A paper on
Bio-Informatics, Bonding Genes With IT

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Introduction
New discoveries are being made in the field of genomics. An area of study which look at the DNA sequence of an organism in order to determine which genes code use for beneficial traits and which genes are involved inherited diseases. With an increasing amount of information generated in this area of study, scientist needs a way of storing and analyzing that information. Computers can really help in this process due to their computing capability. As a result a new research area that combines the study of biotechnology and the use of computer is emerging. This field is referred to as bio informatics and evolves the use of Internet tools, artificial intelligence and other advance computational method to asset in storing and analyzing data generated from DNA sequencing.

Bioinformatics
• Bioinformatics describe any use of computer to handle the biological information.
• Bioinformatics is a synonym for computational molecular biology i.e. the use of computers to Factorize the molecular components of living things.

Classical definitions
• The mathematical, statistical and computing methods that aim to solve biological problems using DNA and amino acid sequences and related information.
• Richard Durbin“, Head of informatics at the welcome trust Sanger Institute, expressed an interesting opinion: “I do not think all biological computing is bioinformatics, e.g. mathematical modeling is not bioinformatics, even when connected with biology-related problems. In my opinion, bioinformatics has to do with management and the sequence use of biological information, particular genetic information”.
• Bioinformatics is the application of information technology to the management of biological data.
• Bioinformatics is first and fore most a biological science. It is often less about developing perfect elegant algorithms than it is about answering practical questions.

The term Bioinformatics has been commandeered by several different disciplines to mean rather different things. In broad sense, we may say this term can be considered to mean information technology applied to the management and the analysis of biological data. In the context of genome initiatives, the term was originally applied to the computational manipulation and analysis of biological sequence data (DNA, protein).
• Bioinformatics is an integration of mathematical statistical and computer methods to analyze biological, biochemical data.
• Bioinformatics is a newly emerging interdisciplinary research area, which may be defined as the interface between biological and computational science.
• Bioinformatics is a bright new field. It is the science of developing computer database and algorithms for the purpose of spring up and enhancing biological research. Bioinformatics is being used most noticeably in the human genome Project, the efforts to identify the 80000 genes in human DNA.
• Bioinformatics is a combination of computer science, information technology and genetics to determine and analyze genetic information. According to Messourie University, Bioinformatics is the science and the technology about learning, managing and processing biological information.
• Bioinformatics is the field of science in which biology, computer science, and information technology merge to form a single discipline. The ultimate goal of this discipline is to enable the discovery of new
biological insights as well as to create a global perspective form which unifying principles in biology can perceive.

Bioinformatics components

Bioinformatics has following three components

1. The creation of DATABASES allowing the storage and management of large biological data sets.
2. The development of ALGORITHMS and STATICS to determine the relationships among members of large data sets.
3. The USE OF THESE TOOLS for the analysis and interpretation of various types of biological data, including DNA, RNA & Protein sequences, proteins structures, gene expression profiles and biochemical’s pathways. The term bioinformatics first term into being in the 1990’s and was originally synonymous with the management and analysis of DNA, RNA & protein sequence data.

General Description

Biologists collect data and then interpret it. We have vast volumes of DNA sequences which data at our fingertips. But how do we figure out which parts of that DNA Control the various chemicals processes of life?

We know the function and structure of some proteins but how do we determine the function of new proteins? And how we predict what a protein will look like based on knowledge of its sequence? So, bioinformatics is the tool we can use to help us answer these questions and many others like them.

How is computing related to Biology?

An organism heredity and functional information is stored as DNA, RNA and proteins, all of which are linear chained composed of smaller molecules. DNA is made up of four deoxyribonucleotides (adenine, thy mine, Cytosine and guanine RNA is made up from the four ribonucleotides (adenine uracil, cytosine and guanine) & Proteins are made up of 20 amino acids because these macro molecules are linear chains of defined components, they can be represented as sequences of symbols. These sequences can then be compared to find similarities that suggest the molecules are related by form or function.

