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Resampling Method for Prediction of Third Structure F. Didehvar ¹, A. Katanforoush², and M. J. Sadeh³

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In many bioinformatics problems we face the problem of insufficient data for statistical analysis of subsequences. This in particular is the case with alignment problems for mapping of two proteins and the prediction of third structure of proteins. In this lecture we describe an application of the bootstrap method for the improvement of the alignment and prediction techniques.