Cellular-Level To Biomass Eidomics Simulation For Hypothesis Generation In Lung Cancer

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Rationale

There has been significant new information regarding biologic sciences in the last decade. This new information is in cell processes and in how cells interact with each other in whole tissues, organs, and the body, in both health and disease states. We created a new approach, termed eidomics ("eidos" means image or form), to managing and communicating all of this complex data through three dimensional and four dimensional interactive pictorial representations.

We postulate that much of biology is actually governed by very simple rules – such as life or death, or when a cell divides it forms two cells – although these simple rules can be made increasingly complex under some circumstances. Thus we set out to create a model using simple rules to recreate complex behaviors.

Methods

We chose to use a combination of computer simulation and animation in order to create the eidomic model. The simulation engine approaches the challenge of simulating a tumor from the ground up, starting with a single cell and growing the tumor to many thousands of cells in size utilizing simple rules that govern cell behavior and interactions, and these rules are modifiable through simulation parameters via a GUI. The simulation results are displayed in a style of animation similar to that used in video games, allowing the user to observe tumor growth over time, to inspect it from different viewpoints. Other cells such as inflammatory cells can be added.

Results

The eidomic model we have developed has produced results that seem to be consistent with findings from bench research done in vivo and in vitro by our and other labs. The model has been able to realistically recreate complex cancer behaviors viewed through direct imaging methods.

Conclusions

The eidomic model has proven useful already in highlighting areas of cancer development where our knowledge is limited. Simulations run using cell movement speeds suggested in literature resulted in rates of metastasis much higher than expected. While the simulation is now at a point where it is useful for hypothesis generation and testing, our future plan is to develop the model into an accurate predictor of tumor growth. In the future, we plan to expand the scope of the model from a single alveolus to the entire lung, as well as to use data from scans of actual tumors in patients as a starting point for generating predictions about the tumor's growth.

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