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genome can be recognized because they affect the sizes or numbers of restriction fragments. Point mutations are more difficult to detect. The ultimate map is to determine the sequence of the DNA. From the sequence, we can identify genes and the distances between them. By analyzing the protein-coding potential of a sequence of the DNA, we can

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Advances in genome sequencing and annotation have eased the difficulty of identifying new gene sequences. Predicting the functions of these newly identified genes remains challenging. Genes descended from a common ancestral sequence are likely to have common functions. As a result, homology is widely used for

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gene function prediction.

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