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RSF without

# 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 follow-up of MM patients (MM).

#### $\underline{\mathbf{Aims}}$

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

### 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].

B. Results

1) Evaluation of the method

## **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.  $Error\ prediction = 1 - C-index$ 

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

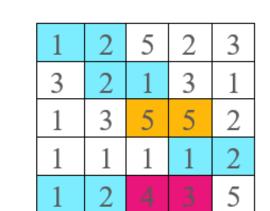
Example of the GLCM (Gray-Level Co-Occurrence) Matrix [3]:

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  $\sigma$ pixels distance and a  $\theta$  angle.



Fig. 1: FDG-PET image of a multiple myeloma patient

For a distance of 1 and an angle of  $0^{\circ}$  (plan horizontal):



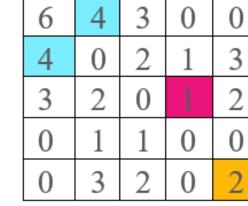


Fig. 3: GLCM Matrix p

 $Energy = \sum_{i=1}^{Np} \sum_{j=1}^{Np} (p(i,j))^2$ with Np \* Np the size of the GLCM ma-

trix

Method Fig. 6: Prediction error for each method. Method Average p-value

0.05

0.27

0.4

0.40

0.24

3) The interest of using textural features

All

0.34

0.45

0.40

0.51

characteristics

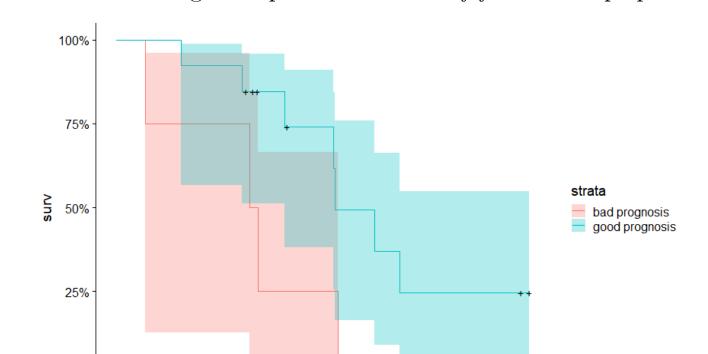


Fig. 7: Optimal number of features kept per method.

clinical

0.45

0.48

0.45

0.52

characteristics

Minimal depth

0.11 Variable-Hunting Tab. 1: Average p-value according to the method.

Our method

Gradient-Boosting Cox

Lasso-Cox

Without selection

Minimal depth

Our method

Minimal depth method

Without selection

Variable-Hunting method

Fig. 8: Kaplan Meier curves of the two groups obtained with the test set (pink: bad prognosis, <u>blue</u>: good prognosis). Error: 0.39, p-value = 0.045

textural and conventional

characteristics

0.36

0.45

0.41

0.67

Tab.2: Influence of the features class on the prediction error, with different selection

methods. There are the same patients in each sub-databases

# 3) The method

Fig. 2: Intensity matrix I

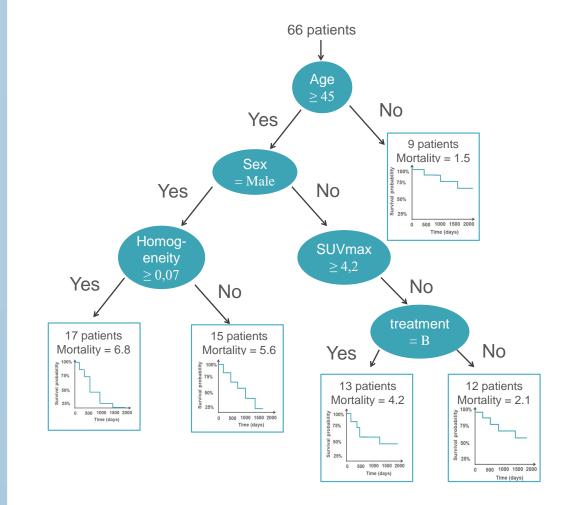
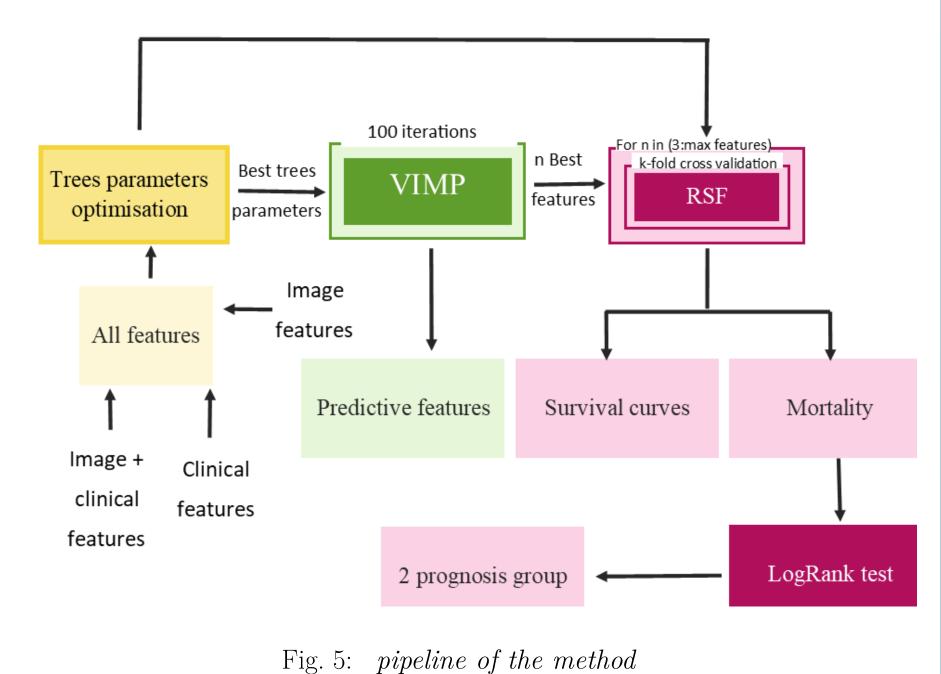
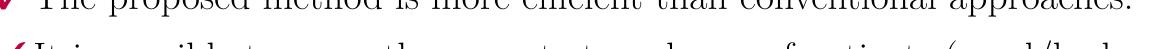


