

Enhancing the Spatial Resolution of Hyperpolarized Carbon-13 MRI of Human Brain Metabolism using Structure Guidance

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Joint work with:

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The Leverhulme Trust

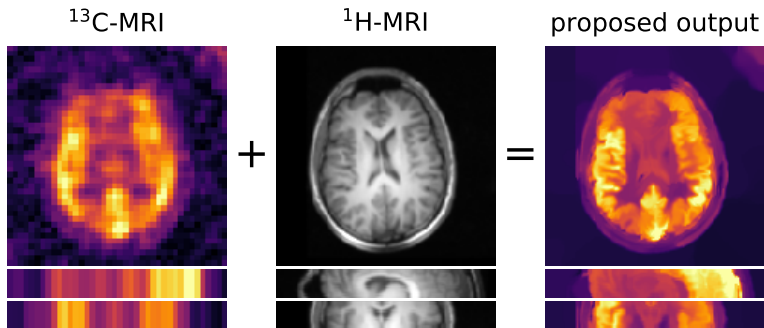


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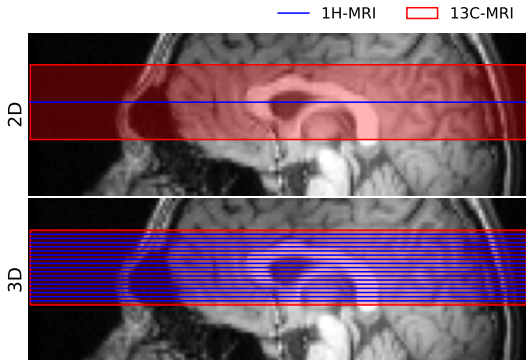
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Motivation



- ▶ **Dynamic nuclear polarization** like Carbon-13 Magnetic Resonance Imaging ($^{13}\text{C-MRI}$) has a relatively **low spatial resolution**
- ▶ **enhance 3D resolution** of $^{13}\text{C-MRI}$ using **structural information** of Hydrogen-1 MRI ($^1\text{H-MRI}$)

Novelty



- ▶ **Superresolution** of 13C-MRI using 1H-MRI gained increased interest recently [Farkash et al. MRM 2019](#), [Dwork et al. Magn Res Mat Phys Bio Med 2021](#), [Ma and Park Tomography 2020](#)
- ▶ Novelty 1: **2D v 3D anatomical data**
- ▶ Novelty 2: **improved mathematical model (dTV)**

Inverse problem

$$Sx = y$$

x : desired high-resolution 13C-MRI image

y : low-resolution 13C-MRI image

S : resolution model: 3D high-res to 2D low-res

$$S : \mathbb{R}^{N \times M \times K} \rightarrow \mathbb{R}^{N/R \times M/R}, \quad (Sx)_{n,m} = \frac{1}{K \cdot R^2} \sum_{k=1}^K \sum_{a,b=0}^{R-1} x_{n+a,m+b,k}$$

Here: $K = 15, R = 4$

Goal: recover x given y

Variational Regularization

Variational regularization

Approximate solution of $Sx = y$ via

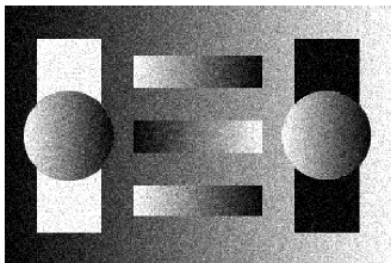
$$\hat{x} = \arg \min_x \left\{ \|Sx - y\|_2^2 + \lambda \mathcal{R}(x) \right\}$$

- ▶ $\|Sx - y\|_2^2$: data fidelity, can be related to noise statistics
- ▶ \mathcal{R} : **regularizer**: penalizes unwanted features, ensures stability and uniqueness
- ▶ λ : **regularization parameter**: $\lambda \geq 0$. If $\lambda = 0$, then an original solution is recovered. As $\lambda \rightarrow \infty$, more and more weight is given to the regularizer \mathcal{R} .

