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Not only is the quantity of life science data expanding, but new types of biological data continue to be introduced as a result of technological development and a growing understanding of biological systems. Methods for analyzing these data are an increasingly important component of modern biological research. In Bioinformatics, leading researchers in the field provide a selection of the most useful and widely applicable methods, able to be applied as is, or with minor variations, to many specific problems. Volume I: Data, Sequence Analysis and Evolution examines a selection of methods involving the generation and organization of data, including sequence data, RNA and protein structures, microarray expression data and functional annotations, methods for discovering the functional components of genomes, whether they be genes, alternative splice sites, non-coding RNAs or regulatory motifs, and several of the most interesting methods in phylogenetics and evolution.