

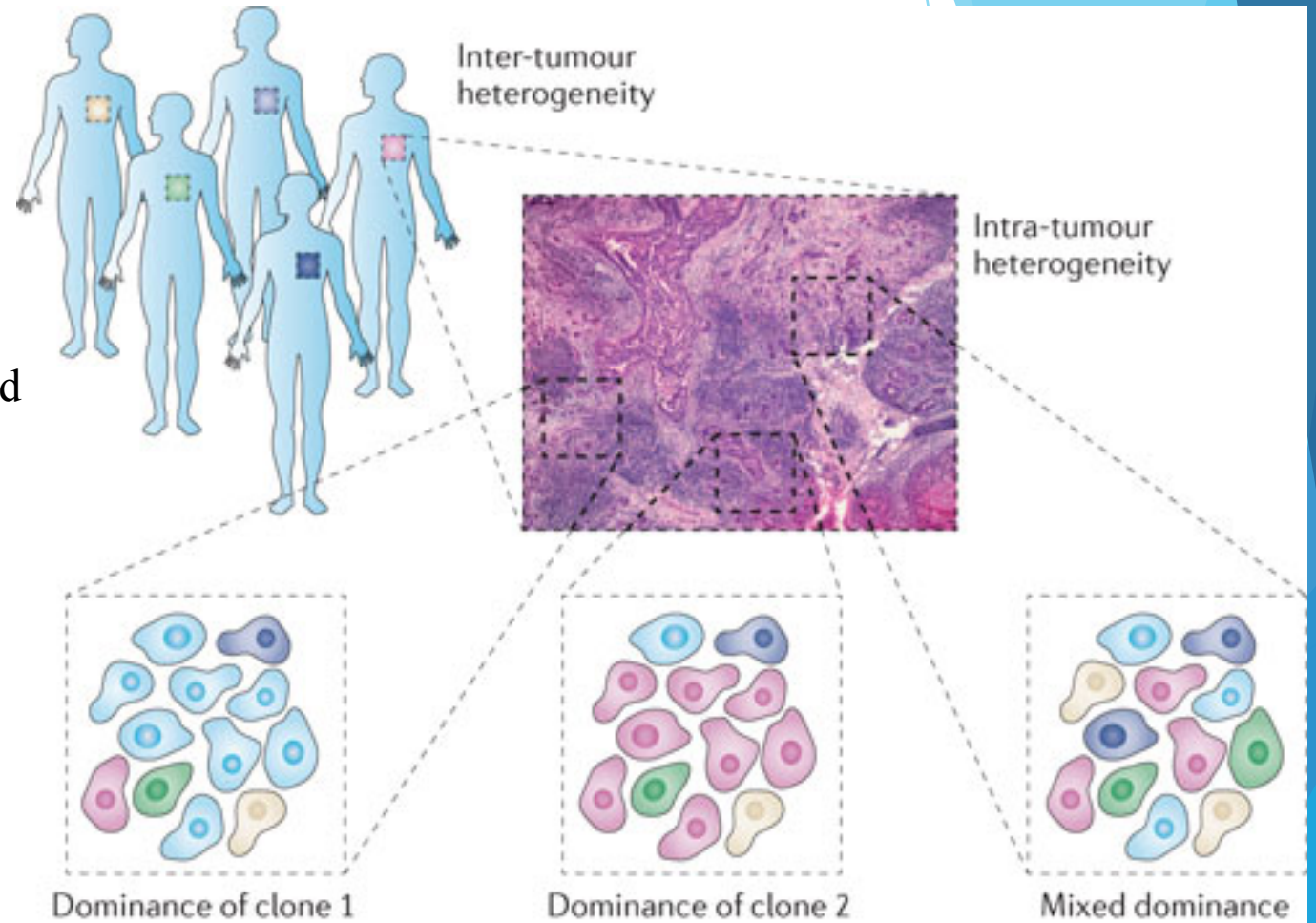
Genomic Data-Guided Mathematical Modeling of Cancer

