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Biology and Data Interpretation Techniques Concepts

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INTRODUCTION

The data analysis is a key factor in the biological research, where every comparison could lead to a new finding. Arranging specific data in an organized ways will be the starting step and it is known as data preparation. This data should be explained and a proper description should be provided. Every data has evaluation criteria and the interpretation would be against this evaluating data and it will be the final step. Here, the quantitative data will be statistically analysed. There are many computational software's available like SPSS or ANOVA for analysing data. When it is quantitative data, the statistical analysis would help in measuring the degree of change in whole process and to predict the consistency of data. When compared quantitative data, qualitative data interpretation is difficult, as it require similar consensus in patterns [1]. In case of quantitative methodology, the testing theory is through the testing of a hypothesis. In qualitative research, you are either exploring the application of a theory or model in a different context or are hoping for a theory or a model to emerge from the data [2].

As stated by Marshall and Rossman (1990) "Data analysis is the process of bringing order, structure and meaning to the mass of collected data. It is a messy, ambiguous, time-consuming, creative, and fascinating process. It does not proceed in a linear fashion; it is not neat. Qualitative data analysis is a search for general statements about relationships among categories of data" [2,3].

BIOLOGICAL DATA MINING

In process of understanding different and difficult biological processes, biologists are working hard in analysing, taking them to next levels of biological and disease causing pathways. Genomic and protein sequences, DNA microarrays, protein interactions, biomedical images has resulted in production of bulk data, leading to interpret disease causing pathways and electronic health records.

This has resulted in a flood of biological and clinical data from genomic and protein sequences, DNA microarrays, protein interactions, biomedical images, to disease pathways and electronic health records. To exploit these data for discovering new knowledge that can be translated into clinical applications, there are fundamental data analysis difficulties that have to be overcome. Practical issues such as handling noisy and incomplete data, processing compute-intensive tasks, and integrating various data sources, are new challenges faced by biologists in the post-genome era. The fundamentals of state-of-the-art data mining techniques used to solve challenges in data analysis problems. Real application would be how biologists and clinical scientists can employ data mining. These studies finally results in making meaningful observations and discoveries. Sequence Analysis, Biological Network Mining, Classification, Trend Analysis and 3D Medical Images, Text Mining and Its Biomedical Applications are important applications of data mining.

COMPUTATIONAL MODELLING

In biological research, the support of computers and algorithms has a major role. When the quantity of data is high this support would be important, whiles it is difficult to analyze by humans. From the relation between two elements to its reaction levels in environment, the biology consists of high levels datasets to be analysed. Usually, models are replica of real process to make research easy and convenient [3-17].

Mathematical models are computerised as an attempt to simplify interpretations, but found to be more thoughtful idea, while many complex biological models were started to solve in an easier way. Thus, the variable data was presumably solved to obtain qualitative and quantitative results. The data interpretation became very easy and thus these models started developing in different dimensions, such as 1) Models Provide a Coherent Framework for Interpreting Data 2) Models Highlight Basic Concepts of Wide Applicability 3) Models Uncover New Phenomena or Concepts to Explore 4) Models Identify Key Factors or Components of a System 5) Models Can Link Levels of Detail (Individual to Population) etc. [17-25].

CONCLUSION

Genetic engineering, microbiology, protein synthesis, protein modelling, enzymology, enzyme kinetics etc. are complicated and the computational models play a major role. Research such as oncology and therapies, imaging is advancement. But, there are number of obstacles and difficulties to be addressed to make a successful scientific model, finally used by a life science expert. Thus, the development of these models would be required and more of this kind could make research get in to next level [3,6].

REFERENCES

[1]. http://www.icap.org/PolicyTools/Toolkits/EvaluationToolkit/4DataAnalysisandInterpretation/tabid/446/Default.aspx

[2]. http://www.uio.no/studier/emner/matnat/ifi/INF4260/h10/undervisningsmateriale/DataAnalysis.pdf data interpretation in research

[3]. Wooley JC, Lin HS, National Research Council (US) Committee on Frontiers at the Interface of Computing and Biology, Washington (DC): National Academies Press (US), 2005.

[4]. Eric B. Lipsky, Brian R. King, Gerard Tromp, Node-Oriented Workflow (NOW): A Command Template Workflow Management Tool for High Throughput Data Analysis Pipelines. Journal of Data Mining in Genomics & Proteomics, Vol. 5, pp.159, 2014.

