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International Journal of Biological Technology (2010) 1(2):60-63
ISSN: 0976 - 4313

Original Article

ABD: Advanced Biotechnological Directory for Protein Sequence and Structure analysis

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Received: 10.5.2010; Revision: 12.7.2010; Accepted: 8.8.2010; Published: 15.8.2010

Abstract

Over the past decades, a number of computational tools for structure prediction have been developed. It is critical that the biological community is aware of such tools and is able to interpret their results in an informed way. Rapid increase in protein sequence information from genome sequencing projects demand the intervention of bioinformatics tools to recognize interesting gene products and associated function often multiple algorithms need to be employed to improve accuracy in prediction and several structure prediction. Here we report the availability of an ABD as a bioinformatics online package dedicated for Insilco analysis of protein sequence and structure analysis (ABD). ABD provides web interface to both in house and widely accepted programmes from major bioinformatic groups organized and five different modules. This database has the potential of becoming a major hub of resources for the biological community.
Key words: ABD; Protein Structure Predication; Sequence Analysis.

Introduction

Protein sequence analysis, structure predications are great interest to the biological community, in order to understand the relationship between different organisms at the molecular level the bioinformatics tool have been used. Comparative analysis of protein sequences and structural are a cornerstone of bioinformatics. The complete genomes of a number of organisms have been sequenced and many more genome-sequencing projects are underway. Structural biology now faces the arduous task of characterizing the shapes and dynamics of the encoded proteins to facilitate the understanding of their functions and mechanisms of action. Recent developments in the techniques of structure determination at atomic resolution, X-ray diffraction and nuclear magnetic resonance spectroscopy, have enhanced the quality and speed of structural studies (Zhang and Kim, 2003).Nevertheless, current statistics still show that the known protein sequences (~1,000,00; Boeckmann *et al.,* 2003) vastly outnumber the available protein structures (~20,000; Berman *et al.*, 2002).

Over the last decade genome wide technologies have been increasingly used to explore biological process in the whole cells (Vastrik,2007). These system biology approaches are essential elucidate the interactions between genes. Proteins and metabolites high throughout content screening and chemicals genetics methods now commonly used to investigate chemical involved cellular functions with the aim of identifying novel drugs or discover the macromolecular targets of chemical compounds (Yildirim 2007). These studies generate large quantities of systems biological/chemical data. Tools are urgently required to facilitate the visualization and analysis of these data to extend our knowledge of biological functions and to examine the relationships between drugs/targets (Xiong *et al* ,.2008)

High throughput experimental techniques have led to the population web accessible databases with vast amounts of biological databases with vast amounts of biological data mathematical models of biological systems are playing an essential in the interpretation of this data. The scientific community now faces the challenge of the mathematical models themselves upcoming increasingly complex and numerous .There is need centralized database to store all these

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International Journal of Biological Technology (2010) 1(2):60-63
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models in standard formats to make them easily accessible and reusable by the research opportunity (Lyoyd, 2008).

Materials and Methods

Hardware requirements

Processor-Intel Pentium IV, Speed - 2.53 GHz, RAM- 256 MB, Hard Disk-80 GB.

Software requirements

Operating System-Windows XP SP2, Primary technology-ASP.NET 2005, Host Server-Mozilla, Opera, Intermediate tool-VB.NET 2005.

ASP.NET 2.0 the latest version of Active Server Pages, is Microsoft's technology for building dynamic, database-driven Web sites. ASP.NET is one of the most popular languages for building scalable, interactive Web sites. Several of the highest traffic Web sites on the Internet employs ASP.NET. ASP.NET uses compiled code written in Common Language Runtime languages such as Visual Basic and C#. Unlike previous versions of Active Server Pages, this version does not use interpreted scripting languages such as VBScript.