- Sequence comparison is the most useful computational tool to emerge for molecular biologists.
- The World Wide Web (www) has made it possible for a single public database of genome sequence data to provide services through a worldwide community of uses.
- Program blast is used to compare an uncharacterized DNA sequence to the entire publicly held collection of DNA sequences.

Example: Fruit files (Drosophilla melanogaster) are a popular model the development of animals from embryo to adult. Fruit files have a gene called eyeless, which, if it’s ‘knocked out’, results in a fruit files with no eyes. It’s obvious that the eyeless genes play a role in eye development. In human anirid gene is responsible for the eye. In human who are missing this gene, the eye develop without irises, could be they’re some similarity in how eyeless and aniridia function, even though flies and human are vastly different organisms? To gain insight into how eyeless and aniridia work together we compare their sequences.

Most scientists compared the respective gene sequences by hand aligning them one under the other in a word processor and looking for matches character by character. Pair wise comparison of biological sequences is the foundation of the most widely used bio-informatics techniques. Pair wise sequence comparison algorithms works as a core element of their function.

These days a biologist can find dozens of sequences matches in second using sequence-alignment programs such as BLAST and FASTA.

COMPARISON EYELESS AND ANIRIDIA WITH BLAST

Query: 24IERLPSLEDASHQGSGVQNLGWSKGNWVPDLPSRSDKIVELAHSGARPCDISRILQVSNRP + M + HSGVNQLGGVGWRPDLSDKKEVLEAHSGARPCDISRILQVSN

Subject: 17IPRPPPANSQMS-HSGVNQLGGVFVNGRPDLPSRSDKIVELAHSGARPCDISRILQVSN

Query: 84GCVSGLRGYETGSRPARAIGGSKPRVA TAEYVVSQGQKCREPSIFAWEniDRLLQENGCVSKILGGRYETGSRPARAIGGSKPRVA EWSKI + QYVKRECPISIFAWEIRDRILE

Subject: 76GCVSGLRGYETGSRPARAIGGSKPRVATPEV VSIAQYKRCPSIFAWERDRLLSE

Query: 144 VCINDNIPSVSINRVLRLNAAEKEQ

Subject: 136 VCTINDNIPSVSSINRVLRLNASEKQQ
In each set of three times, the query sequence is on the top line, and the aniridia sequence is on the bottom line.

Middle lines shows where the two sequence matches

**Case 1:** If there is a letter in middle line, the two sequences matches exactly at that position.

**Case 2:** If there is a plus sign on the middle line, the two sequences are different at that position, but there is some chemical similarity between the amino acids.

**Case 3:** If there is nothing on the middle line, the two sequences don’t match at that position. As, a result, BLAST can detect patterns that are imperfectly replicated from sequence to sequence, and hence display relationship that are inexact but still biologically meaningful.

**Importance of Bioinformatics**

- The central challenge of bioinformatics rationalization of the mass of sequence information, with a view not only to deriving more efficient means of data storage, but also to design more sharp analysis tools. The command that derives this analytical process is the need to convert sequence into information into biochemical and biophysical knowledge to make out meaning of this ‘or’ to decipher the structural, functional and evolutionary clues encoded in the language of biological sequence.
- To extract biological meaning from sequence information is the reason we study it. In essence, we are faced with the task of decoding as unknown language.
- This unknown language may be decompose into sentences (proteins, words (motifs), and letter- its alphabet-s- (amino-acids), and the code may be tackled at a variety of these levels. The letter has no hire meaning, but their particular combination into words its important.
- Sometime a single letter with in a word perhaps, can change its intense meaning (e.g. -Sun-sin) and hence the meaning of the entire sentence, so it is vital to find the meaning of code correctly.
- Consider for example, the single base chain in the human hemoglobin a chain code on for glutamic acid (GAA) to valine (GUA), this minute difference results in a change from a normal healthy state to fatal sickle cell anemia.
- Ultimately, our aim is to be able to understand the words in a sequence sentence is that formed a particular protein structure and perhaps one day to be able to design proteins (‘or’ to write sentences) of our own.
- The science of bioinformatics is essential to the use of genome information in understanding human diseases and in the identification of new molecular targets for drug discovery.

