Scaling of the average crossing number in equilateral random walks, knots and proteins

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Abstract

We compare here the scaling behaviour of the mean average crossing number $\langle \mathrm{ACN} \rangle$ of equilateral random walks in linear and closed form with the corresponding scaling observed in natural protein trajectories. We have shown recently that the scaling of $\langle \mathrm{ACN} \rangle$ of equilateral random walks of length n follows the relation $\langle \mathrm{ACN} \rangle = \frac{3}{16} n \ln n + bn$ and that a similar result holds for equilateral random polygons. Furthermore, our earlier numerical studies indicated that when random polygons of length n are divided into individual knot types, the $\langle \mathrm{ACN}(\mathcal{K}) \rangle$ for each knot type $\mathcal{K}$ can be described by a function of the form $\langle \mathrm{ACN}(\mathcal{K}) \rangle = a(n-n_0)\ln(n-n_0)+b(n-n_0)+c$ where a, b and c are constants depending on $\mathcal{K}$ and n_0 is the minimal number of segments required to form $\mathcal{K}$. Here we analyze in addition natural protein structures and observe that the relation $\langle \mathrm{ACN} \rangle = \frac{3}{16} n \ln n + bn$ also describes accurately the scaling of $\langle \mathrm{ACN} \rangle$ of protein backbones.

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