Improving clinical outcomes using radiomics: the potential of big data in radiotherapy

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Big data has revolutionised the way in which we analyse large amounts of information. When applied to the fields of medical imaging and radiation therapy, big data analytics and data mining can provide healthcare professionals with accurate information about the tumour phenotype and its implications on prognosis and treatment outcomes. The rapidly emerging field of radiomics has attracted more attention due to its potential as a centralised, quantitative method for influencing patient outcomes in terms of delivering precise, personalised radiotherapy treatment. Radiomics is the large-scale extraction and analysis of quantitative features from high-throughput image scan data and aims to support and improve clinical decision support systems. Radiotherapy treatment planning has advanced significantly as technology and methodologies are constantly improving, however, the volume and rate at which image data is produced is overwhelming. Better analytical methods such as machine learning and deep learning algorithms, two branches of artificial intelligence, have led to more accurate radiomics models that can better predict prognosis, treatment response, and treatment outcomes by using selected image biomarkers obtained from mining the data. The radiomics process is extensive and involves data acquisition, tumour segmentation, extraction of radiomic features, data analysis and modelling, and validation of these models. In this review, we detail some of these processes and the importance of reproducibility and standardisation is explained. Some of the challenges and improvements in the field are outlined.

I. INTRODUCTION

Radiomics is the extraction of a large number of quantitative features from images produced by imaging modalities such as computerised tomography (CT), magnetic resonance (MR), positron emission tomography (PET), and ultrasound. In certain terms it is a bridge between medical imaging and personalised medicine. Radiomics is a specialist application of big data to medical imaging; the term "big data" refers to very large datasets that are too large and too complex to be processed or analysed by traditional processing software. Medical imaging is rapidly evolving into a highly quantitative science and therefore it is becoming more than just a diagnostic tool; it has a central role in delivering personalised precision medicine to patients. In this way, radiomics is a valuable quantitative tool that further enables clinicians to adapt a given radiotherapy treatment as appropriate; each patient is different, pathophysiology varies between patients, and therefore the ultimate goal of radiotherapy, which is to deliver enough radiation to the target tumour without damaging surrounding healthy tissue, is attained with higher precision and accuracy without compromising the overall health of the patient.

Imaging algorithms have been used for decades to analyse and enhance medical images using computers; now, image processing and analysis is a multidisciplinary science involving applied mathematics, statistics, physics, computer science, and biomedical science.[1] Radiomics is based on advanced mathematical analysis and data characterisation algorithms that extract a large amount of quantitative features from medical imaging data; the process relies on the transformation of digitally encrypted images to mineable, high-dimensional data.[2] The original images hold valuable information about tumour pathophysiology which can improve clinical decision support systems (CDSS) by revealing disease characteristics and disease-specific processes that would otherwise be difficult to identify.[3]

Whilst computer-aided diagnosis and detection (CAD) systems are able to provide single answers, for example, whether or not a lesion or cancer is present in the region of interest (ROI), analyses using radiomics tools naturally extend on this by extracting many features from the data and placing them in stored databases for subsequent data mining; the latter process is then used for hypothesis generation and testing.[4] The radiomics workflow is split into stages, beginning with the generation of diagnostic image data and ending with a rigorous analysis of the data which is then compiled into a report that evaluates how best to personalise each treatment. Rapid learning healthcare (RLHC) networks that link big volumes of radiomics data from millions of patients is a future goal which is accompanied by significant data management hurdles.[2]

Artificial intelligence (AI) techniques such as machine learning (ML) and deep learning (DL) algorithms are currently used for big data analytics. Over the last decade, there has been an exponential rise in the amount of published literature on ML techniques which, for example, have been shown to successfully identify cancers of the brain.[5] Radiomics may be applied to any type of image modality and can be used in different clinical settings, for example diagnosis, prediction of prognosis, and to evaluate treatment response. Improvements on diagnostic, prognostic, and predictive performance have already been demonstrated by several radiomics studies through identification of novel imaging signatures.[6] This review explores the potential of radiomics as a quantitative tool for personalised precision medicine and we give an overview of the application of radiomics in radiotherapy.

