

1 Reading assignment 9. Section 4.1

Read Section 4.1 and answer the following:

1. What is "Comparative modeling"?

The set of techniques that can be applied when a clear evolutionary relationship between the target and a protein of known structure can be easily detected from the sequence.

2. What is "homologous fold recognition"?

Methods that can be applied when the structure of the target protein turns out to be related to that of a protein of known structure so they could be part of the same family.

3. What is "analogous fold recognition"?

Methods that can be applied when the structure of the target protein turns out to be related to that of a protein of known structure for reasons other than evolution.

4. What is "new fold recognition"?

When neither the sequence nor the structure of the target protein are similar to that of a known protein.

5. In Figure 4.1, where would "new fold recognition" fit?

Fragment based methods.