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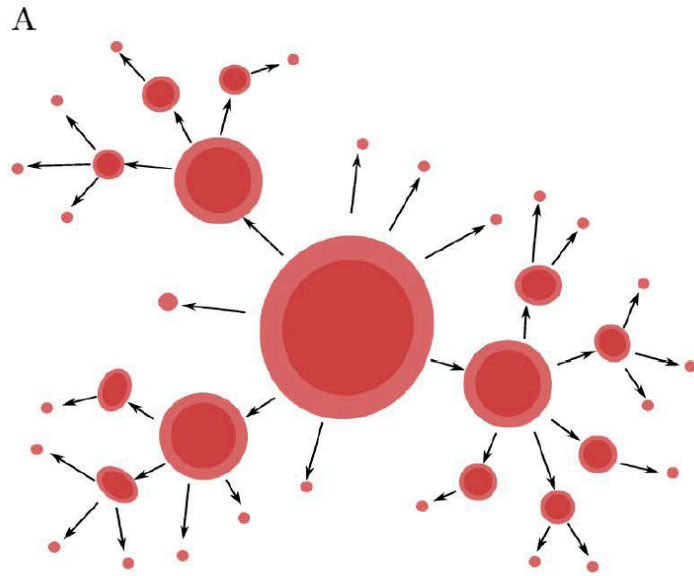
Introduction

- **Cancer:** The uncontrolled growth of abnormal cells in the body.
- It is the second leading cause of deaths in the US.
- In 2014, 2,626,418 deaths were recorded and 22.5 % of these deaths can be attributed to cancer.
- **Intra-tumor heterogeneity** causes:
 1. Spatial restrictions
 2. Composition restrictions
- Diagnoses depend heavily on biopsies, which may/may not accurately reflect the tumor as a whole.

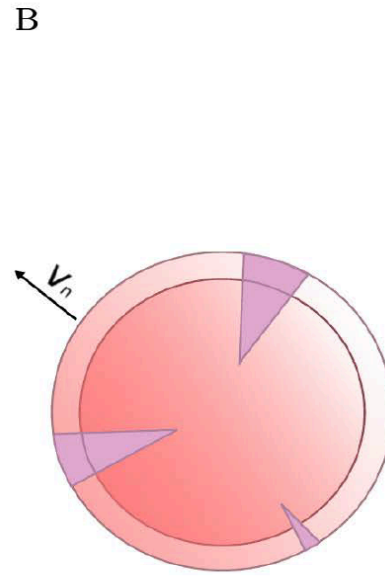


Models Used

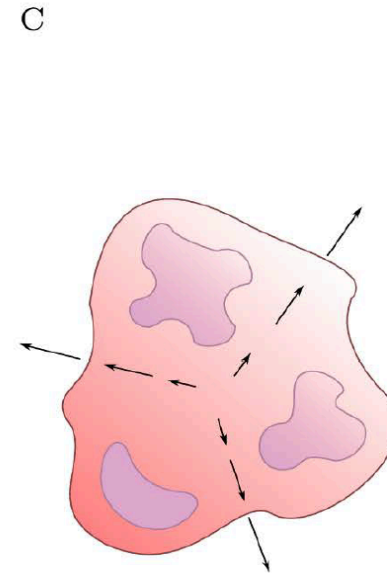
- Based on model and method from Waclaw (2016)



- A. Tumor composed of discrete microlesions.
The microlesions:
1. Increase in size
 2. Seed other microlesions



- B. Surface Growth.
Only a layer on the surface of the cell replicates radially outward.



- C. Volumetric Growth.
Every cell replicates and pushes outward.

Formulas Used

General Formula:

$V_{\text{tot}}(t)$ Total volume of the tumor

$$V_{\text{tot}}(t) = \sum_{n=1}^{\infty} \int_0^{\infty} f_n(a, t) V_n(a) da,$$

$\langle n(t) \rangle$ Average number of drivers per cell

$$\langle n(t) \rangle = \frac{1}{V_{\text{tot}}(t)} \sum_{n=1}^{\infty} n \int_0^{\infty} f_n(a, t) V_n(a) da.$$

In the case of single-driver surface growth,

$$V_{\text{tot}}(t) = \frac{1}{3M} e^{Gt} + \frac{2}{3M} e^{\frac{-Gt}{2}} \cos\left(\frac{\sqrt{3}}{2}Gt\right) - \frac{1}{M},$$

Where:

$f_n(a, t)$: The expected number of microlesions of age a at time t

$V_n(a)$: Total volume of a microlesion of type n at age a

G : Asymptotic growth rate

M : Migration Probability

Results Produced

Figure 1. Volume vs Time using Single Driver-Surface Growth Method

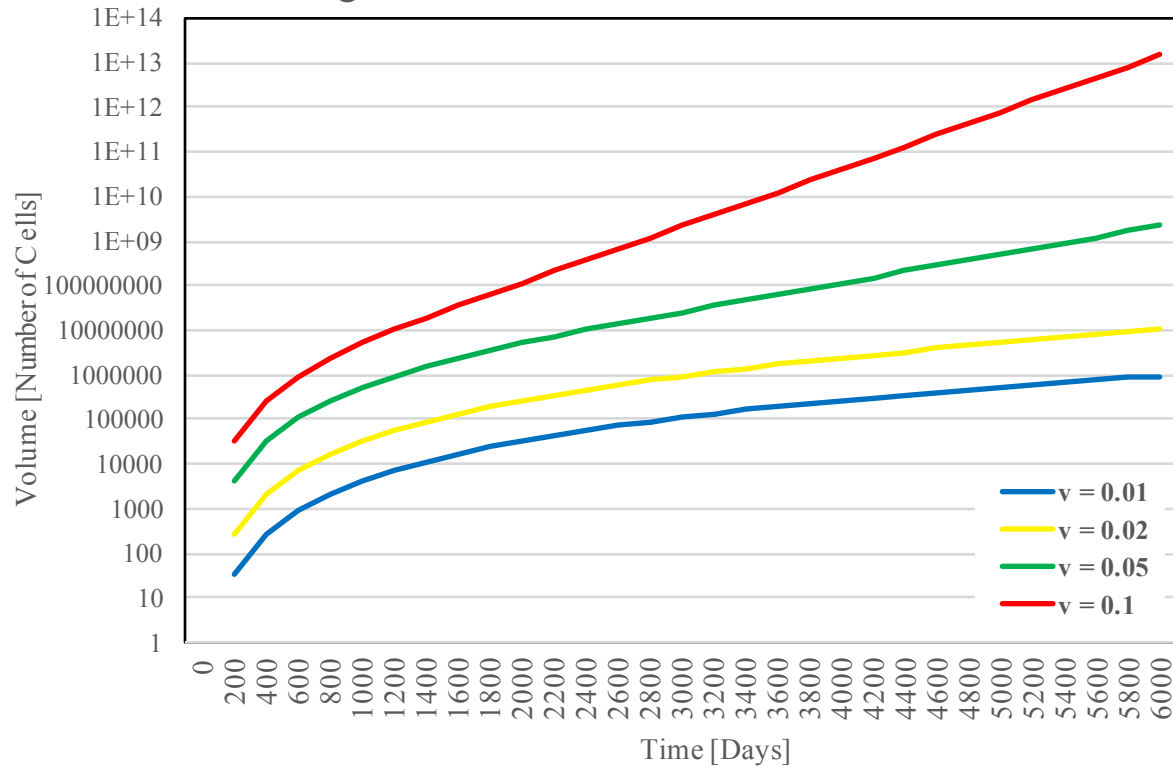


Figure 1. Using the single driver-surface growth method. Figure 1 is a plot of the relationship between volume and time when **velocities vary** and **migration probability is constant**.

Figure 2. Volume vs Time using Single Driver-Surface Growth Method

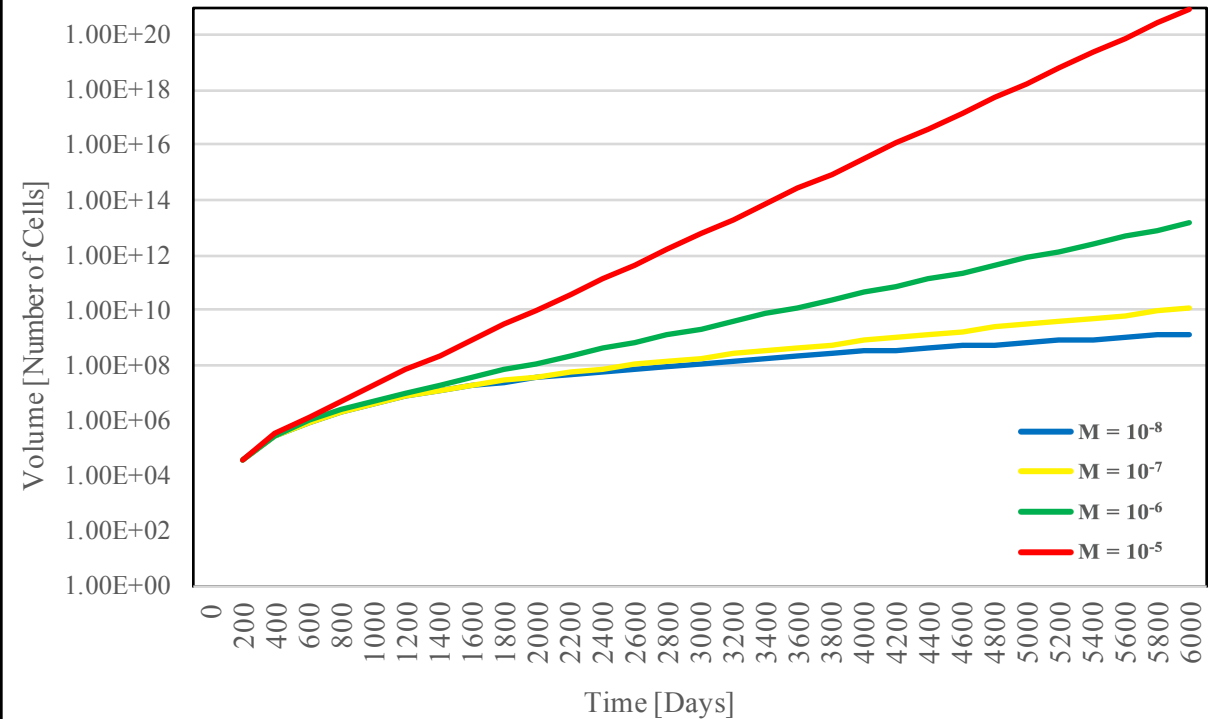


Figure 2. Using the single driver-surface growth method. Figure 2 is a plot of the relationship between volume and time when **migration probabilities vary** and **velocity is constant**.

