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## Proteomics - Bioinformatics Introduction

Bioinformatics is an interdisciplinary field at the junction of several disciplines ranging from biology to mathematics to computer science to information technology. The term was coined by Hwa Lim at the Supercomputer Computations Research Institute at the Florida State University in the late 1980's, to encompass all forms of computational study and analyses of biological problems. The "field" itself is more a tool to analyze and solve various biological problems and thus is becoming a part of the study of biology. Increased research and development efforts directed towards bioinformatics are pushing for bioinformatics to become a sub-discipline of biology in the future.

Several factors have influenced the "evolution" of bioinformatics as a major tool for modern day biology research. Two of the most important of these would be the need to solve complex biological problems and the parallel development of enabling technologies.

The need arose initially from major initiatives from various biotechnology companies in their efforts to make safer and more effective drugs. Bioinformatics was to shorten the process of drug discovery by managing and analyzing huge amounts of data that was generated from the various research efforts. The Human Genome Project created a further need to initially store and manage and later analyze the data that was generated and this heralded the development of problem specific databases and data mining tools to extract the relevant information from these databases. Two parallel fields that evolved along with bioinformatics, namely genomics and proteomics are currently driving further research in bioinformatics. Genomics created the first need, as the analysis of various sequenced genomes over the past decade required extensive computational intervention. Proteomics is the newest among these sub-disciplines requiring extensive services from bioinformatics. The proteomics challenge seems to be more complex than the genomics problem, first because of the much larger number of proteins present in a single organism, second because of the structural complexity of proteins compared to a simpler double helical structure of the DNA, and third because post translational modifications are known to affect the structure and potentially the function of the protein.

Technology has in several forms driven development of bioinformatics applications. Increases in the storage capacity and access speed of various computer databases helped manage the huge volume of data generated. Faster processors and supercomputers helped analyze this data. The internet helped this effort further by globalizing the research efforts with the setting up of large public databases and bioinformatics utilities free to be used by the global research community. Advances in engineering technology helped automate most research processes and build various state-of-the-art instruments such as microarrays and mass spectrometers. These technologies in turn rely extensively on bioinformatics tools to process the data they generate to solve complex problems and increase further understanding of the underlying biology.

Bioinformatics can be broadly described as having applications in at least one of the following four processes:

- Storing, annotating and analyzing DNA sequences from various genomes.
- Structural and Functional Characterization of various protein and RNA samples
- Clustering proteins into families and the development of protein models
- Aligning similar proteins and generating phylogenetic trees to examine evolutionary relationships

Thermo Electron on its part realized that developing efficient bioinformatics tools to enable state-of-the-art proteomics research is a more necessity, than a luxury. It is with this view that Thermo Electron has developed a suite of bioinformatics tools that work in tandem with the wide range of mass spectrometers to provide the proteomics scientist the most valuable of tools in his/her armory to decode the secrets underlying the various proteins ultimately responsible for all cellular



processes. For a further description of various bioinformatics solutions for proteomics provided by Thermo Electron, please visit the mass spectrometry software products page.

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