



Prerequisite Terminologies:

In order to have a better understanding of the main topic, you should have the basic concept of the following terms:

- Coiled Coil Domains
- Hidden Markov Model

Introduction:

MARCOIL is a hidden Markov model-based program that predicts the existence and location of potential coiled-coil domains in protein sequences. The prediction of CCDs is used frequently, and its optimization seems worthwhile. Marcoil is an HMM for the recognition of proteins with a CCD on a genomic scale. A cross-validated study suggests that MARCOIL improves predictions compared to the traditional PSSM algorithm, especially for some protein families and for short CCDs. Potential confounding factors such as differences in the dimension of parameter space and in the parameter values were avoided by using the same amino acid propensities and by keeping the transition probabilities of the HMM constant.

Steps:

- Open the homepage of the Marcoil tool, which you can access from [here](#).

- Enter your query protein sequence in FASTA format or you can upload the FASTA file.
- Click on 'Submit' to get the results.
- It provides results in different sections:
 - **CC-Prob:**
Marcoil generates the Coiled Coil probability graph for your query protein where the position of the coil is represented in the protein sequence.
 - **ProbList:**
In this section, the coiled coil probability list per residue and the sequence of your query protein is provided. You can analyse the coiled coil probability in percent and best heptad phase.
 - **ProbStat:**
The coiled coil probability per residue, compact representation is illustrated in this section. You can analyse the coiled-coil probability in percent and heptad position with highest probability.
 - **Predicted Domains:**
This section provides an overview of predicted coiled coil domains.

Summary:

In this video tutorial of protein databases and analysis, we learned about the Marcoil tool of MPI Bioinformatics Toolkit to predict the coiled coil domains within the protein sequences. We also got to know how to analyse the different sections of results provided by Marcoil and the predicted location of potential coiled-coil domains in protein sequences.