## A Deep Learning Approach for Placing Magnetic Resonance Spectroscopy Voxels in Brain Tumors

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**Supplementary Table 1.** The quantitative results of voxels predicted by the regression models for each fold in cross-validation.  $^{\dagger}$ Value is statistically significant (P < .05). One-way ANOVA for all p-value.

Fold	$f_{tumor}$ (%)			Volume (mL)		
	$v_{\scriptscriptstyle M}$	$oldsymbol{\mathcal{V}}_{DL}$	p	$\nu_{\scriptscriptstyle M}$	$oldsymbol{\mathcal{V}}_{DL}$	p
1	$95.9 \pm 5.6$	$93.2 \pm 12.5$	0.17	$13.5 \pm 9.2$	$12.2 \pm 2.6$	0.32
2	$93.1 \pm 10.0$	$95.2 \pm 6.81$	0.24	$11.5 \pm 5.3$	$13.0 \pm 5.4$	0.18
3	$89.2 \pm 12.7$	84.1 ± 19.1	0.12	$12.5 \pm 7.7$	$13.3 \pm 3.6$	0.55
4	$93.3 \pm 11.8$	$92.9 \pm 13.4$	0.89	$14.5 \pm 7.9$	$11.6 \pm 2.8$	$0.01^{\dagger}$
5	$94.4 \pm 17.3$	$92.7 \pm 18.7$	0.63	$9.6 \pm 6.6$	$10.1 \pm 5.8$	0.62

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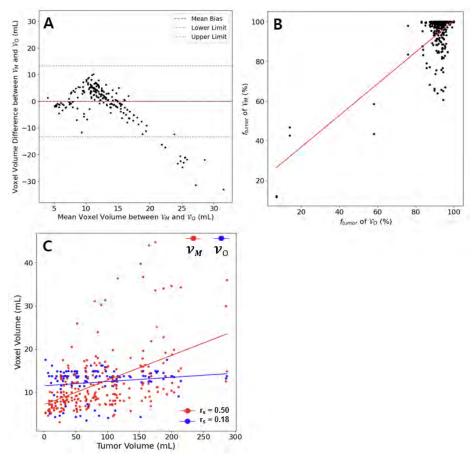
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| Conv1): ResidualBlock(
| (conv1): Conv3d(1, 64, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv2): Conv3d(64, 64, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (residual_conv): Conv3d(1, 64, kernel_size-(1, 1, 1), stride-(1, 1, 1)) (conv2): ResidualBlock(
| (conv1): Conv3d(64, 128, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv2): Conv3d(64, 128, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv2): Conv3d(64, 128, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): ResidualBlock(
| (conv1): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3): Conv3d(256, 256, kernel_size-(3, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3d(256, 256, kernel_size-(3, 2, 3, 3), stride-(1, 1, 1), padding-(1, 1, 1)) (conv3d(256, 256
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Supplementary Fig. 1. Voxel localization regression model architecture.



**Supplementary Fig. 2.** Correlation plot between voxel placement characteristics of tumor volume,  $f_{tumor}$ , and  $V_{tumor}$  between  $\mathcal{V}_{M}$  and  $\mathcal{V}_{O}$ . The grid-like pattern in (A) is due to the discrete search optimization of Ref [8].