Agent-Based Simulation of CAR-T Cell Therapy Using BioDynaMo

Progress update of Google Summer of Code Project 2025



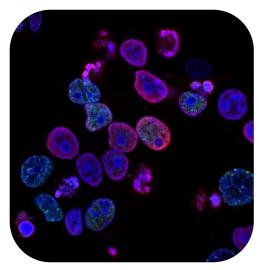
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CAR-T Therapy & the Challenge

CAR-T therapy: A type of immunotherapy that engineers T-cells to recognize and kill cancer cells.

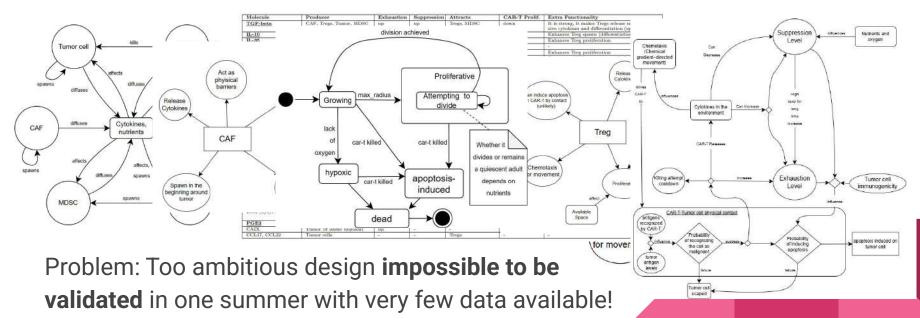
- Proven effective in leukemia and other hematological cancers.
 - In the literature, many robust models—typically based on differential equations—simulate CAR-T treatment in blood cancers.
- However, CAR-T still struggles in solid tumors due to unique tumor microenvironmental factors.
 - Researchers need models to try different treatment techniques and scenarios in order to improve CAR-T performance. However, very few models exist for these types of cancers, and much less data is available.



CAR-T Simulation in BioDynaMo

<u>Objective</u>: Implement solid tumor CAR-T treatment using an agent-based simulation on **BioDynaMo**, a high-performance, open-source simulation platform ideal for capturing these microenvironmental interactions.

In the beginning, I designed an agent-based model on my own, by reading papers and trying to include all relevant biological dynamics. And I even implemented on BioDynaMo a third of it...



The Nature Paper

- Agent-based simulation modeling CAR-T cell therapy in in vitro tumor-derived organoids.
- Aims to allow testing of multiple therapeutic strategies without the cost and time of lab experiments.
- The research team that wrote it spent six months solely tuning hyperparameters with real data!
- <u>Aim</u>: Develop a similar simulation simulation in BioDynaMo and replicate their results.
 - Main advantages of BioDynaMo:
 - Faster simulations -> More scenarios can be tested
 - Code is much more accessible, modular and suitable for future extensions

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scientific reports

(f) Check for updates

OPEN In silico study of heterogeneous tumour-derived organoid response to CART-cell therapy

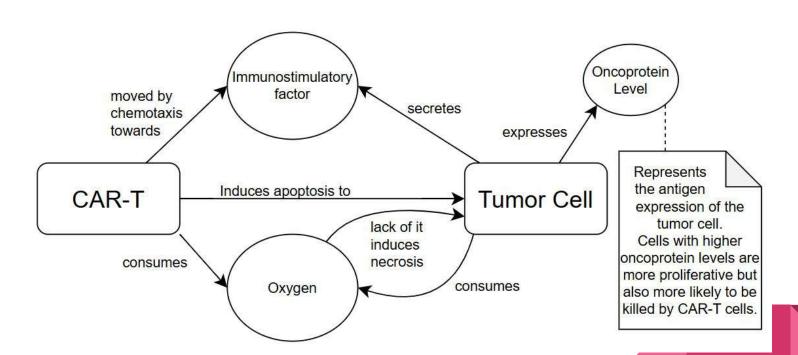
Luciana Melina Luque ¹², Carlos Manuel Carlevaro^{2,3}, Enrique Rodriguez-Lomba⁴ & Enrique Lomba⁵

Chimeric antigen receptor (CAR) T-cell therapy is a promising immunotherapy for treating cancers. This method consists in modifying the patients T-cells to directly target antigen-presenting cancer cells. One of the barriers to the development of this type of therapies, is target antigen heterogeneity. It is thought that intratumour heterogeneity is one of the leading determinants of therapeutic resistance and treatment failure. While understanding antigen heterogeneity is important for effective

Luque, L.M., Carlevaro, C.M., Rodriguez-Lomba, E. et al. In silico study of heterogeneous tumour-derived organoid response to CAR T-cell therapy. *Sci Rep* 14, 12307 (2024).

