

Computational tools for protein and DNA/RNA 3D structure modeling for Cryo-EM maps.

Devashish Prasad², Genki Terashi¹, Xiao Wang², and Daisuke Kihara^{1,2}

1. Purdue University, Biological Sciences
2. Purdue University, Computer Sciences

Abstract -

Cryo-electron microscopy (Cryo-EM) has revolutionized structural biology in recent years, and deep learning-based methods have contributed significantly to determining protein and DNA/RNA structures from Cryo-EM maps.

To assist structure determination, we have been developing computational tools that use deep learning for protein and DNA/RNA 3D structure modeling. We introduce our suite of tools, which includes DeepMainMast, Emap2sec & Emap2sec+, CryoREAD, DAQ Score, and DAQ Refine. These tools are made available at Google Colab, Code Ocean capsules, and as source code at Github.

We hope that this accessibility will allow more researchers to benefit from deep learning-based methods in Cryo-EM and promote further advances in the field. Our tools are available at <https://kiharalab.org/emsuites/> and <https://github.com/kiharalab/>.