Appendix 1

Materials and methods

Computed tomography (CT) scanning protocol

The 29 patients at The Third Affiliated Hospital of Shenzhen University also underwent CT scanning with a 128-slice spiral CT system (Brilliance iCT, Philips System; 120 kV, 280 mA, section thickness 5 and 2 mm, reconstruction interval 1 mm). The scanning protocol included data acquisition in 3 phases: the precontrast phase (PCP), the corticomedullary phase (CMP; 30-second delay after contrast injection), and the nephrographic phase (NP; 90-second delay after contrast injection). Multiplanar reconstruction was performed for axial, coronal, and sagittal planes. After the unenhanced scan, an intravenous bolus injection of nonionic contrast media of 80–100 mL was administered at a rate of 4 mL/s through the median cubital vein.

Feature classification and statistical analysis

To explore the contributions of CT texture features in model decision-making, Shapley additive explanations (SHAP) was used to break down the model's decisions. SHAP connects the optimal credit allocation with local explanations using the classic Shapley values from game theory and their related extensions. To compare whether the predictions were statistically different between the 3 radiologists, we used the Welch two-tailed 2-sample *t*-test ($P<0.05$). These statistical analyses were conducted in Python (v.3.8.0) and R (v.3.6.3).

Results

Explanation of the prediction model

To evaluate the contribution of the extracted texture features to the model prediction, the SHAP value of each feature was calculated for each sample.

The bar plot and beeswarm plot show the SHAP values of the top 20 texture features for pathological tumor stage prediction. The beeswarm plot shows the SHAP values and feature values across the original data set. The shade of the dot represents the different eigenvalue magnitudes, with bluer dots indicating lower eigenvalues and redder dots indicating larger eigenvalues. As shown in the beeswarm plot, a positive SHAP value indicates a higher likelihood for the corresponding prediction. Conversely, a negative SHAP value indicates a lower likelihood for the corresponding prediction.

In *Figure 5A*, the gray-level-related features, including 2t_glszm_LAHGLE (tumor feature of the CMP: gray-level size zone) and the tumor volume-related feature such as 2t_mask_VN (tumor feature of the CMP: mask-original voxel num), played a vital role in the prediction of pathological tumor T1 staging.

In *Figure 5B*, the 3-dimensional size and shape of the region of interest (ROI)-related features, including 2t_shape_SVR (tumor feature of the CMP: surface area to volume ratio) and 2t_shape_MV (tumor feature of the CMP: mesh volume), played a vital role in the prediction of pathological tumor T2 staging.

In *Figure 5C*, the related features, including 3k_glrlm_GLNU (kidney feature of the NP: gray-level run length matrix), 3v_glszm_GLNU (vein feature of the NP: gray-level size zone), and 3t_shape_M2DC [tumor feature of the NP: maximum 2D diameter (Column)], played a vital role in the prediction of pathological tumor T3 staging.

The SHAP value revealed that the texture features of the tumor region in the CMP of the enhanced CT image significantly contributed to determining whether a case was stage T1 or T2. In determining whether a case was stage T3, the texture features of the renal region, venous region, and tumor region in the NP of the enhanced CT image contributed significantly.