**Key components of Bioinformatics**

1. Ability to analyze the databases and conversant with data many tools.
2. Identification of genes of interest to follow-up choosing genes may be a difficult task to new sequences.
3. Establishing function for the genes of interest- function genomics and establishment of model system, a no simple task at this point.

**APPLICATIONS**

Bioinformatics used in many area of application as describe below-


**KEY CHALLENGE**

Today, application of computations methods allows us to recognize by that form characteristics patterns but we do not yet understand the intricate syntax required to peace patterns together and build complete protein structure. A key challenge of bioinformatics is to analyze the wealth of sequence data in order to understand the amassed information in term of protein structure, function and evaluation. These are two basic principles analytical approaches in bioinformatics:

- **Pattern Recognition and Pattern Prediction**

**SOME USEFUL LINKS**

- Http://bioinformatics.org/- an international organization, which promotes freedom and openness in the field of bioinformatics.
- Http://wwwinbios.org/- Bioinformatics society of India.
- Http://www.bioperl.org- The Bioperl Project.
BIOINFORMATICS IN INDIA

Studies IDC points out that India will be a potential star in bioscience field in the coming years after considering the factors like bio-diversity, human resources, infrastructure facilities and government’s initiatives. According to IDC, bioscience includes pharma, Bio-IT (bioinformatics), agriculture and R&D. IDC has been reported that the pharmaceutical firms and research institutes in India are looking forward for cost-effective and high-quality research, development, and manufacturing of drugs with more speed.

This sector is the quickest growing field in the country. The vertical growth is because of the linkages between IT and biotechnology, spurred by the human genome project. The promising start-ups are already there in Bangalore, Hyderabad, Pune, Chennai, and Delhi. There are over 200 companies functioning in these places. IT majors such as Intel IBM. Wipro are getting into this segment spurred by the promises in technological developments.

Government Initiatives

India, as a hub of scientific and academic research, was one of the first countries in the world to establish a nation wide bioinformatics network.

The department of biotechnology (DBT) initiated the program on bioinformatics way back in 1986-87. The Biotechnology Information System Network (BTIS), a division of DBT, has covered the entire country by connecting to the 57 key research centers. BTIS is providing an easy access to huge database to the scientists. Six national facilities on interactive graphics are dedicated to molecular modeling and other related areas. More than 100 databases on biotechnology have been developed. Two major databases namely coconut biotechnology databases and complete genome of white spot syndrome of shrimp has been released for public use. Several major international data bases for application to genomics and proteomics have been established in the form of mirror sites under the National Jai Vigyan Mission.

Advantages India has

India is well placed to take the global leadership in genome analysis, as is in a unique position in terms of genetic resources. India has several ethnic populations that are valuable in providing information about disease predisposition and susceptibility, which in turn will help in drug discovery.

However, as India lacks the records of clinical information about the patients, sequence data without clinical information will have little meaning. And hence partnership with clinicians is essential. The real money is in discovering new drugs for ourselves and not in supplying genetic information and data to the foreign companies, who would then use this information to discover new molecules.

The genomic data provides information about the sequence, but it doesn’t give information about the function. It is still not possible to predict the actual 3-D structure of proteins. This is a key area of work as tools to predict correct folding patterns of proteins will help drug design research substantially. India has the potential top lead if it invests in this area.

Looking at this biotech and pharma companies need tremendous software support. Software expertise is required to write algorithms, develop software for existing algorithms, manage databases, and in final process of drug discovery.

Some major opportunity areas for IT companies include:

1. Improving content and utility of databases.
2. Developing better tool for data generation, capture, and annotation O Developing and improving tools and databases for comprehensive functional studies.
3. Developing and improving tools for representing and analyzing sequence similarity and variation.
4. Creating mechanisms to support effective approaches for producing robust, software that can be widely shared.