Results Produced

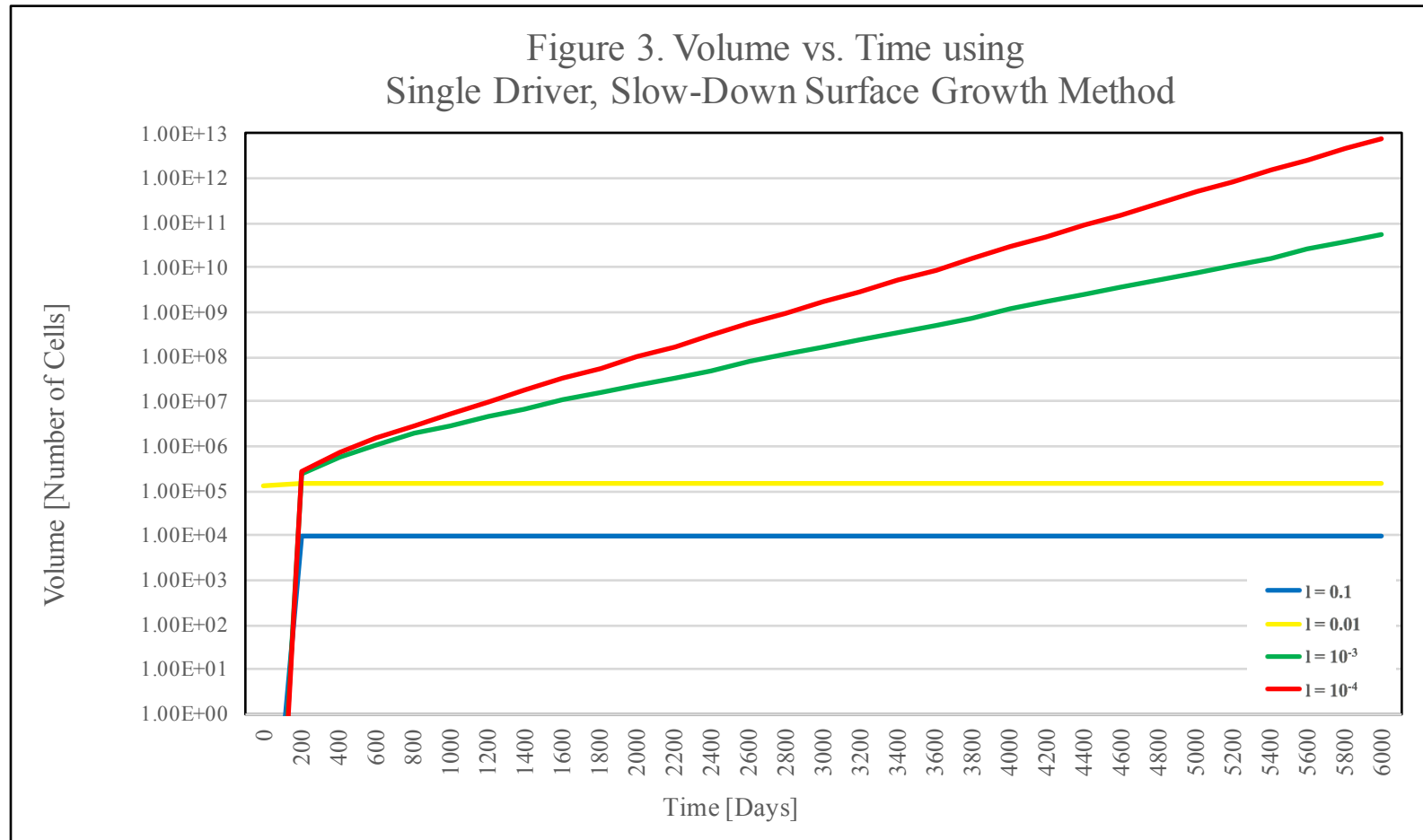
