Lecture 16. Protein Structure Prediction

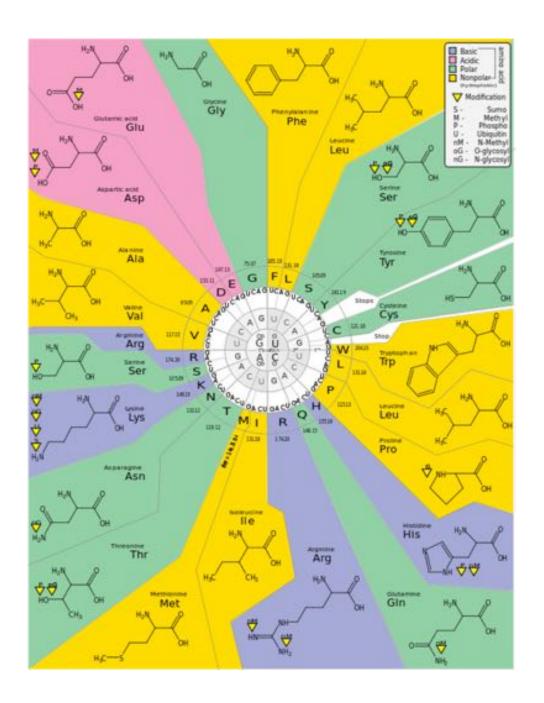
Michael Schatz

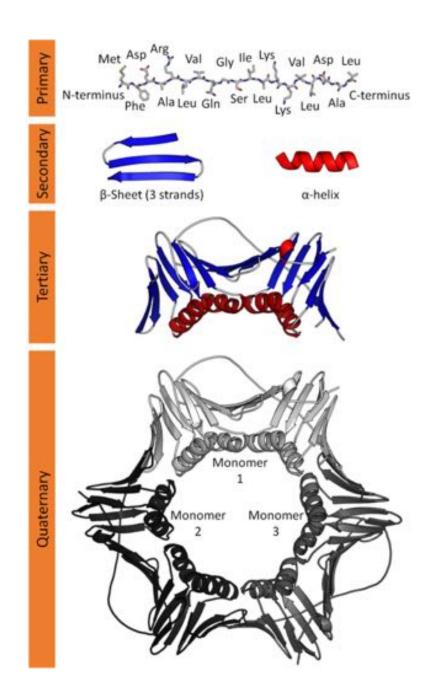
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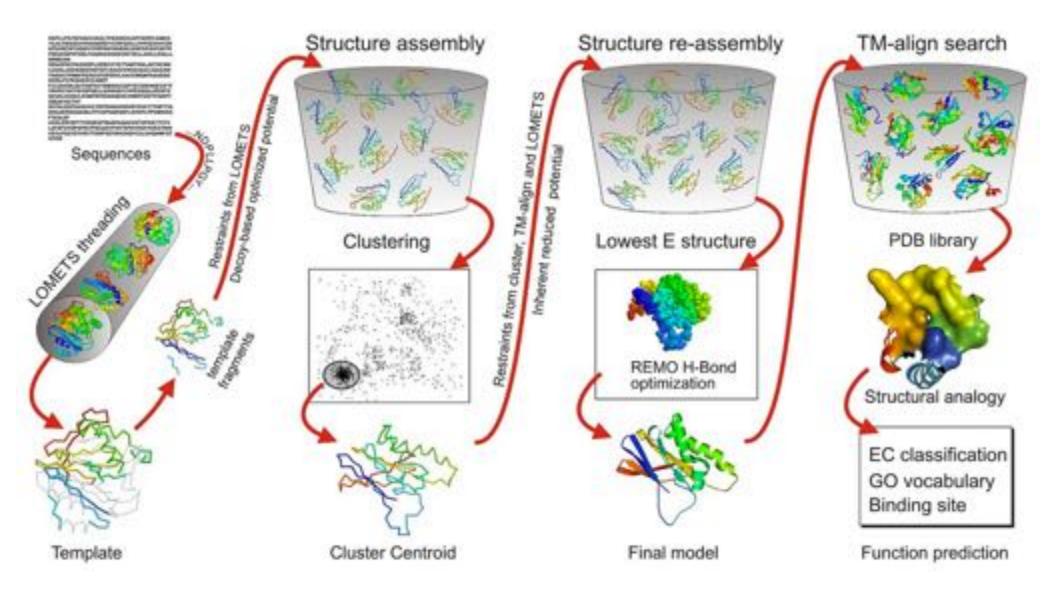


Protein Structure



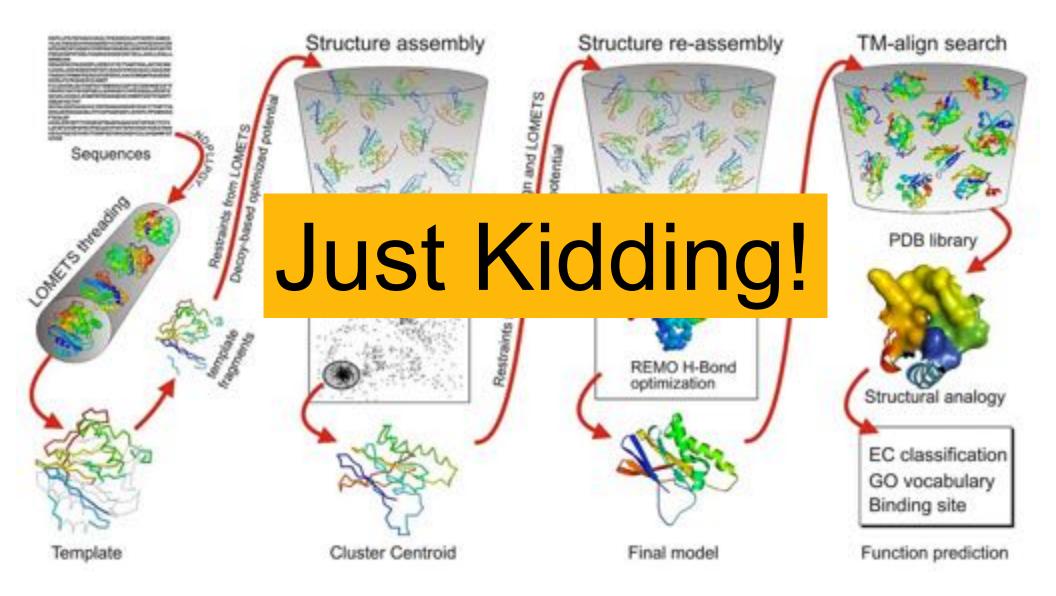


Protein Structure Prediction



I-TASSER: a unified platform for automated protein structure and function prediction Roy et al (2010) *Nature Protocols* 5, 725–738. doi:10.1038/nprot.2010.5

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Review!

Topics

Genomics

- Genomics Technologies
- Genome Assembly
- Whole Genome Alignment
- Phylogenetics
- Read mapping
- Variant Identification
- Gene Finding
- RNA-seq
- Methyl-seq, Chip-Seq, Hi-C
- Genome Annotation
- ENCODE
- Single cell vs bulk sequencing

Quantitative Techniques

- Normal, Poisson, Binomial
- P-value
- de Bruijn and overlap graphs
- Dot pots
- Quality Values (Phred Scale)
- Differential Expression
- Sampling variance
- Expectation Maximization
- Full text indexing & BWT
- Plane Sweep Alg
- Dynamic Programming
- Hidden Markov Models

What is the goal? What is the approach? What are the key challenges?

How did we explore these topics in the homeworks and lectures?