Review Article

A survey of recently emerged genome-wide computational enhancer predictor tools

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ABSTRACT

The race for the discovery of enhancers at a genome-wide scale has been on since the commencement of next generation sequencing decades after the discovery of the first enhancer, SV40. A few enhancer-predicting features such as chromatin feature, histone modifications and sequence feature had been implemented with varying success rates. However, to date, there is no consensus yet on the single enhancer marker that can be employed to ultimately distinguish and uncover enhancers from the enormous genomic regions. Many supervised, unsupervised and semi-supervised computational approaches had emerged to complement and facilitate experimental approaches in enhancer discovery. In this review, we placed our focus on the recently emerged enhancer predictor tools that work on general enhancer features such as sequences, chromatin states and histone modifications, eRNA and of multiple feature approach. Comparisons of their prediction methods and outcomes were done across their functionally similar counterparts. We provide some recommendations and insights for future development of more comprehensive and robust tools.

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Contents

1. Introduction

Our perspective on non-coding regions in the genome had been overturned since King and Wilson (1975) discovered that the non-coding regions are one of the major players in divergent evolution in the animal kingdom almost forty years ago. One of the most

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