Specialty area: Advanced Diffusion Acquisition

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Highlights

- Scan time is a limiting factor for translation of advanced diffusion weighted magnetic resonance imaging (DW-MRI) to clinical practice. Moreover, physical constraints limit the total time that DW-MRI can be acquired for pre-clinical or phantom studies.
- Compressed sensing (CS) is a signal processing perspective that can be applied to circumvent Nyquist criteria and dramatically accelerate DW-MRI acquisitions.
- We will discuss the fundamentals of CS and how CS can be used to reveal complex diffusion-inferred tissue models with limited k-space data and/or with limited diffusion sensitization.

TALK TITLE:

Compressed Sensing for Fast Acquisition

TARGET AUDIENCE

- This presentation targets scientists and researchers who are familiar with basic magnetic resonance imaging (MRI) acquisitions and the contrasts derived from DW-MRI.

OUTCOME/OBJECTIVES

As a result of attending this presentation, participants should be able to:
- Understand the fundamentals of CS theory in relation to Nyquist criteria and the classical spin-echo approach for DW-MRI.
- Discuss strategies for using CS to accelerate DW-MRI acquisition (i.e., while acquiring standard practices for diffusion sensitization of MRI).
- Discuss approaches for CS of diffusion-derived tissues models (i.e., estimating motion probability propagators from limited diffusion sensitizations).
- Compare advantages and limitations of using CS to accelerate acquisition of DW-MRI.

PURPOSE

Diffusion contrasts imbue MRI with exquisite sensitivity to tissue microarchitecture[1], but specificity in the context of complex tissue architecture has been elusive[2]. High-resolution acquisitions reduce the impacts partial voluming and offer the potential to image more homogeneous local environments [3-8], but increasing resolution traditional necessitates increased data acquisition time. Alternatively, moving beyond a typical tensor representation to more complex tissue models at the individual voxel level [9-15] has the potential to resolve long-standing concerns over "cross-fibers" [16, 17]. Yet, complex models required more detailed characterization of changes in MRI signal contrast with changes in applied diffusion weighting; hence, more data are needed.

Since Richard Ernst's NMR Fourier Zeugmatography[18], the fundamental constraints on rapid imaging have been (1) achieving sufficient signal-to-noise ratio for each observed Fourier coefficient and (2) acquiring sufficient Fourier space (k-space) such that Nyquist criteria are satisfied for the reconstruction physical resolution. Simply put, under the Nyquist criteria, the number required observations scales with the product of the voxel dimensions and linearly with

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the number of independent volumes. With both high-resolution diffusion imaging and complex diffusion models, the length of time required is prohibitive for routines clinical applications (i.e., constraints of less than 30 mins to 1 hour of total scan time) and borderline infeasible/impractical for research studies (e.g., due to scanner drift, physiological motion). CS is a signal processing perspective that offers the potential to circumvent Nyquist criteria [19-21]. We will review the fundamental of how CS can be applied to MRI acquisition [22] and how CS can be used to reveal complex diffusion-inferred tissue models with limited data.

METHODS / RESULTS

In 2006, Candes *et al* and Donoho introduced CS to the information theory community, and CS approaches were rapidly translated to a diverse array of signal processing and sensing application from signal pixel image[23] to MRI[22], as reviewed in a 2008 IEEE Spectrum special issue[24]. The key idea in CS is that data can be represented in two basis sets (with low coherence), one during sensing and another during reconstruction. When the signals under consideration can be sparsely represented in the reconstruction basis, one recover the signal from sparse (and noisy) observations taken with the sensing basis. Random sampling has attractive statistical properties, but randomization is not required. CS efforts in the MRI community followed Lustig's work in which Fourier space (k-space) was sparsely sampled in space and time (for dynamic sequences) while sparsifying transform were developed to increase sparsing in the reconstruction basis, e.g., [25-27].

It was quickly realized that the process of computing diffusion-inferred tissue models (e.g., tensors[1], spherical harmonics[14], tensor mixtures[28, 29], fiber orientation distributions[30, 31], etc.) was a sensing process in itself. Using CS theory, it is not strictly necessary to regularly sample the space of diffusion sensitization parameters in order to recover these models. In 2008, we presented the first, simple approach using CS to recover multiple tensors from traditional diffusion tensor imaging data (which are sparsely sampled relative to modern high angular resolution sequences)[32]. These approaches have been generalized [33-35] and extended to encompass a broad range of possible diffusion models from diffusion spectrum imaging [36-39], orientation diffusion functions (ODF) [40, 41], ensemble average propagators (EAP) [42], and multi-shell propagators [43].

DISCUSSION

Under specific conditions (incoherent sensing and reconstruction basis), CS offers exact reconstruction with the number of samples proportional to the number of parameters required to represent the object (i.e., "sparsity"). From a practical perspective, CS is a special case of regularized regression and is commonly implemented using a fast L1-L2 numerical optimizers. Contrary to some expectations, CS is not a magical spell that offers perfect reconstruction with negligible data. Rather, it is a principled approach for projecting limited information into a defined space. CS grew out of regularized regression and dictionary bases. These approaches have been (and continue to be) applied outside of the CS context for learning for regularizing deconvolution of orientation diffusion functions into fiber orientations [14, 28, 30, 31].

CONCLUSION

CS enables rapid MRI sequences where the amount acquired information scales with the *complexity of the image* as opposed to the *Fourier resolution of the reconstructed image*. Real-time and on-scanner CS reconstruction are emerging capabilities[44] and will likely be widely adopted for non-diffusion sequences (e.g., vascular imaging) when the target image is known to sparse in a simple transform of the voxel-domain. Meanwhile, CS of the motion probability propagators is undergoing rapid innovation and expansion in a manner that has paralleled development of models of intra-voxel structure [40, 45-50]. Direct sensing of intra-voxel

structure has enabled reasonable estimation of crossing fiber structure using traditional DTI acquisitions (which are feasible for clinical imaging, e.g. our work[32-35]). Improvements in CS reconstruction and empirical optimality criteria are promising to improve both approaches to advanced diffusion weighted imaging.

Fundamental challenges remain in understanding and interpreting CS acquired images because well-accepted measures of image quality (i.e., signal-to-noise, contrast, resolution) are not necessarily constant for all possible target images. For example, it is straightforward to create a straw-man CS sequences such that a set of healthy brains is reconstructed with near perfect accuracy where as a brain with a tumor would be constructed as normal. Therefore, particular care must be exercised in determining the domain of target images for a CS method is designed and these assumptions should be carefully validated.

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