

Supplementary Material for TINC: Tree-structured Implicit Neural Compression

1 Imaging system

The HD-fMOST system was used to perform whole-brain *Neurons* and *Vessels* imaging at a voxel size of $0.32 \times 0.32 \times 1\mu m^3$. The whole-brain dataset size of *Neurons* is ~ 2.82 TB, containing $\sim 12,000$ coronal slices with 29005×24486 pixels for each. The whole-brain dataset size of *Vessels* is ~ 10.9 TB, containing 5160 coronal slices with 28692×20005 pixels for each.

2 Data access

The HiP-CT dataset can be accessed from <https://mecheng.ucl.ac.uk/hip-ct/>. The *Neurons* and *Vessels* data were partially uploaded in the attachment named as “biological data example.zip”.

3 Reproducible code

We provided the code for reader to reproduce our conclusion with detailed instruction in the attachment named as “reproducible code.zip”.

4 Supplementary Figures

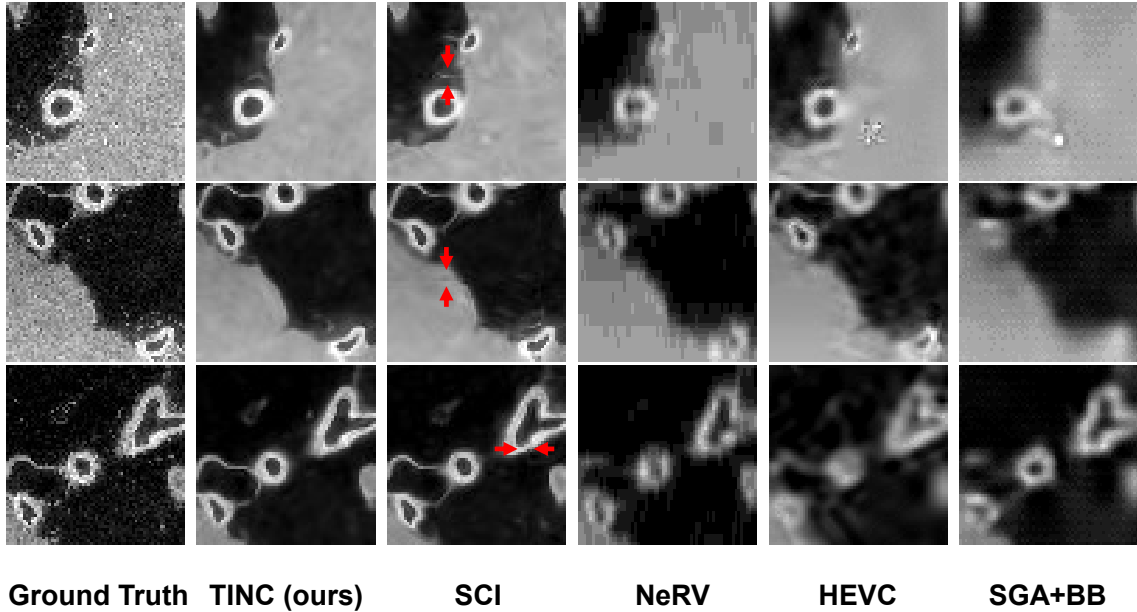


Figure 1: Visual comparisons with state-of-the-arts on *Kidney* data—2D slices from 3D volumes around $256\times$ compression ratio. The red arrows highlight the blocking artifacts produced by SCI.

