Editorial

Radiomics and Precision Medicine

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Breakthroughs in image acquisition and interpretation have substantially enhanced diagnostic value using radiological imaging. Furthermore, with the advent of artificial intelligence (AI), there have been substantial advances in the quantitative analysis of radiological images (1). Therefore, a new sophisticated term called" Radiomics" has emerged recently, which has been created by the combination of two topics including 'radio' (radiological images) and 'omics' (genomics, transcriptomics, proteomics, and metabolomics) to extract precise quantitative information from diagnostic images using advanced mathematical algorithms, which is challenging to be recognized by unaided eyes (2). Radiomics is classified into two types: Feature-based and deep learning-based radiomics. In the feature-based radiomics pipeline, there are four main steps, including data collection and preprocessing; segmentation of the region of interest (ROI); radiomics features extraction, screening, and quantitative analysis; and model selection and validation, through which tissue and lesion properties on radiological images are extracted. These properties, referred to as the radiomics features, include heterogeneity, size, shape, and serial changes during follow-up. For a more efficient interpretation, these features used for clinical problem-solving can be combined with other biomarkers such as demographic, histologic, genomic, or proteomic data.

Image processing is often used as a preprocessing technique to enhance image quality by normalizing and harmonizing the medical images obtained from multiple facilities and suppliers. This step is mainly conducted to negate the effect of diverse qualities and ensure that consistency and uniformity are maintained across the dataset. Afterward, the ROI is segmented (manually or automatically) using 2D or 3D images. Hence, highly discriminative and quantitative features are extracted from the segmented part fed into machine learning algorithms to establish a mathematical relationship and perform meaningful predictions analysis. Intensity (histogram), shape, and texture features are the most widely used radiomics features (3). These features are often enhanced using preprocessing techniques, e.g., wavelet transform and Gaussian filtering, increasing the number of extracted features.

Regarding radiomics model selection and validation, there are three correlated aspects, i.e., feature size, model complexity, and evaluation metrics. For instance, while new data are captured as more features are added, the complexity of the model should be adjusted accordingly. On the other hand, complex models are prone to overfitting and often require larger datasets. Moreover, adding more data can make the dataset unbalanced, which needs proper evaluation metrics, e.g., precision, recall, or f1-score instead of accuracy. Therefore, to achieve a superior ML model, one should carefully choose model evaluation features, model complexity, and metrics. In this regard, using artificial intelligence, the extracted features are used to train machine learning models (neural networks, random forest, decision trees, and support vector machine [SVM]) for practical purposes among which histopathologic diagnosis, therapy response, tumor grade, gene mutations, patient survival, and complications can be mentioned (4). To evaluate the model, the training phase should be followed by validation and testing phases to measure the performance of each trained model in terms of accuracy, sensitivity, specificity, receiver operating characteristic (ROC) curve, and area under the ROC curve (AUC).

Contrary to feature-based models that require rich features as input, deep learning-based radiomics have solved the problem by adding deep layers of artificial neurons, constructing a deep neural network that can be fed raw signals or images, and training to output the prediction directly. Over the past decade, many deep-learning network architectures, including convolutional neural net-

works (CNNs), auto-encoders, and generative adversarial networks (GANs), have been introduced by scientists. These deep neural networks are robust and highly nonlinear mathematical models capable of finding the essential characteristics of the radiological images. The deeper network has multiple advantages and challenges. For example, having more layers means higher nonlinearity and capacity of the network to solve more complex problems. On the other hand, this comes with various problems such as vanishing gradient, over-fitting, and the need for more significant quality data. To overcome these issues, techniques such as skip connections, regularization, dropout layers, and data augmentation were also introduced. Although data augmentation is widely used in deep learning radiomics solutions, having large enough quality data often prevents it from being applied to specific areas such as neuro-oncology. Another well-known technique to solve the data size problem is the transfer learning method. The main idea behind transfer learning, as the name suggests, is to transfer the knowledge acquired from a source significant dataset (better to be close to the target application domain) into the target dataset and fine-tune the model to better suit the problem.

Usually, a pre-trained model is preferred to start the model training instead of randomly initializing the model's parameters. For example, one could use a model obtained from automated glioma segmentation as the starting point to further train the network for brain metastases segmentation ([5], [6]). As the radiological images are often discerned via visual analysis in conventional radiology, many valuable features may not be adequately extracted. Indeed, radiomics has emerged to address this issue. For instance, survival chances might vary between two patients suffering from tumors with differences in size, heterogeneity, and shape; however, they would be histopathologically similar. Hence, each patient needs specific treatments based on various prognostic factors. This concept is the aim of precision medicine ([7]).

While personalized medicine was still the main medical procedure, in 2008, the term precision medicine was defined by Clayton Christensen, a business strategist from Harvard Business School to help physicians diagnose the cause of a disease with high certainty using molecular diagnostics. However, it took three more years for precision medicine to be officially endorsed by a committee formed by the US National Research Council. Finally, in 2011, the committee released a plan, called Toward Precision Medicine, to modernize the taxonomy of disease based on the cause, e.g., genetic variants instead of the symptoms ([8]). Then, the National Institute of Health (NIH) introduced precision medicine as a novel method designed to select unique treatments for groups of patients by recognizing similarities in genetic or molecular profiling, individuals' lifestyles, and environment ([9]). Precision medicine aims to give tailored therapy to patients and diseases based on genomics, proteomics, radiomics, and other related technologies. Moreover, precision medicine attempts to guide healthcare decision-makers toward determining the best approach to prevent iatrogenic damages and reduce medical expenditure ([10]).

Personalized medicine is a type of medical care based on tailoring treatment instead of the one-size-fits-all approach. Indeed, clinicians should adopt a specific approach to treat and care for each patient according to individual characteristics, such as lifestyle, age, diet, body mass index, gender, and environment, to achieve the best outcome. Regarding differences between precision medicine and personalized medicine, the former focuses on proper care and intervention for similar subpopulations classified based on meeting unique characteristics and is originally research-oriented by creating big data (collecting molecular and clinical information) and fundamentally detecting the causes of the disease ([11]).

All in all, as artificial intelligence (AI) has advanced during the 21st century, by utilizing quality data, applying various ML techniques, and training deep neural networks or machine learning models, distinctive characteristics of a disease can be revealed; thus, this can improve conventional image evaluation for the overall management of the disease. Furthermore, the correlation of these features with clinical, demographic, and therapeutic profiles will help us better understand the disease with less human error and save time and money.

Footnotes

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