APPLICATION OF BIOINFORMATICS IN MEDICINE pdf

1: Application of Bioinformatics in Medicine

Application of bioinformatics in which preventive medicine or preventive care are taken to prevent diseases, rather than curing them or treating their symptoms. The development of diagnostic tests are needed which provides precise details of the genetic mechanism of disease to measure an individual's inclination to different diseases which may.

It chiefly involves the building, updating and care of the database incorporating a wealth of biological information and at the same clip enable the users to analyse and research the information. The term medical information sciences trades with the application of fast turning computing machine engineering to the field of medical specialty ; it could be either medical instruction or for the intent of medical research which finally enhances our apprehension in the intervention of disease. Health information sciences With the promotion of scientific discipline and engineering, bioinformatics now emerges as a new aspect of scientific discipline which combines the Fieldss of Molecular Biology and Genetics, Biotechnology and Microbiology doing them interpreted and explored by agencies of computing machine engineering. The constitution of NCBI national Centre for biotechnology information in as a public database, has helped in circulating information across the universe thereby facilitates in tracking out the molecular procedures of the disease Fig 2a. In the ulterior stage many other databases were created such as Ensembl helping in tracking the familial mechanism responsible for the pathogenesis of the disease. Figure demoing the NCBI database page. The page shows the constitution of database in the twelvemonth and the assorted parametric quantities that can be explored utilizing this database. Bioinformatics, genomics and Disease Cracking the human genome codification and the publication of 3. It helps the other scientist and physicians to understand the molecular DNA codification the design of an person in item. The findings of the genome undertaking are: Single nucleotide polymorphism SNP contributes to the 0. They are functioning as a familial markers in correlating the drug efficaciousness and toxicity potency of any single Fig 3a. Bioinformatics packages are in current usage to track these concealed Single nucleotide polymorphism in human genome. Copy figure fluctuations CNVs are besides the other factor adding up another part in 0. The microarray engineerings along with the array algorithm are in current usage to track out these fluctuations. Figure demoing the human chromosomes 1, 2, 3 and 4 with the cistron venue mapped responsible for the diseases. VHL cistron on chromosome 3 mapped for illustration is a factor that participates sometimes in the pathogenesis of malignant neoplastic disease. The look degree of any peculiar cistron is non correlated with the degree of mRNA nowadays in the cell. Hence analyzing messenger RNA and DNA sequences entirely are non able to give the right look position of the cistrons ruling in a peculiar disease. Besides the human cistrons undergo alternate splice and RNA redacting mechanism which enhances a cistron potency in coding different proteins. Now the Fieldss of bioinformatics have besides collaborated with the scientific discipline of proteins to analyse and research every protein in the human organic structure Fig 4a. With the coming of X-ray crystallography and NMR Natural Magnetic Resonance , it is possible to capture and analyze proteins on the screen in their 3D construction. Today scientists are on the brink of making human proteome map and if they will be successful in their proteome map there will be a better quality of life functioning to minute inside informations. Figure demoing the diagnosing of nephritic carcinoma utilizing the 2D-Gel cataphoresis technique. Bioinformatics and Pharmacology The baronial award victor for decrypting cellular signaling mechanism, Alfred Gilman, a pharmaceutical chemist is now working on a undertaking to follow the cellular signaling mechanism map and transcribed that cognition on the computing machine screen. Now all the drug companies are utilizing the engineering of bioinformatics to develop more algorithms that can be used to foretell the map of proteins encoded by freshly discovered cistrons. These have been possible by the usage of assorted multiple alliance package that is in current usage to set up the phyletic relationships of the proteins under survey. Drug moorage is the most powerful engineering, possible through the bioinformatics cognition are in most common usage to happen the docking site of the drug in the active cleft of the proteins. The proteins take parting in the pathogenesis of diseases can be easy mapped out and docked on the computing machine screen which has revolutionized the filed of pharmacological medicine. Scientists presents are able to map the mutants in proteins giving drug-resistant belongings to the cells. This will

decidedly heighten the cognition of better understanding the drug resistant mechanism which are the common scenario observed in AIDS, Cancer and Tuberculosis. For TB, the genome of Mycobacterium TB has been sequenced and mapped to research the ABC transporters proteins present in the bacteriums giving drug immune belongings. Red coloring material indicates the mutants in the active site of the enzyme while violet colour indicates accessary alterations. Figure demoing the drug immune potency of HIV I resistant drugs. From the event in the history taking to the find of exchange of DNA strands by homologous chromosomes Joshua Lederberg in ensuing in familial fluctuation till the present twenty-four hours find by the Mario Capecchi and Oliver Smithies in who have applied the homologous recombination in mammalian cells, homologous recombination can happen between introduced DNA and the cell chromosomes besides repair with the aid of induced cistrons. They have conspicuously focused to aim the cistrons which are involved in mammalian organ development. Several congenital mistakes that arise in the event of deformity can besides be corrected. If the experiments successful on the mouse theoretical account as a cistron therapy beginning, the art of medical specialty will be enriched with biological science as a beginning of future developments in medical specialty. Current Technologies in complete meeting of information sciences with medical specialty: The map of many cistrons encoded by the human genomes is yet to be determined. Bioinformatics failed to decrypt the maps of some novel cistrons which does non exhibit homology sequence form with the other cistrons published in the database. For this in vitro research wet lab is required to execute the necessary uses. The human genomes submitted by both public and private sectors have gaps in them. Bio-informatics failed to mean the importance of these non-coding sequences and their being. We still do hold complete look libraries that are a expression signature of the cistrons present in a tissue or organ. Proteins, their location and alteration are non characterized. Not all diseased cistrons have been characterized so far and the familial differences between normal and disease province are non known. NMR and X-ray crystallography techniques are labour intensive and required a month or two. Bioinformatics failed to foretell the maps of fresh proteins whose construction are non similar to that of the other proteins present in the databases. The process of molecular moorage is really much clip devouring. Gene patenting should be banned because it halt the outshining hereafter of the patented cistron. Bio-informatics coder should be encouraged among pupils from MSc and PhD field. The writer is Dr.

