

Received:  
29 April 2021

Revised:  
13 October 2021

Accepted:  
17 November 2021

<https://doi.org/10.1259/bjr.20210539>

Cite this article as:

Cho H, Kim CK, Park H. Overview of radiomics in prostate imaging and future directions. *Br J Radiol* 2022; **95**: 20210539.

## INNOVATIONS IN PROSTATE CANCER SPECIAL FEATURE: REVIEW ARTICLE

# Overview of radiomics in prostate imaging and future directions

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### ABSTRACT

Recent advancements in imaging technology and analysis methods have led to an analytic framework known as radiomics. This framework extracts comprehensive high-dimensional features from imaging data and performs data mining to build analytical models for improved decision-support. Its features include many categories spanning texture and shape; thus, it can provide abundant information for precision medicine. Many studies of prostate radiomics have shown promising results in the assessment of pathological features, prediction of treatment response, and stratification of risk groups. Herein, we aimed to provide a general overview of radiomics procedures, discuss technical issues, explain various clinical applications, and suggest future research directions, especially for prostate imaging.

### INTRODUCTION

Over the past decade, the assessment of tumor characteristics through medical imaging and advanced analysis techniques has undergone transformative changes towards personalized medicine. In particular, radiomics extracts high-dimensional features from raw imaging data and builds an analytical model based on data mining to improve clinical decision-making.<sup>1,2</sup> Initial efforts focused on quantifying intratumoral heterogeneity using various texture features from imaging modalities such as X-ray, ultrasound, CT, and MRI, which span the lung, breast, and prostate.<sup>3–7</sup> The current set of radiomics features goes beyond texture and includes 2D/3D shape features, signal intensity features from the histogram, and deep learning (DL) inspired features.<sup>1</sup> Some studies have added new features that reflect prior knowledge to enhance the feature set. For example, features specific to the tumor margins have been proposed for lung cancer.<sup>8</sup> After appropriate data mining and model building procedures, radiomics offers improvements in the assessment of pathological features, prediction of treatment response, stratification of risk groups, etc.

Radiomics and radiogenomics have made significant contributions to all subdisciplines in radiology; urologic radiology is no exception. In this study, we aimed to provide

a general overview of radiomics procedures, discuss technical issues, explain various clinical applications, and suggest future research directions, especially for prostate imaging. We mainly focused on radiomics.

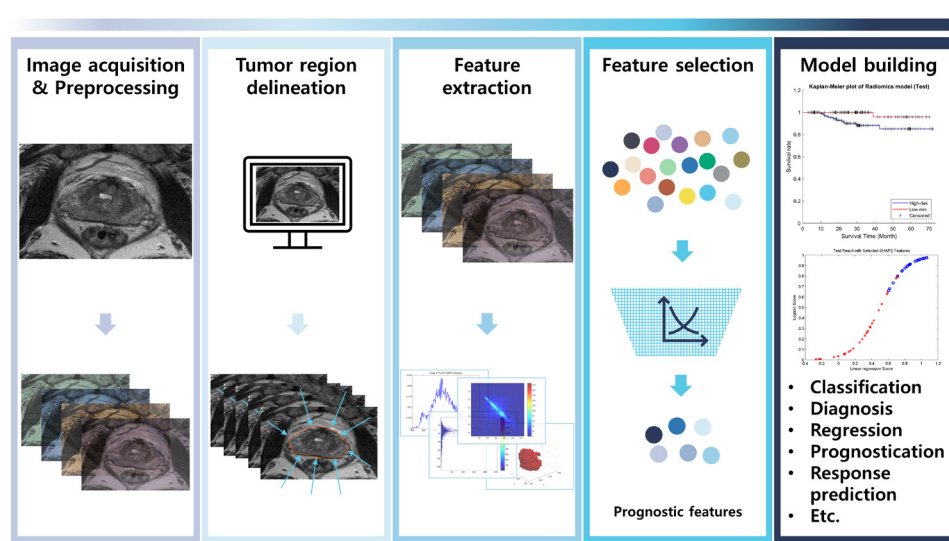
#### General overview of radiomics procedures

This section outlines the standard steps involved in radiomics studies, as shown in [Figure 1](#). We first start with procedures common to all subdisciplines in radiology and then describe prostate-specific issues.

