## **SUPPLEMENTARY MATERIAL**

## Correlation-weighted <sup>23</sup>Na magnetic resonance fingerprinting in the brain

Lauren F. O'Donnell<sup>1</sup>, Gonzalo G. Rodriguez<sup>1,2</sup>, Gregory Lemberskiy<sup>1</sup>, Zidan Yu<sup>1,3,4</sup>, Olga Dergachyova<sup>1</sup>, Martijn Cloos<sup>1,5</sup>, Guillaume Madelin<sup>1,3,\*</sup>

<sup>1</sup>Center for Biomedical Imaging, Department of Radiology, NYU Grossman School of Medicine, New York, NY, USA

<sup>2</sup>NMR Signal Enhancement, Max Planck Institute for Multidisciplinary Sciences, Göttingen, Germany

<sup>3</sup>Vilcek Institute for Graduate Biomedical Studies, NYU Langone Health, New York, NY, USA

<sup>4</sup>Department of Medicine, John A. Burns School of Medicine, University of Hawaii, Honolulu, HI, USA

<sup>5</sup>Donders Centre for Cognitive Neuroimaging, Donders Institute for Brain, Cognition and Behaviour, Radboud University, Nijmegen, The Netherlands

<sup>\*</sup>Corresponding author: guillaume.madelin@nyulangone.org

December 12, 2024



Figure S1. Images of the center axial slice of the 7-compartment phantom acquired after each of the 23 pulses in the <sup>23</sup>Na MRF acquisition (global normalization). The pulse train is shown in Figure 1(B). These images were normalized to the brightest pixel over all 23 images for the slice shown here. The first three pulses form a 90°–180°–90° inversion composite block that was used to increase T<sub>1</sub> sensitivity and improve RF homogeneity of the magnetization inversion. In the composite block,  $\tau_1 = \tau_2 = 7.5$  ms. The next 20 pulses form the variable flip angle and phase angle train with  $\tau_3 = ... = \tau_{23} = 15$  ms. Acquisition parameters were TR = 511 ms, isotropic resolution = 5 mm, isotropic FOV = 320 mm, FLORET trajectory (3 hubs/45°, 100 interleaves/hub) and 16 averages, for a total scan time of 40:52 min.



Figure S2. Images of the center axial slice of the brain of volunteer 5 acquired after each of the 23 pulses in the <sup>23</sup>Na MRF acquisition (individual normalization). The pulse train is shown in Figure 1(B). These images were normalized to the brightest pixel in each of the 23 individual images for the slice shown here. The first three pulses form a 90°–180°–90° inversion composite block that was used to increase T<sub>1</sub> sensitivity and improve RF homogeneity of the magnetization inversion. In the composite block,  $\tau_1 = \tau_2 = 7.5$  ms. The next 20 pulses form the variable flip angle and phase angle train with  $\tau_3 = ... = \tau_{23} = 15$  ms. Acquisition parameters were TR = 702 ms, isotropic resolution = 5 mm, isotropic FOV = 320 mm, FLORET trajectory (3 hubs/45°, 100 interleaves/hub), 4 scans, 2 averages/scan, for a total acquisition time of 31:06 min.



Figure S3. Images of the center axial slice of the brain of volunteer 5 acquired after each of the 23 pulses in the <sup>23</sup>Na MRF acquisition (global normalization). The pulse train is shown in Figure 1(B). These images were normalized to the brightest pixel over all 23 images for the slice shown here. The first three pulses form a 90°–180°–90° inversion composite block that was used to increase T<sub>1</sub> sensitivity and improve RF homogeneity of the magnetization inversion. In the composite block,  $\tau_1 = \tau_2 = 7.5$  ms. The next 20 pulses form the variable flip angle and phase angle train with  $\tau_3 = ... = \tau_{23} = 15$  ms. Acquisition parameters were TR = 702 ms, isotropic resolution = 5 mm, isotropic FOV = 320 mm, FLORET trajectory (3 hubs/45°, 100 interleaves/hub), 4 scans, 2 averages/scan, for a total acquisition time of 31:06 min.



Figure S4. Scatter plots of  $T_1$ ,  $T_{2,long}^*$ ,  $T_{2,short}^*$  and SD measured with <sup>23</sup>Na MRF versus the reference method (RM). Mean values and standard deviation (STDV) for  $T_1$ ,  $T_{2,long}^*$ ,  $T_{2,short}^*$  are given in Table 1. The SD reference values were taken from the ground truth in the 7-compartment phantom composition with  $\pm 5\%$  STDV. The error bars correspond to  $\pm 1$  STDV.



Figure S5. <sup>23</sup>Na MRF maps produced after matching with different numbers of correlation coefficients (k) used as average weighting factors in a 7-compartment phantom. The "Maximum" label above the left column indicates the result of mapping between the fingerprint dictionary and the image signal using only the highest correlation coefficient (k = 1). The values above each column indicate the number of highest correlation coefficients included in the map calculations. The maps for k = {10, 20, ..., 1000} therefore correspond to the weighted average of signals with the k highest correlation coefficients, where the value of the correlation coefficient itself was used as the weighting factor.



Figure S6. <sup>23</sup>Na MRF maps produced after matching with different numbers of correlation coefficients (k) used as weighting factors in brain for volunteer 5. The "Maximum" label above the left column indicates the result of mapping between the fingerprint dictionary and the image signal using only the highest correlation coefficient (k = 1). The values above each column indicate the number of highest correlation coefficients included in the map calculations. The maps for k = {10, 20, ..., 1000} therefore correspond to the weighted average of signals with the k highest correlation coefficients, where the value of the correlation coefficient itself was used as the weighting factor.

## **Correlation Coefficient**



**Figure S7. Boxplots of**  $T_1$ **,**  $T^*_{2,long}$ **,**  $T^*_{2,short}$  **and SD measured in the 7-compartment phantom.** Blue boxes represent data from <sup>23</sup>Na MRF. Red boxes represent data from the reference method (RM) for relaxation times, and from ground truth for SD. Boxplots are grouped by column for k = {1 (maximum), 20, 50, 100, 200} highest correlation coefficients used for the weighed average of each map parameter.



**Figure S8. Maximum number of fingerprint dictionary matches in the 7-compartment phantom.** The plots show the maximum number of fingerprint dictionary matches made to the subset of pixels within a reference range for  $T_1$ ,  $T_{2,long}^*$  and  $T_{2,short}^*$  versus the number of k = {1, 2, 3 ..., 1000} correlation coefficients included in the matching. The limits were imposed using the reference method (values are shown Table 1).



**Figure S9. Maximum number of fingerprint dictionary matches in brain.** The plots show the maximum number of fingerprint dictionary matches made to the subset of pixels within a reference range for  $T_{2,long}^*$  in CSF, GM and WM and  $T_{2,short}^*$  in GM and WM versus the number of k = {1, 2, 3 ..., 1000} correlation coefficients included in matching. Ranges for relaxation were determined by literature values shown in Table 3. We omitted  $T_1$  from this analysis because we did not find enough reports of <sup>23</sup>Na  $T_1$  at 7 T in the literature to impose limits for our computation.



**Figure S10.** Comparison of brain maps for a single axial slice reconstructed with and without Gaussian filtering (volunteer 5). Gaussian filtering (smoothing) was applied prior to matching using a heuristically determined window executed in MATLAB. The filter was applied over individual slices, in plane, on the image acquired after each of the 23 pulses of the <sup>23</sup>Na MRF pulse train. After filtering, fingerprint dictionary matching was carried out as described in the Methods section. The maps shown here correspond to: signal with maximum correlation coefficient (k = 1) only, with and without filtering; average over k = 20 signals with the highest correlation coefficients, but without the correlation coefficient weighting (simple averaging with weighting = 1 for all k signals), with and without filtering; and average over k = 20 signals with the highest correlation coefficient weighting.