supported by a Backpropagation (BP) approach and classified as a Support Vector Machine (SVM) and Multi-Layer Perceptron (MLP) was created. The pre-processing steps involved restoring of the image, sharpening and smoothening, contrast enhancement method which helped in denoising. The above process was able to achieve high accuracy and performance by including level set segmentation during denoising of the images.

J. Yogapriya et al. [21] have done a comparative analysis by considering some of the pre-trained models like GoogleNet, ResNet-18, VGG16, a CNN model (Convolutional Neural Network). The dataset used are GIT (GastroIntestinal Tract) images from Norway's VV health trust taken with endoscopic equipment. The small data sizes issue was resolved by using transfer learning to fine-tune the developed model. The analysis made it clear that, from the pre-trained models considered, the VGG16 model was able to achieve better performance with 96.33% accuracy, 96.5% precision, 96.5% F1-measure, and 96.37% recall. The requirement of manually updating the information which is then used as the dataset, is the weakest point of the algorithm. By using larger datasets, the above-mentioned issue can be solved.

Deiva Nayagam et al. [22] have recommended utilizing digitized H&E stained histology slides to do deep learning to identify colorectal cancer. He claims that, when compared to all other methods and techniques, the CNN model's classification of images of colon cancer tissues has the highest accuracy and the shortest computation time. Accuracy of 99.7% was achieved using CNN as the main model. The model provides a 99.9% median accuracy for normal slides and 94.8% median accuracy for cancer slides. The model's predictions were comparatively better than that of a pathologist. Use of supervised techniques for image classification outperformed the unsupervised techniques.

Eiichiro Uchino et al. [23] focused primarily on the seven pathological characteristics necessary for a diagnosis, including segmental sclerosis, crescent, endocapillary proliferation, global sclerosis, and structural modifications to the basement membrane and crescent. Using the information mentioned, an AI based model was developed to classify the above findings. The dataset used for this model development consisted of the WSIs from 283 renal biopsy patients who had their procedures approved by the Kyoto University Hospital for research use. The model performed well, with an AUC of more than 0.98, which was virtually identical to nephrologists' results. A weak point of the model could be that it becomes tough to predict accurately when the input deviates from the data largely. Another limitation of this model is that the dataset considered were involving only PAS and PAM staining.

3. PROPOSED METHODOLOGY

3.1 Datasets

In this study, we considered three different datasets, first is Dartmouth Kidney Cancer Histology Dataset, second is Histopathological images of Colon and Lung Cancer and third is Gastric Slice Dataset. The detailed description of these datasets is given below.

The Pathology and Laboratory Medicine Department at Dartmouth-Hitchcock provided this dataset of 563 whole-slide pictures of renal cell carcinoma (RCC) Formalin-fixed paraffin embedded (FFPE) and hematoxylin and eosin (H&E) stained images (DHMC).

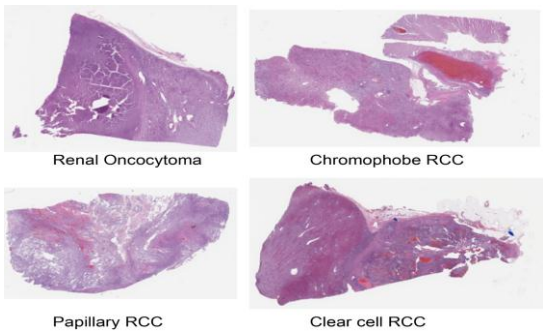

Fig. 3.1 Kidney Pathology Images

Histopathological Pictures of Lung and Colon Cancer - This collection includes 25,000 histopathological images divided into 5 groups. JPEG files with a resolution of 768 by 768 pixels make up each image. The original sample of verified sources that complied with HIPAA was used to create the 500 photos of colon tissue and 750 images of lung tissue (including 250 each of benign, adenocarcinoma, and squamous cell carcinomas) (250 benign colon tissue and 250 colon adenocarcinomas). The Augmentor programme was then used to enhance these photos to 25,000.

