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Some remarks on protein attribute prediction and pseudo amino acid composition. (English)

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Summary: With the accomplishment of human genome sequencing, the number of sequence-known proteins has increased explosively. In contrast, the pace is much slower in determining their biological attributes. As a consequence, the gap between sequence-known proteins and attribute-known proteins has become increasingly large. The unbalanced situation, which has critically limited our ability to timely utilize the newly discovered proteins for basic research and drug development, has called for developing computational methods or high-throughput automated tools for fast and reliably identifying various attributes of uncharacterized proteins based on their sequence information alone. Actually, during the last two decades or so, many methods in this regard have been established in hope to bridge such a gap. In the course of developing these methods, the following things were often needed to consider: (1) benchmark dataset construction, (2) protein sample formulation, (3) operating algorithm (or engine), (4) anticipated accuracy, and (5) web-server establishment. In this review, we are to discuss each of the five procedures, with a special focus on the introduction of pseudo amino acid composition (PseAAC), its different modes and applications as well as its recent development, particularly in how to use the general formulation of PseAAC to reflect the core and essential features that are deeply hidden in complicated protein sequences.

Reviewer: [Reviewer \(Berlin\)](#)

MSC:

92D20 Protein sequences, DNA sequences

92-02 Research exposition (monographs, survey articles) pertaining to biology

Cited in **126** Documents

Keywords:

PseAAC; functional domain mode; gene ontology mode; sequential evolution mode; cross-validation

Software:

Cell-PLoc; Euk-mPLoc; Euk-PLoc; EzyPred; Gneg-mPLoc; GPCR-2L; GPCR-CA; GPCR-GIA; Gpos-PLoc; Hum-mPLoc; Hum-PLoc; Memtype-2L; Pfam; Plant-mPLoc; ProtIdent; PseAAC; Quat-2L; QuatIdent; SecretP; SMART ; SubChlo; Virus-ploc

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