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Magnetic resonance spectroscopy (MRS) probes tissue biochemistry in a completely non-invasive manner. However, *in vivo* applications are constrained by severe signal to noise ratio (SNR) limitations due to the low physiological concentrations of metabolites. With heteronuclei, e.g.  $^{31}\text{P}$ , the low gyromagnetic ratios compared to  $^1\text{H}$  and long transverse relaxation times increase the difficulty. Magnetic resonance imaging is now routinely performed using array receive coils, which give increased SNR over a wider field of view than a single coil. Similar benefits may be expected for MRS [Ref. 1]. We report a general purpose Bayesian algorithm that is quick to run and easy to implement for combining spectra from the elements of an array receive coil. We test it in the frequency domain on  $^{31}\text{P}$  cardiac spectra from a new 8-element array and on  $^1\text{H}$  spectra from body and head arrays.

**Methods:** Data were acquired using a TIM Trio (3T Siemens) scanner using an 8-element  $^{31}\text{P}$  array, a 12-element  $^1\text{H}$  head array and a 6-element body matrix coil in combination with 6-elements from a spine array. Localisation was achieved using 3D CSI (for  $^{31}\text{P}$ ) and single voxel spectroscopic (SVS) methods (STEAM for  $^1\text{H}$  liver spectra and PRESS for  $^1\text{H}$  brain spectra).

**Model:** A typical MRS experiment is illustrated in Fig. 1. For each voxel, the complex spectrum detected by the  $i^{\text{th}}$  element is

$$\bar{s}_{i,k} = \bar{\alpha}_i q_k + \text{partially correlated noise} \quad (1)$$

where  $\bar{\alpha}_i$  are element scaling/phasing parameters,  $q_k$  are the “true” spectrum and the noise is partially correlated between elements of the array due to mutual inductance. The challenge is to recover robustly the true spectrum  $q_k$  from the measured spectra  $\bar{s}_{i,k}$ .

**Noise whitening:** When the SNR is low, it is important to note that mutual inductance correlates the noise between elements in the array. We characterise the noise by calculating the covariance matrix  $\Sigma$  from a region of the spectrum devoid of signal. We calculate matrices of eigenvectors  $X$  and eigenvalues  $D$  of the covariance matrix. Using these, we apply the transformation  $W = X(2D)^{-1/2}$  to the acquired spectra  $\bar{s}$  and the unknown coil scaling factors  $\bar{\alpha}$  giving “channel spectra”  $s$  and sensitivities  $\alpha$ :

$$s_{i,k} = \sum_j W_{ij} \bar{s}_{j,k} \quad \text{and} \quad \alpha_i = \sum_j W_{ij} \bar{\alpha}_j \Rightarrow s_{i,k} = \alpha_i q_k + \text{uncorrelated noise with standard deviation } \sqrt{1/2} \quad (2)$$

**Maximum likelihood solution by the Singular Value Decomposition:** Since the noise in the channel spectra is not correlated, we model their real and complex parts as normal distributions with standard deviation  $\sqrt{1/2}$ . Thus, the Bayesian “likelihood” is

$$L = P(\{s_{i,k}\} | \{q_k\}, \{\alpha_i\}) = \prod_{i,k} \exp(-|s_{i,k} - \alpha_i q_k|^2) / \pi \quad (3)$$

Since  $\exp$  increases monotonically, it is apparent that the maximum likelihood occurs at the minimum value of  $\sum_{i,k} |s_{i,k} - \alpha_i q_k|^2$ . If we consider the spectra from each channel to be the rows of a complex matrix  $\mathbf{S}$ , this is equivalent to saying that the maximum likelihood values of the vectors of channel amplitudes  $\alpha$  and sample magnetisations  $q$  are found when  $\alpha q^T$  most closely approximates  $\mathbf{S}$  in the Frobenius norm. Hence, the maximum likelihood values may be found using the singular value decomposition  $\mathbf{S} = \mathbf{U}\mathbf{\Psi}\mathbf{V}^T$  where the columns of  $\mathbf{U}$  are the left and  $\mathbf{V}$  the right singular vectors of  $\mathbf{S}$  and  $\mathbf{\Psi}$  is a diagonal matrix of singular values arranged in non-increasing order. The SVD decomposes  $\mathbf{S}$  into a series of contributions of increasing rank with maximum power at each step [Ref. 2, Theorem 5.9]. Hence, the maximum likelihood reconstruction has  $\alpha_i = \psi_{i,1}^*$  and  $q_k = \psi_{1,1} u_{k,1}$ . The quality of the reconstruction is measured by  $\Gamma = (\psi_{1,1} \sqrt{N_i} / \sum \psi_{i,1}^2 - 1) / (\sqrt{N_i} - 1)$  which varies from 1 (“perfect”) to 0 (“pure noise”). If desired, the same algorithm can be applied in the time domain to the free induction decays from each element.

**Results:** Fig. 1 presents  $^{31}\text{P}$  cardiac spectra acquired from the interventricular septum of a volunteer as described above. Apodized spectra from each element, the results of our SVD combination method and the standard Siemens method are compared. Our method gives SNR  $\sim$ 60% greater than the standard Siemens method. In other tests on  $^1\text{H}$  SVS spectra from the liver and brain acquired with 12-elements, the SVD recombination is again better than the standard Siemens method. For  $^1\text{H}$ , the quality of the SVD recombination is comparable to that obtained using a prescan without water suppression, fitting the water peak and scaling each element’s spectra accordingly. Numerical simulations further demonstrate the power of this method.

**Conclusion:** We present a method for combining spectra from array receive coils that improves on all previous methods. It is fast, accurate, easy to implement, fully automatic, doesn’t require the presence of a reference signal (although it can use one that is present), and correctly handles arrays that have correlated noise. We believe that this powerful and simple algorithm offers an excellent solution for combining spectra acquired with array receive coils.

1. Wright and Wald, *NMR in Biomedicine* (1997); 2. Trefethen and Bau, *Numerical Linear Algebra*.

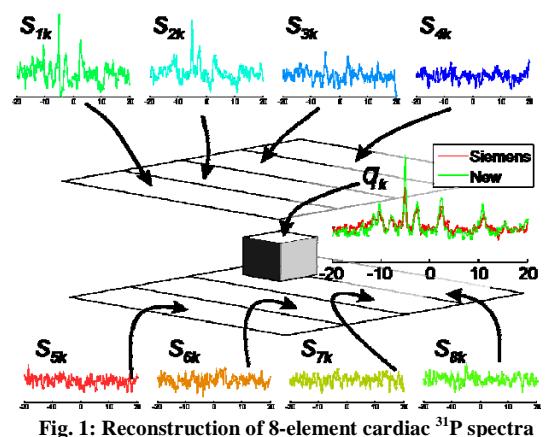


Fig. 1: Reconstruction of 8-element cardiac  $^{31}\text{P}$  spectra