

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.



Fig. 1 SPROM workflow diagram

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

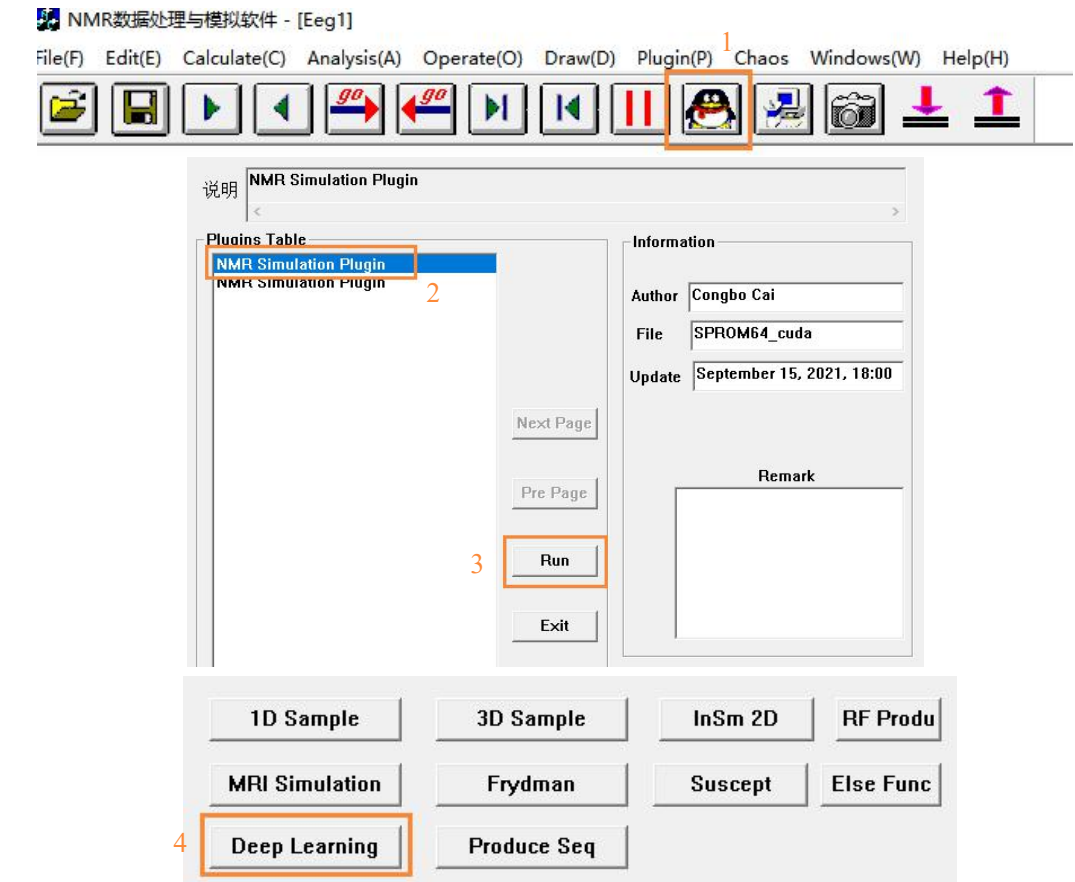


Fig. 2 The initial interface of eeg

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

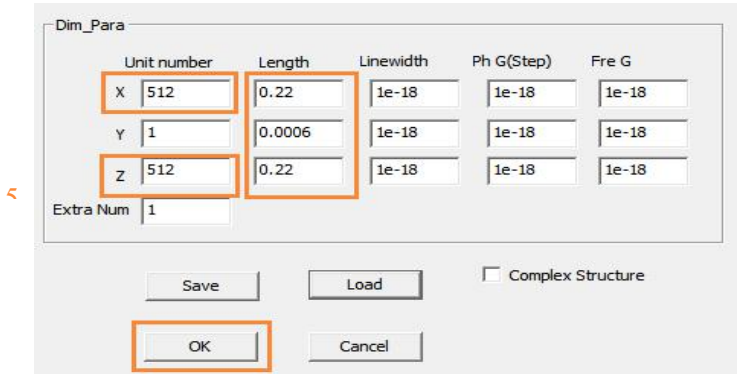
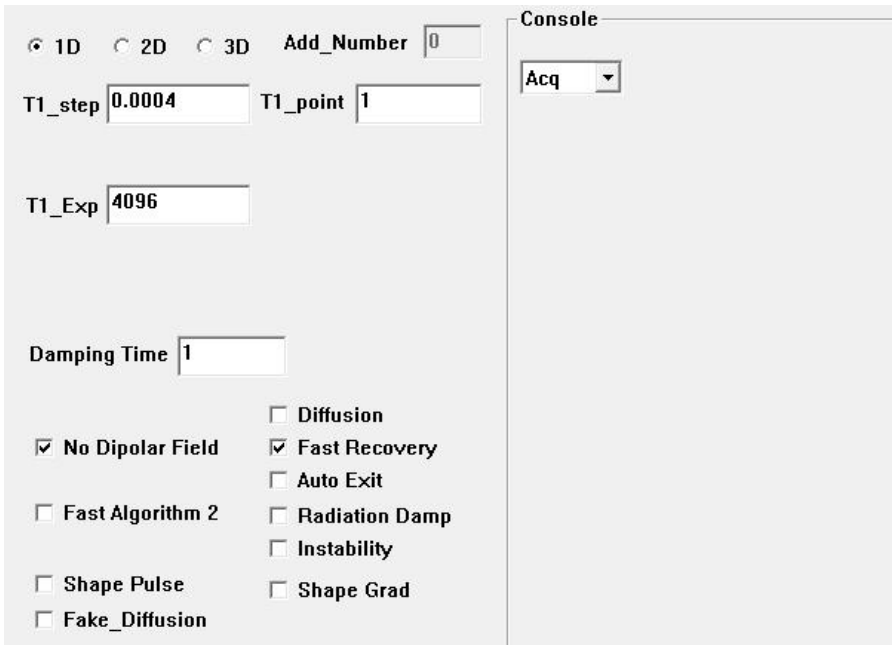