II. DISCUSSION

A. What is big data?

Big data is a rapidly emerging field that has broad applications and implications across many disciplines, including healthcare, banking and security, energy and utilities, manufacturing, science, technology and more. The advent of computer systems has led to an accumulation of data that is so significant; both the quantity of information and speed at which it is growing is increasing. The larger the volume of data, the more difficult it is to process due to limitations

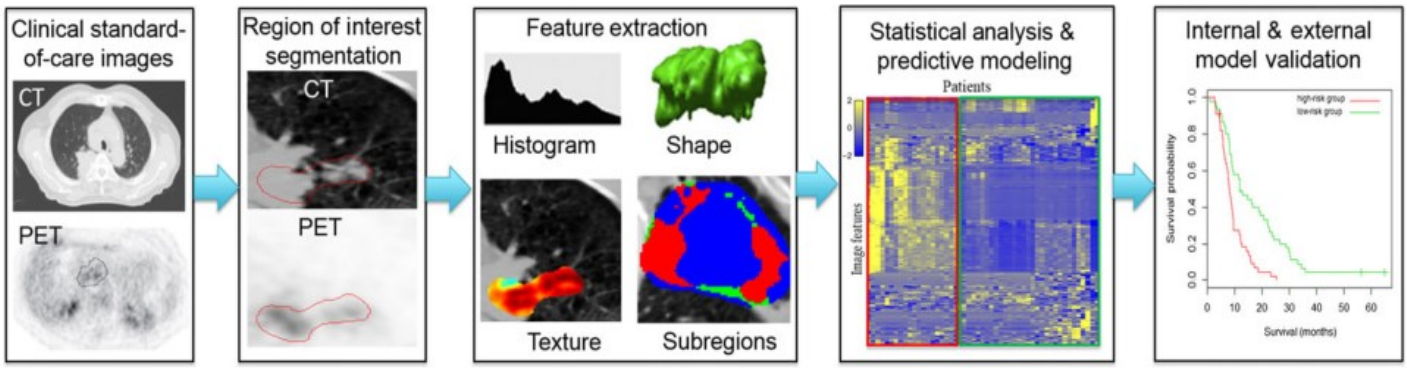

Fig. 1: The generalised radiomics workflow. Segmentation is the most rigorous stage. Selection algorithms are applied to the features to choose the most useful ones in the clinical context. Statistical analysis produces cluster heat maps and predictive models are produced to link image data with non-radiomic data. The model is validated first internally and then externally.

in computing resources, making it difficult to extract value from the data. Big data aims to extract meaningful information from very large and complex datasets; the volume of the data, however, is not the only characteristic of big data. IBM have identified four characteristics - "the four V's of big data" - that makes big data distinguishable; these are:

1. Volume: The quantity of data determines how much value can be extracted from it. The size of the volumes that characterise big data are usually of the order of petabytes and larger.

2. Velocity: The speed at which data is generated, collected, analysed, retrieved, and also the rate of flow of this data.

3. Variety: The many types of data available, categorised as either structured, semi-structured, or unstructured. Structured data can be easily stored, queried, analysed and retrieved by machines - examples include Excel files and SQL databases. Medical imaging data is raw and disorganised and is therefore unstructured, examples of which include No-SQL databases, audio and video files. Semi-structured data is a mix of structured and unstructured data such as JSON and XML.

4. Veracity: This determines the quality of the data, that is, how truthful and reliable it is and whether the analytics and outcomes are error-free and credible. Veracity is a future goal but data quality in healthcare is a particularly sensitive issue and unstructured data such as translations of poor handwriting on medicine prescriptions is an example of how data quality varies.[7]

In healthcare, big data can originate from internal sources (personal medical records, CDSS) and external sources (laboratories, pharmacies, governments), all found in different file formats, from multiple locations. Figure 1 illustrates the passage of big data from its source to its analytical applications.[6] Data is initially pooled into a raw state which subsequently requires processing and transformation. Repositories called data warehouses integrate data from multiple sources into a single place; data warehouses are built using the extract, transform, and load (ETL) process, which cleanses the data so that it qualifies for querying and analysis. After the data has been transformed, big data analytics platforms that possess enormous processing power, such as Hadoop, distribute a query (a large problem) across multiple separate servers that each solve different parts of the query and the results are conglomerated into a final result, providing near real-time results.[8]

B. Radiomics - big data in medical imaging

Two clinical radiotherapy outcome models, namely tumour control probability (TCP) for predicting tumour response, and normal tissue complication probability (NTCP) for predicting radiation-induced toxicities, are two of the main ways in which the principle of radiotherapy is illustrated, usually in the form of sigmoid curves as a function of radiation dose absorbed. Initially, these models were simplistic and only included a few volume and dose metrics that summarised the treatment plan and prognostic risk factors.[9] Recently, attention has been placed on developing more data-driven analytical models due to the advent of big data. The application of big data analytics to medical imaging can have a significant impact on radiotherapy treatment planning and thus the associated clinical outcomes.

