Pure Shift NMR Covariance

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Introduction

The development of novel experimental strategies to significantly enhance signal resolution by broadband **homodecoupling is a current topic of high interest in ^{1}H NMR spectroscopy**[1]. A number of different building blocks have been implemented into 1D and 2D homo- and heteronuclear experiments in order to provide resolution-enhanced pure chemical shift ^{1}H NMR spectra, where signals appear collapsed to singlets. On the other hand, Covariance processing methods have been used to generate challenging NMR spectral representations[2]. We present here the first attempts towards a general solution to generate ***Pure Shift NMR spectra by using Generalized Indirect Covariance* (psGIC**) co-processing[3,4]. The current strategy is based on the calculation of a new 2D psGIC spectrum from the combination of a parent homo- or heteronuclear spectrum and a reference 2D F1-homodecoupled ^{1}H-^{1}H correlation spectrum only showing diagonal cross-peaks (DIAG), which share a common ^{1}H frequency dimension. Using psGIC, the F1 dimension in the DIAG spectrum is transferred to the F2 dimension of the parent spectrum, thus generating a new pure shift 2D spectrum.

Methodology

The key point of this proposal is a highly resolved 2D DIAG spectrum that can be obtained by two methods: i) experimentally, from a modification of the recent 2D PSYCHE-TOCSY pulse sequence with omission of the DIPSI-2 pulse train[5] (Fig. 1A); ii) a faster method reconstructs it from an experimental 1D broadband homodecoupled ^{1}H spectrum[6] followed by the *make2D** reconstruction (Mnova) (Fig. 1B). As proof of concept, the conventional 2D HSQC and 2D DIAG spectra of strychnine were combined following the GIC formalism (λ=1). This co-processing directly provides a reconstructed pure shift HSQC (psGIC-HSQC) spectrum showing well defined singlet signals for all cross-peaks (Fig. 2).

