

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

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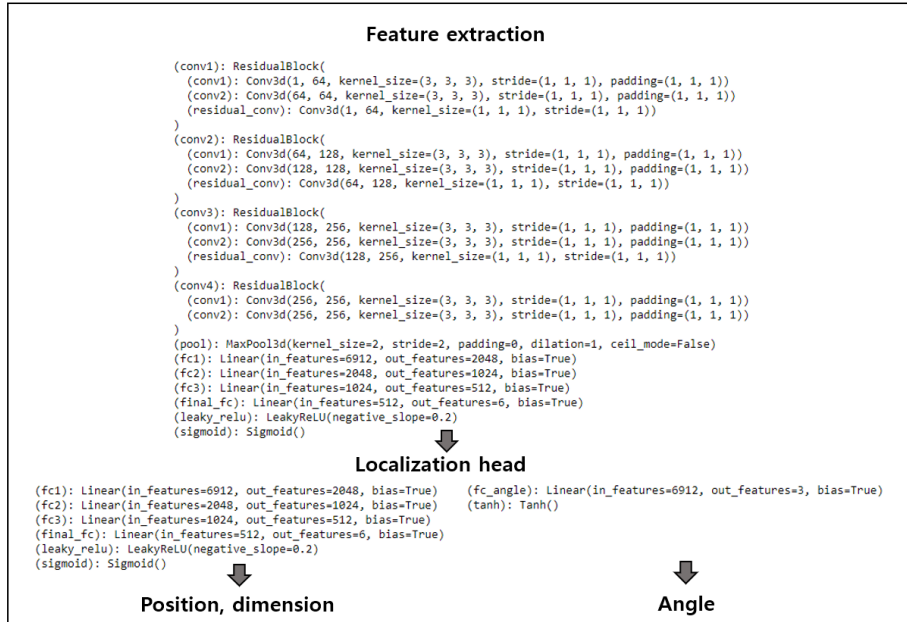
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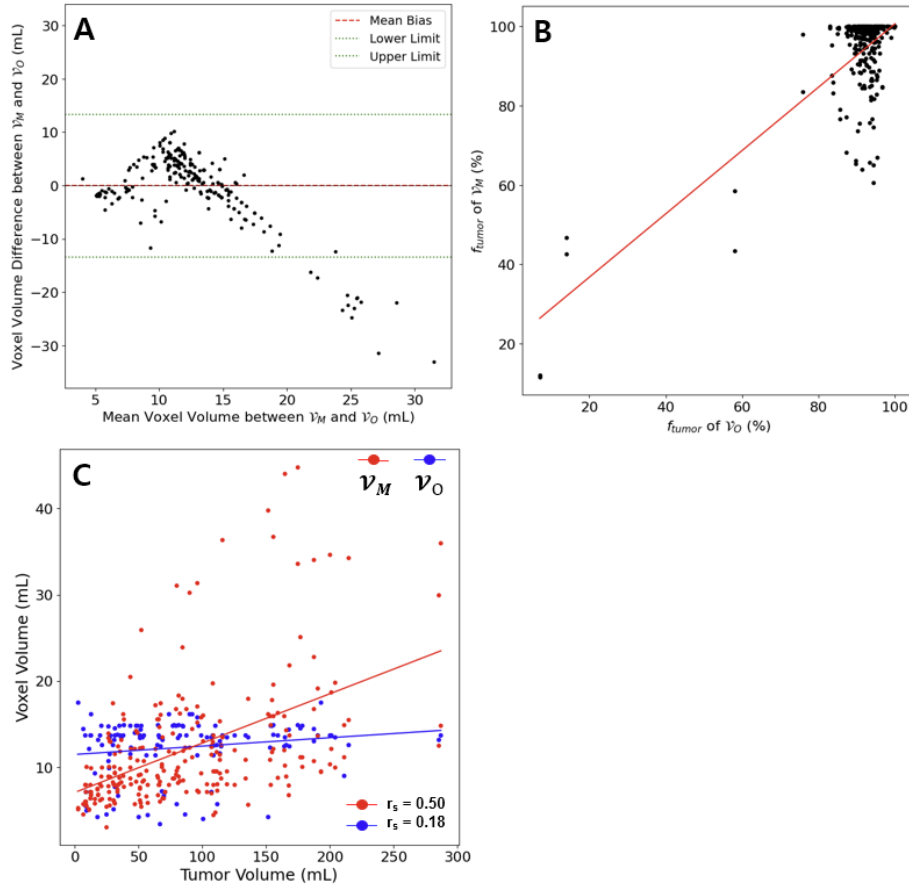
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Supplementary Table 1. The quantitative results of voxels predicted by the regression models for each fold in cross-validation. †Value is statistically significant ($P < .05$). One-way ANOVA for all p -value.

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



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].