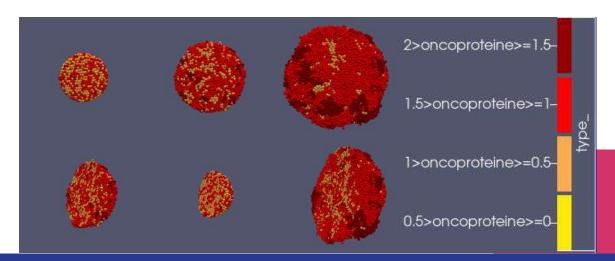
https://doi.org/10.1038/s41598-024-63125-5

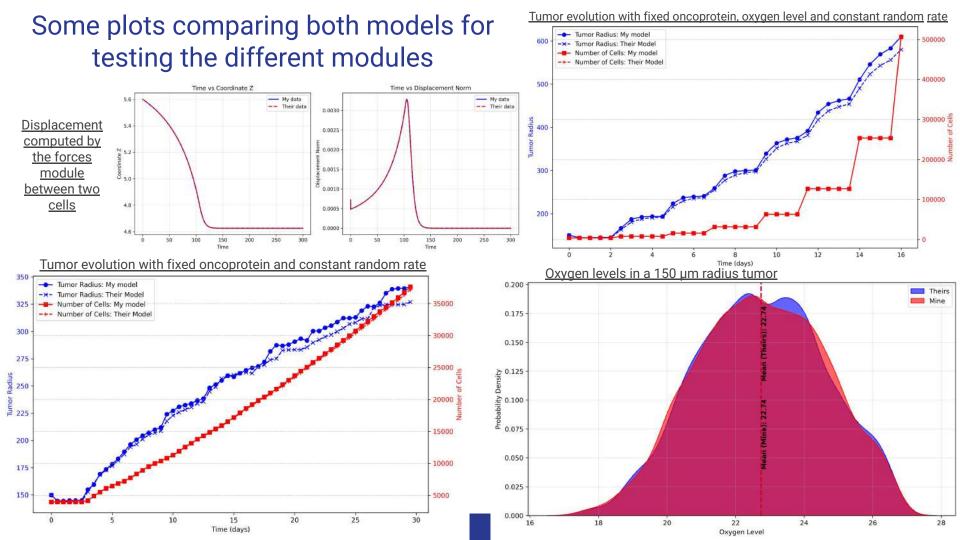
The model



What have I achieved so far?: Tumor Replication

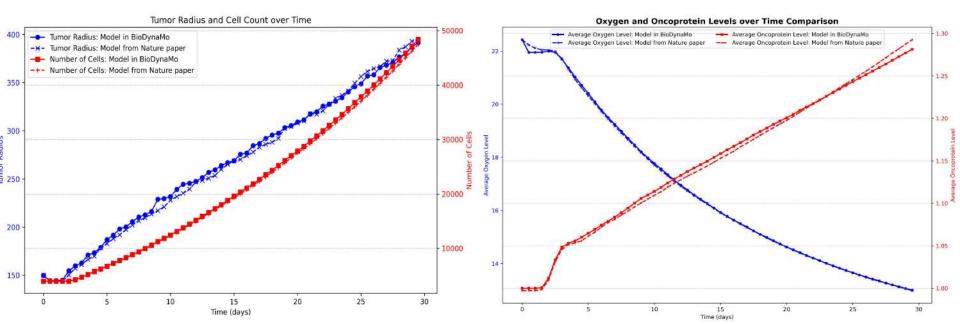
- Tumor inspired by and calibrated using liver carcinoma data.
- Main components already implemented:
 - Chemical diffusion module solving the corresponding differential equations, with agents consuming and secreting substances.
 - Forces module computing repulsion between overlapping cells and adhesion dynamics.
 - Tumor cell agent with state control, volume changes, and division influenced by oxygen and oncoprotein levels, as well as apoptosis and necrosis with swelling and lysis phases.





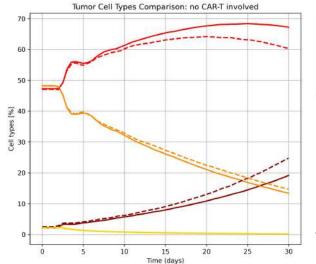
Evolution of a 150 µm radius tumor with no CAR-T treatment: models comparison

- As the tumor grows:
 - The oxygen levels lessen: more cells means more oxygen consumption.
 - The average oncoprotein level increases: cells with higher levels are more proliferative and since the oncoprotein is inherited in division the average value goes up in time.



Oncoprotein levels are continuous, but cells are grouped into four types $(1-4, high \rightarrow low)$.

- <u>Type 1</u> cells: they are the most proliferative so their proportion in the tumor increases.
- Type 3-4 cells: divide less frequently and lose oxygen in a resource-competitive environment. Therefore become less and less common.



Type 1 (Model in BioDynaMo)
Type 2 (Model in BioDynaMo)
Type 3 (Model in BioDynaMo)
Type 4 (Model in BioDynaMo)
Type 4 (Model in BioDynaMo)
Type 1 (Model from Nature paper)
Type 2 (Model from Nature paper)
Type 3 (Model from Nature paper)
Type 4 (Model from Nature paper)

Differences are because of the random initialization in the oncoprotein levels of the first 3960 tumor cell.

Performance Comparison:

Preliminary execution time comparison for a 30 days simulation (AMD Ryzen 5 3600, 6 cores / 12 threads, 16 GB RAM):

- Mine: ≈ 8,982 hours
- Theirs: ≈ 18,848 hours
 - → My (yet unoptimized) model in BioDynaMo is more than **twice as fast**.

What's the next goal?

- Add CAR-T (already in progress)
- Add parameter files to allow modification without recompiling
- Clean and polish the code
- Write a scientific-style document describing the model, and results replicating the Nature paper findings.
- In the long term: Extend the simulation to include immunosuppressive chemicals and secreting agents (T-regs). Compare different patient and treatment scenarios for example:
 - Reduce oxygen levels to study hypoxia and necrosis (already implemented).
 - Study higher proliferation rates, as occurs in pediatric tumors.
 - Some people present with more rigid tissues, which result in higher cell forces that can affect CAR-T tumor infiltration.

