Abstract

Extracellular matrix (ECM) proteins are those secreted to the exterior of the cell, which act as
mediators between resident cells and the external environment. These proteins not only maintain cellular structure but also play a part in diverse processes, including growth, hormonal response, homeostasis, and disease progression. Regardless of their importance, current knowledge of the number and functions of ECM proteins is limited. Deregulation of ECM proteins may cause diseases, including developmental abnormalities and cancer. Recent studies say that some of these proteins in body fluid may be considered as disease specific markers. Therefore, identification of ECM proteins is a significant step in understanding cancer progression and providing effective therapeutic targets or diagnostic markers. Despite their importance, current knowledge of the number and functions of ECM proteins is limited. Experimental identification of ECM is labor as-well-as time intensive. Here, propose a computational and novel method to predict ECM proteins. The dataset used in this study for training and testing was obtained from Uniprot database. Specific features such as PSI-BLAST derived PSSM and amino acid composition were utilized for training the models. Based on this newly generated features and the discriminatory characteristics of Hidden Markov Model were determined, which significantly improved the performance of SVMhmm classification.

References

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