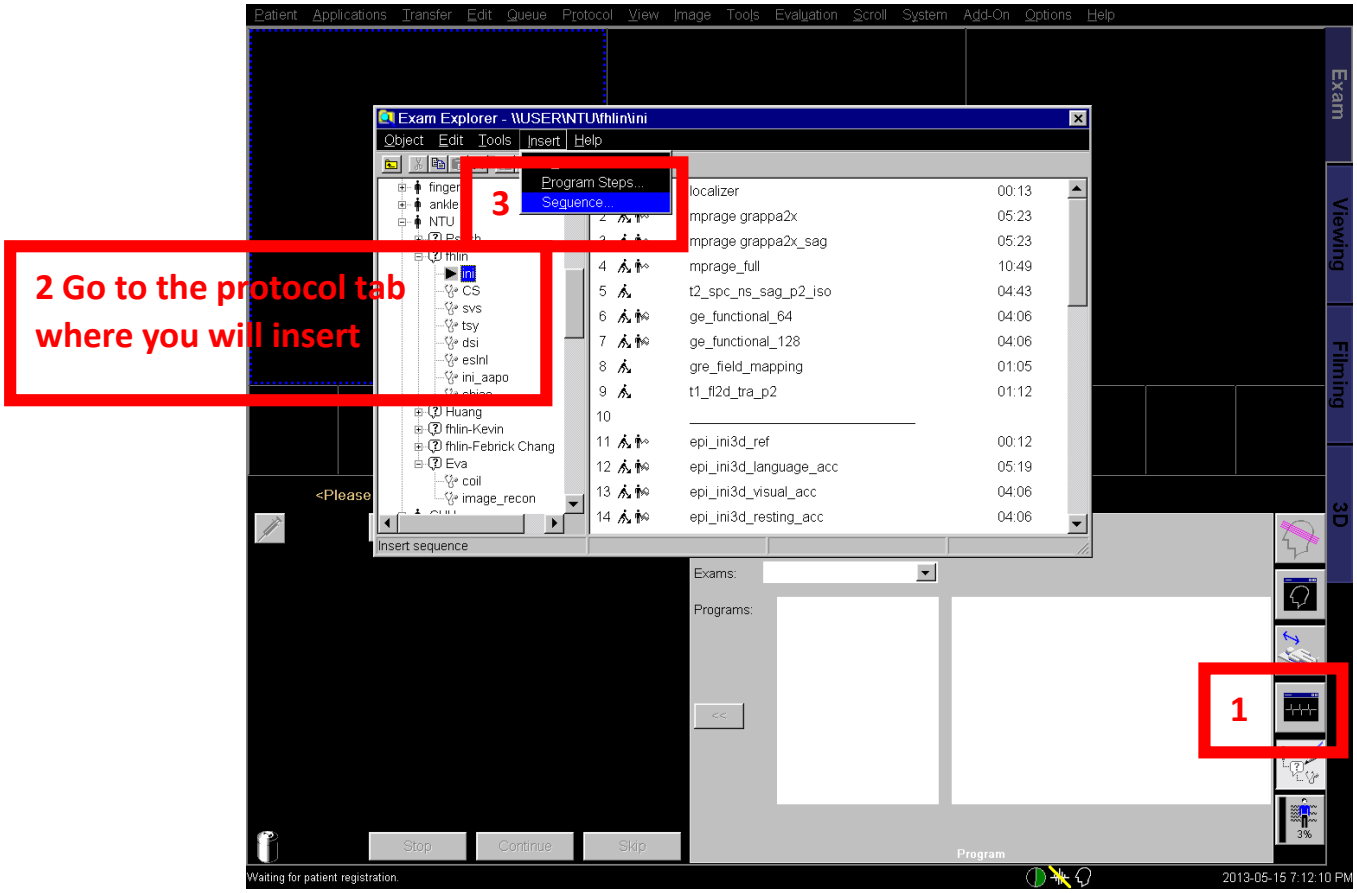
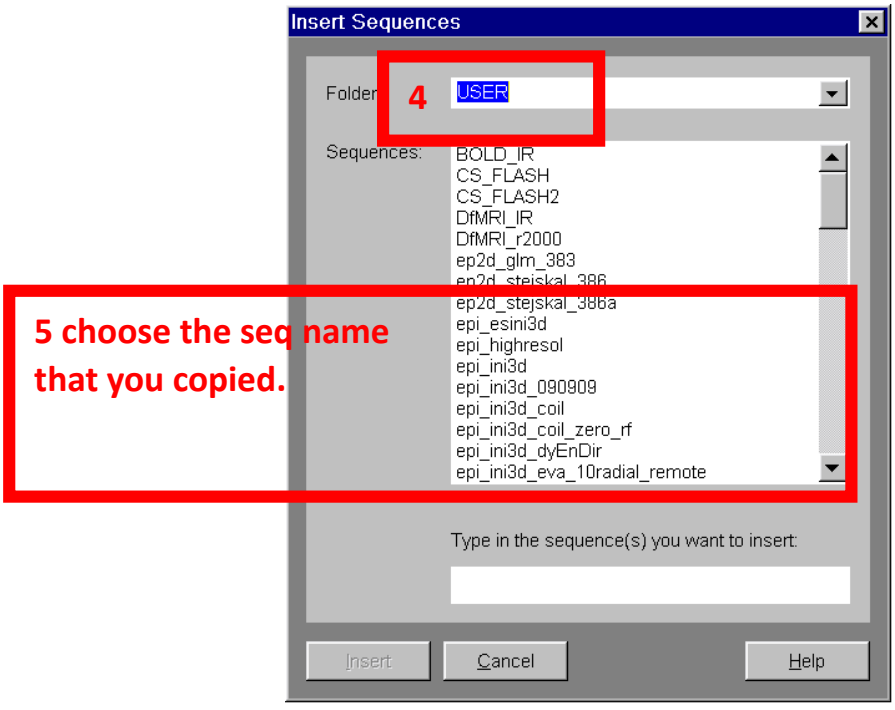
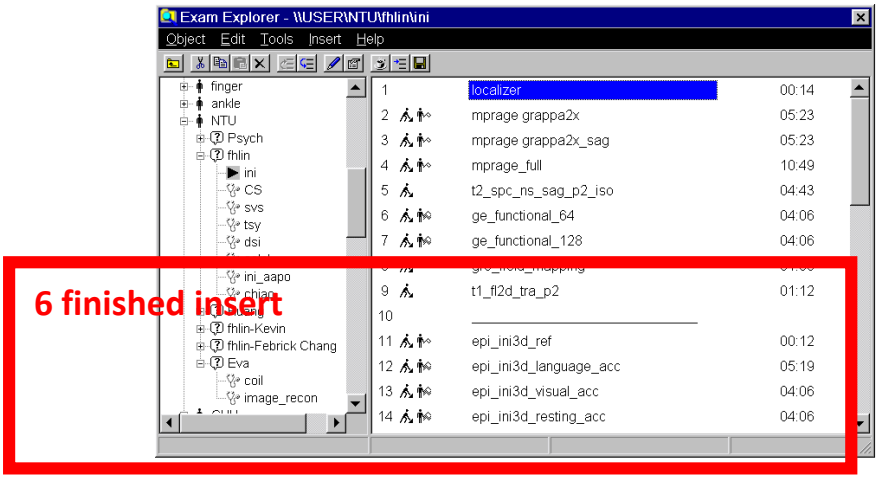
Sequence import (binary files are in dir: "*seq*")

