X²-Gaussian: 4D Radiative Gaussian Splatting for Continuous-time Tomographic Reconstruction

Supplementary Material

1. Details of Dataset

DIR Dataset We collected 4D CT scans from the DIR dataset [4], which were acquired from patients with malignant thoracic tumors (esophageal or lung cancer). Each 4D CT was divided into 10 3D CT volumes based on respiratory signals captured by a real-time position management respiratory gating system [7]. For each patient, the CT dimensions are 256×256 in the x and y axes, while the z-axis dimension varies from 94 to 112 slices. The z-axis resolution is 2.5 mm, and the xy-plane resolution ranges between 0.97 and 1.16 mm. The CT scan coverage encompasses the entire thoracic region and upper abdomen. Following the approach in literature [3, 13], we preprocessed the original data by normalizing the density values to the range of [0, 1]. We simulated the classical one-minute sampling protocol used in clinical settings by uniformly sampling 300 paired time points and angles within a one-minute duration and a 0 to 360 angular range. Based on the respiratory phase corresponding to each timestamp, we selected the appropriate 3D CT volume, and then utilized the tomographic imaging toolbox TIGRE [1] to capture 512×512 projections.

4DLung Dataset 4D CTs in 4DLung dataset [6] were collected from non-small cell lung cancer patients during their chemoradiotherapy treatment. All scans were respiratory-synchronized into 10 breathing phases. For each patient, the CT scans have dimensions of 512×512 pixels in the transverse plane, with the number of axial slices varying between 91 and 135. The spatial resolution is 0.9766 to 1.053 mm in the transverse plane and 3 mm in the axial direction. Following the same pipeline as DIR dataset, We captured 300 projections with sizes of 1024×1024 .

SPARE Dataset The 4D CT images from the SPARE dataset [11] have dimensions of 450×450 pixels in the transverse plane and 220 slices in the axial direction, with an isotropic spatial resolution of 1.0~mm in all directions. Following the same methodology as the DIR dataset, we acquired 300 projections, each with dimensions of 512×512 pixels.

2. Implementation details of baseline methods

We conducted comparison with various 3D reconstruction methods, which were directly applied to 4D reconstruction under the phase binning workflow. Traditional algorithm FDK [10] was implemented using the GPU-accelerated TI-GRE toolbox [1]. We evaluated five SOTA NeRF-based

tomography methods: NeRF [9] (using MLP-based volumetric scene representation), IntraTomo [12] (using a large MLP for density field modeling), TensoRF [5] (utilizing tensor decomposition for efficient scene representation), NAF [13] (featuring hash encoding for faster training), and SAX-NeRF [3] (employing a line segment-based transformer). The implementations of NAF and SAX-NeRF used their official code with default hyperparameters, while NeRF, IntraTomo, and TensoRF were implemented using code from the NAF repository. All NeRF-based methods were trained for 150,000 iterations. We also evaluated three SOTA 3DGS-based methods: 3DGS [8] (introducing realtime rendering with 3D Gaussians), X-GS [2] (incorporating radiative properties into Gaussian Splatting), and R²-GS [14] (proposing a tomographic reconstruction approach to Gaussian Splatting). Since 3DGS and X-GS lack the capability for tomographic reconstruction, following [2], we leveraged their novel view synthesis abilities to generate an additional 100 X-ray images from new viewpoints for each 3D CT. These synthesized views, together with the training data, were used with the FDK algorithm to perform reconstruction. All 3DGS-based methods used their official code with default hyperparameters. All experiments were executed on a single NVIDIA RTX 4090 GPU.

3. More Quantitative Results

Tab. 1 and Tab. 2 present the comparative results for each patient in the 4DLung dataset and DIR dataset, respectively. Our method achieved optimal reconstruction results for nearly all patients across both datasets.

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Table 1. Comparison of our X²-Gaussian with different methods on the 4DLung dataset.

Method	Patient1		Patient2		Patient3		Patient4		Patient5		Average	
	PSNR	SSIM	PSNR	SSIM								
FDK [10]	27.36	0.646	22.98	0.410	28.48	0.662	28.76	0.654	27.59	0.684	27.03	0.611
IntraTomo [12]	30.39	0.926	35.73	0.930	34.99	0.938	35.29	0.941	35.02	0.960	34.28	0.939
TensoRF [5]	30.42	0.907	36.67	0.931	34.64	0.933	35.14	0.944	35.86	0.969	34.55	0.937
NAF [13]	30.76	0.901	37.46	0.932	34.69	0.934	35.47	0.947	36.30	0.964	34.94	0.936
X-GS [2]	30.62	0.709	25.16	0.526	31.45	0.722	30.88	0.773	29.98	0.792	29.62	0.705
R^2 -GS [14]	33.19	0.918	39.22	0.972	37.90	0.960	37.29	0.939	38.96	0.970	37.31	0.952
Ours	34.49	0.929	40.44	0.957	39.94	0.966	38.10	0.943	40.06	0.973	38.61	0.957

Table 2. Comparison of our X²-Gaussian with different methods on the SPARE dataset.

Method	Patient1		Pati	ent2	Pati	ent3	Average	
111001100	PSNR	SSIM	PSNR	SSIM	PSNR	SSIM	PSNR	SSIM
FDK [10]	9.85	0.232	11.85	0.229	21.04	0.616	14.25	0.359
IntraTomo [12]	27.55	0.889	27.83	0.864	26.48	0.860	27.29	0.871
TensoRF [5]	26.88	0.863	27.21	0.832	26.64	0.877	26.91	0.857
NAF [13]	28.67	0.908	29.25	0.880	27.39	0.892	28.44	0.893
X-GS [2]	14.16	0.328	17.37	0.356	23.06	0.652	18.20	0.442
R^2 -GS [14]	30.04	0.907	32.06	0.901	31.26	0.916	31.12	0.908
Ours	31.38	0.920	32.47	0.907	32.87	0.939	32.24	0.922

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