# Autocalibrated Parallel MR Spectroscopic Imaging without Extra Autocalibrating k-space Lines

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**Introduction:** Hyperpolarized $^{13}C$ applications (1) require rapid imaging to combat signal loss due to RF saturation, T1 decay and metabolism. Parallel imaging can reduce imaging time (2,3), but the need for coil sensitivity callibration information is a major challenge. External sensitivity references can be impractical due to low natural abundance of $^{13}C$. Self-calibrating parallel MR techniques are attractive because necessary coil sensitivity information is acquired as part of the acquisition (3-5), but most rely on dense sampling of the center of k-space which can impose a significant time burden for MR spectroscopy. For example, a typical spectroscopic acquisition with 16 x 16 phase encode steps and a desired undersampling factor of 3 demands an extra 43 phase encode steps to fully sample the central 8 x 8 k-space points. This extra calibration data represents 31% of the total imaging time.

We present a new acquisition strategy for undersampled MR spectroscopic imaging with parallel reconstruction that eliminates the need for extra auto-callibrating lines. This approach relies on joint spatial and spectral undersampling, with select chemical species aliasing to unused portions of the spectra. As long as there is a small portion of the spectrum without significant *spectral* aliasing, then that data can be used as a *spatial* sensitivity reference to reconstruct the remaining undersampled data.

**Theory:** This new approach to parallel acquisition is illustrated by considering the numerical phantom in Fig 1a, with five spectral peaks (fig 1b) commonly observed following simultaneous injection of $^{13}C$-labeled hyperpolarized urea and pyruvate. The pulse sequence used for joint spatial-spectral acquisition is based on a flyback echo planar spectroscopic imaging (EPSI) sequence, where a short phase encode blip is applied so that each echo occurs at a different spatial phase encoding line (6). Constant phase encode blips are chosen so that the spatial and spectral dimensions are undersampled uniformly. A sample undersampling pattern in the kx-kf plane with reduction factor of 3 is shown in Fig 2a. Conventional phase-encode undersampling, by contrast, is shown in Fig 2b.

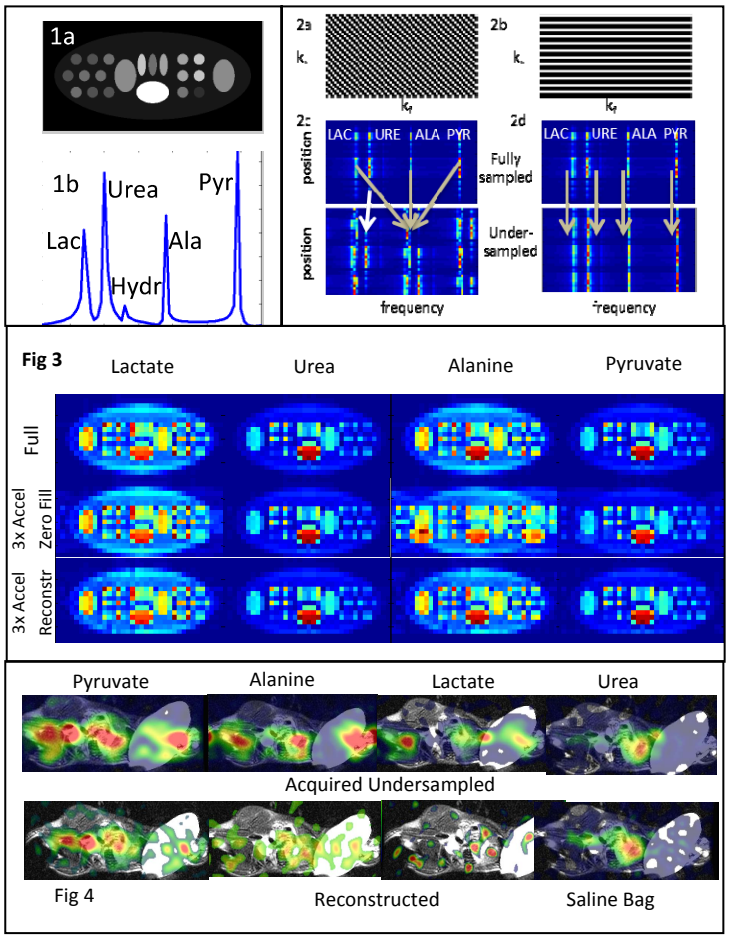
When data are undersampled in only the spatial domain (Fig 2d), each spectral component aliases independently and expected spatial foldover is observed. By contrast, the joint spectral-spatial patern in Fig 2a yields data that alias in both the spatial and spectral dimensions. The pyruvate peak (for example) *folds spatially* onto the *spectrally aliased* lactate peak. For the spectral bandwidth chosen in Fig 1b, the spectrally undersampled urea peak does not overlap any of the other peaks. As a consequence, the undersampled urea peakrepresents a *full FOV spatial data set.* This full FOV urea data set can be used as a sensitivity reference to reconstruct the remainder of the folded peaks.