Radiomics is an emerging field of oncology which aims to establish links between medical imaging and personalised precision medicine. The suffix -omics originated in molecular biology to characterise biologic molecules - genomics for DNA, transcriptomics for RNA, proteomics for proteins, metabolomics for metabolites.[4] Radiomics involves the extraction of a large number of quantitative features from a region of interest (ROI) in images obtained by CT, MRI, and PET scans. The quantitative features relevant to radiotherapy include lesion shape, intensity, texture, wavelet, and location; all of these features are extracted by mining the data from tomographic images which most likely contain millions of voxels (volume elements). It is not surprising, then, that hundreds of quantifiable features may be extracted from a single tumour.[4,10,11] This additional patient-specific information can be used to build on existing TCP and NTCP models to attain a more comprehensive representation of radiation response by improving their predictive power.[9]

The application of big data analytics which can discern significant trends and patterns that would be impossible to observe using human observer studies alone is called data mining and it is not limited to radiomics; in fact, all high-throughput -omics data are mineable. After the large datasets have been cleansed and transformed, any number of mining processes can be used to discover patterns in the

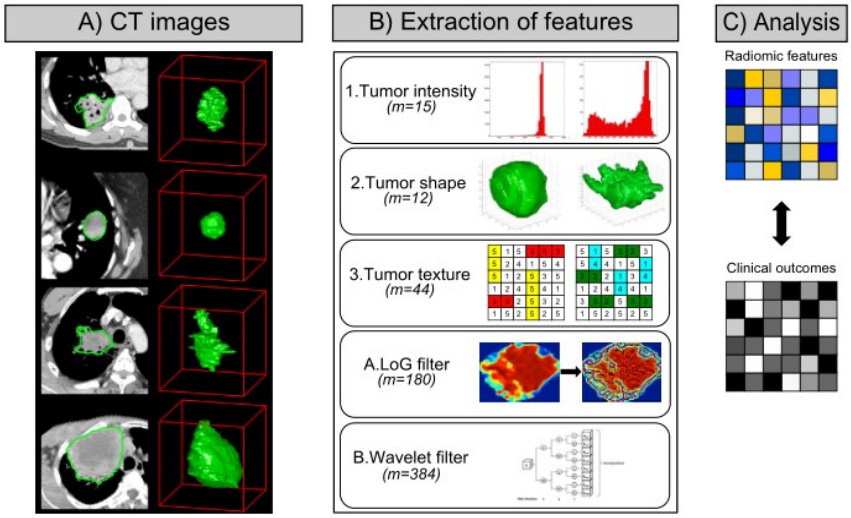

Fig. 2: Workflow of a CT radiomics study. (A) Image acquisition, enhancement, segmentation is performed; (B) numerous features are extracted; (C) the most relevant, reproducible features are selected and forwarded as inputs for statistical analysis and machine learning models.

data, including AI and statistical methods such as regression analysis.[4] Clinicians who use advanced data analytics instead of substandard data-processing software may be able to identify important characteristic features of the data, which can be used to create a CDSS to aid decision-making.[12] Data on treatment outcomes such as survival are linked to analyses of the whole primary tumour. Additionally, radiomics analyses may be performed on tumour subregions (habitats), metastatic lesions, and also normal tissues, to reveal various radiosensitive phenotypes exhibited by the cancer cells[2]. The significance of radiomics is that the tumour phenotypes can be quantified comprehensively to improve decision support in radiotherapy and other cancer treatments, at a low financial cost.[13]

C. Workflow of radiomics

The workflow of a radiomics study is a step-by-step process, as shown in Figure 1; the main steps after image acquisition are tumour region segmentation, feature extraction, feature selection/dimension reduction, quantitative data analyses, modelling, and model validation.[2–4,6,10,14] Figure 2 shows the workflow for a CT-based radiomics study, highlighting in particular the complex feature extraction stage.[15]

1. Image acquisition, reconstruction, enhancement

All radiomics studies and analyses begin with a choice of imaging modality and ROI, and an event prediction (prediction target). Different anatomical and molecular imaging protocols have been incorporated into radiomics studies, including CT, MRI, PET, and combinations or variations of these. The modality of choice depends largely on the ROI and the standard of care varies for each situation and type of cancer; the standard of care for gliomas is MRI and for head, neck, and lung cancers it is CT and PET; most of the radiomics studies thus far have used CT for the assessment for tissue density, shape, and texture. PET imaging has gained significant traction in applied radiomics due to the functional nature of PET images which are related to the underlying biology of the tumour.[10,16,17] Image acquisition is both time-consuming and costly due to the sheer amount and inherent heterogeneity (thus requiring texture analysis) of the image data.[18] It is hoped that radiomics can overcome some of these heterogeneities by using large datasets for feature extraction, consequently improving upon current texture analysis processes.

