

# The effect of different segmentation methods on the performance of prognostic models for early-stage non small cell lung cancer

Katleen Claesen  
Master of Nuclear Engineering Technology

## Introduction

**Lung cancer** is the **leading cause of cancer-related death** worldwide, with non-small cell lung cancer (NSCLC) being the most common type [1]. To increase survival, an early diagnosis and accurate staging are necessary (Fig. 1). **Radiomics**, the extraction of quantitative features from medical images, can provide insight into detection, staging, and prognosis by identifying patterns that cannot be observed by the human eye. The outcome of these **prognostic models can be influenced by tumor segmentation**, the process of outlining tumors. This research investigates whether different PET segmentation methods affect the performance of prognostic NSCLC models.

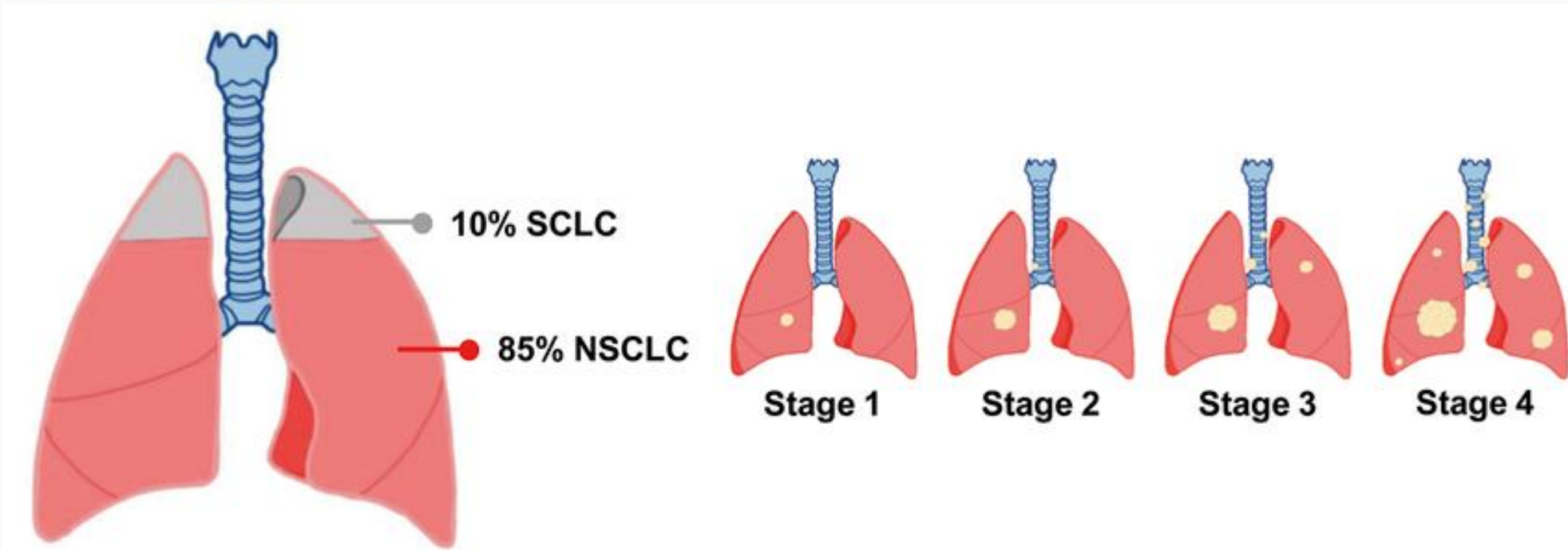
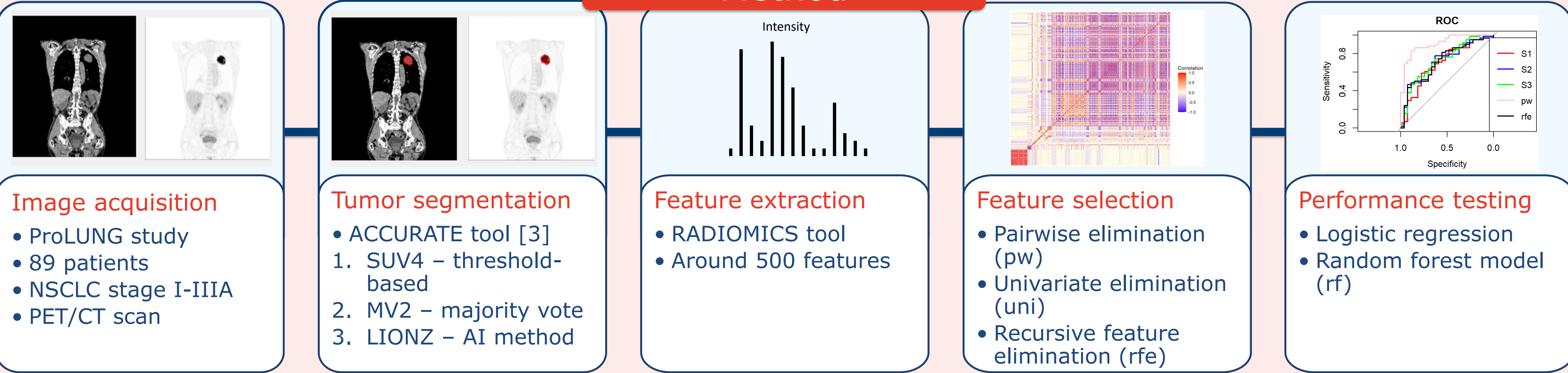


Fig. 1: Types and stages of lung cancer [2]. NSCLC: non-small cell lung cancer; SCLC: small cell lung cancer.

