Linewidth constraints in Matlab AMARES using per-metabolite T_2 and per-voxel ΔB_0

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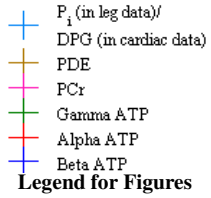
TARGET AUDIENCE: In-vivo MR spectroscopists

PURPOSE: The AMARES spectroscopic fitting algorithm[1] was re-implemented in Matlab (The MathWorks Inc., MA) to improve its performance, to allow integration into a joint fitting and post-processing pipeline and in order to facilitate the inclusion of new kinds of prior knowledge. This abstract focuses on linewidth constraints to illustrate the improvements in ^{31}P-MRS fitting that are achievable with more sophisticated prior knowledge. The prior knowledge we use here is motivated by the following linewidth relationship:

$$1/T_2^* = 1/T_2 + 1/T_2^{*}\text{□} \quad \text{i.e. } LW = LW_{intrinsic} + LW_{\Delta B0} \text{ [Eq. 1]}$$

where $LW_{intrinsic}$ is an intrinsic property of each metabolite and $LW_{\Delta B0}$ depends primarily on the B_0-inhomogeneity in a given voxel. It ought therefore to be possible to fix $LW_{intrinsic}$ for each peak and fit only a single line-broadening term ($LW_{\Delta B0}$) per voxel. Theory shows that in least-squares fitting of a Lorentzian peak[2], uncertainty in the fitted peak area (amplitude) is dominated by errors in fitting the linewidth. We hypothesise that constraining linewidths according to Eq. 1 will make the fitted peak amplitudes less susceptible to noise.



Legend for Figures 1&3

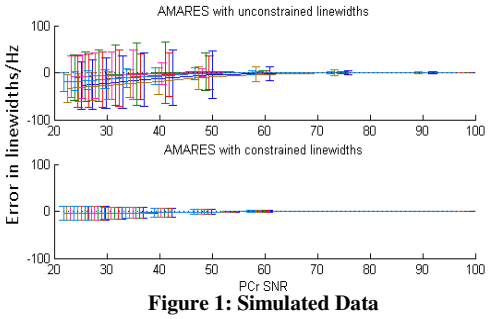


Figure 1: Simulated Data

METHODS:

Matlab AMARES: The minimization of the AMARES model function was accomplished using the Trust-Region-Reflective algorithm[3] as implemented in Matlab's "lsqcurvefit" function using pure Matlab code to compute the AMARES model function and its analytical Jacobian at each iteration. The results of this code were validated against AMARES in jMRUI and by Monte Carlo simulations. Despite being implemented purely in Matlab, the time to fit spectra in a 16x16 CSI slice in Matlab on the author's PC was less half that in jMRUI.

Determination of $LW_{intrinsic}$: The constrained fitting approach requires the (differences in) intrinsic linewidth for each metabolite as prior knowledge (see Eq. 1). To determine these, AMARES fitting with unconstrained linewidths was first run on a 5x5x3 subset of voxels centred around the mid-intraventricular septum from 9 cardiac CSI data sets acquired with a 10cm ^{31}P TR loop at 7T (Siemens)[4]. Each voxel's PCr linewidth was plotted against the linewidths of the ATP, DPG and PDE peaks in turn. These 10 plots (not shown) were fitted to a straight line of gradient 1 using the Matlab robust bisquares weighting fitting function "fit". The intercept defines the additional linewidth of the peak compared to that of PCr, i.e. $\Delta LW_{intrinsic}$. These values were then incorporated into the prior knowledge of the constrained fitting algorithm.

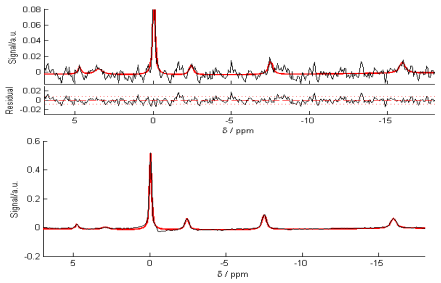


Figure 2: Top: AMARES fit with constrained linewidths. Bottom: Gold standard data used to determine $LW_{intrinsic}$.

