DYNAMIC FIELDMAP ESTIMATION FOR RESPIRATION CORRECTION BASED ON SINGLE SHOT 3D IMAGES

B. Zahneisen[1], T. Grotz[1], M. Zaitsev[1], and J. Hennig[1]
[1]University Hospital Freiburg, Freiburg, Germany

Introduction: MR-encephalography (MREG) [1] has been shown to allow extremely fast (TR < 100ms) and highly sensitive monitoring of physiological changes in the brain. It is based on the use of highly undersampled isotropic 3D single shot trajectories (e.g. Rosette, Concentric Shells) in combination with regularized multi-coil reconstruction. Because of the long readout times, the method is sensitive to off-resonance effects. The acquisition of a (static) field map prior to the actual measurement allows an off-resonance corrected reconstruction that reduces the trajectory specific off-resonance artifact. However, dynamic fluctuations of the field map cause changes in the point spread function (PSF) resulting in signal variations. The major source of dynamic field map changes is respiration. Methods for dynamic field map estimation are given in [2] and [3]. [1] (referred to as DORK) estimates a global variation of the resonance frequency from k-space centers acquired at two different times. DORK can therefore only perform a 0-order correction and is restricted to the use of a 2D multi-slice sequences. [2] proposes to perform a joint regularized reconstruction and estimation of the unknown underlying field map. In our case of a highly undersampled volumetric acquisition, both methods are not optimal. The aim of this work is to estimate dynamic changes of local precession frequencies (off-resonance map) from dynamic changes of the image phase of a reconstructed time series. The dynamic changes are measured relative to a reference time point.

Theory: The off resonance map F can be separated into a static and a dynamic component: $F(\mathbf{r},t) = F_0(\mathbf{r},t_0)+dF(\mathbf{r},t)$. The methods aims to estimate and correct for the dynamic component $dF(\mathbf{r},t)$. It is assumed that the reconstructed image phase $\Phi(\mathbf{r},t)$ is determined by the object's phase at the echo time TE. With that, the image phase of time frame n can be written as $\Phi_n(\mathbf{r},t)=[F_0(\mathbf{r})+dF(\mathbf{r},t_n)]\cdot TE$. The dynamic field at time point t_n is then given by $dF(\mathbf{r},t)= (\Phi_n-\Phi_0)/TE$. The calculation of $dF(\mathbf{r},t)$ is restricted to regions of the brain that are not affected by CSF pulsation and/or strong static off-resonances. If the exact TE is unknown, it can be determined iteratively by optimizing the output of the applied correction with respect to TE.

Materials and methods: All experiments were performed on a 3T scanner (Trio, Siemens) using a 32 channel head coil array for signal reception. The correction was applied to 3D-MREG functional imaging data with a repetition time of 100ms and full coverage of the brain. For k-space acquisition a single shot, variable density, concentric shells trajectory was used [4] in combination with regularized reconstruction. For demonstration purposes, only 0th and 1st order components were corrected by applying a frequency shift to the data and adding a linear ramp to the trajectory.

Results: Fig.1 displays a dynamic field map for a single time point from the time series (top). The residual dynamic field map after correction of global and linear components is shown in b). Fig.2a shows the time course of the estimated global resonance frequency together with the phase of an arbitrary voxel. Fig.2b shows the time course of the linear components in the dynamic field maps. Especially the z-gradient varies with the respiration cycle. As an example, three time courses (raw, corrected) of voxel intensities at various positions are plotted in Fig.3. For every pixel, the respiration contribution was calculated as the spectral power P_{resp} at the respiration frequency. The respiration contributions (corrected vs. raw) of all pixels together with the linear regression are plotted in Fig.4 for dataset 1. In the table the regression coefficient of the proposed method is displayed for all 3 datasets (#1-3) and compared to DORK correction.

