This document describes how to use SPROM to generate the training samples. The platforms and configurations we used are Windows 7/8.1/10/11 and CUDA 9.0 respectively. The overall workflow is shown in Fig.1.

Start simulation		Parameter setting	Sequence loading	 Data generation]▶	END
	, -				_	

Fig. 1 SPROM workflow diagram

1. Open eeg64.exe and click the following buttons in sequence to start it.

NN	IR数据处理	里与模拟软件 -	[Eeg1]				- 1		
File(F)	Edit(E)	Calculate(C)	Analysis(A)	Operate	e(O) Draw	D) Plugi	n(P) Chaos	Windows(W)	Help(H)
Z					N N		8	8 🙆 🛓	1
		说明 <mark>NMR S</mark>	Simulation Plugi	n				>	
		Plugins Tab	e lation Plugin	1	11	Inform	ation		
		NMH SIMU	iation Plugin	2		Author	Congbo Cai		
						File	SPROM64_cu	da	
						Update	September 15	, 2021, 18:00	
					Next Page]			
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				3	Run]			
					Exit				
		1D S	ample	3	D Sample		InSm 2D	RF Produ	
		MRI Si	mulation		Frydman		Suscept	Else Func	
		4 Deep l	earning	Pr	oduce Seq				

Fig. 2 The initial interface of eeg

2. Set the size of templates or load the parameters file (./para/model.par3d) directly.

			Lengui		-	
	x	512	0.22	1e-18	1e-18	1e-18
	Y	1	0.0006	1e-18	1e-18	1e-18
	z	512	0.22	1e-18	1e-18	1e-18
Extra	ra Num 1					
		Save		Load	Complex	Structure

Fig. 3 The templates size setting interface

3. Set scan parameters or simply click "Load Param" button to load the parameter file (./para/scanpar.sav) directly.

0.0004	Add_Number 0	Acq -	
4096			
ng Time 1			
N: 1 F: 11	Diffusion		
Dipolar Field	Fast Recovery Auto Exit		
t Algorithm 2	□ Radiation Damp □ Instability		
ipe Pulse	🗖 Shape Grad		
e_Diffusion			
	C 2D C 3D 0.0004 4096 1g Time 1 Dipolar Field t Algorithm 2 ope Pulse e_Diffusion	C 2D C 3D Add_Number 0 0.0004 T1_point 1 4096 Diffusion Dipolar Field Fast Recovery Auto Exit t Algorithm 2 Radiation Damp Instability upe Pulse Shape Grad e_Diffusion	C 2D C 3D Add_Number 0 Acq ▼ Acq ♥ Acq ♥

Fig. 4 The scan parameters setting interface

4. Sequence Loading.



Fig. 5 The sequence loading interface

- 4.1 Click "Load Seq" button to load the sequence file (SEMOLED_singe_train.seq), and then click "Add Seq" button to accept this sequence loading.
- 4.2 Click "Display Seq" to show the sequence and check whether the sequence parameters are correct.



Fig. 6 A preview of MOLED sequence

4.3 Go to "New Task" to create a new task and repeat Step 4.1. Notice that select sequence files (SEMOLED_single_train_shift_gradient.seq) if gradient fluctuation for MOLED echo-shifting gradients is needed.

Setup Panel		
GID C2D C3D Add Number	Console	
T1 eten 0.0004 T1 noint 1	Pulse v Evolve v	
II_step	Evolve - Evo	
	Evolve - Evo	
T1_Exp 4096	Pulse v Evolve v	
	Evolve - Evo	
	Evolve v	
Damping Time 1	Pulse v Evolve v	
-	Evolve v	
Diffusion Diffusion Experimental Fast Recovery	Evolve v	
☐ Auto Exit	Pulse * Evolve *	
🗖 Fast Algorithm 2 🛛 🧮 Radiation Damp	Evolve *	
⊢ Instability	Evalve +	
□ Snape Pulse □ Shape Grad	Evalve +	
1 Take_Dilusion	Pulse X Evolve X	
	Fundre v Evalue v	
Save Param Array Simul	Evolve v	
Add Seq Load Param Display Seq		
	Fundre v Eventre v	
Append Seq Save Seq Start	Convert Conv	
New Task Load Seg Exit	Endrée Fondrée Fondrée Fondrée Fondrée Fondrée Fondrée Fondrée Fondrée Fondrée	
	Evalve v	
Insert Seq Deep Samples Deep Cuda	Evolve T Evolve	
	Evolve +	
	Evolve v	
	Evolve -	

Fig. 7 The Main sequence design panel

- 5. Data generation
- 5.1 click "Deep Cuda"

