Fully-Learned Features for Lung Cancer Overall Survival Prediction

Danny Francis, Vladimir Groza, Benoit Huet, Nozha Boujemaa*
Median Technologies, France
**corresponding author e-mail: danny.francis@mediantechnologies.com*

Background

Overall survival prediction is an important task in oncology. Treatments can be personalized with respect to patients thanks to such predictions. Medical imaging can offer a non-invasive way to assess the survival probability of a patient with lung cancer. Visual features extracted from computed tomography (CT) scans can have a high prognostic value.

Recently, it has been shown that convolutional neural networks (CNN) were extremely efficient at analyzing images. Our work is based on such CNN, which we apply to CT scans to extract relevant information for overall survival prediction.

Approach

We propose an end-to-end method to predict the Overall Survival (OS) time for patients with non-small cell lung cancer (NSCLC). The model we introduce here outputs a High/Low OS score for high/low-risk patients based on a CT scan.

Unlike previous works where authors use common radiomics [1] or where features are learned in an unsupervised manner [2], this work is based on features learned in a supervised fashion to predict OS.

Dataset

Patient scans were manually annotated in order to provide slice-based 2D patches containing the tumors. The training dataset was split evenly with respect to patients' death time, thus obtaining high/low risk subsets H and L. Only patients with known death time are kept.

Pipeline and Methods

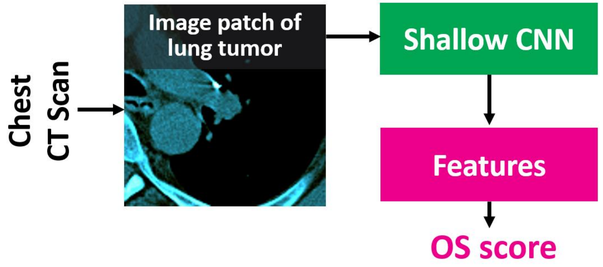
Based on 2D patches centered on tumors, a custom shallow CNN with three convolutional layers followed by a normalized dense layer (a dense layer without bias where the output is divided by the norms of the input vector and of its weights) learns OS-specific visual features to derive the OS score.

The figure below sums up how our OS score is computed. The objective function used to train our models was defined as follows:

$$\mathcal{L} = E_{X \in L, Y \in H}\left[\exp\left(\frac{\text{score}(X) - \text{score}(Y)}{K}\right)\right]$$

where K is the standard deviation of the score on $L \cup H$.

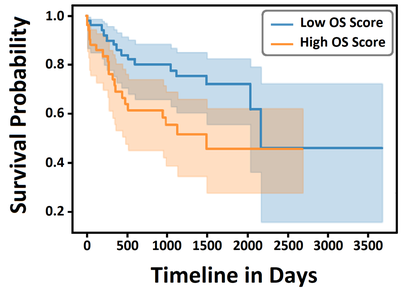
When minimizing this objective function, the result is that patients with low risk, who belong to set L, will have a lower OS score than patients from the high-risk set H. The proposed model was trained five times with different weights initializations. The optimization algorithm we used was RMSprop with a learning rate of 0.0001 and minibatches of 24 data samples.



The obtained models were used to get predictions on the test cohort. The latter was split evenly into two groups based on predicted OS score to obtain a low-risk group and a high-risk group. The OS score for a given patient is derived as the median OS score of all tumor patches extracted for that patient.

Results

The evaluation of our models by deriving the Hazard Ratio (HR) between the low-risk and high-risk groups gave a HR of **2.03** (**p-value = 0.04**, 95% confidence interval = [1.04, 3.96]) for ensembled models. The obtained OS score can therefore significantly split patients between a low-risk group and a high-risk group.
The figure below is a Kaplan-Meier plot showing the difference between the low-score test population and the high-score test population.



Low OS score patients have clearly **better survival probabilities** than high OS score patients. Our OS score can **predict** with statistical significance the **survival probability of patients with non-small cell lung cancer**.

Conclusions

Numerical experiments of the proposed shallow model demonstrate that fully-learned features can significantly separate low-risk patients from high-risk patients, providing some insights about the importance of the learned visual features for clinical information predictions, such as OS in this case. Even though our results must be validated on bigger independent cohorts, they can be considered as promising. On top of that, with more training data, the power of deep learning should significantly improve predictions by extracting more useful visual information.

References

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