#### Image acquisition and preprocessing

As with any study, the first step is to acquire the appropriate imaging data. Sufficient samples should be collected to obtain statistically valid results.<sup>9</sup> This is important because we deal with hundreds to thousands of features in radiomics, which makes it especially vulnerable to small n, large p issues. Different imaging parameters and scanner types affect the raw data and thus lead to increased feature variability. The best practice is to adhere to a strict imaging protocol to reduce variability in imaging parameters. However, this could be unrealistic in multicenter studies, where differences in imaging parameters are expected. One can use a similar data setting between multicenter cohorts or apply a retrospective harmonization method to reduce

Figure 1. The overall workflow of radiomics.



intercenter variability.<sup>10–13</sup> To handle differences in image resolution, the data can be resampled to a common isotropic resolution (e.g.  $1 \times 1 \times 1 \text{ mm}^3$ ). If different imaging protocols were used in one study, it should be noted to improve the reproducibility of future studies.

In the preprocessing step, registration, filtering, and intensity normalization are commonly performed.<sup>14,15</sup> Image registration is typically performed to align multimodal images. Filtering, in the form of smoothing, can be performed to reduce noise. Intensity normalization can be used for stable feature extraction.<sup>16–18</sup> It is important to ensure that the inherent property of the imaging modality is retained after preprocessing. Dynamic contrast-enhanced MRI should be normalized considering all phases because normalizing individual phases might remove the time-varying enhancing pattern. The application of inhomogeneity correction for MRI is controversial because it may change the intensity profile.<sup>19,20</sup> However, it might increase the feature stability across patients; thus, some studies still adopt it.<sup>21,22</sup>

#### Delineation of the region of interest

Radiomics is a focal analysis method in which regions of interest (ROIs) should be specified. Typically, the tumor region is specified by manual, automatic, or semi-automatic methods. However, normal regions could be analyzed based on the study goals. Manual specification fully reflects expert knowledge but may suffer from inter- and intraobserver variability. The automatic method applies a computer-based segmentation algorithm; thus, it is fast and leads to no or reduced variability. From classical computer vision, region-growing, watershed, active contour algorithms have been widely used for segmentation.<sup>23–25</sup> Recently, U-net-based deep learning has been adopted for prostate segmentation.<sup>26</sup> The semi-automatic method allows users to interactively modify the algorithm-generated ROI, and thus, is the middle ground between the manual and automatic methods. Additionally, this is the preferred method because it is faster than the manual method and allows modification of the results by experts.

Recent radiomics studies went beyond the tumor region and attempted to quantify the peritumor region so that the surrounding microenvironment could be modeled.<sup>3,27–32</sup> This was performed by expanding the tumor ROI. Prostate radiomics can certainly benefit from this; a recent study reported that peritumoral radiomics can yield results that are independent predictors for risk stratification in prostate cancer.<sup>33</sup> Active research is ongoing regarding the extent to which we probe (*i.e.* 1 to 5 mm) beyond the tumor boundary.

#### Feature extraction

In the feature extraction step, researchers extracted hundreds to thousands of features belonging to different categories from the prespecified ROIs. Most studies have the following three categories, as shown in Table 1<sup>34,35</sup>: histogram-based features, texture features, and morphological features. In addition to the standard set of features, each study might consider additional options, such as margin features. The features are defined mathematically; this lends the possibility of interpreting features physically and biologically.

The histogram-based features are computed from the intensity histogram of the ROI and include the mean, variance, kurtosis, etc. Texture features are the main focus of radiomics studies since they quantify intratumoral heterogeneity. Typically, they are computed from the gray-level co-occurrence matrix (GLCM) and gray-level size zone matrix, which model intervoxel heterogeneity.<sup>36</sup> The morphological features (*e.g.* roundness) quantify the tumor shape in 2D or 3D. They are direct extensions of semantic features measured by experts, except that they are mathematically defined and continuous-valued. For example, roundness is measured in a binary fashion (round vs non-round) in semantic features, while roundness in radiomics is a continuous value between 0 and 1 defined mathematically.