[5]. Jacob Varghese B, Khai Bui, Naomi Divall, Alexander Egan, Ali Kermani, et al. A New Dimension of Codons for Protein Synthesis. Journal of Metabolic Syndrome vol. 1, pp.117, 2012.

[6]. Wenlong Tang, Jigang Zhang, Dongdong Lin, Pleiotropic Enrichment Analysis with Diverse Omics Data. Adv Genet Eng vol.3, pp.e113, 2014.

[7]. Davuluri RV, Bioinformatics for mining the data from next generation biotechnology platforms,The Wistar Institute, USA, 2011.

[8]. Abrukov V, Abrukov S, Smirnov A, Polykarpov A, A new material's experiment: Data mining for modeling and creation of knowledge base, 3rd International Conference and Exhibition on Materials Science & Engineering-2014.

[9]. Simenvova K, Nanoscale materials (nanocomposites, nanowires, carbon nanotubes, nanoparticles): Computational modeling and applications in molecular, cell biology and nanomedicine, International Expo and Conference on Analytrix & HPLC-2012.

[10]. Li J, Advanced understanding of the nor wood physiology and postoperative management, International Conference & Exhibition on Clinical Research Dermatology, Ophthalmology & Cardiology-2011.

[11]. Zhang W, Computational models to integrate transcriptomic and proteomic data for predict abundance of undetected proteins, International Conference and Exhibition on Metabolomics & Systems Biology-2012.

[12]. Abrukov V, A new material experiment: Data mining for modeling, data mining for presentation, 2nd International Conference and Exhibition on Materials Science & Engineering-2013.

[13]. Simeonova KM, Mathematical models for study of stem cells dynamics of neurological disorders and some cancer computational models, based on nanobiotechnology, 4th World Congress on Biotechnology, DoubleTree by Hilton Hotel Raleigh-Durham Airport at RTP, NC, USA, 2013.

[14]. Abrukov V, Knowledge base is a future of nanomaterials world, 3rd International Conference on Nanotek & Expo-2013.

[15]. Zhang W, Computational models to integrate transcriptomic and proteomic data for predict abundance of undetected proteins, International Conference and Exhibition on Metabolomics & Systems Biology-2012.

[16]. Firer MA, Interpreting Data from in Vitro Methods for Determining Cellular Cytotoxicity of Anticancer Drugs and Therapies, International Conference & Exhibition on Analytical and bioanalytical techniques-2010.

[17]. Warner RA, Color-coded Z scores for the display and analysis of biomedical data, 2nd World Congress on Biomarkers & Clinical Research-2011.

[18]. Mc Auley MT, Proctor CJ, Corfe BM, Cuskelly GCJ, Mooney KM, Nutrition Research and the Impact of Computational Systems Biology, J Comput Sci Syst Biol vol.6, pp.5, 2013.

[19]. Gigrich JS, System engineering tools and analysis to leverage signaling pathways of hepatocytes to determine toxicity risk, 4th International Conference and Exhibition on Metabolomics & Systems Biology-2015.

[20]. Panwar VK , Choudhary DK, Application of Two-Level Half Factorial Design Technique for Developing Mathematical Models of Bead Penetration and Bead Reinforcement in SAW Process, International Journal of Innovative Research in Science, Engineering and Technology Vol. 2, Issue 6, 2013.

[21]. Khalil HS, Tummala H, Chakarov S, Zhelev N, Lane DP, Targeting ATM pathway for therapeutic intervention in cancer, BioDiscovery, vol.3, issue 1, 2012.

[22]. Bianca C, From Physics to Living Systems- Applicable Mathematical Models, J Applied Computat Mathemat, vol. 1, pp.e123, 2012.

[23]. Gamit AD, Shah SA, Shah DR, Tiwari S, Micro-porous membrane controlled release systems for sustained delivery of Venlafexine hydrochloride: Development and evaluation, 3rd International Conference and Exhibition on Pharmaceutics & Novel Drug Delivery Systems-2013.

[24]. Wittum G, In silico modeling penetration of xenobiotics through human skin, 4th International Conference and Exhibition on Pharmaceutics & Novel Drug Delivery Systems-2014.

[25]. Hernandez AS, Process integration of computer driven wargames in support of fiscal policy decisions, International Summit on Industrial Engineering-2014.

