

Build a **protein secondary structure classifier** with 3 classes H/E/C.

Each protein (i.e. a string of 20 amino acid codes) should be orthogonally encoded –see articles

A sliding window of the selected length should be used for context encoding - see articles

A classifier (**Naive Bayes, Logistic Regression, SVM, Random Forest**) should be composed of binary classifiers using selected combining scheme.

Performance Measures Q3 and SOV - see articles

Only **R language**