Role of Bio-informatics in Molecular Medicine

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INTRODUCTION-

Bioinformatics is the application of tools of computation and analysis to the capture and interpretation of biological data .Bioinformatics is essential for management of data in modern biology and medicine .The bioinformatics toolbox includes computer software programs such as BLAST and Ensembl, which depend on the availability of the internet .Analysis of genome sequence data, particularly the analysis of the human genome project, is one of the main achievements of bioinformatics to date .Prospects in the field of bioinformatics include its future contribution to functional understanding of the human genome, leading to enhanced discovery of drug targets and individualised therapy . Bioinformatics is the field of endeavor that relates to the collection, organization and analysis of large amounts of biological data using networks of computers and databases (usually with reference to the genome project and DNA sequence information) .Bioinformatics studies two important aspect of modern biology.

1.One is the flow of genetic information from DNA of individual organism up to the characteristics of a population of such organisms (with an eventual passage of information back to the genetic pool, as encoded within DNA).

2.The flow of experimental information from observed biological phenomena to models that explain them, and then to new experiments in order to test these models. The science of Bioinformatics has their own base in the number of molecular activities like organization of DNA sequence and protein three-dimensional structural data collections in the 1960's and 1970's. It has become a major academic and industrial enterprise with the introduction of biological experiments that rapidly produce huge amounts of data like the multiple genome sequencing projects, the large scale analysis of gene expression, and the large scale analysis of protein-protein interactions. Basic biological science always play a key role in the clinical medicine (and clinical medical information systems), and is creating a new generation of epidemiologic, diagnostic, prognostic, and treatment modalities.

Bioinformatics efforts that appear to be wholly geared towards basic science are likely to become relevant to clinical informatics in the coming decade. For example, DNA sequence information and sequence annotations will appear in the medical chart with increasing frequency. The algorithms developed for research in bioinformatics will soon become the part of clinical as well as basic information systems.

ROLE OF BIOINFORMATICS IN FUNCTIONAL GENOMICS – Genomics will make three major contributions to drug therapy. In the first place, new genes, which code for secreted proteins, will continue to be identified. Second, genomic sciences are about to identify the most suitable targets for drug intervention. Although current drug therapy rests on approximately 500 such targets, the emerging number is estimated to be in the range of 5,000 to 10,000 target

molecules. Third, we are learning why patients respond differently to drugs. The genetic patterns that define these responses are being identified and used to target drugs more effectively during their development. This approach will also allow for individualized drug therapy. The existence of these genes does, of course, not detract from the importance of environmental influences. These 1000 disease genes might not always guide the synthesis of proteins that are good drug targets. However, it appears reasonable to assume that each of these disease genes, or rather proteins that are specified by the disease genes connects with at least 5-10 proteins that represent feasible levels for drug intervention. On the basis of these calculations, one can assume that there are 5000-10,000 gene products that can be used as targets for drug interventions. Even if the lower number would turn out to be the proper approximation, the utilization of information stemming from the Human Genome Project and from other related programs would allow for a tenfold increase in the number of drug targets, compared with the current situation. Such an expansion of the operational possibilities of drug therapy would lead to more specific therapies and into therapeutic methods that are much closer to the molecular causes of diseases than current therapies .There are few reason due to which bio-informatics become permanent part of genomics.These are –

1.Due to need of improved software that align two genomic sequences and has a authentic statistical basis

2.A strong system for the prediction about the gene , that can combine the genomic sequence compression , intrinsic sequence properties and result from database search of protein sequence and ESTs

3.Automated and reliable software for aligning three or more sequence alignments

4.Better methods for displaying and browsing genomic sequence alignments

5.Good quality of data setting and protocol for evaluation of the accuracy and performance of the genomic alignment software.

IN PHARMACOGENOMICS USING SNPs– Pharmacogenomics is improving the drug discovery process by accelerating target discovery and by helping to select the most promising drug candidates. High Throughput Screening (HTS) is now a days proved to be an excellent bioinformatics tool in during discovery . A-Switch from descriptive to causal Diagnostics- Define Genes and Gene Products which are causally responsible for the pathogenic process Determine Gene Products which are suited as Drug Targets B- Two Data Sets have to be known Gene Sequences Profiles of Gene Product Expression

The role of single nucleotide polymorphism in understanding of these diseases is that SNPs can cause a diseases like Sickle cell anemia and further they can be used a s a marker for a diseases .these can be used to denote the prevalence of a diseases . SNP is more frequently found in diseased humans than in non affected individuals .Likewise Apo E is a SNPs marker for Alzheimer ,[S] Diseases. They are different sites for the study related to SNPs-

http://lpg.nci.nih.gov/GAI

http://www.genome.wi.mit.edu/cvar_snps

http://snp.cshl.org

http://www.ncbi.nlm.nih.gov/SNP

http://hgbase.interactiva.de

SNPs and Diseases- following are the well known diseases -

Migraine headaches

Muscular dystrophy

Sickle cell anemia

Type-II diabetes

Beta-thalassemia

Phenyl ketonuria

Fibro muscular displasia

Hypertension

A disorder associated with Apo E2

LIST OF GENES WITH SNPs STUDY ALREADY REPORTED –

Catechol-O.methyltransferase (COMT)

Cytochrome P450 1B1 (CYP1B1)

Cytochrome P450 17 (17-Alpha-Hydroxylase)

Glutathione Peroxidase (GPX1)

Glutathione S-transferase P1 (GSTP1)

Methylguanine-DNA Methyltransferase (MGMT, AGT)

Myeloperoxidase (MPO)

Tumor Necrosis Factor-alpha (TNF-a)

Xeroderma Pigmentosum, Complementation Group D (XPD)

Xeroderma Pigmentosum, Complementation Group F (XPF, ERCC4)

X-ray Repair, Complementing Defective, in Chinese Hamster, 1 –XRCC1

There are few more sites if someone else want to things in detail gain study the in detail

http://www.aacc.org/pharmacogenetics/.

http://www.newchemicalentities.com/ ,

http://www.orchid.com/, and http://www.genescreen.com/.

FUTURE OF BIOINFORMATICS –The practice of studying genetic disorders is changing from investigation of single genes in isolation to discovering cellular networks of genes, understanding their complex interactions, and identifying their role in disease. As a result of this, a whole new age of individually tailored medicine will emerge. Bioinformatics will guide and help molecular biologists and clinical researchers to capitalise on the advantages brought by computational biology. The clinical research teams that will be most successful in the coming decades will be those that can switch effortlessly between the laboratory bench, clinical practice, and the use of these sophisticated computational tools.