

# Mathematical Modeling of Tumor-Immune Interactions: Methods, Applications, and Future Perspectives

Chenghang Li<sup>1</sup> and Jinzhi Lei<sup>1,2,\*</sup>

<sup>1</sup> School of Mathematical Sciences, Tiangong University, Tianjin 300387, China.

<sup>2</sup> Center for Applied Mathematics, Tiangong University, Tianjin 300387, China.

Received 16 October 2024; Accepted 11 February 2025

---

**Abstract.** Mathematical oncology is a rapidly evolving interdisciplinary field that uses mathematical models to enhance our understanding of cancer dynamics, including tumor growth, metastasis, and treatment response. Tumor-immune interactions play a crucial role in cancer biology, influencing tumor progression and the effectiveness of immunotherapy and targeted treatments. However, studying tumor dynamics in isolation often fails to capture the complex interplay between cancer cells and the immune system, which is critical to disease progression and therapeutic efficacy. Mathematical models that incorporate tumor-immune interactions offer valuable insights into these processes, providing a framework for analyzing immune escape, treatment response, and resistance mechanisms. In this review, we provide an overview of mathematical models that describe tumor-immune dynamics, highlighting their applications in understanding tumor growth, evaluating treatment strategies, and predicting immune responses. We also discuss the strengths and limitations of current modeling approaches and propose future directions for the development of more comprehensive and predictive models of tumor-immune interactions. We aim to offer a comprehensive guide to the state of mathematical modeling in tumor immunology, emphasizing its potential to inform clinical decision-making and improve cancer therapies.

**AMS subject classifications:** 92C42, 92B05, 92B10

**Key words:** Tumor immunology, mathematical oncology, tumor-immune interaction, mathematical model, computational simulation.

---

## 1 Introduction

Cancer, often described as a malignant tumor, represents a complex and dynamic ecosystem [12, 51, 66]. This ecosystem, known as the tumor microenvironment (TME) (Fig. 1),

---

\*Corresponding author. *Email addresses:* jzlei@tiangong.edu.cn (J. Lei), lichenghang@tiangong.edu.cn (C. Li)

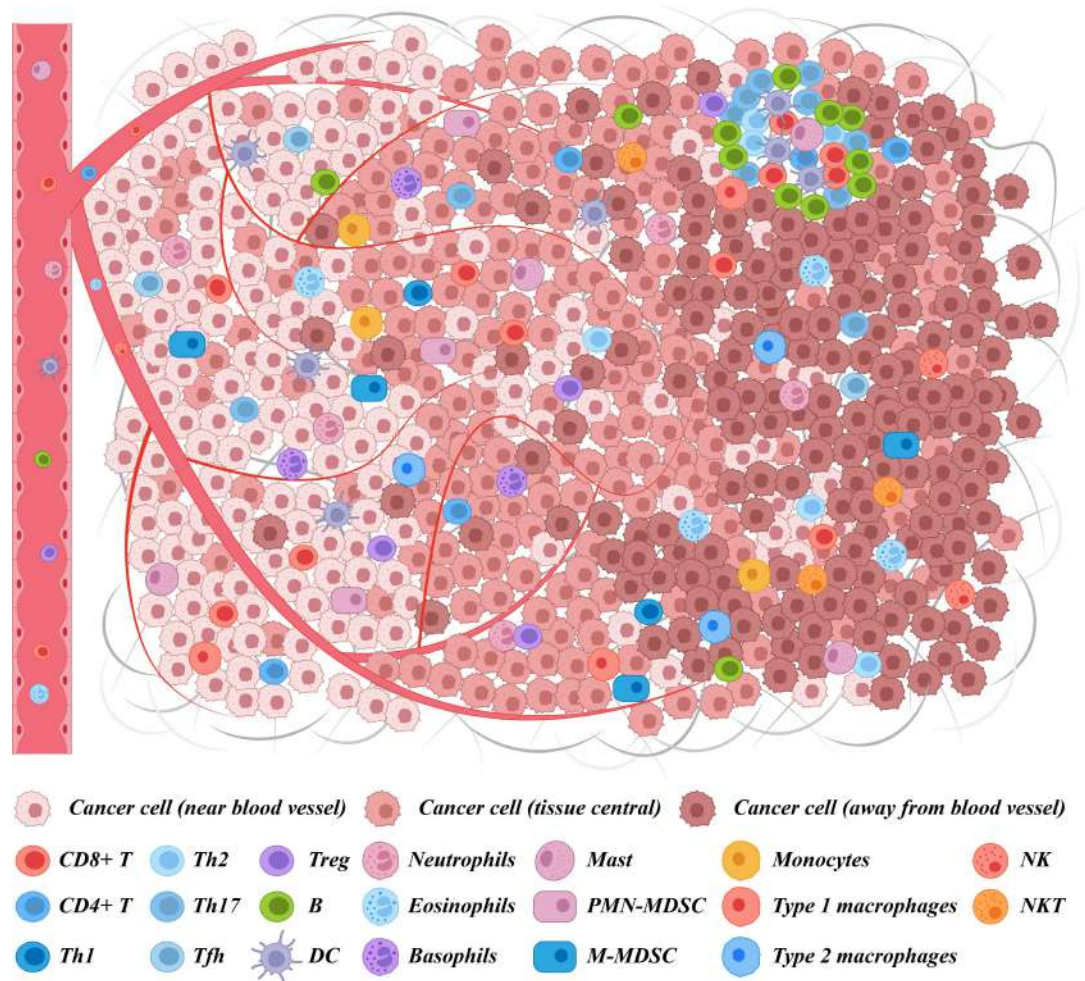


Figure 1: A global map of the tumor microenvironment.

comprises not only malignant tumor cells capable of rapid proliferation and metastasis but also includes various non-cancerous components such as immune cells, stromal cells, fibroblasts, and vascular endothelial cells [12, 66, 89, 119]. The TME plays a pivotal role in the processes of tumor growth, progression, metastasis, and drug resistance [66, 89, 119, 204, 239]. Within this environment, tumors actively shape conditions favorable to their survival and proliferation through mechanisms such as the secretion of cytokines, immune-modulating factors, and the expression of immune checkpoint molecules [133,240]. Meanwhile, immune cells infiltrate tumor tissue via migration, chemotaxis, and recruitment, influencing tumor development [133,218,227].

Tumor-immune system interactions are marked by a dynamic and complex interplay of mutual promotion, competition, and adaptation [93,236]. These interactions not only influence tumor growth, metastasis, and regression but also modulate the immune sys-