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LEVERAGING RANDOM SURVIVAL FOREST (RSF) AND PET IMAGES FOR PROGNOSIS OF MULTIPLE MYELOMA AT DIAGNOSIS

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Context

Multiple myeloma (MM) is a bone marrow cancer that accounts for 10% of all haematological malignancies. It was reported that full-body FDG PET imaging provides prognostic information for both baseline and therapeutic

Contribution

There is yet much to discover in the survival analysis of MM. However, the **Random Survival Forest (RSF)**[2] has demonstrated robustness but is not studied in the PET imaging and MM context.We developed a two-stage computerassisted method based on PET imaging features towards **assisting current diagnosis and treatment decisions** for MM patients, with RSF and "Variable importance" (VIMP) [2].

Definitions

Right censoring: When no event (death/relapse) has taken place at the end of the evaluation period.

C-index: The concordance probability is the frequency of concordant pairs among all pairs of subjects. Error prediction = 1 - C-index

follow-up of MM patients (MM).

Aims

- \checkmark Predict Progression-Free Survival (PFS).
- \checkmark Provide predictive features (Clinics and Radiomics).

Survival curve: Survival rates of a specific population, over a period of time.

A. Material and method

1) The data

✓ Prospective multi-centric french IMAJEM study [1], 66 patients✓ 132 Clinical and imaging features (textural and conventional).

2) The textural features : Radiomics

Example of the GLCM (Gray-Level Co-Occurrence) Matrix [3]:

Translate the joint probability $\mathbf{P}(\mathbf{i},\mathbf{j}|\sigma,\theta)$ of the ROI. The position (i,j) represents the number of times that the **combination of the pixels with i and j levels** appears in the I matrix, separated by σ **pixels distance** and a θ **angle**. Fig. 1: *FDG-PET image of a*

For a distance of 1 and an angle of 0° (plan horizontal):



$Energy = \sum_{i=1}^{Np} \sum_{j=1}^{Np} (p(i,j))^2$

B. Results

1) Evaluation of the method





Fig. 2: Intensity matrix I

Fig. 3: GLCM Matrix p

3) The method



Fig. 4: The RSF differs from the random forest in the target value (the ensemble mortality) but also in the way to separate branches (log-rank test on the mortality)



Fig. 5: *pipeline of the method*

Our method0.05Gradient-Boosting Cox0.27Lasso-Cox0.4Without selection0.40Minimal depth0.24Variable-Hunting0.11

Tab. 1: Average p-value according to the

method.



Fig. 8: Kaplan Meier curves of the two groups obtained with the test set (\underline{pink} :

bad prognosis, <u>blue</u> : good prognosis). Error : 0.39, p-value = 0.045

3) The interest of using textural features

	All	textural and conventional	clinical
	characteristics	characteristics	characteristics
Our method Minimal depth method Variable-Hunting method Without selection	$\begin{array}{c} 0.34 \\ 0.45 \\ 0.40 \\ 0.51 \end{array}$	$\begin{array}{c} 0.36 \\ 0.45 \\ 0.41 \\ 0.67 \end{array}$	$\begin{array}{c} 0.45 \\ 0.48 \\ 0.45 \\ 0.52 \end{array}$

Tab.2: Influence of the features class on the prediction error, with different selectionmethods. There are the same patients in each sub-databases

3) The predictive features



C. Conclusions and perspectives

- The proposed method is more efficient than conventional approaches.
 It is possible to correctly separate two classes of patients (good/bad prognosis).
 It is possible to determine the features that are the most predictive.
 It shows the interest of using textural features.
 The relative resampling is more predictive than absolute resampling
- \checkmark This approach can be generalised to other diseases.
- \checkmark Thereafter, more patients will be included.

References

[1] P. Moreau, et al., Prospective evaluation of magnetic resonance imaging and [18f] fluorodeoxyglucose positron emission tomography-computed tomography at diagnosis and before maintenance therapy in symptomatic patients with multiple myeloma included in the ifm/dfci 2009 trial : Results of the imajem study. Journal of Clinical Oncology, 35(25).
[2] H. Ishwaran, et al. Random surival forest. The annals of applied statistics, 2(3).
[3] M. Vallières et al. Image biomarker standardisation initiative. Journal of Clinical Oncology, 35(25) :2911–2918.

Fig. 8 : Histogram of the features found as predictive with the VIMP method. <u>Yellow:</u> clinical, <u>purple</u>: Imaging. OMRR (One Matrix relative resampling), OMAR (absolute resampling), Heq (histogram equalization), equalsize (equal size of voxels)

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