	Save Param	Array Simul
Add Seq	Load Param	Display Seq
Append Seq	Save Seq	Start
New Task	Load Seq	Exit
Insert Seq	Deep Samples	Deep Cuda

Fig. 8 The initial interface for generating data

5.2 Set the number of the generated samples (Here, the maximum value should not exceed 20000):

N	Imber	2
12	Input Number	r
	ОК	1

Fig. 9 The number setting interface

5.3 Enter the name of the storage path:

	Input Name	
13	scan_SEMOLED	

Fig. 10 The storage path setting interface

- 5.4 Set environment parameters:
- B1: inhomogeneous RF field
- Brain Pattern: select the human brain parametric templates
- Rand Pattern: parametric templates randomization
- Has Motion: subject movement
- Max_Vx(m/s): velocity of x direction
- Max_Vy(m/s): velocity of y direction
- Max_rot(rad/s): angular velocity.

Of course, you can simply import the parameters file (./para/motion.dlp) directly. Anyway, click the "OK" button at the end.

I Rand Pattern		nplex Inhomo Inter_F	Result Not_Empty_Insi	de I✔ OLED type
□ T2* □ Do	uble T2	Phantom 🔽 Brain P	attern 🔲 Save Seq Para	✓ Has Motion
□ Shape Pul □	Sensitive	Map Homo_Acq C	Chem Shift 🦵 Vary_Motion	1
Max_Mean_Devia	0.2	Smooth Factor 2	Null_X	T2 range
Max_Var_Devia	0.4	Extra Num 1	32 Null_Y	Median T2
Shape number	600	Smooth Times 0	32	C Large T2
Local B0 times	0	Max_Vx 0.0	5	C Human T2
Block num	8	Max_Vy 0.0	5	C Smallest T
Block Size	1024	Max_rot 0.5		

Fig. 11 The Simulation Settings Panel.

5.5 Enter the size of parameter templates, click "OK", and then select M0 template (.m0 file) and T2 template (.t2 file) in sequence. After the selection, the simulation starts.

	X_num	512
	Y_num	512
	Slice_num	10
15	Person_num	550
	O*	
	Can	cel

Fig. 12 The size of parameter templates setting interface

Output Files:

T2 templates: .T2 file • Team0.B1 M0 templates: .M0 file . Team0.m0 B1 field inhomogeneity templates: .B1file Team0.rot Velocity of x direction: .vx file • Team0.T2 Velocity of y direction: .vz file Team0.vx Angular velocity: .rot file • Team0.vz Complex-value MRI signal: .ccb file tempd Team0.ccb •

Example code (MATLAB) for reading the outputs:

```
% .ccb file
fid_file = `tempd_Team0.ccb';
origin_1D_data=load(fid_file, '-ascii');
origin_1D_complex=origin_1D_data(:,1)+1.0i*origin_1D_data(:,2);
origin_2D_complex=reshape(origin_1D_complex,[fre_num,phase_num]);
% parameters file
fid_file = `Team0.T2';
fip_dif=fopen(fid_file,'rb');
[Array_2D_dif,num]=fread(fip_dif,inf,'double');
data_temp=Array_2D_dif(:,:);
data_temp=reshape(data_temp,model_num_x,model_num_y);
fclose(fip_dif);
```

Example code (MATLAB) for saving the parametric template:

```
T2=single(template_t2); % template_t2 is a 512*512*(slice*n) array
[fid,msg]=fopen('template.T2','wb');
fwrite(fid,T2,'float');
fclose(fid);
```

Reference:

[1] C. B. Cai, M. J. Lin, Z. Chen, X. Chen, S. H. Cai, and J. H. Zhong, "SPROM - an efficient program for NMR/MRI simulations of inter- and intra-molecular multiple quantum coherences," *C.R.Physique*, vol. 9, no.1, pp. 119-126, Jan. 2008.

[2] C. B. Cai, C. Wang, Y. Q. Zeng *et al.*, "Single-shot T2 mapping using overlapping-echo detachment planar imaging and a deep convolutional neural network," *Magn. Reson. Med.*, vol. 80, no. 5, pp. 2202-2214, Nov. 2018.

[3] J. Zhang, J. Wu, S. J. Chen *et al.*, "Robust single-shot T2 mapping via multiple overlapping-echo acquisition and deep neural network," *IEEE Trans. Med. Imag.*, vol. 38, no. 8, pp. 1801-1811, Aug. 2019.

[4] Q. Q. Yang, J. C. Wang, J. F. Bao *et al.*, "Model-based synthetic data-driven learning (MOST-DL): Application in single-shot T2 mapping with severe head motion using overlapping-echo acquisition," 2021. [Online]. Available: <u>https://arxiv.org/abs/2107.14521</u>.