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Stability of Ramachandran Plots under Small Perturbations of Bond and Dihedral Angles of a Backbone Protein Structure

The existence of Amide Planes of Protein Structures has been confirmed recently by a Mathematical Programming Approach [1]. The proposed cost function is the expression of a dihedral angle in terms of three variables: two bond angles, and the angle corresponding to alpha-carbon geometry. The average value of this dihedral angle is calculated to be 180 degrees by exhaustive statistical analysis of dipeptide structures [2] and this was the first indirect confirmation of Pauling's insight on the existence of amide planes of Protein Structure [3]. In this work we show how the methods of Mathematical Programing can be applied to derive the same average value which we believe to be the first of a series of introductory results belonging to a new modelling process of biomolecular structure. We then consider the small perturbation of the three variables above and we introduce the expressions of the two remaining dihedral angles.

From the observation of some regularities on the distances between atom sites along a protein backbone, we start our modelling by considering 3-dimensional curves through sequences of evenly spaced atom sites, according to an Euclidean definition of distance. This will lead to the introduction of elementary Ansätze for the coordinates of the position vectors of these evenly spaced atom sites and we make the assumption of local equilibria on the configuration of an atom site and its nearest neighbors. This assumption is enough for deriving the position of the central atom site from a generalized Fermat's problem, since it also means the minimization of the potential energy function [4]. There are two interesting previous results coming from these Ansätze and the equilibrium condition. The first one is that they preclude the existence of atom sites with more than 4 links to their nearest neighbors which is a known fact of protein structure. The other result is that they also imply that the curves quoted above should be right circular helices, which corresponds to another Pauling's insight – the alpha helices.

In order to summarize, it was found that from three known facts about the protein structure: evenly spaced atom sites, alpha helices and a maximum of 4 links of an atom site to its nearest neighbors, any two of them imply the third. In a first example of this modelling, we have chosen helices through the sequences of alpha-carbon, hydrogen and oxygen as well as through the sequences of nitrogen and carbonyl [4]. The results, albeit introductory, are in good agreement with the literature [1]. The study of the perturbations of the two remaining dihedral angles allows for checking the stability of Ramachandran Plots and to test its efficiency to predict new protein structures. Work along these lines is now in progress and will be presented on this talk.

References

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