ERRATUM

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This is a correction to Yogananda CG, Shah BR, Nalawade SS, et al. **MRI-based deep-learning method for determining glioma *MGMT* promoter methylation status.** *AJNR Am J Neuroradiol* 2021;42:845–52 [10.3174/ajnr.A7029] [33664111]

There was an error in the Python code for the 3-fold cross-validation procedure. This resulted in the use of the training cases instead of the set-aside test cases for the testing procedure for molecular marker accuracy. This caused our reported accuracies from the TCIA/TCGA data set to be artificially inflated. The corrected accuracies for the Table (computed using nnU-Net[1]), along with the updated receiver operating characteristic (ROC) curve for Fig 3 are provided here. The updated accuracies do not outperform other reported methods for *MGMT* molecular marker prediction using MR imaging.

Cross-validation results

	MGMT-Net		
Fold Description	**% Accuracy**	**AUC**	**Dice Score**
Fold no.			
Fold 1	59.75	0.4966	0.7906
Fold 2	73.49	0.6588	0.7725
Fold 3	64.63	0.5854	0.7874
Average	65.95 (SD, 0.06)	0.5802 (SD, 0.081)	0.7835 (SD, 0.009)

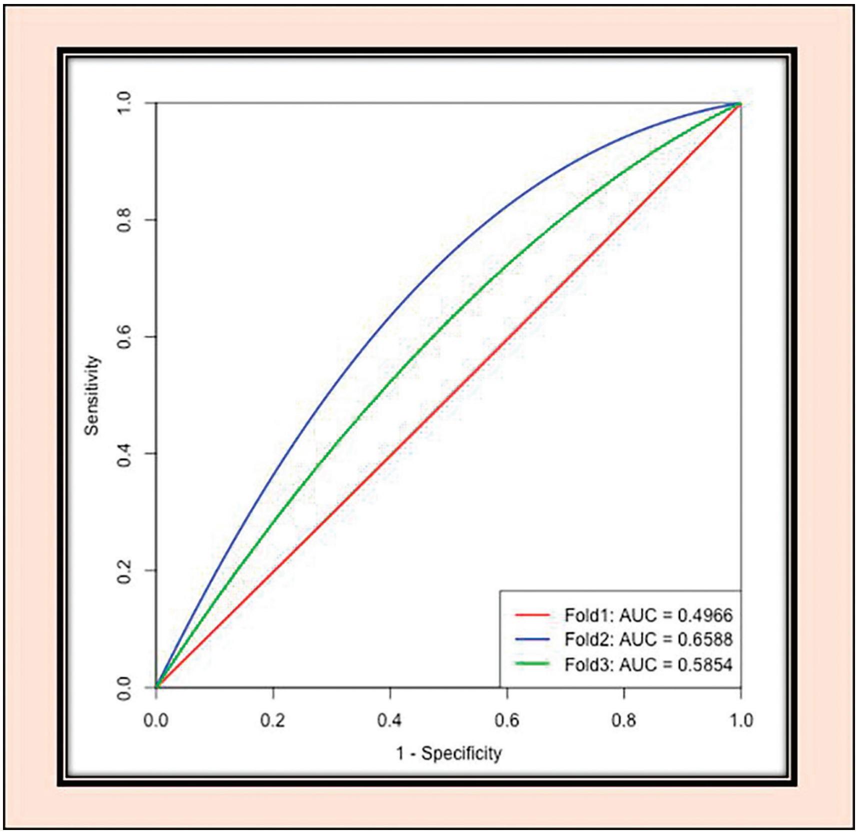

FIG 3. ROC analysis for *MGMT*-net. Separate curves are plotted for each cross-validation fold along with corresponding area under the curve (AUC) values.

REFERENCE

1. Isensee F, Jaeger PF, Kohl SAA, et al. **nnU-Net: a self-configuring method for deep learning-based biomedical image segmentation.** *Nat Methods* 2021;18:203–11 CrossRef Medline

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