Abstract

Identifying the cooperation between transcription factors is crucial and challenging for uncovering the mystery behind the complex gene expression patterns. In this contribution, we proposed a novel computational method relying on functional domain compositions to infer the cooperation between transcription factors. For our testing dataset, the overall prediction accuracy reaches 84.3%, a fairly good result, and outperforms the prediction by both amino acid composition method and BLASTP based approach. The computational method we developed can help the researches on transcription regulatory mechanism. The corresponding online service TFIPS is available on http://pcal.biosino.org/.

Key words: Transcription factor cooperation, Functional domain composition, the Nearest Neighbor Algorithm, Jackknife cross-validation test