For parallel reconstruction, we employ a modified version of the Cartesian SENSE reconstruction (7). The signal from coil *l*, $s_l$, can be represented the sum of the spin density at spectral and spatial aliased locations:

$$s_l(x,\omega) = \sum_j C_l(x + j\Delta x)\rho(x + j\Delta x, \omega - j\Delta\omega) \equiv \mathbf{A}\rho$$

$C_l(x)$ is the coil sensitivity. The image, ρ, is recovered by inverting **A.**

**Simulation:** Coil array data corresponding to eight receiver elements were generated from the numerical phantom in Fig 1 using a Biot-Savart model of the surface coil reception patterns. Reconstruction results are shown in Fig 3. The top row of Fig 3 shows the reference lactate, urea, alanine and pyruvate. The second row shows the result of joint spectral-spatial undersampling. The reconstructed data (third row) matches the original data with minimal residual aliasing artifact.




**In Vivo:** The above approach was tested *in vivo* using the blipped EPSI pulse sequence described above, with undersampling pattern shown in Fig 2a. A normal Sprague-Dawley rat was placed supine in between an eight-element carbon-tuned coil array. 3 mL of approximately 100 mM $^{13}C$ pyruvate and 100 mM $^{13}C$ urea were injected following co-polarization for 1.5 hours using a HyperSense polaraizer (Oxford instruments) and imaged on a clinical MR scanner at 3T (GE Medical Systems). MRSI images were obtained 30 s following injection. The full FOV phase encode matrix size was 24 x 6, with 16 frequency encode points and 59 spectral points in the EPSI direction. Voxel size was 1 $cm^3$. Total scan time was 11 s (acceleration factor of 3). Coronal color overlays of metabolite peak areas are shown in Fig 4. Images are independently normalized.

**Summary:** We have described a new approach to parallel MR spectroscopy that uses joint spectral-spatial undersampling to reconstruct parallel MR data without extra autocalibrating lines. This technique exploits the sparsity of hyperpolarized $^{13}C$ spectra and requires only that some portion of the spectrum alias without spectral overlap (urea in our example). In other applications, adjustment of the bandwidth may be needed to ensure this criterion is met, which requires some *a priori* knowledge about the spectra. In general practice, the spectral composition is usually well known and so this is usually not a particularly burdensome requirement. This technique is applicable to both proton and carbon spectroscopy.

**Acknowledgments** K. Scott for technical assistance, funding from NIH grant P41EB013598 and UC Discovery grant ITLbio 178688 with GE Healthcare. **References** **1.** Ardenkaer-Larsen et al PNAS 2003 100:10158 **2.** Tropp et al JMR 2010 208:171 **3.** Arunachalama et al NMR Biomed 2009 22:867 **4.** McKenzie et al MRM 47:529 (2002) **5.** Griswold et al MRM 47:1202 (2002) **6.** Hu et al MRM 192:258 **7.** Pruessmann et al MRM 1999 42:952 **Acknowledgments** K. Scott (technical assistance) and NIH grant P41EB013598 and UC Discovery grant ITLbio 178688 with GE Healthcare.