

The native structure of proteins is stabilized by both local and non-local interactions. The available phase space is highly reduced in size due to the local interactions, but non-local interactions determine the final physiologically active native structure. Although it is well-known that these two types of interactions are the key factors in determining the tertiary structure, their relative contributions is open for debate. This study will lay the groundwork for the investigation of relative contributions of these interactions. The contribution of both local and non-local neighbors to the Ramachandran map of the residue in question is examined by using statistical weight matrices (U) constructed according to the Markov assumption. An efficient matrix multiplication scheme based on rotational isomeric states model is introduced for studying realistic conformations of all-alanine, tryptophan, and valine short chains in the denatured state. This scheme is based on U 's obtained from dipeptide and tripeptide simulations. By using these matrices one can obtain the Ramachandran plot for longer sequences, such as tetra-peptides. Comparison of explicit tetra-peptide simulations with the Markov model shows that the Markov assumption fails to capture interactions specific to the tetra-peptide. Here, a systematic correction is proposed for efficient calculation of realistic protein conformations. Preliminary results suggest that the Markov assumption can be improved significantly by adding the contributions from hydrogen bonds and hydrophobic contacts, which are only present in the tetra-peptide sequence. Such a coarse-grained model will help elucidate the protein folding problem and improve secondary structure prediction algorithms.