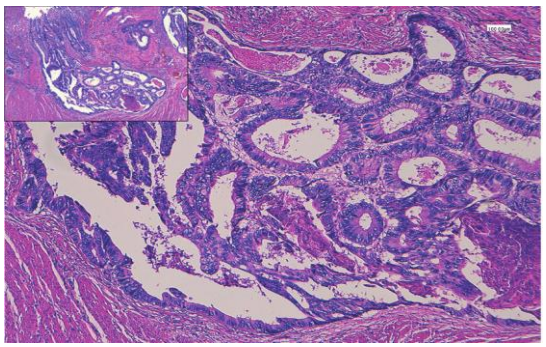

Fig. 3.2 Colon Pathology Images

Gastric Slice Dataset - The gastric slice dataset contains 140 normal pictures and 560 images of malignancy.

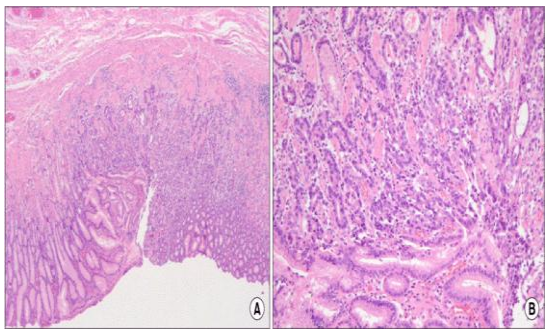

Fig. 3.3 Stomach Pathology Images

3.2 Image Preprocessing

Since we are using relatively small datasets to have a robust performance, we will first apply data augmentation on the datasets and combine them. Since the WSI images are very large we will perform slide tiling by extracting square tiles with a fixed stride from tissue regions and traverse them in a sliding window fashion while training the model.

3.3 Deep learning model

We will use Transfer Learning on EfficientNetB7 architecture [24] and finetune it to our dataset. EfficientNet offers Compound Scaling which combines the Depth, Width and Resolution Scaling in an efficient manner providing a model with smaller size and higher accuracy. The reason for using a pretrained model instead of training a model from scratch is the faster training time with a similar model performance.

We will take advantage of Partial Transfusion [6] and fine-tune only the trainable weights of the batch normalization layers as it leads to similar performance as to fine-tuning all of the weights along with faster training. This means that we can only train the parameters scale and offset, instead of all the parameters and reduce the overall training time once again. The model will be trained with the Adam optimisation algorithm [25] and cross entropy loss function.

In order to perform transfer learning with the given model few changes need to be made to the pretrained model. First, we need to remove the final classification layer as it outputs the labels for the ImageNet dataset. Then we apply a Global-Average-Pooling (GAP) layer followed by a dropout layer. A softmax activated dense layer at the end will be added to classify into our target labels.

4. CONCLUSIONS

In this study, we have done a lot of research work about pathology classification, we have explored numerous research papers related to pathology and its statistics. We came to know that among various diseases the cancers related to the digestive system are some of the most frequent, especially gastric cancer, colon cancer and renal cancer. Pathologists find it very difficult to detect these diseases manually with existing systems. Therefore, a lot of work needs to be done to help pathologists to reduce the time-consuming workflow of identifying diseases and diagnosing the disease. Furthermore, we have learned about various existing systems and proposed systems in the research papers which helps us in building our new proposed model that helps pathologists to detect the disease very quickly and easily.

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REFERENCES

[1] Siegel RL, Miller KD, Fuchs HE, Jemal A. "Cancer statistics, 2022". CA Cancer J Clin. 2022; 72(1): 7– 33.

