Predicting Subcellular Localization of Proteins by Bioinformatic Algorithms

When predicting the subcellular localization of proteins from their amino acid sequences, there are basically three approaches: signal-based, global property-based, and homology-based. Each of these has its advantages and drawbacks, and it is important when comparing methods to know which approach was used. Various statistical and machine learning algorithms are used with all three approaches, and various measures and standards are employed when reporting the performances of the developed methods. This chapter presents a number of available methods for prediction of sorting signals and subcellular localization, but rather than providing a checklist of which predictors to use, it aims to function as a guide for critical assessment of prediction methods.

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