A probabilistic approach to pancreatic cancer.

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1 Abstract

Within the pancreas 'normal' cells undergo genetic mutation and as a result divide uncontrollably, in many regards this growth is considered to be a completely random process and predicting the way and the extent to which a tumour may grow out of control is not accurately done using Bayesian methods[1] - considering the prior nature of growth and applying those statistics to new growth is not likely to be effective as the overall makeup of genetic mutation is likely to be affected heavily by numerous factors such as diet, sleep patterns, general levels of acidity and chemical compositions of the surrounding environment. As a result previous exploits in trying to predict cell mutation especially within the pancreas have been deemed unsuccessful.

This paper discusses a potential risk-factor based, probabilistic, approach into cell growth, and using knowledge of random processes, trying to determine where and how far growth will occur within a given time period. However, it is safe to assume that trying to predict how a mutated cell divides is an extremely challenging task and current mathematical techniques are proven to be inaccurate, as a result it is my belief that a new emphasis be made in using new mathematical techniques in order to model growth.

2 Understanding the behaviour of pancreatic cancer

Within the pancreas the composition of DNA remains the same as through the entire human body, each strand of nucleotides (repeating units) are made up of the phosphate group, deoxyribose sugar and nitrogenous base, (ACTG). The sequence of the pairings of the nitrogenous bases determines the behaviour of the cells including its growth. As cells divide, it is possible for the bases that are encoded to change and as a result the encoded growth commands change and ultimately leads to uncontrolled cell division, leading to the development of malignant or benign tumours[2]. Pancreas in the cancer is of particular difficulty to detect and treat as symptoms only become prevalent during the latter stages of the cancer's lifecycle and as a result pancreatic cancer can be considered to be one of if not the most deadly forms of the disease.

[3]Pancreatic cancers are mainly classified into different based upon where the mutated cells originate from, exocrine and endocrine tumors. With exocrine tumors being the most common and a particular excocrine tumour adenocarcinoma being the most notable 'subtype'. Pancreatic adenocarcinoma accounts for the majority of pancreatic cancer cases and the tumours typically arise within the cell lines of the pancreatic ducts.

2.1 Risk factors associated with pancreatic adenocarcinoma's

When calculating the likelihood of new growth it is vital to consider pre-existing risk factors that patients have, we will look at how we can numerically analyse these factors later on within the paper. The analysis will focus on 3 risk factors with potential to look at more in order to get a holistic application of the patients history. The 3 that are included in this model include:

Stress: Although not definitively proven to contribute to any growth, it can be shown to an increase in pancreatis or inflammation within the pancreas, another prominent risk factor. Additionally, stress has proven to potentially damage DNA repair which in turn increases the risk of genetic mutation. In this writing I will be using the measure of blood pressure in my formula, blood pressure is typically measured against arterial blood flow and its units are in millimeters of mercury where 1 mm HG is roughly equal to 133 pascals or 133 Newtons per metre.

Diet/unhealthy weight gain: It is proven that unhealthy diet and nutritional habits contribute in gaining unwarranted illness. As a result I have decided to include blood-sugar measurements of the patient in the predictive model. Although the research behind this relationship between blood sugar levels and cancer growth indicates a complex relationship that cannot be easily deciphered, it is a personal belief of mine that what we eat is what we are and so unhealthy snacks and

foods will no doubt produce unhealthy cells, it is just the variations with what we consume that is so complex to track and find a definitive pattern.

Age: Inevitably the changes in cell signalling and the accumulation of cell damage throughout the lifetime of an individual means that susceptibility to uncontrolled division and growth also grows,this continually increases with age and as a result it is a crucial risk factor and has been incorporated into the predictive model.

As of yet modern scientific research has struggled to define a clear mathematical relationship between such risk factors and variations in the rates of growth, however it is suggested with an extremely heavy hand, that lifestyle choices especially in the areas of diet and exercise will inevitably contribute to the development of malfunctioning cells/ cell codes.

2.2 The Growth of Pancreatic Cancer

4 Pancreatic Cancer has one of the worst survivable percentages of all known disease with roughly a 9 % chance of surviving post-diagnosis. According to a medical research team from Purdue University, it typically takes 10-20 years for pancreatic cancer to develop within a patient, and the model they emulated on a petri dish, took several months to grow into a recognisable form. Hence the challenge of being able to track and predict accurately the next stages of growth is extremely complicated and is beyond my own research capacities as an undergraduate. [5]However, the benefits of being able to somewhat predict the growth levels of the cancer will reap uncounted benefits in catering treatments and drug applications, which is almost guaranteed to help improve the treatment of the cancer.

3 Probabilistic modelling of growth

$$G \cdot P = \frac{\mu^2 \left(e^{-\alpha} + \beta^{-1}\right)}{\phi}$$

This is a basic formula derived from the risk factors described previously. Where μ is the blood sugar levels that are measured in mmoL/L or millimoles per litre. α is the age of the patient in years, β is the blood pressure levels of the patients - most obvious indicator of high stress within the blood is high blood pressure, and this is typically measures in mmHG or millimetres of mercury and the pressure that will be used is systolic pressure (where your heart pushes out). Where ϕ is representative of the golden ration, occurring frequently in nature= and a probable factor in the nature of growth within the pancreas.

3.1 Growth Potential

The entire concept of growth potential is built upon two ideas, to predict the future you need to understand the past and the risk factors we have taken into account paint a fair picture, despite the lack of detail that may appear. The other principle is the need for a numerical representation of the rate at which

3.2 The probability function:

$$\Omega_t = \frac{\zeta(s).n}{t}$$

[6]This is a simple probability function combining the Riemann - Zeta function $\zeta(s)$, the existing number of cells within the tumour space (n) (which can be calculated using simple arithmetic and a rough approximation of the current size of a tumour. The time(t) in months is used to find the average growth of said tumour per month. The numerator gives an overall average in the increase in the number of cancer cells within a specific area, whilst the growth time period is the required or said time that one is looking to see where the growth of the cancerous cells within that specific area of the pancreas is.

3.2.1 The Riemann - Zeta function:

The function is used within numerous mathematical fields including complex analysis and analytical continuation, as a result I believe that it can also be used to decipher the growth of cancerous cell areas.

$$\zeta(s) = \sum_{s=1}^{t} 1/n^s$$

Here time (t) is taken to be in seconds instead of months and as a result yields a more accurate representation of cell growth. And instead of an upper limit of s, we take the upper limit to be t.

3.3 Final Formula:

$$\xi = \frac{\mu^2 \left(e^{-\alpha} + \beta^{-1}\right)}{\phi} . \frac{\zeta(s).n}{t}$$

Where ξ is the rough estimate of the number of cells after the growth period, and the area of growth can then be calculated by finding the average size of said cancer cell and multiplying the two. The new area can be calculated by subtracting the previous area before the growth time period.

3.4 Final Remarks:

This brief note is not meant to be used in real applications as the level of detail within the model is not up to the standards required to match the levels of accuracy modeled by other modern models. This is a brief glimpse into my ideas of the future of modelling, where I believe that ordinary differential equations are limited in modelling the random nature of cell division. A probabilistic model, one that takes into account rates of change of protein folding done within the DNA is what I believe to be the future of cancer modelling, especially with the emergence of machine learning techniques within the protein folding research space. Although, it may feel as though I have pulled variables and functions out of thin air, the mathematical proof behind this is far too complicated and long winded to be included in this paper, and there is not a large enough data set that has been fed to the model to provide any sort of validity.

3.5 References:

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