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2: Bioinformatics Basics: Applications in Biological Science and Medicine - CRC Press Book

Bioinformatics is defined as the application of tools of computation and analysis to the capture and interpretation of biological data. It is an interdisciplinary field, which harnesses computer science, mathematics, physics, and biology (fig (fig1). 1).

This is an open access article distributed under the Creative Commons Attribution License , which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. Introduction Next-Generation Sequencing NGS technology, often seen as the foundation of precision medicine, has been successfully applied in oncology diagnostics and immunotherapy. With advances in gene diagnostics and immunotherapy, there may be a chance to control the development of cancers and alleviate the suffering of patients undergoing chemotherapy. To promote the translation of precision medicine from bench to beside and from application of genetic testing to personalized medicine, new analysis methods for NGS and genetic data need to be developed. For example, the NGS panel is quite different from whole genome sequencing WGS , focusing on fewer genes or regions but requiring greater precision and efficiency. For complex diseases, such as cancers, the driver genes are usually a cluster of genes in a regulatory network. Graph theories, such as shortest path analysis and random walk algorithms, will help dissect genomewide interactions into key modules or paths whose dysfunction is associated with disease progression. In this special issue, we have received 32 papers, out of which 19 has been accepted for publication. These papers could be generally divided into 3 categories including 1 computational models in identifying key biomarkers, pathways, and network modules associated with cancers and other diseases, 2 validations of the mechanisms of key biomarkers and their applications in tumor diagnosis and treatment, and 3 other studies in predicting tumor evolution, drug-disease association, disease sequence alignment, and so on. Na first identified survival-related gene network modules. By selecting representative genes from survival-related modules, they developed a deep learning-based risk stratification model for lung cancer. Their model showed high predictability for prognosis in independent datasets and its predictive value was independent of clinical and pathological features of lung cancer. Briefly, it firstly builds a biological pathway network, and then the GeneRank algorithm was used to select disease-associated pathways. The results by gene expression data of breast cancer show that the method proposes an effective way to identify reliable disease-associated pathways. The AUC of 0. Based on microarray data of influenza A disease, genes are selected as DNB and the 7th time period is defined as predisease state. This study provides a better understanding about gene expression in drug resistance samples, which is potentially useful for the treatment of osteosarcoma. They also demonstrated that p16 expression is significantly associated with early stage primary OPSCCs and the patients with p16 expression tend to show better survival following surgery and radiotherapy. Their results suggest that HMGB1 expression is significantly associated with lung cancer progression and might be a potential prognosis and therapeutic marker for lung cancer. In their experiments, the knockdown of IL-6 induced apoptosis and reduced cell proliferation and tumorigenicity and remarkably promoted the antitumor effect of gemcitabine. The results suggest that combining shRNA targeting IL-6 and gemcitabine is a potential clinical approach for pancreatic cancer therapy. They found that PD-L1 expression levels were correlated with disease progression. This is a potential mechanism by which glycyrrhizin can inhibit the progression of lung cancer. They showed that biochemical analyses of liver function tests at the initial diagnosis of colorectal liver metastases enable the stratification of patients into low- and high-risk groups, which may help clinicians to determine promising treatment strategies. The constructed phylogenetic trees have great performance in characterizing tumor development process, which outperforms other similar algorithms. The authors also implemented the method with an interactive web tool and applied the method to real microarray and RNA-seq datasets. In summary, we expect that this special issue updates novel NGS-based computational methods in predicting key genes, pathways, and network modules associated with diseases like cancers and experimental validations of their mechanisms, as well as their applications in disease diagnosis and treatment. The studies will serve as a bridge to connect computational models in mining clinical NGS data and translation of the findings into personalized

therapies for diseases. Acknowledgments We are grateful to the authors for contributing their valuable work to this special issue and the reviewers for this constructive comments. We also thank the editorial board for approving this topic and hope this issue will advance the research in disease-associated biomarker identification and its applications in translational research.

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3: Bioinformatics Applications in Life Sciences and Technologies

Applications of Bioinformatics in Medicine and Biotechnology August 3, Tanmoy Ray Leave a comment In simple words, bioinformatics is the application of information technology to study living things (or biological processes) at the molecular level (gene or protein level).