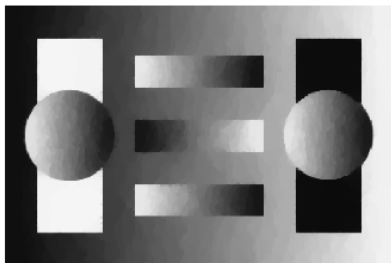
Example: Regularizers

- ▶ Total Variation [Rudin, Osher, Fatemi 1992](#)

$$\mathcal{R}(x) = \|\nabla x\|_{2,1} = \sum_{\beta} \|(\nabla x)_{\beta}\|_2 = \sum_{\beta} \sqrt{(\partial_1 x)_{\beta}^2 + (\partial_2 x)_{\beta}^2 + (\partial_3 x)_{\beta}^2}$$



Noisy image



TV denoised image

How to incorporate the 1H-MRI image into the regularization?

Example: Regularizers

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- ▶ Directional Total Variation [Ehrhardt and Betcke 2016](#)

$$\mathcal{R}(x) = \sum_{\beta} \|D_{\beta}(\nabla x)_{\beta}\|_2$$

$$D_{\beta} = I - \gamma \xi_{\beta} \xi_{\beta}^T \in \mathbb{R}^{3 \times 3}, \quad \xi_{\beta} = \frac{(\nabla v)_{\beta}}{\sqrt{\|(\nabla v)_{\beta}\|_2^2 + \varepsilon^2}} \in [-1, 1]^3 \subset \mathbb{R}^3$$

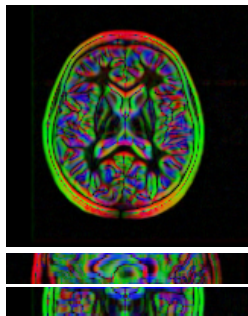
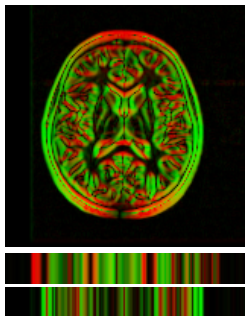
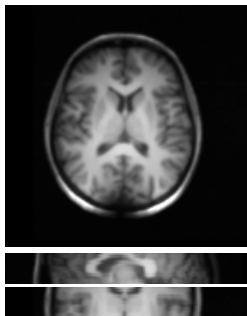
Default values: $\gamma \approx 0.9995, \varepsilon \approx 0.01 \cdot \max_{\beta} \|(\nabla v)_{\beta}\|_2$

2D v 3D directional total variation

$^1\text{H-MRI}$

vector field ξ (2D)

vector field ξ (3D)



- Directional Total Variation [Ehrhardt and Betcke 2016](#)

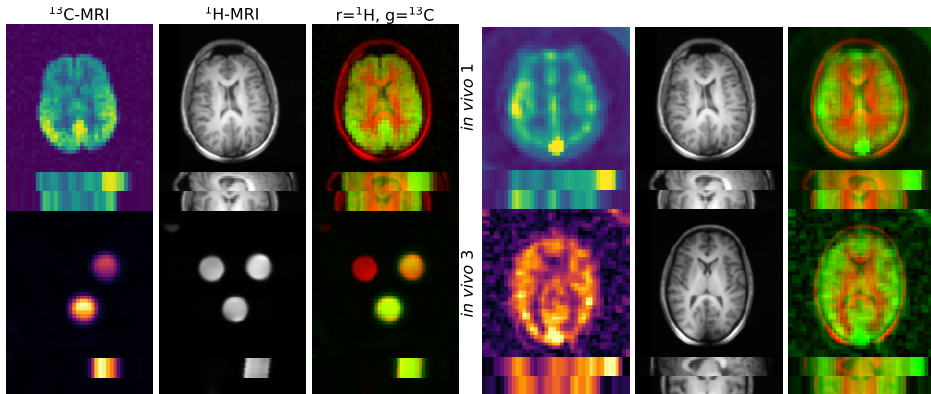
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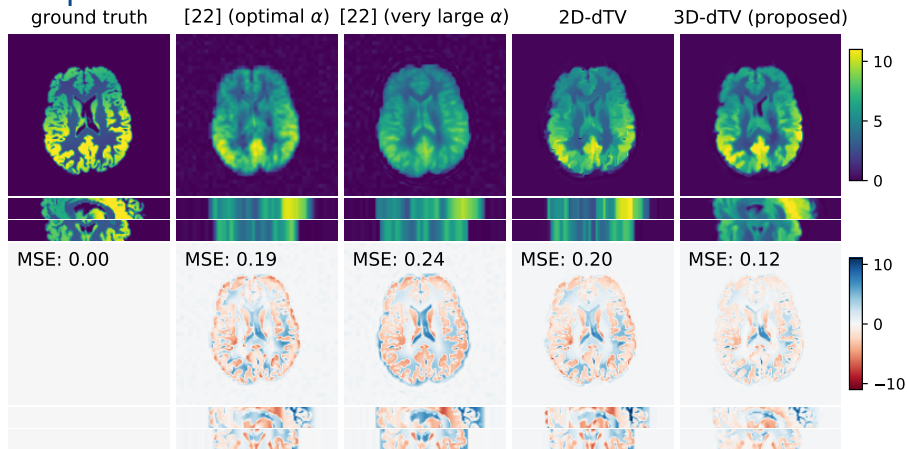
Overview of Data

