

Ontology based Image Analysis for Clinical Care Pathways

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Abstract— In oncology treatment, clinical care pathways play a major role in the prognosis of the disease. Based on the significant research collaboration between academic bodies and government agencies, standard clinical care pathways are available in the form of standard ontologies. Standard disease ontologies cover possible treatment options for patient-specific conditions. In this work, we have designed a framework to automatically segment kidney cancer/tumor to estimate the T staging and convert the T stage and other patient-specific clinical information to a standard Resource Definition Format (RDF). Converting patient-specific information in the form of ontologies will help to map with the standard ontologies to extract clinical care pathways. For kidney tumor segmentation in CT images, an unet-based deep learning architecture was used, and hyper parameters were tuned to get the tumor segmentation. Based on the size of the tumor, T-stage information was derived, and from patient electronic medical records, patient-specific clinical information was extracted. Using T-stage and clinical information, patient-specific clinical information was converted to RDF file format for each patient and stored in a Graph DB database that can be queried via Spark QL queries. To extract clinical care pathways for a specific condition of the patient, owl language was used to develop mapping functions for mapping patient-specific ontologies with standard ontologies. Proposed methodologies were tested on 209 patients, and we were able to achieve kidney segmentation and tumor segmentation accuracy of 0.9 and 0.86 IOU scores, respectively. Further owl functions were used to extract the clinical care pathways by mapping patient-specific ontologies to standard ontologies.

Index Terms— Ontologies, Clinical care pathways, Deep Learning, tumor segmentation

I. INTRODUCTION

An ontology is a formal representation of knowledge within a specific domain, typically describing the concepts, relationships, and properties relevant to that domain. It provides a structured and organized way to model a particular area of interest, enabling better understanding, communication, and reasoning about that domain. Ontologies are used in various fields, including computer science, information science, artificial intelligence, and knowledge engineering. Clinical care pathways, also known as care pathways, clinical pathways, or care plans, are structured, multidisciplinary plans that outline the key steps and interventions involved in the care of patients with a specific health condition or undergoing a particular medical procedure. These pathways are designed to improve the quality, efficiency, and consistency of care by providing a standardized approach to the diagnosis,

treatment, and management of patients. Kidney cancer, also known as renal cancer, refers to the uncontrolled growth of abnormal cells in one or both kidneys. Clinical care pathways are essential in managing kidney cancer by providing standardized procedures for diagnosis, staging, and treatment. They guide healthcare professionals in recommending tests like CTscans and tailoring treatment plans, such as surgery, targeted therapy, immunotherapy, or radiation, based on the cancer's stage and characteristics. Our paper focuses on two critical aspects of healthcare: organizing patient information and analyzing CT images to aid in cancer diagnosis. In the proposed work, we are using ontologies to represent patient information in the form of a resource description file (RDF) and using owl language to map patient information to the standard ontologies where clinical care pathways are given. RDF (Resource Description Framework) serves as a comprehensive representation for aggregating information about patients from diverse data sources, encompassing images, signals, text, and signals. Through this specific RDF structure, we effectively organize and store patient-specific details extracted from various sources, such as images (including 3D CT images) and text (including clinical reports). The integration of RDF and ontology in managing healthcare data promises a more interconnected, interoperable, and insightful method for comprehending and leveraging patient information. This has the potential to make substantial contributions to enhanced diagnostics, personalized medicine, and overall improvements in healthcare outcomes. Image analysis of 3D computer tomography (CT) Images with computer vision and deep learning techniques can derive clinical insights that can be very useful for the patient's disease diagnosis. In this work, we are analyzing CT images to determine and compute the size of the tumor that exists in the kidney region. Estimating the size of the kidney tumor and deriving T-stage information from images will be a very useful addition to the patient-specific ontologies.

