Predicting Structure: Current Techniques and Challenges

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TASSER Techniques

- This is a family of structure prediction techniques.
- I-TASSER is a server based program.
  - User submits an amino acid
  - Program returns several possible structures based on known ones.
- M-TASSER is a program specifically designed for tertiary structure prediction and is more accurate

QUARK

- QUARK is a program attempting to fold small proteins ab initio.
- QUARK represents proteins by their side-chain center of mass and peptide backbone..
- QUARK does not fix bond lengths and angles.
- Searches through conformational space allow one-third of short proteins (<100 residues) with TM-ratios of >.5 to be successfully folded

Challenges (cont.)

- Analysis is generally done on fragments instead of the whole protein.
- Larger proteins (120 amino acids or more) are hard to accurately predict.

Fold-It

- Fold-It is a game designed to teach people about protein structure
- This online game uses rosetta structure prediction methodology
- This is an example of crowdsourcing scientific research.

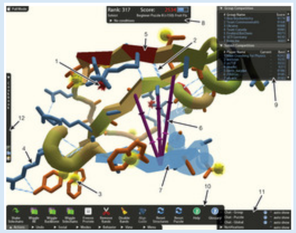

Figure 1: This is a screenshot of the Foldit game.

Challenges

- Most accurate programs require template structures to predict protein folding.
- Knowledge of the temperature and other thermodynamic properties of a protein-solution system is difficult to predict.
- The ‘Search Space’ of all possible conformations of a protein is large when not constraining the search.

Bibliography

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