Gene prediction In the context of genomics , annotation is the process of marking the genes and other biological features in a DNA sequence. This process needs to be automated because most genomes are too large to annotate by hand, not to mention the desire to annotate as many genomes as possible, as the rate of sequencing has ceased to pose a bottleneck. Annotation is made possible by the fact that genes have recognisable start and stop regions, although the exact sequence found in these regions can vary between genes. The first description of a comprehensive genome annotation system was published in [19] by the team at The Institute for Genomic Research that performed the first complete sequencing and analysis of the genome of a free-living organism, the bacterium Haemophilus influenzae. Most current genome annotation systems work similarly, but the programs available for analysis of genomic DNA, such as the GeneMark program trained and used to find protein-coding genes in Haemophilus influenzae , are constantly changing and improving. Following the goals that the Human Genome Project left to achieve after its closure in , a new project developed by the National Human Genome Research Institute in the U. The so-called ENCODE project is a collaborative data collection of the functional elements of the human genome that uses next-generation DNA-sequencing technologies and genomic tiling arrays, technologies able to automatically generate large amounts of data at a dramatically reduced per-base cost but with the same accuracy base call error and fidelity assembly error. Computational evolutionary biology[edit] Further information: Computational phylogenetics Evolutionary biology is the study of the origin and descent of species , as well as their change over time. Informatics has assisted evolutionary biologists by enabling researchers to: The area of research within computer science that uses genetic algorithms is sometimes confused with computational evolutionary biology, but the two areas are not necessarily related. Comparative genomics The core of comparative genome analysis is the establishment of the correspondence between genes orthology analysis or other genomic features in different organisms. It is these intergenomic maps that make it possible to trace the evolutionary processes responsible for the divergence of two genomes. A multitude of evolutionary events acting at various organizational levels shape genome evolution. At the lowest level, point mutations affect individual nucleotides. At a higher level, large chromosomal segments undergo duplication, lateral transfer, inversion, transposition, deletion and insertion. The complexity of genome evolution poses many exciting challenges to developers of mathematical models and algorithms, who have recourse to a spectrum of algorithmic, statistical and mathematical techniques, ranging from exact, heuristics , fixed parameter and approximation algorithms for problems based on parsimony models to Markov chain Monte Carlo algorithms for Bayesian analysis of problems based on probabilistic models. Many of these studies are based on the detection of sequence homology to assign sequences to protein families. Pan-genome Pan genomics is a concept introduced in by Tettelin and Medini which eventually took root in bioinformatics. Pan genome is the complete gene repertoire of a particular taxonomic group: It is divided in two parts- The Core genome: Set of genes not present in all but one or some genomes under study. Many studies are discussing both the promising ways to choose the genes to be used and the problems and pitfalls of using genes to predict disease presence or prognosis. Oncogenomics In cancer , the genomes of affected cells are rearranged in complex or even unpredictable ways. Massive sequencing efforts are used to identify previously unknown point mutations in a variety of genes in cancer. Bioinformaticians continue to produce specialized automated systems to manage the sheer volume of sequence data produced, and they create new algorithms and software to compare the sequencing results to the growing collection of human genome sequences and germline polymorphisms. New physical detection technologies are employed, such as oligonucleotide microarrays to identify chromosomal gains and losses called comparative genomic hybridization , and single-nucleotide polymorphism arrays to detect known point mutations. These detection methods simultaneously measure several hundred thousand

sites throughout the genome, and when used in high-throughput to measure thousands of samples, generate terabytes of data per experiment. Again the massive amounts and new types of data generate new opportunities for bioinformaticians. The data is often found to contain considerable variability, or noise , and thus Hidden Markov model and change-point analysis methods are being developed to infer real copy number changes. Two important principles can be used in the analysis of cancer genomes bioinformatically pertaining to the identification of mutations in the exome. First, cancer is a disease of accumulated somatic mutations in genes. Second cancer contains driver mutations which need to be distinguished from passengers. These new methods and software allow bioinformaticians to sequence many cancer genomes quickly and affordably. This could create a more flexible process for classifying types of cancer by analysis of cancer driven mutations in the genome. Furthermore, tracking of patients while the disease progresses may be possible in the future with the sequence of cancer samples. Analysis of protein expression[edit] Protein microarrays and high throughput HT mass spectrometry MS can provide a snapshot of the proteins present in a biological sample. Bioinformatics is very much involved in making sense of protein microarray and HT MS data; the former approach faces similar problems as with microarrays targeted at mRNA, the latter involves the problem of matching large amounts of mass data against predicted masses from protein sequence databases, and the complicated statistical analysis of samples where multiple, but incomplete peptides from each protein are detected. Cellular protein localization in a tissue context can be achieved through affinity proteomics displayed as spatial data based on immunohistochemistry and tissue microarrays. Bioinformatics techniques have been applied to explore various steps in this process. For example, gene expression can be regulated by nearby elements in the genome. Promoter analysis involves the identification and study of sequence motifs in the DNA surrounding the coding region of a gene. These motifs influence the extent to which that region is transcribed into mRNA. Enhancer elements far away from the promoter can also regulate gene expression, through three-dimensional looping interactions. These interactions can be determined by bioinformatic analysis of chromosome conformation capture experiments. Expression data can be used to infer gene regulation: In a single-cell organism, one might compare stages of the cell cycle , along with various stress conditions heat shock, starvation, etc. One can then apply clustering algorithms to that expression data to determine which genes are co-expressed. For example, the upstream regions promoters of co-expressed genes can be searched for over-represented regulatory elements. Examples of clustering algorithms applied in gene clustering are k-means clustering , self-organizing maps SOMs , hierarchical clustering , and consensus clustering methods. Analysis of cellular organization[edit] Several approaches have been developed to analyze the location of organelles, genes, proteins, and other components within cells. This is relevant as the location of these components affects the events within a cell and thus helps us to predict the behavior of biological systems. A gene ontology category, cellular compartment, has been devised to capture subcellular localization in many biological databases. Microscopy and image analysis[edit] Microscopic pictures allow us to locate both organelles as well as molecules. It may also help us to distinguish between normal and abnormal cells, e. Protein localization[edit] The localization of proteins helps us to evaluate the role of a protein. For instance, if a protein is found in the nucleus it may be involved in gene regulation or splicing. By contrast, if a protein is found in mitochondria , it may be involved in respiration or other metabolic processes. Protein localization is thus an important component of protein function prediction. There are well developed protein subcellular localization prediction resources available, including protein subcellualr location databases, and prediction tools. Analysis of these experiments can determine the three-dimensional structure and nuclear organization of chromatin. Bioinformatic challenges in this field include partitioning the genome into domains, such as Topologically Associating Domains TADs , that are organised together in three-dimensional space.

