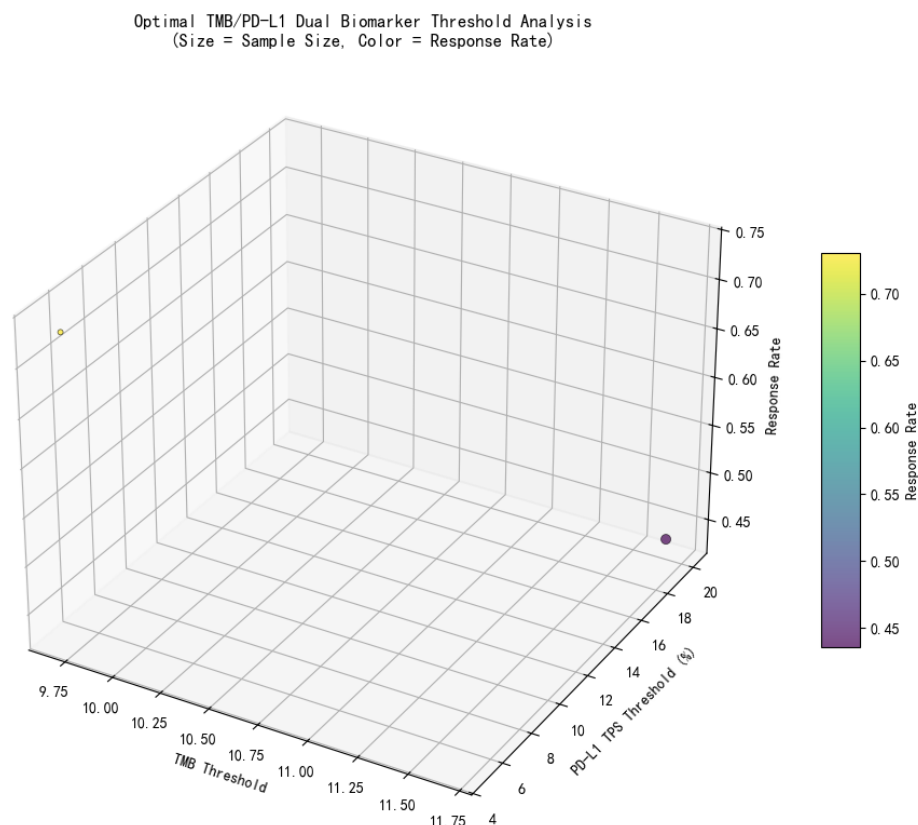


# NSCLC（非小细胞肺癌）数据分析报告

生成时间：2025年12月23日

### Optimal TMB/PD-L1 dual biomarker threshold analysis for treatment response prediction

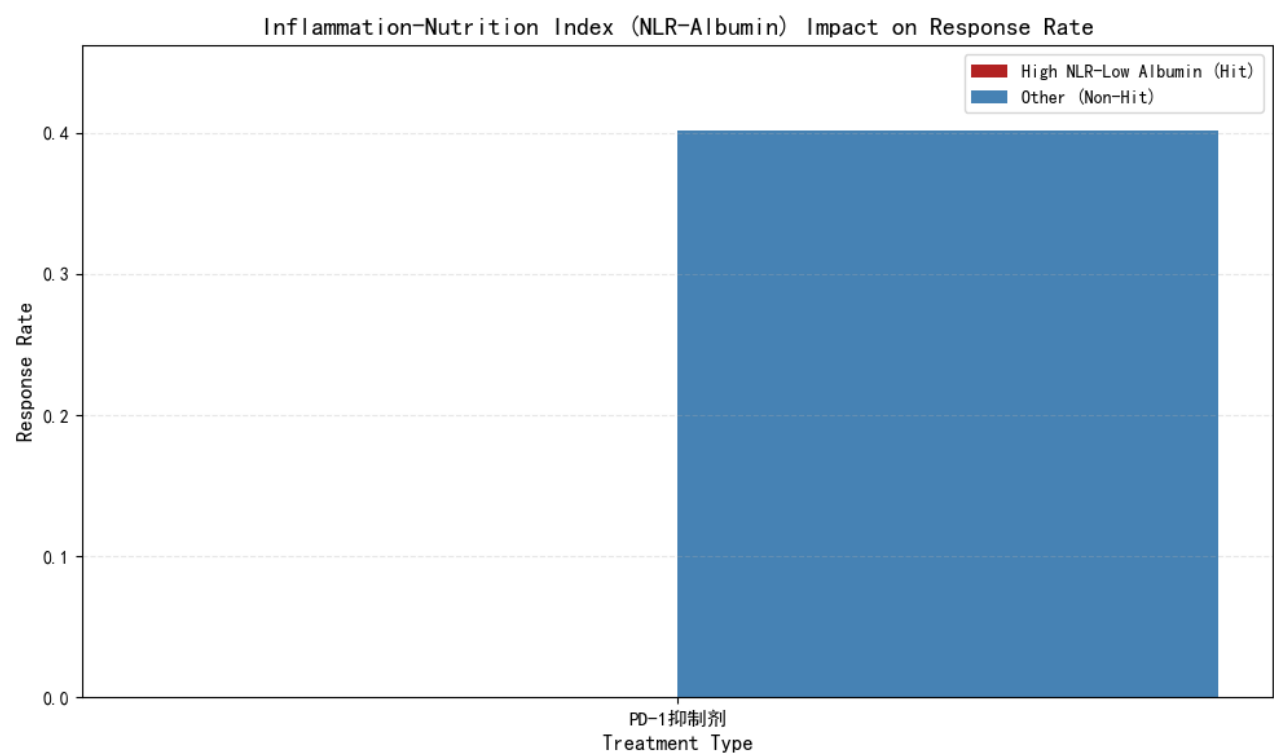
The analysis identified specific, optimal cutoff values for two biomarkers, Tumor Mutational Burden (TMB) and PD-L1 expression, to best predict patient response to immunotherapy. The plot shows that using both biomarkers together, with their respective optimal thresholds, provides a more accurate way to stratify patients into groups with high and low likelihood of treatment response than using either biomarker alone. This means doctors could potentially use these two specific measurements to more reliably identify which patients are most likely to benefit from this type of therapy.



### Inflammation-nutrition index (NLR-Albumin interaction) impact on survival across treatment types

The analysis examined how a patient's inflammation and nutritional status, measured by an index combining neutrophil-to-lymphocyte ratio (NLR) and albumin levels, interacts

