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A study and Analysis of CNN approach for the Lung Cancer Detection Using Deep Domain Adaption Technique and Image Processing

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Abstract

Medical imaging provides non-invasive assessments of phenotypic diversities in a number of cancer types. Medical images have the potential to offer insights into the patterns of disease spread and treatment response. Furthermore, advances in computerized medical image analysis enable the extraction of tumor's visual representation (features) to facilitate characterizing tumour phenotypes. The association between tumor imaging biomarkers and existing genetic foreknowledge lead to the emergence of image-genomics.

In this paper we review a deep domain adaptation learning framework for associating image features to tumour genetic information. Our approach exploits the potential of domain adaptation technique for image-genomics to quantify image features based on similar knowledge domains. This is accomplished by facilitating the learning of tumour image representations with larger datasets from similar domains to reduce the reliance on large volumes of disease-specific datasets for image-genomics research.

In addition, our proposed framework enables the extraction of additional tumour visual descriptors to provide abstract image representations for associating with gene expressions. It leverages the current state-of-the-art in image object recognition to provide image features which encode subtle variations of tumour phenotypic characteristics. The quantification of such features is facilitated by the employment of domain adaptation techniques. We evaluated our proposed deep domain adaptation learning framework by comparing with current state-of-the-art in: (i) tumour histopathology image classification and; (ii) the degree of image-genomics associations compare with human-crafted tumour image descriptors.

Keywords: Cancer Detection, Image processing, CNN, Machine Learning, Deep learning.

Introduction

Current practices for the treatment of human cancers rely upon the establishment of accurate diagnosis, which may involve a series of complex medical procedures comprising of patient screening for symptom evaluation, non-invasive imaging for disease localization and histopathology analysis of tissue specimens. In recent years, genetic sequencing is becoming an increasingly important addition to the existing diagnostic pipeline. Cancer diagnosis may be the result of analysis of data generated through each medical examinations; the integration of such data contributes towards the understanding of the diseases and hence exhibit potentials to offer optimal cancer therapy at individual patient level [1]. Although medical imaging and general pathology are becoming more routine in current cancer diagnosis, genetic sequencing is not always practical. This is due to human cancers exhibits strong phenotypic and genetic heterogeneity, where disease develops at multiple sites with genetic differences [2]. It is not practical or feasible to obtain tissue samples from all sites of disease as invasive biopsies have the potential to induce tumor proliferation. Further, the cost of genetic examination is high in addition to its limited accessibility.

As an alternative, medical images provide non-invasive assessments of phenotypic diversities in a number of cancer types and contribute to clinical decision- making, e.g., tumor detection, subtype characterization and treatment responses [3, 4]. Advances in computerized medical image analysis allow the extraction of tumor's visual representations (features) to facilitate the characterization of tumor phenotypic differences, which offers insights into the patterns of disease spread and prognosis. The association between tumor imaging features and genetic foreknowledge allows the derivation of imaging surrogates to genetic biomarkers, and ultimately lead to the emerging field of image-genomics [5].

Image-genomics aims to associate the tumor imaging trait and clinical data (e.g., the underlying tumor gene expression) to provide an alternative approach that contributes to a non-invasive and accurate cancer diagnosis [6]. As such, the discovery and extraction of optimized tumor imaging descriptors represent a major challenge in the current image-genomics research.

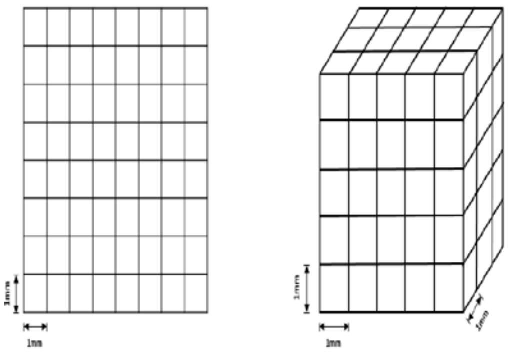
Medical Imaging and Image Processing

A Medical imaging is a fundamental component of the modern healthcare system and is essential for the accurate diagnosis and staging of cancers. Medical images provide a fast and non-invasive assessment of phenotypic diversity in many cancers [12] through a variety of different imaging modalities (or techniques). Medical image processing, in turn, allows the extraction of meaningful information which offers insights of different aspects of patients' conditions. In this chapter, we provide an overview of medical imaging and the theoretical background in image processing techniques that are crucial for cancer diagnosis.

