Data-driven and physics-informed learning of efficient acquisition protocols

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Target audience: Researchers interested in reducing MRI acquisition time while maintaining the most relevant measurements to characterise tissue properties.

Purpose: Long acquisition times hamper the translation of microstructural (diffusion) MRI to clinical applications. Various approaches have been proposed for designing optimal diffusion MRI protocols to acquire the most informative measurements in the shortest possible time,[1-3] most of them based on a priori assumed models or representations and parameter values. This work aims to develop and compare data-driven machine learning approaches that select an optimal subset of measurements from a larger set to ultimately reduce acquisition time while maintaining the maximum information content. Specifically, we compare the performance of autoencoder neural networks trained to subselect measurements and subsequently predict all the measurements with minimal error, and are either 1) agnostic to the signal model and parameters of interest, or 2) "physics-informed", i.e., including a signal model to drive the subselection.

Methods: Five healthy controls were scanned on a 3T 40mT/m scanner with a 5D Diffusion-T1-T2* protocol varying b-value (b), gradient direction (Θ_g, Φ_g), inversion time (TI) and delay time (TD) in an asymmetric spin echo[1,4] (1344 unique settings). Repetition time (TR) and b-tensor anisotropy (b_Δ) were 7500 ms and 1, respectively. The data were preprocessed as previously described.[1] The selection of the most representative set of measurements was based on a concrete autoencoder, which has shown superior performance in reconstructing the full set of measurements compared to other approaches.[1,5] The autoencoder included a concrete selection layer (CL) as encoder with the size indicating the maximum number of selected measurements.[5,6] The decoder was either 1) a neural network (coined CL+NN) or 2) a physics-informed neural network with a forward signal equation (coined CL+eq):[4,7]

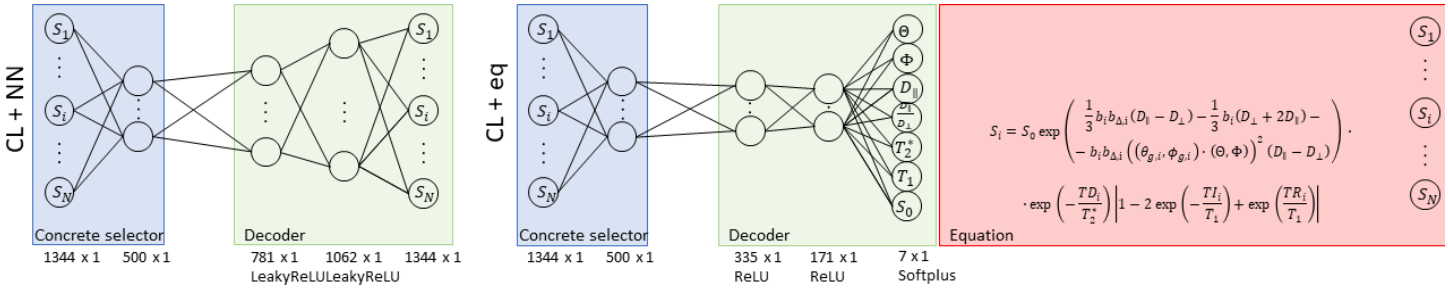

***Figure 1**. Networks employed to select the optimal subset of measurements and predict back all the measurements with minimal error. The decoder in CL+eq incorporates a forward signal equation which is a function of the first eigenvector direction (Θ and Φ), parallel ($D_\parallel$) and perpendicular diffusivity ($D_\perp$), T2*, T1 and S_0.*

Both networks were trained on voxels from the whole brain to select unique 500 measurements using a specific regularisation method,[8] based on leave-one-out cross-validation using the Adam optimiser with learning rate 0.001, batch size 256, and mean-squared error (MSE) loss. We investigated differences on validation data in i) the subset of selected measurements, ii) errors of predicted measurements, and iii) accuracy of parameter estimates. All experiments were conducted on synthetic data obtained from maps estimated on the full dataset using a network similar as CL+eq but without the selector layer, with added Gaussian noise (signal-to-noise ratio SNR = 30). Maps from subselected measurements identified by the CL+NN and CL+eq were estimated in a similar way and compared to the ground truth (GT).