2. Image segmentation

Segmentation algorithms are a modern analysis approach to the detection and extraction of specific objects with anatomical structures from the image, for example, malignant lesions in mammograms.[1] Segmentation is used to delineate a ROI (in 2D) or VOI (in 3D) to distinguish them from background tissue, allowing for calculation of radiomics features.[3,19] However, segmentation requires much rigour and is the most challenging component of a radiomics study, particularly because the borders of tumour regions and subregions are often ambiguous.[14] The analysed voxels within the image depend on the segmentation algorithm and this introduces some bias in the derivation of radiomic features due to variability in segmentation; it has been suggested that a multiple-segmentation based approach could limit this bias to an extent.[2] An example of manual segmentation from a CT image is shown in Figure 2 which demonstrates that inter-reader variability accounts for a difference in choice of tumour boundaries. Semi-automatic segmentation methods can overcome both the labour intensiveness and high inter-reader variability of manual segmentation whilst providing more consistent tumour contouring, however some of these algorithms still require some degree of user correction for inhomogeneous lesions.[20] An ideal image segmentation algorithm should meet some kind of feasibility criteria and it has been proposed that four basic features determine how good the algorithm is: accuracy, automation, consistency, and reproducibility.

At present, there is no universal segmentation algorithm that can be used with all types of medical images.[10,18] However, many semi-automatic algorithms have been implemented to investigate their robustness for feature extraction, some of which include GrowCut and SCES. Recently, the

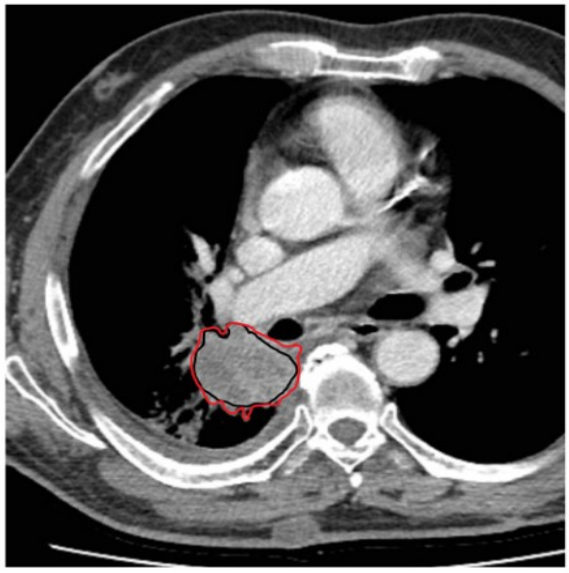

Fig. 3: Manual segmentation of lung cancer on a CT image. Black and red ROIs differ due to inter-reader variability.[20]

emergence of DL image segmentation algorithms based on convolutional neural networks (CNN) have been trained to fully automate the segmentation process, though only for entire organs and skeletal elements, not for dedicated tumour regions[3,4,21]; a recent study[22] proposed an automatic segmentation method based on a CNN which achieved a dice similarity coefficient (DICE score) of 0.88, indicating strong segmentation performance.[23]

3. Feature extraction

Image segmentation is followed by high-throughout extraction of more than a thousand quantitative and qualitative image features that characterise the ROI/VOI, such as tumour shape, intensity, location, texture, and wavelet from the images; this information should be useful enough but not redundant, for the purposes of reproducibility.[10,14] Figure 4 is a visualisation of feature descriptors obtained through computation.[23] Radiomics features are categorised as semantic or agnostic. Semantic features are well-known descriptors of lesions in radiology, for example, shape, location vascularity, spiculation (which measures the degree of pointedness or spikiness of the tumour surface), and necrosis (tissue death).[4] Agnostic features do not form part of radiologists' common language to communicate diagnostic results and are defined as quantitative computational metrics that are mathematically extracted from an image.

