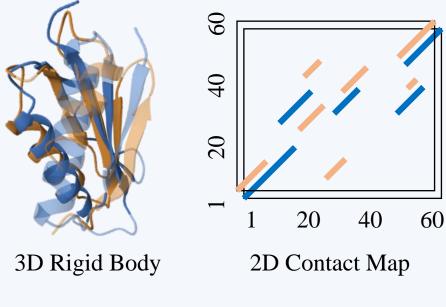
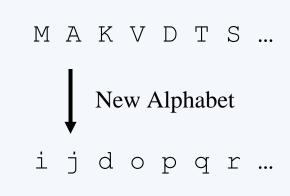
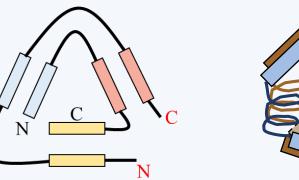
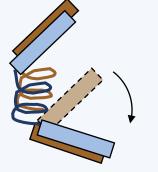
Structure Alignment Methods

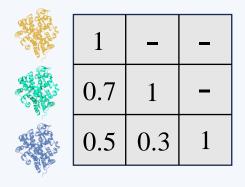




DL-based 1D String







Flexible Alignment

Multiple Alignment

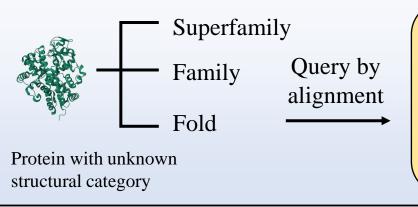
Questions of Interest

- Do structure-based methods have comparable performance on previous sequence-based tasks?
- What factors affect performance of various structure alignment tools on downstream tasks?
- How to effectively utilize structure information when sequence information exist?
- What is the running time and memory consumption of these tools?



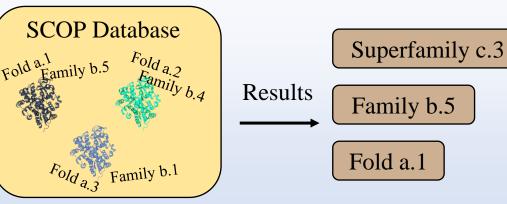
Homology Detection

Fragment Permutation



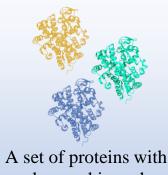
Pairwise

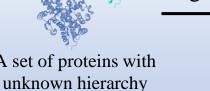
alignment

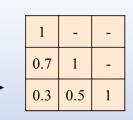


Task 2

Phylogeny Reconstruction (Evolution)

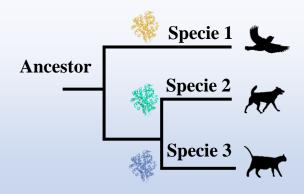






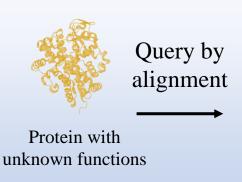
Scoring

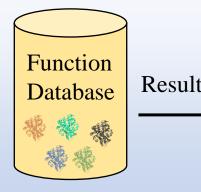
Construct evolution tree



Task 3

Function Inference





		Similarity	Functional terms	Scores
ts →		0.3	ATP hydrolysis activity	0.3
		0.8	Nucleotide binding	0.8
		0.1	Catalytic activity	0.1
	•••	•••	•••	•••