[2] Shinohara S, Bychkov A, Munkhdelger J, Kuroda K, Yoon HS, Fujimura S, Tabata K, et al. "Substantial improvement of histopathological diagnosis by whole-slide image-based remote consultation". Virchows Arch. 2022 Aug;481(2):295-305. doi: 10.1007/s00428-022-03327-2. Epub 2022 Jun 7. PMID: 35672584; PMCID: PMC9172976.

[3] Chetan L. Srinidhi, Ozan Ciga, Anne L. Martel, "Deep neural network models for computational histopathology: A survey", Medical Image Analysis (2020), doi: https://doi.org/10.1016/j.media.2020.101813

[4] Van der Laak, J., Litjens, G. & Ciompi, F. "Deep learning in histopathology: the path to the clinic". Nat Med 27, 775–784 (2021). https://doi.org/10.1038/s41591-021-01343-4

[5] Baqui, M. N., Rozhana, S., Rajib, R. C., Huda, M. M., Mohammad Mesbahuzzaman, .-., & Paul, T. K. (2019). "Frequency of Mislabeled Specimen in a Histopathology Laboratory". Journal of Surgical Sciences, 17(2), 80–83. https://doi.org/10.3329/jss.v17i2.43726

[6] Kanavati, F.; Tsuneki, M. Partial transfusion: "On the expressive influence of trainable batch norm parameters for transfer learning". arXiv 2021, arXiv:2102.05543.

[7] Iizuka, O., Kanavati, F., Kato, K. et al. "Deep Learning Models for Histopathological Classification of Gastric and Colonic Epithelial Tumors". Sci Rep 10, 1504 (2020). https://doi.org/10.1038/s41598-020-58467-9

[8] Tsuneki, M.; Kanavati, F. "Deep Learning Models for Poorly Differentiated Colorectal Adenocarcinoma Classification in Whole Slide Images Using Transfer Learning". Diagnostics 2021, 11, 2074. https://doi.org/10.3390/diagnostics11112074

[9] Ahmad, N., Asghar, S. & Gillani, S.A. "Transfer learning-assisted multi-resolution breast cancer histopathological images classification". Vis Comput 38, 2751–2770 (2022). https://doi.org/10.1007/s00371-021-02153-y

[10] Byeon, Sj., Park, J., Cho, Y.A. et al. "Automated histological classification for digital pathology images of colonoscopy specimen via deep learning". Sci Rep 12, 12804 (2022). https://doi.org/10.1038/s41598-022-16885-x

[11] BingluHuang,ShanTian,NaZhan,JingjingMa,ZhiweiHuang, ChukangZhang,HaoZhang,FanhuaMing,FeiLiao,MengyaoJi,JixiangZhang,YinghuiLiu,PengzhanHe,BeiyingDeng,JiamingHu,WeiguoDong: "Accurate diagnosis and prognosis prediction of gastric cancer using deep learning on digital pathological images: A retrospective multicentre study"

[12] Xiaodong Wang, Ying Chen, Yunshu Gao, Huiqing Zhang, Zehui Guan, Zhou Dong, Yuxuan Zheng, Jiarui Jiang, Haoqing Yang,

Liming Wang, Xianming Huang, Lirong Ai, Wenlong Yu, Hongwei Li, Changsheng Dong, Zhou Zhou, Xiyang Liu & Guanzhen Yu: "Predicting gastric cancer outcome from resected lymph node histopathology images using deep learning" https://doi.org/10.1038/s41467-021-21674-7

[13] Hisham Abdeltawab, Fahmi Khalifa, Mohammed Ghazal, Liang Cheng, Dibson Gondim & Ayman El-Baz: "A pyramidal deep learning pipeline for kidney whole-slide histology images classification" https://doi.org/10.1038/s41598-021-99735-6

[14] Yasmine Abu Haeyeh, Mohammed Ghazal, Ayman El-Baz, Iman M. Talaat: "Development and Evaluation of a Novel Deep-Learning-Based Framework for the Classification of Renal Histopathology Images" https://doi.org/10.3390/bioengineering9090423

