DNpro: A Deep Learning Network Approach to Predicting Protein Stability Changes Induced by Single-Site Mutations

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Abstract : A single amino acid mutation can have a significant impact on the stability of protein structure. Thus, the prediction of protein stability change induced by single site mutations is critical and useful for studying protein function and structure. Here, we presented a deep learning network with the dropout technique for predicting protein stability changes upon single amino acid substitution. While using only protein sequence as input, the overall prediction accuracy of the method on a standard benchmark is >85%, which is higher than existing sequence-based methods and is comparable to the methods that use not only protein sequence but also tertiary structure, pH value and temperature. The results demonstrate that deep learning is a promising technique for protein stability prediction. The good performance of this sequence-based method makes it a valuable tool for predicting the impact of mutations on most proteins whose experimental structures are not available. Both the downloadable software package and the user-friendly web server (DNpro) that implement the method for predicting protein stability changes induced by amino acid mutations are freely available for the community to use.

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