nMapping: High speed, high SNR fMRI using direct mapping of functional networks

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Target Audience: MR physicists and Neuroscientists interested in advanced fMRI imaging methodology.

Introduction: In BOLD fMRI, image acquisition/reconstruction and data analysis are implemented as two separate steps, with a 4D (XYZT) data set as the output of the former and the input to the latter. In most applications, fMRI data is processed and reduced to timeseries associated with brain nodes or networks. Direct mapping of nodes or networks from highly undersampled raw fMRI k-space data (nMapping) (1) was introduced to provide dramatic increases in SNR efficiency when the geometry of the nodes/networks is known. In (1), the theoretical basis for nMapping is described, and using synthetic data, increases in SNR per unit time of over an order of magnitude are anticipated for nMapping of several hundred nodes/networks, when compared to conventional fMRI using the Human Connectome Protocol (HCP) (2). We demonstrate here the use of fully sampled human fMRI data, undersampled to simulate nMapping data acquisition, to determine the degree to which undersampled nMapping data captures the relevant variance in the fMRI signal.

Methods: The requirements for the nMapping process are 1) a parcellation of the brain; and 2) a 3D k-space trajectory. The linear relationship between the coefficients of the parcels (the nMap) and the MR signal can be expressed by a simple encoding matrix which is derived directly from the MR signal equations integrated over the parcels. For a k-space trajectory *k* and nMap coefficients *x*, the MR signal *S* can be expressed as $S = Ax$ where the elements of the encoding matrix *A* are $\boldsymbol{A_{ij} = \int_{V_i} w_i(r) e^{ik_j \cdot r}\, dV}$, where the integral is over the volume V_i of the *i*th parcel, the weight w_i is the relative weight of the element over space, and *j* indexes over the k-space points acquired. For parcels V_i that fall over a uniform Cartesian grid, *A* reduces to the Fourier encoding matrix. When there are more k-space points than parcels, this represents an over-determined set of equations that can be directly solved for the nMap coefficients x using least squares estimation. A 278 parcel functional atlas from Shen (3) was used, and a single shot 'yarn ball' 3D k-space trajectory, shown in **Figure 1**, was used to simulate nMap data acquisition. The trajectory is parameterized by: $x(t)=r\bullet\sin(\phi)\sin(\theta)$; $y(t)=r\bullet(\cos(\phi)\sin(\theta)\cos(\gamma)-\cos(\theta)\sin(\gamma))$; $z(t)=r\bullet(\cos(\phi)\sin(\theta)\sin(\gamma)+\cos(\theta)\cos(\gamma))$, where θ ranges from 0-48$\bullet 2\pi$, $\phi=0.236\,\theta$, $\gamma=0.0204\,\theta$, $r=0.62\text{cm}^{-1}(\theta/\theta_{max})^{0.614}$, and θ (t) was time optimized using (4). The parameters were numerically optimized to minimize the condition number of the encoding matrix. The duration of the trajectory was 23.6 ms, compared to a 720ms TR for the HCP protocol. Resting state and motor task BOLD fMRI data was downloaded from the WU-Minn HCP database. The mean signal over each parcel was calculated and used as reference timecourses. Simulated nMap k-space data *S* was calculated by integration of the MR signal equation for each k-space point. The signals *x* in each parcel were then calculated from this signal by direct least squares estimation: *x~A\S*, and compared to the reference signal.

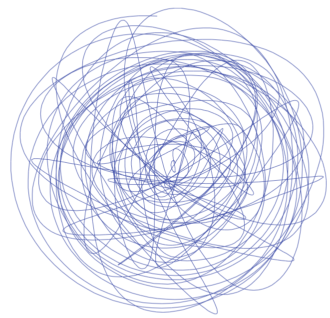

Figure 1: 'Yarn ball' trajectory.

Results: The parcel time courses estimated using nMapping agreed well with the corresponding reference signals, with a mean correlation of 0.84 for both the resting state and motor task data sets. A correlation matrix of reference vs nMap timecourses is shown in **Figure 2a**, demonstrating the expected symmetry and high values along the diagonal. A map of the correlation coefficients by parcel, viewed from above the brain, is shown in **Figure 2b**. Representative images of the reference and nMap estimated signals across parcels are shown in **Figure 3**, demonstrating similar patterns.

Discussion: We demonstrate here that using a generic parcellation of the brain, a large fraction of the information that is present at the parcel level in BOLD data is captured by an nMapping process that uses less than one tenth of the data acquisition time of the HCP protocol. The residual discrepancy is likely dominated by inaccuracy of the assumption that the signal across each parcel is uniform. Per-subject parcellation is expected to improve the validity of this assumption. This work does not yet take advantage of parallel imaging, which should afford additional acceleration. The highly accelerated nMap data acquisition can be used to increase SNR per unit time, increase statistical power, and employ multi-echo methods to increase BOLD specificity (5). This approach shares high temporal resolution with MR Encephalography (6) and Inverse Imaging (7), but the use of prior information about the functional geometry allows for the problem to be highly over-determined and SNR efficient. Incorporating the principles of spatio-temporal separability (8) may allow for simultaneous estimation of both parcel geometry and temporal signals.

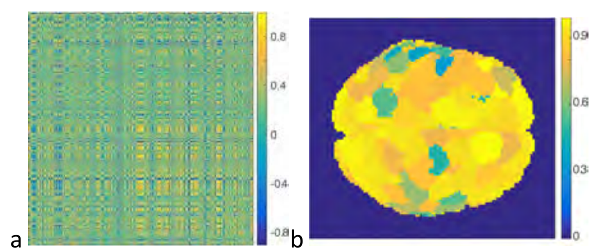

Figure 2: **a**) Correlation matrix between fully sampled and nMap parcels; **b**) Correlations by parcel (diagonal elements of **Fig. 2a**).

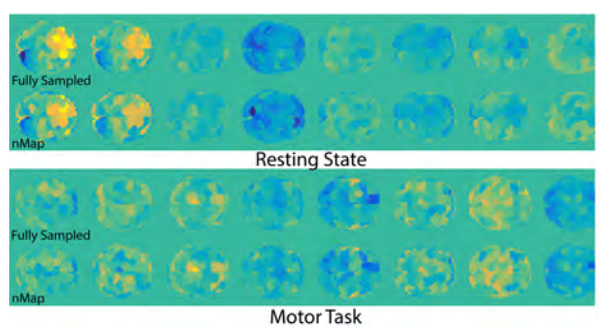

Figure 3: Example time frames of parcel maps reconstructed from fully sampled data, and from nMap estimates.

References: 1. Wong EC. Brain connectivity 2014;4(7):481-486. 2. Van Essen et al. Neuroimage 2013;80:62-79 3. Shen et al. Neuroimage 2013;82:403-415. 4. Lustig et al. IEEE TMI 2008;27(6):866-873. 5. Kundu et al. Neuroimage 2012;60(3):1759-1770. 6. Lee et al. Neuroimage 2013;65:216-222. 7. Chang et al. Neuroimage 2014;91:401-411. 8. Zhao et al. IEEE TMI 2012;31(9):1809-1820.