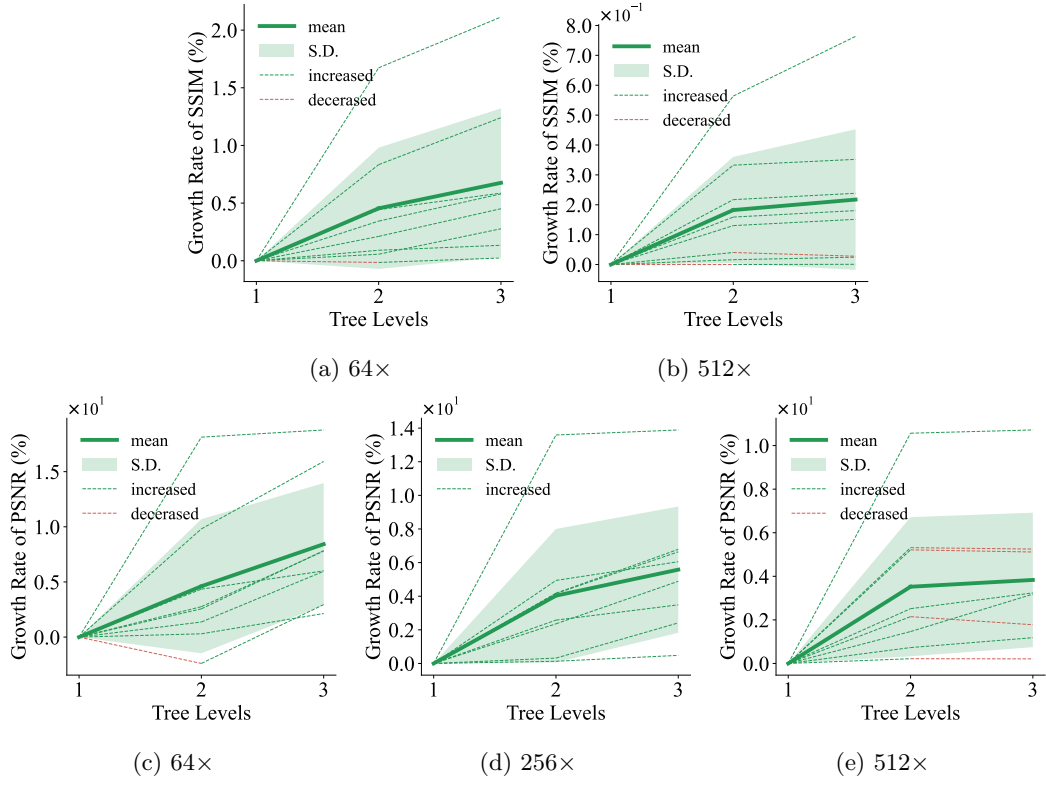


Figure 2: The growth rate of SSIM and PSNR for each data when increasing the tree levels under different compression ratios. The compression ratios are labeled at the bottom of each sub-figure. The dashed lines represent the change in each data. The solid line represents the mean of changes, and the filled area represents the standard deviation, where the positive and negative change are highlighted with green and red respectively.

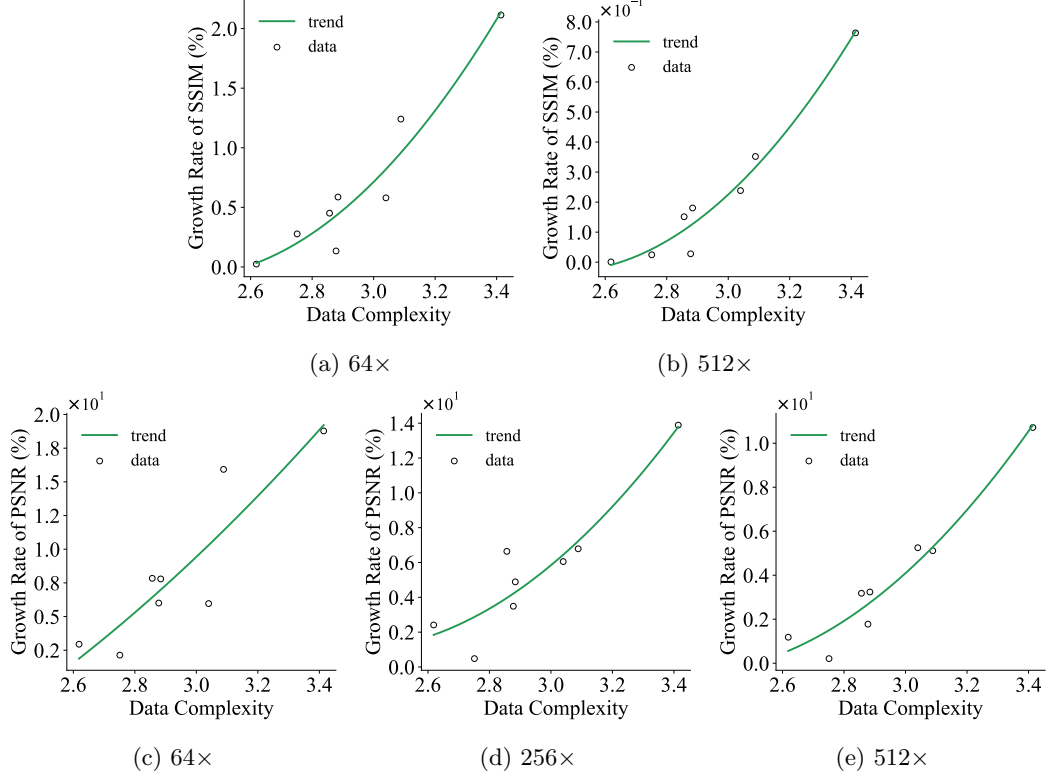


Figure 3: The scatter plot of each data's complexity and the growth rate of SSIM and PSNR when increasing tree levels from 1 to 3 under different compression ratios. The compression ratios are labeled at the bottom of each sub-figure. The solid line represents the trend of change, estimated by a quadratic fit.

