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Research Paper Information Technology

GENE Prediction

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1. INTRODUCTION

1.1 Introduction to Bio-informatics

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 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(e.g. DNA computing, neural computing, evolutionary computing, immuno-computing, swarm-computing, cellular-computing).

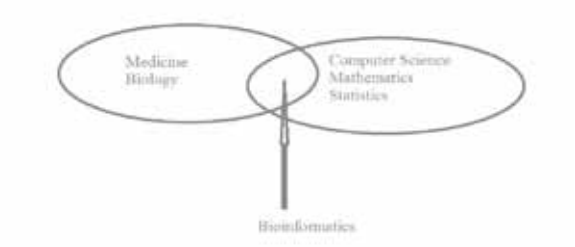

Figure 1.1: Bioinformatics-A cross between Biological rules and Computational mathematics

1.2 GENE Structure

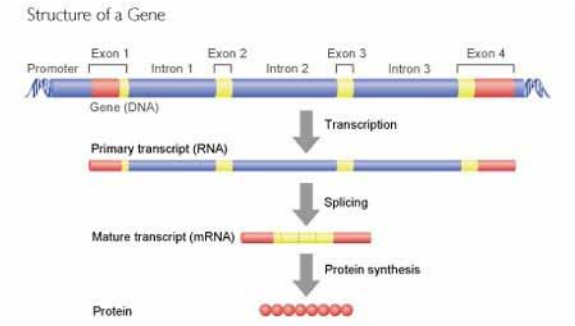

Figure 1.2: GENE Structure

There are two general types of gene in the human genome:

- Non-coding RNA genes
- Protein-coding genes.

Non-coding RNA genes represent 2-5 per cent of the total and encode functional RNA molecules.

Many of these RNAs are involved in the control of gene expression, particularly protein synthesis. They have no overall conserved structure.

Protein-coding genes represent the majority of the total and are expressed in two stages: transcription and translation (Gene expression). They show incredible diversity in size and organization and have no typical structure.

1.2.1 GENE Structure Prediction

In computational biology gene prediction or gene finding refers to the process of identifying the regions of genomic DNA that encode genes. This includes protein-coding genes as well as RNA genes, but may also include prediction of other functional elements such as regulatory regions. Gene finding is one of the first and most important steps in understanding the genome of a species once it has been sequenced.

In its earliest days, “gene finding” was based on painstaking experimentation on living cells and organisms. Statistical analysis of the rates of homologous recombination of several different genes could determine their order on a certain chromosome, and information from many such experiments could be combined to create a genetic map specifying the rough location of known genes relative to each other. Today, with comprehensive genome sequence and powerful computational resources at the disposal of the research community, gene finding has been redefined as a largely computational problem.

- The objective of gene prediction is to identify regions of genomic DNA that encodes protein.
- This includes protein-coding genes as well as RNA genes, but may also include prediction of other functional elements such as regulatory regions.

Gene finding is one of the first and most important steps in understanding the genome of a species once it has been sequenced.

1.2.2 GENETIC Diversity

The aim is to predict the Genetic Diversity of all organisms for cross breading. The project will help the researchers to select the organism so that the database predicts the gene. The proposed system scans the available databases and narrows down the options available to the researchers drastically. The ample time and resources will be saved. This study is undertaken to cover the gene applications in existing knowledge buried in large biological texts and to infer results from them.

2. METHODOLOGY

The methodology for the work will involve the use of pattern matching technique to analyze the given database and retrieve the desired information.

In this project we use visual basic 2010 front end in this we made form.1st form we made for login page the enter into next form in this we predict gene bye gene sequences.3rd form we add new gene and in 4 form we add new use.

In backend we use SQL 2005 in this we made database for sequences of gene

In this we use websites for database are:
http://www.cbs.dtu.dk/biolinks/pserve2.php
http://www.ncbi.nlm.nih.gov/sites/gquery?itool=toolbar
http://www.genedb.org/Homepage
http://www.genome.jp/kegg/genes.html

www.hprd.org

and use server for find out netglyserver.3.0. In this we use the concept of pattern matching for finding out the gene sequences. In this work, we use to store the information in database and those database we use are to collect the information are:



Figure 2.1: Write organism name in search parameter



Figure 2.2: Write organism name in search parameter



Figure 2.3: Select Particular Items for Database

3. SCREEN SHOTS



Figure 3.1: Login Page



Figure 3.2: Add GENE



Figure 6.3: GENE Data Entered

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