New radiomics features have been actively developed. Features tailored to tumor margins have shown promising results.<sup>8</sup> Texture based on the orientation of the intensity gradient

Table 1. Radiomics features based on pyradiomics<sup>34</sup> documentation

Category	Measure	Features
Histogram	Histogram	10Percentile, 90Percentile, Energy, Entropy, Interquartile Range, Kurtosis, Maximum, Mean Absolute Deviation, Mean, Median, Minimum, Range, Robust Mean Absolute Deviation, Root Mean Squared, Skewness, Total Energy, Uniformity, Variance
Texture	GLCM	Autocorrelation, Cluster Prominence, Cluster Shade, Cluster Tendency, Contrast, Correlation, Difference Average, Difference Entropy, Difference Variance, Inverse Difference, Inverse Difference Moment, Inverse Difference Moment Normalized, Inverse Difference Normalized, Informational Measure Of Correlation1, Informational Measure Of Correlation2, Inverse Variance, Joint Average, Joint Energy, Joint Entropy, Maximal Correlation Coefficient, Maximum Probability, Sum Average, Sum Entropy, Sum Squares
Texture	GLSZM	Gray Level Non-Uniformity, Gray Level Non-Uniformity Normalized, Gray Level Variance, High Gray Level Zone Emphasis, Large Area Emphasis, Large Area High Gray Level Emphasis, Large Area Low Gray Level Emphasis, Low Gray Level Zone Emphasis, Size Zone Non-Uniformity, Size Zone Non-Uniformity Normalized, Small Area Emphasis, Small Area High Gray Level Emphasis, Small Area Low Gray Level Emphasis, Zone Entropy, Zone Percentage, Zone Variance
Morphological	-	Elongation, Flatness, Least Axis Length, Least Axis Length, Maximum 2D Diameter Column, Maximum 2D Diameter Row, Maximum 2D Diameter Slice, Maximum 2D Diameter, Mesh Volume, Sphericity, Surface Area, Surface Volume Ratio, Voxel Volume

GLCM, gray-level co-occurrence matrix; GLSZM, gray-level size zone matrix.

might add complementary information in addition to the conventional GLCM.<sup>37</sup> One study quantified the structural deformation of tumors according to tumor progression.<sup>38</sup> Some studies have extracted vessel features based on tubular structure analysis.<sup>39,40</sup> These new features are relatively under-explored for prostate imaging and are promising avenues for future research.

### Feature selection

The feature selection step involves selecting important features from a pool of hundreds to thousands of features. This is because it is infeasible to use many potentially correlated features from the extraction step. The goal is to obtain a compact set of features with low redundancy. The selected features are sometimes referred to as radiomics signatures. Borrowing from machine learning, there are four feature selection methods: filter, wrapper, embedded, and dimension reduction methods.<sup>41</sup> The filter method selects the most meaningful features by measuring the direct associations between the features and outcomes. This does not consider collinearity among the selected features and could be undesirable. The wrapper method seeks optimal features by evaluating possible feature sets using machine learning models. It has high computational costs and tends to overfit the training data. Support vector machine-based recursive feature elimination<sup>42</sup> and stepwise regression<sup>43</sup> are widely used. The embedded method has explicit feature selection during the model-building procedure. Typically, regularized regressions in the form of the least absolute shrinkage and selection operator (LASSO)<sup>44</sup> and ridge regression belong to this category. LASSO theoretically guarantees the maximum orthogonality between features and derives sparse results. Therefore, it is widely used in radiomics. Dimension reduction projects high-dimensional features onto a different computational space where a compact representation is possible. Methods such as principal component analysis<sup>45</sup> are widely used. However, once the radiomics features are mapped onto a different space, it is difficult to interpret them.