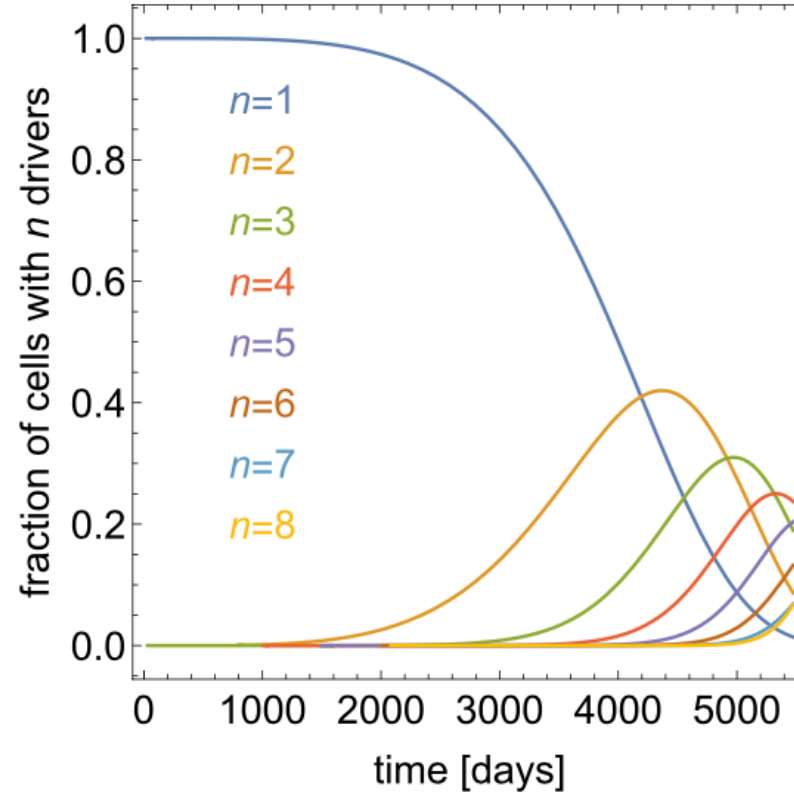
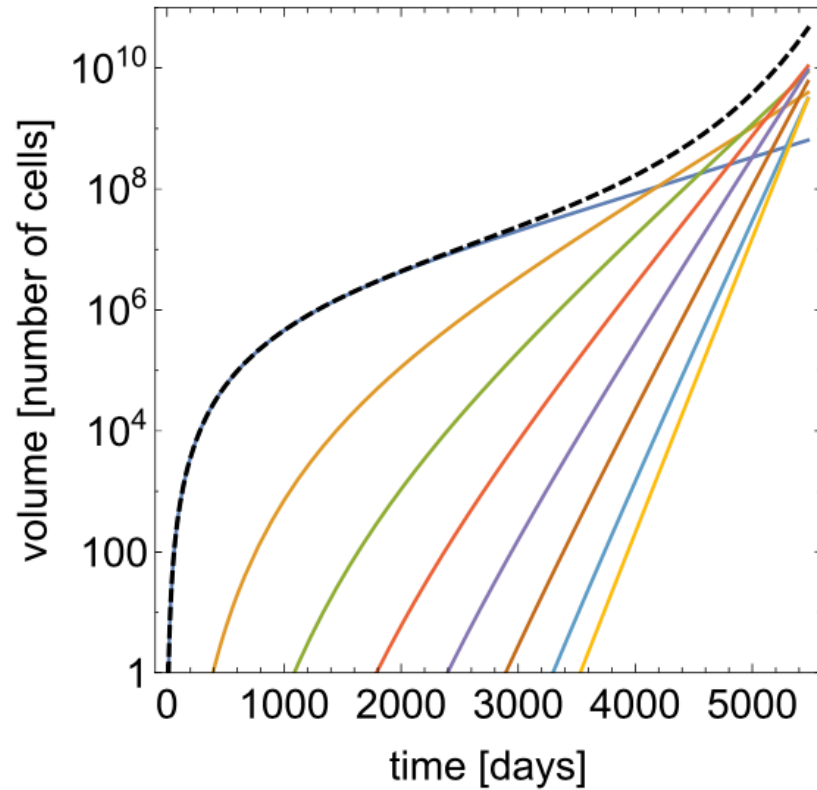


