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On the relevance of structural annotations for disulfide bridge prediction

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Disulfide bridges strongly constrain the native structure of many proteins and predicting their formation is therefore a key sub-problem of protein structure and function inference. A large body of approaches for this prediction problem rely on different kinds of classifiers and slightly differ in their experimental protocol. Therefore, the comparison of the conclusions of these works is difficult.

In this talk, I will propose an extensive study which aims at establishing the relevance of various structural-related annotations in the context of a disulfide pattern predictor. In order to achieve this goal, I will introduce a tractable and interpretable feature selection methodology, based on forward selection of feature functions. We will show that only a very limited number of annotations are sufficient to construct a high performance disulfide pattern predictor.

Host:
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