**Protein Secondary Structure Prediction**

**What is Secondary Structure?**

* **Secondary structure = local folding patterns** in proteins.
* Main types:
  + **α-helix** → coiled structure stabilized by H-bonds.
  + **β-sheet** → sheet-like arrangement, parallel/antiparallel.
  + **Turns/loops** → connect helices and sheets.
* Role in stability and function of proteins.

**Analogy:**

* Think of protein as a long ribbon.
* Folding into helices = curling ribbon.
* Folding into sheets = flattening ribbon back-and-forth.

**Principles of Prediction**

1. **Chou–Fasman Method**
   * Statistical analysis of amino acid propensities.
   * Some residues prefer helix (Ala, Glu), others prefer sheets (Val, Ile).
2. **GOR Method (Garnier–Osguthorpe–Robson)**
   * Uses information from surrounding residues, not just one.
   * More accurate than Chou–Fasman.
3. **Modern Approaches**
   * Machine learning & neural networks.
   * Example: PSIPRED, DeepCNF.

**Applications of Secondary Structure Prediction**

* Useful when experimental 3D structure is unavailable.
* Guides tertiary structure prediction.
* Helps identify active/binding sites.
* Disease study: mutations that disrupt helices/sheets.

**🧪 Lab Session: Predicting Protein Secondary Structure**

**Objective:** Use tools to predict secondary structure from sequence.

**Steps:**

1. Take hemoglobin α-chain sequence from UniProt.
2. Use **PSIPRED** (online secondary structure prediction tool).
3. Upload/paste sequence → Run prediction.
4. Interpret results:
   * “H” = helix.
   * “E” = β-sheet.
   * “C” = coil/turn.
5. Compare predicted output with known PDB structure.

Tasks**:**

* Predict structure for two different proteins (e.g., hemoglobin vs insulin).
* Discuss: *Why does insulin have fewer helices compared to hemoglobin?*

**📝 Quick Review Questions**

1. What are the main types of secondary structure?
2. What is the difference between Chou–Fasman and GOR methods?
3. Why is secondary structure prediction important in bioinformatics?