Fig. 4: The RSF differs from the random forest in the target value (the ensemble mortality) but also in the way to separate branches (log-rank test on the mortality)



- ✓ 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.
- ✓ This approach can be generalised to other diseases.

# C. Conclusions and perspectives



- ✓ It shows the interest of using textural features.
- ✓ The relative resampling is more predictive than absolute resampling
- ✓ Thereafter, more patients will be included.

# References

[1] P. Moreau, et al., Prospective evaluation of magnetic resonance imaging and [18f] fluorodeoxyglucose positron emission tomographycomputed 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.

# 3) The predictive features

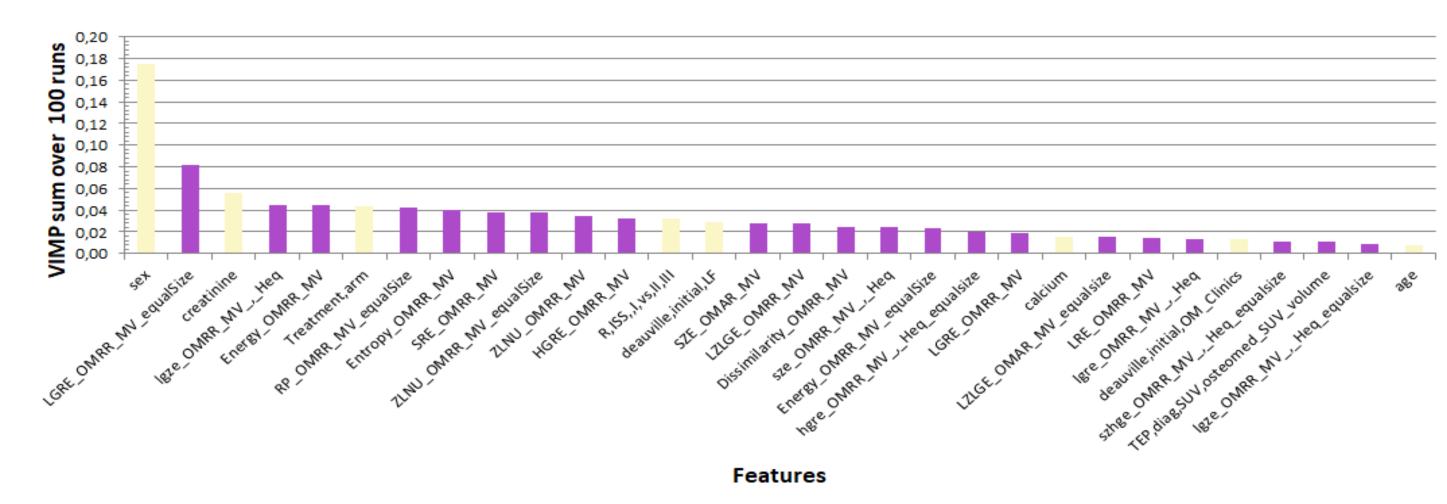


Fig. 8: Histogram of the features found as predictive with the VIMP method. Yellow: clinical, purple: Imaging.

OMRR (One Matrix relative resampling), OMAR (absolute resampling), Heq (histogram equalization), equalsize (equal size of voxels)

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