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4: Bioinformatics - Wikipedia

Bioinformatics is being used in following fields: Microbial genome applications Molecular medicine Personalised medicine Preventative medicine Gene therapy.

Published online May 4. Sanches , 3 Jasjit S. Martins Find articles by Raul C. Suri Find articles by Jasjit S. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. Life sciences researchers collect and analyse a high amount of different types of scientific data, including DNA, RNA, and amino acid sequences, in situ and microarray gene expression data, protein structures and biological pathways, and biological signals and images of diverse origin. In recent years, a wealth of bioinformatics applications in the fields of basic and applied life sciences has changed the paradigm of both research and exploitation of knowledge. The development of novel and powerful bioinformatics tools dedicated to biological data acquisition, data mining, and analysis empowered both the basic and applied life sciences research. These bioinformatics developments span from tools for genome annotation and function prediction, gene expression analyses, and databases of biological information, to the emerging fields of biomedical applications of research, including the development of new bioinformatics-based devices and predictive applications. This special issue is composed of five original research papers selected after in-depth peer review. Understanding the genetic control of complex dynamic traits is of fundamental importance to agricultural, evolutionary, and biomedical genetic research. A statistical mapping framework, called functional mapping, has been developed and extensively used to characterize the quantitative trait loci QTLs or nucleotides QTNs that underlie a complex dynamic trait. However, this tool is not well suited when the curves are complex, especially in the case of nonmonotonic curves. Therefore, to overcome this problem, in their work J. Qi and colleagues propose the earliness index E-index to cumulatively measure the earliness degree to which a variable or dynamic trait increases or decreases its value. The authors show by both theoretical proofs and simulation studies that E-index is more general than functional mapping and can be applied to any complex dynamic trait, even those with nonmonotonic curves. RNA-Seq experiments are nowadays extensively used in a wide range of studies, spanning from genome-wide gene expression and regulatory mechanisms underlying basic physiological traits to human pathologies, including cancer. However, RNA-Seq data analyses are complex and require the use of several different tools to manipulate and process the retrieved data. The work presented by F. Russo and collaborators shows recent advancements and novelties introduced in RNASeqGUI, a graphical interface that allows the user to handle and analyse big data sets collected from RNA-Seq experiments in a fast, efficient, and reproducible way. The here presented version of RNASeqGUI combines graphical interfaces with tools for reproducible research, such as literate statistical programming, human readable report, parallel executions, caching, and interactive and web-exploitable tables of results. The Cancer Genome Atlas TCGA data portal is a platform containing tumor gene expression data, together with clinical information, enabling researchers to gather information on significant genomic alterations that occur during the development and metastasis of a tumor. To help biomedical researchers to identify gene expression patterns related to breast cancer survival, H. The authors believe that the use of TCGA4U will inspire more biomedical researchers to explore the biological mechanisms of those genes and more precisely explain their role in breast cancer development, paving the way for the discover of more targeted therapies and help more breast cancer patients. Predicting blood-brain barrier BBB permeation is essential for drug design of molecules that act in the central nervous system CNS. On the other hand, peripherally acting drugs must show limited ability to cross the BBB and therefore be devoid of action in the CNS. As an alternative to invasive animal experiments, in silico screening methods have been introduced to assist in the development of central nervous system active drugs. In their paper, D. Zhang and colleagues describe the design and implementation of a genetic algorithm to predict the BBB permeation ability of a given molecule, achieving more accurate results than currently available models. A single nucleotide polymorphism SNP is the result of the variation of a single nucleotide at a specific position in the genome. Besides introducing some degree of genetic variation

within a population, certain SNPs have been associated with the susceptibility of the individual to specific diseases. The accumulated knowledge resulting from the availability of human genome sequences and the association of specific SNPs with certain diseases prompted the development of the so-called predictive preventive personalized medicine. In their article, P. The development of bioinformatics tools have changed the paradigm of research in both basic and applied biological sciences, as illustrated by the papers published in this special issue. While these tools enable scientists to gain knowledge of complex biological systems, they also allow envisioning the exploitation of results towards novel developments in biomedical applications, thus contributing to promote both individuals and populations welfare.

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5: Applications of Bioinformatics

Bioinformatics is the use of information technology in biotechnology for the data storage, data warehousing and analyzing the DNA sequences. There is a tremendous application of bioinformatics in the field of homology and similarity tools, protein function analysis, personalised medicine, Gene therapy, Drug development, Comparative Studies and.

