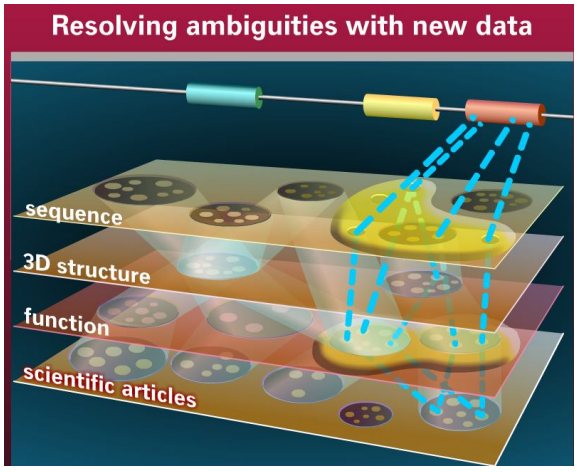
Next generation bioinformatics for biomedical research

While traditional bioinformatics has evolved from simple data management to data-interpretation, the emphasis today has shifted to high-throughput data collection, personal medicine and the analysis of complex systems. This tendency is accompanied by an unprecedented development of new computer architectures and cloud computing that bring the power of supercomputers within arm's reach of bench scientists and clinical practicioners. At the same time, bionic devices and on-line diagnostic tools open up new areas of applications.



In this fast evolving scene of new technologies, integrating heterogeneous bioinformatics data is perhaps one of the most challenging tasks. Databases increase both in volume and in complexity, and public resources available on the Internet can not cope with a growing number of user groups, especially medical and industrial users concerned with data confidentiality. On the other hand many, if not most biomolecular mechanisms that translate the human genomic information into phenotypes are not known and as a consequence, most of the molecular and cellular data cannot be interpreted in terms of biomedically relevant conclusions. While personalized diagnostics and cures are likely to remain a dominant trend, the temperate view suggests biomedical applications relying on the comparison of biomolecular sequences and/or on the already known biomolecular mechanisms may have even greater chances to enter clinical practice. Developing stand-alone tools for genome annotation, personalized medicine and high throughput technologies is especially important in the analysis of complex diseases such as neurological and psychiatric disorders.

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