Chapter 41

Importance of Information Working With Colon Cancer Research

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ABSTRACT

Modern science helps us to understand the changing world around us, across fields such as biology, computer science, mathematics, statistics, chemistry, computational biology, biotechnology, biochemistry, and many others. An important branch of science that has had a large impact on the medical field is bioinformatics. This chapter introduces the importance of information science into colon cancer research. According to the American Cancer Association, in the United States in 2018, 97,220 new cases of colon cancer (CC) were identified. The research into this topic area is an immediate need to save many lives and improve people's living standards.

1. INTRODUCTION

Modern science helps us to understand the changing world around us, across fields such as biology, computer science, mathematics, statistics, chemistry, computational biology, biotechnology, biochemistry, and many others. An important branch of science that has had a large impact on the medical field is bioinformatics. This field has recently attracted the attention of academia and medical professionals

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(Chavan, 2008; Poe et al., 2009; Simon, 2005; Umarji et al., 2009). Bioinformatics, a new science, aims at assisting the medical field when choosing correct treatments, detecting diseases, and supporting drug development. A particularly challenging disease is cancer, a genomic disease in which human cells lose their ability to follow the chronological phases of a normal cell cycle. Thus, those cells lose their regulation process, divide uncontrollably, and alter their chromosomal constituency, forming cancer cells (Al-Rajab & Lu, 2012).

Computerised models can employ gene expression data and related information to estimate the clinical state of a patient or the amount of cancer tissues or cells inside the body (Al-Rajab & Lu, 2012; Ardekani, Aslani, & Lakpour, 2007, Guo et al, 2021). Bioinformatics has shown positive impact during the treatment of cancer as professionals continually strive to control tumour growth in ways that were impossible in the past. Moreover, many studies have demonstrated that cancer-cell gene expression is essential to effective remediation (Fenstermacher, 2005; Kihara, Yang, & Hawkins, 2006). Cancer studies also employ bioinformatics to record cancer-cell expression from datasets and to identify tumour and drug responses (Kihara, Yang, & Hawkins, 2006). Until recently, bioinformatics studies have succeeded in identifying two types of cancer: ovarian and breast. The future of bioinformatics will certainly contribute to the therapy of other types of cancer (Ardekani, Aslani, & Lakpour, 2007). Additionally, with bioinformatics, it is possible for therapists to analyse immune system responses to permit a better understanding of the alterations in both controlled and uncontrolled tumours and to provide patients with better treatment. Moreover, bioinformatics, with the help of mathematical models, has demonstrated success in describing the effects of radiation therapy and chemotherapy on the human body.

Cancer is classified as a critical disease in modern civilisation that causes great suffering. There are many carcinogens and different causes of cancer (e.g., radiation, smoking, artificial chemicals, microbes, dirty water, polluted air), all of which accelerate changes in cells. Certainly, there are many causes yet undiscovered (Shah & Kusiak, 2007). However, traditional methods of diagnostics have depended mainly on the clinical appearance and the morphologic structure of cancer. However, these attributes have limited influence because cancer results from many different factors. Moreover, there is an overwhelming need to find informative genes from information in huge datasets, wherein researchers eliminate unrelated genes, reduce noise and complexity and present opportunities for disease detection (Shah & Kusiak, 2007). An informative gene is suitable and beneficial for classifying cancer (Mohamad et al., 2008). The most challenging task for cancer diagnosis is recognising relevant gene expressions from massive datasets, which can help determine the disease phenotype (Liu, Liu, & Zhang, 2010). The insertion and evolution of array diagnostic technologies aid the early prediction and accurate diagnosis of cancer (Al-Rajab & Lu, 2016). For example, the instantaneous retrieval and analysis of thousands of gene expression levels instantaneously and would greatly benefit cancer classification (Park & Cho, 2003). Cancer classification plays a vital role in enhancing patient health care and can greatly improve quality of life. Classification, therefore, is crucial for drug assignment (Liu, Liu, & Zhang, 2010). Cancer classification and detection uses a microarray dataset to discriminate samples within a given model (Mohamad et al., 2007). The aim of using microarray data in cancer classification is to distinguish body cells into relevant classes of observations, such as normal versus cancerous (Al-Rajab & Lu, 2016; Osareh & Shadgar, 2010).

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