Tisdall, Beginning Perl for Bioinformatics, The huge mass of genomic data generated by high performance technologies are impossible to handle without a parallel development in computational resources enabling the storage, management and analysis of genomic information. Bioinformatics has acquired a fundamental role in the genomic era. The millions DNA sequences fragments produced by new generation sequencers are sorted and assembled with sophisticated bioinformatics software. Annotation software search for functional signals in the genomes to infer coding genes in the sequence and other type of functional non-coding sequences. Multidisciplinary and complementary teams Genomics has changed the sociology of biological research. The size and complexity of the genome projects require large collaborative scientific networks with complementary and multidisciplinary teams. Many of the publications about genomes are signed by dozens, even hundreds, of scientists coming from various research centers of different countries, and this trend is steadly growing. Small laboratories will continue existing, but its relative weigth will diminish in research. Comparative and evolutionary genomics The comparison of genomes either the close or distant species is a very useful approach to unravel the evolutionary processes that occur in the genome. This also makes it possible to know, from the conserved sequences between species, which are the genome functional parts. Comparing the human genome with the chimpanzee has allowed us to quantify the differences that have accumulated in both genomes since they diverged about six million years from their common ancestor. Functional genomics and other omics Functional genomics is the comprehensive analysis of function, expression and interaction of all genes in an organism. The transcriptome the sequences and expression patterns of all transcripts , the proteome the sequences and expression patterns of all proteins , the interactome the complete set of physical interactions between proteins, DNA sequences and RNA , the epigenome the complete set of epigenetic modifications on the genetic material of a cell , are some examples. Genome Wide Association analysis To find out what genetic variants make us different each other within our specie, it is necessary to study the genomes of many individuals. The HapMap project was the next milestone after the genome sequencing. His goal was to characterize genetic variation patterns in different ethnic groups of the human species, as a preliminary step to take on genome-wide studies able to associate genetic variants with different aspects on the phenotype, especially those that confer susceptibility to disease. The joint application of genetic variation efficient technologies, bioinformatics tools and statistical analysis make possible the comprehensive catalog of genetic variants affecting human phenotype, with their enormous implications arising for prevention, diagnosis and personalized treatment of diseases. Biomedicine The human genome will have profound effects on the fields of biomedical research and clinical medicine. Almost every disease has a genetic component. The completion of the human genome means that we can search for the genes directly associated with different diseases and begin to understand the molecular basis of these diseases more clearly. This new knowledge of the molecular mechanisms of disease will enable better treatments, cures and even preventative tests to be developed. Drug discovery Using computational tools to identify and validate new drug targets, more specific medicines that act on the cause not merely the symptoms of the disease can be developed. Personalized medicine Clinical medicine will become more personalized with the development of the field of pharmacogenomics. Today, doctors have to use trial and error to find the best drug to treat a particular patient as those with the same clinical symptoms can show a wide range of responses to the same treatment. Preventive actions such as change of lifestyle or having treatment at the earliest possible stages when they are more likely to be successful, could result in huge advances in our struggle to conquer disease. Gene therapy In the not too distant future, the potential for using genes themselves to treat disease may become a reality. Microbiology By studying microorganisms genome scientists can begin to understand these microbes at a very fundamental level and isolate the genes that give them their unique abilities to survive

under extreme conditions. The arrival of the complete genome sequences and their potential to provide a greater insight into the microbial world and its capacities could have broad and far reaching implications for environment, health, energy and industrial applications.

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6: Centre for Molecular and Biomolecular Informatics

Applications of Bioinformatics in Medicine and Biotechnology. Genomics: Bioinformatics plays a vital role in the areas of structural genomics, functional genomics, and nutritional genomics.

Bioinformatics plays a vital role in the areas of structural genomics, functional genomics, and nutritional genomics. Genetics is the study of individual genes and their roles in inheritance. In contrast, genomics aims at the collective characterization and quantification of genes, which direct the production of proteins with the assistance of certain enzymes and messenger molecules. The field of genomics generates a vast amount of data from gene sequences, their interrelation, and functions. Bioinformatics plays a very important role to manage this vast amount of data. Bioinformatics provides both theoretical bases and practical methods for detecting systemic functional behaviors of the cell and the organism. It covers emerging scientific research and the exploration of proteomes from the overall level of intracellular protein composition protein profiles , protein structure, protein-protein interaction, and unique activity patterns e. Proteomics is an important component of functional genomics, genetics, biochemistry, and molecular biology. Proteomics involves systematic, high-throughput approach to protein expression analysis of a cell or an organism. Typical results of proteomics studies are inventories of the protein content of differentially expressed proteins across multiple conditions. This can be achieved by deploying peptide mass fingerprinting and peptide fragmentation fingerprinting, gel technology, HPLC, and mass spectrometry. The vast protein data proteomics results can be managed and access easily by using bioinformatics tools, software, and databases. The microarray technique generates a vast amount of data, a single run generates thousands of data value and one experiment requires hundreds of runs. Bioinformatics is used for transcriptome analysis where mRNA expression levels can be determined. Cheminformatics involves organization of chemical data in a logical form to facilitate the retrieval of chemical properties, structures and their relationships. Bioinformatics is used to identify and structurally modify a natural product, to design a compound with the desired properties and to assess its therapeutic effects, theoretically. Cheminformatics analysis includes analyses such as similarity searching, clustering, QSAR modeling, virtual screening, etc. Bioinformatics tools are very effective in prediction, analysis and interpretation of clinical and preclinical findings. Computational methods and bioinformatics tools are used to predict the drug-likeness. It basically means the identification and elimination of candidate molecules that are unlikely to survive the later stages of discovery and development. More importantly, bioinformatics is also laying the foundation for the evolution of the field of Computation Synthetic Biology CSB. Drugs are often given in combination in order to improve the therapy success rate. The relationship between the molecular data pertaining to a patient and their disease phenotype are complex and cannot be determined manually. Bioinformatics is an essential component in basic research, in the development of new concepts for diagnosis and therapy as well as in clinical practice. Bioinformatics can play a central role in interpreting the molecular data and as an instrument for providing recommendations for the practicing physician. Agricultural Science Crop Improvement.