[15] MichaelFenstermaker, Scott A.Tomlins, KarandeepSingh, JennaWiens, Todd M.Morgan: "Development and Validation of a Deep-learning Model to Assist With Renal Cell Carcinoma Histopathologic Interpretation" https://doi.org/10.1016/j.urology.2020.05.094

[16] Amit Kumar Chanchal, Aman Kumar, Shyam Lal, Jyoti Kini: "Efficient and robust deep learning architecture for segmentation of kidney and breast histopathology images" https://doi.org/10.1016/j.compeleceng.2021.107177

[17] Giovanna Maria Dimitri , Paolo Andreini, Simone Bonechi , Monica Bianchini, Alessandro Mecocci, Franco Scarselli, Alberto Zacchi Guido Garosi, Thomas Marcuzzo andSergio Antonio Tripodi, "Deep Learning Approaches for the Segmentation of Glomeruli in Kidney Histopathological Images" https://doi.org/10.3390/math10111934

[18] F. Li et al., "Correlation-Guided Network for Fine-Grained Classification of Glomerular lesions in Kidney Histopathology Images," 2020 42nd Annual International Conference of the IEEE Engineering in Medicine & Biology Society (EMBC), 2020, pp. 5781-5784, doi: 10.1109/EMBC44109.2020.9176234.

[19] Shubham, S., Jain, N., Gupta, V. *et al.* "Identify glomeruli in human kidney tissue images using a deep learning approach". *Soft Comput* (2021). https://doi.org/10.1007/s00500-021-06143-z

[20] Fuzhe Ma, Tao Sun, Lingyun Liu, Hongyu Jing, "Detection and diagnosis of chronic kidney disease using deep learning-based heterogeneous modified artificial neural network", Future Generation Computer Systems, Volume 111, 2020, Pages 17-26, ISSN 0167-739X. https://doi.org/10.1016/j.future.2020.04.036.

[21] J. Yogapriya, Venkatesan Chandran, M. G. Sumithra, P. Anitha, P. Jenopaul, C. Suresh Gnana Dhas, "Gastrointestinal Tract Disease Classification from Wireless Endoscopy Images Using Pre-trained Deep Learning Model", Computational and Mathematical Methods in Medicine, vol. 2021, Article ID 5940433, 12 pages, 2021. https://doi.org/10.1155/2021/5940433

[22] Deiva Nayagam R, Aarthi K, Mirra S, 2022, "Colon Cancer Classification on Histopathological Images using Deep Learning Techniques", INTERNATIONAL JOURNAL OF ENGINEERING RESEARCH & TECHNOLOGY (IJERT) ETEDM – 2022 (Volume 10 – Issue 08).

[23] Eiichiro Uchino, Kanata Suzuki, Noriaki Sato, Ryosuke Kojima, Yoshinori Tamada, Shusuke Hiragi, Hideki Yokoi, Nobuhiro Yugami, Sachiko Minamiguchi, Hironori Haga, Motoko Yanagita, Yasushi Okuno, "Classification of glomerular pathological findings using deep learning and nephrologist–AI collective intelligence approach", International Journal of Medical Informatics, Volume 141, 2020, 104231, ISSN 1386-5056, https://doi.org/10.1016/j.ijmedinf.2020.104231

[24] Tan, M.; Le, Q. "Efficientnet: Rethinking model scaling for convolutional neural networks". In Proceedings of the International Conference on Machine Learning, Long Beach, CA, USA, 9–15 June 2019; pp. 6105–6114.

[25] Kingma, D.P.; Ba, J. Adam: "A method for stochastic optimization". arXiv 2014, arXiv:1412.6980.

[26] Song, Z., Zou, S., Zhou, W. et al. Clinically applicable histopathological diagnosis system for gastric cancer detection using deep learning. Nat Commun 11, 4294 (2020). https://doi.org/10.1038/s41467-020-18147-8