### Model building

Important features were identified and are used to build various machine-learning models suitable for each study. They can be broadly grouped into classification, regression, and survival models.<sup>1</sup> The classification assigns category labels (*e.g.* non-responding vs responding) to patients, and thus could be used for many purposes, including treatment response, tumor staging, and subtyping. Common models include the support vector machine,<sup>46</sup> random forest,<sup>47</sup> linear discriminant analysis,<sup>48</sup> and logistic regression.<sup>49</sup> Regression is used when the target is continuously valued (*i.e.* prostate antigen levels). Depending on the characteristics of the target, nonlinear regression can be applied. Survival analysis is mostly performed using Cox's proportional hazard model with the selected features.<sup>50</sup>

### Integrating genomics information with radiomics

Radiogenomics itself is a distinct research topic; thus, a comprehensive review is beyond the scope of this study.<sup>51,52</sup> Still, we explain a few methods for integrating genomic features during the various steps of radiomics. First, radiogenomics is widely used to obtain an in-depth understanding of tumors by exploring the association between radiomics and genomics. It is possible to explore genomic characteristics based on the radiomics signature.<sup>53–55</sup> Similarly, it is also possible to conduct radiomics modeling based on genomics signature.<sup>56–58</sup> Both approaches fix one set of information and use it to explore another set of information. Second, after separately performing radiomics and genomics modeling, the final modeling can be performed by combining the results of the two models.<sup>59</sup> In addition, enrichment scores may be added as an additional feature in classification or regression models.

### TECHNICAL ISSUES

In this section, we discuss some technical issues and limitations of radiomics. First, the most well-known issue is feature reproducibility stemming from variability in the imaging protocol.<sup>9–12,17,60</sup> Unstandardized imaging parameters, scanner-dependent

characteristics, and variability in contrast agents lead to changes in the raw data, resulting in decreased feature reproducibility. This problem is particularly serious in MRI because CT can guarantee a basic level of stability due to the physical unit of Hounsfield.<sup>61</sup> General structural MRI has no standardized units that can be shared by different sites. Even MRI images with the same sequence may have differences in the raw imaging data.<sup>62</sup> These limitations can be partially overcome by quantitative MRI such as apparent diffusion coefficient imaging.<sup>63</sup> Still, we should strive towards a standardized imaging protocol so that radiomics built from one setting can be generalized to other scenarios. There are methods to improve the reproducibility of the features. Retrospective harmonization to regress out imaging protocol-related covariates is widely used.<sup>13</sup> Normalizing the intensities using histogram equalization is another common approach. In addition, dynamic MRI should be performed to ensure accurate timing of the various phases. In a real clinical setting, it is difficult to avoid feature reproducibility problems; however, we should strive to reduce it as much as possible towards a reproducible and generalizable radiomics model.

The second issue is commonly referred to as the curse of dimensionality.<sup>64–66</sup> Radiomics features can be hundreds to thousands or more, depending on the goal of the study. The feature dimension grows quickly if genomics is involved, resulting in millions of features. The incredibly high dimensionality of the feature

space requires large data samples for proper modeling. However, owing to practical clinical limitations, we rarely have sufficient samples. There are a few radiomics studies in which the sample size exceeded 500.<sup>67</sup> One way to tackle this problem is to limit the number of features. Many researchers believe that more features are always better. However, this is only valid if sufficient samples are available. With limited samples, researchers can choose important categories of features that worked well in previous studies instead of using the full suite of features. Another side-effect of insufficient samples is overfitting. Using limited samples might lead to modeling results that overfit the given training data. This can be partly mitigated by cross-validation, but the better option is to use independent external validation data.<sup>68</sup> Overfitting is a major issue that is beyond the scope of this study, and readers can study other excellent literature.<sup>1,67</sup>

## APPLICATION OF RADIOMICS IN PROSTATE CANCER

### Classification of pathological features

In this section, we survey recent studies of radiomics in prostate imaging (Table 2). Many studies have applied radiomics to prostate-related classification tasks. Bernatz et al<sup>69</sup> adopted radiomics features and principal component analysis to discriminate groups stratified by Gleason scores using multiparametric MRI. Chaddad et al<sup>70</sup> conducted a similar study using intermodality

