

Abundance of Pseudoknots in the RNA World

Daniel P. Aalberts (aalberts@williams.edu)

Evan M. Miller

Williams College, Williamstown, MA 01267, USA

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An RNA world likely predated today's more complicated biology with DNA, RNA, and protein. The emergence of life in an RNA World requires catalytic RNA. Pseudoknots (see Fig 1) are the most plausible early catalysts given their prevalence in present-day RNA enzymes and in the directed-evolution experiments which select for catalytic properties. Pseudoknots are important not because they are the most common RNA folds, but because when they do appear, they function as enzymes or regulate genetic pathways.

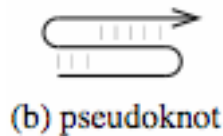


Figure 1. DNA has base pairs linking its two complementary strands while base pairs in RNA occur between complementary regions of its single strand. Hairpin or tree-like folds (Fig 1a) are most frequent for RNA, but occasionally the more complicated pseudoknot fold (Fig 1b) emerges. The figures depict the RNA molecular backbones and the base pairs.

Using a statistical physics theory, we predict how abundant pseudoknot folds are among the ensemble of all possible RNA sequences. Since RNA pseudoknots are so often catalytic, our computation addresses what is, for most people, the most implausible step in an evolutionary tale, that from raw material to self-replicating life. The theory agrees beautifully with measurements of known folds across a wide range of species, drawn from all domains of life.