Improved Elastic Rod Model of 3D RNA Structure Formation

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1 Introduction

The spatial shape of biological molecule is known to be one of the important determinants of its biochemical properties. Therefore, the specification and prediction of three-dimensional folding of biological macromolecules is one of the most challenging and fundamental problems of molecular biology. This work is devoted to the search of the proper technique for solution of this problem within the important class of biopolymers - ribonucleic acids.

2 Materials and Methods

An approach proposed for investigation and analysis of RNA spatial shape combines theoretical methods well adopted to DNA tertiary structure prediction [6, 2], biochemical data on 3D structure of single-stranded RNA regions and both experimental and theoretical data on thermodynamic stability of RNA structural elements [3, 5, 7]. The continuous mathematical model applied describes tertiary structure of RNA molecule as a number of linked basic structural elements with known spatial configuration. We study formation of dangling ends - non-closed single-stranded parts, stems - double-stranded regions of the molecule where adjacent nucleotides form base pairs and loops of various types.

Each basic element may be represented as a closed contour consisting of a corresponding number of continuously linked thin curvilinear elastic rods with absolutely rigid cross-bounds simulating Watson-Crick interactions. With adequate choice of the parameters of the rod its shape approximates the large-scale 3D structure of the structural element of the RNA molecule. It is assumed that initially all rods constitute the single-stranded helix structure of the RNA in A-form.

We consider dangling ends and stems as fixed straight twisted rods in the relaxed state represented by single or double-stranded RNA helixes. The other singlestranded parts of the molecule are treated as stressed. The determination of the statically stable spatial shape of single-stranded basic structural elements is concluded from the solution of the boundary value problem that determines the rod configuration satisfying the geometrical constraints at its ends. The 3D form of the rod is defined by the system of classical ODE of the equilibrium [6, 2]:

$$Ap' = Br(q - q_0) - Cq(r - r_0) + F_2 \qquad F_1' = rF_2 - qF_3$$

$$Bq' = Cp(r - r_0) - Ar(p - p_0) - F_1 \qquad F_2' = pF_3 - rF_1$$
$$Cr' = Aq(p - p_0) - Bp(q - q_0) \qquad F_3' = qF_1 - pF_2$$

These equations include six parameters: A, B, C, - two bending and one twisting stiffness coefficients of the rod; p_0, q_0, r_0 - geometrical parameters of the rod in the relaxed state (the projection of the curvature and the twist on the principal axes of the strain tensor), $F = (F_1, F_2, F_3)$ is an external force applied to the ends of the rod.

3 Results

Three dimensional structures of RNA molecules of different types were reconstructed by means of this technique, in particular, Yeast Phenylalanine Transfer RNA (Fig. 1), its tertiarily structure was determined by X-ray analysis (Fig. 1) and described in details in [4]. The comparison of this RNA with our rod model reveals a good correspondence. In the figures the view direction is chosen approximately perpendicular to the molecular plane.

Figure 1: Yeast Phenylalanine Transfer RNA.

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