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7: Bioinformatics: Medical Applications | The Center for Translational and Basic Research (CTBR)

Bioinformatics. Bioinformatics involves the application of computer science to biological and medical research. With the vast amount of research and discoveries being made every day, it is necessary to involve extremely powerful computers to categorize, organize, analyze and keep track of all the information.

History[edit] Translational bioinformatics is a relatively young field within translational research. However, this attempt was largely unsuccessful as preliminary attempts for automation resulted in misinformation. TBI needed to develop a baseline for cross-referencing data with higher order algorithms in order to link data, structures and functions in networks. The past decade has also seen the development of personalized medicine and data sharing in pharmacogenomics. These accomplishments have solidified public interest, generated funds for investment in training and further curriculum development, increased demand for skilled personnel in the field and pushed ongoing TBI research and development. Currently, it is partially deployed in drug development , regulatory review, and clinical medicine. General topics that appear in recent conferences include: Since the completion of the human genome , new projects are now attempting to systematically analyze all the gene alterations in a disease like cancer rather than focusing on a few genes at a time. In the future, large-scale data will be integrated from different sources in order to extract functional information. The availability of a large number of human genomes will allow for statistical mining of their relation to lifestyles, drug interactions, and other factors. Translational bioinformatics is therefore transforming the search for disease genes and is becoming a crucial component of other areas of medical research including pharmacogenomics. This suggests that cloud-computing technologies might be a valuable and economical technology for facilitating large-scale translational research in genomic medicine. For instance, the GenBank database, funded by the National Institute of Health NHI , currently holds 82 billion nucleotides in 78 million sequences coding for , species. The equivalent of GenBank for gene expression microarrays, known as the Gene Expression Omnibus GEO , has over , samples from 7, experiments and this number doubles or triples each year. All together, TBI has access to more than a quarter million microarray samples at present. In the data consolidation approach, data is extracted from various sources and centralized in a single database. This approach enables standardization of heterogeneous data and helps address issues in interoperability and compatibility among data sets. However, proponents of this method often encounter difficulties in updating their databases as it is based on a single data model. In contrast, the data federation approach links databases together and extracts data on a regular basis, then combines the data for queries. The benefit of this approach is that it enables the user to access real-time data on a single portal. However, the limitation of this is that data collected may not always be synchronized as it is derived from multiple sources. Data warehousing provides a single unified platform for data curation. Data warehousing ingrates data from multiple sources into a common format, and is typically used in bioscience exclusively for decision support purposes. Currently, numerous software and methodologies for querying data exist, and this number continues to grow as more studies are conducted and published in bioinformatics journals such as Genome Biology , BMC Bioinformatics , BMC Genomics, and Bioinformatics. Data integration serves to utilize the wealth of information available in bioinformatics to improve patient health and safety. An example of data integration is the use of decision support systems DSS based on translational bioinformatics. DSS used in this regard identify correlations in patient electronic medical records EMR and other clinical information systems to assist clinicians in their diagnoses. Second- and third-generation versions of sequencing systems are planned to increase the amount of genomes per day, per instrument, to According to the CEO of Complete Genomics Cliff Reid, the total market for whole human genome sequencing around the world has increased five-fold during and , and was estimated to be 15, genomes for This caused a significant drop in sequencing costs. The overarching goal for TBI is to "develop informatics approaches for linking across traditionally disparate data and knowledge sources enabling both the generation and testing of new hypotheses". Furthermore, analytic and storage capabilities are hindered due to large volumes of data present in current research. This problem is projected to increase with personal genomics as it will create an even greater accumulation of data. It is also seen as a

means to shift clinical trial designs away from case studies and towards EMR analysis. A collection of predictions is as follows: Lesko states that strategy must occur in the European Union to bridge the gap between academic and industry in the following ways â€" directly quoted: What information consumes is rather obvious: Hence a wealth of information creates a poverty of attention and a need to allocate that attention efficiently among the overabundance of information sources that it might consume. Associations, conferences and journals[edit] Below is a list of existing associations, conferences and journals that are specific to TBI. By no means is this an all-inclusive list, and should be developed as others are discovered. Associations American Medical Informatics Association:

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8: Translational bioinformatics - Wikipedia

Accordingly, bioinformatics has become an essential component of all biomedical projects and a core competency for all biomedical scientists. This symposium featured distinguished bioinformatics scientists from the United States and around the world, who presented some of the latest applications of bioinformatics in medicine and health care.

