Chapter 6
Application of Uncertainty Models in Bioinformatics

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ABSTRACT

This chapter provides the information related to the researches enhanced using uncertainty models in life sciences and biomedical Informatics. The main emphasis of this chapter is to present the general ideas for the time line of different uncertainty models to handle uncertain information and their applications in the various fields of biology. There are many mathematical models to handle vague data and uncertain information such as theory of probability, fuzzy set theory, rough set theory, soft set theory. Literatures from the life sciences and bioinformatics have been reviewed and provided the different experimental & theoretical results to understand the applications of uncertain models in the field of bioinformatics.

INTRODUCTION

Bioinformatics is the application of computer technology to the management of biological information. Computers are used to gather, store, analyze and integrate biological and genetic information which can then be applied to gene-based drug discovery and development. The need for Bioinformatics capabilities has been precipitated by the explosion of publicly available genomic information resulting from the Human Genome Project.

The goal of this project – determination of the sequence of the entire human genome (approximately three billion base pairs) – will be reached by the year 2002. The science of Bioinformatics, which is the melding of molecular biology with computer science, is essential to the use of genomic information in understanding human diseases and in the identification of new molecular targets for drug discovery.

Figure 1. The cost of sequencing has fallen from $100,000,000/genome in 2001 to $10,000/genome in 2011. The cost of genomics is estimated to fall to $2,000 a genome within the next few years.
Courtesy of the National Human Genome Research Institute
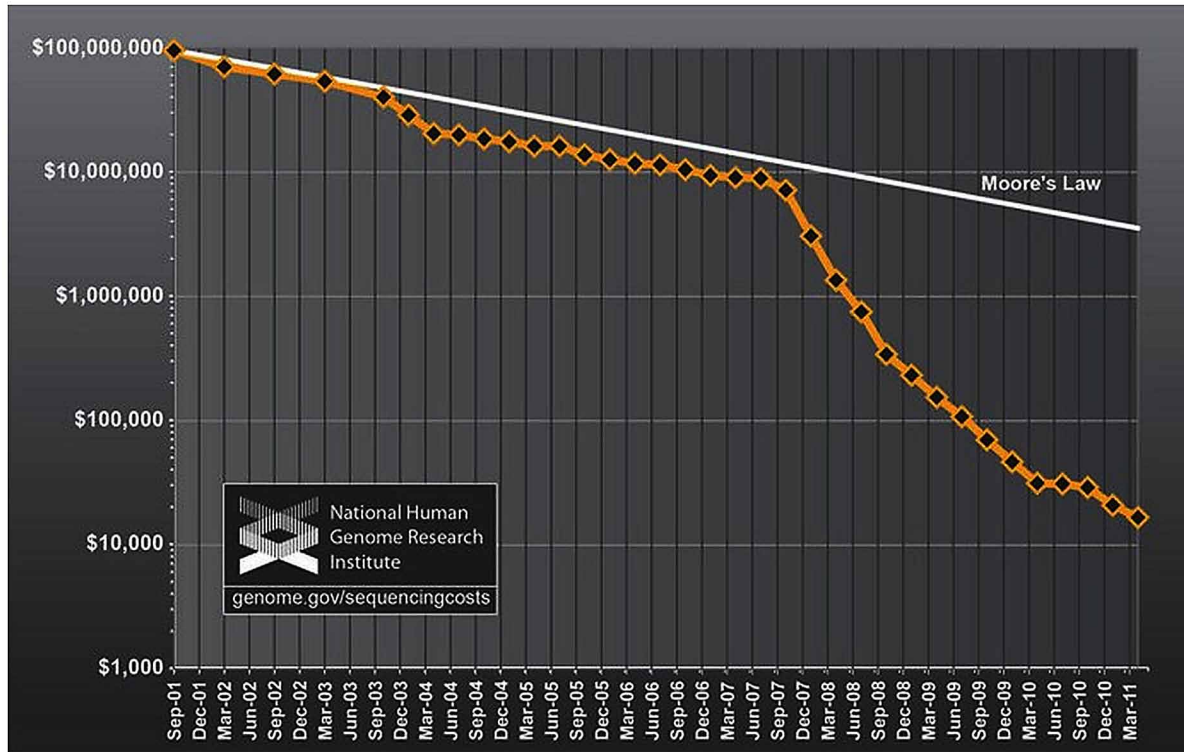
Many times biotechnology and bioinformatics are taken as synonymous. But, bioinformatics combines molecular biology, computer science, mathematics, statistics and engineering to store, maintain, organize, process and analyze biological and chemical data in order to advance medicine and healthcare whereas biotechnology brings together biological sciences with engineering technologies to manipulate living organisms and biological systems to produce products that advances healthcare, medicine, agriculture, food, pharmaceuticals and environmental control.

This analytical branch of genomic research mines large sets of data to answer new research questions and throw light on older ones. Bioinformatics analysis will support the next revolution in genomic science to address fundamental areas of natural history research (Schuh, 2005) including:

- Basic investigations of the phylogenetic relatedness of all life.
- Tracing the geographic distribution of biodiversity across varied environments and regions.
- Unravelling the developmental history of organisms from initial embryonic cellular stages of life to the functional complexity of mature multi-cellular individuals.
- Defining population-level processes of natural selection.
- Initiating landscape-based environmental comparisons of varied habitats around the world.
- Speeding-up species discovery.

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