II. LITERATURE REVIEW

In the pursuit of developing a method for kidney and tumor segmentation for obtaining T-stage information, various studies have been conducted, each employing different approaches and techniques for performing the segmentation. One study [6] utilized deep convolutional neural networks, specifically two U-Net architectures (U-Net and Attention U-Net), for precise kidney tumor segmentation in CT scans. The KiTS19 dataset, consisting of 210 NIFTI-formatted abdomen CT volumes, was used for experimentation. The study demonstrated the effectiveness of deep convolutional neural networks in accurately segmenting kidney tumors in CT scans, although it had limitations in detecting edge cases or tumors in border cases. Another study [7] focused solely on kidney segmentation using a U-Net 2D model on the KiTS19 dataset. The method involved preprocessing, scope reduction, kidney segmentation, and false-positive reduction. The results showed excellent accuracy, with an average Dice coefficient of 96.33%, an average Jaccard index of 93.02%, an average sensitivity of 97.42%, an average specificity of 99.94%, and an average accuracy of 99.92%. In contrast, a different study [8] introduced a deep learning approach for classifying kidney cysts on CT scans as benign or malignant, using 2.5D ResUNet and 2.5D DenseUNet models. Although it focused on the initial kidney segmentation task, the proposed method outperformed other models with a Dice coefficient of 0.975 on the KiTS19 dataset. However, domain shifting was identified as a limitation affecting generalization across different datasets. A study [9] from 2014 aimed to predict clinical query trends by analyzing radiologists' and physicians' queries for text and medical images. The authors utilized ontologies like FMA, RadLex, ICD, and the NCI Cancer Thesaurus to statistically analyze domain ontology concepts and establish relationships, effectively anticipating clinical query trends. The Kidney Precision Medicine Project (KPMP) [10] seeks to map the entire kidney by integrating clinical, histological, and genetic data using ontologies such as KTAO and OPMI. These ontologies aim to enhance precision medicine by providing a roadmap for their utilization, facilitating the description of kidney disease, and supporting community-based development for widespread acceptance and annotation of public kidney data. In the realm of chronic kidney disease (CKD) diagnosis [11], a study based on data from 109 UK general practitioners' offices utilized laboratory tests, clinical codes, and ontologies to improve case detection accuracy. The results emphasized the potential utility of ontology-derived codes in identifying CKD patients. Another paper [12] introduced T2R, a system designed to automatically generate RDF triples representing relations among terms in textual documents. It highlighted the potential of utilizing laboratory tests, clinical codes, and ontologies to identify patients with CKD, including those with end-stage renal disease. The study suggested the need for future research to validate CKD coding in specific patient populations.

III. METHODOLOGIES

A. Dataset and Experimental Setup

The dataset in our work is the KiTS19 Challenge Data [2]. This is a collection of multi-phase CT imaging, segmentation masks, and comprehensive clinical outcomes for 209 patients who underwent nephrectomy for kidney tumors between 2010 and 2018. The experimental setup used is a workstation with Ubuntu 20.04 as the operating system, containing an NVidia Quadro RTX 5000 16GB graphics card.

B. Extract Tumor staging information from CT images

The methodologies we follow up on are pre-processing, deep learning-based tumor segmentation, computing the t-stage of a tumor, clinical data conversion to a resource description file (RDF), and finally, owl mapping for extracting standard clinical care pathways.

Pre-processing of CT image data

The pre-processing step involves the conversion of 3D volume to 2D slices of images and masks. The steps followed are:

- Step 1: Loading KiTS-19 209 patient volumes and masks in NIFTI format.
- Step 2: Slice extraction of 2D CT image and mask slices from 3D image and mask volumes.
- Step 3: 2D image slices are normalized considering the HU value range of $[-250, 250]$ [3].
- Step 4: Normalized 2D image slices and mask slices are saved in PNG format.
- Step 5: Normalized image and mask slices are resized to 128 x 128 pixels.
- Step 6: Ground truth labels are encoded with the values 0, 1, and 2 (corresponding to background, tumor, and organ for kidney organs).

C. Deep learning-based kidney and tumor segmentation

In order to gain Insights from CT image analysis we perform Kidney organ segmentation, Kidney tumor segmentation and generate t-stage of tumor. In our work, we are pursuing a semantic voxel-based approach to segmenting [4] the kidney and tumor regions in 2D CT images. In the approach of semantic voxel-based we perform classification-based segmentation that provides both tumor and kidney segmentation results into one model giving individual segmentation results. We employ a U-Net as the backbone, followed by encoder weights of EfficientNetB4, wherein we perform transfer learning—a popular concept in deep learning that involves reusing features from a pretrained network for a new problem. Our dataset comprises 45,424 images and masks encoded with 0, 1, and 2 (representing background, tumor, and kidney, respectively). The training split is 80%, and the validation split is 10%. Additionally, we have an unseen test set consisting of 10% of the dataset.