About Current Bioinformatics and Medicine Bioinformatics will have a series of important roles in the medicinal sciences. Biology and medicine are living in a time of rapidly increasing involvement of knowledge about processes at the molecular level, and bioinformatics can help cope with this rapid increase of required skills. An important function for bioinformatics is explaining things at the molecular level. To do so, enzymes from pathogens or mutated native enzymes can be modelled by homology. These models can be used to explain the effects determined by molecular biology. P63 mutations The human genome will be known and properly annotated in a few years. At that moment we know nearly all targets for medicins. Getting the same information for a parasite will enable us to make better medicins against infections with less side effects. After all, such a medicin should block a process that is crucial for the parasite, but it should of course not block the equivalent process in the host. Parasite and active site Many research projects are aiming at the discovery of information about molecules or molecular interactions. Bioinformatics can help here. Correlated mutation analysis CMA is a technique to find co-variation in pairs of sequences. Bioinformaticists originally thought that CMA could be used to solve the protein folding problem, but it became clear that co-variation is a much better indicator for functional dependencies and inter-molecular contacts. It is more important for the medicinal sciences, however, to get an overview of entire process and not just about one or a few steps. Putting the pieces of the big jigsaw puzzle together, to get an overview of networks of interconnected steps is a typical task for bioinformatics. Networks and regulation Information about a molecule, or even a complicated network of interactions between proteins, is just the beginning. We want to understand the entire interplay of networks, and all forms of communication inside cells, between cells, between organs, and between organisms. Bioinformatics is the ideal tool to integrate data at all levels from molecule to man. It includes all known sequence, structure and mutation data with a large number of ligand binding studies and computational results. In the future we will extend this system with more data which will be automatically extracted from literature. We will also add new data types, such as expresion profiling data and automatically selected literature references. Expression data is collected with gene chips. A gene chip is an array of thousands of pieces of nucleic acid that all are complementary to a gene one wants to monitor. Adding a drop of cell extract will lead to hybridization, and if this hybridization is quantitative, one gets data about expression levels. In real life things are a bit more complicated, but from a bioinformatics point of view this is the minimal required knowledge. Bioinformatics can help with the selection of probes to put on the chip, with the extraction of data from the chip, but most interestingly, a lot of bioinformatics will be needed An array spotter Bioinformatics and medicine will meet mainly in two ways. First, collaborations on the research topics listed above will bring researchers together. Not only can bioinformatics be used to explain experimental results, but when used properly, bioinformatics can also generate ideas for new experiments to answer old questions, or stronger even, bioinformatics can raise new questions. Second, bioinformatics will have to become part of the curriculum of all medical students. And what better way to generate this computer savvyness with a course that teaches the student skills he or she will use regularly throughout the career? Bioinformatics will provide just that: The faculty of medical sciences It is not an exaggeration to state that the CMBI plays a leading role in the Dutch bioinformatics field, and probably also in Europe. This opens up beautiful opportunities for students and scientists. In Nijmegen a student can get in contact with this science of the future called bioinformatics, but it is also possible to become a well-trained bioinformatician, ready for the challenges that come with the better jobs. Experimental scientists in Nijmegen have better opportunities than at other universities in the Netherlands to discuss their research with bioinformaticians, and to collaborate with them. This potentially gives our experimental scientists a significant step ahead that "comes for free".

APPLICATION OF BIOINFORMATICS IN MEDICINE pdf

9: Applications of Bioinformatics in Medicine and Biotechnology

While the promise of this kind of personalized medicine is still distant, researchers like FÃ¡tima Al-Shahrour, head of the Translational Bioinformatics Unit in the clinical research program at.

Application of Bioinformatics in various Fields Application of Bioinformatics in various Fields Molecular medicine The human genome will have profound effects on the fields of biomedical research and clinical medicine. Every disease has a genetic component. The completion of the human genome means that we can search for the genes directly associated with different diseases and begin to understand the molecular basis of these diseases more clearly. This new knowledge of the molecular mechanisms of disease will enable better treatments, cures and even preventative tests to be developed. Personalised medicine Clinical medicine will become more personalised with the development of the field of pharmacogenomics. At present, some drugs fail to make it to the market because a small percentage of the clinical patient population show adverse affects to a drug due to sequence variants in their DNA. As a result, potentially life saving drugs never make it to the marketplace. Today, doctors have to use trial and error to find the best drug to treat a particular patient as those with the same clinical symptoms can show a wide range of responses to the same treatment. Preventative medicine With the specific details of the genetic mechanisms of diseases being unravelled, the development of diagnostic tests to measure a persons susceptibility to different diseases may become a distinct reality. Preventative actions such as change of lifestyle or having treatment at the earliest possible stages when they are more likely to be successful, could result in huge advances in our struggle to conquer disease. Gene therapy In the not too distant future, the potential for using genes themselves to treat disease may become a reality. Gene therapy is the approach used to treat, cure or even prevent disease by changing the expression of a persons genes. Currently, this field is in its infantile stage with clinical trials for many different types of cancer and other diseases ongoing. Drug development At present all drugs on the market target only about proteins. With an improved understanding of disease mechanisms and using computational tools to identify and validate new drug targets, more specific medicines that act on the cause, not merely the symptoms, of the disease can be developed. Microbial genome applications Microorganisms are ubiquitous, that is they are found everywhere. They have been found surviving and thriving in extremes of heat, cold, radiation, salt, acidity and pressure. They are present in the environment, our bodies, the air, food and water. Traditionally, use has been made of a variety of microbial properties in the baking, brewing and food industries. The arrival of the complete genome sequences and their potential to provide a greater insight into the microbial world and its capacities could have broad and far reaching implications for environment, health, energy and industrial applications. For these reasons, in , the US Department of Energy DOE initiated the MGP Microbial Genome Project to sequence genomes of bacteria useful in energy production, environmental cleanup, industrial processing and toxic waste reduction. By studying the genetic material of these organisms, scientists can begin to understand these microbes at a very fundamental level and isolate the genes that give them their unique abilities to survive under extreme conditions. Scientists are interested in this organism because of its potential usefulness in cleaning up waste sites that contain radiation and toxic chemicals. Climate change Studies Increasing levels of carbon dioxide emission, mainly through the expanding use of fossil fuels for energy, are thought to contribute to global climate change. One method of doing so is to study the genomes of microbes that use carbon dioxide as their sole carbon source. Alternative energy sources Scientists are studying the genome of the microbe Chlorobium tepidum which has an unusual capacity for generating energy from light Biotechnology The archaeon Archaeoglobus fulgidus and the bacterium Thermotoga maritima have potential for practical applications in industry and government-funded environmental remediation. These microorganisms thrive in water temperatures above the boiling point and therefore may provide the DOE, the Department of Defence, and private companies with heat-stable enzymes suitable for use in industrial processes Other industrially useful microbes include, Corynebacterium glutamicum which is of high industrial interest as a research object because it is used by the chemical industry for the biotechnological production of the amino acid lysine. The substance is employed as a source of protein in animal nutrition. Lysine is one of

