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	Ug'ur Sezerman and Aytiil Ercal; 1 Introduction 2 Methods
Sommario/riassunto	High-throughput sequencing and functional genomics technologies have given us the human genome sequence as well as those of other experimentally, medically, and agriculturally important species, thus enabling large-scale genotyping and gene expression profiling of human populations. Databases containing large numbers of sequences, polymorphisms, structures, metabolic pathways, and gene expression profiles of normal and diseased tissues are rapidly being generated for human and model organisms. Bioinformatics is therefore gaining importance in the annotation of genomic sequences; the understan