Introduction:
# Integrative modeling of molecular complexes

CS/CME/Biophys/BMI 371

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Molecular complexes

- Proteins (and other biomolecules such as RNA) often come together to form large complexes

- Determining structures for these complexes is difficult

  – Getting a crystal is very hard

  – Electron microscopy is more feasible but often leads to low-resolution structures, where it's not clear which blob is which protein
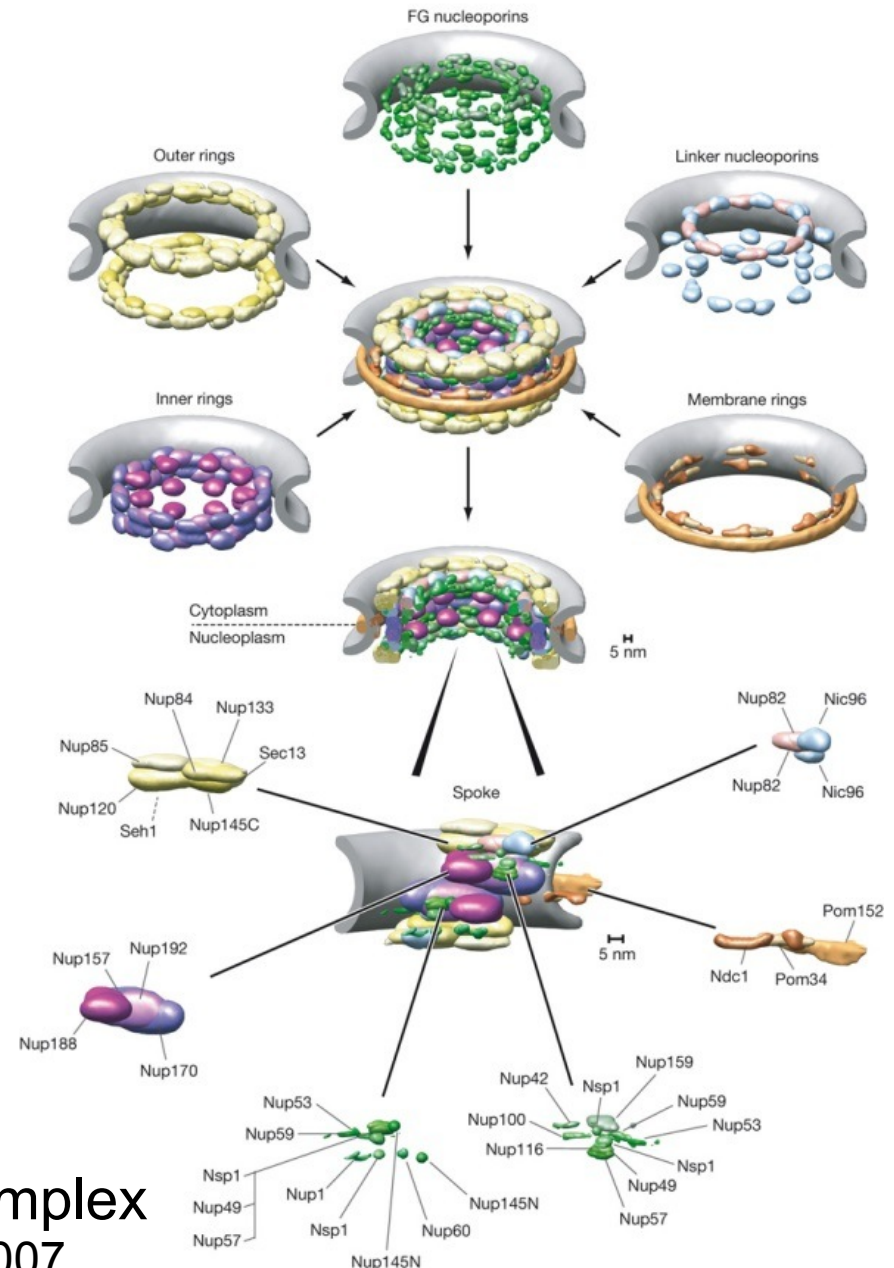
Nuclear Pore Complex
Alber et al., *Nature* 2007

Idea: supplement traditional structure determination methods with other forms of data

- Example: using techniques such as affinity purification or cross-linking + mass spectrometry, one can determine small sets of proteins that are in direct physical contact

- One can combine all of this information computationally to deduce structure (and in some cases, even multiple conformations) of these large complexes