## Method



## Results

Model performance was **compared across the different segmentation** methods and was found to be consistent across all three methods. The area under the curve (AUC) values from the receiver operator characteristic curves showed **minimal differences** between the different segmentations (Fig. 2). This indicates little impact on the performance of prognostic radiomics models.

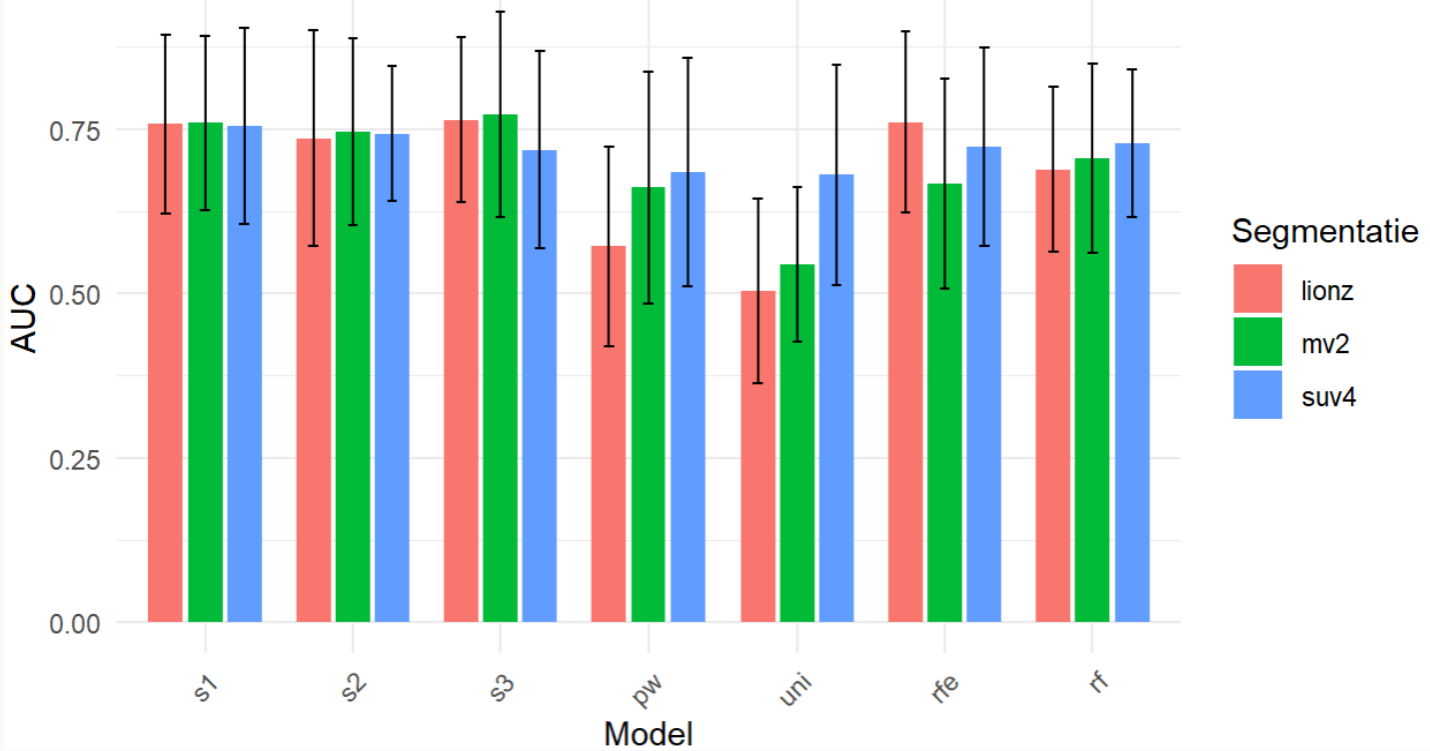


Fig. 2: The AUC for every segmentation method per prognostic model for an overall survival of 36 months.

When **comparing different models**, more differences were observed (Table 1). **Simple models**, such as model s1 using only the TLG radiomic feature ( $AUC\ 0.76 \pm 0.14$ ), were the **most reliable overall**. In contrast, more complex machine learning models, such as random forest, did not result in better prognostic accuracy.

Table 1: AUC values per segmentation method, per prognostic model. The models that were used are s1 (TLG-only), s2 (TLG and SUVmax), s3 (TLG, SUVmax and DmaxBulk), pw (after pairwise elimination), uni (after univariate elimination), rfe (after recursive feature elimination) and rf (random forest).

	LIONZ	MV2	SUV4
s1	0.76 ± 0.14	0.76 ± 0.13	0.75 ± 0.15
s2	0.74 ± 0.16	0.75 ± 0.14	0.74 ± 0.10
s3	0.76 ± 0.13	0.77 ± 0.16	0.72 ± 0.15
Pw	0.57 ± 0.15	0.66 ± 0.18	0.68 ± 0.17
uni	0.50 ± 0.14	0.54 ± 0.12	0.68 ± 0.17
rfe	0.76 ± 0.14	0.67 ± 0.16	0.72 ± 0.15
rf	0.69 ± 0.13	0.70 ± 0.13	0.72 ± 0.12

## Conclusion

The results of this research indicate that the **choice of PET segmentation method does not significantly affect the performance** of prognostic models for early-stage NSCLC. This supports the robustness and flexibility of radiomics workflows in clinical practice. In contrast, **model selection plays an important role**, with simple models based on key radiomic features performing best.

Supervisors / Co-supervisors / Advisors: Prof. Dr. Brigitte Reniers (UHasselt)  
Prof. Dr. Liesbet Mesotten (ZOL)  
drs. Jill Meynen (UHasselt)

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