



GFT NMR experiments for polypeptide backbone and $^{13}\text{C}^\beta$ chemical shift assignment

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Abstract

(4,3)D, (5,3)D and (5,2)D GFT triple resonance NMR experiments are presented for polypeptide backbone and $^{13}\text{C}^\beta$ resonance assignment of $^{15}\text{N}/^{13}\text{C}$ labeled proteins. The joint sampling of $m = 2, 3$ or 4 indirect chemical shift evolution periods of 4D and 5D NMR experiments yields the measurement of $2^m - 1$ linear combinations of shifts. To obtain sequential assignments, these are matched in corresponding experiments delineating either intra or inter-residue correlations. Hence, an increased set of matches is registered when compared to conventional approaches, and the 4D or 5D information allows one to efficiently break chemical shift degeneracy. Moreover, comparison of single-quantum chemical shifts obtained after a least squares fit using either the intra or the interresidue data demonstrates that GFT NMR warrants highly accurate shift measurements. The new features of GFT NMR based resonance assignment strategies promise to be of particular value for establishing automated protocols.

Introduction

Recently introduced GFT NMR spectroscopy (Kim and Szyperski, 2003) provides high-dimensional spectral information with both accuracy and speed. The phase-sensitive joint sampling of several indirect dimensions of a high-dimensional NMR experiment leads to largely reduced minimum measurement times when compared to FT NMR. This allows one to avoid the ‘sampling limited’ data collection regime (Szyperski et al., 2002). Concomitantly, the analysis of the resulting chemical shift multiplets, which are edited by the G-matrix transformation, yields increased accuracy for the measurement of the chemical shifts. To indicate that a combined G-matrix and Fourier transformation (FT) is employed, the approach was named ‘GFT’ NMR spectroscopy (Kim and Szyperski, 2003).

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GFT NMR spectroscopy is derived from ‘modules’ that were developed in the 1990s, triggered by the invention of two-spin coherence spectroscopy (Szyperski et al., 1993a) and its generalization, reduced-dimensionality (RD) NMR spectroscopy (Szyperski et al., 1993b). Two-spin coherence spectroscopy has also been named MQ (Simorre et al., 1994) or ZQ/DQ NMR spectroscopy (Rexroth et al., 1995), and was employed for measuring scalar couplings (Rexroth et al., 1995), dipole-dipole (Reif and Hennig, 1997) and dipole-CSA cross-correlated relaxation (e.g., Brutscher et al., 1998). It has been suggested (Ding and Gronenborn, 2002; Bersch et al., 2003) that RD NMR represents a variant of ‘accordion spectroscopy’ (Bodenhausen and Ernst, 1982), which was previously designed to jointly sample a chemical shift evolution and the mixing time employed in exchange spectroscopy (EXSY). However, the time evolution of longitudinal magnetization during the mixing time in EXSY (or NOESY) differs from the jointly incremented chemical shift time evolution in RD NMR. Thus, the two approaches lack similarity in terms of