# Homology-Based Prediction of Eukaryotic Gene Structures

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We have developed a method for prediction of eukaryotic gene structures (exon-intron organizations) based on sequence homology together with several lines of statistical information such as coding potential and signal strength around exon-intron boundaries and translational start sites. Based on testing upon sets of human and *C. elegans* genes of known structures, we found that the method predicts coding nucleotides at an accuracy of 96% or more, when the amino acid identity between the reference and target sequences exceeds 50%. Using this method, we are attempting to identify all genes involved with drug metabolism in organisms whose entire genomic sequences have been determined.
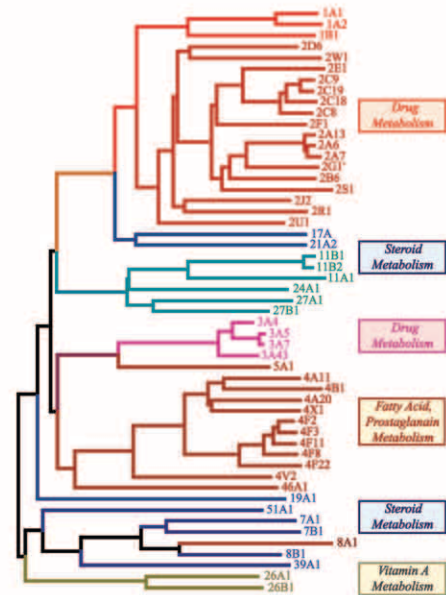
A phylogenetic tree of human cytochrome P450 genes