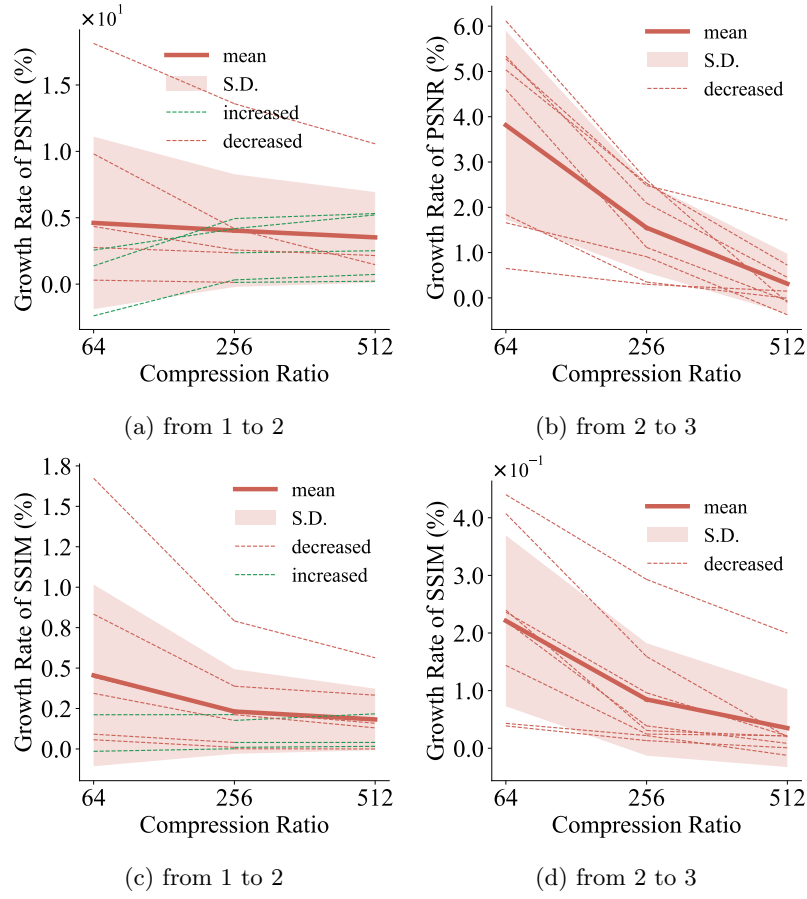


Figure 4: The growth rate of SSIM and PSNR when increasing tree levels from 1 to 2 and from 2 to 3 for each data on different compression ratios. The changes of tree levels are labeled at the bottom of each sub-figure. The dashed lines represent the change in each data. The solid line represents the mean of changes, and the filled area represents the standard deviation, where the positive and negative change are highlighted with green and red respectively.

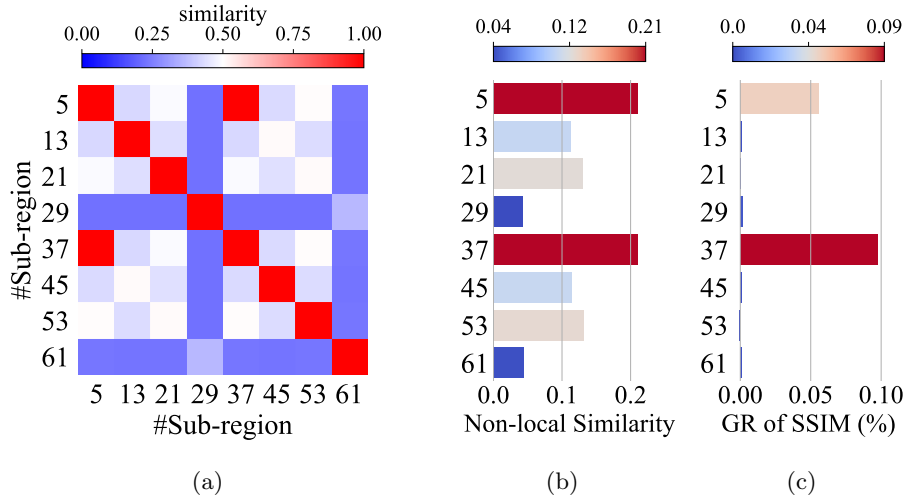


Figure 5: Effect of allocating more parameters to the shallow level on TINC's compression fidelity for each sub-regions in a *Brain* data under $256\times$ compression ratio. All sub-figures share the same y-axis label. (a) The heatmap of similarities between 8 equally spaced distant sub-regions. The serial numbers of the regions represent their z-curve order. (b) The non-local similarity of each region. (c) The growth rate of SSIM for each region when allocating more parameters to the shallow level.