Agnostic features are categorised as either first-, second-, or higher-order statistical outputs; each output determines the complexity of the feature. First-order outputs are usually single values such as mean, median, minimal and maximal, range, skewness, and kurtosis, all derived from 3D data that is condensed into a single tumour intensity histogram.[4,10] Second-order outputs are texture descriptors which quantify the statistical relationships between neighbouring voxels with the same or different contrast values, thus providing crucial texture analysis needed to determine the heterogeneity of habitats within the tumour, that is, intra-lesion heterogeneity.[20] There is a large body of literature that reviews the hundreds of output values generated from texture analysis.[4] Higher-order outputs are obtained by placing filter grids on the image or by applying mathematical transforms to the image to determine and extract repetitive or non-repetitive patterns, highlight specific details, or to optimise the contrast-to-noise ratio by suppressing noise.[20]

Collections of features that possess predictive and prognostic value are called radiomics signatures or quantitative imaging biomarkers (QIB). Computational feature extraction can be performed using a number of different software packages, including the Imaging Biomarker Explorer (IBEX), and CGITA and Mazda are used for texture analysis on user-defined VOIs.[17] Prototype algorithms for radiomics feature extraction have been provided on the open source, MATLAB-based software platform CERR which can combine RT treatment plans and model RT outcomes.[6,24,25]

The features mentioned thus far - even mathematical transforms and filters - are a few decades old and thus do not present any significant turning points in the context of radiomics research; the innovation therefore lies in manipulating large amounts of feature parameters, extracted from a single lesion, and applying advanced statistical methods in the hope that appropriate combinations of these parameters can provide clinicians with valuable information on tissue properties that may be therapeutically beneficial on an individual basis (personalised RT). Due to the huge amount of methods available for the calculation of radiomics features, there should be strict adherence to the guidance given by the Image Biomarker Standardisation Initiative (IBSI).[3]

Shape and size

Characteristic shape and size features such as surface area, tumour volume (TV), tumour compactness, sphericity, maximum diameter, and effective diameter all define the size of the ROI/VOI.[18] The surface-to-volume ratio determines how spherical or spiculated the lesion is and this is clinically relevant because variations in tumour shape during RT can be quantified; the aggressiveness of a highly spherical lesion with sharp edges is less than that of a more spiculated lesion.[10] Several studies in the literature have explored the potential of computational methods, in terms of their accuracy and reproducibility, for the extraction of characteristic tumour shape and texture information from brain tumour MR imaging. For example, the scale-invariant feature transform (SIFT) shown in Figure 5 is a quantitative computational image feature descriptor with potential clinical relevance: it can measure the spatial characteristics of a tumour.[23] The smaller the TV, the better the prognosis compared to a large lesion. A 2013 review of the literature cites many publications on the predictive and prognostic value of the TV from PET images of solid tumours, confirming its importance as a first-order quantitative imaging feature.[26]

Intensity

Intensity histograms are first-order radiomics features which display the voxel values for the selected ROI/VOI. A single intensity histogram is generated from 3D TV data and is used to predict the nature of the lesion by assessing the distribution of individual voxels in the image, to obtain

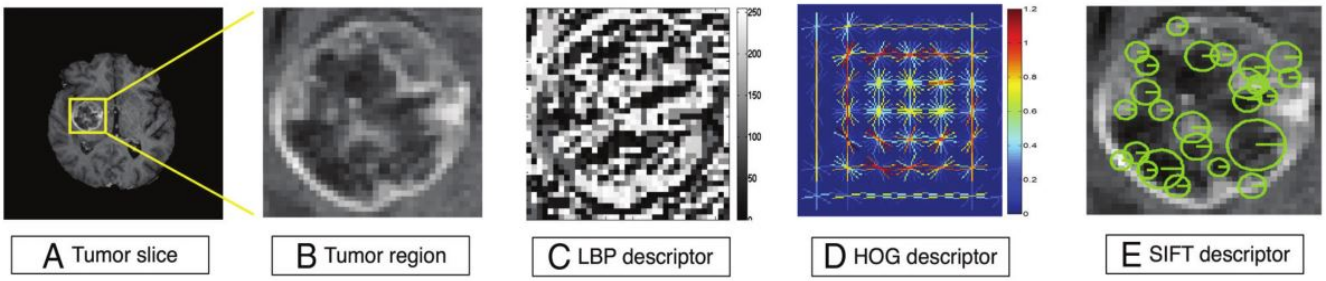

Fig. 4: Computational feature descriptors are shown. Each quantitative feature descriptor has potential clinical relevance, for example, in measuring the tumour microenvironment or spatial characteristics.

