IT Driven 'Omics' Technology in Health Management

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***Abstract* —Emergence of information technology into the field of biology has promoted cosmic understanding of complex nature of life at all levels of understanding including sub cellular, cellular, molecular as well as system level. Knowledge at the gene, protein, protein- protein interaction leads to the different interdisciplinary areas such as bioinformatics, nanoinformatics and other areas with the suffixes 'omics'. Omic' technologies espouse a holistic view of the molecules that make up a cell, tissue or organism and can be applied for the greater understanding of normal physiological processes in screening, diagnosis and prognosis as well as aiding our understanding of the aetiology of diseases**

Keywords — Information technology, omics technology, health management

I.INTRODUCTION

Emergence of information technology into the field of biology has promoted cosmic understanding of complex nature of life. As Cheney (2003) states: "Understanding the role of IT for science is important because of the central role of science in today's information society. Advances in science affect economic performance and the achievement of societal goals, from health to national security. As a result, it is important for policy makers to understand how IT affects the quality and productivity of science [1].Even though information technology has been used in the relm of biological science for a long time, many of them were hesitating to adopt computational models in life science. But in the present scenario, attitude towards the application of computer assisted technologies in bioscience changed transforming biology with a new visage. Lander et al. (1991) observed that biology had been going through major changes driven by computing for the previous ten years [2]. Since the discovery in the 1950s of how genetic information is coded in DNA, the biosciences have increasingly become much more dependent on IT. Now biology is much more reliant on information technology as it renders its services at all levels of understanding including sub cellular, cellular, molecular as well as system level.

II.'OMIC ' TECHNOLOGIES

Omic' technologies adopt a holistic view of the molecules that make up a cell, tissue or organism. They are aimed primarily at the universal detection of genes (genomics), mRNA (transcriptomics), proteins (proteomics) and metabolites (metabolomics) in a specific biological sample in a non-targeted and non-biased manner. This can also be referred to as high-dimensional biology; the integration of these techniques is called systems biology[3,4]. Omic technology can be applied not only for the greater understanding of normal physiological processes but also in disease processes where they play a role in screening, diagnosis and prognosis as well as aiding our understanding of the aetiology of diseases. [5]

A. Genomics

Genomics is the methodical study of an organism's genome. There are different databases that allow the submission, storage, analysis and data mining of gene sequences. International Nucleotide Sequence Databases (INSD) consisiting of DNA Data Bank of Japan (National Institute of Genetics), EMBL (European Bioinformatics Institute) , GenBank (National Center for Biotechnology Information) are repositories for nucleotide sequence that exchange new and updated data on a daily[6]. BioGraph, ConsensusPathDB, Entrez, mGen containing four of the world leading databases GenBank, Refseq, EMBL and DDBJ. EcoCyc a database that describes the genome and the biochemical machinery of the model organism, Ensembl, Repbase, integrall,EuPathDB[6] are some of the other commonly entrusted genomic databases .

Microarray technology that advanced significantly in recent years has made gene analysis faster and easier.DNA microarrays measure differences in DNA sequence between individuals and the expression of thousands of genes can be analyzed simultaneously. They can reveal abnormalities such as chromosomal insertions and deletions or abnormal chromosomal numbers in a process called comparative genomic hybridization. [5] Availability of genome sequences of pathogens has provided a incredible amount of information that can be constructive in drug target and vaccine target recognition

B. Proteomics

The proteome is defined as the set of all expressed proteins in a cell, tissue or organism.[7] Proteomics aims to characterise information flow within the cell and the organism, through protein pathways and networks,[8] with the eventual aim of understanding the functional relevance of proteins.[9]Proteomics Identifications Database (PRIDE), ProteomeScout, MitoMiner,are some of the major proteomics databases and UniProt , Swiss-Prot, PROSITE, Pfam etc are some of the protein sequence databases widely accepted all over the world. The proteome is a dynamic reflection of both genes and the environment and is thought to hold special promise for biomarker discovery because proteins are most likely to be ubiquitously affected in disease and disease

response.[10]This is reflected in the many protein disease biomarkers already available (e.g. CA125 and alpha-fetoprotein)

C. Metabolomics

Metabolomics can generally be defined as the study of global metabolite profiles in a system (cell, tissue or organism) under a given set of conditions.[11] The metabolome is the final downstream product of gene transcription and, therefore, changes in the metabolome are amplified relative to changes in the transcriptome and the proteome.[12] Studying the reaction of various organisms to diverse stresses and environments at the genetic, transcript, protein, and metabolite levels by means of different methods and comparing these results with those of other organisms will fortify their incorporation into a systems biology scaffold. Recent progress in this field reveals that integrated metabolomic analyses can provide information on the stage, subtype and grade of breast tumors and give mechanistic insights [13]

D. Pharmacogenomics

Pharmacogenomics the intersection of genomics and pharmacology is the study of the role of inheritance in individual variation in drug response which can potentially be used to individualise and optimise drug therapy.[14] Pharmacogenomics is particularly significant for oncology, as severe systemic toxicity and unpredictable effectiveness are hallmarks of cancer therapies.[14] Systems approaches to anomalies such as cancer, cardiovascular disease and obesity give the chance to facilitate greatly the achievement of selecting new targets for treatments and drug development.

III. COMPUTATIONAL DRUG DESIGNING

The completion of the human genome project has revolutionised the field of drug-discovery against threatening human pathogens [15].The strategies for drug design and development are progressively shifting from the genetic approach to the genomic approach [16]. For Example Some ALL patients have evidently characterized chromosomal aberrations and the practical cost of these aberrations are not fully understood. Bioconductor tools were used to build up a new characterization of the disparity in gene expression between ALL patients with two specific forms of chromosomal translocation[17]. It is evident that diseases in biological organisms are caused by malfunction of a protein which is a product of a particular gene in performing its function in general. The control of the biological system is made possible when a drug molecule interacts with the active site of the target protein [18].

Computational drug design involves finding the molecular structures that will create a strong interaction with the active site of the target protein and chemical activities that leads to protein folding. Modified forms of ‘Gleevec’a drug against Chronic myeloid leukaemia is a product of computational drug designing, that is effective against later stages of CML. [19]. The influence of the completed genome sequence on vaccine design approaches has been effective for organisms like *Mycobacterium tuberculosis* [20] Molecular profiling through metabolomics has made its presence in gynaecological oncology in which proteomic profiling was initially applied to human serum to find out ovarian cancer by Petricoin *et al*.[21] Gadducci *et al*.[22] that give a good overview of the markers associated with ovarian, endometrial and cervical cancer and the role proteomic profiling has to play. CA125 is the most reliable marker in ovarian cancer. In recent times the autoantibody against the S100A7 protein has been found to be elevated in early and late-stage ovarian cancer but the clinical usefulness has yet to be investigated[23] .There is Computer Aided Drug Design (CADD) Three dimensional database system runs to find out best suited pharmacophore for its availability, solubility and toxicity determination through what atom connected with other atom in what manner and how these two atoms close together in spatial three dimensional sense [24].

IV. CONCLUSION

Information technology has great impact on diverse area of medical and biological research as well as practice for its new direction and perspective of ideas with cost effective design and protocol. Development of new softwares is enabling betterment of medical field. There are so many options to test drugs, vaccines using computational modelings of biological systems. As natural as well as anthropogenic reasons causes pollution, new diseases are emerging even at the genetic level perplexing the whole humanity. Here Computational simulations, biomodellings are inevitable for the better understanding, and treatment of the diseased world. Computational studies in biology make it possible to detect the rules of protein structure, function and protein-protein interactions. These will certainly speed up the drug design.

V. REFERENCES

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