Accepted Manuscript

RBSURFpred: Modeling Protein Accessible Surface Area in Real and Binary Space using Regularized and Optimized Regression

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PII: S0022-5193(17)30576-3
DOI: 10.1016/j.jtbi.2017.12.029
Reference: YJTBI 9311

To appear in: *Journal of Theoretical Biology*

Received date: 12 October 2017
Revised date: 11 December 2017
Accepted date: 28 December 2017

Please cite this article as: Sumit Tarafder, Md. Toukir Ahmed, Sumaiya Iqbal, Md Tamjidul Hoque, M. Sohel Rahman, RBSURFpred: Modeling Protein Accessible Surface Area in Real and Binary Space using Regularized and Optimized Regression, *Journal of Theoretical Biology* (2017), doi: 10.1016/j.jtbi.2017.12.029

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Highlights

- We have presented a new predictor RBSURFpred, which extends a previous predictor, REGAd^{3}p on several dimensions by incorporating 58 physicochemical, evolutionary and structural properties into 9-tuple peptides via Chou's general PseAAC, which allowed us to obtain higher accuracies in predicting both real-valued and binary ASA.
- The proposed tool named RBSURFpred is built using the regularized exact regression technique with higher-order polynomial function as kernel to fit non-linear feature space.
- We have incorporated 3 important features of a protein residue to predict its exposure to solvent that have not been explored before for this application.
- RBSURFpred resulted in promising performance when compared with two other existing state of the art predictors in the literature.

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