

Metabolite Concentration Estimations in the Brain Using 7 T MRSI

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Objective

Magnetic resonance spectroscopic imaging (MRSI) is an imaging modality capable of non-invasively quantifying different metabolites and mapping their distributions over a volume of interest based on spectroscopic MRI data. One of its drawbacks is the lack of standardized units; generally, only relative signal intensities in different positions as well as ratios between metabolites are used. The goal of this study was to move away from arbitrary institutional units towards the estimating the concentration of various metabolites. For this purpose, concentration values were estimated in various regions of interest (ROIs) and then compared to literature values.

Methods

A whole-brain 3D-CRT-FID-MRSI (matrix size 64x64x39, 3.4 mm isotropic resolution, FOV = 220x220x133 mm, TR = 450 ms, AD = 1.3 ms, flip angle 39°, WET water suppression) was acquired in 15 minutes in 24 healthy volunteers using a 32Rx/1Tx head coil and a Siemens at 7 T Magnetom scanner. [1] In addition to this sequence, the protocol contained an unsuppressed MRSI acquisition with the same geometric properties in order to measure a water signal which could be referenced to literature values, as well as a T1 weighted anatomical scan for segmentation and a B_1^+ map for determining the transmitter voltage.

The MRSI data were quantified using LCModel [2] in the ranges of 0.2-1.2 ppm and 1.8-3.88 ppm. The basis set contained various metabolites including creatine and phosphocreatine (tCr), phosphocholine and glycerophosphocholine (tCho), N-acetyl aspartate (NAA), glutamate (Glu) and myo-inositol (mIns).

Together with the amplitude each individual metabolite signal A_{Met} and the water signal amplitude A_{Water} , literature water concentration values (C_{Water}) in grey and white matter were used to estimate the metabolite concentrations C_{Met} according to [3]:

$$C_{Met} = C_{Water} \frac{A_{Met}}{A_{Water}}$$

For analysis, 55 different brain regions were defined based on the segmentation of the T1w MRI. The various metabolite concentrations were estimated in each region, and the estimations' reliability was assessed based on Cramér-Rao lower bound values (CRLB) of NAA, tCr, tCho and mIns as delivered by LCModel. The reproducibility of the acquired data was evaluated by calculating coefficients of variations between volunteers.

Results

44 of the 55 segmented regions were deemed to be of acceptable quality and the rest was discarded. The best performing ROIs (i.e. the ROIs with the highest proportion of voxels within the selected quality criteria) were the parietal cortex, the motor cortex and the cingulate cortex.

While 15 different metabolites were evaluated, the metabolites choline, creatine, glutamate, myo-inositol and N-acetylaspartate yielded the highest overall quality, and over all ROIs, the concentration values were between 1.37-2.42 mM for tCho, 5.93-9.36 mM for tCr, 6.18-10.14 mM for Glu, 4.31-6.60 mM for mIns, and 7.12-10.86 mM for NAA.

The average CVs for those metabolites were relatively low at around 9% to 11%. Furthermore, concentration estimates of almost all metabolites were in good agreement with literature values.

Conclusion

This study successfully established a baseline for future research by acquiring, evaluating and publishing a large amount of data. Data quality may be further improved through the implementation of metabolite-specific B_1^+ corrections. Lastly, the stability and reproducibility of MRSI within subjects should also be a focus of future research.

ROI	tCho	tCr	mIns	NAA	Glu
Subcortical WM (bilateral)	1.92 ± 0.73	7.24 ± 2.62	5.24 ± 1.85	9.73 ± 3.61	7.67 ± 3.29
Motor cortex/subcortex GM+WM	1.87 ± 0.50	7.78 ± 1.83	5.42 ± 1.43	10.48 ± 2.44	8.13 ± 2.41
Cortical GM (bilateral)	1.69 ± 0.71	7.07 ± 2.85	5.26 ± 2.12	9.33 ± 4.05	8.23 ± 3.70
Subcortical GM (bilateral)	2.17 ± 0.97	7.99 ± 3.72	5.28 ± 2.51	8.66 ± 4.35	7.72 ± 4.15
Mean of all good and acceptable regions	1.88	7.37	5.23	9.43	7.85

Table 1: Example concentration estimate values in selected ROIs in mM.

References

- Hangel G, Spurny-Dworak B, Lazen P et al. Inter-subject stability and regional concentration estimates of 3D-FID-MRSI in the human brain at 7 T, 2021. NMR in Biomed. DOI: 10.1002/nbm.4596
- Provencher SW. Automatic quantitation of localized in vivo H spectra with LCModel. NMR Biomed. DOI: 10.1002/nbm.698
- Gasparovic C, Song T, Devier D, et al. Use of tissue water as a concentration reference for proton spectroscopic imaging. Magn Reson Med. 2006;55(6):1219-1226. DOI: 10.1002/mrm.20901

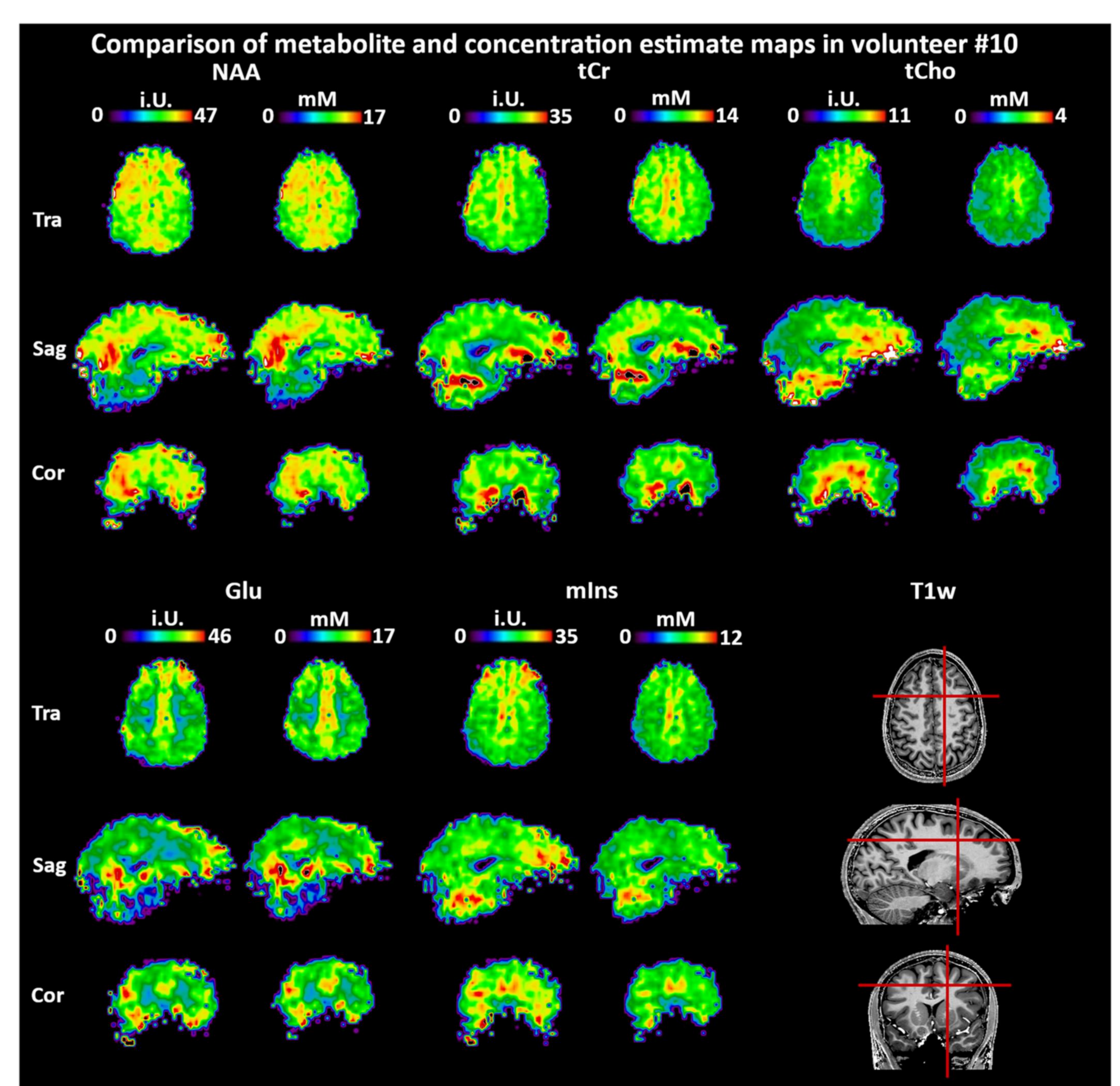
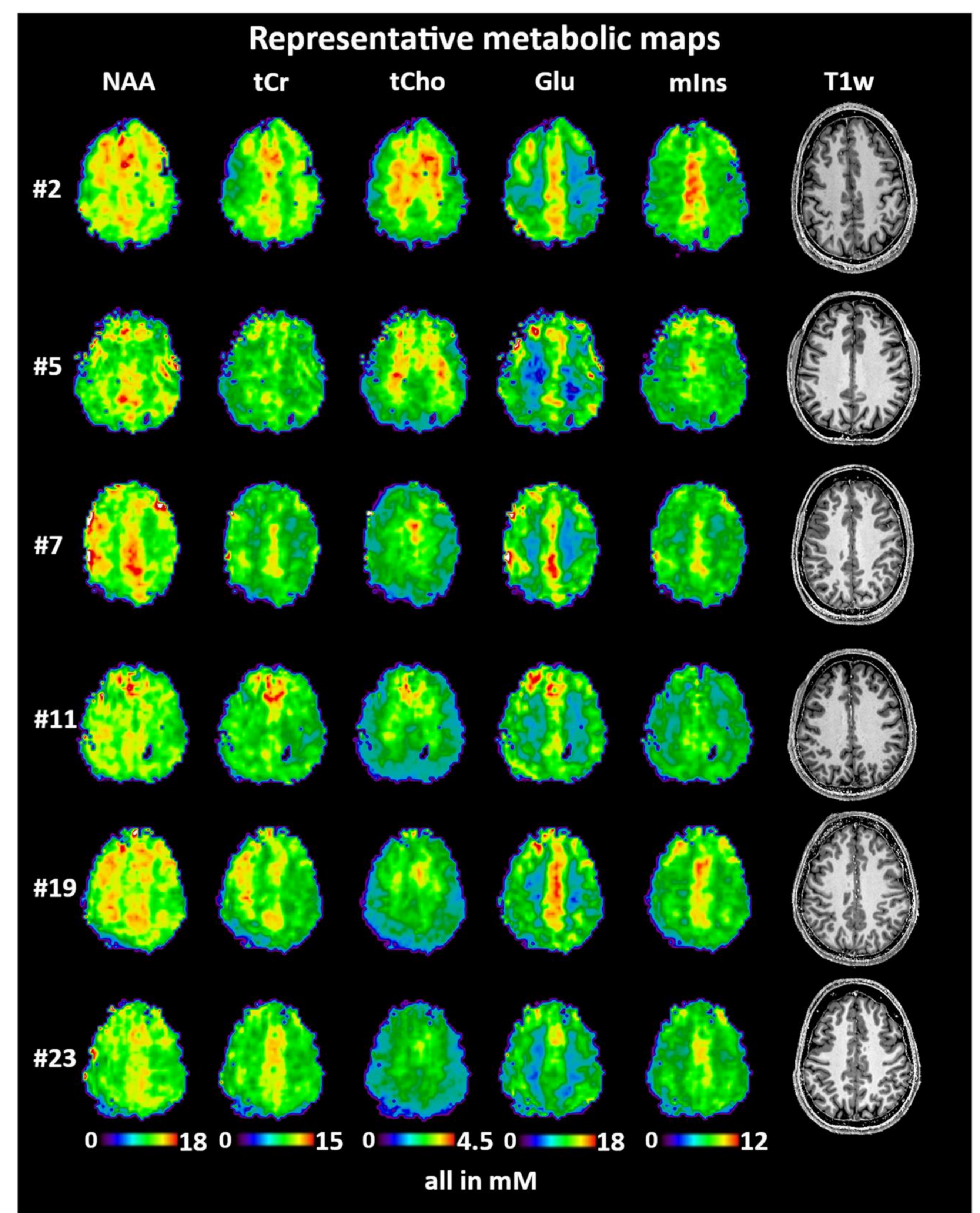


Figure 1 (top): Transversal slices of the concentration estimate maps of five different metabolites (NAA, tCr, tCho, Glu, mIns) in 6 volunteers, as well as the respective T1 weighted images.

Figure 2 (bottom): Comparison of 3D metabolite maps in institutional units and the respective concentration estimate maps in milli-molar for the five metabolites NAA, tCr, tCho, Glu and mIns.