and report first-order statistics such as mean, median, maximum, minimum, skewness, kurtosis, entropy, and uniformity.[10,18,20] The intensity of the voxel is a basic, first-order feature which corresponds to Hounsfield units (HU) in CT and the standardised uptake value (SUV) in FDG-PET. The risk of relapse of tumour habitats for patients with non-small cell lung cancer (NSCLC) can be indicated by areas of high-FDG uptake during RT pre-treatment scans.[26] Intensity features and shape and size features are usually used in parallel and are complimentary to one another. The open source software package PyRadiomics, written in Python code, was engineered to extract large amounts of these features from medical images.[16,27] The first-order statistics we have mentioned do not take into account important spatial information; modern radiomics studies rely on more sophisticated methods. For example, single or combination image filters are used to perform tasks such as edge enhancement to highlight regions in which the intensity changes rapidly. The most complex mathematical agnostic radiomics features include Laplacian transforms and Minkowski functionals.[4,16]

Wavelet

Wavelet features are higher-order statistical features that capture the intensity and texture information by the process of wavelet decomposition - a mathematical transform - which decomposes the original image. Wavelet transforms belong to the group of mathematical methods mentioned in the previous section; these can extract image areas with increasingly coarse texture patterns.[10,20] The coefficients of the wavelet transform are arranged into a transformation matrix which is applied to a raw data vector. In-depth mathematical analysis of the wavelet transform in wavelet analysis is beyond the scope of this review but can be found in textbooks and in the literature.[28,29] The properties of wavelets are ideal for detecting intensity and texture features in images because the wavelet decomposition decomposes the image, focussing these features on different spatial frequency domains to selectively emphasise the configuration of individual voxel intensities in that domain.[17,20] In other words, focussing on different frequency ranges within the TV can provide detailed texture information which may quantify intra-tumour heterogeneity. This detailed texture information can only be revealed by computer generation of the relevant high-frequency components of the 2D/3D image; it is virtually impossible for a human to achieve this.[10] A 2014 publication analysed 440 radiomics features extracted from the CT scans of 1,019 patients with head-and-neck cancer or lung cancer, and found that a wavelet feature known as Grey Level Non-Uniformity performed well in the quantification of intra-tumour heterogeneity of lung cancer.[10,13] A 2020 reference manual provides an extension of the original IBSI reference manual and details the mathematical formalisms used to define wavelets and other image biomarkers based on convolutional filters, and also addresses the issue of inconsistency across organisations, by standardising those biomarkers; this work is yet another step forward in achieving better reproducibility of radiomics results across institutions.[28]

Texture

Texture features belong to the class of second-order statistical outputs that use intra-tumour texture details to evaluate intra-tumour heterogeneity. The distinct non-uniformity of the TV can be assessed from these texture features, allowing clinicians to differentiate between cancerous and non-cancerous lesions.[10] Texture features compare and consider the spatial locations of each voxel relative to surrounding voxels.[13] One study performed using patients with NSCLC showed that CT texture analysis has potential for predicting prognosis and survival; another CT-based radiomics study found longer survival in patients with more homogeneous tumours.[14] One of the largest, most rigorous studies was conducted to decode the tumour phenotype using a sample size of 1,019 patients, which created a QIB composed of only four radiomics features (based on shape, size, texture, and wavelets); the QIB was combined with tumour-node-metastasis (TNM) staging, the gold standard of cancer staging, showing improvements in the ability to define the tumour phenotype compared with TNM staging alone.[4,13,14]

4. Feature selection/dimension reduction

This next step in the radiomics workflow follows from the extraction of hundreds of features that must be treated with statistical or machine learning (ML) selection algorithms to select the most useful features that can classify patients in terms of their predicted treatment outcome. To achieve a good radiomics performance, the focus must be on determining the most useful information; some extracted features may be unnecessary depending on the end goal and this will subsequently affect the analytical power of the radiomics model.[10] The number of extracted features usually exceeds the sample size, likely leading to overfitting of the data, where the model essentially fails to fit newer data because the trained

