

Comparison of different tools for the prediction of protein interaction specificity - (session: Other)

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We decided to compare a set of procedures for their ability to predict the binding specificity of SH3 protein modules starting from their binding peptide lists. We chose to analyze: regular expressions, position weight matrices, position specific scoring matrices (PSSMs) or profiles and the SPOT procedure (Brannetti *et al.*, 2000, Brannetti *et al.* 2001).

We first measured the ability of these methods to recognize the peptides able to bind a given SH3 domain in the whole database of SH3-binding peptides. Then we wondered if the information contained within the available peptide sequences is good enough to represent the recognition specificity of an SH3 domain, and tried to identify the best way of handling this information in order to obtain a better correlation with interaction data (natural partners) derived from the [MINT](#) database of protein interactions.

To this aim, we used the above mentioned techniques to search for the natural binding partners within the SWISSPROT database, for each chosen SH3 domain.

We measured the performance of each method for a set of SH3 domains, and the predictive power of each matrix applying the ROC analysis. The results on the SWISSPROT database show that all the methods but the regular expressions perform rather well. Details about the different performances will be discussed in the poster.