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Improving the automatic diagnosis of hepatocellular carcinoma with contrastive learning

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Purpose or Learning Objective:

Several deep learning methods have been proposed to automatically classify liver lesions in MRI or CT, with good performance [1,2,3]. They all share a classical training procedure. Contrastive learning (CL) is a novel deep learning paradigm where pairs of cases, instead of cases taken in isolation, are leveraged to train the model. CL methods can be either trained without labels, in this case it learns global mathematical representations of the input images [4], or it can use labels during training in order to help to discriminate input images based on a specific characteristic [5]. In this study, we evaluate the potential of CL to improve the automatic classification of hepatocellular carcinoma (HCC) in CT-scans. We formulate it through a binary classification problem (HCC versus no HCC).

Methods or Background:

We work with 2-phase CT-scans (arterial/venous) in 2D, by choosing slices where concerned lesion is the largest, as well as lesion segmentations manually computed. We stack each image to obtain $512 \times 512 \times 4$ inputs. We work with a private dataset that contains 1853 lesions in the training set (418 HCC, 1435 no-HCC), and the test set contains 551 lesions (134 HCC, 417 no-HCC). As a baseline, we train a convolutional neural network with 5 convolutional layers and 2 final dense layers, with a total number of parameters of 1,131,506. Our network architecture is detailed in figure 1.

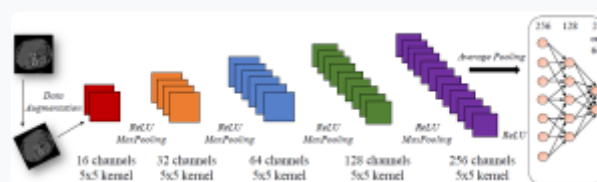


Fig 1: The deep network architecture used to train our models.

To increase performances, we propose to use a pretraining method, named Supervised Contrastive Learning (SupCon)

which is a self-supervised learning method. Our pipeline consists in a first pretraining step in which our model learns global representations of the images with the training images, and a second step in which the frozen weights are re-used to infer representations on the test set and compute a logistic regression to predict HCC probabilities. The full pipeline is detailed in figure 2.

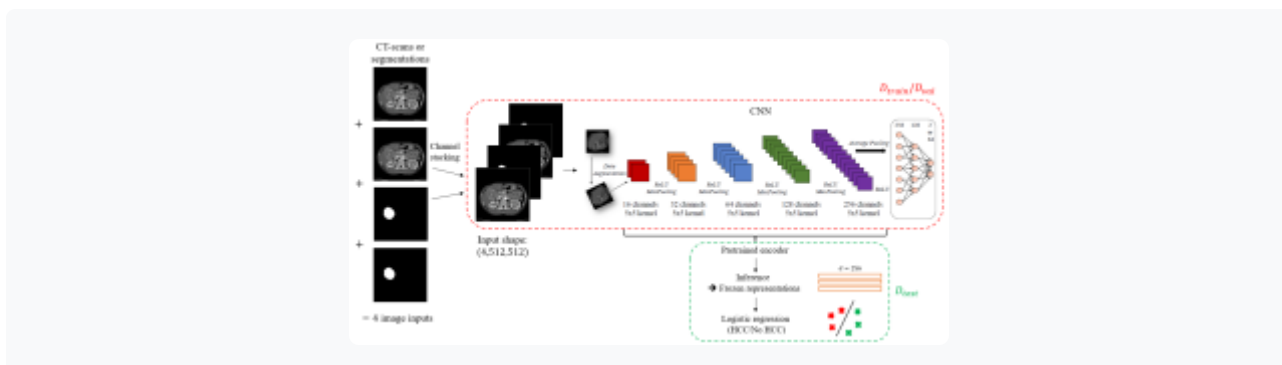


Fig 2: The full pipeline of our method.