- ▶ *In vitro* 3 tubes Daniels et al. NMR Biomed 2016
- ▶ *In vivo* 4 healthy volunteers Grist et al. NeuroImage 2019
- ▶ *In silico* GM/WM ≈ 4 , smooth variations



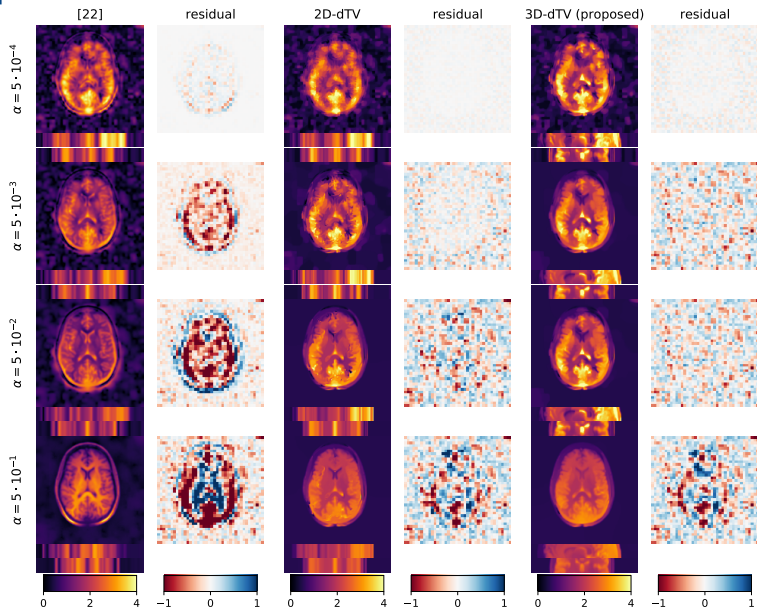
Images need to be **registered!**

Compare methods: *In Silico*



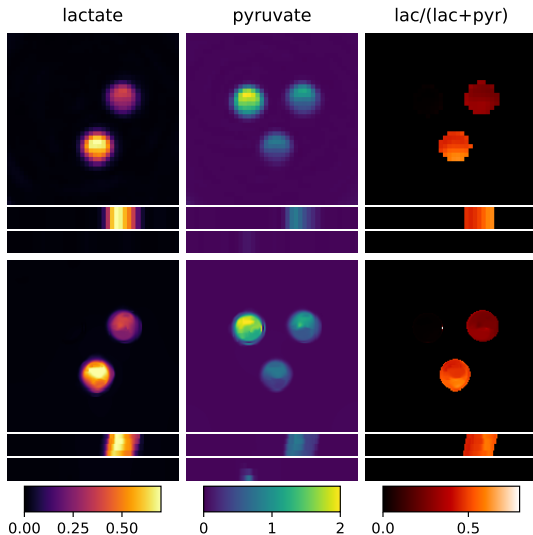
- ▶ [22] = [Dwork et al. 2021](#) enforces ^{13}C -MRI and ^1H -MRI globally to **either have positive or negative correlation** (see CSF for large α)
- ▶ **3D-dTV** leads to **anatomically better-defined structures** compared to **2D-dTV**

