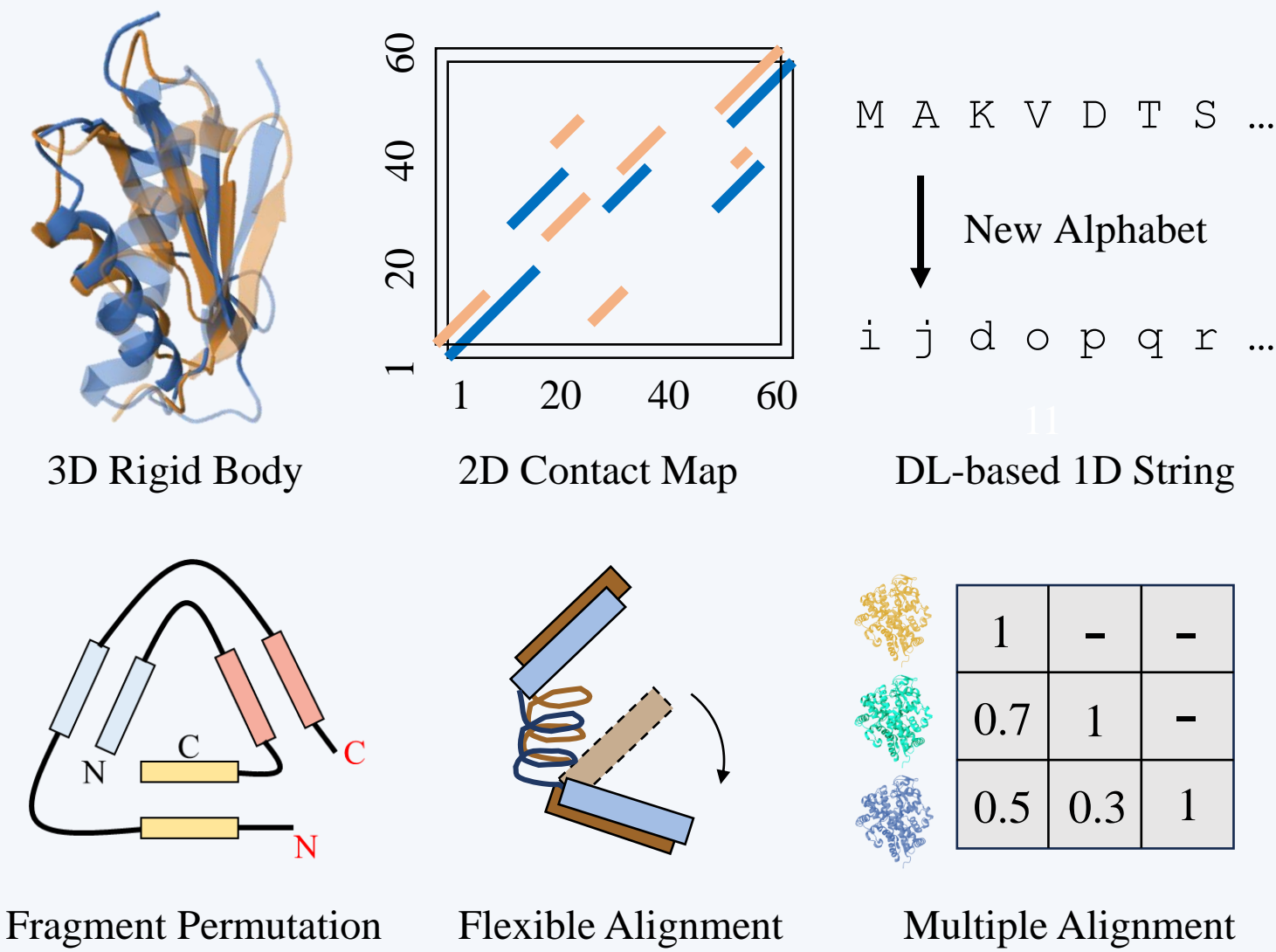


# Structure Alignment Methods

# Questions of Interest

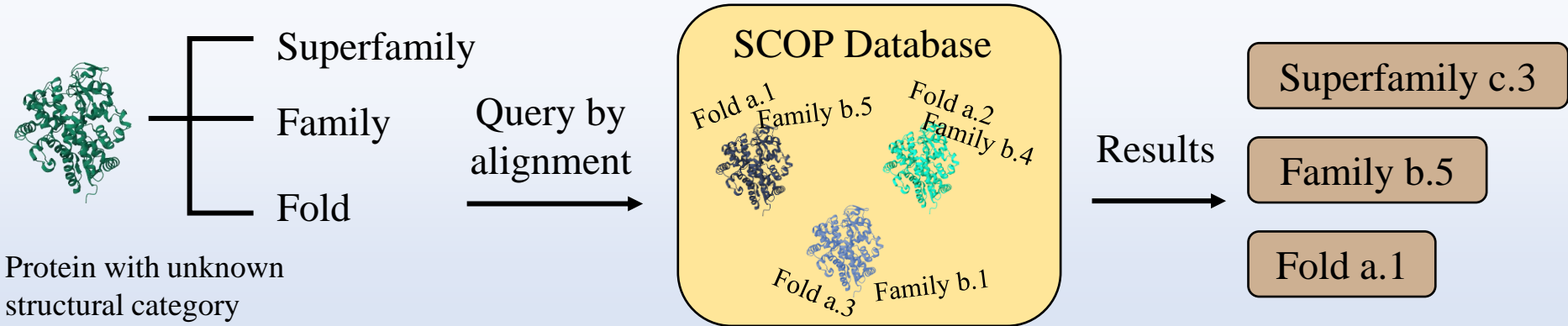


- Do structure-based methods have comparable performance on previous sequence-based tasks?
- What factors affect performance of various structure alignment tools on downstream tasks?