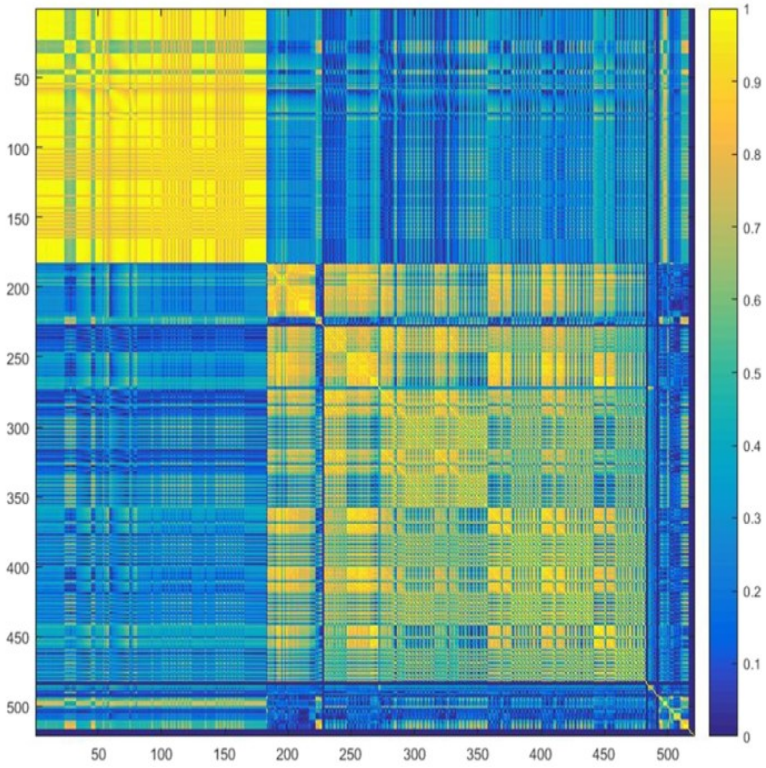

Fig. 5: Radiomics feature clustering shown as a heat map. The scale on the right hand side of the map refers to the degree of correlation between pairs of radiomic features, shown as numbers on the abscissa and ordinate. Features can be grouped together within the same cluster if a high correlation between them is observed. The yellow squares along the diagonal represent clusters of highly correlated features and blue squares represent cluster of features exhibiting lower degrees of correlation.

model has learned to detect patterns specific only to the data it was trained with.[6,14] To mitigate the risk of overfitting, highly correlated features should be grouped together to form a single archetypal feature.[2,14]

The two most commonly used approaches to feature selection/dimensionality reduction are cluster analysis and principal component analysis (PCA).[20] Cluster analysis can be used to generate a cluster heat map, shown in Figure 5, which is a visual representation that differentiates groups of radiomics features with different degrees of correlation. Many publications have mentioned the use of test-retest datasets to rank features with a specific emphasis on ensuring repeatability, reproducibility, robustness, and stability. Test-retest data are data obtained from two image datasets acquired in a short time frame (a few minutes to a few days) from just one sample of patients;[14,20] these data are not available for all tumours, but the Reference Image Database to Evaluate Therapy Response (RIDER) test-retest dataset which used lung CT scan data from 26 NSCLC patients is publicly accessible.[12,17]

Emerging tools for feature selection include ML models that use the feature datasets as their input and can perform pattern recognition tasks to detect patterns from the datasets to find the most relevant features.[16,20] The minimum redundancy maximum relevance (mRMR) algorithm is available as a package in the R programming language and computes mutual information between the feature datasets to find features that are both relevant and complementary.[15,30]

5. Data analysis and model development

This stage of the workflow is an extension of the previous stage and involves (1) unsupervised approaches to feature selection/dimension reduction, and (2) supervised approaches to determine whether the selected radiomics features are associated with one or more specific outcomes.[20] The main difference between these approaches is that unsupervised analysis only applies to unlabelled data and produces graphical representations and summaries of the data, whereas supervised analysis involves the development of multivariate predictive models that incorporate all the selected radiomics features to enable predictions of treatment outcome, prognosis, treatment response, tumour phenotype and genotype, metastatic potential, and more.[11,16,18,31] Both unsupervised and supervised approaches use statistics and machine learning. Machine learning algorithms are extremely useful for developing classifier models. Computational tools such as R and MATLAB are used for advanced statistical analysis of the radiomics data.[18]

