Downsampling Strategies for MRS data

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Introduction

On many NMR and MRI systems the acquired analog signals are digitized at sampling frequencies much higher than the Nyquist condition would demand. This is done mainly to improve the dynamic range and the sensitivity [1, 2] of the acquired signals but also to relax the requirements for anti-aliasing filters. To reduce problems related to increased storage requirements and processing time data is usually downsampled to manageable amounts. Depending on the actual method applied, unwanted artifacts can be introduced into the final signal. In this work two common downsampling approaches are investigated and problems are identified that negatively impair quantification of magnetic resonance spectroscopy (MRS) data. An additional third approach is introduced which does not suffer from theses artifacts and thus leads to more accurate and artifact free downsampled FIDs.

Materials & Methods

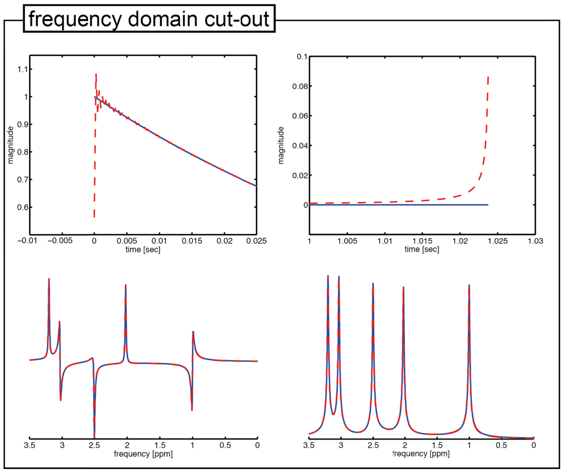
All downsampling procedures were tested in Matlab on a set of simulated FIDs. All signals were simulated with an original bandwidth of 32kHz, duration of 1s and an exponential linewidth of 5Hz. The oversampling factor was set to 8, which lead to a target bandwidth after sample decimation of 4kHz. These values resemble a typical situation on a Philips human MR systems. First a noise-free FID containing a single peak at 4.7 ppm was simulated. The second data set contained 5 different peaks at 1.0, 2.02, 2.5, 3.03 and 3.2ppm, covering the frequency range of brain metabolites. The phases of these peaks were set to arbitrary values (-102, 0, 150, 90, 0 degrees) to simulate J-coupling induced phase evolution. Both signals were processed with each algorithm and compared to an ideal FID calculated at the final reduced sample rate (shown in blue in all Figures). The first downsampling algorithm (Fig. "frequency domain cut-out") consisted of a FFT in the first step, followed by an IFFT of only data points within the limited bandwidth of interest. A second commonly used procedure (Fig. "moving-average TD") was applied in the time domain by averaging every 8 samples, corresponding to the oversample factor, to form a new data point of the sample reduced FID. The proposed improved method for downsampling ("LP TD-filtered") is performed in the time domain and in a first step involves extrapolating the FID by 256 data points at the beginning and at the end of the FID using a Linear Prediction filter. Subsequently the data was filtered by a 257 order Nuttall filter with 4kHz bandwidth. In the last step the downsampled FID is recovered by cutting out every 8th data point starting from the original echo top that was shifted by 384 (256 samples due to linear prediction extrapolation + 128 samples due to filter groupdelay) samples.

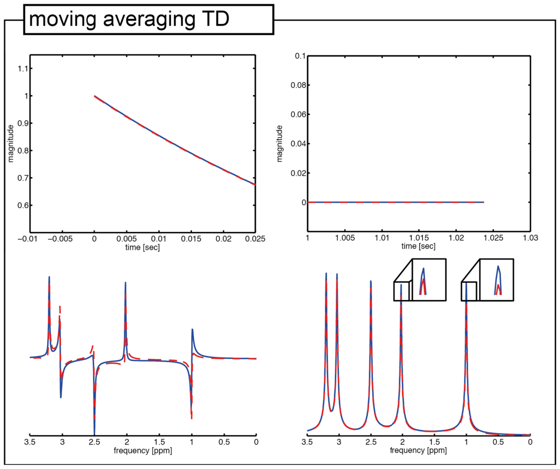
Results & Discussion

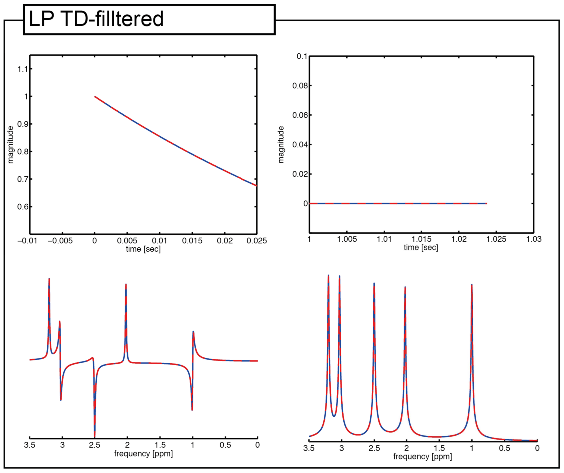
From the processed data three main artifacts can be identified. First, the widely used "cut out" algorithm can introduce wiggles at the beginning and at the end of the FID. These are a consequence of the periodic nature of the DFT algorithm and originate due to the signal jump between the last point of the FID and the first FID point of half echo sampled data. These oscillating can have impact on data quality in processing steps like zero-filling or time domain fitting were the initial points of the FID are proportional to the concentrations present. Furthermore the initial data points especially from water scans might have influence on processing steps like eddy current correction or fast coil combination algorithms based on the phase of the initial point in each channel. Moving average filter avoid the wiggle artifacts but nevertheless introduces amplitude distortions in the final spectrum due to smooth frequency response. As an example peaks like NAA at 2.02 ppm would experience a damping of about 0.58dB (6.4%), which is unsatisfactory in quantitative evaluations. Furthermore moving average filtered data experience a group delay (3.5 samples in case of 8 fold oversampling), which appears as small linear phase in the frequency domain. This needs to be corrected either by linear phase correction or by forward-backward filtering, which leads to zero phase delay but also to squared magnitude response. As a consequence the damping problem with respect to off-center frequency components like NAA gets amplified even more. The novel downsampling scheme "LP TD-filtered" prevents all of the described artifacts. Linear prediction was used to model a smooth artificial extension only to absorb distortions due to the filter's step response. The subsequently applied filter has sharp frequency response over the spectral range of interest and an odd filter order was chosen to easily correct for linear phase due to the groupdelay. In conclusion, a novel downsampling scheme is introduced that avoids truncation wiggles, phase distortions and frequency dependent damping. It hence enhances quantification reliability of in vivo and in vitro MRS data.

References

[1] R A de Graaf, in-vivo NMR Spectroscopy, Wiley 2007
[2] J C Hoch & A S Stern, NMR Data Processing, Wiley 1996


frequency domain cut-out


moving averaging TD


LP TD-fillltered

Figures: The first row of subplots in each section corresponds to the beginning and the end of the magnitude time signal from a single peak at 4.7ppm. The second row shows the real and the magnitude spectra of the second simulated data set. The blue line in all figures represents the ideally downsampled signal.