Table 2. Recent studies of radiomics/radiogenomics on prostate cancer

Application	Reference	Imaging modality	Study target	RQS
Classification				
	Bernatz et al. <sup>69</sup>	T2, ADC, DCE-T1, T1	Gleason Grade Group (1,2 vs 3,4,5)	12
	Chaddad et al. <sup>70</sup>	T2, ADC	Gleason Grade Group (1 vs 2 vs 3,4,5)	13
	Chen et al. <sup>71</sup>	T2, ADC	Gleason Score Group (>6 or not)	14
	Gong et al. <sup>72</sup>	T2, ADC	Gleason Score Group (>7 or not)	15
	Shiradkar et al. <sup>21</sup>	T2, ADC	Biochemical recurrence	17
	Zamboglou et al. <sup>73</sup>	PET	Cancer or not, Gleason Score Group (>7 or not), Stage (pN1 vs pN0)	16
Regression				
	Hectors et al. <sup>74</sup>	T2, ADC	Gleason Score, Gene signature association	16
	Krauss et al. <sup>22</sup>	T2	Prostate-specific antigen serum level	14
Survival analysis				
	Bourbonne et al. <sup>75</sup>	DCE-T1, T2, ADC	Biochemical relapse-free survival	15
	Mo et al. <sup>76</sup>	CT (Con/non-Con)	Progression-free survival after chemotherapy	18
Radiogenomics				
	McCann et al. <sup>77</sup>	DCE-T1, T2, ADC	Radiomics-Gene expression association	-
	Stoyanova et al. <sup>78</sup>	DCE-T1, T2, ADC	Radiomics-Gene expression association	-
	Kesch et al. <sup>79</sup>	Ga-PSMA-PET/CT	Radiomics-Genomic index association	-
	Fischer et al. <sup>80</sup>	T2	Combining pretreatment, clinical, genomics pathway, and radiomics feature to predict pathological stage	-

ADC, apparent diffusion coefficient; DCE, dynamic contrast-enhanced; PET, positron emission tomography; PSMA, prostate-specific membrane antigen.

RQS, radiomics quality score



texture features in addition to conventional GLCM texture features to classify groups stratified by Gleason scores using  $T_2$  weighted MRI images and apparent diffusion coefficient (ADC) maps. Chen et al<sup>71</sup> compared prostate imaging reporting and data system (PI-RADS) with radiomics in differentiating high-grade and low-grade Gleason score groups using  $T_2$  images and ADC maps. In this study, the authors adopted an augmentation technique, called the synthetic minority oversampling technique, to boost samples in the minority class. Results have shown that the radiomics model was better than the conventional PI-RADS. Additionally, Gong et al<sup>72</sup> also performed the same classification task using additional clinical information and showed that both radiomics and clinical information lead to better classification. This study also used  $T_2$  and ADC maps. Shiradkar et al<sup>21</sup> showed that it is feasible to predict biochemical recurrence using recently proposed texture features based on the orientation of the intensity gradient in  $T_2$  images and ADC maps. Many studies have used MRI, but some have used position emission tomography (PET). Zamboglou et al<sup>73</sup> demonstrated the effectiveness of radiomics modeling obtained from the gross tumor volume of PET images. In this study, the authors showed that PET radiomics can be used to distinguish between cancer and non-cancer groups, groups stratified by Gleason scores, and different stages.

### Regression and survival models

Some studies performed regression tasks using radiomics for prostate imaging (Table 2). Hectors et al<sup>74</sup> confirmed a linear association between radiomics features from  $T_2$  and ADC maps, and as well as clinical outcomes such as Gleason scores. Krauss et al<sup>22</sup> built a radiomics model to predict antigen serum levels and compared it with conventional volume measurements in the transition zone using  $T_2$  MRI. Some studies have shown that survival analysis using a radiomics approach is feasible. Bourbonne et al<sup>75</sup> built a multivariate Cox model using radiomics features to evaluate recurrence risks from MRI. It was shown that prediction of biochemical recurrence was possible; stratification of risk groups for biochemical relapse-free survival was also possible. Similarly, Mo et al<sup>76</sup> showed that radiomics using both contrast-enhanced and regular CT images can be used to create a progression-free survival model after chemotherapy for stratifying risk groups.

### Radiogenomics

Radiogenomics combines high-dimensional radiomics features with genomic features, another high-dimensional feature, to better probe tumor characteristics.<sup>51,52</sup> This approach allows us to establish links between macroscale imaging and microscale genetic information, which might lead to a better understanding of the underlying tumor biology.