	#1	#2	#3
DORK	0.61±0.15	0.53±0.13	0.57±0.12
new	0.35±0.09	0.37±0.13	0.33±0.08

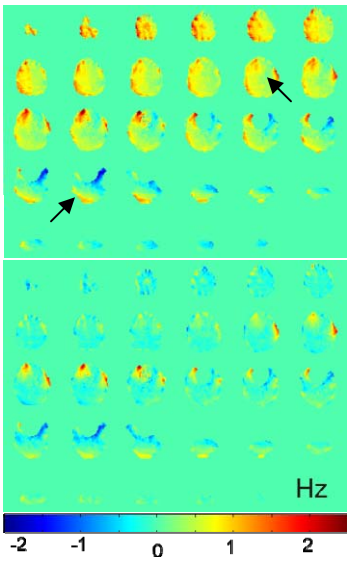
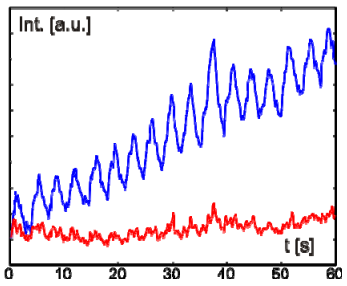


Fig.1) Dynamic field maps before (top) and after (bottom) correction of 0th and 1st-order components.

Discussion: We have shown that for 3D single shot acquisition the estimation of a dynamic field map from the changes of the image phase of a time series relative to a reference time point is feasible. Feeding back the dynamic off-resonance map to the reconstruction results in a ~64% reduction of respiration fluctuations in the signal time series compared to ~40% for the DORK-method. The method requires twice the computation time. Compared to a k-space based method, our approach allows one to restrict the calculation of the field map to a ROI and exclude unwanted regions that also influence the phase of a measured signal by providing a spatial map of the off-resonances. Future work will investigate a correction method by using the full dynamic map (conjugate phase reconstruction) and validation on fast event related fMRI experiments.

[1] Hennig J, Zhong K, Speck O. Neuroimage 34(1):212-219(2007).
[2] Pfeuffer J, Van de Moortele P, Glover G MRM 47:344 –353 (2002)
[3] Sutton B, Noll D, and Fessler J., MRM 51:1194 –1204 (2004)
[4] … ISMRM 2011 (submitted)
This work is part of the INUMAC project supported by the German Federal Ministry of Research, grant #13N9208.



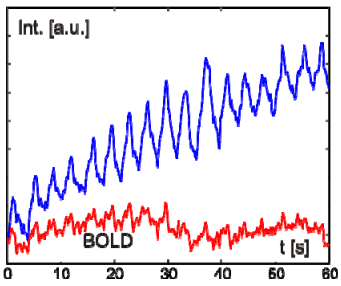


Fig.3 Uncorrected (blue) and corrected (red) voxel time series (arrows fig.1)

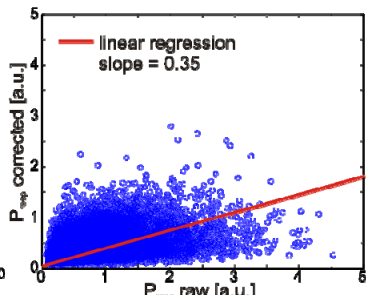


Fig.4 Respiration Contribution

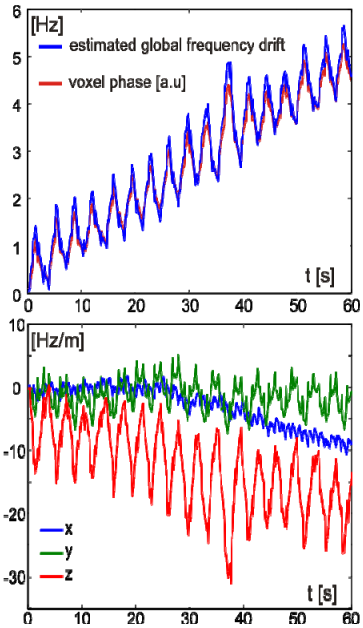


Fig.2 a) global frequency fluctuations (blue) and phase of a voxel (red). b) estimated gradients