

## **Brett Koenig**

Computer Science

Year in School: Junior

Hometown: St. Louis, Mo.

Faculty Mentor: Dr. Dmitry Korkin, Computer Science

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### **Prediction of superhelical proteins using machine learning methods**

Brett Koenig & Dmitry Korkin

The main objective is to use three state of the art machine learning methods to find the most efficient way for predicting and characterizing the superhelical proteins based solely on their sequence information. To achieve this goal we will first apply each method individually and then integrate all three methods to obtain the most efficient and accurate prediction. We first apply the support vector machine (SVM), a feature-based approach that requires training on the set of positive and negative examples. As the second method, we will use the Bayesian inference approach. Finally, we will employ the Hidden Markov Model (HMM), another popular machine learning technique widely used in bioinformatics. Expectations for the research are that combining all three learning methods at different prediction stages will result in superior performance and accuracy when compared to each individual approach.