Article type: Editorial

Home Page URL: https://www.alliedacademies.org/immunology-case-reports/

Harnessing artificial intelligence to predict immune response in cancer.

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Received: *02-Aug-2025, Manuscript No. AAICR-25-171208;* ***Editor assigned:*** *03-Aug-2025, Pre QC No. AAICR-25-171208(PQ);* ***Reviewed:*** *18-Aug-2025, QC No. AAICR-25-171208;* ***Revised:*** *24-Aug-2025, Manuscript No. AAICR-25-171208(R);* ***Published:*** *30-Aug-2025, DOI: 10.35841/aaicr-8.3.208*

Introduction

The advent of immunotherapy has revolutionized cancer treatment, offering durable responses in malignancies once considered intractable. Yet, only a subset of patients benefits from these therapies, and predicting who will respond remains a major clinical challenge. The immune system's interaction with tumors is complex, dynamic, and influenced by myriad factors—from genetic mutations and tumor microenvironment to systemic inflammation and microbiome composition. Enter artificial intelligence (AI): a transformative tool capable of decoding this complexity and forecasting immune responses with unprecedented precision. Artificial intelligence encompasses machine learning (ML), deep learning (DL), and other computational techniques that enable systems to learn from data and make predictions. In oncology, AI has already demonstrated utility in imaging diagnostics, drug discovery, and treatment planning. Its application to immuno-oncology—particularly in predicting immune responses—marks a new frontier in personalized cancer care [1].

By integrating diverse datasets, AI can identify patterns and biomarkers that escape traditional statistical methods. These insights can guide treatment selection, monitor therapeutic efficacy, and uncover novel targets for intervention. The tumor microenvironment (TME) plays a pivotal role in shaping immune responses. It comprises cancer cells, stromal cells, immune infiltrates, cytokines, and extracellular matrix components. AI algorithms can analyze high-dimensional data from single-cell RNA sequencing, spatial transcriptomics, and multiplex immunohistochemistry to characterize the TME. For instance, deep learning models have been used to classify tumors as "hot" (inflamed and immunogenic) or "cold" (immune-excluded or immunosuppressed), which correlates with response to checkpoint inhibitors. AI can also quantify immune cell densities, spatial arrangements, and phenotypic states—providing a comprehensive map of immune activity within tumors [2].

Checkpoint inhibitors targeting PD-1, PD-L1, and CTLA-4 have transformed treatment for cancers such as melanoma, non-small cell lung cancer (NSCLC), and renal cell carcinoma. However, response rates vary widely. AI models trained on genomic, transcriptomic, and clinical data can predict which patients are likely to benefit. AI can assess TMB from sequencing data and correlate it with neoantigen load and immunogenicity. Machine learning algorithms can quantify PD-L1 levels from histopathological images more accurately than manual scoring. AI can identify immune-related gene clusters predictive of response, such as interferon-gamma signaling or cytolytic activity scores [3].

These predictive models are being validated in clinical trials and may soon inform routine decision-making. Cancer immunology is inherently multi-layered. AI excels at integrating multi-omics data—including genomics, epigenomics, proteomics, and metabolomics—to build holistic models of immune response. For example, combining microbiome profiles with host genetics and immune cell phenotypes has revealed microbial signatures associated with immunotherapy outcomes. Similarly, integrating metabolomic data can uncover metabolic constraints on immune cell function within tumors. AI-driven multi-omics integration enables the discovery of composite biomarkers that outperform single-parameter

Citation: Campbell R. Harnessing artificial intelligence to predict immune response in cancer. Immunol Case Rep. 2025;8(3):208.

predictors, enhancing precision in patient stratification. AI is not limited to static predictions—it can support dynamic monitoring of immune responses during treatment. By analyzing longitudinal data from blood tests, imaging, and wearable devices, AI can detect early signs of response or resistance. AI extracts quantitative features from medical images to track tumor changes and immune infiltration [4].

Machine learning models can interpret circulating tumor DNA (ctDNA), cytokine levels, and immune cell counts to assess treatment efficacy. AI can analyze serial biopsies to monitor immune cell dynamics and tumor evolution. These capabilities pave the way for adaptive immunotherapy, where treatment is tailored in real time based on evolving immune responses. Despite its promise, AI in immuno-oncology faces several hurdles: Heterogeneous datasets with variable quality can impair model performance. Black-box models may lack transparency, limiting clinical trust and regulatory approval [5].

Conclusion

Artificial intelligence is poised to revolutionize cancer immunotherapy by predicting immune responses with precision and speed. By decoding the complexities of the tumor microenvironment, integrating multi-omics data, and enabling real-time monitoring, AI empowers clinicians to tailor treatments, improve outcomes, and reduce toxicity. While challenges remain, the convergence of computational power, biological insight, and clinical need ensures that AI will be a cornerstone of future oncology care—transforming the tug-of-war between cancer and the immune system into a guided, strategic battle.

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