Results and Discussion

The database can be accessed over the internet. A screenshot of the home page is shown in (Figure 1). ABD is a compilation of in-house databases, web servers and web. Interface for various programs related to protein sequence and structure analyses clusters five modules. ABD is an easy to use web server, which will enable the novice as well as the expert users to carry out protein sequence and structure analysis rapidly and easily. ABD provides various tools and database related to protein sequence and structure analysis classified into five difference modules. Database and web server(Fig.2), software (Fig.3) Sequence analysis, secondary structure prediction, structure analysis, homology modeling and structure validation, database (Fig.4) More than, 128 tools for protein sequence and structure analysis is available from ABD. This database provides a mechanism by which researchers and students can transform the information about protein sequence and structure into knowledge about a protein structure prediction. ABD is simple on-line database, the Advanced Biotechnological Directory, ABD facilitates the access to several database and web server, open access journal, links related to biotechnology &bioinformatics . Its single and user-friendly WWW interface. ABD provides various tools and database related to protein sequence alignment and structure analysis

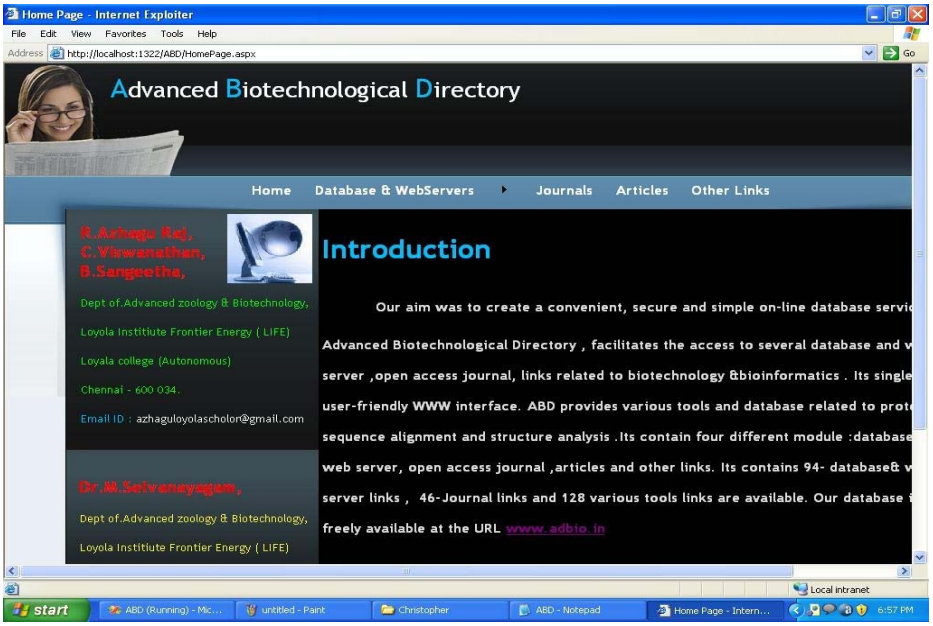

Fig.1: A screenshot of the home page introduction

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International Journal of Biological Technology (2010) 1(2):60-63
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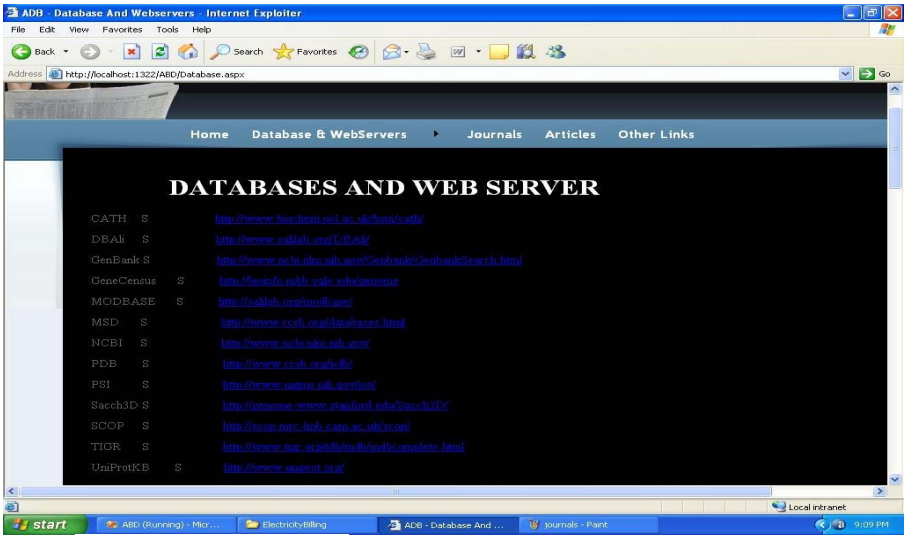