Figure 3. Using the single driver-slow-down surface growth method. Figure 3 is a plot of the relationship between volume and time with **constant migration probability**, **constant velocity**, and **varying time scales of growth decrease**.

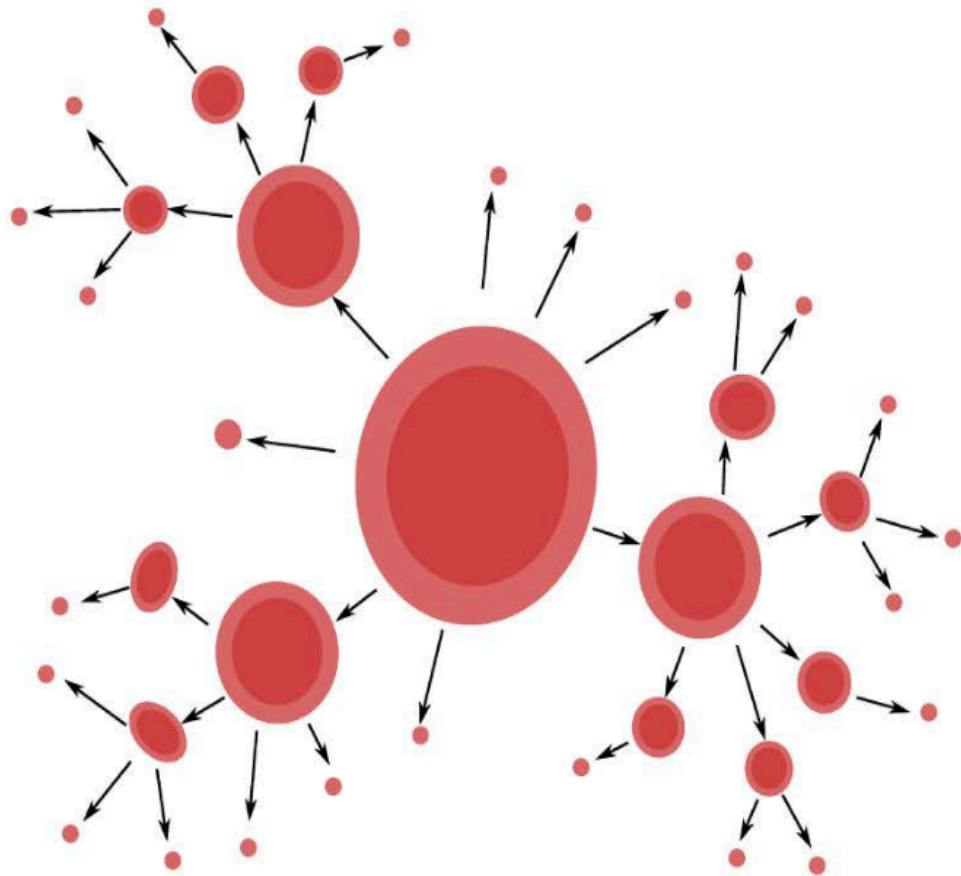
Work in Progress



- Total volume and fraction of cells with n drivers in the case of surface growth.
- Colored lines represent subpopulations of cells within a tumor with n number of mutations.

