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Cutting edge computational solutions for large scale high-dimensional data sets arising out of new biology

New biology is a branch of biology that that deals with the nature of biological phenomenon at the molecular level. In post genomic era a new language has been created for new biology viz.,Genomics,Functional Genomics, Proteomics,cDNA,microarrays, Global Gene Expression Patterns .New Computational Tools are used for Sequencing, Analyzing experimental data, Searching, Pattern matching, Data mining, Gene discovery, Function discovery aiming to Classify, Identify patterns, predictions, Create models & Prediction, Assessment and Comparison,Optimization,Better utilize existing knowledge. The new wave of high-throughput technologies in genomics and proteomics are constantly improving and generating an unprecedented amount of data that can be termed as Big Data means large data sets in terms of volume, variety, velocity, variability, veracity, & complexity. Bioinformatics researchers are currently confronted with a huge challenge of handling, processing and moving these large-scale biological data, a problem that will only increase in coming years. Therefore, cloud computing bears great promise for effectively addressing issues of large-scale data generated by high-throughput technologies in the fields of genomics, proteomics and other biological research areas. Cloud-based bioinformatics resources have changed the approaches toward huge datasets, providing much faster data acquisition, analysis rates and storage. New cloud-based bioinformatics computing tools, algorithms, and workflows are consistently being developed and successfully deployed. Basically, the cloud refers to software and services that run on the internet instead of one's computer. The increased use of next generation sequencing has led to challenges in data analysis, large-scale data storage and management, multi-site data integration, validation for quality and scale-up of informatics. It is integral to overcome these analysis and informatics challenges to successfully translate NGS research and data from the lab to clinical stage. Success in the life sciences will depend on our ability to properly interpret the large-scale, high-dimensional data sets that are generated by these technologies, which in turn requires us to adopt advances in informatics. New technological advances and the availability of 'big data' enable us to probe deep into the origin of life and to further understand evolutionary processes. This paper reviews the current development of cloud based computational technologies that can be applied and pinpoints their potential beneficial applications as well as implications for Life Sciences. Big data Analytics platforms that offer implementations of the Map Reduce computational pattern e.g., Hadoop make it easy for developers to perform data-intensive computations at scale is also highlighted. The New Biology approach has the potential to meet critical societal goals in food, the environment, energy, and health.

Biography

Ajit Kumar Roy is an acclaimed researcher, Consultant, and award-winning Keynote Speaker. He served at CIFA, ICAR, as Principal Scientist and was involved in R&D activities in ICT, Statistics, Bioinformatics and Economics. At international level, he served as a Computer Specialist at SAARC Agricultural Information Centre (SAIC), Dhaka, Bangladesh for over 3 years. He published over 100 articles in refereed journals, conference proceedings. His recent best-sellers are *'Applied Big Data Analytics'*; *'Impact of Big Data Analytics on Business, Economy, Health Care and Society'*; *'Web Resources for Bioinformatics, Biotechnology and Life Sciences Research'*; *'Self Learning of Bioinformatics Online'*; Data Science – A Career Option for 21st Century; *'Applied Bioinformatics, Statistics and Economics in Fisheries Research'* and *'Applied Computational Biology and Statistics in Biotechnology and Bioinformatics'*.

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