Some studies have applied radiogenomics to prostate imaging. McCann et al<sup>77</sup> and Stoyanova et al<sup>78</sup> explored the relationships between radiomics features and prognostic gene expression in the form of gene-associated radiomics signatures. Using a more advanced technique, Kesch et al<sup>79</sup> found that a cluster formed by grouping similar radiomics features was related to a well-known genomics index. Fischer et al<sup>80</sup> integrated three types of pretreatment information, clinical information, genomics pathway, and

Table 3. Adherence rate according to the 6 key categories and 16 items of RQS

Category/Item	Adherence rate
Average of 16 items	41.9%
<b>Category 1: Protocol quality and stability in image and segmentation</b>	34.0%
Protocol quality	50.0%
Test-retest	0.0%
Phantom study	0.0%
Multiple segmentation	70.0%
<b>Category 2: Feature selection and validation</b>	66.3%
Feature reduction or adjustment of multiple testing	100.0%
Validation	46.0%
<b>Category 3: Biologic/clinical validation and utility</b>	86.7%
Multivariate analysis with non-radiomics features	90.0%
Biologic correlates	50.0%
Comparison to 'gold-standard'	90.0%
Potential clinical utility	100.0%
<b>Category 4: Model performance index</b>	54.0%
Discrimination statistics	90.0%
Calibration statistics	10.0%
Cut-off analysis	70.0%
<b>Category 5: High level of evidence</b>	0.0%
Prospective study	0.0%
Cost-effective analysis	0.0%
<b>Category 6: Open science and data</b>	5.0%

RQS, radiomics quality score.

radiomics features to predict the pathological stage. The molecular characteristics of each stage were evaluated through the analysis of genes and miRNAs; the association between biomarkers and imaging features was also analyzed. Radiogenomics studies in prostate imaging are relatively scarce compared to other organs and thus, are a rich avenue for future research exploring radiomics-genomics associations.

### FUTURE DIRECTIONS

#### Evaluation of existing literature

To provide objective interpretations, we evaluated the studies in Table 2 with radiomics quality score (RQS).<sup>81</sup> We evaluated RQS for pure-radiomics studies because it may be not appropriate to evaluate radiogenomics studies, which mainly focus on the assessment of radiomics-genomics association. The RQS of the studies were median 15 with a range of 12 ~ 18. The RQS has 16 items grouped into 6 major categories and we assessed whether a study met the requirements of each category. We further explored the adherence rate according to the 6 key categories and 16 items (Table 3). We observed that the "high level of evidence" category was the least satisfied one and suggest future studies to move towards prospective study designs to confirm

existing retrospective design-based studies. A longitudinal study design and independent validation over many institutions are other directions that could improve the level of evidence. The “open science and data” category was the second least satisfied category. Satisfying this category is also related to the “high level of evidence” and more academic journals are mandating the policy of open data and codes.<sup>82–84</sup> Thus, we believe more studies will satisfy the “open science and data” category in the future.

### Integration of deep learning

Radiomic studies rely heavily on machine learning and the field of machine learning is rapidly moving toward DL.<sup>85–90</sup> This trend also applies to medical imaging; thus, an increasing number of radiomics studies have adopted DL as the major methodological component.<sup>91–96</sup> Almost all conventional steps in radiomics can be replaced with DL equivalent versions. In the image acquisition step, DL can be applied to learn features that are less affected by the variability in imaging parameters.<sup>97</sup> In the specification of ROIs, various DL approaches, including U-net-based segmentation methods, have already been used to perform automatic tumor segmentation.<sup>98</sup> The performance of tumor segmentation can be measured with standard dice coefficient factoring in inter-rater variability.<sup>99</sup> However, the results of the DL-based automatic segmentation are still required to be confirmed by a human expert. Radiomics features are handcrafted features that are predefined based on expert knowledge. DL is capable of learning specific features from the data themselves; thus, there is no need to specify predefined features.<sup>85</sup> This implies that one could apply the same DL approach to solve many different tasks. However, DL can properly learn features from the data only if sufficient samples are available to train the model.<sup>86,89,90</sup> This could be difficult to apply in practice because the sample size requirements for deep learning are larger than those of conventional machine learning studies.

