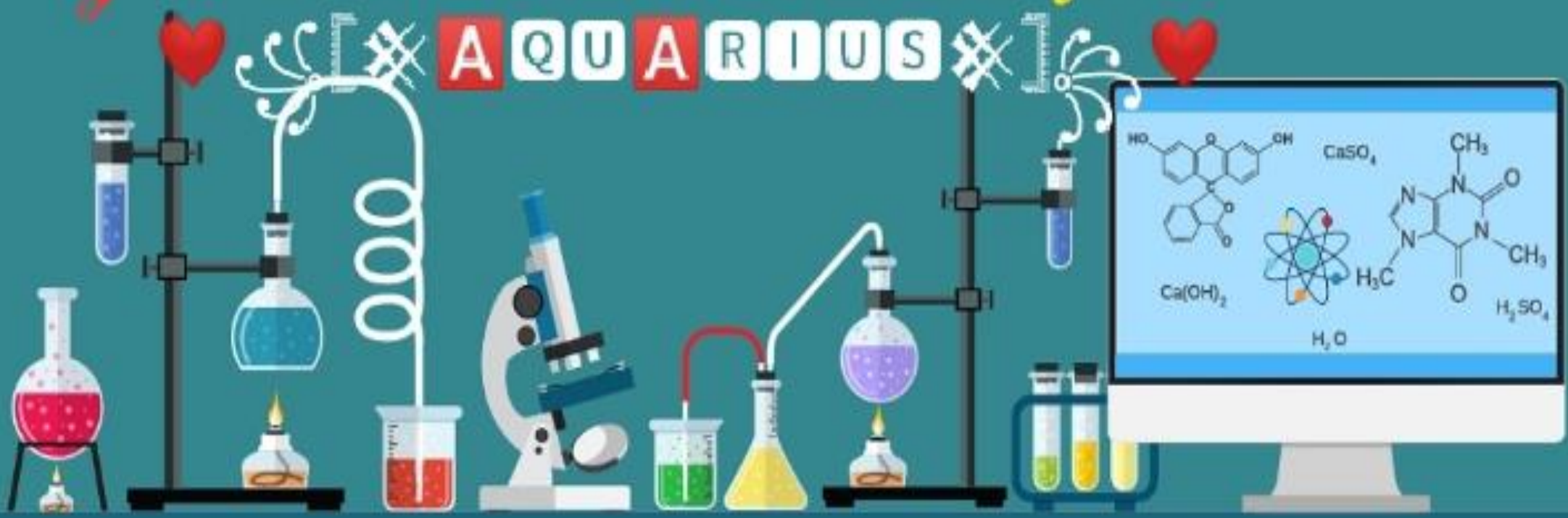


G D B BIF-401 Bioinformatics I

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AQUARIUS



Solution:

Biological research is the most fundamental research to understand complete mechanism of living system. In recent decades, bioinformatics methods, with the use of knowledge accumulated in public databases such as NCBI, Pubmed and other databases, make it possible to systematically dissect large gene lists in an attempt to assemble a summary of the most enriched result in current biology which is able to provide a huge contribution to biological research. In the same contrast, bioinformatics scanning approaches are emerging as alternative technologies that allow investigators to simultaneously measure the changes and regulation of genome-wide genes under certain biological conditions. These high-throughput technologies usually generate large gene of biological research interest lists as their final outputs. If we see earlier traditional biological researches, we were able to study one gene or a few genes at a time.

But after introduction of bioinformatics and regularly generation of research database around world and keeping them publically available online to support biological researchers was a very unique idea and beneficial for new researcher as well as the scientists working in same research interest in different geographical location in this world. Initially the complete aim of bioinformatics was just to handle data in biological research, but with increasing popularity and involvement of tool development to analyze data in a lesser time to complete research in fast and efficient manner. Bioinformatics has acquire a bigger place than it was expected to. In later segment of review we can see how these tools and techniques have affected our biological research. It is a complete bridge which relates mathematics, computer and statistical science to biological research.

Some major examples of modern Bioinformatics contributions in biological science that force the researchers headed to use Bioinformatics tools and methods in modern biological research are

Tools and Technique

Bioinformatics is partly based on tools and technique used earlier to get complete analysis of biological experiments in a shorter period of time. The main aim of developing these tools was to perform those analysis tasks, which were very much time consuming and without which research cannot be taken further. We can see a very small example of sequence alignment, where we have developed a tool for basic local alignment of sequence called “BLAST”. to perform this before showing any structural and functional similarity between two genes. After that so many tools were also designed to perform multiple sequence alignment like “Clustal W” to get analysis report for more than two genes at a time. Similarly for phylogenetic analysis also bioinformatics tools were developed and they were capable of generating various tree based on algorithms like UPGMA, and Neighbor joining methods etc.

Human Genome Sequencing

Human genome sequencing was the basic foundation for origin and evolution of this particular domain of biological research tool. This experiment was very big and time consuming and expected to reach its completion at some later point of time, but still it was completed 2 years early than it was expected.

Molecular Biology Data

World has seen enormous amount of data generated by molecular biologists and the difficulties to handle them in previous decades during 20th century. After human genome project, there was a flood of biological research in field of molecular biology and biotechnology started, which was a great source of huge experimental data and to handle that bioinformatics came in existence. Bioinformatics made all the data available online and very efficiently able to manage, modify and replace the complete data in a very shorter duration.

Biotechnology

Bioinformatics has surely reduced the time consuming experimental procedure and it is bringing a huge difference in complete time taken in biotechnological research earlier. It is also working in field of simulation of experiments online based on data models created with previous experimental lab data to predict the most probable result within a short span.

Regards:

BIF-401 Expert Zoologists