

# A Library of Generalized Fourier Sampling Theorems for Irregular 2D Regions of Support

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**Introduction:** We have presented elsewhere [1,2] a generalization of the Fourier sampling theorem, called “multiple region” MRI (mrMRI), which dramatically increases  $k$ -space sampling efficiency when the object or its edges are confined to small, possibly non-adjacent portions of the field of view (FOV). This report describes the numerical generation of a library of such sampling patterns for thousands of irregular 2D regions of support. This library could be used to facilitate the clinical application of mrMRI; once the supporting region geometry is known (*e.g.* from a scout scan), the appropriate sampling pattern can simply be looked up in the library.

**Method:** MrMRI is implemented by covering the FOV with an array of rectangular cells. Assume that the object (or its edges) is known to be supported on only  $C$  cells. Samples in  $k$ -space are acquired on a small number  $A$  ( $A \geq C$ ) of sparse, slightly displaced cartesian grids. Each of these sparse grids has the usual (Nyquist) spacing necessary for Fourier reconstruction of a rectangular FOV with the dimensions of a single cell. The mrMR image can be constructed from the data on all of these sparse grids by using small FTs together with a simple linear transformation. During reconstruction, the average image variance (*i.e.* the “noise”) over the supporting cells is amplified by a factor equal to the trace of a matrix that depends only on the relative locations of the supporting cells and the  $k$ -space offsets of the sparse grids. If the supporting cell locations are known *a priori*, the  $k$ -space offsets can be chosen to minimize this trace. The resulting mrMRI sampling pattern is optimal in the sense that it produces images with the lowest possible global variance. In the special case where the cells coalesce into one rectangular region and  $A = C$ , the optimal mrMRI pattern reduces to the conventional (Nyquist) sampling pattern, and the global variance reaches its lower bound, which is associated with no noise amplification.

For arbitrary cell configurations with  $C = 2$  or  $3$ , we previously found analytic solutions for the optimal sampling patterns. We now seek numerical solutions for  $C \geq 4$ . Note that it is computationally expensive to directly minimize the matrix trace over the space of all possible  $k$ -space offsets. However, the matrix trace reaches its lower bound whenever the determinant of the inverse of the same matrix reaches its upper bound. Because this determinant is a periodic, bandlimited function of the  $k$ -space offsets, its maximum can be found with less computational effort by performing gradient ascents from a relatively small number of seed points. Thus, if the determinant reaches its upper bound for a particular set of  $k$ -space offsets, we will have found a set of offsets that cause the trace to reach its lower bound, and noise will not be amplified during reconstruction. If the determinant does not reach its upper bound, we can still use the  $k$ -space offsets producing the maximum determinant.

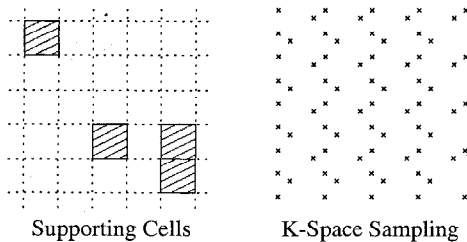


Figure 1

At last year’s ISMRM meeting, we presented a library of mrMRI sampling patterns for 1D cell configurations, along with some isolated 2D examples [3]. Here we present a library of sampling patterns for thousands of 2D arrangements of supporting cells. It took 5,000 CPU hours for R10000 CPUs (SGI) to generate these solutions. If a pair of 2D cell configurations were related to one another by rotation, translation, reflection, and/or cell shearing transformations, it sufficed to numerically compute the mrMR sampling pattern of one of them, because the sampling pattern of the other configuration could be analytically derived from it. In addition, 2D cell arrangements which formed 1D (or sheared 1D) patterns could be reconstructed using sampling patterns derived from the 1D library. These redundancies made it possible to avoid the numerical computation of the mrMR sampling patterns for the majority of cell configurations. For example, out of all the 53,130 different arrangements of five cells fitting within a  $5 \times 5$  cell array ( $\binom{25}{5} = 53,130$ ), only 2,889 (5%) are truly distinct 2D patterns and need to be subjected to the above-described numerical computation.

**Results:** Figure 1 shows a typical optimal mrMRI sampling pattern in the library. Figure 2 shows a histogram of the noise amplification for the 17,392 geometries in the 2D library for 4–7 supporting cells (excluding those which were equivalent to 1D problems). A large majority of the solutions resulted in a very small amount of noise amplification — 30% did not amplify noise, 97% gave noise amplifications of less than 13%, and the maximum noise amplification over all geometries was 18%. The average noise amplification over all 2D geometries in this library was only 4%.

**Conclusions:** We have generated a library of sparse  $k$ -space sampling patterns that can be used to reconstruct objects which have their edges or intensity confined to thousands of different irregular 2D regions of support. Image reconstruction is computationally cheap (small FTs and small linear transformations), and there is little or no noise amplification. These results may be used to dramatically reduce imaging time or to increase spatial resolution in some clinical settings (*e.g.* some applications of MRA [2] and interventional MRI).

## References:

- [1] S.K. Nagle, D.N. Levin, and V.Y. Kuperman, ISMRM, 1998, p. 187.
- [2] S.K. Nagle and D.N. Levin, MRM, 41:774–786, 1999.
- [3] S.K. Nagle and D.N. Levin, ISMRM, 1999, p. 1645.

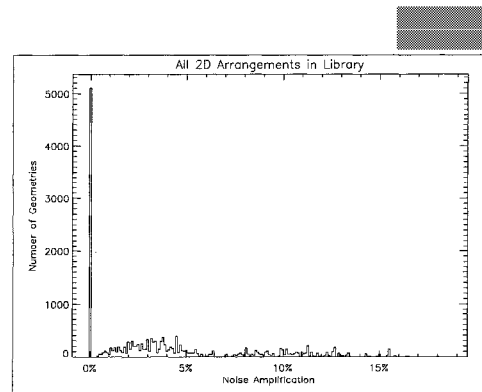


Figure 2