Off-Lattice Parallel Algorithm for Tumor Immunosurveillance Based on Cess-Finley Model

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1 Abstract

Agent-based models (ABMs) are powerful tools for simulating tumor-immune interactions. The Cess-Finley model, originally implemented in an on-lattice framework, simplifies computation but limits spatial resolution. This work presents an off-lattice parallel algorithm based on an extended version of the Cess-Finley model, allowing cells to move in continuous space for more realistic simulations. Parallelization using OpenMP improves performance, enabling large-scale experiments. A Multi-Parameter Sensitivity Analysis (MPSA) identifies influential parameters in tumor-immune dynamics, supporting future model calibration and therapeutic exploration.

2 Introduction

• **Cess-Finley model** simulates macrophage and T cell dynamics via cytokine-driven interactions in the tumor microenvironment [1].

• **Off-lattice**, **center-based models** provide more realistic simulations by allowing agents to move in continuous space but are computationally intensive [2].

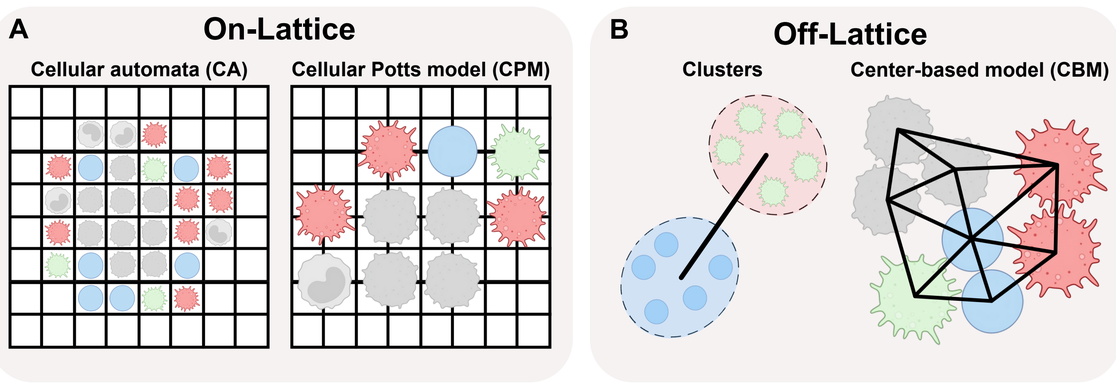


Fig 1. Examples of On-Lattice and Off-Lattice Agent-Based Models (ABMs).
(A) On-lattice models, where cells are restricted to fixed positions on a grid.
(B) Off-lattice models, where cells are represented in continuous space, allowing free movement without grid constraints [2].

