Bioinformatics Services Section Front Page

Biological data are being produced at a phenomenal rate. For example as of August 2000, the GenBank repository of nucleic acid sequences contained 8,214,000 entries and the SWISS-PROT database of protein sequences contained 88,166. On average, these databases are doubling in size every 15 months. In addition, since the publication of the H. influenzae genome, complete sequences for over 40 organisms have been released, ranging from 450 genes to over 100,000. Add to this the data from the myriad of related projects that study gene expression, determine the protein structures encoded by the genes, and detail how these products interact with one another, and we can begin to imagine the enormous quantity and variety of information that is being produced. As a result of this surge in data, computers have become indispensable to biological research. Such an approach is ideal because of the ease with which computers can handle large quantities of data and probe the complex dynamics observed in nature. **Bioinformatics**, is a subject often defined as the application of computational techniques to understand and organise the information associated with biological macromolecules.