Integrative modeling: combining diverse experimental data to deduce structures of large complexes

Alber et al., *Nature* 2007

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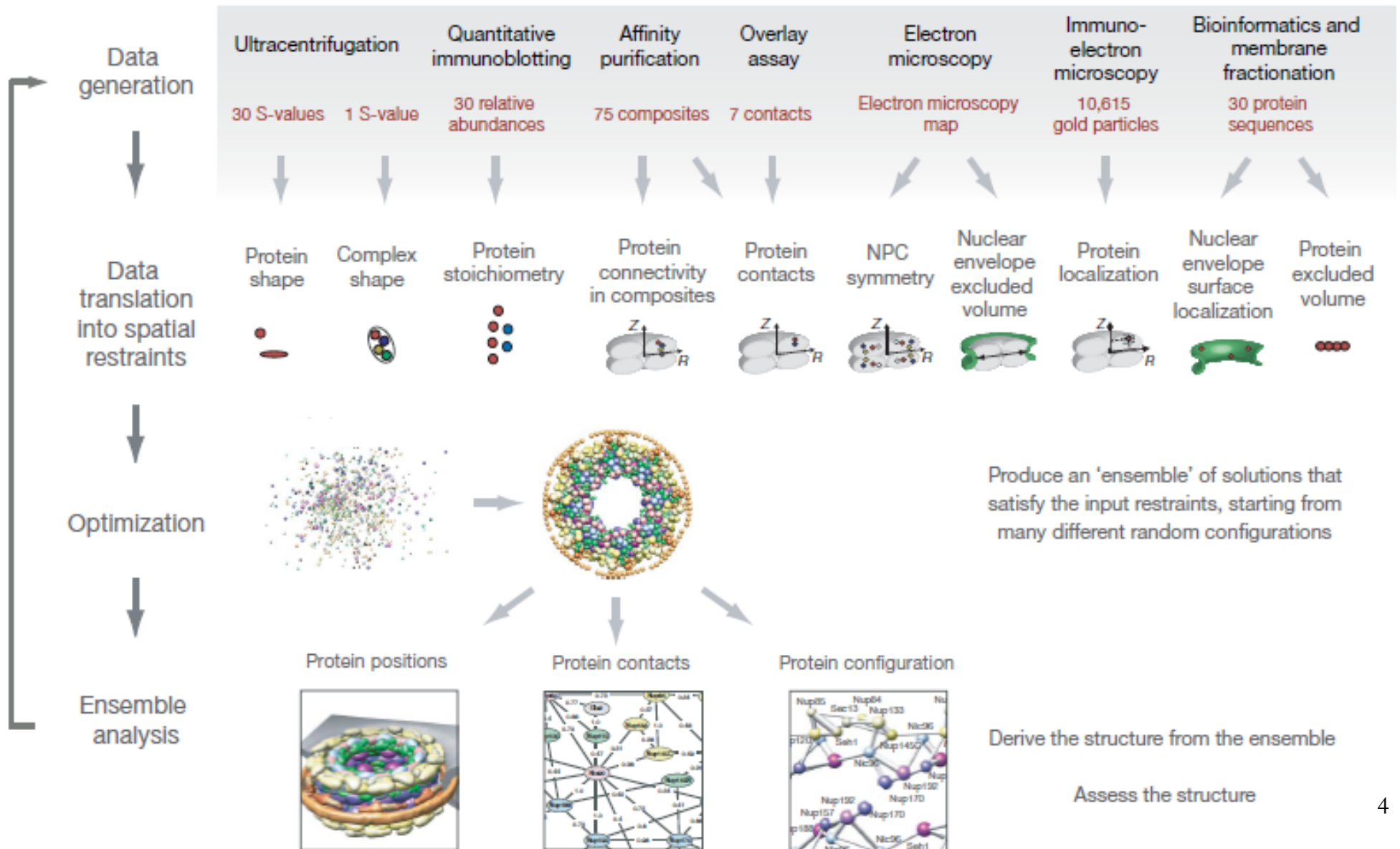
Background information

- ## Review article

  - Advances in integrative modeling of biomolecular complexes (*Methods* 59:372–381, 2013)

    - http://www.sciencedirect.com/science/article/pii/S1046202312003052

- ## Software article

  - Putting the Pieces Together: Integrative Modeling Platform Software for Structure Determination of Macromolecular Assemblies (*PLOS Biology* 10:e1001244, 2012)

    - http://dx.doi.org/10.1371/journal.pbio.1001244