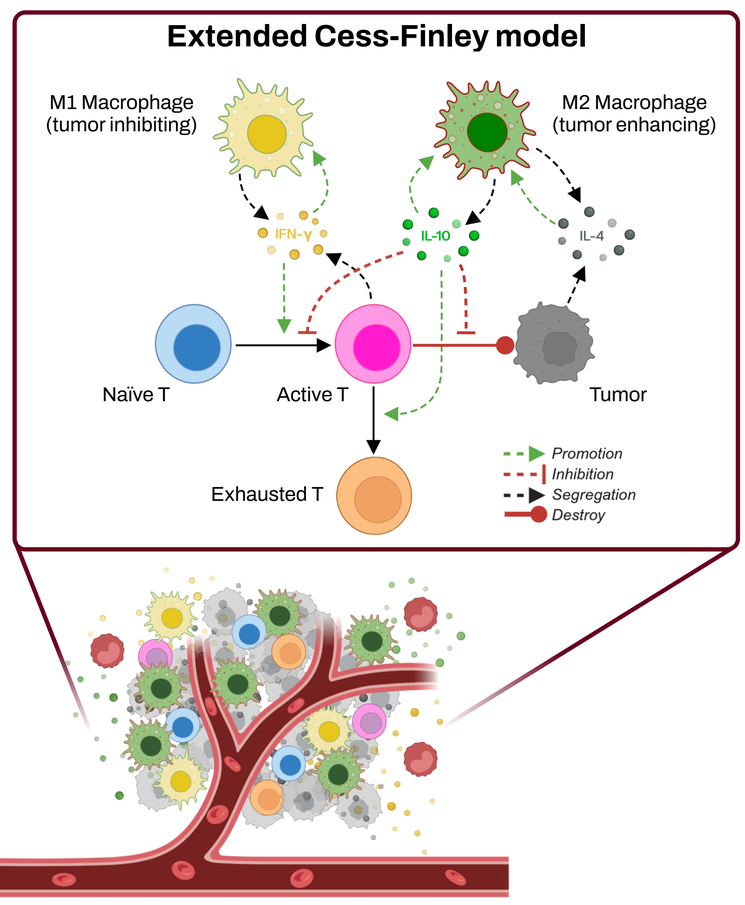
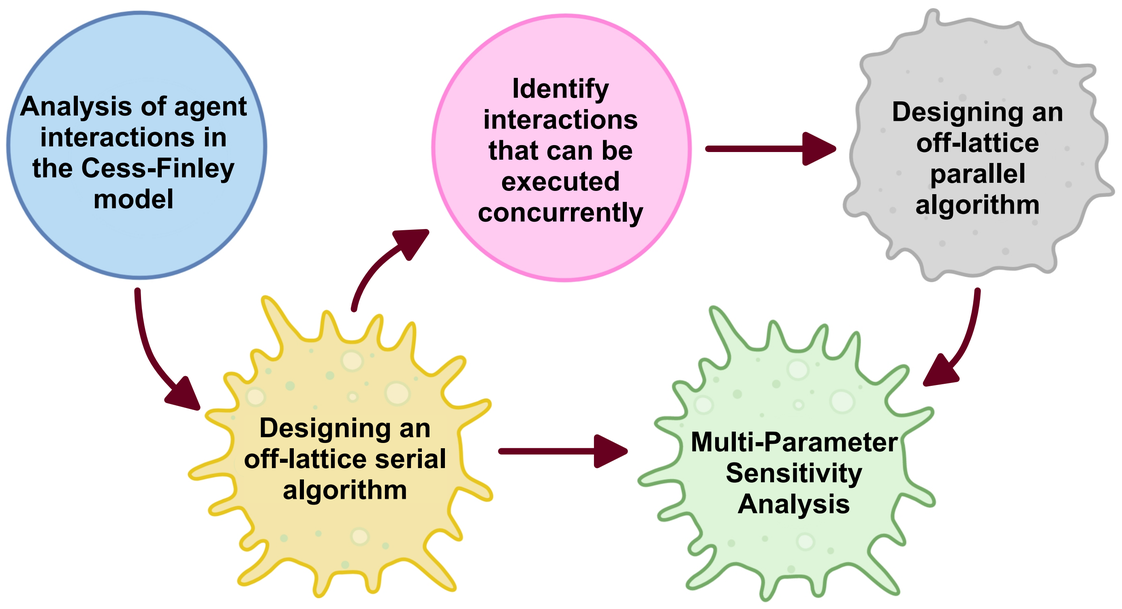


Fig. 2. Extended Cess-Finley Model in the Tumor Microenvironment (TME).
Cytokine-mediated interactions among macrophages, T cells, and tumor cells. Arrows indicate promotion, inhibition, segregation, or destruction [1][3].

3 Objective

• Design an off-lattice parallel algorithm using a center-based method for tumor immunosurveillance based on an extended Cess-Finley model.

4 Methodology



5 Results

PhysiCell uses **OpenMP** for multi-core parallelization [4]. We evaluated performance through **strong** and **weak** scaling experiments.