Results or Findings:

With a classic supervised classifier, we obtain an area under the curve (AUC) of 89%, a sensitivity of 86% and a specificity of 79%. With our proposed method, we increase the AUC and sensitivity, reaching a performance AUC of 91% (+2 pts), a sensitivity of 87% (+1 pt) for the same specificity threshold of 79%. To compute sensitivity and specificity, we use the Youden threshold value on the test set [6]. The receiver operating characteristic curves of both methods are presented in figure 3.

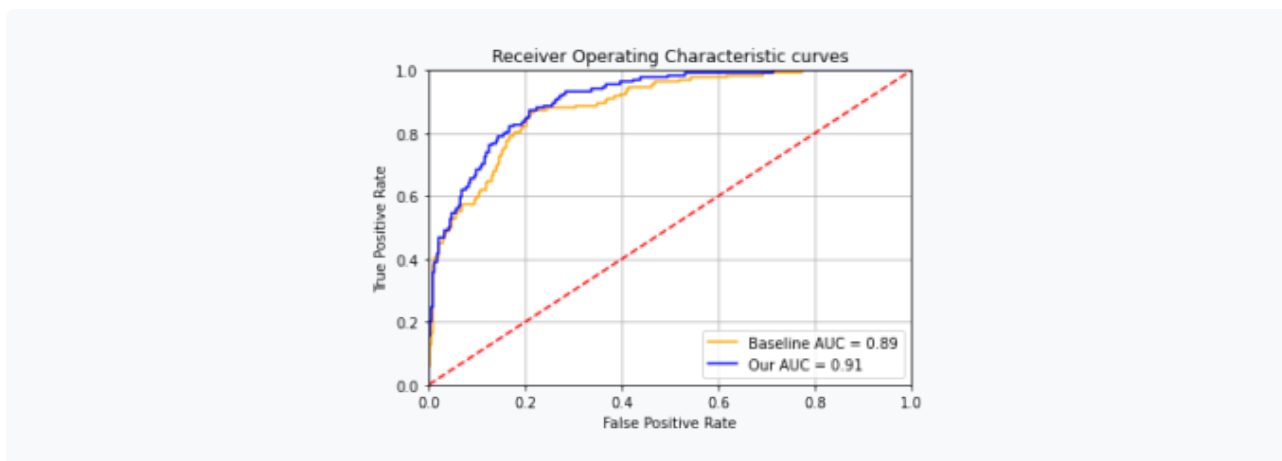


Fig 3: ROC curves for the baseline classification method and our proposed method. The red dotted line represents an arbitrary classification for HCC.

Conclusion:

We proposed to use a state-of-the-art CL method to improve the performance of HCC classification obtained with a baseline classifier. This method improves the AUC of 2% and opens perspectives for future work using other CL methods in the literature. Notably, the self-supervised learning paradigm allows to train models with unlabelled or partially labelled datasets and therefore can be easily applicable in the medical domain, due to the difficulty of obtaining large amounts of annotated scans. These preliminary results would however need to be confirmed with a prospective study.

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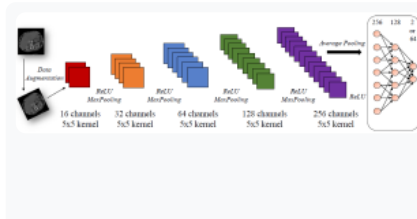


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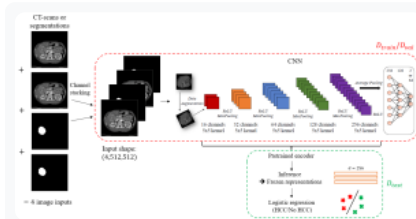


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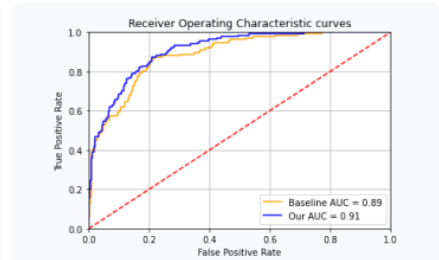


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