Errata

In the article "MIRD Pamphlet No. 25: MIRDcell V2.0 Software Tool for Dosimetric Analysis of Biologic Response of Multicellular Populations" (*J Nucl Med.* 2014;55:1557–1564), the methods incorrectly state that the 2-D and 3-D cell geometries are close-packed square lattice and close-packed cubic lattice, respectively. Rather, they are simple square lattice and simple cubic lattice, respectively. The authors regret the incorrect statement.

In the article "Borderline Findings in *O*-(2-[^{18}F]-Fluoroethyl)-L-Tyrosine PET of Patients with Suspected Glioma Relapse: Role in Clinical Practice" (*J Nucl Med.* 2025;66:187–193), a systematic error in calculations, leading to an overestimation of sensitivity and negative predictive values in Table 2 and Supplemental Tables 2 and 3, was discovered. Revised Table 2 is provided below, and revised Supplemental Tables 2 and 3 are provided in the supplemental materials of the original article. In addition, in the abstract on page 187, final diagnoses of tumor relapse were confirmed by histopathology in 263 [not 175] patients and by clinical course in 176 [not 264] patients. On page 191 in the Discussion, the diagnostic performance showed a lower sensitivity (69%–73%) and a lower specificity (67%–70%) [not a higher sensitivity (94%–95%) but a lower specificity (67%–70%)]. The authors regret the errors.

TABLE 2
Diagnostic Performance of Quantitative Parameters of ^{18}F-FET Uptake in Visual Analysis

Parameter	AUC	Sensitivity	Specificity	Accuracy	PPV	NPV	Cutoff	*P**
All patients (*n* = 439)								
TBR_{mean}	0.76	0.69	0.70	0.69	0.90	0.37	1.95	<0.001
$\text{TBR}_{\text{max-2mL}}$	0.78	0.73	0.67	0.72	0.89	0.40	1.95	<0.001
TBR_{max}	0.78	0.69	0.78	0.71	0.92	0.40	3.05	<0.001
TTP	0.63	0.67	0.58	0.65	0.86	0.32	36 min	<0.001
Slope	0.65	0.58	0.67	0.60	0.87	0.30	0.2 SUV/h	<0.001
Intercept	0.76	0.71	0.67	0.70	0.89	0.38	2.00	<0.001
Patients with clearly positive or clearly negative findings (*n* = 301)								
TBR_{mean}	0.84	0.82	0.78	0.81	0.94	0.52	1.95	<0.001
$\text{TBR}_{\text{max-2mL}}$	0.86	0.85	0.81	0.84	0.95	0.57	1.95	<0.001
TBR_{max}	0.86	0.88	0.76	0.85	0.94	0.60	2.85	<0.001
TTP	0.66	0.67	0.59	0.66	0.87	0.31	36 min	<0.001
Slope	0.65	0.61	0.68	0.62	0.88	0.30	0.2 SUV/h	<0.001
Intercept	0.84	0.89	0.71	0.86	0.93	0.63	1.76	<0.001
Patients with borderline readings (*n* = 138)								
TBR_{mean}	0.46	0.38	0.55	0.42	0.73	0.22	1.95	ns
$\text{TBR}_{\text{max-2mL}}$	0.45	0.59	0.33	0.53	0.74	0.20	1.85	ns
TBR_{max}	0.59	0.43	0.67	0.49	0.80	0.27	2.95	ns
TTP	0.58	0.68	0.55	0.64	0.83	0.35	36 min	ns
Slope	0.66	0.86	0.48	0.77	0.84	0.52	0.65 SUV/h	0.005
Intercept	0.51	0.47	0.55	0.49	0.77	0.24	2.00	ns

**P* value according to ROC analysis.

AUC = area under the ROC curve; NPV = negative predictive value; PPV = positive predictive value; TBR_{max} = maximum SUV in tumor divided by mean SUV of background region; $\text{TBR}_{\text{max-2mL}}$ = mean SUV of 2 mL ROI centered on tumor maximum divided by mean SUV of background region; TBR_{mean} = mean SUV of tumor area (>1.6) divided by mean SUV of background region; TTP = time-to-peak; ns = not significant.

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