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ACCEPTED MANUSCRIPT

iACP-GAEnsC: Evolutionary genetic Algorithm based Ensemble Classification of Anticancer Peptides by utilizing Hybrid Feature space

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Highlights

- Computational model is developed for Anti-cancer peptides.
- Three discrete feature extraction methods are used.
- Ensemble feature space is formed
- Simple majority and GA based majority are used
- Obtained quite promising results than existing methods.

Abstract

Cancer is a fatal disease, responsible for one-quarter of all deaths in developed countries. Traditional anticancer therapies such as, chemotherapy and radiation, are highly expensive, susceptible to errors and ineffective techniques. These conventional techniques induce severe side-effects on human cells. Due to perilous impact of cancer, the development of an accurate and highly efficient intelligent computational model is desirable for identification of anticancer peptides. In this paper, evolutionary intelligent genetic algorithm-based ensemble model, 'iACP-GAEnsC', is proposed for the identification of anticancer peptides. In this model, the protein

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