

Computational Biology Program at USC

Today molecular biology is driven to a large extent by computer science and statistics. Having in many respects already become an **informational** science, molecular biology is rapidly becoming a **computational** science as well. *Computational molecular biology* is developing at an amazing rate. In 1989 the first “big science” project in biology (the *Human Genome Project*) was launched. It is aimed at determining the 100,000 genes that comprise the entire 3 billion letters of the human genome. “Raw” genetic texts are likely to become the main research tools of biologists over the next decades. The spectrum of computational techniques used in computational molecular biology ranges from graph theory and statistics to flows in networks and computer vision. A number of newly developing experimental techniques are likely to further widen this spectrum. Applications of computational molecular biology are also rapidly broadening and now include DNA sequence comparison, DNA physical mapping, DNA sequencing, molecular evolution, DNA fingerprinting, predictions of protein secondary and tertiary structure, prediction of genes in raw genetic texts, DNA linguistics, fast search in biological databases, RNA secondary structure predictions, etc. The group headed by Dr. Michael Waterman and which includes Dr. Pavel Pevzner and Dr. Simon Tavaré, has pioneered computational molecular biology research in many of these areas. They work closely with several experimental groups both in academia and in the biotechnology industry, to develop computational biology for the 21st century. Main cooperation: Affymetrix, National Center for Biotechnology Information.

