

# To Pool or Not to Pool?

## Comparability of Multi-Protocol Ultra-High-Resolution qMRI in Healthy Brain Aging

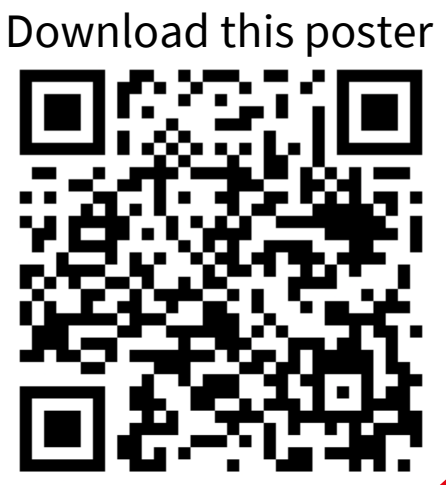
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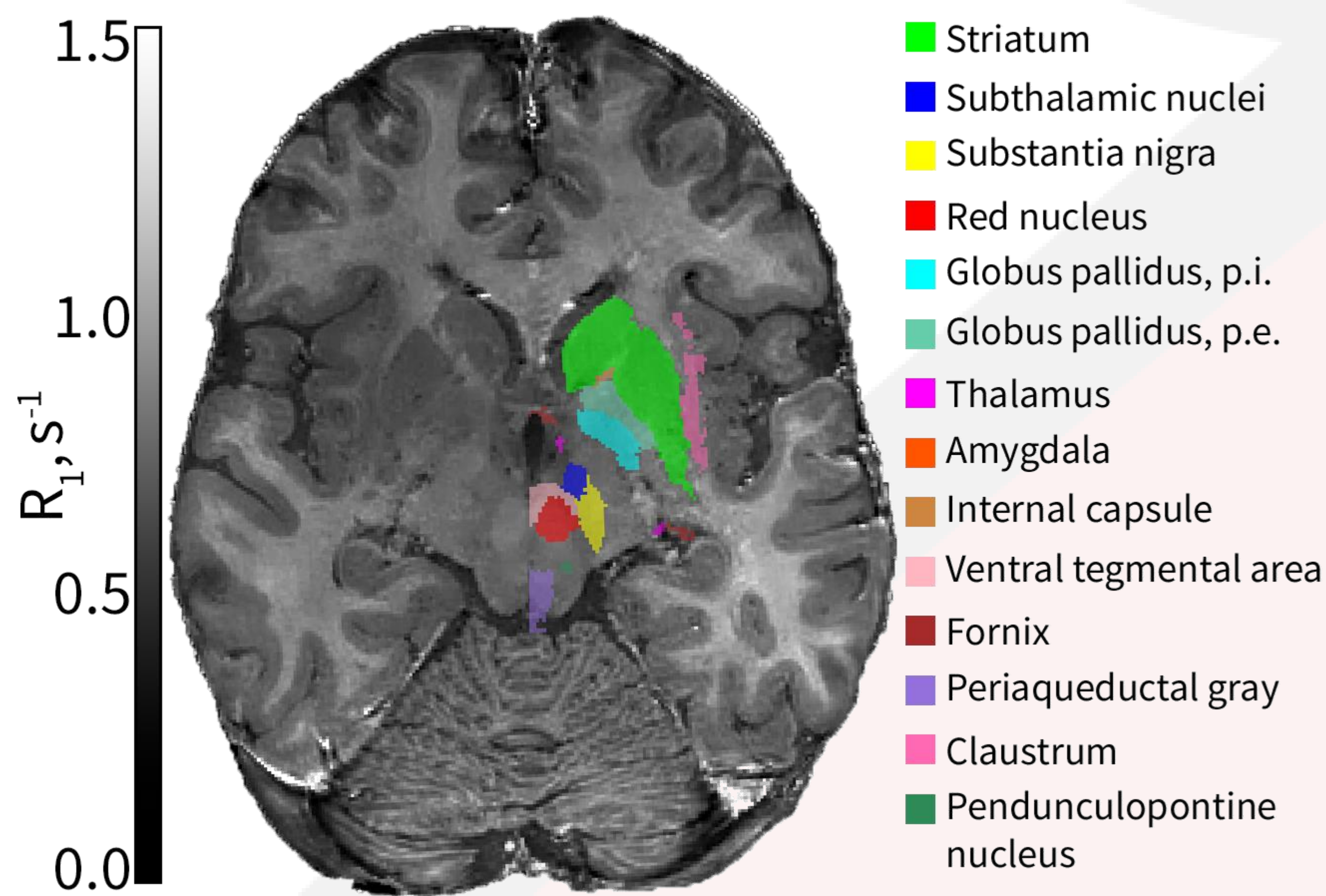
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## Introduction

We aim to investigate how variations in the scan protocol and hardware affect ultra-high-resolution ultra-high field (UHF) qMRI data. We do so by examining how pooling datasets impacts the qMRI metrics of subcortical structures in the context of healthy ageing.

