

Seminar

Integrative structure determination: methods and applications

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Structures of macromolecules are key to understanding biological processes. Currently, no single experimental method is universally applicable for direct observation of structures of large protein assemblies. Integrative structure determination fills this gap by combining data from complementary experimental methods with physical theories and statistical inference to inform the structure.

The yeast centrosome (spindle pole body) is an example of an assembly whose structure we recently determined by an integrative approach, using data from X-ray crystallography, FRET, EM, SAXS, yeast two-hybrid experiments, bioinformatics predictions and physical principles. The structure sheds light on centrosome assembly and size regulation during the cell cycle. Further, the above modeling effort inspired the development of new methods for (1) validating integrative models, and (2) making modeling more accurate and applicable to larger systems, which will be discussed next.

Finally, I will discuss future directions focusing on integrative methods development, and applying integrative modeling to uncharacterized systems and new sources of data.

Wednesday, Dec 5th 2018

11:30 AM (Tea/Coffee at 11:00 AM)

Seminar Hall, TIFR-H