Problems in the sector

The major issue for India is its transition from, a recognized global leader in software development to areas of real strength upon which it can capitalize in the biosciences. The identifiable areas are in computation biology and bioinformatics, where a substantial level of development skills are required to develop custom applications to
knot together and integrate disparate databases (usually from several global locations), simulations, molecular images, docking programs etc.

The industry people, meanwhile, say that the mushrooming of bioinformatics institutes is creating a problem of finding talented and trained individuals in this industry. While many of them have a superficial knowledge and a certificate, India lacks true professionals in this area. Most people, who opt for bioinformatics are from the life sciences areas that do not have exposure to the IT side of bioinformatics, which is very important. Another issue is that some companies face shortage of funds and infrastructure. The turn around time for an average biotech industry to breakeven would be around three to five years.

**BIOLOGICAL DATABASES:**

A biological database is a large, organized body of persistent data, usually associated with computerized software designed to update, query and components of the data stored with in the system. A single database might be a single file containing many records, each of which includes the same set of information.

For example, a record associated with a nucleotide sequence database typically contains information such as contact name, the input sequence with a description of the type of molecule, the scientific name of the source organism from which it was isolated, and often literature citations associated with the sequence.

*For researches to benefit from the data stored in a database, to additional requirement must be met:*

1. Easy access to the information and
2. A Method for extracting only that infraction needed to answer scientific biological questions

**Biological Databases**

*These are three types of biological databases:*

1. Flat File database  
2. Relational database  
3. Object oriented database

**1. Flat File database:** A flat file database is simply an ordered collection of similar files usually conforming to a standard format for their content. The emphasis in formatting data for a flat file database is at the character level i.e., at the level of how the data would appear if it were printed on a page. Flat file database are often made searchable by indexing. An index pulls out a particular attribute from a file and pairs the attribute value in the index with a file name and location. It’s just analogous to book index.

Many of the popular biological databases began as a flat file database. PDB (protein Data Bank) is the best example of flat file database. The PDB began by using flat files in a well known PDB formal. The format of their flat files was designed to be read easily by FORTRAN.

**2. Relational database:** In a relational database, the information is stored in a collection of tables. The flat file that describes a protein structure is like a bound book. These are chapter about the origin of the sample, how the database was collected, the sequence the secondary structure and the position of the atoms. In relational database, the information in each chapter is put into separate tables, and instead of having its own books, each protein has its own set of tables. So, there are tables of experimental conditions, second structure elements, atomic positions etc.

**3. Object oriented database:** An object oriented data base system is a DBMS that is consistent with object oriented programming principles. The practical upshot of the object oriented approach in the database world is the emergence of DBMS’s that are flexible enough to the store more than just table and to handle functions behind those in a rigidly defined query language vocabulary. Since object oriented database handle data as object rather than as table. An object oriented database can provide access to image and video files within the same database. Object oriented database don’t force the use of SQL (structure query language), but rather provide flexible binding to programming languages.

**Biological database Management Systems:** Database don’t just happen, they are maintained by database management systems. There are flat file indexing system, RDBMS’s, object oriented (ODBMS’S) and object relational hybrids.

**Biological Database Searching**

There are two types of biological database search:

1. **Boolean search**  
2. **Fuzzy search**

**1. Boolean search:** All search engine use some form of Boolean logic, as the query forms for most of the public biological databases. Boolean queries join a series of search terms with the operators ‘AND ‘or’ and ‘NOT’. The meaning of these operators is straight forward.
Joining two keyword with ‘AND’ finds document that contain only keyword 1 and keyword 2, using ‘OR’ finds document that contain either keyword 1 ‘or’ keyword 2 (or both); and using NOT finds documents that contain keyword 1 but not keyword 2.

Search engine differ in how they interpret a space or an implied operator. Some search engines consider a space an ‘OR’ so when you type protein structure, you are really asking for proteins structure. Eg. Excite search engine defaults to ‘OR’. Similarly google defaults to ‘AND’, so you will find only reference that contain protein and structure. Boolean queries are read from left to right just like text.