## Methods

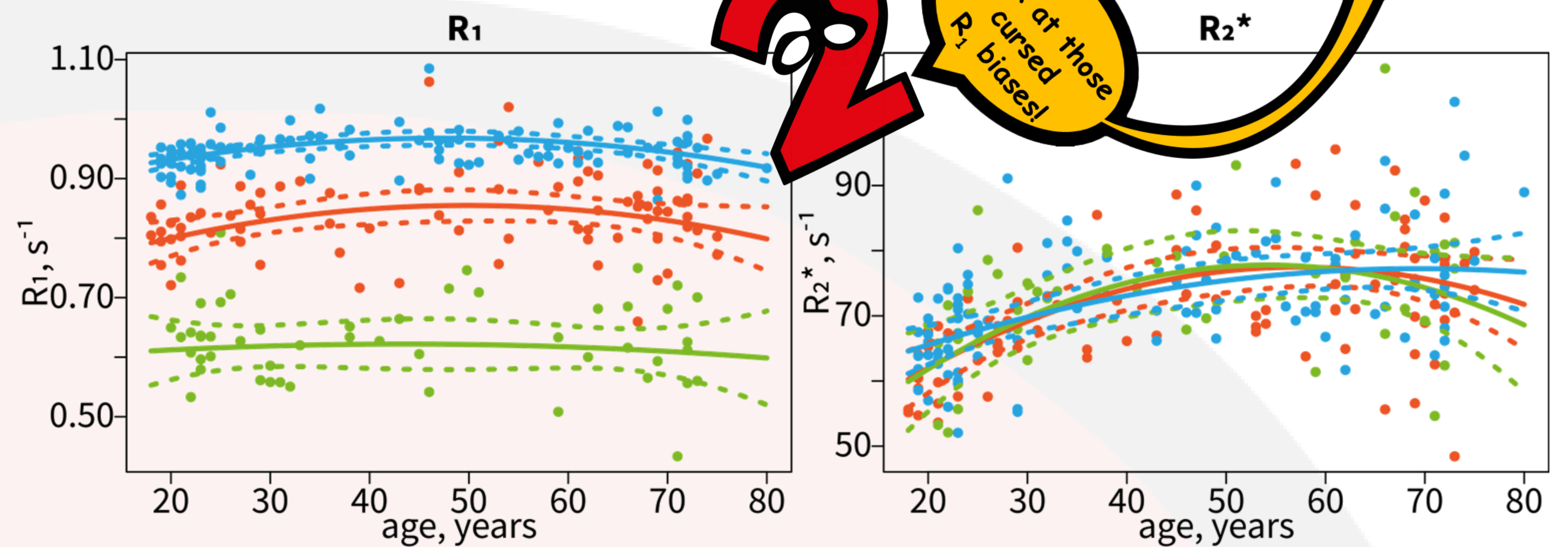
We combined the openly available UHF (7T) AHEAD dataset<sup>1</sup> built using a multi-echo MP2RAGE sequence, with two datasets acquired at GIGA-CRC Human Imaging Unit making use of the 7T multiparameter mapping (MPM<sup>2</sup>) protocols based on the MT-enabled 3DFLASH sequences. One of the MPM datasets was acquired using single transmit (sTx) configuration and the other one with the parallel transmit (pTx) setup. The acquired 0.6 mm (non-interpolated) isotropic data was denoised using LCPA method, and qMRI metrics ( $R_1$ ,  $R_2^*$ ) were extracted using hMRI toolbox<sup>3</sup>, hmri.info. The subcortical structures were then segmented using the MASSP 1.0 toolbox<sup>4</sup>. Linear models, accounting for age, age<sup>2</sup>, sex and dataset source were fit to the combined data to examine the age dependence and potential biases in the pooled dataset.



Above: Subcortical structures segmentation example (only structures in the left hemisphere are shown) overlaid over the pTx-MPM  $R_1$  map.