Fig. 3 The templates size setting interface

3. Set scan parameters or simply click “Load Param” button to load the parameter file ([./para/scanpar.sav](#)) directly.

6



The interface shows a configuration window for scan parameters. At the top, there are radio buttons for 1D, 2D, and 3D, with 1D selected. Next to them is an 'Add\_Number' field with the value 0. Below this are input fields for 'T1\_step' (0.0004), 'T1\_point' (1), and 'T1\_Exp' (4096). A 'Damping Time' field is set to 1. A group of checkboxes includes 'No Dipolar Field' (checked), 'Diffusion' (unchecked), 'Fast Recovery' (checked), 'Auto Exit' (unchecked), 'Fast Algorithm 2' (unchecked), 'Radiation Damp' (unchecked), 'Instability' (unchecked), 'Shape Pulse' (unchecked), 'Shape Grad' (unchecked), and 'Fake\_Diffusion' (unchecked). On the right, a 'Console' panel has a dropdown menu set to 'Acq'.

Fig. 4 The scan parameters setting interface

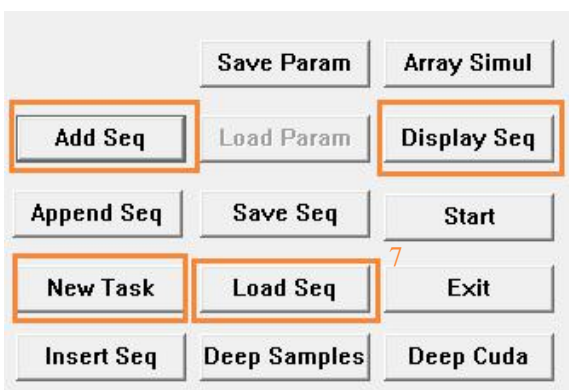
4. Sequence Loading.

8

9

10

7



The interface is a grid of buttons for sequence management. The buttons are: 'Save Param', 'Array Simul', 'Add Seq' (highlighted with an orange box and labeled 8), 'Load Param', 'Display Seq' (highlighted with an orange box and labeled 9), 'Append Seq', 'Save Seq', 'Start', 'New Task' (highlighted with an orange box and labeled 10), 'Load Seq' (highlighted with an orange box and labeled 7), 'Exit', 'Insert Seq', 'Deep Samples', and 'Deep Cuda'.

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.