the essential amino acids in animal nutrition. Biotechnologically produced lysine is added to feed concentrates as a source of protein, and is an alternative to soybeans or meat and bonemeal. Lactococcus lactis is one of the most important micro-organisms involved in the dairy industry, it is a non-pathogenic rod-shaped bacterium that is critical for manufacturing dairy products like buttermilk, yogurt and cheese. This bacterium, Lactococcus lactis ssp. Researchers anticipate that understanding the physiology and genetic make-up of this bacterium will prove invaluable for food manufacturers as well as the pharmaceutical industry, which is exploring the capacity of L. Antibiotic resistance Scientists have been examining the genome of Enterococcus faecalis-a leading cause of bacterial infection among hospital patients. The discovery of the region, known as a pathogenicity island, could provide useful markers for detecting pathogenic strains and help to establish controls to prevent the spread of infection in wards. Forensic analysis of microbes Scientists used their genomic tools to help distinguish between the strain of Bacillus anthryacis that was used in the summer of terrorist attack in Florida with that of closely related anthrax strains. The reality of bioweapon creation Scientists have recently built the virus poliomyelitis using entirely artificial means. They did this using genomic data available on the Internet and materials from a mail-order chemical supply. The research was financed by the US Department of Defence as part of a biowarfare response program to prove to the world the reality of bioweapons. The researchers also hope their work will discourage officials from ever relaxing programs of immunisation. This project has been met with very mixed feeelings Evolutionary studies The sequencing of genomes from all three domains of life, eukaryota, bacteria and archaea means that evolutionary studies can be performed in a quest to determine the tree of life and the last universal common ancestor. Crop improvement Comparative genetics of the plant genomes has shown that the organisation of their genes has remained more conserved over evolutionary time than was previously believed. These findings suggest that information obtained from the model crop systems can be used to suggest improvements to other food crops. At present the complete genomes of Arabidopsis thaliana water cress and Oryza sativa rice are available. Insect resistance Genes from Bacillus thuringiensis that can control a number of serious pests have been successfully transferred to cotton, maize and potatoes. This new ability of the plants to resist insect attack means that the amount of insecticides being used can be reduced and hence the nutritional quality of the crops is increased. Improve nutritional quality Scientists have recently succeeded in transferring genes into rice to increase levels of Vitamin A, iron and other micronutrients. This work could have a profound impact in reducing occurrences of blindness and anaemia caused by deficiencies in Vitamin A and iron respectively. Scientists have inserted a gene from yeast into the tomato, and the result is a plant whose fruit stays longer on the vine and has an extended shelf life. Development of Drought resistance varieties Progress has been made in developing cereal varieties that have a greater tolerance for soil alkalinity, free aluminium and iron toxicities. These varieties will allow agriculture to succeed in poorer soil areas, thus adding more land to the global production base. Research is also in progress to produce crop varieties capable of tolerating reduced water conditions. Vetinary Science Sequencing projects of many farm animals including cows, pigs and sheep are now well under way in the hope that a better understanding of the biology of these organisms will have huge impacts for improving the production and health of livestock and ultimately have benefits for human nutrition. Comparative Studies Analysing and comparing the genetic material of different species is an important method for studying the functions of genes, the mechanisms of inherited diseases and species evolution. Bioinformatics tools can be used to make comparisons between the numbers, locations and biochemical functions of genes in different organisms. Organisms that are suitable for use in experimental research are termed model organisms. They have a number of properties that make them ideal for research purposes including short life spans, rapid reproduction, being easy to handle, inexpensive and they can be manipulated at the genetic level. An example of a human model organism is the mouse. Manipulation of the mouse at the molecular level and genome comparisons between the two species can and is revealing detailed information on the functions of human genes, the evolutionary relationship between the two species and the molecular mechanisms of many human diseases. Bioinformatics Analysis Tools Links.

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