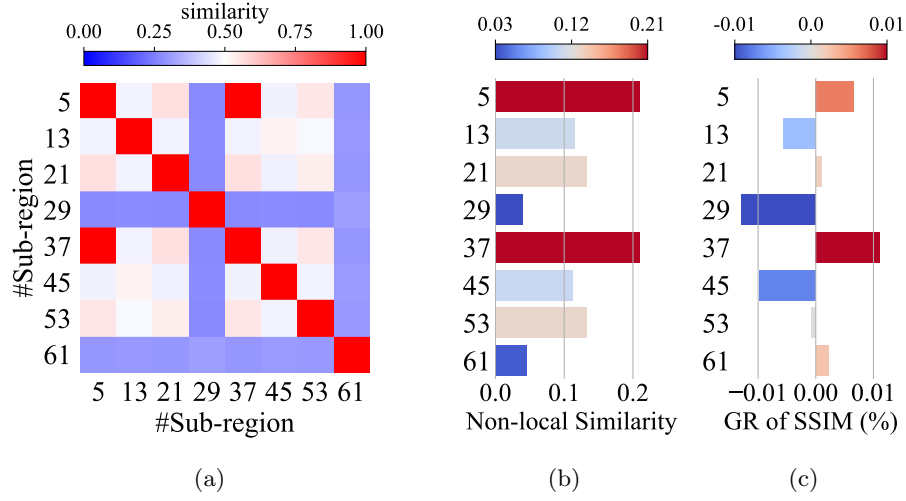


Figure 6: Effect of allocating more parameters to the shallow level on TINC's compression fidelity for each sub-regions in a *Heart* data under $512\times$ compression ratio, with the same layout in Figure. 5

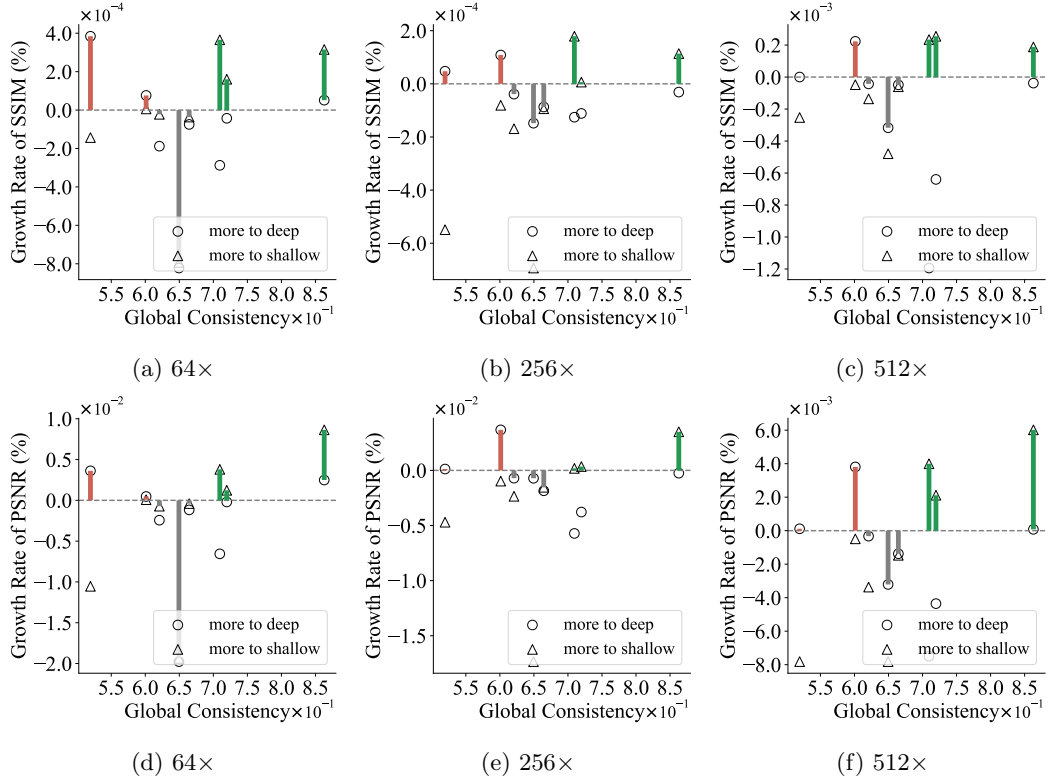


Figure 7: Effect of three inter-level parameter allocation approaches on TINC's compression fidelity for medical data with different global consistency under different compression ratios. The compression ratios are labeled at the bottom of each sub-figure. We used the even allocation as baseline and calculated the growth rate of SSIM and PSNR for the other two approaches, represented as squares and triangles. We marked the gap between the best and second-best approaches, and use red, gray, and green colors to indicate the three cases of allocation more to the deep being the best, even allocation being the best, and allocation more to the shallow being the best, respectively

