

**Online Table 1. Variation in segmentation volumes and variability for BraTumIA 2.0 across 25 repetitions on identical datasets**

Segmented region	Mean Segmentation volumes, mL	Mean Standard Deviation in segmentation volumes, mL (range)	Mean Coefficient of Variation, % (range)	Mean Generalized Conformity Index (range)
Enhancing	24.1	0.5 (0.07 – 1.3)	3.7 (0.7 – 19.3)	0.84 (0.55 – 0.92)
Edema	92.3	1.7 (0.4 – 4.8)	2.2 (0.5 – 8.0)	0.85 (0.74 – 0.92)
Non-enhancing	2.7	0.3 (0.007 – 1.2)	19.5 (4.6 – 67.1)	0.47 (0.19 – 0.73)
Necrotic	6.9	0.3 (0.07 – 1.0)	14.4 (1.0 – 67.3)	0.66 (0.23 – 0.90)
Total Tumor-related Abnormality	126.1	1.8 (0.8 – 5.0)	1.7 (0.5 – 7.5)	0.89 (0.78 – 0.94)
Total Non-enhancing Tumor-related Abnormality	101.9	1.7 (0.7 – 4.9)	2.0 (0.5 – 7.7)	0.86 (0.74 – 0.92)
Non-enhancing Non-necrotic Tumor-related Abnormality	95.1	1.7 (0.6 – 4.8)	2.1 (0.5 – 7.6)	0.86 (0.74 – 0.92)
White Matter	547.6	4.7 (1.1 – 29.4)	0.9 (0.2 – 6.1)	0.93 (0.87 – 0.97)
Gray Matter	605.8	6.7 (1.5 – 25.3)	1.1 (0.3 – 4.9)	0.89 (0.83 – 0.95)

**Online Table 2. Mean Volumes, within-subject standard deviations and total standard deviation for Automatically Segmented Volumes (in mL).**

Segmented region	Mean Volumes (range)		Within-subject Standard Deviation		Total Standard Deviation	
BraTumIA Version	1.2	2.0	1.2	2.0	1.2	2.0
Enhancing	25.2 (0.2 - 66)	23.9 (0.4 - 64)	2.5	1.9	17	17
Edema	95.6 (46 - 180)	92.2 (43 - 176)	8.7	11	36	35
Non-enhancing	3.0 (0.01 - 12)	2.7 (0 - 10.0)	0.77	0.71	3	2.4
Necrotic	5.8 (0.1 – 55)	6.8 (0.2– 55)	1.1	0.74	12	12
Total Tumor-related Abnormality	130 (53 – 252)	126 (50 – 241)	9	11	53	49
Total Non-enhancing Tumor-related Abnormality	104 (46 – 189)	102 (44 – 182)	8.5	11	40	37
Non-enhancing Non-necrotic Tumor-related Abnormality	98.7 (46 – 189)	94.8 (44 -179)	8.7	11	38	36
White Matter	544 (446 – 644)	547 (448 – 649)	15	17	50	53
Gray Matter	596 (497 – 685)	610 (521 – 711)	17	16	54	55

**Online Table 3. Intraclass Correlation Coefficient and Concordance Correlation Coefficient for Automatically Segmented Volumes.**

Segmented region	ICC (95% CI) <sup>a</sup>		CCC (95% CI) <sup>b</sup>	
BraTumIA Version	1.2	2.0	1.2	2.0
<b>Enhancing</b>	0.98 (0.95 - 0.99)	0.99 (0.97 - 1)	0.97 (0.94 - 0.99)	0.98 (0.96 - 0.99)
<b>Edema</b>	0.94 (0.87 - 0.98)	0.91 (0.79 - 0.96)	0.94 (0.87 - 0.98)	0.91 (0.79 - 0.96)
<b>Non-enhancing</b>	0.94 (0.85 - 0.97)	0.92 (0.80 - 0.97)	0.94 (0.85 - 0.97)	0.91 (0.80 - 0.96)
<b>Necrotic</b>	0.99 (0.98 - 1)	1 (0.99 - 1)	0.99 (0.98 - 1)	1 (0.99 - 1)
<b>Total Tumor-related Abnormality</b>	0.97 (0.93 - 0.99)	0.95 (0.88 - 0.98)	0.97 (0.94 - 0.99)	0.95 (0.89 - 0.98)
<b>Total Non-enhancing Tumor-related Abnormality</b>	0.96 (0.89 - 0.98)	0.92 (0.81 - 0.97)	0.96 (0.90 - 0.98)	0.92 (0.82 - 0.97)
<b>Non-enhancing Non-necrotic Tumor-related Abnormality</b>	0.95 (0.88 - 0.98)	0.91 (0.80 - 0.97)	0.95 (0.89 - 0.98)	0.91 (0.80 - 0.96)
<b>White Matter</b>	0.92 (0.81 - 0.97)	0.90 (0.77 - 0.96)	0.92 (0.81 - 0.97)	0.90 (0.77 - 0.96)
<b>Gray Matter</b>	0.91 (0.79 - 0.96)	0.92 (0.80 - 0.97)	0.91 (0.78 - 0.96)	0.92 (0.81 - 0.97)

Abbreviations: CCC = Concordance Correlation Coefficient; CI = Confidence Intervals; ICC = Intraclass Correlation Coefficient

<sup>a</sup> CIs calculated using F-distribution

<sup>b</sup> CIs calculated using Fisher's Z-transformation