We utilize the Adam optimizer with a learning rate of 0.0001. For activation functions, Leaky ReLU is employed for kidney segmentation and tumor segmentation. The batch size is set to 8, and the loss function comprises both dice loss and focal loss. Our chosen training metric is the dice score. This approach enables the evaluation of both kidney and tumor segmentation with respect to the ground truth marked by the radiologist. Our evaluation metrics is IOU on the test dataset giving results for each class individually.

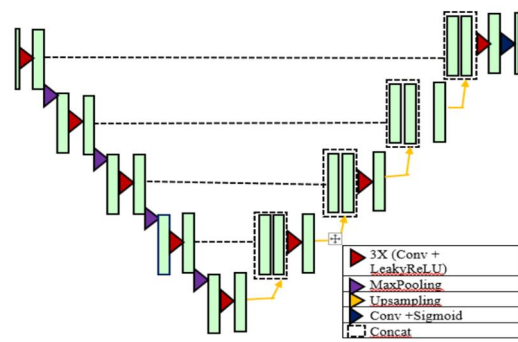


Figure1. 2D U-net architecture for tumor segmentation [4]

D. Algorithm to generate Tumor Staging Information

To generate tumor staging from the segmented tumor, we compute the largest diameter of the tumor class(label encoded 1), and based on the diameter size, we categorize the tumor for each patient into different stages as defined in the flow chart in Figure 2. The extracted tumor staging information will be added to patient-specific ontologies to get better mapping with standard ontologies for clinical care pathways

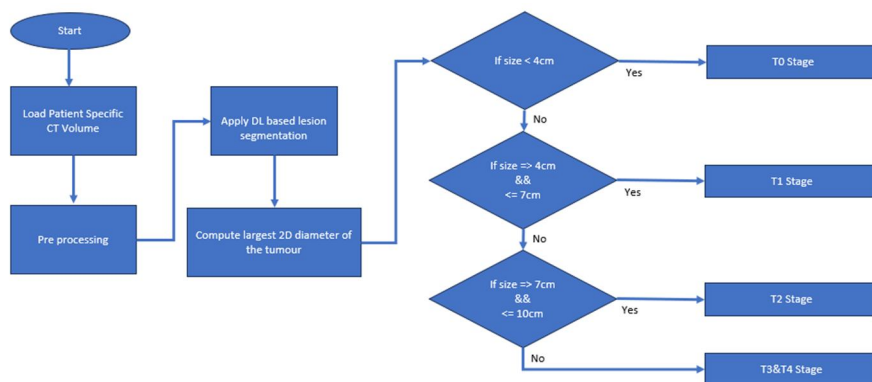


Figure2. Algorithm flow for computing t stage of tumor from CT image analysis

F. Clinical data conversion to resource description file (rdf)

To glean patient clinical history and diagnosis from clinical reports, each patient's information is converted into a JSON file. In this file, every anatomical term associated with kidney carcinoma is meticulously mapped with Radlex [5]. Radlex terminologies, developed and maintained by the Radiological Society of North America (RSNA), are specifically tailored to the needs of the radiology community. RadLex plays a vital role in standardizing reporting and communication in radiology, fostering information exchange among radiologists, aiding decision-making in medical imaging, and contributing to the development of image informatics. The JSON file comprises 20 attributes for each of the 209 patients, each linked to a unique case ID. These attributes are mapped with Radlex terminology, utilizing a unique RID (RadLex Identifier) specified for each term. The mapping is represented with triples, or RDF, identified by a URI (Uniform Resource Identifier). In this RDF structure, the patient node serves as the subject, the RID of the patient is the predicate, and the case ID is the object. This RDF format offers a comprehensive representation of the clinical report in the form of a knowledge graph. This graph facilitates the integration of data from diverse sources and systems, promoting interoperability in healthcare. It enables the storage and representation of clinical information about the patient, including tumor staging from the CT image, patient history from the clinical reports, medical ontologies from Radlex, and other pertinent clinical data in a format that is easily shareable and linkable, as shown in Figure 3. The RDF data can be stored in the GaphDB database and queried using the SPARQL query language, allowing for advanced searches and retrieval of relevant information.

