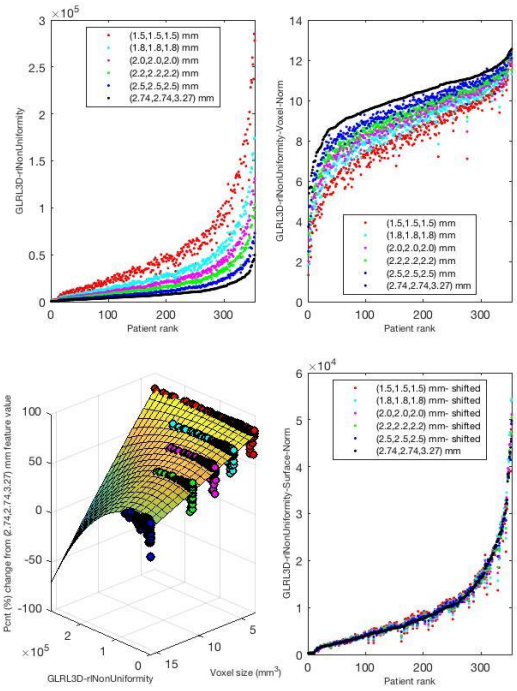

Fig.1: Results for RLNU (training). **TOP**: (left) feature calculated at each voxel dimension against patient rank. (right) Feature normalised by voxel number in ROI. **BOTTOM**: (left) Surface model to calculate feature change. (right) Surface model shifted result.

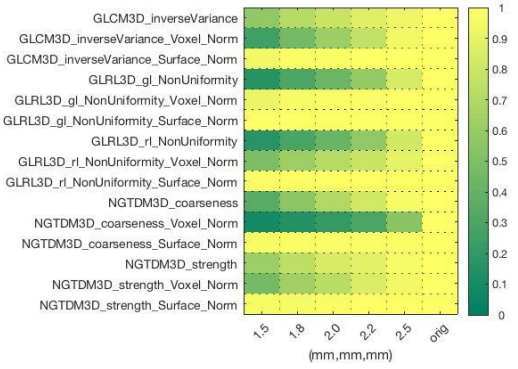

Fig.2: CCC heatmap for each feature (validation dataset)

Conclusion

We developed, tested and validated a novel normalisation technique for voxel size dependent radiomic features. On-going work aims at validating the proposed approach on other imaging modalities.

References

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[3] K. G. Foley *et al.*, "Development and validation of a prognostic model incorporating texture analysis derived from standardised segmentation of PET in patients with oesophageal cancer," *Eur. Radiol.*, 2017.

PO-0964 Stability and prognostic significance of CT radiomic features from oesophageal cancer patients

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Purpose or Objective

Radiomics aims at extracting quantitative features from medical images. Several studies focussed on the potential value of radiomic analysis in predicting tumour response for oesophageal cancer (OC) patients using contrast enhanced CT images. However, in clinical practice contrast agents are not always administrable, making the development of a new radiomic model necessary. In this work, we investigated the usefulness of radiomic features extracted from contrast and non-contrast enhanced CT scans in the development of a prognostic model in OC.

Material and Methods

CT images and radiotherapy volumes of 213 patients from a clinical trial in OC[1]were processed with the CERR package[2]. Patients were divided into 3 groups: mixed group (MG) with contrast and non-contrast enhanced CT images (n=213), contrast group (CG) with contrast enhanced CT scans (n=138) and non-contrast group (nCG) with non-contrast enhanced CT data (n=75). Radiomic features were automatically extracted in 2D and 3D in compliance with the IBSI[3], using in-house developed data analytics software[4]. Stable features were selected as the ones with similar intra-groups distributions (Kruskal-Wallis test). Corresponding 2D and 3D stable features within each group were evaluated for differences (Wilcoxon signed rank test). Remaining filtered features and clinical characteristics were used to develop a prognostic model with the Cox regression method.

Results

A total of 119 2D and 3D features were computed from each group. The Kruskal-Wallis test excluded 82, 3 and 6 unstable features obtained from MG, from CG and from nCG, respectively (Fig. 1). Some stable features (6 for MG, 15 for CG and 17 for nCG) did not show a significant difference if extracted considering 1 tumour layer at a time or considering the whole tumour volume. Among stable features, 4 features showed no difference if obtained from 3D or 2D data and were stable in all the 3 groups. The Cox regression model, constructed with 8 clinical and radiomic variables, identified 1 feature (GLDZM zone distance variance) associated with survival (Table 1).

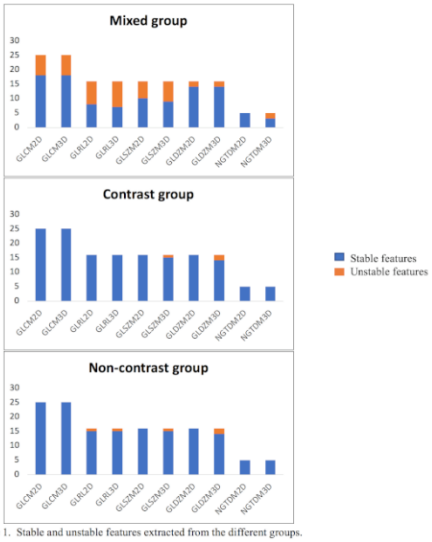

Figure 1. Stable and unstable features extracted from the different groups.

Conclusion

The prognostic model has identified 1 texture significantly and independently correlated with overall survival. This

feature can add value over and above currently known prognostic factors if computed in 2D or 3D and independently from administration of CT contrast agents.

Prognostic variable	p-value	Parameter estimate	Hazard Ratio	95% Confidence Intervals	
				Lower	Upper
GLDZM zone distance variance	0.005	0.274	1.315	1.085	1.593

Table 1. Results of the Cox regression model

References:

1. Hurt CN et al.SCOPE1:a randomised phase II/III multicentre clinical trial of definitive chemoradiation,with or without cetuximab,in carcinoma of the oesophagus.BMC Cancer.2011 Oct 28;11:466
2. Deasy JO et al.CERR:a computational environment for radiotherapy research.Med Phys.2003 May;30(5):979-85
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PO-0965 How to find the best radiomics features for prediction of overall survival in SBRT for HCC?

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Purpose or Objective

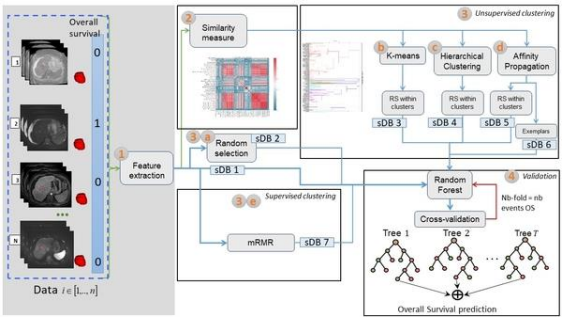
One of the major issues in radiomics is the very large amount of tested extracted features, compared to the often-reduced sample size and the low number of events. Reduction of dimensionality may be therefore an important preliminary step to improve the prediction capability of the predictive models.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

PO-0966 Prediction of Locoregional Control in Hepatocellular Carcinoma After SBRT with Deep Learning

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