

Convolutional neural network learning from RT dose distribution and images improves predicting locoregional recurrence for head and neck cancer

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INTRODUCTION

Head and neck (H&N) cancer is a common malignancy in the world, and locoregional recurrences (LR) is one of the main causes of poor prognosis for H&N cancer. Assessing tumor risk and then selecting an individualized treatment schedule before treatment is critical to improving patient prognosis. Some studies have successfully established tumor risk assessment models from medical images and radiation dose distribution by the radiomics method [1-2]. However, radiomics features are artificial, which may be biased and may limit the performance of the predicted model. Fortunately, deep learning network, such as the convolutional neural network (CNN), can extract features with high predictive performance automatically by adaptive feature learning, and has been successfully used for medical image analysis. In particular, for the prognosis problem with “time-to-event” survival data, the survival CNN (SCNN) composed of CNN and Cox proportional hazards regression model were presented[3]. But it has not been widely applied to medical image analysis, such as CT, PET, etc. This study is aimed to investigate the feasibility and performance improvement of introducing SCNN into LR prediction from radiotherapy dose distribution, CT and PET for H&N cancer cases.

METHOD

The VGG-19 CNN and the Cox proportional hazards regression model were combined to establish the SCNN framework (Fig. 1). Four SCNN models were trained by inputting the slices with the maximum GTV pixels (denoted as the center slice) of dose distribution, CT, PET and the integration of these three matrices, respectively. The model output was the patient LR risk.

A negative partial log-likelihood was used for the loss function:

$$Loss = - \sum_{j:\delta_j=1} \left(R_j - \log \sum_{i:t_i \geq t_j} e^{R_i} \right)$$

where t is the survival time, j is a sample with LR, i is an at-risk sample with $t_i \geq t_j$, and R is the LR risk outputted from SCNN. The adam algorithm was chosen to minimize the loss function. 1000 epochs were used with each minibatch containing 30 patient data during model training. At each epoch, images and dose at 256×256 were reinforced by randomly flipping (horizontally and vertically) and rotating a random amount (-10° – 10°) before fed into SCNN.

A cohort of 237 patients with H&N cancer was obtained from The Cancer Imaging Archive [4]. 141 were used to train the models and the other 96 were to validate. The SCNN-based models were assessed by C-index, the Kaplan–Meier curves analysis and Log-Rank test, and then compared with the traditional radiomics-based models built by our previous work [2].

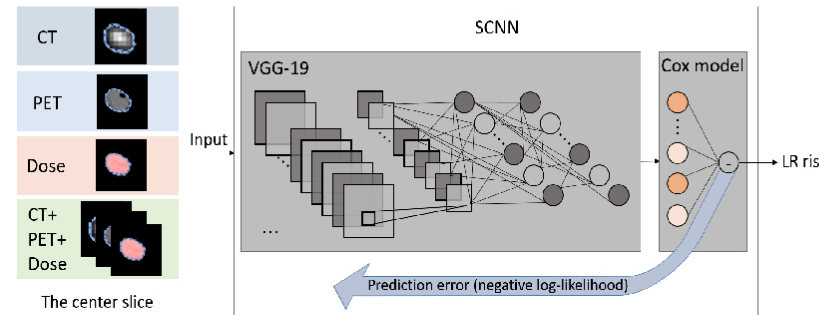


Fig. 1. The framework of SCNN.

CONCLUSIONS

The SCNN models were established with the capability of automatically extracting features from dose distribution, CT and (or) PET images, and it can improve the prediction accuracy of LR for H&N cancer compared to traditional radiomics models.

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RESULTS

In the validation set, the C-index of SCNN-based models were significantly higher than that of radiomics-based models for model_CT (0.61 vs. 0.54, $p < 0.05$) and model_CT+PET+dose (0.70 vs. 0.66, $p < 0.05$); and it was equivalent for model_PET and model_dose (0.60 vs. 0.59, 0.60 vs. 0.60, both $p > 0.05$) (Table 1). Furthermore, for SCNN-based models, model_PET and model_CT+PET+dose could successfully differentiate the Kaplan–Meier curves of high- and low-risk groups ($p < 0.05$); but for radiomics-based models, only model_CT+PET+dose ($p < 0.05$) could realize this differentiation (Fig. 2). Overall, the performance of the SCNN models was superior to that of the radiomics model.

