#### **Supplementary Material**

### A detailed description of radiomics parameter

In this study, a total of 485 radiomics features were generated from contrast-enhanced CT images. All feature extraction methods were implemented using A.K. (Artificial Intelligence Kit, GE Healthcare, China) software. The 485 features were divided into six types: histogram parameters, texture parameters, form factor parameters, GLCM parameters, RLM parameters, GLZSM parameters.

### **Histogram Parameters**

Histogram parameters are concerned with properties of individual pixels. They describe the distribution of voxel intensities within the CT image through commonly used and basic metrics. The following twenty first order statistics were extracted, such as energy, entropy, maxIntensity, minIntensity, meanValue, mean absolute deviation, medianIntensity, range, root mean square (RMS), standard deviation, stdDeviation Uniformity, variance, volume count, voxelvalue sum, RelativeDeviation, frequency size, quantiles, percentiles, skewness, kurtosis.

# **Texture Parameters**

Texture is one of the important characteristics used in identifying objects or regions of interest in an image, texture represents the appearance of the surface and how its elements are distributed. It is considered an important concept in machine vision, in a sense it assists in predicting the feeling of the surface (e.g. smoothness, coarseness ...etc.) from image. Various texture analysis approaches tend to represent views of the examined textures form different perspectives, and due to multi-dimensionality of perceived texture, there is not an individual method that can be sufficient for all textures. Therefore, AK software is mainly concerned with texture classification accuracy improvement using textures features statistical based methods. The radiomics features in the texture parameters mainly consisted of energy, entropy, correlation, inertia, cluster shade, cluster prominence.

### **Form Factor Parameters**

These group of features includes descriptors of the three-dimensional size and shape of the tumor region. We determined the following shape and size based features: sphericity, surface area, compactness 1, Compactness 2, Maximum 3D diameter, Spherical disproportion, surfacetovolumeratio, volume, volumeCC and VolumeMM.

#### **GLCM Parameters**

The Grey level co-occurrence matrix (GLCM) represents the joint probability of certain sets of pixels having certain grey-level values. The advantage of the co-occurrence matrix calculations is that the co-occurring pairs of pixels can be spatially related in various orientations with reference to distance and angular spatial relationships, as on considering the relationship between two pixels at a time. As a result, the combination of grey levels and their positions are exhibited apparently. Therefore, it is defined as "A two dimensional histogram of gray levels for pair of pixels, which are separated by a fixed spatial relationship". However, the matrix is sensitive to rotation. With the change of different offsets define pixel relationships by varying directions.

The rotation angle of an offset: 0°, 45°, 90°, 135° and displacement vectors (distance to the neighbor pixel: 1, 2, 3 ...), different co-occurrence distributions from the same image of reference. GLCM of an image is computed using displacement vector d defined by its radius, (distance or count to the next adjacent neighbor preferably is equal to one) and rotational angles. Following GLCM parameters were extracted in our study: energy of GLCM, entropy of GLCM, Inertia of GLCM, correlation, inverse difference moment and Haralick features. Furthermore, Haralick features including: Haralick correlation, angular second moment, contrast Haralick entropy, HaraVariance, sumAverage, sumVariance, sumEntropy, differenceVariance, differenceEntropy, inversedifferencemoment.

# **RLM Parameters**

The grey level run-length matrix (RLM)  $Pr(i,j|\theta)$  is defined as the numbers of runs with pixels of gray level i and run length j for a given direction  $\theta$ . RLMs is generated for each sample image segment having directions (0°,45°,90° &135°), then the following ten statistical features were derived: short run emphasis, long run emphasis, grey level nonuniformity, run length non-uniformity, low grey level run emphasis, high grey level run emphasis, short run low grey level emphasis, short run high grey level emphasis, long run low grey level emphasis and long run high grey level emphasis(32).

# **GLZSM Parameters**

The gray level Size Zone Matrix (SZM) is the starting point of Thibault matrices(33). For a texture image f with N gray levels, it is denoted GSf(s, g) and provides a statistical

representation by the estimation of a bivariate conditional probability density function of the image distribution values. It is calculated according to the pioneering Run Length Matrix principle: the value of the matrix GSf(s, g) is equal to the number of zones of size s and of gray level g. The resulting matrix has a fixed number of lines equal to N, the number of gray levels, and a dynamic number of columns, determined by the size of the largest zone as well as the size quantization.

The more homogeneous the texture, the wider and flatter the matrix. SZM does not required computation in several directions, contrary to RLM and co-occurrences matrix (COM). However, it has been empirically proved that the degree of gray level quantization still has an important impact on the texture classification performance. For a general application it is usually required to test several gray level quantization in order to find the optimal one with respect to a training dataset. Empirically, 32 provides often the best result. More precisely, this matrix is particularly efficient to characterize the texture homogeneity, non-periodicity or speckle like texture; it had provided betters characterizations than granulometry (or COM, RLM, etc.) for the classification of cell nuclei, dermis, road quality (bitumen condition) and some textures in PET images(33). The following quantities are defined in AK software: the normalized GLSZM, small zone emphasis, large zone emphasis, gray-level zone emphasis, small zone low gray-level emphasis, small zone high gray-level emphasis, large zone low gray-level emphasis, large zone high gray-level emphasis, gray-level emphasis, large zone low gray-level emphasis, large zone high gray-level emphasis, large zone high gray-level emphasis, gray-level variance, zone-size variance.

### **Feature selection**

Principal component analysis (PCA) is a statistical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components. The number of distinct principal components is equal to the smaller of the number of original variables or the number of observations minus one. This transformation is defined in such a way that the first principal component has the largest possible variance (that is, accounts for as much of the variability in the data as possible), and each succeeding component in turn has the highest variance possible under the constraint that it is orthogonal to the preceding components. The resulting vectors

are an uncorrelated orthogonal basis set. PCA is sensitive to the relative scaling of the original variables.

PCA is mostly used as a tool in exploratory data analysis and for making predictive models. Also, PCA is the simplest of the true eigenvector-based multivariate analyses. Often, its operation can be thought of as revealing the internal structure of the data in a way that best explains the variance in the data. If a multivariate dataset is visualized as a set of coordinates in a high-dimensional data space (1 axis per variable), PCA can supply the user with a lower-dimensional picture, a projection of this object when viewed from its most informative viewpoint. This is done by using only the first few principal components so that the dimensionality of the transformed data is reduced.

PCA is used to summarize matrix data, such as found in transcriptome, proteome or metabolome and medical examinations, into fewer dimensions by fitting the matrix to orthogonal axes. In this study, 15 principal components were obtained by using PCA method to convert 65 original features.