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Internal Seminar

Improved Version of TATAPRO Algorithm

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Sequence-specific resonance assignment is a prelude for the 3D structure determination of proteins using NMR spectroscopy. The automated algorithm, Tracked AuTomated Assignments in PROteins (TATAPRO) proposed earlier utilizes the protein primary sequence and peak-lists from a set of triple-resonance spectra, which correlate $^{1}H^{N}$ and ^{15}N chemical shifts with those of ^{13}CA, ^{13}CB and ^{13}CO. We have made this algorithm more robust by increasing the number of amino acid residues, which could be identified uniquely. In my presentation, I will demonstrate the utility of a graphical method for efficient pattern recognition in this assignment procedure. I will present all the improvisations that we have incorporated into the TATAPRO algorithm.

Thursday, Oct 20th 2016

2:00 PM (Tea/Coffee at 1:45 PM)

Seminar Hall, TCIS