Digital images consist of a collection of numerical picture elements, called pixels. The term pixel resolution refers to the number of pixels in an image, which can be represented as a single number or by the number of pixels in each dimension. For example, an image that contains 8,294,400 pixels can also be referred to as having a resolution of 8.3 megapixels or 3840 ×2160 (width × height) pixels.

Many medical imaging techniques consist of sampling 2D images along a third spatial axis to form 3D images, known as volumetric images or image volumes. These 3D volumetric images encode the spatial relationships between 3D pixels, called voxels, which both 2D and 3D images allow the extraction and interpretation of the encoded information through the use of image processing techniques. Both pixels and voxels exhibit spatial resolutions, which describe the size of the details captured by individual pixels or voxels. For instance, a spatial resolution of 10.00mm × 10.00mm × 5.00mm means that a voxel depicts a region with a volume of 500.00 mm.

Contrast resolution refers to the range of distinct intensity or a set of intensities for red, green and blue (RGB) channels that can be distinguished in grayscale and colored images respectively. A relatively low contrast resolution can be interpreted as pixel/voxel intensities that are similar in an image and are difficult to distinguish.



(a) A 2D image (b) A 3D image volume

Fig 1 : illustrates an example of a 2D image and a 3D volumetric image. Pixels and voxels are visualized in forms of 2D and 3D arrays of grids respectively

In medical image processing, a region of interest (ROI) consists collections of pixels in 2D images that represent an area which encodes important information for particular domain or application in cancer diagnosis. The corresponding term volume of interest (VOI) refers to the emphasized anatomical structures that encode important knowledge for clinical uses.

Modern healthcare utilizes different medical imaging modalities to capture different aspects of the human body for cancer diagnostic and treatment. Medical image modalities can be categorized into two classes based on their technique and process in visualizing different aspects of the diseas: (i) Anatomical and (ii) Physiological (functional) imaging. Anatomical medical images capture and visualize the anatomical structures of the ROI in the form of 2D or 3D images. Anatomical medical images allow physicians to interpret and evaluate the disease conditions for diagnosis purposes, and can also be used for the monitoring of treatment responses [4]. Functional imaging, on the other hand, captures the metabolic status of the ROI, which allows physicians to assess the physiological status of patients, and to identify structures with abnormalities, such as tumors.

Common anatomical medical image modalities include X-ray, computed tomography (CT), magnetic resonance imaging (MRI). Common functional imaging includes single-photon emission computed tomography (SPECT) and positron emission tomography (PET). Such image techniques produce a single type of image or image volumes that are referred as single-modality medical imaging.

Similar to CT images, digital WSI enables medical image analysis techniques to be applied to extract image features of abnormal cells. Image traits can then be exploited to correlate to genetic profiles of the tumor.

Methodology

Machine learning techniques for medical image processing are a well-established field. The ability of machine learning to quantify the representation features of the input medical image empowers numerous automated medical image processing algorithms for different clinical applications. However, machine learning systems were limited due to its requirement of domain expertise with careful engineering to be able to learn and transform the input data. Deep learning is a class of machine learning technique which allows learning of data representations with multiple layers of abstraction. Convolution neural networks (CNNs) are a deep learning technique that extracts image features from imaging data to learn the sophisticated underlying representations with deep networks.

Machine Learning

Machine learning is a major field of computer science that has been utilized to serve many aspects of modern healthcare systems. With carefully engineered mathematical models, machine-learning systems have been applied in pattern recognition, image classification, medical image retrieval and tumor image segmentation. Compare to the rule-based systems, the core of machine learning techniques are based on the development of models from statistical and artificial intelligence approaches. It is essential for the machine learning model to "learn" to recognize the distinguishing characteristics of the patterns within the data to produce meaningful outputs. Generally, the learning approaches for machine learning models are divided into the following: supervised learning, unsupervised learning and reinforcement learning.

