



A Deep Multi-task Network to Learn Tumor Pathological Representations for Lymph Node Metastasis Prediction

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97



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Introduction









Lung cancer is the leading cause of cancer-death worldwide.

Accurate lymph node metastasis staging is critical for initial treatment decision-making. 38% patients' clinical N stages disagreed with their pathological N stages

(1) Sung H, Ferley J, Siegel RL, Laversanne M, Soerjometarem I, Jemal A. et al. Global cancer statistics 2020: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. CA: A Cancer Journal for Clinicians. 2020. (2) Navani N, Fisher DJ, Tierney JF, Stephens RJ, Burdett S, Rydzewska LHM, et al. The Accuracy of Clinical Staging of Stege I-HIB Non-Small Cell Lung Cancer: An Analysis Based on Individual Participant Data. Chest 2019;55(3):502-9.

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Related Works







Radiomics methods

Deep learning methods

DL with auxiliary segmentation task

(1) Wang X. Nan, W. Yan S, Li G, Guo N, Guo Z. MADS II Radiomics Analysis Using SIM Predicts Mediastinal Lymph Nodes Status of Squamous Cell Lung Cancer by Pre-Treatment Chest CT Scan. Journal of Thoracic Oncology. 2018;13(10):S374-S. (2) Aba X. Wang X. Xia W. Li Q. Tau Li Q. Tau Li A cross-model 30 deep learning for accurate lymph node metastasis prediction in clinical stage II lung denoncarcinoma. Lung Cancer. 2020;45(10)-7. (3) Aba X. Wang X. Xia W. Juang L. Linu. J. Zmat J. Li D. Status Status Construction and Cancer Status Constructing Cancer Status Construction and Cancer S

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Methods







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Experiments and Results

- 681 patients
- Demographics, tumor biomarkers, disease histories, and CT images
- 10-fold cross validation for test
- Another 5-fold cross validation for hyperparameter tuning and early stopping
- Repeating 10 times with different random seeds

Table 1. The LNM prediction performances of the proposed model and baseline models.

Methods	AUC		AP	AP	
	Mean	SD	Mean	SD	
Logistic regression	0.760	0.073	0.433	0.116	
Single-task model	0.760	0.079	0.448	0.118	
Multi-task model	0.768	0.073	0.448	0.113	

Table 2. The paired t test of the performances of the proposed model and baseline models.

Methods	Pair t test of AUC	Pair t test of AP
Logistic regression vs Single-task model	0.99	<0.01
Logistic regression vs Multi-task model	<0.01	<0.01
Single-task model vs Multi-task model	<0.01	0.89





Discussion

- The proposed method does not require ROI annotations. And the pT labels are usually recorded in the pathology reports and easily obtained.
- As many types of cancer are evaluated by the TNM stage system, we can also extend this strategy to LNM prediction for other types of cancer.
- Instead of the multi-task learning, we can also extract the pT stage representations separately and then integrate them with other clinical features like traditional radiomics methods, which may be more clinically acceptable.
- Combining the cfDNA features with clinical and image features to achieve more precise LNM prediction.
- Exploring how to predict the LNM in the lymph node station granularity to provide more detailed information for clinicians.



Conclusion

In this study, we proposed a deep multi-task network for LNM prediction. Experimental results show that the deep tumor pathological representations learned using the auxiliary task can significantly improve the LNM prediction performance.















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