Fig. 2: Database and classification

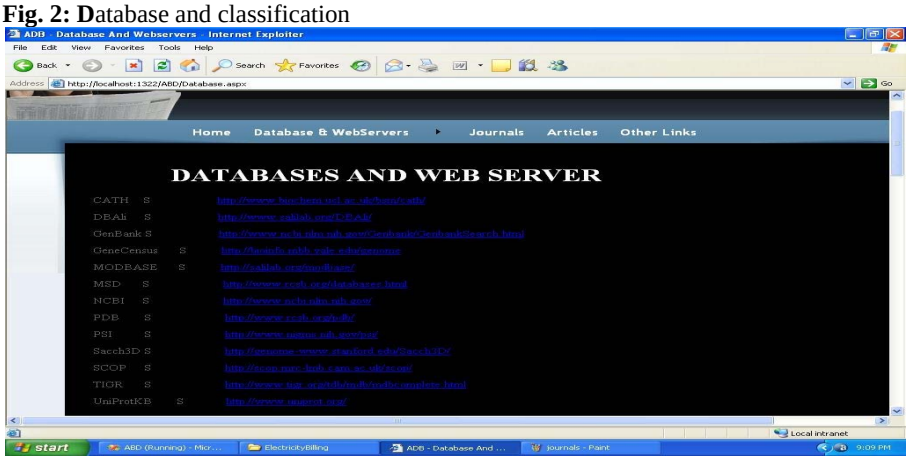

Fig.3: A screenshot of the software page

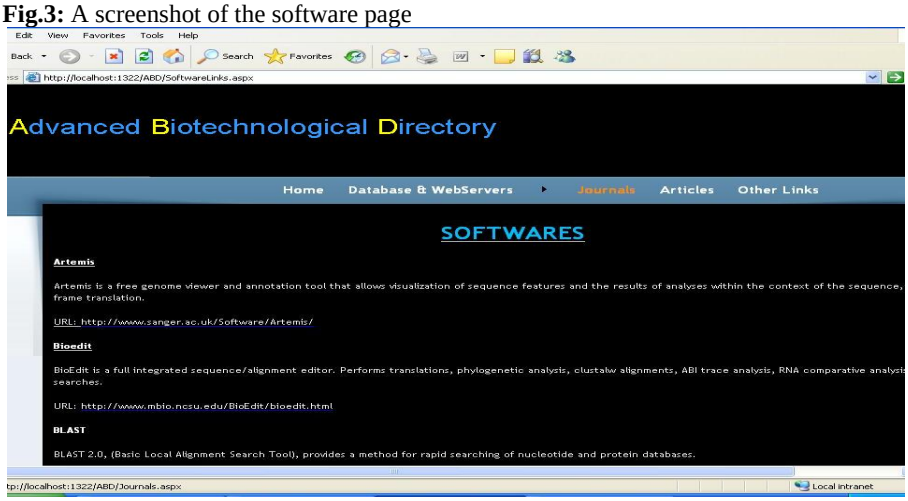

Fig. 4: A screenshot of the databases

Discussion

Comparative analysis of protein sequences and structure are cornerstone of bioinformatics. It is now in a transition state from a data centric science to knowledge based science, analysis and extraction of relevant information from huge amount of data from various high thorough experiments remains as the major challenge in bioinformatics (Collins,2003). Rapid increase in data generation has left us with many genes and proteins as unknown or hypothetical ones, as it is impossible to validate all the sequence data by means of biochemical experiments for confirmation of the likely associations, bioinformatics approaches can play an important role as a filter for recognizing potential gene products that can represent new fold or novel function. Computational approaches enable the recognition of potential gene products of a family and to rationally design mutation experiments. Along with rapid incoming data the availability of various resources to analyze the data has also increased (Gowthaman *et al*., 2006; Shameer and Sowdhamini, 2007).

The complete genomes of a number of organisms have been sequenced and many more are under way structural biology now faces the arduous task of characterizing the shapes and dynamics of the encoded protein to facilitate the understanding of their functions and mechanisms of action. Finding answers to the complexity of questions emerging in modern biology requires the use of quantitative computational approaches. For example the experimental and mathematical modeling of biochemical networks in systems biology has a strong theoretical component. However the use and applicability of computational methods in systems biology is often compared by the complexity of the software tools available to support the modeling tasks. One efforts towards offering a better support to the user in the application of several different tools available is the system biology workbench (Sauro *et al.,* 2003)

Conclusion

We have explained about the ABD (Advanced Biotechnological Directory). ABD will be a useful resource for researchers and academic communities interested in protein sequence and structure analysis.

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