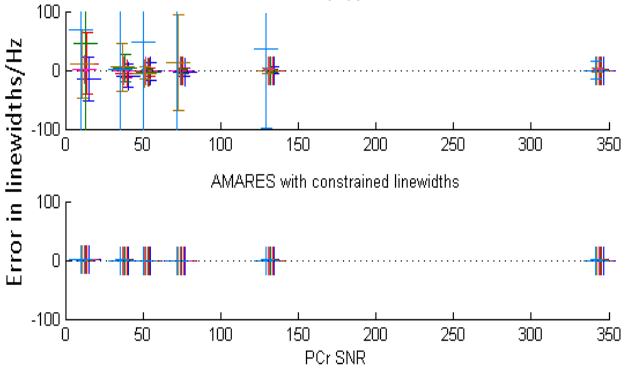


Figure 3: In Vivo Leg Data

Validation: A Monte Carlo simulation was then run on 1000 samples of simulated cardiac spectra with different levels of noise. The deviation of the fitted linewidths from the true values is plotted against SNR in Fig. 1, for AMARES with independent linewidths and with constrained fitting. A range of Monte Carlo simulations were also run where the $LW_{intrinsic}$ prior knowledge was deliberately set wrongly for one peak to assess the potential bias that could be caused by this approach (not shown). Bias was only seen when $LW_{intrinsic}$ was set larger than the actual linewidth. As a demonstration of this method in vivo, CSI data was acquired in the thigh using a 16-element ^{31}P array (Rapid Biomedical) at 7T. 112 scans were run with various numbers of averages (from N=1–100) and voltages (100–531V). The relative intrinsic linewidths were calculated using the two scans with 100 averages (i.e. a PCr SNR >150) and thereafter used as prior knowledge. A single voxel was then chosen for analysis and the data from several receive elements was fitted separately to increase the number of independent samples. We assumed that the metabolite concentrations remained constant, so any changes seen are due to noise. Fitting the spectra gave 112 data points for each AMARES method. The two scans with 100 averages were averaged and used as the gold standard against which all other fits were compared. Visual inspection of these spectra (Fig. 2) and the AMARES residuals confirmed that this was reasonable. Finally, the data were binned against the average SNR of each segment and plotted in Fig. 3.

RESULTS & **DISCUSSION**: In the Monte Carlo simulation of constrained fitting, the deviation is the same for all of the peaks because only $LW_{\Delta B0}$ can vary. The actual fitted linewidths depend also on the intrinsic linewidths $LW_{intrinsic}$ in the prior knowledge. In a typical ^{31}P-MRS spectrum, constrained fitting is more reliable because the stronger PCr signal effectively determines the linewidths for the low SNR peaks, which does not happen with independently fitted linewidths. In vivo, both the fit with independent linewidths and the constrained fit deteriorate at lower SNR, as expected. For all peaks except PCr at SNR=12.5 and α-ATP at SNR=35.6, the constrained linewidth fit has a tighter standard deviation than the unconstrained linewidth (F-test with α=0.001). These SNRs may be compared to 30min cardiac data from our standard UTE-CSI protocol. SNR=12.5 is comparable to 3T cardiac data and SNR=35.6 is comparable to 7T cardiac data. This approach is expected to be particularly valuable to improve fitting of a whole set of low SNR (<30) data such as arises in an exercise response study, or in a saturation- or inversion-recovery experiment because all data can be summed to give excellent initial values for the peak intrinsic linewidths, chemical shifts and relative phases before fitting each individual low SNR spectrum with linewidth constraints.

CONCLUSION: A pure-Matlab implementation of AMARES runs rapidly and makes it straightforward to include arbitrary types of prior knowledge. Linewidth constrained fitting particularly improves low SNR ^{31}P spectra, which will be useful for exercise protocols and for saturation- and inversion-recovery.

REFERENCES: 1.Vanhamme, L., et al., JMR, 1997. **129**(1): p. 35-43. 2. Cavassila S, et al. JMR 2000;143:311-20. 3. Coleman, T.F. et al., Siam J Optim, 1996. **6**(2): p. 418-445. 4. Rodgers, C.T., et al., MRM, 2013.

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