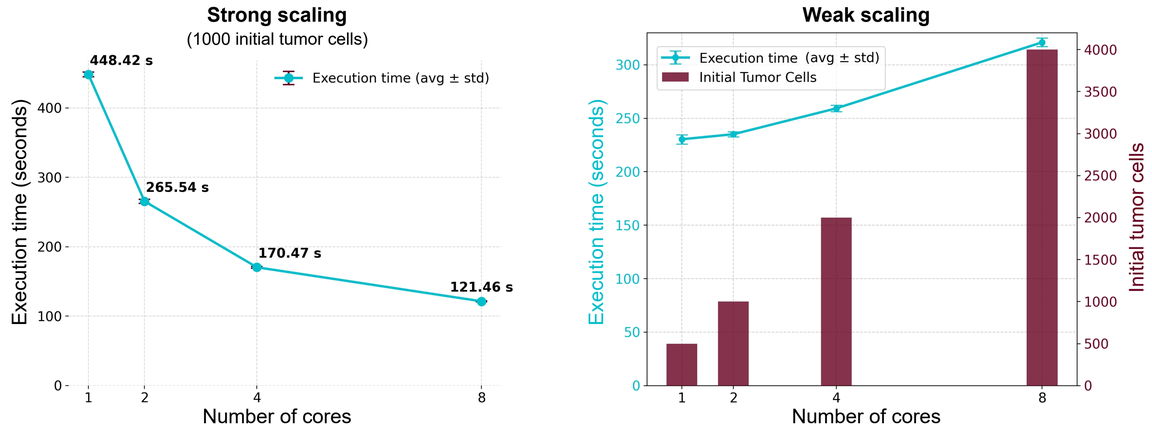


Fig. 3. Strong scaling: Execution time decreases with more cores for a fixed cell count.
Weak scaling: The number of cells increases proportionally with the number of cores. Execution time grows moderately as the computational load grows.

To explore how signal sensitivity affects cell behavior, we modulate the **half-max** parameter in the Hill function. By multiplying half-max by different factors (0.2, 0.5, 2.0, 5.0), we simulate varying sensitivity levels.

This parametrization enables us to systematically analyze how variations in the sensitivity of individual rules or their combinations influence tumor growth outcomes.

Therefore, we applied a **Multi-Parameter Sensitivity Analysis (MPSA)** to evaluate the impact of these factors on tumor-immune dynamics [5].

