


Bioinformatics  [/baɪ.ouˈɪnfərˈmætɪks/](#) is an [interdisciplinary](#) field that develops methods and [software tools](#) for understanding [biological data](#). As an [interdisciplinary](#) field of science, bioinformatics combines [computer science](#), [statistics](#), [mathematics](#), and [engineering](#) to analyze and interpret [biological data](#). Bioinformatics has been used for *in silico* analyses of [biological queries](#) using [mathematical](#) and statistical techniques.

Bioinformatics is both an [umbrella term](#) for the body of biological studies that use [computer programming](#) as part of their methodology, as well as a reference to specific analysis "pipelines" that are repeatedly used, particularly in the field of [genomics](#). Common uses of bioinformatics include the identification of candidate genes and [nucleotides \(SNPs\)](#). Often, such identification is made with the aim of better understanding the genetic basis of disease, unique adaptations, desirable properties (esp. in agricultural species), or differences between populations. In a less formal way, bioinformatics also tries to understand the organisational principles within [nucleic acid](#) and [protein](#) sequences, called proteomics.

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Introduction [\[edit \]](#)

Bioinformatics has become an important part of many areas of biology. In experimental [molecular biology](#), bioinformatics techniques such as [image](#) and [signal processing](#) allow extraction of useful results from large amounts of raw data. In the field of genetics and genomics, it aids in sequencing and annotating genomes and their observed [mutations](#). It plays a role in the [text mining](#) of biological literature and the development of biological and gene [ontologies](#) to organize and query biological data. It also plays a role in the analysis of gene and protein expression and regulation. Bioinformatics tools aid in the comparison of genetic and genomic data and more generally in the understanding of evolutionary aspects of molecular biology. At a more integrative level, it helps analyze and catalogue the biological pathways and networks that are an important part of systems biology. In structural biology, it aids in the simulation and modeling of DNA,^[1] RNA,^{[1][2]} proteins^[3] as well as biomolecular interactions.^{[4][5][6]}