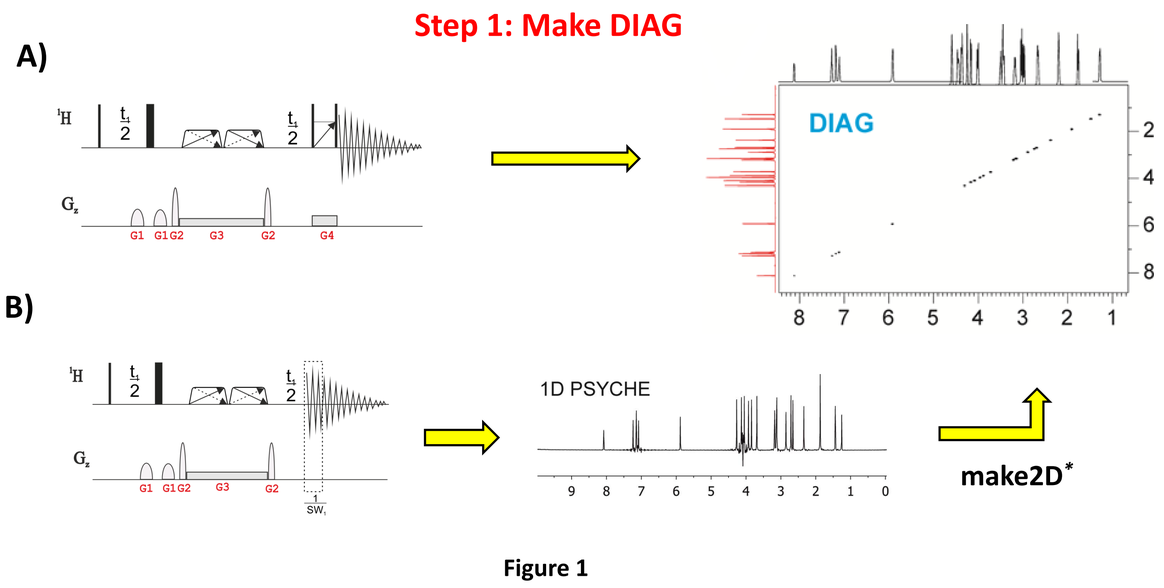


Figure 1

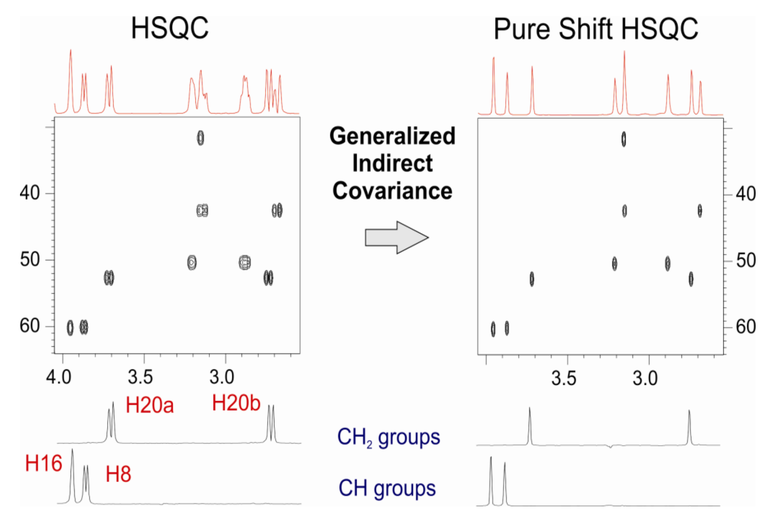


Figure 2

* **make2D** is Mnova script (available in Mnova 11) that synthesizes 2D-DIAG spectra by automatically deconvolving a ps-1D spectrum and generating 2D diagonal peaks using Lorentzian-type lineshapes

Pure-Shift NMR Spectra

This GIC procedure can be used to reconstruct any pure shift spectrum, even for some experiments that can be **very challenging** or **impossible to acquire** through experimental pulse schemes. Some examples are illustrated by the psGIC-HSQC-TOCSY (Fig. 3) and psGIC-HSQMBC (Fig. 4) spectra.

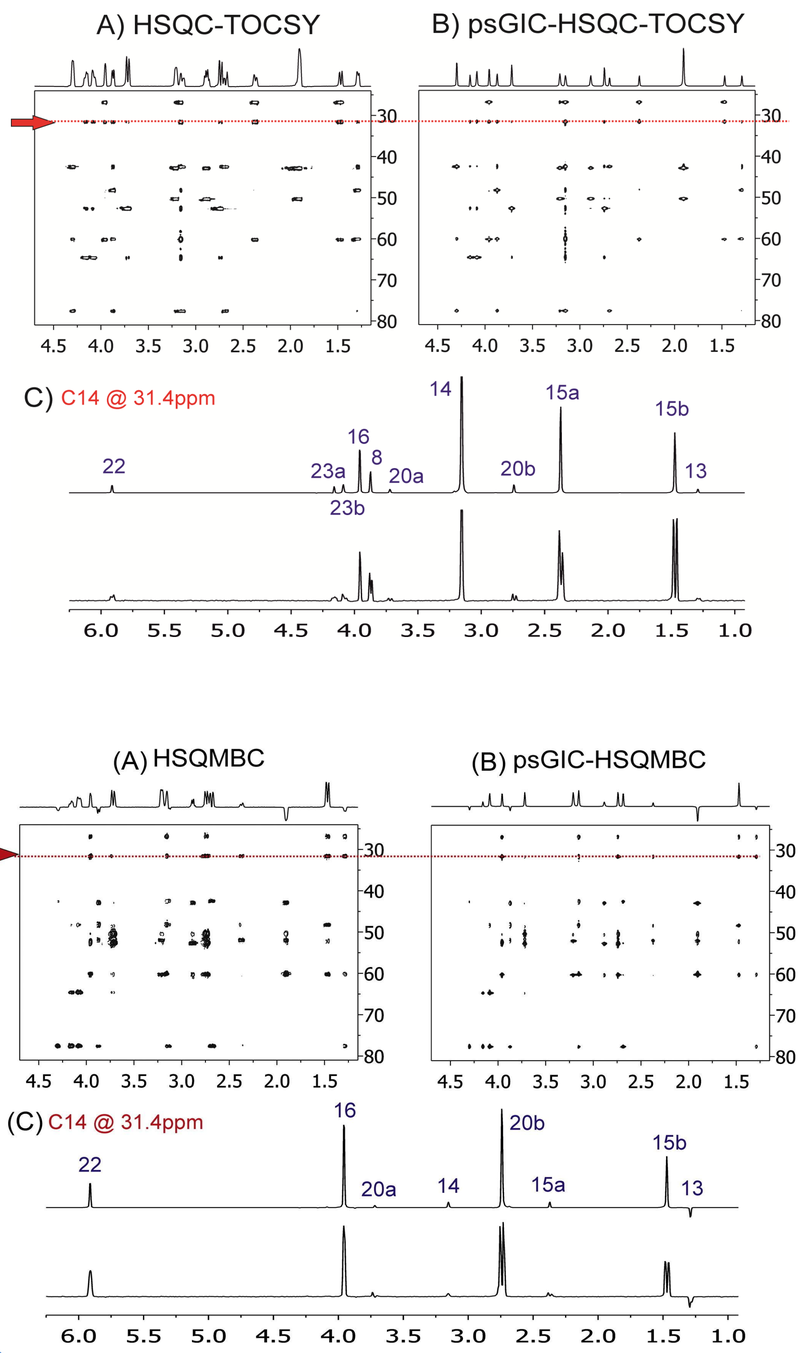


Figure 3.
Aliphatic region corresponding to (A) the regular 2D HSQC-TOCSY and B) the psGIC-HSQC-TOCSY spectra of strychnine generated by GIC. A comparison of the internal F2 projections at the top of each 2D spectrum and the selected C14 rows in C) shows the absence of *J* multiplicity and the excellent reproducibility of signal intensities for all cross-peaks.