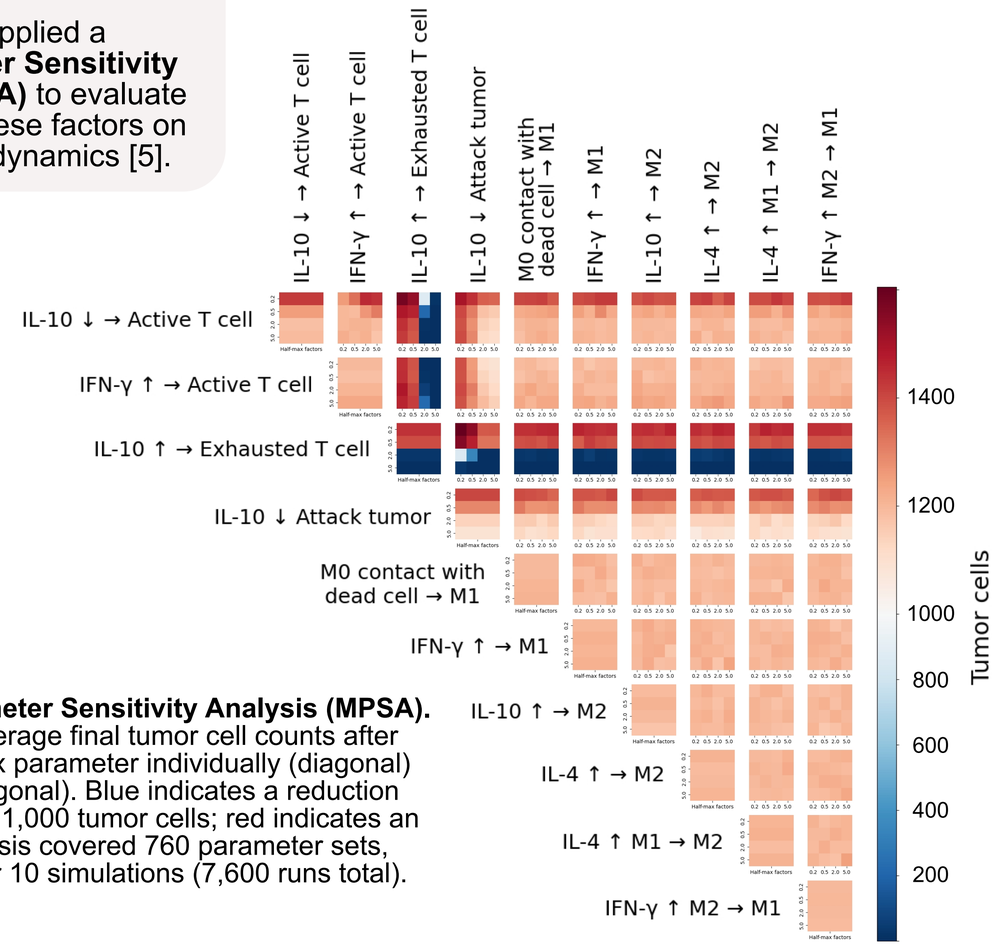


Fig. 4. Multi-Parameter Sensitivity Analysis (MPSA).
Heatmaps show average final tumor cell counts after varying the half-max parameter individually (diagonal) and in pairs (off-diagonal). Blue indicates a reduction relative to the initial 1,000 tumor cells; red indicates an increase. The analysis covered 760 parameter sets, each averaged over 10 simulations (7,600 runs total).

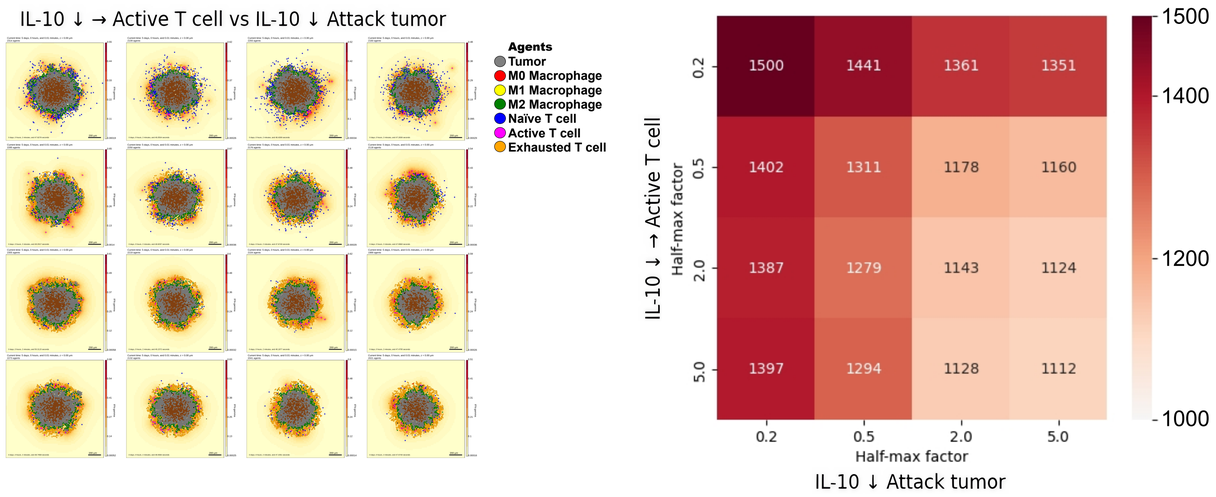


Fig. 5. Simulation snapshot and average tumor cell counts for IL-10 rule combinations.
(Left) Final snapshot of a single simulation for each of the 16 combinations between two IL-10 related rules: IL-10 reducing T cell activation vs IL-10 reducing attack rate on tumor cells. Each panel shows the spatial distribution of agents at the end of the simulation [4].
(Right) Average final tumor cell count across 10 runs for each of the 16 rule combinations.

6 Conclusions

• Parallelization with **OpenMP** improved computational performance, supporting larger-scale and more complex simulations.

• Multi-parameter sensitivity analysis (**MPSA**) revealed key parameters driving immune-tumor interactions, aiding future efforts in model calibration and therapeutic design.

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Note: Images depicting cellular interactions were created with BioRender.com