

COMPUTATIONAL PREDICTION OF REGULATORY ELEMENTS BY COMPARATIVE SEQUENCE ANALYSIS

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With many vertebrate genomes now completely sequenced, the most promising methods for predicting functional sequence elements are based on comparison of sequences from multiple species. We focus on problems that arise when using such tools on a genome-wide scale in the vertebrates. These problems include difficulties in finding reliably homologous promoter sequences, difficulties in choosing the best tool and parameters to apply to these sequences, and difficulties in assessing the significance of the predictions produced. Solutions are offered to each of these problems, though they are far from complete.