

Worldwide competitions and the RNA folding problem

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Abstract

The discovery and design of biologically important RNA molecules has lagged behind proteins, in part due to the general difficulty of three-dimensional RNA structural characterization. What are the prospects for an 'AlphaFold moment' for RNA? I'll describe some recent progress in modeling RNA structure from old-fashioned and new machine learning, cryoelectron microscopy, and current and upcoming internet-scale competitions hosted on the Eterna, Kaggle, and CASP platforms.

Biography

Dr. Das is a Professor of Biochemistry at Stanford University School of Medicine. After training in particle physics and cosmology at Harvard, Cambridge, University College London, and Stanford, Dr. Das did postdoctoral research in computational protein folding at the University of Washington with David Baker. On returning to Stanford, Dr. Das set up his lab to focus on computer modeling and design of RNA molecules, which underlie important molecular machines in biology and medicine. As a core part of this research, Dr. Das leads Eterna, an open science platform that crowdsources intractable RNA design problems to 250,000 players of an online videogame and provides scoring feedback based on actual wet-lab experiments. Dr. Das has been recognized by the Burroughs-Wellcome Career Award at the Interface of Science, the Stanford Medicine Endowed Faculty Scholar award, and selection as an investigator of the Howard Hughes Medical Institute.