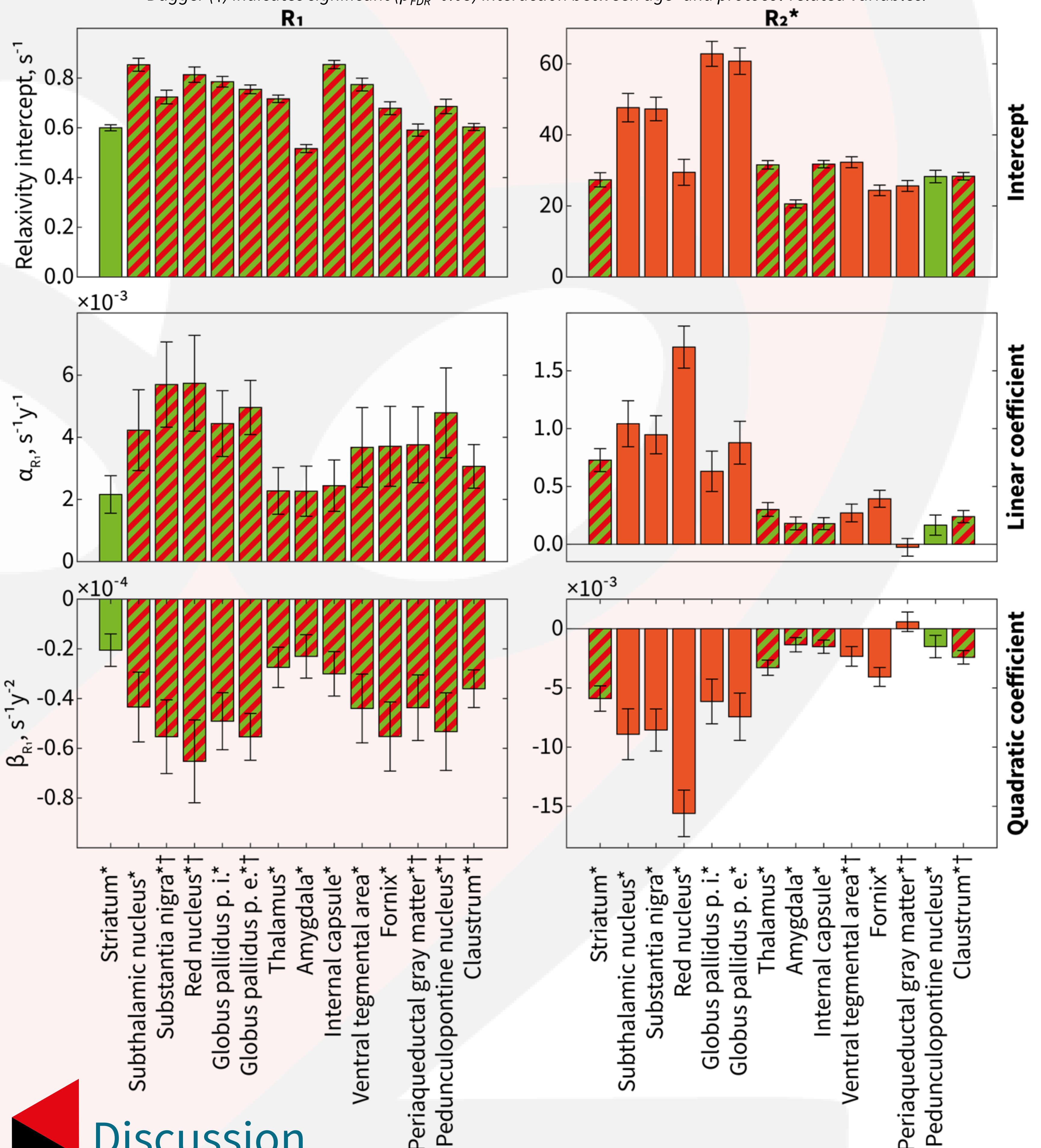
## Results

The fitted models indicated positive linear and negative quadratic terms in age dependence of  $R_1$  and  $R_2^*$  in most segmented structures, while also indicating biases in the same metrics driven by protocol and hardware differences.



Above: An example of  $R_1$  and  $R_2^*$  age dependence in Subthalamic nucleus. Blue markers indicate AHEAD data, red markers – sTx-MPM data, green markers – pTx-MPM data. Lines indicate per-protocol fitted models.

Below: Summary of findings in relaxivity models:  $R \sim \text{Intercept} + \alpha \cdot \text{age} + \beta \cdot \text{age}^2 + \gamma \cdot \text{sex} + \varepsilon \cdot \text{protocol}$ . The Intercepts, linear and quadratic age-related coefficients for pooled  $R_1$  and  $R_2^*$  data are presented for each segmented subcortical structure. Asterisk (\*) indicates significant age dependence, red bars indicate significant ( $p_{\text{FDR}} < 0.05$ ) bias of sTx-MPM against AHEAD data, green bars – of the pTx-MPM against AHEAD data. Dagger (†) indicates significant ( $p_{\text{FDR}} < 0.05$ ) interaction between age- and protocol-related variables.



## Discussion

Our findings indicate that pooling datasets can provide reliable qMRI metric age dependence despite protocol differences. Pooling data must nevertheless be done with caution to account for biases between datasets mostly exhibited by  $R_1$  and less so by  $R_2^*$ .

## References

- [1] A. Alkemade et al., NeuroImage 221 (2020) 117200.
- [2] N. Weiskopf et al., Frontiers in Neuroscience 7 (2013).
- [3] K. Tabelow et al., NeuroImage 194 (2019) 191–210.
- [4] P.-L. Bazin et al., eLife 9 (2020) e59430.