How to find the best radiomics features for prediction of overall survival in SBRT for HCC?

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Purpose or Objective

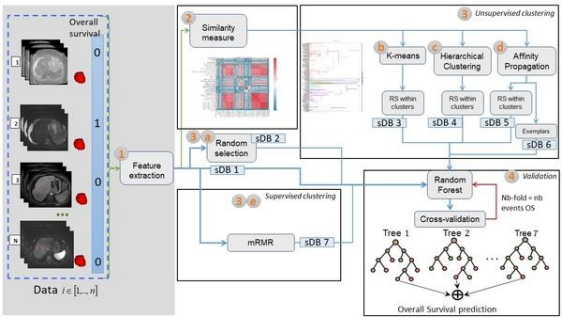
One of the major issues in radiomics is the very large amount of tested extracted features, compared to the often-reduced sample size and the low number of events. Reduction of dimensionality may be therefore an important preliminary step to improve the prediction capability of the predictive models. The aims of the study were:

- to propose methods for reducing redundancy by selecting the more informative features from -multimodal images;
- to evaluate and compare the prediction capability of the models when using these methods.

The considered example was MRI based radiomics to predict overall survival after SBRT for hepatocellular carcinoma (HCC).

Material and Methods

Eighty-one patients underwent SBRT for inoperable HCC. For each patient, 7 modalities of MR images were acquired. A total of 273 features were extracted from manually delineated tumours belonging to 4 radiomics categories (geometrical, first order, gradient-based and second order) in each modality. As we follow the workflow [Figure 1]



, a similarity measure based on Spearman correlation was computed across the features. Four methods for feature selection were then assessed namely three unsupervised (K-means, Hierarchical clustering (HC) and Affinity propagation (AP)) and a supervised (mRMR) clustering and compared random selection (RS) and no selection (using all the features). Affinity propagation clustering yields a set of exemplars which better represented each cluster. Finally, in order to assess the predictive capabilities of each one of the feature selection method, a random forest classifier was trained and tested via a stratified-K-fold (K=19 the occurrence of decease event) cross-validation. This process was repeated 1000 times. Feature importance as assessed by aggregation of the performance at each try. The performance is evaluated by computing the precision (True positive / True positive + True negative) of prediction.

Results

The table displays the selected predictive feature depending on the selection methods. Unsupervised clustering algorithms allowed to select a non-redundant set of features able to significantly better predict HCC overall survival [Exemplars from AP: Precision= 0.76 ± 0.01, (p-value < 0.001)], in comparison to the other methods [All features: Precision = 0.73 ± 0.001; RS from all features : Precision = 0.71 ± 0.3 ; RS from K-means clustering : Precision = 0.715 ± 0.1; RS from HC: Precision = 0.74 ± 0.02; RS from AP clustering: Precision = 0.735 ± 0.01 and exemplars from mRMR: Precision = 0.735 ± 0.01] . The most reproducible predictive features are related with the shape of the tumour [Figure 2]

	All features	Random selection	Random Selection HC
1	T1_Tardif_Flatness	T1_Gado_Least_Axis_Length	T1_Gado_Least_Axis_Length
2	T1_Gado_Least_Axis_Length	T1_Tardif_Flatness	T1_Tardif_Flatness
3	T1_Tardif_Least_Axis_Length	T1_Tardif_Least_Axis_Length	T1_Tardif_Least_Axis_Length
4	T1_Tardif_Canny_std	T2_LoG_mean	T2_LoG_mean
5	T2_LoG_mean	T1_Tardif_Canny_std	T1_Tardif_Canny_std
6	T2_Sobel_mean	T2_LoG_std	T2_Sobel_mean
7	T2_LoG_std	T2_Sobel_mean	T2_LoG_std
8	T2_mean	T2_mean	T2_mean
9	T2_max	T2_max	T2_max
10	ADC_skewness	T1_Gado_Compactness1	T1_Gado_Sphericity
	Exemplars AP	Random selection Kmeans	Random selection AP
1	T1_Tardif_Flatness	T1_Gado_Least_Axis_Length	T1_Gado_Least_Axis_Length
2	T2_mean	T1_Tardif_Flatness	T1_Tardif_Flatness
3	ADC_mean	T1_Tardif_Least_Axis_Length	T1_Tardif_Least_Axis_Length
4	T1_Gado_Compactness1	T2_LoG_mean	T2_LoG_mean
5	Diffusion_DWI_1_Sphericity	T1_Tardif_Canny_std	T1_Tardif_Canny_std
6	T1_Gado_Information_Measures_of_Correlation_2	T2_LoG_std	T2_Sobel_mean
7	T2_Sum_Average	T2_Sobel_mean	T2_LoG_std
8	T1_Tardif_Elongation	T2_mean	T2_mean
9	Diffusion_DWI_1_Elongation	T2_max	T2_max
10	T2_Sphericity	T1_Gado_Sphericity	T1_Gado_Compactness1

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Conclusion

A framework for feature selection in a radiomics workflow is presented. Unsupervised methods allow to cluster together groups of features increasing the prediction capabilities and reducing redundancy. AP outperforms the other features selection method suggesting the use of the exemplars as representative feature of each cluster.