

## Identifying Promoters and Their Types Based on a Two-Layer Approach

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**Abstract :** Prokaryotic promoter, consisted of two short DNA sequences located at in -35 and -10 positions, is responsible for controlling the initiation and expression of gene expression. Different types of promoters have different functions, and their consensus sequences are similar. In addition, their consensus sequences may be different for the same type of promoter, which poses difficulties for promoter identification. Unfortunately, all existing computational methods treat promoter identification as a binary classification task and can only identify whether a query sequence belongs to a specific promoter type. It is desired to develop computational methods for effectively identifying promoters and their types. Here, a two-layer predictor is proposed to try to deal with the problem. The first layer is designed to predict whether a given sequence is a promoter and the second layer predicts the type of promoter that is judged as a promoter. Meanwhile, we also analyze the importance of feature and sequence conversation in two aspects: promoter identification and promoter type identification. To the best knowledge of ours, it is the first computational predictor to detect promoters and their types.

**Keywords :** promoter, promoter type, random forest, sequence information

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