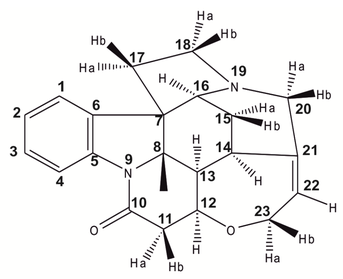
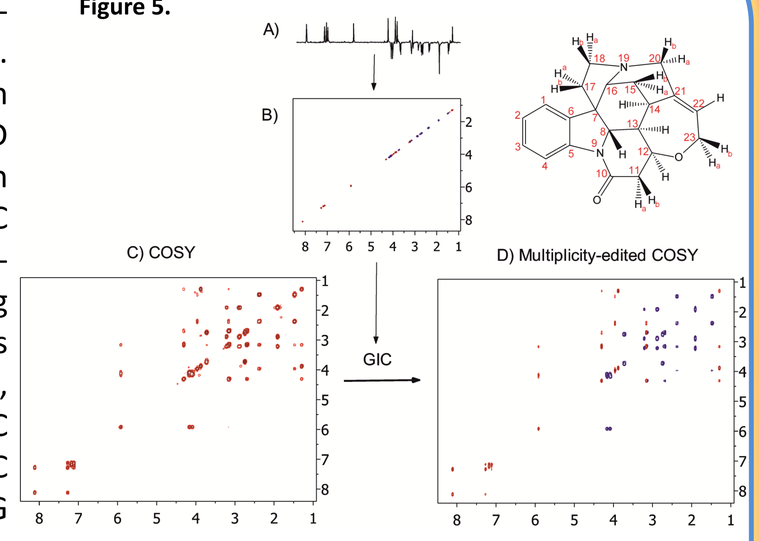


Figure 4.
Aliphatic region corresponding to (A) the regular HSQMBC and (B) the psGIC-HSQMBC spectra of strychnine generated by GIC. A comparison of the internal F2 projections at the top of each 2D spectrum and the selected C14 rows in (C) shows the absence of *J* coupling pattern and the excellent reproducibility of signal intensities for all cross-peaks.

Multiplicity-edited NMR Spectra

The same approach can be applied using the ^{1}H-^{1}H 2D pure shift ME-DIAG (ME-psDIAG) spectrum (Fig. 5B) synthetically generated from the internal F2-projected 1D spectrum (Fig. 5A) of an experimental 2D ME-psHSQC spectrum recorded with BIRD-based homodecoupling during acquisition. Thus, ME-GIC versions of the classical COSY (Fig. 5D), TOCSY, HSQC-TOCSY or HMBC spectra can be obtained from GIC combination with the ME-psDIAG spectrum.

Figure 5.



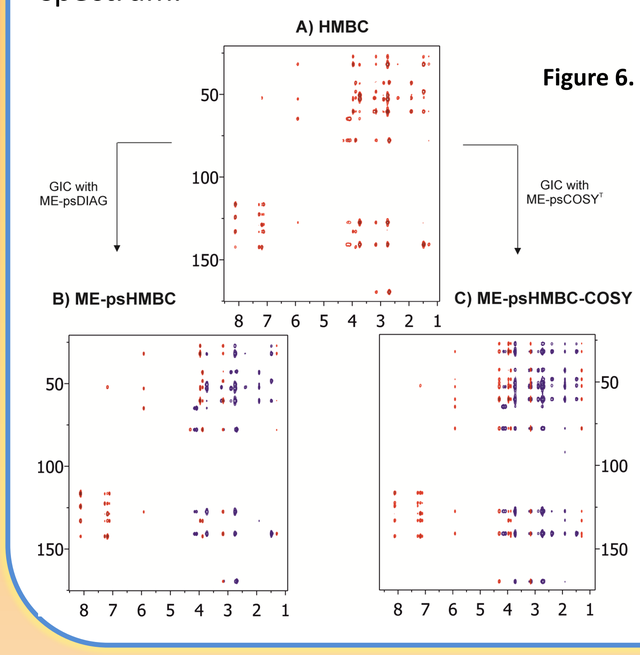


Figure 6.

On the other hand, a ME-psHMBC-COSY spectrum could be reconstructed by GIC between the standard HMBC and the transposed ME-psCOSY spectra (Fig. 6), giving a major number of correlations that can be useful to observe missing two-bond correlations in the original HMBC spectrum or to detect up to four- and five bonds away long-range correlations.

- ✓ Simple and fast processing tool.
- ✓ Complement for conventional dataset analysis
- ✓ General application to a broad range of NMR experiments.
- ✓ Generation of novel synthetic pure-shift spectra, even for NMR experiments that are "impossible" nowadays.
- ✓ Access to unfeasible multiplicity-edited COSY, TOCSY or HMBC spectra

References:

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