Compare methods: *In Vivo*



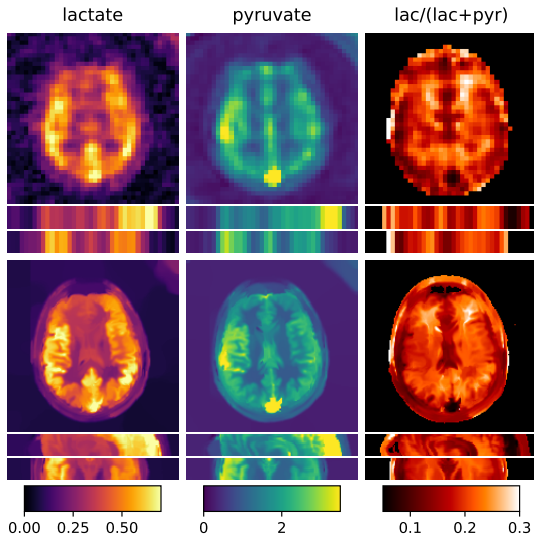
► Similar observations as for *in silico* data

Qualitative evaluation: *In Vitro*



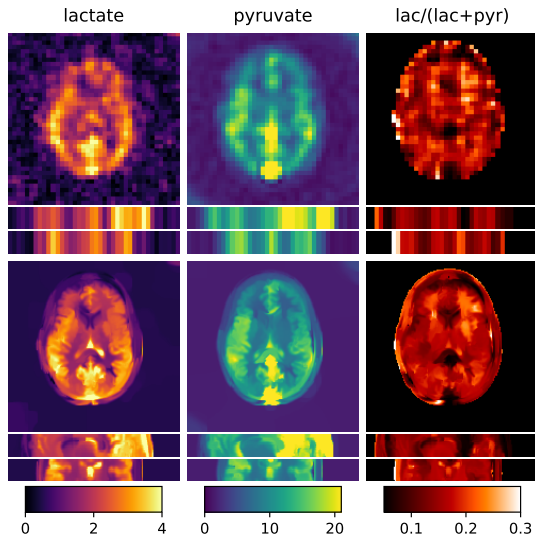
► Higher resolution but preserves smooth variations

Qualitative evaluation: *In Vivo* 1



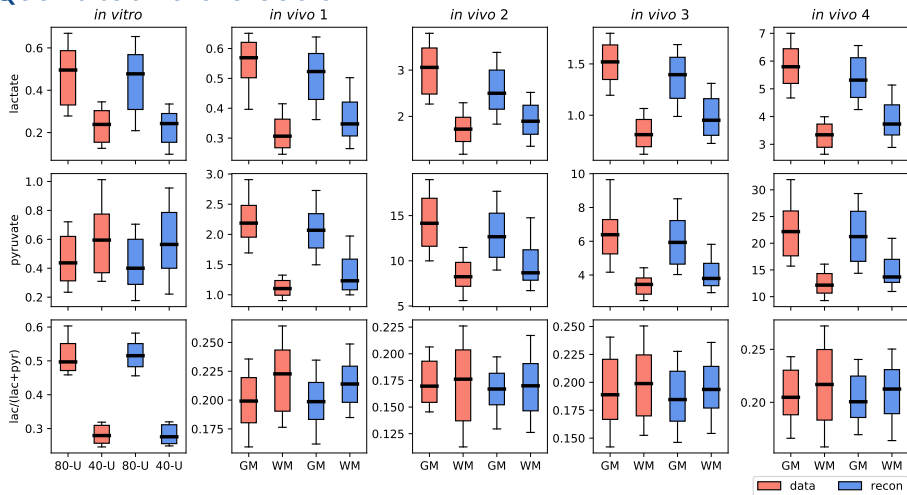
- ▶ **Anatomically well-defined images**
- ▶ **not constant within anatomical regions (e.g. GM, WM)**

