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Evolutionary based Optimal Ensemble Classifiers for HIV-1 Protease Cleavage Sites Prediction

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**Highlights:**

- Optimal ensemble framework for HIV-1 protease cleavage site prediction.
- Optimal formation of encoding-classifier pair selection by evolutionary algorithm.
- Natural selection in number of base learners and optimal data-learner mapping.
- Credibility of proposed ensemble model in cross-domain prediction.
- Experiment on benchmark data and statistical comparison with current state of art.

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