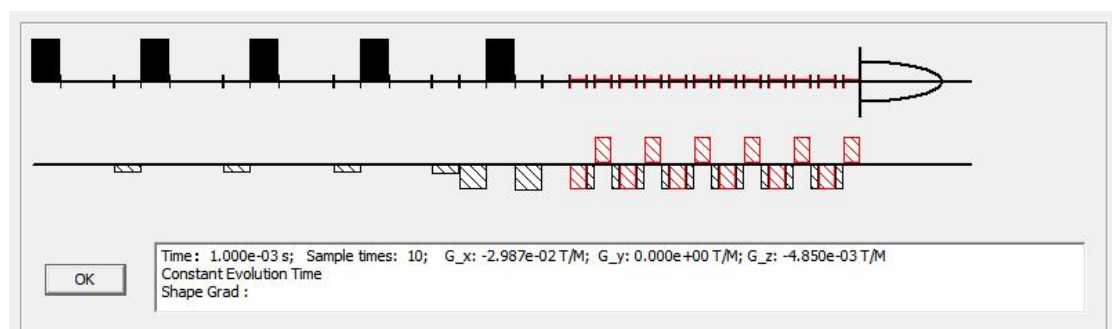


Fig. 6 A preview of MOLED sequence

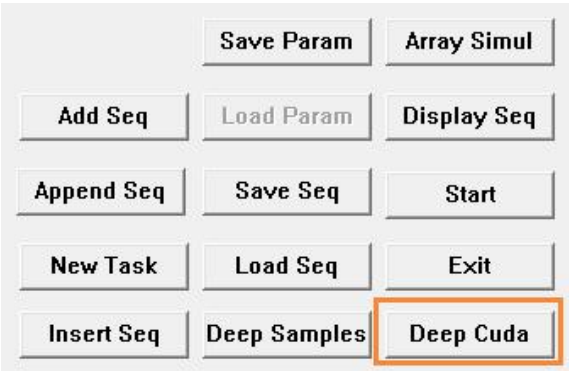
4.3 Go to “New Task” to create a new task and repeat Step 4.1. Notice that select sequence files ([SEMOLED\\_single\\_train\\_shift\\_gradient.seq](#)) if gradient fluctuation for MOLED echo-shifting gradients is needed.



Fig. 7 The Main sequence design panel

5. Data generation

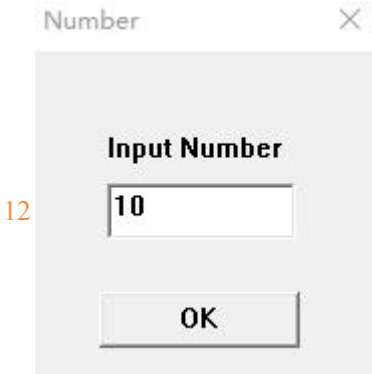
5.1 click “Deep Cuda”



11

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):



12

Fig. 9 The number setting interface

5.3 Enter the name of the storage path:

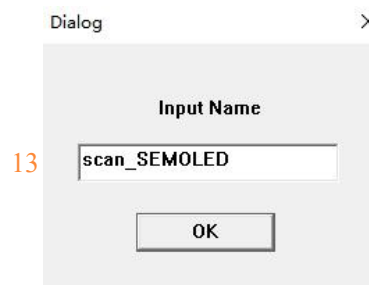


Fig. 10 The storage path setting interface

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.

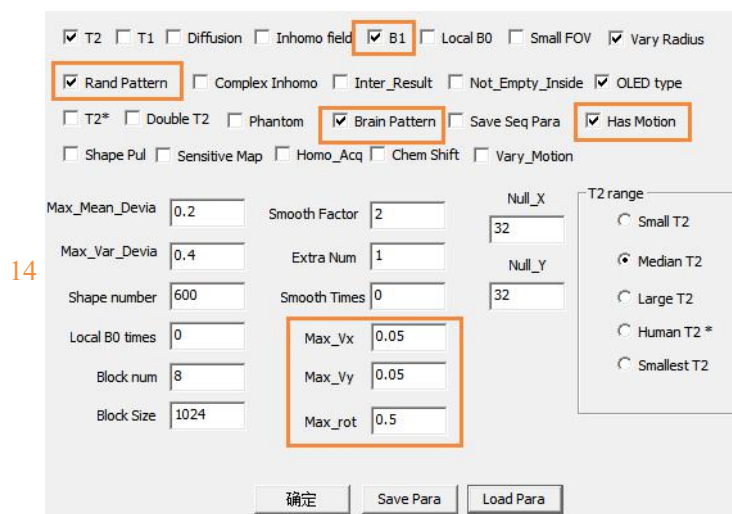


Fig. 11 The Simulation Settings Panel.

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.

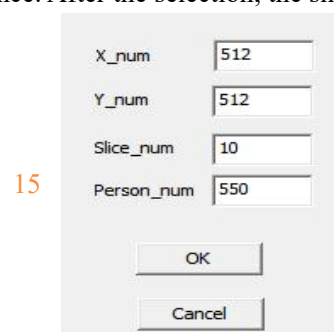









Fig. 12 The size of parameter templates setting interface

### Output Files:

 Team0.B1	• T2 templates: .T2 file
 Team0.m0	• M0 templates: .M0 file
 Team0.rot	• B1 field inhomogeneity templates: .B1 file
 Team0.T2	• Velocity of x direction: .vx file
 Team0.vx	• Velocity of y direction: .vz file
 Team0.vz	• Angular velocity: .rot file
 tempd_Team0.ccb	• Complex-value MRI signal: .ccb file

### 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: <https://arxiv.org/abs/2107.14521>.