Qualitative evaluation: *In Vivo* 2



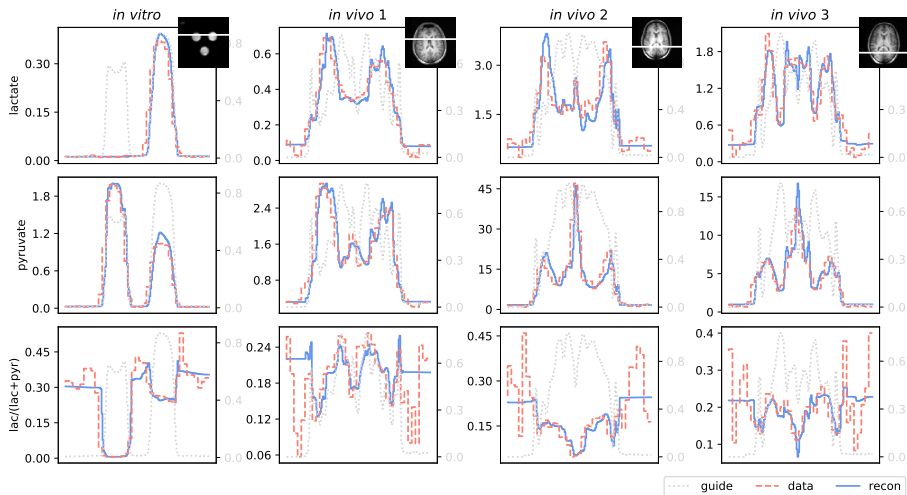
- ▶ **Similar observations** as for the 1st *in vivo* data set

Quantitative evaluation



- ▶ **Similar mean values** in low and high-resolution ^{13}C -MRI images
- ▶ **Variation within** and **difference between** anatomical regions **reduced** (good? bad? just reflecting truth?)

Line plots



► Further visual evidence that **quantification is preserved**

Conclusions and Outlook

Conclusions

- ▶ Aim: **increase resolution** of ^{13}C -MRI
- ▶ **Directional total variation well-suited** for this task (allows locally changing correlations)
- ▶ **3D guide image** works much better than 2D as it better reflects anatomy
- ▶ **Higher resolution** with **preserved quantification**
- ▶ **Computationally efficient:** takes less than 2 minutes on 3 year old MacBook Pro
- ▶ **Robust to parameter choices:** simple to tune the 3 model parameters and 2 algorithm parameters

Conclusions and Outlook

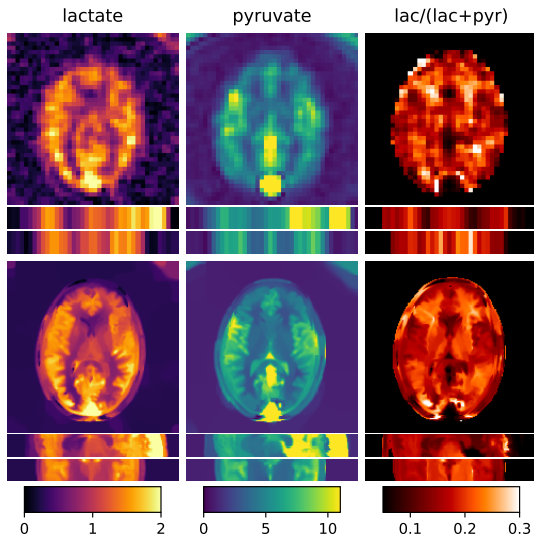
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Future work

- ▶ **Validation, validation, validation ...** e.g. *in vivo* data sets with tissue samples
- ▶ **Better modelling of data**, e.g. by using k-space data

Qualitative evaluation: *In Vivo* 3



Qualitative evaluation: *In Vivo* 4