2. Fuzzy search: Fuzzy search lets the users to find documents even if the word being searched are misspelled. The term first literally means a different word or something blurred. Suppose we want to search for an expression DAVID in a database version. OWL29.6. We see that for the expression DAVID we get exact ‘71’ matches. Now, if we introduce one fuzzy position (Eg. Let us say that the final D may belong to the group DEQN), then we find ‘252’ matches in this version of the database, with two fuzzy positions, we retrieve, ‘925’ matches with three fuzzy positions, the number increases to ‘2739’, and with tolerance at all five positions, ‘51506’ matches are retrieved. Thus, more fuzzy the pattern become, the more matches are retrieved:

<table>
<thead>
<tr>
<th>Expression</th>
<th>No. of exact matches (OWL29.6)</th>
</tr>
</thead>
<tbody>
<tr>
<td>D-A-V-I-D</td>
<td>71</td>
</tr>
<tr>
<td>D-A-V-[DEQN]</td>
<td>252</td>
</tr>
<tr>
<td>[DEQN]-A-B-I-[DEQN]</td>
<td>925</td>
</tr>
<tr>
<td>[DEQN]-A-[VLI]-I-[DEQN]</td>
<td>2739</td>
</tr>
</tbody>
</table>

DATA ANALYSIS (WITH PERL & PYTHON)

A vast assortment of software tools exists for bio-informatics. In bioinformatics, that often means writing programs that sift-through mountains of data to extract just the information you require. Perl, the practical extraction and reporting language, is ideally suited to this task.

Why perl/phyton used: There are a lot of programming languages out there. In the survey of bioinformatics software, we have programs written in Java, C and FORTRAN. So why we use PERL? The **answer in efficiency** i.e., it takes for less programming time to extract data with perl than with ‘C’ or with Java.

Perl has following merits that make it an obvious choice:

1. Its efficiency, *i.e.*, programming time to extract data.
2. Perl, with its highly developed capacity to detect patterns in data, and especially strings of text, is the most obvious choice.
3. Perl has a flexible syntax, or grammar, so if you are familiar with programming in other language such as ‘C ‘or BASIC, it is easy to write perl code in a C-like ‘or’ BASIC-like dialect.
4. Perl also takes care of much of the dirty work involved in programming, such as memory allocation.
5. it’s often the case that programming problems requiring many lines of code in C ‘or’ Java may be solved in just a ten lines of perl.
6. Perl has a mountain of features, and it’s unrealistic to assume you can master it without a serious commitment to learning the art of computer programming.

String contained in a block of sequence data. To do this, you need a slightly more complex Perl program that might look like this:

```perl
#!/usr/bin/perl -w
# Look for nucleotide string in sequence data
my $target = "ACCCTG";
my Search-string =
  'CCACACCACACCCACACACCACACCACACCACACCACACCACACCACACCACACCACACACAC;
  'CATCCCTAACACTACCCTAACACAGCCCTAATCTAACCCTGGCCAACCTGTCTCTAACTT";
my @matches;
# Try to find a match in letters 1-6 of $ search string then look at letters 2-7,
# and so on. Record the starting offset of each match.
For each my $i (0. . length $search_string) {
  if ($target eq substr ($search_string, $i, length $target)) {
    push @matches, $i;
  }
}
# Make @matches into a comma-separated list for printing
```
print “My matches occurred at the following offsets : @matches. \n”;
print “done\n”;

This program is also short and simple, but it’s still quite powerful. It searches for the target string “ACCCTG” in a sequence of data and keeps track of the starting location of each match. The program demonstrates variables and loops, which are two basic programming constructs you need to understand to make sense of what is going on.

The next obvious choice would probably be python. Python is a fully object-oriented scripting language introduced by Guido van Rossum in 1988. Python has some outstanding contributed code, including a library of functions of structure biology.

A Bioinformatics Example : One of the strengths of Perl—and the reason that bioinformaticians love it—is that with a few lines of code, you can automate a tedious task such as searching for nucleotide Variables

A variable is a name that is associated with a data value, such as a string or a number. It is common to say that a variable stores or contains a value. Variables allow you to store and manipulate data in your programs; they are called variables because the values they represent can change throughout the life of a program.

