Computed Tomographical Abdominal Image Analysis Correlating Renal Lesions with Subsequent Histologic Findings

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Abstract

We propose a graphical model method that can effectively use X-ray computed tomography imaging data to automatically diagnose patients with the appropriate renal carcinoma subtype. The method should be able to first, recognize the kidneys from a CT scan of the loser torso and determine the appropriate region of interest. Furthermore, it should be able to determine which of the two kidneys has an abnormality (unless both do). From this, we can group patients based on carcinoma subtype, which would allow for us to compare variants and to extrapolate from the differences. The ultimate goal then, is to determine a distinguishing characteristic or set of characteristics that can successfully predict and differentiate benign oncocytomas from non-benign variants of renal cell carcinoma. The intention is that this could prove useful in preventing hazardous surgical procedures that would otherwise be unnecessary.

1 Introduction

Renal Cell Carcinoma (RCC) is a fairly common cancer with global incidence of more than 200,000 cases a year with approximately half of diagnosed cases resulting in death [3].

RCC historically presents with a triad of clinical symptoms: flank pain, hematuria, and tumor palpation [3]. However, during the past 15 years, increased use of Computed Tomography (CT) has eliminated this traditional clinical presentation and given rise to the incidental renal mass (IRM). Indeed, 70% of renal tumors are detected incidentally [4]. An IRM is an unsuspected tumor that was identified on an abdominal CT ordered for another purpose, for example an pneumonia diagnosis. An example CT is shown in Figure 1, where the arrow denotes the location of a tumor mass. Because these tumors are identified without the classical corresponding clinical symptoms, it is unclear whether they are malignant or benign. However, because the consequences of a malignant mass are obvious and severe, the preferred treatment is surgical removal and histological diagnosis. The post-surgical histological breakdown of the IRM is 70% Clear Cell Carcinoma, 14% Papillar Type 1 and 2, 8% Chromophobe, and 8% Oncocytoma. [2] Oncocytoma is a benign variant of RCC and does not require surgical intervention [1]. Therefore, if diagnosis of malignancy could be determined from radiologic and other evidence then surgery could be avoided. There may also be other treatment or diagnostic implications to identifying and staging the additional RCC subtypes.

2 Problem Description

In general, this is task of classifying blocks of an image. We must establish the likelihood that individual blocks are located within a kidney cross-section and whether they belong to healthy tissue

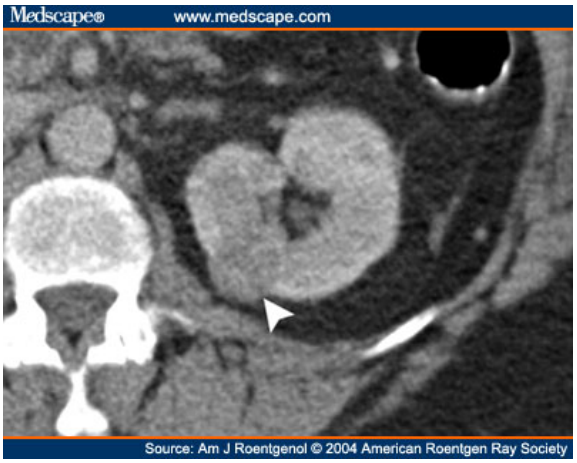

Figure 1: Example of a Renal Lesion

or to an abnormal mass. The factors which influence this likelihood, such as absolute position or identity of neighboring blocks, must be encoded in a graphical model.

The true complexity revolves around the image recognition component. Specifically, image registration, kidney identification, and subsequent tumor identification will involve a great deal of computational effort. Some aspects of image registration will be simplified by the presentation of the highly structured CT images which are ordered, aligned, and oriented in the same fashion for all patients. Additionally, the CT set will be of the contrast enhanced phase allowing for better delineation of tissue structures. We expect to identify the kidney in its broadest cross-section and use the expectation of a relationship between adjacent slices to step out from the widest cross-section.

While the problem of kidney identification is made more difficult by the lack of spacial symmetry between kidneys, we do expect to be able to use each patients contra-lateral kidney for comparison purposes to ease identification of the mass. The population of healthy contra-lateral kidneys can be used as a baseline, obviating the need for a set of healthy patients.

A supervised learning framework based on a generative model learning from this course will be exploited to a) identify kidneys from the CT images, b) categorize the whole kidney, and c) recognize lesions within the kidney. Images are projected onto a feature space that best encodes the variation among known lesion images. The framework provides the ability to learn to recognize new lesion in a supervised manner.

3 Data Source

The data sources that will be leveraged include two database. The first is a curated research data repository for the Department of Urology (Urologic Oncology Research Database). This repository is linked with the clinical enterprise through billing and registration systems. Additionally, the Urology repository pulls patient data from the NewYork-Presbyterian Hospital (NYP) Central Data Warehouse (CDW). Text data corresponding to pathological observations has been manually curated and dissected into structured data. The main variables that we intended to extract include: date of birth, gender, race, hypertension, CVD, smoking, obesity, CKD (chronic kidney disease), preoperative eGFR (Creatine Clearance, race age, and sex) radical or partial nephrectomy date, and corresponding tumor histology. To obtain CT imaging data, this list will be cross referenced with the University Radiology department PACS system. We will be referencing the most recent CT image prior to surgery. Analysis of CT images may provide diagnostic features such as kidney size, lesion size, 3D volumetric shape, fat density, fat location, tissue density, Hounsfield units, among other.

4 Expected Conclusions

We expect, upon conclusion of this effort, to identify a set of factors from background and radiologic evidence which are associated with mass malignancy. It is not known at this time whether the resulting model will have high enough precision to recommend against surgical intervention with acceptably low risk of mis-classifying a malignant mass.

References

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