DL-derived features can lead to improved performance in many tasks, but they are difficult to interpret.<sup>86,89,90</sup> This “interpretability” issue is especially important in the medical domain for DL models to gain expert’s trust. Recent approaches to improve “interpretability” have been actively applied in medical imaging, including gradient-weighted class activation mapping and layer-wise relevance propagation.<sup>100</sup> Finally, the DL method can be applied in an end-to-end manner.<sup>85</sup> Instead of replacing each radiomics step with a DL-based step, one big DL network can handle all steps at the same time. This can be a universal solution to the radiomics approach; however, future research is needed on the performance and the “interpretability” of this approach.

Several studies have applied DL to prostate imaging. Chaddad et al<sup>101</sup> created a DL model that could predict the Gleason score. Shao et al<sup>102</sup> developed a model that can identify tumor slices and ROIs using deep reinforcement learning. They automatically determined the most critical slice among the identified tumor slices and predicted the Gleason grades. Khosravi et al<sup>103</sup> conducted a study to diagnose malignancy using MRI and DL. The developed model showed results that exceeded the performance of the PI-RAD.

DL has a high potential to improve prostate radiomics. However, the issues of sample size and interpretability must be overcome. Radiomics features are mathematically defined and thus are more interpretable than data-driven DL features. A lung cancer study aiming to optimize radiotherapy dose included a neural network that tried to synthesize radiomics features in an auxiliary task.<sup>104</sup> Although they did not correlate DL features with radiomics features, this is one way to incorporate radiomics features into a DL network. We believe integrating or guiding the DL neural network with more interpretable radiomics features is an important future direction. In another lung cancer study, the authors tried to reduce the burden on the sample size by using a shallow network for prognosis.<sup>105</sup> Deep and wide networks have more capacity to learn complex representations, but for some small field of view objects, a shallow network could be suitable to extract low-level texture and edge features.<sup>85</sup> Thus, we believe exploring shallow networks to reduce the sample size requirements is an important direction to move forward.

### Habitat and clustering

A tumor is heterogeneous in nature; one hypothesis is to assume that it consists of many subregions.<sup>106,107</sup> Subregions are sometimes referred to as habitats. Analyzing the subregions separately can provide more detailed information about the tumor, as compared to analyzing the whole tumor.<sup>108–110</sup> Habitat is commonly created by clustering; *i.e.* joining pixels with similar features. There is rich literature on how to perform clustering for various modalities and features. The concept of habitat has shown promising results in brain and breast cancer and is a promising venue for prostate radiomics.<sup>108–110</sup> The habitat concept can be expanded to include various prostate zones (*i.e.* anterior fibromuscular stroma and central/transitional/peripheral zones).<sup>111</sup> Features from the tumor habitat and the various prostate zones can be compared. The interactions among them could be a rich source of information for prostate radiomics.

### Incorporating histology

The prostate is one of the few organs where whole-mount histology information is available after prostatectomy. The histology images could be reformatted into a stack of slices that can be registered on *in vivo* imaging, such as pelvic MRI. With the registration, rich features derived from the histology could be used to provide additional features for the radiomics approach. Jamshidi et al<sup>112</sup> showed that the combination of histological images and *in vivo* imaging enables a more in-depth understanding of tumors. This is another promising avenue for prostate radiomics.

## CONCLUSION

Radiomics has made a significant impact in radiology research, including urologic radiology. It has the potential to be used as a surrogate marker in precision medicine. The studies reviewed here show that prostate radiomics is promising for many different tasks using routine imaging. However, radiomics is hampered by difficulties, as described previously. Nonetheless, recent advancements in imaging technology and machine learning will improve radiomics, making it more acceptable for clinical use. There are underexplored options in prostate radiomics such as defining

habitats or integrating imaging information from histology compared to those in other organs. Thus, these may be considered as rich avenues for future research.

## FUNDING

This research was supported by the National Research Foundation (NRF2020M3E5D2A01084892), Institute for Basic Science

(IBS-R015-D1), Ministry of Science and ICT (IITP-2020-2018-0-01798), IITP grant funded by the AI Graduate School Support Program (2019-0-00421), ICT Creative Consilience program (IITP-2020-0-01821), and Artificial Intelligence Innovation Hub program (2021-0-02068).

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