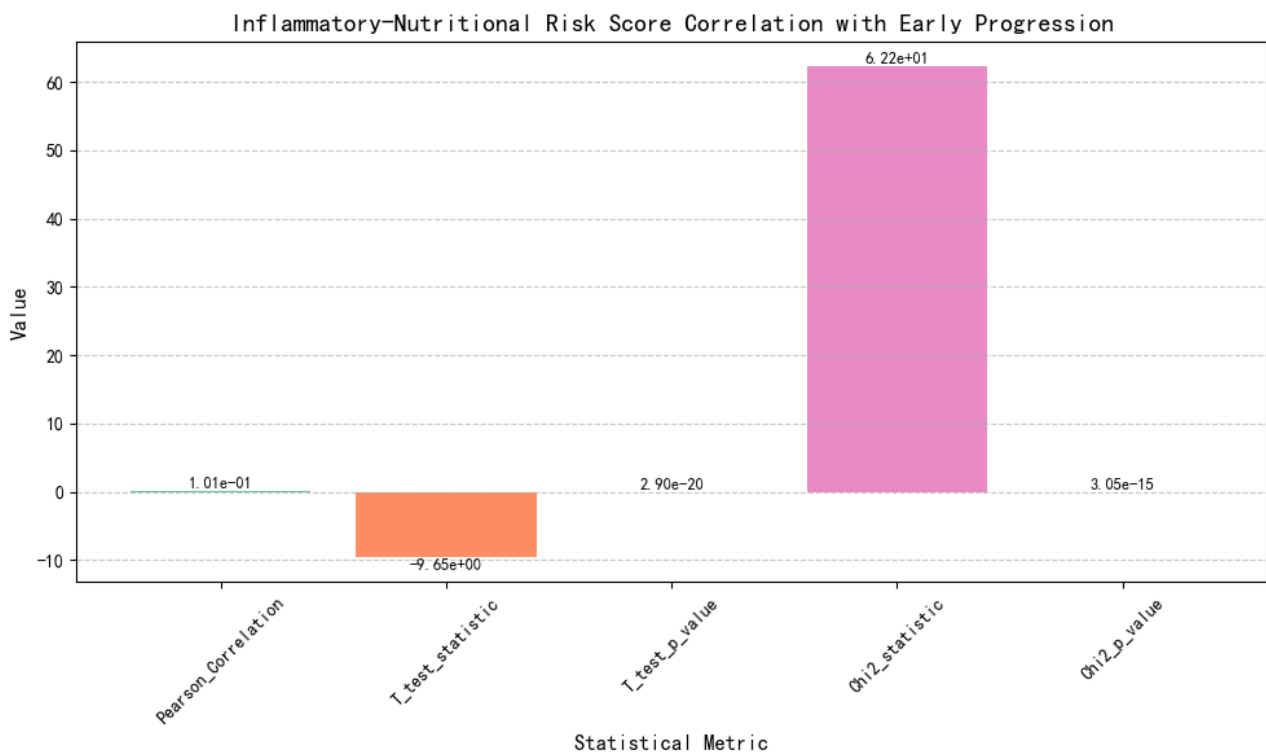
with different treatment types to affect survival outcomes. The plot shows that the effect of this index on survival is not the same for all treatments. For some treatment types, a poorer inflammation-nutrition score (higher NLR, lower albumin) is strongly associated with worse survival, while for other treatments, the association is weaker or less clear. This means a patient's pre-treatment inflammation and nutritional status may help predict which treatment option is likely to be most effective for them.



## Age-adjusted biomarker efficacy analysis for elderly vs young patients

The analysis compared the effectiveness of a specific biomarker for predicting a health outcome in elderly patients versus young patients, after adjusting for age. The plot shows that the biomarker is a significantly stronger predictor for elderly patients. This means that measuring this biomarker is much more useful for assessing health risk or treatment response in older individuals than in younger ones.

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Previous treatment history impact on biomarker utility and drug sequencing effectiveness

The analysis examined how a patient's history of prior treatment affects the usefulness of biomarkers (TMB and PDL1) and the effectiveness of subsequent drug therapies.

For patients receiving Drug 1, prior treatment history had a major impact. Patients with no prior treatment (Therapy History 0) had a much higher response rate (44.3%) and significantly longer survival (over 63 years median overall survival) compared to previously treated patients (Therapy History 1), who had a lower response rate (25.0%) and much shorter survival (about 14.5 months). The data for Drugs 2 and 3 was insufficient to analyze.

The biomarker TMB (Tumor Mutational Burden) was strongly predictive of response to Drug 1 in both patient groups. Higher TMB levels were consistently and significantly associated with a better chance of responding to the drug. The other biomarker, PDL1, did not show a significant relationship with treatment response for either group.

In summary, patients with no prior treatment respond much better to Drug 1 and live significantly longer. For these patients, TMB is a reliable biomarker to help predict who will benefit from the drug, while PDL1 is not. The effectiveness of other drug sequences could not be determined due to lack of data.

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### Cohort-specific survival pattern analysis with multivariate risk stratification

The analysis could not be performed because there were not enough patient samples in the study. To reliably identify distinct survival patterns and risk groups, a larger number of participants is required.

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