

## Non-Cartesian Calibrationless Parallel Imaging Reconstruction: Application to Hyperpolarized <sup>13</sup>C Imaging

Markus Durst<sup>1,2</sup>, Ulrich Koellisch<sup>1</sup>, Jonathan I. Sperl<sup>2</sup>, Eliane Weidl<sup>3</sup>, Florian Wiesinger<sup>2</sup>, Axel Haase<sup>1</sup>, and Rolf F. Schulte<sup>2</sup>

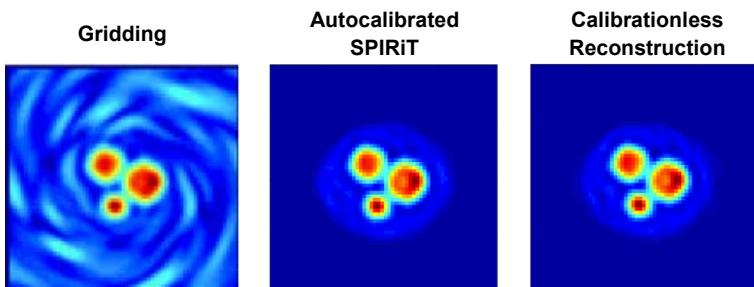
<sup>1</sup>IMETUM, Technische Universität München, Munich, Bavaria, Germany, <sup>2</sup>GE Global Research, Munich, Bavaria, Germany, <sup>3</sup>Department for Nuclear Medicine, Technische Universität München, Munich, Bavaria, Germany

### Introduction:

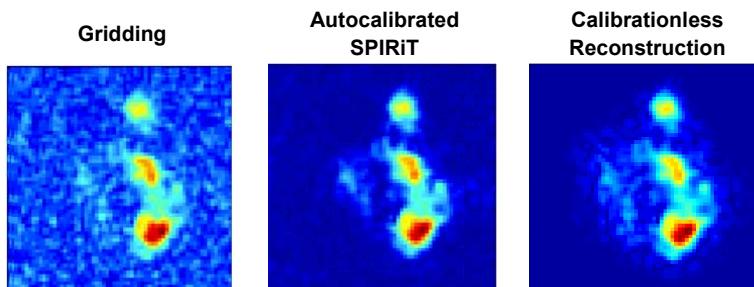
The signal enhancement achieved with hyperpolarized <sup>13</sup>C imaging agents allows unique insight into biochemical processes by detecting the cellular uptake and conversion of <sup>13</sup>C labeled substances with spectroscopic MR. Because of the irreversible T1-decay and the depletion of the hyperpolarized magnetization with each excitation, scan time and the number of excitations are crucial for these measurements. Therefore, the combination of rapid calibrationless parallel imaging, where the time consuming acquisition of a fully sampled calibration area can be omitted, with fast spiral pulse sequences seems to be promising for these measurements. In this work, a fast calibrationless parallel imaging approach, which has been demonstrated for proton imaging [1], was implemented and applied to metabolic imaging with hyperpolarized [1-<sup>13</sup>C]pyruvate.

### Theory and Methods:

The calibrationless parallel imaging algorithm exploits the low-rank property of the fully sampled k-space data. For this purpose, a Hankel-structured k-space data matrix is constructed from the undersampled multicoil data, consisting of overlapping blocks. Those overlapping blocks are linearly dependent, therefore a data matrix without missing entries has a lower rank and can be calculated using matrix completion by thresholded singular-value-decomposition [2] without the need of acquiring a fully sampled calibration area. For non-Cartesian acquisition schemes, the goal is to find a low-rank matrix which is consistent with the acquired data after interpolation back onto the non-Cartesian grid. This problem is solved in an iterative manner [1]. The k-space trajectory for simulation purposes was designed consisting of 12 spiral interleaves (Fig.1). Due to SNR-constraints the nominal matrix-size was reduced to 23x23 covering a FOV of 80mm. The decomposition of the metabolites was performed using least squares CSI (LSCSI) [3], requiring only a minimal number of acquisitions by using prior knowledge about the metabolites' resonance frequencies. Simulation data was generated and modulated with T2\* decay (T2\*=30ms), measured coil sensitivities of a four-channel array and three metabolite concentrations (simulating pyruvate, alanine and lactate), in order to examine the performance of the calibrationless reconstruction. Additionally, an *in vivo* IDEAL spiral [4] parallel MRI (pMRI) measurement [5] of a male buffalo rat, which was acquired on a HDx 3T scanner (GE Healthcare, Milwaukee, WI, USA) using a four-channel coil (Rapid Biomedical, Würzburg, Germany), served as a first test to analyze the performance of the algorithm under *in vivo* conditions. The trajectory was designed with two-fold oversampling in the center, and a smooth transition to four-fold undersampling in the outer k-space (duration 65ms, FOV=80mm, nominal matrix-size 36 x 36, flip angle 10°, TR=250ms, slice thickness 1cm), hence allowing to compare the calibrationless method to autocalibrated SPIRiT [6].

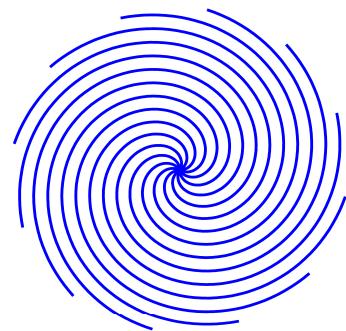


**Fig.2:** Comparison of calibrationless reconstruction of simulated data with a reduction factor of R=3



**Fig.3:** In-vivo lactate maps of a rat, reconstructed with different methods; the same data was used for reconstruction

**Acknowledgements:** Funded from BMBF grants # 01EZ0826/7, 01EZ1114B



**Fig. 1:** k-space trajectory with 12 spiral interleaves.

### Results and discussion:

The reconstruction of the simulated dataset was performed with different reduction factors R. Up to R=3, aliasing noise could almost completely be removed, whereas the image information was preserved by choosing an adequate threshold for the singular values (about 8% were kept with a blocksize of 5x5x4). The results were comparable to autocalibrated SPIRiT (as shown in Fig.2), for R=4 minimal aliasing artefacts occurred. The calibrationless reconstruction of the *in vivo* data shows very high resemblance with the autocalibrated SPIRiT reconstruction (Fig. 3).

### Conclusion:

Calibrationless pMRI with undersampled spiral trajectories was successfully applied to hyperpolarized <sup>13</sup>C metabolic imaging, the performance of this method was shown to be comparable to existing autocalibrated pMRI reconstruction methods like SPIRiT. As the acquisition time is further reduced by avoiding additional scan time for acquiring a calibration area, this method offers great potential for time-critical hyperpolarized <sup>13</sup>C metabolic imaging.

### References:

- [1] Lustig et al. ISMRM 2011, 483;
- [2] Cai et al. arXiv: 0810.3286, 2008;
- [3] Reeder et al. JMRM 2007, 26:1145-1152;
- [4] Wiesinger et al. MRM, in press;
- [5] Schulte et al. ISMRM 2011: 1522;
- [6] Lustig et al. MRM 2010, 64: 457-471;