Abstract

Background

Cellular respiration is a catabolic pathway for producing adenosine triphosphate (ATP) and is the most efficient process through which cells harvest energy from consumed food. When cells undergo cellular respiration, they require a pathway to store and transport electrons (i.e., the electron transport chain). The electron transport chain produces a transmembrane proton electrochemical gradient because of oxidation-reduction reactions. If protons flow back through the membrane, ATP synthase converts this mechanical energy into chemical energy by producing ATP, which provides energy in many cellular processes. In the electron transport chain process, flavin adenine dinucleotide (FAD) is one of the most vital molecules for carrying and transferring electrons. Therefore, predicting FAD binding sites in the electron transport chain is vital for helping biologists understand the electron transport chain process and energy production in cells.

Results

We used an independent data set to evaluate the performance of the proposed method, which had an accuracy of 69.84%. We compared the performance of the proposed method in analyzing two newly discovered electron transport protein sequences with that of the general FAD binding predictor presented by Mishra and Raghava and determined that the accuracy of the proposed method improved by 9%–45% and its Matthew's correlation coefficient was 0.14–0.5. Furthermore, the proposed method enabled reducing the number of false positives significantly and can provide useful information for biologists.

Conclusions

We developed a method that is based on PSSM profiles and SAAPs for identifying FAD binding sites in newly discovered electron transport protein sequences. This approach achieved a significant improvement after we added SAAPs to PSSM features to analyze FAD binding proteins in the electron transport chain. The proposed method can serve as an effective tool for predicting FAD binding sites in electron transport proteins and can help biologists understand the functions of the electron transport chain, particularly those of FAD binding sites.