Protein Sorting Prediction

Many computational methods are available for predicting protein sorting in bacteria. When comparing them, it is important to know that they can be grouped into three fundamentally different approaches: signal-based, global-property-based and homology-based prediction. In this chapter, the strengths and drawbacks of each of these approaches is described through many examples of methods that predict secretion, integration into membranes, or subcellular locations in general. The aim of this chapter is to provide a user-level introduction to the field with a minimum of computational theory.