

Machine Learning, Artificial Intelligence and Computational Modeling

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PRETREATMENT PREDICTION OF ANTI-PD-1 IMMUNOTHERAPY RESPONSE USING MACHINE LEARNING IN PATIENTS WITH METASTATIC MELANOMAS USING TARGETED TRANSCRIPTOMICS IN CIRCULATING CD8 CELLS

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Background The aim of this study is to assess the role of machine learning in identifying patients that will respond to anti-PD1 from expression data from circulating CD8 T-cells in patients with metastatic melanoma.

Methods Normalized RNA expression data was obtained from gene expression omnibus (GEO) a public functional genomics data repository.¹ All project files for GSE166181 were downloaded in clinical, RNA sequencing data, and metadata for each of these patients. Pretreatment data were extracted for each patient labeled "T0" which was used in the prediction. All normalized expression data that had no values were deleted and a final profile of the expression profiles was obtained. The expression of these genes was assigned as high or low. The patients were divided into 70/30 for training and test set. The overall accuracy of each cell and total accuracy for individual patients.

Results A total of 20 patients with 11 responders and 9 non-responders a total of 18250 cells were identified at the pretreatment stage. A training set of 9 responders and 6 non-responders was used to train the deep learning algorithm for the test set 3 responders and non-responders each were kept out. A 5-layer deep learning algorithm was trained. In the test set, a total of 2237 cells were classified with a total of 1085 cells (48.5%) correctly identified among all test-set patients. In total 3 out of 6 patients (50%) were correctly identified with a threshold of 50% cells were correctly identified see table 1. Two patients were non-responders and 1 was a responder. While the one non-responder and two responders were.

Conclusions The algorithm was partially successful in identifying non-responders in the pretreatment group in this small cohort of patients. However, a larger dataset is required to train and test to develop a more accurate algorithm for patients that will or will not respond to anti-PD-1 treatment prior to treatment.

REFERENCE

- De Biasi S, Gibellini L, Lo Tartaro D, Puccio S *et al.* Circulating mucosal-associated invariant T cells identify patients responding to anti-PD-1 therapy. *Nat Commun* 2021;**12**(1):1669. PMID: 33723257

Abstract 1269 Table 1 Test set cellular classification

	Non-responders			Responders		
	Patient 3	Patient 30	Patient 5	Patient 13	Patient 23	Patient 7
Correct	225(56.8%)	57(60.6%)	349(47.9%)	154(65%)	195(44.7%)	105(38.2%)
Incorrect	178(44.2%)	56(49.6%)	380(52.2%)	126(45%)	242(65.4%)	170(61.9%)
Total	403(100%)	113(100%)	729(100%)	280(100%)	437(100%)	275(100%)

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