

## Chapter 9

# Application of Bioinformatics in Cancer Prediction and Prognosis

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### ABSTRACT

*Informatics and internet technologies are becoming extremely popular in today's healthcare system. The emergence of the worldwide web has affected the way in which health-related information is distributed and accessed over cyberspace. The internet is rapidly gaining importance, not just for healthcare professionals, but also for patients, by enabling them to search for drug- and other health-related information. Bioinformatics is the combination of biology and information technology. The term bioinformatics was coined by Paulien Hogeweg in 1979 for the study of informatic processes in biotic systems. Its primary use since the late 1980s has been in genomics and genetics, particularly in those areas of genomics involving large-scale DNA sequencing.*

### INTRODUCTION

Informatics and Internet technologies have become very common in today's healthcare system. The emergence of the web around the world has affected the way health-related information is distributed and accessed through cyberspace. The Internet is rapidly gaining importance, not only for healthcare professionals, but also for patients, by enabling them to search for information health (Whitman, 2022). So in this chapter we will see a definition bioinformatics and the components of bioinformatics and The value of Bioinformatics in ML and Tumor image segmentation.

Bioinformatics is the combination of biology and information technology. (Anderson, 2002). The term bioinformatics was coined by Paulien Hogeweg in 1979 for the study of informatic processes in biotic systems. It was primary used since late 1980s has been in genomics and genetics, particularly in those areas of genomics involving large-scale DNA sequencing.

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## ***Application of Bioinformatics in Cancer Prediction and Prognosis***

Bioinformatics can be defined as the application of computer technology to the management of biological information. Bioinformatics is the science of storing, extracting, organizing, analyzing, interpreting and utilizing information from biological sequences and molecules. It has been mainly fueled by advances in DNA sequencing and mapping techniques. Over the past few decades rapid developments in genomic and other molecular research technologies and developments in information technologies have combined to produce a tremendous amount of information related to molecular biology. The primary goal of bioinformatics is to increase the understanding of biological processes. (Whitman, 2022)

**The Components of Bioinformatics:** The discipline encompasses any computational tools and methods used to manage, analyze and manipulate large sets of biological data in order to:

- The creation of databases, allowing the storage and management of large biological data sets
- The development of algorithms and statistics to determine relationships among members of large data sets
- The use of these tools for the analysis and interpretation of various types of biological data, including DNA, RNA and protein sequences, protein structures, gene expression profiles, and biochemical pathways (Whitman, 2022).

The Bioinformatics focuses on the development of algorithms and software for the transfer, storage, analysis, and development of genomics databases. Machine learning (ML) belongs to the branch of computer science that provides self-learning capability to the machines without explicit programming. The ML algorithms are being extensively used for the tasks of prediction, classification, and feature selection in bioinformatics. The ML approaches are very good for solving problems such as distinguishing between DNA sequences and classification of DNA sequences. Currently, the ML in bioinformatics has become significant due to the advent of deep learning (Guo, 2018).

Bioinformatics represents an interdisciplinary branch for developing improved methods for retrieving, analyzing, storing, and organizing the biological data. It focuses on the development of algorithms and software for the transfer, storage, analysis, and development of genomics database. Machine learning (ML) belongs to the branch of computer science that provides self-learning capability to the machines without explicit programming. The ML algorithms are being extensively used for the tasks of prediction, classification, and feature selection in bioinformatics. The ML approaches are very good for solving problems such as distinguishing between DNA sequences and classification of DNA sequences. Currently, the ML in bioinformatics has become significant due to the advent of deep learning (Malik, 2021)

The ML algorithms are used for selecting relevant features in bioinformatics application as biological data are high dimensional in nature (Malik, 2021). The second major application of ML in bioinformatics has been found in classification of biological data. The third major application of ML in bioinformatics was found to be prediction of biological data (Malik, 2021).

## **TUMOR**

An abnormal mass of tissue that forms when cells grow and divide more than they should or do not die when they should. Tumors may be benign (not cancerous) or malignant (cancerous). Benign tumors may grow large but do not spread into, or invade, nearby tissues or other parts of the body. Malignant tumors

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