

University of Hull

600093 - Computational Science

Report

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1 | Introduction

This report shall show the steps taken to simulate the growth of cancer cells in a tissue using the Gompertz Equation to model growth.

Growth for individual cells can be modelled using a differential equation so that the number of cells is a function of time. The Gompertz Model of Cell Growth works well in this application because it can accurately model the non exponential nature of cell growth (Tatro n.d.). Once an area has reached it's capacity no more tumour cells can form, hence the cells must begin to move through a tissue. This movement can be simulated using simple random walk algorithm or more complex genetic algorithms.

This paper specifically shall analyse the computational complexity of such models and evaluate the differences between simulation techniques. The underlying implementation shall be investigated, including random algorithms and accuracy of simulations on computer systems.

2 | Methodology

2.1 Task1

The random movement of cells must be modelled using a probability distribution.

There are several probability distributions that can be classified as discrete or continuous, we will analyse uniform, bernoulli and beta.

The uniform distribution is usually regarded as a continuous distribution but can also be used to model discrete variables.

Area under the graph is one.ss

$$f(x) = \begin{cases} a & \text{if } x = 1 \\ b & \text{if } x = 0 \end{cases}$$

$$f(x) = \begin{cases} 1 & \text{for } 0 \leq x \leq 1 \\ 0 & \text{otherwise} \end{cases}$$

Uniform distribution Definition of distributions Uniform distributions Bernoulli Distribution

Movement directions

'Complexity of direction methods'

2.2 Task2

$$\frac{dN}{dt} = kN \ln\left(\frac{M}{n}\right)$$

3 | Conclusion

Some text

List of Figures

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Bibliography

Tatro, Dyjuan (n.d.). “The Mathematics of Cancer: Fitting the Gompertz Equation to Tumor Growth”. In: ().