- How to effectively utilize structure information when sequence information exist?
- What is the running time and memory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

...

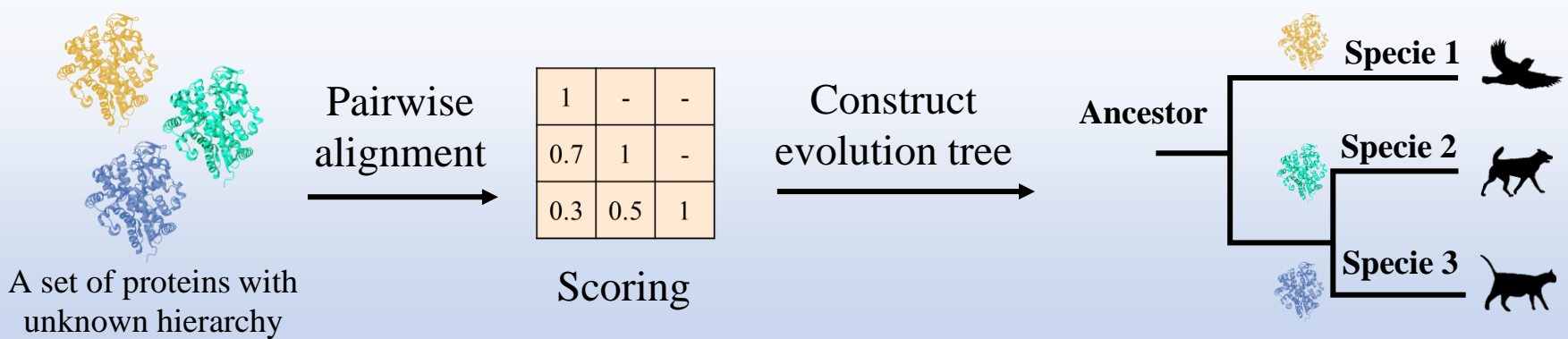
## Task 1

Homology Detection



## Task 2

Phylogeny Reconstruction (Evolution)



## Task 3

Function Inference

