Packing Problems in Protein Folding

Dorothee Liebich, Theo Mevissen, Ralf Zimmer, and Thomas Lengauer

Institute for Algorithms and Scientific Computing (SCAI)
GMD – German National Research Center for Information Technology
Schloß Birlinghoven, D-53754 Sankt Augustin, Germany
E-mail: Dorothee.Liebich@gmd.de

Voronoi tessellations of proteins define a description of amino acids by the corresponding Voronoi cells. Based on this model, the protein folding problem, i. e. predicting the three-dimensional structure of a protein from its amino acid sequence, can be considered as a three-dimensional packing problem.

For a representative test set of proteins contained in the PDB Voronoi tessellations have been constructed using the classical Voronoi method. The resulting amino acid cells have been analysed and described by various criteria including geometrical as well as chemical features, e. g. volume of the cells, position and area of faces, or position of functional groups. In order to obtain a classification with only a few representative cells that lead to compact packings of proteins, different similarity measures based on these criteria, such as the intersection volume of cells or the distance of corresponding functional groups, have been introduced and used for clustering the amino acid cells of the test set with different clustering methods. By a combination of these clusterings, which we call "multiple-criteria-clustering", we have determined a classification of the amino acid cells of the same size as standard rotamer libraries, which appears to be well suited for investigations of protein packing.

For the analysis of packing paths, i. e. intermediate states a protein assumes during the folding process, protein conformations have been studied in lattice models. We have developed a method for constructing conformations satisfying certain restrictions, which are given by contacts between amino acids that have to be realized, and analysed the influence of chain length and number of predefined contacts on the uniqueness of conformations.

References

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