Lux: Computational Tools for Tumor Analysis

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Abstract

Computational modeling can be an expensive task, especially for healthcare institutions. Moreover, current mathematical analysis tools for oncology-related complexities can be inefficient and costly. Lux is a mobile application programmed to simplify statistic forecasting for tumor growth, heterogeneity, and various immunotherapies, including Chimeric antigen receptor (CAR) T-cell therapies, Cytotoxic T lymphocyte (CTL/$CD8^+$ T) treatments, and CTL/$CD8^+$ T-cell treatments assisted by $CD4^+$ T-cell stimulation.

1 Introduction

Lux is the first software program in the Luminosity project series. The main objective of Luminosity is to expose the uncertainties of cancer progression in the human body in order to minimize potential risks. Tumor growth is complex and involves various factors that must be taken into consideration in order to accurately predict its development. Examples include the tumor microenvironment (TME) and angiogenesis. The intrinsic diversity present in cancer tissue, however, is effectively represented by spatial heterogeneity and biological entropy. This is why Lux was designed to analyze entropy values for gradient densities.

In addition, immunotherapy can involve many kinds of cell types, including lymphocytes T and B, natural killer (NK) cells, and tumor-infiltrating lymphocytes (TILs). The first version of Lux has been programmed to model three case scenarios, which have been studied to be choice therapies for various tumor types. The combination of these growth factors can describe at the basic level how tumors mature and reduce with applied treatment plans.

2 Methods

2.1 Tumor Growth

Matured tumors experience decreased nutrient consumption due to the finite nature of its growth. To capture the asymptotic-like behavior of late-stage cancers, two models are directly considered: logistic and logarithmic functions. Logarithmic functions can model the decelerated growth of exhausted tumor progressions because it is naturally concave down within its domain.

However, such models are not fit to describe the exponential tumor size increase during the initial stages of a cancer. The logistic model does, however, more accurately represent this characteristic. The mathematical model used in Lux to quantify tumor growth is the Gompertz sigmoidal function:

$$V(t) = V_0 e^{\frac{\alpha}{\beta}(1-e^{-\beta t})}$$

Let V_0 be the initial tumor size (in mm^3, cm^3, or cells), α the intrinsic growth rate (per day), β the deceleration rate (per day), and t as the time (in days) at which to forecast the tumor size. Supporting research is taken from Vaghi, Cristina, et al. [5].

2.2 Tumor Heterogeneity

The Shannon entropy formula is used by Lux to solve the "spatial heterogeneity of tumor density within each tumor region" [3]. The model receives two parameters. The first parameter is the total number of discrete cell types or density levels, which shall be greater than one. In a study by Kleinberger et al., heatmaps were produced using Gaussian blurring to determine which areas of a tissue sample were tumorous and non-tumorous [3]. After processing the density map, a Shannon entropy model may be used to compute the level of heterogeneity or randomness within a particular tumor region. The model is defined as:

$$H(x) = -\sum_{i=1}^{n} p(x_i) \log_2 p(x_i)$$

Let n be the total number of cell type intensities within a tumor region, $p(x_i)$ be the probability or proportion of intensity for a cell type i, x as the intensity level of one cell type, and H as the Shannon entropy value.

For consistency, Lux was also designed to normalize the entropy value using a min-max function so that the solution is bounded between 0 and 1. A normalized H value of 0 means the tumor has no heterogeneity, and a value of 1 means the tumor is completely heterogeneous. This is achieved to determine whether the computed heterogeneity is low, moderate, or high for a certain tumor region. The model used to normalize the heterogeneity constant has been proposed in a paper by Wilcox [6].

2.3 CAR-T Cell Therapy

The CAR-T treatment efficacy model used by Lux is a simplified version of an equation proposed in a paper by Barros et al. [1]. The ordinary differential equation (ODE) provided can be organized into two terms: the logistic tumor growth term and the CAR-T killing term. Lux uses the base equation, but modifies the CAR-T killing term into the form of a Michaelis-Menten kinetics model. The complete equation programmed into Lux is:

$$\frac{dT}{dt} = rT(1 - \frac{T}{K}) - k\frac{CT}{s+T}$$

Let r be the tumor growth rate (per day), k be the CAR-T kill rate (per cell per day), s be the half-saturation constant (in number of cells), T be the tumor cell population (in cells), C be the CAR-T cell population (in cells), and K as the carrying capacity (in cells).