Although unsupervised and reinforcement learning exhibit strong potentials in multiple disciplines, our contribution rely on labeled medical imaging data to explore the region-specific genetic association. As the contributions of this thesis involve mainly supervised approaches, we will only cover those approaches here. Supervised training approaches require several different types of database, defined as follows:

Training data: refers to a collection of data that are used to train the machine learning model. The machine learning model learns the representation of the training data and its predictive relationship to the output labels. Validation data: refers to a separate collection of data that are used in addition to the training data to adjust or guide the training process. This process involves the comparison between the predicted output with the training data labels. This provides an indication of the performance of the model on unseen data during the training process, and allows tuning of model parameters.

Test data: refers to a collection of withheld data which is used to evaluate the performance of the model at the after the completion of the training process. Test data indicates the performance of the trained model with new examples. Test data are not involved in the training process.

Supervised Learning

Supervised learning is one of the most common approaches for medical image processing and analysis. It refers to the approach where the model is trained with labeled data sets so that the model learns the internal representation of the input data to make predictions on the labels [13]. The resulting model from supervised learning is typically used to assign class labels with known predictive features for future data sets. Supervised learning is capable of performing classification or regression with training data set with discrete or continuous properties, respectively.

Artificial Neural Network

Artificial Neural Networks (ANNs) are a machine learning approach that was inspired by the biological neural networks that constitute human brains [20]. An ANN consists a collection of connected nodes or "artificial neurons" in a directed graph in the form of networks. ANNs are commonly used in machine learning to learn the complex non-linear relationships from the dataset. This is achieved through the ANN's mechanisms where each neuron receives, processes and transmits a signal from one to another in a similar way to the biological synapse. To achieve the optimized learning outcome, ANN requires the design of an appropriate network structure and learning approach to tune the weights and biases of the network.

Neurons are the fundamental building blocks of many ANNs. Fig 2 illustrates the structure of a single neuron where multiple inputs values are processed in the neuron to produce a single output value, where X is a vector of inputs with n elements, W is the vector of the weights with a corresponding number of elements.

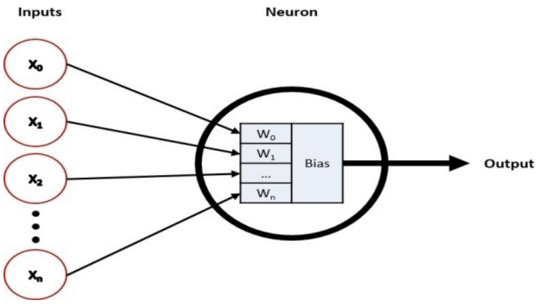


Fig 2: Representation of a single model neuron

The training of an ANN can be explained by illustrated single neuron model. For each element in the training dataset, its features are extracted and transmitted into the neuron in the form of a feature vector. Assuming that the classification task involves only two classes, the neuron processes the input feature vector by multiplying with its internal weights. A class prediction is based on whether the value of the product is above a threshold. If the predicted class does not match the corresponding label, each weight within the neuron is adjusted individually to refine the prediction process. Additionally, the training dataset is typically divided into collections of batches which allows the weight adjustment after training of each batch. An epoch refers to the full pass of the entire training dataset; robust weights for classification tasks are the outcome of hundreds of training epochs.

Deep Learning

Deep learning can be categorized as a class of techniques of machine learning, which allows the computation models with multiple processing layers to learn the internal representation of the input data with multiple levels of abstraction. Deep learning was proposed to address the limited performance of traditional machine learning approaches to process natural data in their raw form. Deep learning resolves this issue by utilizing the multiple processing layers to learn and interpret the low level, abstract representations from the high-level understandings of the input dataset [12]. This is achieved by feeding the raw data through the successive multilayer architecture in a sequential manner, where deeper layers learn the abstract representation from the representation in the previous layers.