Results: Regarding the selected measurements, the lowest TI values were consistently selected across b-values for both approaches, while medium-high TIs were more frequently selected for CL+NN and b-values equal or lower than 1000 s/mm^2 for CL+eq (Fig. 2A). The reconstructed signal MSE distributions were similar for white matter and grey matter (Fig. 2B left), while when considering the selected and not-selected measurements separately, the CL+eq MSE was higher for the selected volumes and lower for the not-selected volumes (Fig. 2B right). The maps estimated from the subselected measurements presented lower error compared to the synthetic GT for the indices selected with the CL+eq approach across tissue types for parallel and perpendicular diffusivity, T2* and S_0 (Fig. 2B bottom shows absolute error distributions in grey matter), although this difference was not immediately apparent in the estimated maps (Fig. 2C).

Discussion & Conclusion: In this work, two data-driven subset selection strategies were compared, one based on a full data-driven method (CL+NN) and another informed by a signal equation (CL+eq). CL+eq indices yielded higher accuracy for the estimation of quantitative parameters, but estimation on CL+NN selected measurements also achieved high accuracy despite being agnostic to the parameters of interest. Notably, for both selection strategies, volumes with low SNR, i.e., high b-values and low TI values, were consistently sampled, suggesting that the optimal subset may be related to the difficulty of reconstructing those measurements. Moreover, the MSE values from the measurements selected by CL+eq and CL+NN were similar, despite the former network being substantially smaller. In summary, this work shows that data-driven protocol optimisation provides useful information on measurement redundancy and can be informed by prior knowledge on the signal equation. Future work will investigate diverse network structures, loss functions (e.g., directly minimising the parameter errors), and extension to other multi-contrast databases.

References: 1. Pizzolato, M., et al. (2020). CDMRI. Mathematics and Visualization. Springer, Cham. 2. Grussu, F., et al. Front Phys 9, 752208 (2021). 3. Alexander, D.C. Magn Reson Med 60, 439-48 (2008). 4. Hutter, J., et al. Sci Rep 8, 15138 (2018). 5. Abid, A., et al. Concrete Autoencoder for Differentiable Feature Selection and Reconstruction. ArXiv (2019). 6. Tax, C.M.W, et al. Optimising multi-contrast MRI experiment design using concrete autoencoders. ISMRM 29th Annual Meeting and Exhibition (2021), p. 1240. 7. Grussu, F., et al. CDMRI 2020, pp. 159-172. 8. Strypsteen, T., & Bertrand, A. J Neural Eng 18, 0460a9 (2021).

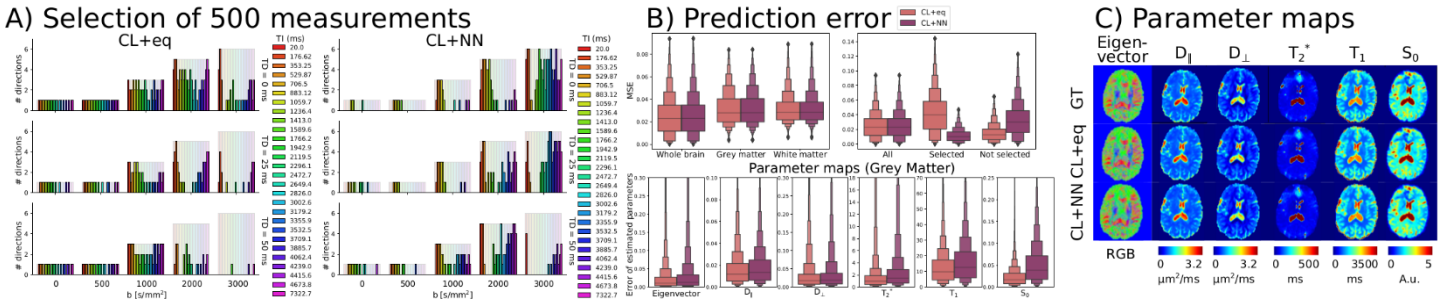

***Figure 2**. Comparison between the networks employed to select the optimal subset of MRI measurements. A) Histogram of the selected measurements according to b-value (0, 500, 1000, 2000 and 3000 s/mm^2), TD (0, 25 and 50 ms) and TI (28 values from 20 to 7322.7 ms). The transparent bars represent the original distribution. B) Box plots of the MSE values per tissue type and measurement set (top), and absolute error of the estimated synthetic maps (bottom, outliers removed for visualization). C) Top: Ground Truth (GT) maps of the parameters used to predict the MRI signal. The eigenvector is presented as Red-Green-Blue (RGB) value corresponding to left-right, anterior-posterior and top-down axes. A.u. = arbitrary units.*