Self-supervised learning for Renal Cell Carcinoma classification

The context

Renal cell carcinoma (RCC), which typically emerges from the renal tubules, is currently categorized into five main histological subtypes: clear cell, papillary, chromophobe, collecting duct, and unclassified RCC. Among them, the three most common RCCs types are clear cell, papillary, and chromophobe, including 70% to 80%, 14% to 17%, and 4% to 8% of all RCCs, respectively [1]. Collecting duct carcinoma is the most uncommon class of RCC (1%), and unclassified RCCs gathers those alien types which do not fit, morphologically or cytogenetically, into any of the above four subtypes [1]. Approximately 10% of renal tumours belong to the benign entities of RCC parenchymal neoplasms, sub-divided into oncocytoma, angiomyolipoma, and papillary adenoma [2].

The prognosis and outcome of RCC rely on an accurate determination of the histological subtype [1]. Unfortunately, histological RCC sub-typing typically shows a poor to fair agreement between pathologists, with a mean inter-observer value in the range 0.32– 0.55 [4].

Furthermore, existing research recognises the critical role played by the differential diagnosis between chromophobe and oncocytoma, which is known to be difficult and prone to errors due to overlapping immunohistochemical and morphological characteristics [1, 6, 7].

The gold standard for RCC categorization is the microscopic visual assessment of Haematoxylin and Eosin (H&E) stained slides (WSIs) of biopsies histological samples, performed by pathologists.

Deep learning (DL) methodologies, in particular convolutional neural networks (CNNs), have recently been applied also in several histological categorization tasks, among which RCC sub-typing [17, 4, 19, 3].

The self-supervised representation learning (SSRL) paradigm has also recently received increasing attention in the research community. Nevertheless, current literature has primarily exploited SSRL on general category object classification tasks (e.g. ImageNet classification).

Surprisingly, there has been very little attention on how to extend SSRL methodologies to other domains like computational biology or medicine, which paradoxically are among the ones that are most affected by the lack of labelled

training data [5, 8]. In this sense, for contexts distant from the standard natural image benchmarks, finding a pretext task capable of learning a reliable and robust data representation is of particular concern. A longitudinal investigation by Wallace et al. [5] shows how traditional SSRL feature embedding fails in several biological downstream tasks. The authors suggest that the absence of canonical orientation, coupled with the textural nature of the problems, prevents SSRL popular methods from learning a pertinent representation space. They conclude that finding an optimal SSRL feature embedding for fine-grained, textural and biological domains is still an open question.

Project aim and requirements

This project aims at finding an application-independent and potentially reusable data representation to mitigate the needing of annotations of the WSIs. Specifically, you are required to implement and compare four different self-supervised solutions, which basically do not require an explicit annotation. Comparison with pretrained and finetuned CNNs is required. The considered solutions should try to discern 4 different subtypes of RCC neoplastic lesions, namely: clear cell RCC (ccRCC), papillary RCC (pRCC), chromophobe RCC (chRCC), and renal oncocytoma (ONCO). Please note two aspects:

1. Not only tumoral class is present in a generic WSI: also, not tumoral tissue may be found indeed. Specific annotations are done by the pathologist (fiber, necrosis and normal renal parenchyma) if needed. All these not-tumoral classes must be grouped in a class, called for instance not-tumour.
2. The final classification label is given at the patient level. Nonetheless, the WSIs must be cropped into thousands of crops to be fed to the SSRL models. Hence, the final decision at the patient level comes from a majority voting among the predicted crops associated with the same patient, and excluding those crops predicted as not-tumour.

The following models must be compared:

1. Four state-of-the-art SSRL strategies.
2. A fully trained supervised solution (i.e., a CNN).
3. A transfer learning-based solution.

For all the models always optimize hyper-parameters (this includes, if used, also transfer learning parameters: which layer? How many features?)

Dataset

Please consider the dataset provided here. Given its large size, down sampling is permitted. For example, you may choose to include only 5 patients per class (refer to the README for details).

References

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