

Chapter 28

Applying CI in Biology through PSO

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ABSTRACT

Conventional computing methods face challenges dealing with real world problems, which are characterised by noisy or incomplete data. To find solutions for such problems, natural systems have evolved over the years and on analysis it has been found these contain many simple elements when working together to solve real life complex problems. Swarm Intelligence (SI) is one of the techniques which is inspired by nature and is a population based algorithm motivated by the collective behaviour of a group of social insects. Particle swarm optimization (PSO) is one of the techniques belonging to this group, used to solve some optimization problems. This chapter will discuss some of the problems existing in computational biology, their contemporary solution methods followed by the use of PSO to address those problems. Along with this several applications of PSO are discussed in few of the relevant fields are discussed having some future research directions on this field.

INTRODUCTION

A massive growth is seen in gathering biological information by scientific communities in these years. This information comes in the form of genomes, protein sequences and gene expression data and so on which causes a need for and efficient computational tools to store, analyze and construe these data. The term bioinformatics and CB always used interchangeably in the field of computer science, which literally means the science of informatics as applied to biological research. Informatics on the other hand is the management and analysis of data using various advanced computing techniques. Hence, in other words, bioinformatics can be described as the application of computational methods to make biological discoveries and explorations (Clote & Backofen, 2000). It can also be defined as the appliance of

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computer technology to the management of biological information, encircling a study of the inherent genetic information, underlying molecular structure, resulting biochemical functions, and the exhibited phenotypic properties (Sushmita Mitra, Yoichi Hayashi,(2006)). The final goal and attempt of this area is to create new insights into the science of life as well as developing a global perspective (Das, Abraham & Konar, 2008). Three major objectives of bioinformatics can be put forward as to develop:

- Algorithms and mathematical models for searching the relationships among the members of huge biological dataset.
- Analyze and interpret the variety of heterogeneous data including nucleotide and amino acid sequences, protein domains and protein structures.
- Tools that enable proficient and effective storage, retrieval and management of high-volume biological databases.

In recent times, large number of biologically motivated algorithms have been developed and are being used for handling many complex problems. For instance, neural computing (Haykin, 1999) attempts to imitate the biological nervous systems of the living creatures inspired by the amount of parallel and distributed processing done inside the brain of a human. Genetic algorithm (GA) is inspired by the Darwinian evolutionary process through cross-over and mutation of biological chromosomes. They have successfully been used in many bioinformatics tasks that need intelligent search, optimization and machine learning approaches. Sushmita Mitra and Yoichi Hayashi, (2006) provide a comprehensive survey of the research in this direction. For the past few years there has been a slow but steady increase of research papers reporting the success Computational Intelligence (CI) based searching, classification and clustering techniques applied to the field of **CB** (Das, Panigrahi & Pattnaik, 2009). CI is constituted with the study of a set of nature-inspired computational methodologies, techniques and approaches to address complex real-world problems to which traditional approaches are ineffective or infeasible. While traditional models often fail to handle uncertainty, noise and the presence of an ever-changing context, CI provides solutions for complicated real problems. It primarily includes artificial neural networks (ANN), evolutionary computation (EC) and fuzzy logic (FL). In addition, CI also embraces biologically inspired algorithms such as SI, artificial immune systems, which can be seen as a part of EC.

This chapter presents some fundamental problems present in **CB**, the existing and traditional solution methods to answer these problems, the issues and challenges associated with these. Some of the contemporary problems solving approaches based on CI are then discussed.

BACKGROUND

To understand bioinformatics in any meaningful way, it is necessary for a computer scientist to understand some basic biology. In this chapter a short and basic introduction to the fundamentals and relevant to computational thing is given which are illustrated below.

Genetic Material: An Overview

Biology at the microscopic level began in 1665 when, Robert Hooke discovered that organisms are composed of individual compartments called cells. A cell's traits were inherent in its genetic information,

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