

**Abstract:**

DNA-protein interactions are essential parts of cell life and cell cycle. Prediction of these interactions requires knowledge of DNA and a protein structure. Because machine learning approaches show adequate results in biological predictions, we chose to use it for the prediction of protein-DNA interactions. In this thesis, we use the machine learning tool P2Rank that was originally designed for prediction of ligand-binding sites and adapt it to predict DNA-binding sites. Apart of that, the thesis serves as a summary of existing prediction tools/methods and includes suggestions for further modifications of P2Rank.