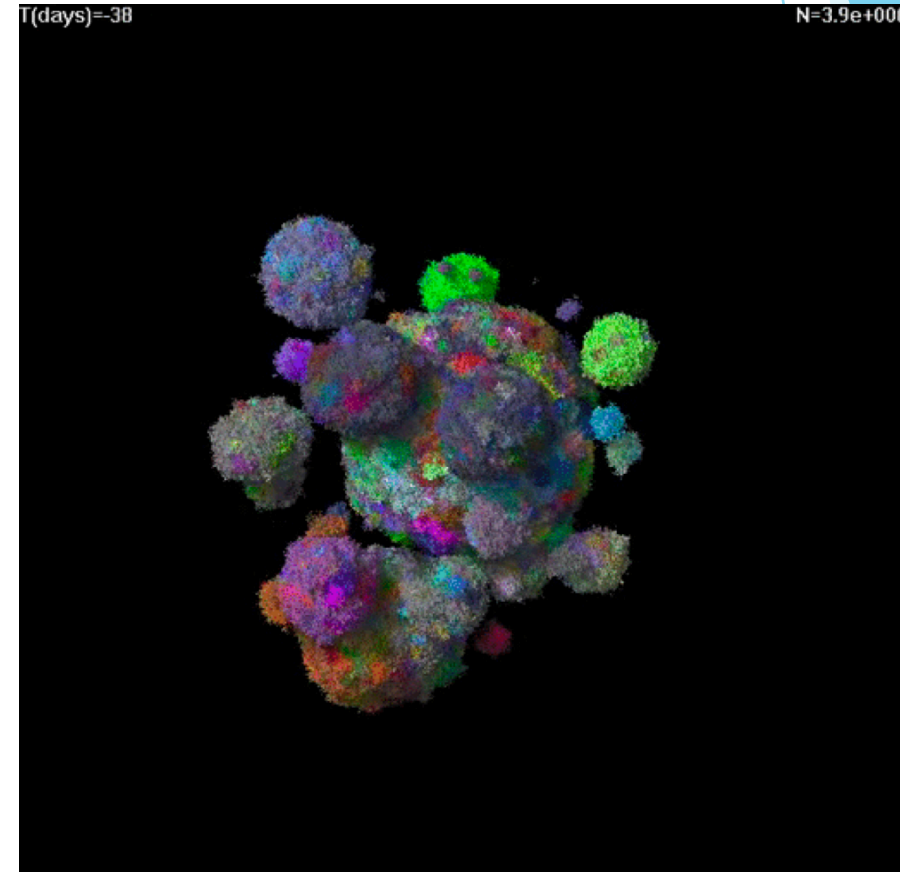
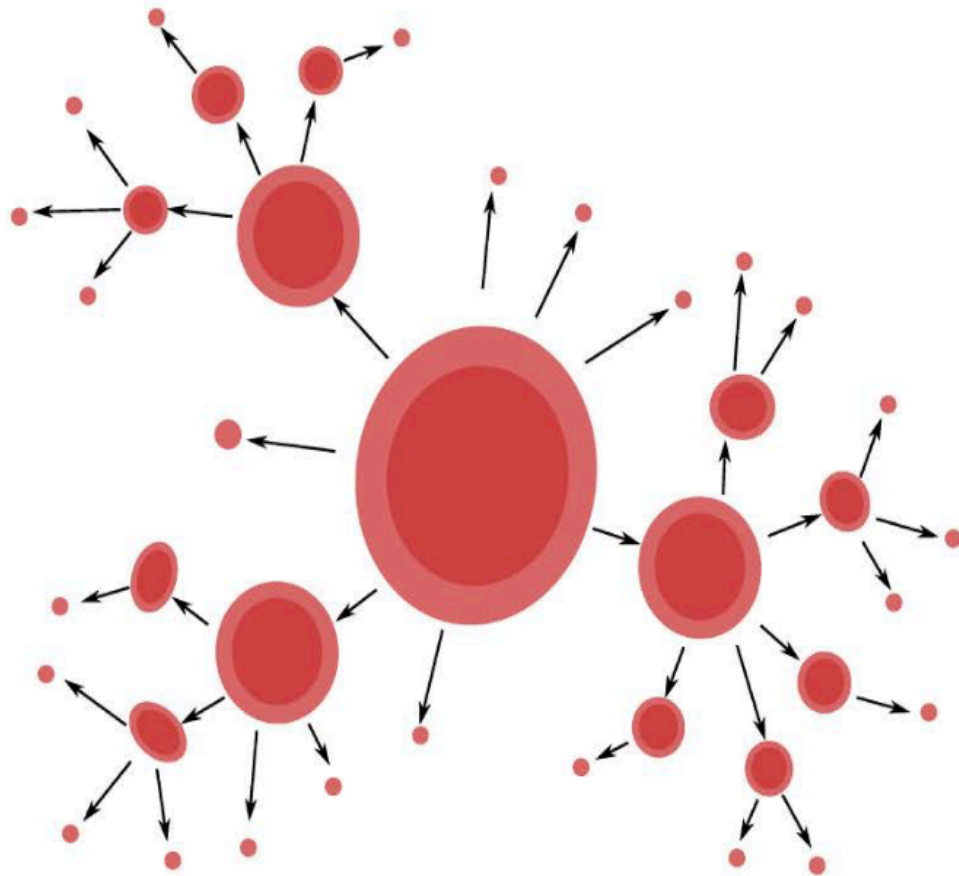
Future Plan

- Research on cancer growth is limited to 2D.
- 3D models of tumors, today, do not accurately represent the true nature of the tumor.



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Acknowledgements

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Works Cited

- Marusyk, A. et al. "Intra-tumor heterogeneity : a looking glass for cancer?" *Nature Reviews Cancer*, vol. 12, no. 5, 2012, pp. 323-334.
- Nichols, Hannah. "The top 10 leading causes of death in the United States." *Medical News Today*. MediLexicon, Intl., 23 Feb. 2017. Web. 11 Jul. 2017. <http://www.medicalnewstoday.com/articles/282929.php>
- Paterson, C. et al. An exactly solvable, spatial model of mutation accumulation in cancer. *Sci. Rep.* 6, 39511; doi: 10.1038/srep39511 (2016).
- Waclaw, Bartek. "Spatial models of cancer." Homepage of Bartek Waclaw, <https://bartekwaclaw.wordpress.com/biophysics/spatial-models-of-cancer/>