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Observations of simple RNA suboptimal structures including pseudoknots suggests that the folding landscape is often funnel shaped¹ WAYNE DAWSON², GOTA KAWAI, Chiba Institute of Technology — Many RNA structure are known to fold up into complex function structures such as ribosomal RNA, transfer RNA (tRNA), riboswitches, etc. We are currently developing a novel theoretical approach for predicting the base pairing topology of folded RNA structures [1,2], a term known as RNA secondary structure. A good prediction of this base pairing can significantly speed up computation of the full 3D structure of these complex molecules. In recent work, we reported a pseudoknot prediction application using this model [3]. We have now upgraded this application to also predict suboptimal structures. The results of this model suggest that structures like tRNA often have a folding landscape of suboptimal structures that is essentially funnel shaped; similar to what is known to be the case for many simple proteins. This model has also been applied to simple protein structure topology prediction in a similar fashion. [1] Dawson, et al. (2001). J Theor Biol. 213, 359-386 and 387-412. [2] Dawson, et al. (2006). Nucleosides, Nucleotides, and Nucleic Acids 25, 171-189. [3]Dawson, et al. (2007). PLoS One, 2, 905.

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