**1.3.1 Sequence Based Methods**

Predicting domains based on the sequence information only and without the knowledge of their 3D structure is a tough task. Some of the early approaches to the problem ranged from

assembling secondary structure elements into domains[1] to identifying domains as those areas having high residue contact density[2]. A more recent approach guesses the number of domains based on their size based distribution[3]. Unfortunately, these methods had poor results and were unreliable.

Current methods rely more on the fact that a domain is a continuous sequence of amino acids that recurs in the protein space. Thus, domains are evolutionary in nature and are those segments of protein that are conserved and reused throughout evolution. Hence, most of the methods employ multiple sequence alignments such as FASTA[4] and BLAST[5] to identify these conserved regions in a protein sequence. This method is very efficient but relies on the existence of homology. In addition to sequence alignments, some methods employ machine learning to further enhance their prediction. Some of the methods using the above techniques are discussed below.

**References**

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