

<p>Image protocol quality - well-documented image protocols (for example, contrast, slice thickness, energy, etc.) and/or usage of public image protocols allow reproducibility/replicability</p> <p><input checked="" type="checkbox"/> protocols well documented</p> <p><input type="checkbox"/> public protocol used</p> <p><input type="checkbox"/> none</p>
<p>Multiple segmentations - possible actions are: segmentation by different physicians/algorithms/software, perturbing segmentations by (random) noise, segmentation at different breathing cycles. Analyse feature robustness to segmentation variabilities</p> <p><input checked="" type="radio"/> yes</p> <p><input type="radio"/> no</p>
<p>Phantom study on all scanners - detect inter-scanner differences and vendor-dependent features. Analyse feature robustness to these sources of variability</p> <p><input type="radio"/> yes</p> <p><input checked="" type="radio"/> no</p>
<p>Imaging at multiple time points - collect images of individuals at additional time points. Analyse feature robustness to temporal variabilities (for example, organ movement, organ expansion/shrinkage)</p> <p><input type="radio"/> yes</p> <p><input checked="" type="radio"/> no</p>
<p>Feature reduction or adjustment for multiple testing - decreases the risk of overfitting. Overfitting is inevitable if the number of features exceeds the number of samples. Consider feature robustness when selecting features</p> <p><input checked="" type="radio"/> Either measure is implemented</p> <p><input type="radio"/> Neither measure is implemented</p>
<p>Multivariable analysis with non radiomics features (for example, EGFR mutation) - is expected to provide a more holistic model. Permits correlating/inferencing between radiomics and non radiomics features</p> <p><input type="radio"/> yes</p> <p><input checked="" type="radio"/> no</p>
<p>Detect and discuss biological correlates - demonstration of phenotypic differences (possibly associated with underlying gene-protein expression patterns) deepens understanding of radiomics and biology</p> <p><input checked="" type="radio"/> yes</p> <p><input type="radio"/> no</p>
<p>Cut-off analyses - determine risk groups by either the median, a previously published cut-off or report a continuous risk variable. Reduces the risk of reporting overly optimistic results</p> <p><input checked="" type="radio"/> yes</p> <p><input type="radio"/> no</p>

<p>Discrimination statistics - report discrimination statistics (for example, C-statistic, ROC curve, AUC) and their statistical significance (for example, p-values, confidence intervals). One can also apply resampling method (for example, bootstrapping, cross-validation)</p> <p><input checked="" type="checkbox"/> a discrimination statistic and its statistical significance are reported</p> <p><input checked="" type="checkbox"/> a resampling method technique is also applied</p> <p><input type="checkbox"/> none</p>
<p>Calibration statistics - report calibration statistics (for example, Calibration-in-the-large/slope, calibration plots) and their statistical significance (for example, P-values, confidence intervals). One can also apply resampling method (for example, bootstrapping, cross-validation)</p> <p><input type="checkbox"/> a calibration statistic and its statistical significance are reported</p> <p><input type="checkbox"/> a resampling method technique is applied</p> <p><input checked="" type="checkbox"/> none</p>
<p>Prospective study registered in a trial database - provides the highest level of evidence supporting the clinical validity and usefulness of the radiomics biomarker</p> <p><input type="radio"/> yes</p> <p><input checked="" type="radio"/> no</p>
<p>Validation - the validation is performed without retraining and without adaptation of the cut-off value, provides crucial information with regard to credible clinical performance</p> <p><input type="checkbox"/> No validation</p> <p><input checked="" type="checkbox"/> validation is based on a dataset from the same institute</p> <p><input type="checkbox"/> validation is based on a dataset from another institute</p> <p><input type="checkbox"/> validation is based on two datasets from two distinct institutes</p> <p><input type="checkbox"/> the study validates a previously published signature</p> <p><input type="checkbox"/> validation is based on three or more datasets from distinct institutes</p>
<p>Comparison to 'gold standard' - assess the extent to which the model agrees with/is superior to the current 'gold standard' method (for example, TNM-staging for survival prediction). This comparison shows the added value of radiomics</p> <p><input checked="" type="radio"/> yes</p> <p><input type="radio"/> no</p>
<p>Potential clinical utility - report on the current and potential application of the model in a clinical setting (for example, decision curve analysis).</p> <p><input checked="" type="radio"/> yes</p> <p><input type="radio"/> no</p>
<p>Cost-effectiveness analysis - report on the cost-effectiveness of the clinical application (for example, QALYs generated)</p> <p><input type="radio"/> yes</p> <p><input checked="" type="radio"/> no</p>
<p>Open science and data - make code and data publicly available. Open science facilitates knowledge transfer and reproducibility of the study</p>

- scans are open source
- region of interest segmentations are open source
- the code is open sourced
- radiomics features are calculated on a set of representative ROIs and the calculated features and representative ROIs are open source

Total score **16** (44.44%)