For clarification, s represents the number of tumor cells at which CAR-T cells become ineffective. When the number of tumor cells equals the half-saturation constant, it means the CAR-T cells are operating at half their original effectiveness. Moreover, the carrying capacity value K represents the maximum tumor size (in mm^3, cm^3, or cells) at which the human body can biologically sustain.

2.4 CTL/CD8$^+$ T Therapy

To effectively model immunotherapy treatments using Cytotoxic T lymphocytes (CTLs), the Kuznetsov model, as discussed in a paper by Mahlbacher et al. [4], is implemented in Lux to compute the tumor growth rate when CTL effector cells are activated and employed. Similar to the CAR-T therapy model, the CTL-based tumor growth ODE is comprised of two main parts: the logistic tumor growth term and the CTL killing term. The complete equation programmed in Lux is:

$$\frac{dT}{dt} = rT(1 - \frac{T}{K}) - nET$$

Let r be the tumor growth rate (per day), n be the CTL kill rate (per cell per day), T be the tumor cell population (in cells), E be the CTL effector cell population (in cells), and K be the carrying capacity of the tumor (in mm^3, cm^3, or cells).

2.5 CTL-CD4$^+$ Response

The mathematical ODE model used by Lux to describe the interaction between CTLs and CD4$^+$ T helper cells has also been discussed by Mahlbacher et al. [4]. CD4$^+$ T helper cells are important because they stimulate CTL activation and promote macrophage and interleukin (IL) employment [4]. The complete equation models the growth rate of CTL effector cells:

$$\frac{dE}{dt} = kET - dE + pEH$$

Let k be the CTL cell proliferation rate (per cell per day), d be the CTL death rate (per day), p be the CTL activation rate (per cell per day), T be the tumor cell population (in cells), E be the CTL effector cell population (in cells), H be the CD4$^+$ cell population (in cells).

3 Discussion

The CAR-T therapy model uses a simplified version of the originally proposed ODE since the T and C cell population parameters were dynamic variables. The parameters have been treated as constants in implementation. Future versions of Lux may propose to include relevant growth models for an improved coverage of more case scenarios.

Tumor biomarkers are another area of exploration for this project. I propose a set of correlation and regression models to analyze and forecast tumor progression using biomarker data. This type of analysis is often more effective in a tumor region with low heterogeneity.

A study done by Jiang et al. suggests the use of Dijkstra's shortest path algorithm to find cancer-related genes in a protein-protein interaction (PPI) network [2]. A future implementation for Lux may use Dijkstra's algorithm to map out likely pathways for metastatic growth to occur using graph theory. Potential usage may include the prediction of malignant lymphoma progressions using a graph network to simulate the lymphatic system.

4 Conclusion

With the goal of informing medical professionals and patients of potentially increasing tumor complexities, I genuinely hope that Lux, and the Luminosity series as a whole, can be a light to those who have none, whose hope rests in obscurity and uncertainty. May this project series be of service to the betterment, treatment, and recovery of cancer patients around the world.

References

[1] Barros, Luciana, et al. *CARTmath—A Mathematical Model of CAR-T Immunotherapy in Preclinical Studies of Hematological Cancers*, https://doi.org/10.3390/cancers13122941.

[2] Jiang, Yang, et al. *Identifying Gastric Cancer Related Genes Using the Shortest Path Algorithm and Protein-Protein Interaction Network*, https://doi.org/10.1155/2014/371397.

[3] Kleinberger, Markus, et al. *Density and entropy of immune cells within the tumor microenvironment of primary tumors and matched brain metastases*, https://doi.org/10.1186/s40478-025-01939-8.

[4] Mahlbacher, Grace, et al. *Mathematical Modeling of Tumor-Immune Cell Interactions*, https://doi.org/10.1016/j.jtbi.2019.03.002.

[5] Vaghi, Cristina, et al. *Population modeling of tumor growth curves and the reduced Gompertz model improve prediction of the age of experimental tumors*, https://doi.org/10.1371/journal.pcbi.1007178.

[6] Wilcox, Allen. *Indices of Qualitative Variation*, Oak Ridge National Lab, https://doi.org/10.2172/4167340.