Deep learning technique employs backward propagation of error or “back propagation” to train the multilayer model for supervised learning [11]. Back propagation calculates the gradient of the error function of the ANN with respect to its weights and passes the gradient backwards through the neural network. Compared to the traditional approach where the gradient of the error function is calculated for each layer separately, the backflow of error gradient allows more efficient computation of gradience for ANNs.

The implementation of deep learning technique utilizes specialized GPUs to improve the performance of training process by 10 to 20 times compared to the traditional training approach on standard CPUs. Recent advances in deep learning have lead to the improved state-of-the-art in various domains such as visual object recognition, speech recognition and also in medical image analysis.

Convolutional Neural Networks

Convolutional Neural Networks (CNNs) is a particular type of ANN and designed to process input data that is in the form of multidimensional arrays, e.g., colored 2D images which consist of 2D arrays for each RGB (color) channel. Compared with traditional ANNs with fully connected adjacent layers, CNNs are much easier to train and are more generalized. CNNs are structured in a series of stages where each stage consists of specialized layers with unique functions. The building blocks of a CNN consists three types of specialized layers: Convolution, pooling and activation layers, e.g., rectified linear unit (ReLU) layers.

Convolution layers consist of organized units in the form of feature maps, where each unit is connected to local patches from the previous layer through a set of weights which is referred as filter. This design allows the Convolution layers to detect local conjunctions of features from the previous layer, as local values are often highly correlated and are invariant to the location in an image input.

Pooling layers are designed to merge features in spatial proximity which share semantic similarities into one. The principle behind pooling layers is to detect the position of motifs that are typically formed by highly correlated features through a coarse-grained approach. An example pooling layer calculates the maximum of a local patch in one or more feature maps. Pooling layers act to reduce the dimensions of the representations and to create an invariance to small distortions and shifts.

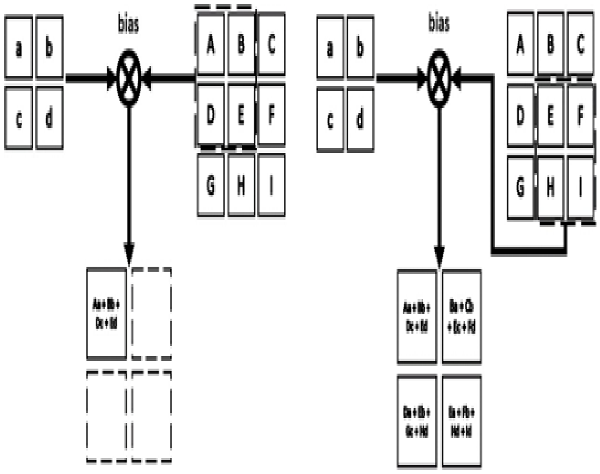


Fig 3: An example 2D convolution of a 3 × 3 input using a 2 × 2 filter with the 2 × 2 output feature map

Results

Results demonstrated that domain adaptation technique facilitates the learning of image representations of abnormalities in medical images by extending or refining existing knowledge from similar domains. The quantification of such image features hence improves the accuracy of tumor image classification tasks, compared to traditional approaches where deep learning models were trained from scratch on limited volumes of domain-specific datasets. Our results also demonstrated that the proposed framework offers additional deep image features to encode abstract representation of tumor phenotypic characteristics which exhibit stronger associations to patient-specific genetic information, compared to human-crafted image features.

Domain adaptation is the ability to apply an algorithm trained in one or more "source domains" to a different (but related) "target domain". Domain adaptation is a subcategory of transfer learning. In domain adaptation, the source and target domains all have the same features space (but different distributions); in contrast, transfer learning includes cases where the target domain's feature space is different from the source feature space or spaces.

Conclusion

In this paper, we presented novel deep domain adaptation learning framework for image-genomics analysis to improve image-genomics association. Our proposed framework emphasized the employment of domain adaptation of deep learning in image-genomics research to offer additional deep image features that encode abstract image representations of subtle variation in tumor medical images. Our domain adaptation approach reduces the dependency on large volumes of annotated medical image dataset for deep learning models to learn the tumor image representation.

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