

Bioinformatics and health: an overview

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Ever increasing datasets, new frontiers in science, the development of new approaches for data analysis and representation, and the tackling of new, complex questions, those are the main driving forces for bioinformatics. The availability of faster and more powerful hardware tools and the further developing field of computer sciences are one of the main underlying supporting forces.

Bioinformatics was not a very popular new discipline in the early '80s. Seen by biologists as indulgence with a new toy, and by computer scientists as a very distant and foreign field of application, the discipline found few adepts amongst biologists. However, finding restriction sites, performing composition analysis and do FASTA searches against very small databases became a practical tool that soon proved its usefulness. Academic packages such as Staden, Wisconsin University Genetics Computer Group (GCG), and a few commercial packages gave bioinformatics a boost. In other applications such as phylogeny, with public domain software, computer assisted analysis soon became essential. However, it was not until the rather dramatic increase in the number and sizes of databases with genome projects, that bioinformatics became really recognized as a key discipline for the new era of genetics, biotechnology and

systems biology. Molecular modeling, biostatistics, and other fields were already fully under development, and there was a growing interest from computer scientists to apply methodologies, algorithms, database structuring and querying to the exotic field of biology, resulting in current multidisciplinary teams.

Bioinformatics was also recognized as a field where developing country scientists could compete on an equal standard with scientists. Although not completely true, it should be recognized that bioinformatics is far less sensitive to economic and bureaucratic hurdles that slow down so terribly basic and applied science in developing countries.

The current Supplement of RECIIS is dedicated to different aspects of bioinformatics. It is not possible to give a wide overview of the field, but several aspects that are relevant to research groups in the field are illustrated. This supplement illustrates aspects regarding the establishment of a regular bioinformatics technological platform in a research institution, discussions on different aspects of functional genomics (ex. dengue, leptospira), new methodologies and tools for analysis, and the use of grammatical rules and linguistics for analysis of biological regulatory regions. 

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Holds a degree in chemistry, and a Ph.D in Molecular Biology from the Federal University in Ghent, Belgium, in 1985. Since 1985, he is a senior researcher at Fiocruz and has worked at the Pasteur Institute, Paris in 1999-2000 as a visiting scientist. He is head of the Laboratory for Functional Genomics and Bioinformatics at the Oswaldo Cruz Institute, and also coordinator of funding and infrastructure programs at the Vice-Presidency for Research and Technological Development of Fiocruz since 2002. His main research interests are functional genomics, bioinformatics and biotechnology.

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