High-resolution diffusion-weighted MRI using variable density spiral acquisition

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Synopsis:
A self-navigated multi-shot MR pulse sequence based on variable density spiral trajectory was implemented for high-resolution diffusion-weighted MRI. The k-space trajectory design was calculated on-line using a simple analytical approximation and the sampling density follows a hanning window function. Due to the over sampling of the center k-space, this 2D self-navigator allows more robust motion correction and the high resolution diffusion-weighted images (256x256) acquired using 8 spiral interleave is of high quality even without elaborate correction schemes.

Introduction:
Spiral trajectory has been very attractive for high resolution diffusion-weighted MRI because of its overall merits against motion artifacts and the capability to use the readout itself as a navigator. However, with the constant density spiral trajectory design (Fig. 1a) the estimate of phase differences between interleave using a single central k-space data point is not reliable. The inadequate phase compensation between interleave can result in non-uniform sampling of k-space and render the diffusion-weighted images useless. In this study, we implemented a variable density spiral trajectory design to heavily oversample the inner k-space portion (the first 100 data points of each interleave cover less than 0.5% of the k-space radius) and the motion-induced phase shift between interleave can be reliably estimated from the multiple data point average. An advantage of this trajectory design is that the sampling density profile followed a hanning window function and the calculation of the trajectory can be calculated using a simple analytical solution, which enables flexible prescription of the scanning parameters.

Methods:
The diffusion-weighted MRI pulse sequence with variable density spiral trajectory was implemented on a GE Signa 1.5T using EPIC LX 9.0. The desired trajectory for a given matrix size (N) and FOV was calculated using the following equations:

\[ K(t) = (N/2/FOV) t^2 \exp(i\omega t), \]

\[ \tau(t) = \frac{S_y \gamma}{k \omega} (\alpha/2 + 1) t^{-\alpha} \]

for \( 0 \leq t \leq \min(t_s, t_{end}) \), and \( \tau(t) = \frac{k \omega}{2} \) for \( t_{end} \leq t \leq t_{end} \)

where \( S_y \) and \( g_m \) are the gradient slew rate and amplitude limits, respectively, \( t_s \) is the transition time when the trajectory switches from the slew-rate limited regime to the gradient amplitude limited regime. The value of \( \alpha \) used was 4. For comparison, with a given acquisition prescription the sequence has the option to choose either variable or constant \( \alpha \) density spiral trajectory. The sequence was first extensively tested using an agar gel phantom at \( b=6000s/mm^2 \) and matrix size \( N=256 \). In vivo measurements were then performed in two healthy volunteers using the following protocol: 8 spiral interleave with 19.94 ms readout window per interleave, \( b=910s/mm^2 \), \( N=256 \), FOV=240mm, TR=6s, BW=100kHz, and 4 different diffusion weighting directions (xyz, -x-y+z, x-y-z, -x+y-z). A whole brain trace mapping based on this protocol takes about 3min.

Results:
With the constant density spiral trajectory (Fig. 1a), the diffusion-weighted MR images collected from the gel phantom and human brains have severe motion artifacts (Fig. 1c). For this design a provisional motion correction mechanism based on the phase shift estimate of the central k-space data point is not reliable. The inadequate phase compensation between interleave can be reliably estimated from the multiple data point average. An advantage of this trajectory design is that the sampling density profile followed a hanning window function and the calculation of the trajectory can be calculated using a simple analytical solution, which enables flexible prescription of the scanning parameters.

Discussion:
The experimental results from this work demonstrate that using the variable density spiral trajectory can substantially improve the image quality of the high resolution diffusion-weighted MRI. It should be pointed out this k-space sampling method is highly time efficient and can be directly used for clinical applications and high-resolution diffusion-tensor imaging. We are currently in the process of testing more elaborate mechanisms for motion and eddy current artifact correction.

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References: