Deep Magnetic Resonance Fingerprinting of the Chemical Exchange Relayed Nuclear Overhauser Effect in the Mouse and Human Brain (rNOE-MRF)

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INTRODUCTION:

Noninvasive imaging of the relayed nuclear Overhauser effect (rNOE) has provided biological and clinical insights into cancer, stroke, liver, and spinal cord injury imaging [1]. In the typical settings, rNOE contrast-weighted images are obtained following a full Z-spectrum acquisition. Distilling the pure rNOE signal from confounding factors, such as water relaxivity, direct saturation, and semisolid magnetization transfer (MT) contrast is challenging. While several previous works were able to mitigate/eliminate the T_1, T_2, and semisolid MT contributions from rNOE signals [2,3], they either required a lengthy acquisition or were still affected by the saturation pulse settings employed. In any case, the resulting signals still represented a combined contribution from the proton volume fraction and exchange rate, hindering the direct extraction of the compound of interest concentration. Since the establishment of magnetic resonance fingerprinting (MRF), it has been further developed to quantify various biophysical parameter, including the amide and semisolid MT exchange parameters [4]. Here, we designed an rNOE-MRF approach aimed at the rapid acquisition and simultaneous reconstruction of quantitative rNOE and semisolid MT maps in-vivo.

METHODS:

Two MRF acquisition protocols were designed and applied subsequently, aiming to gradually quantify the semisolid MT and rNOE parameters. A fully connected serial NN architecture was realized and trained using millions of synthesized signal trajectories to output the proton volume fraction and exchange rate of both proton pools. Glycogen and BSA phantoms, as well as wild-type mice (n=7) and healthy human volunteers (n=5) were imaged at a preclinical 7T scanner (Bruker, Germany) and a 3T clinical scanner (Prisma, Siemens Healthineers), respectively.

RESULTS AND DISCUSSION:

The total scan time was 120 / 210 / 282 sec, for phantoms, mice, and 3D whole brain human imaging, respectively, and the reconstruction took less than 2 sec. The quantitative phantom parameter maps (**Fig. 1a,c**) were in excellent agreement with ground truth (Pearson's r>0.98, p<0.001). The in-vivo parameter maps demonstrated a significant difference between white matter/gray matter ROIs (p<0.01) for both mice (**Fig. 1b**) and humans (**Fig. 1d**). The quantitative proton exchange parameters values (**Fig. 1e-h**) were in agreement with the trend reported in previously published studies [5,6].

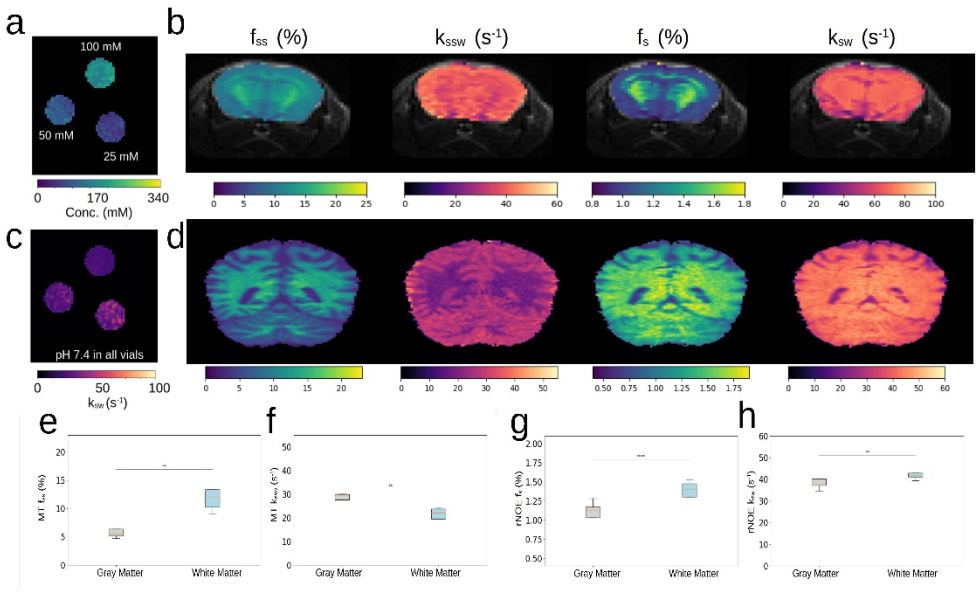

Fig. 1. Quantitative glucose-unit concentration (**a**) and rNOE proton exchange rate (**c**) maps of a representative glycogen phantom. **b**, **d**. Semisolid MT and rNOE proton volume fraction (f_{ss}, f_s) and proton exchange rate (k_{ssw}, k_{sw}) maps, obtained in mice (**b**) and humans (**d**), respectively. (**e-h**). Statistical analysis of the 4 above examined proton exchange parameters obtained in the white/gray matter of the in vivo human brains (n=5).

CONCLUSION:

With its demonstrated ability to rapidly extract quantitative molecular maps, deep rNOE-MRF can potentially serve as a valuable tool for the characterization and detection of molecular properties dynamics, including in vivo abnormalities.

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