Table 1. The C-index of SCNN-based models and radiomics-based models.

Model	C-index		p value (Wilcoxon test)
	SCNN	Radiomics	
CT	0.61	0.54	$< 2.2 \times 10^{-16}$
PET	0.60	0.59	0.11
Dose	0.60	0.60	0.51
CT+PET+dose	0.70	0.66	7.1×10^{-13}

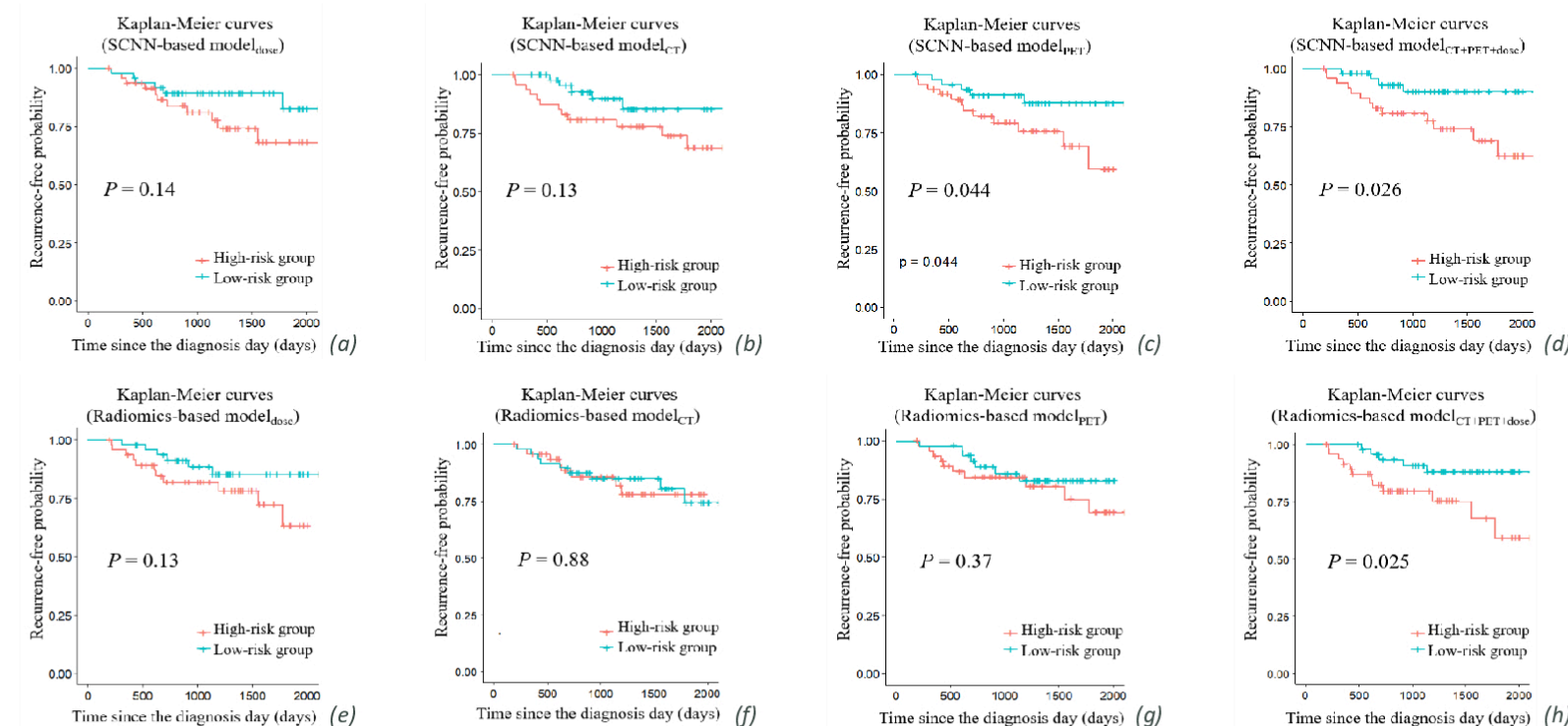


Fig. 2. The Kaplan–Meier survival curves of the high- and low-risk groups predicted by (a)-(d) SCNN-based models and (e)-(h) radiomics-based models in the validation dataset. Patients with predicted risk > median were classified into the high-risk group, and those with predicted risk ≤ median were classified into the low-risk group. The p value was generated using the log-rank test.

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