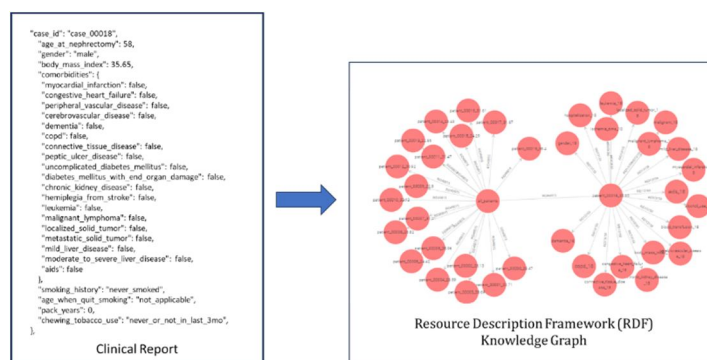


Figure3. Converting patient specific clinical information to standard ontology

G. Owl mapping for extracting standard clinical care pathway

The Web Ontology Language (OWL) language can be used to define classes for clinical concepts (e.g., Patient, Disease, Medication), properties to represent relationships (e.g., has disease, takes medication), and individuals to represent specific instances of these concepts (e.g., Patient1, DiseaseX, MedicationY). This helps to derive a semantically rich representation of clinical knowledge. We have used namespace to include in the graph the standard ontologies defined by SNOMED, LOINC, MEDDRA, MESH, NCIT, etc., as shown below.

Namespaces



Figure6. The training loss curve and validation loss curve

TABLE I. THE TABULAR RESULTS OF THE MODEL

		Background - Class	Kidney Tumor Class	Kidney Organ Class
Model		Efficient NetB0(Encoder) with Unet	Efficient NetB0(Encoder) with Unet	Efficient NetB0(Encoder) with Unet
Dataset Sample Size		45424	45424	45424
(IOU Score)	Validation	0.99	0.85	0.907
	Test (Unseen)	0.99	0.86	0.908

Based on the test set, we were able to achieve a 0.9 IOU score for kidney organ segmentation and a 0.86 IOU score for kidney tumor segmentation. Sample images are shown in Figure 4. From the segmented tumor diameter was calculated, and t-stage information was extracted for all the patient data.

Ontology Mapping

After converting patient-specific clinical and staging information into an RDF graph, All the RDF graphs were stored in GraphDB. Further Owl-ready Python modules were used to map patient-specific ontologies to standard ontologies to extract clinical care pathways. A sample example is given in Figure 5.

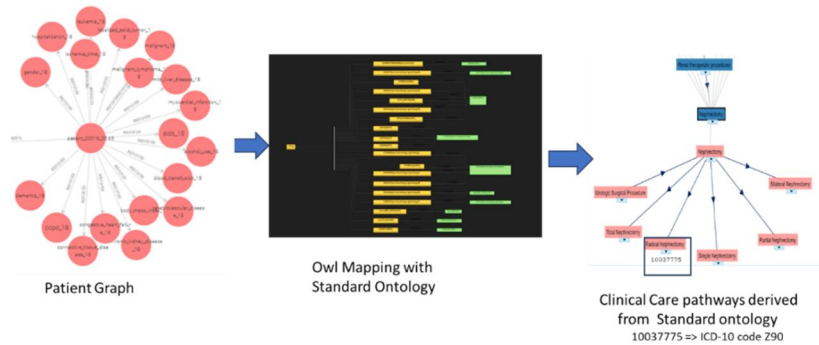


Figure8. Algorithmic flow for mapping patient specific information to standard ontologies

V. DISCUSSION AND CONCLUSIONS

Based on the experiments conducted on the proposed methodologies, we observed that the algorithm for tumor staging is performing reasonably well with a semantic segmentation score of 0.9 IOU on kidney organ segmentation and a 0.86 IOU score on tumor segmentation. Most of the existing DL techniques use instance-based segmentation, where we need to develop multiple models for different objects, and they report IOU scores between 0.6 – 0.75 [] which is far lesser than the performance obtained from proposed tumor segmentation. With instance-based tumor segmentation, though we were able to achieve better performance in kidney organ and tumor segmentation, there is a scope to improve the tumor segmentation at the border of the kidney organ. Further, 3D connectivity information can be utilized for the tumor segmentation by incorporating 2.5D approach and expected improve the segmentation IOU score accuracy, whereas the proposed model used only 2D images. In the proposed methodology, we have used only t stage information, for better clinical care pathway mapping inclusion of Node (N) and Metastasis (M) stage is required. Estimation of N and M stage information can be incorporated with the use of PET images that comes along with PET CT machine. With respect to ontology mapping, identifying the

right standard ontology for clinical care pathways is quite crucial for the accurate treatment suggestions from the algorithm. However, active research work is in progress in this area from well-known academic and government healthcare departments. Further validation of the algorithm has to be conducted on a larger data set to prove the efficacy of the proposed algorithms.

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