A prime example of unsupervised analysis is data clustering which produces the type of cluster heat map shown in Figure 5.[20] To elaborate, this heat map is a covariance matrix of radiomics features which graphically represents the clustering of features with similar R^2 values (the square of the Pearson correlation coefficient and also known as the coefficient of determination in regression analysis, expressed as a fraction within the range $0 \leq R \leq 1$); the numbers on the abscissa and ordinate represent the radiomic feature whilst the scale on the right hand side of the map indicates the degree of correlation between two pairs of features. The yellow squares in Figure 5 highlight groups of features with

high values ($R^2 \geq 0.95$, within the 95% confidence interval) and are redundant;[4] these features should be discarded and the remaining informative, non-redundant, and reproducible features are used to develop classifier models that prove informative for clinicians.[10]

To create the best radiomics model it is crucial to incorporate both radiomics and non-radiomics features and the model should begin with a well-defined endpoint, for example, overall survival, or progression-free survival and disease-free survival (exact endpoints).[4] The non-radiomics features that the model should also incorporate include clinical, molecular, and genomic data such as age, TNM stage, serum markers, gene expression, mutation status, treatment time, fractionation, and more.[14] If insufficient data is available to represent all patients, data sparseness should be a key parameter in the model design. All radiomics models must reflect the size and quality of the data for the radiomics model to have maximum analytical power. In this regard, we stress the importance of data sharing across institutions for data mining efforts and to ensure that the models have maximum statistical power; some data - such as exact endpoints - are not readily available.[4]

6. Model validation

The performance and accuracy of a radiomics model depends on how well it can discriminate between patients. Discrimination analysis computes the sensitivity, specificity, and area under the ROC curve (AUC) to test the discriminator's performance.[32] The discriminator performance can also be measured using the concordance correlation coefficient (CCC or c-index) which ranges from -1 to 1, indicating perfect negative agreement and perfect positive agreement, respectively.[12]

D. Challenges, issues and improvements

Perhaps the most significant challenges in radiomics studies are both technical and practical, including standardisation of imaging protocols, reproducibility of features, and data sharing.[6] Institutions must work collaboratively to standardise the best-practice framework, irrespective of differences in IT infrastructure (software and hardware). To qualify for routine clinical use, the validated radiomics signature or QIB should be fit-for-purpose and demonstrate optimal reproducibility and stability across institutions.[2]

The speed at which the radiomics field is growing presents an urgent need for evaluation criteria that assesses the quality of past and present radiomics studies. When we mention study quality, we acknowledge compliance with best-practice procedures. Studies should mention design, methods, quality assurance (QA), and standard operating procedures (SOP). Clear indications as to how the study adds value to the field should also be included. A 2017 review provides some guidance on these points and proposed a radiomics quality score (RQS), consisting of 16 key components, to assess the quality of radiomics studies.[6] The report concluded that the reporting quality of several prediction model studies is poor based on overwhelming evidence; the authors referred to the TRIPOD initiative, the Transparent Reporting of multi-variable prediction models for Individual Prognosis Or Diagnosis.[2]

The latest breakthroughs in ML algorithms have been DL methods such as CNNs, which combine the graphical processing power of graphics processing units (GPU) with big data.[16] As GPU technologies advance, breakthroughs in medical imaging will become more frequent. GPUs can be leveraged for image processing to maximise image contrast between normal and diseased tissues, and to reduce the effect of image artefacts.[6] A 2018 publication explored the NVIDIA OptiX ray-tracing engine as a new tool for multiple applications, including ray-tracing of X- and gamma-rays for tomographic reconstruction algorithms and as Monte Carlo simulators of photon attenuation in patients.[33]

III. CONCLUSIONS

Radiomics is a promising application of big data analytics which can be used for assessing treatment response and outcome depending on the size, quality, and availability of the data, and the analytical method used. With the emergence of artificial intelligence, novel methods such as fully automated segmentation can simplify the radiomics workflow significantly, meaning that clinicians and experienced radiologists can devote more effort to the analytical and model development stage. The scientific community must focus on workflow standardisation and the reproducibility of results to increase confidence in model outputs such as survival outcome. The sheer number of radiomics and non-radiomics features available can be larger than the study sample size, which can lead to overfitting. Mitigating the probability of overfitting is important to ensure that new data can be added to the model without reference to the data it was trained with. In conclusion, radiomics analysis has the potential to reveal clinically relevant tumour phenotypes by linking quantitative and qualitative features together in a single model possessing powerful predictive and prognostic capability. It is hoped that radiomics analysis can be applied for routine clinical use one day, to create personalised radiotherapy treatment plans for each patient.

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