Our sequence matching program declares four variables $starget, $search_string, @matches, and $i. The $ and @ characters indicate the kind of variable each one is. Perl has three kinds of variables built into the language: scalars, arrays, and hashes.

DATABASE SEARCHES

White sequence alignments can be invaluable tool for comparing two know sequences, a far more common use of alignments is to search though a database of many sequences, to retrieve those that are similar to a particular sequence. In performing database searches, the size and sheer number of sequences to be searched (at the time of the writing of this text, there were more then 13 million sequence in GenBank) often precludes the obvious and direct approach of aligning a query sequence with each sequence in the database and returning the sequences with the highest alignment scores. Instead, various indexing schemes and heuristics must be used to speed the search process. Many of the commonly used database search algorithms are not guaranteed to produce the best match from the database, but rather have a probability of returning most of the sequences that align well with the query sequence. Nevertheless, the efficiency of these tools in finding sequences similar to a query sequence from the vast repositories of available sequence data has made them invaluable tools in the molecular biology.

Blast and its relatives

One of the most well-known and commonly used tools for searching sequence databases is the BLAST algorithm, introduce by S. Alychul in the early 1990s. The original BLAST algorithm searches a sequence database for maximal ungapped local alignments. In other words, BLAST finds subsequences from the database that are similar to subsequence in the query sequence. Several variations of the BLAST algorithm are available for searching protein or nucleotide sequence databases using protein or nucleotide query sequences.

A FASTA search begins by breaking the search sequence into words. For genomic sequences a word size of 4 to 6 nucleotide is generally used, while 1 to 2 residues are generally used for polypeptides. Next a table is constructed for the query sequences showing the locations. By comparing the offset tables for two sequences, area of identity can be found quickly. Once these areas are found, they are joined to form larger sequences, which are then aligned using a full Smith-Waterman alignment. However, because the alignment is constrained to known region of similar sequence, FASTA is much faster than performing a complete dynamic programming alignment between query sequence and all possible targets.
PATTERN RECOGNITION AND PREDICTION

In investigating the meaning of sequences two distinct analytical themes have emerged: In the first approach, PATTERN RECOGNITION techniques are used to induce similarity between sequences and hence to inner related structure and functions.

In the second approach, PREDICTION methods are used to deduce 3D structure directly from the linear sequence. The development of more powerful pattern recognition and structure prediction techniques will continue to be a dominant theme in bioinformatics research while the number of experimentally determined protein structure remains small. The entire outset, it is important to high list the distinction between pattern recognition and prediction. As mentioned above, these are the principal analytical approaches in bioinformatics, and the concepts are often used interchangeably. However, in terms both of what they attempt to achieve and of what, in fact, they can achieve, these methods are really quite different and should not be confused.

Pattern Recognition

Methods, as the name suggests, are built on the assumption that some underlying characteristics of a protein sequence, or of a protein structure, can be used to identify similar traits in related proteins. In other words, if part of a sequence or structure is preserved of conserved (whether because it is important to the activity of the protein, or because it is critical to its fold), this characteristic may be used to diagnose new family members. If such concord traits are distilled from known protein family, and stored in databases, then newly sequenced proteins may be rapidly analyzed to determine whether they contain these previously recognized family characteristics. Searches pattern databases, and of fold template database, are now routinely used to diagnose family relationships, and hence to infer structures and function of newly determined sequences.

Prediction

By contrast, prediction, the Holy Grail of bioinformatics, is still not possible, and is unlikely to so for decades to come. Prediction stems from the idea that a functional site, or indeed a complete structure, need a complete structure, need not have ‘seen’ before, but can be deduced directly from acid sequence. This approach obviates the need to create reference databases of functional site or structural templates, but requires instead the design of sophisticated software capable of meaning-fully addressing the folding problem.

References:

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<th>Author/Authors name</th>
<th>Publication House</th>
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