Advances in high-throughput NMR spectroscopy of proteins at CESG, NMRFAM, and BMRB
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Abstract
Continued development of our probabilistic approach to NMR data collection has led to the combination of adaptive, reduced dimensionality data collection (HIFI-NMR) with automated assignment (PINE). The new approach is called HIFI-PINE. In response to requests from PINE users, we have added additional experiments to those supported. More robust and efficient methods for spectral data collection and signal recognition are being implemented. Data collection and analysis are supported on both Varian and Bruker spectrometers. Intermediate and final results can be analyzed graphically, respectively, with HIFI-Enhancer and PINE-SPARKY. Final results are submitted to the TARA software tool, which generates probabilistic torsion angle constraints for entry into structure determination programs. A high-throughput server (powered by Condor) for CS-Rosetta is now available from the BMRB website.

HIFI-PINE
HIFI-NMR (fast data collection) and PINE (automated chemical shift assignment and secondary structure determination) are two of the major data collection approaches to NMR spectroscopy. HIFI-NMR aims to integrate automated and adaptive data collection (HIFI-NMR) with automated data analysis (HIFI-PINE). The iterative approach combines feedback from the assignment module to ensure the acquisition of adequate NMR signal/noise and high quality chemical shift information (peak lists); these, in turn, yield superior backbone and sidechain resonance assignments, and secondary structure prediction in less time. The correlation of associated peaks across spectra, along with the HIFI-Enhancer visualization tool, alleviates the need for post-processing in the fast data collection approach. The main core of PINE-SPARKY (yellow boxes) has been successfully tested on small proteins. The final integrated tool (with incorporation of the green boxes) will support fully automated protein structure determination from chemical shifts data alone.

TARA
TARA predicts an area in $\phi$, $\psi$ (Ramachandran) space for each residue. TARA output (including multiple ambiguous torsion angle constraints) can be used as input to CYANA for better structure calculation through our TARA-CYANA interface.

References