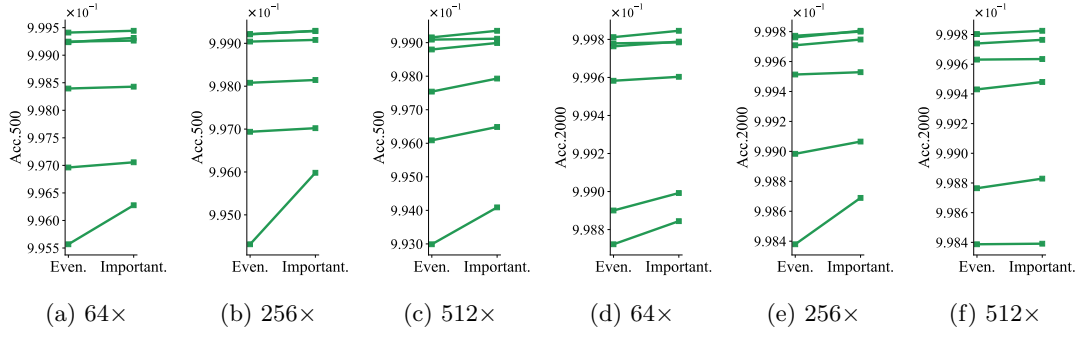


Figure 8: Comparison of different intra-level parameter allocation approaches for 6 *Neurons* data under different compression ratios. The compression ratios are labeled at the bottom of each sub-figure.

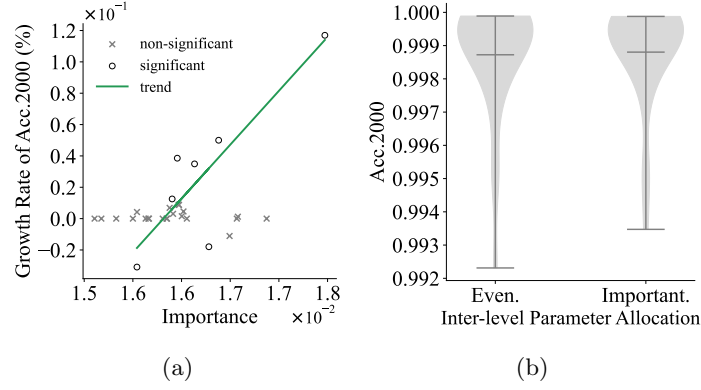


Figure 9: Effect of important allocation on TINC's compression fidelity, in terms of Acc.2000 on a *Neurons* data under 512 \times compression ratio. (a) The growth rate of Acc.2000 for each region. The regions with and without significant growth rate are represented as cross marker and square respectively. The solid line represents the trend of change, estimated by a linear fit. (b) The violin plots of Acc.2000 for all these regions. The shaded area represent the distribution of Acc.2000 across all regions. The three horizontal lines from top to bottom represent the maximum, average and minimum values respectively.

5 Supplementary Tables

Table 1: The compression time and decompression time for each method on medical data under around $512\times$ compression ratio. JPEG was excluded due to lower compression ratio. The decompression time were multiplied by 1,000 to simulate the real situation where the data needs to be decompressed frequently for processing and analysis

Methods	INR based				Commercial		Data driven		
	TINC(ours)	SCI	NeRV	NeRF	H.264	HEVC	DVC	SGA+BB	SSF
Compression (seconds)	2310	2913	2392	489.2	1.670	1.000	58.82	2701	7.086
Decompression *1k(seconds)	217.4	160.8	195.3	99.15	370.1	276.8	183.0	280.0	400.0

Table 2: The compression time and decompression time for each method on biological data under around $512\times$ compression ratio, with the same layout in Table. 1

Methods	INR based				Commercial		Data driven		
	TINC(ours)	SCI	NeRV	NeRF	H.264	HEVC	DVC	SGA+BB	SSF
Compression (seconds)	1999	1445	1603	769.6	0.900	2.414	38.99	3231	3.940
Decompression *1k(seconds)	216.3	201.1	98.64	84.43	448.6	501.1	295.6	279.3	127.7