1) Copy 2 binary files under the dir: *C:/MedCom/MriCustomer/seq/*
2) insert the sequence






Exam Explorer - \\USER\NTU\fhlin\ini
Object Edit Tools Insert Help
finger
ankle
NTU
Psych
fhlin
ini
CS
svs
tsy
dsi
ini_aapo
chiao
fhlin-Kevin
fhlin-Febrick Chang
Eva
coil
image_recon
1 localizer 00:14
2 mprage grappa2x 05:23
3 mprage grappa2x_sag 05:23
4 mprage_full 10:49
5 t2_spc_ns_sag_p2_iso 04:43
6 ge_functional_64 04:06
7 ge_functional_128 04:06
9 t1_fl2d_tra_p2 01:12
10
11 epi_ini3d_ref 00:12
12 epi_ini3d_language_acc 05:19
13 epi_ini3d_visual_acc 04:06
14 epi_ini3d_resting_acc 04:06
6 finished insert

Sequence protocols:

Copy the *seq (smsini)* in protocol tab and rename (one for ref and one for acc)

1) Reference scan (2 segments, takes few sec, size ~ 200MB)

1. Slice = 20
2. Phase enc. Dir = R>>L
3. Fov read = 210 mm
4. TR = 50 ms
   TE = 27.5 ms
5. Flip angle = 25 deg
6. Measurements = 10
7. Base resolution = 42
8. Bandwidth = 3970 Hz/px
9. Reference Scan box checked

2) Acc scan (2 segments, takes few mins, size ~ XX GB)

1. Slice = 20
2. Phase enc. Dir = R>>L
3. Fov read = 210 mm
4. TR = 50 ms (the whole brain sampling rate is 10Hz = 0.1 sec),
   TE = 27.5 ms
5. Flip angle = 25 deg
6. Measurements = 2460 (= 60 dummy scan + 2400 scan = 246 sec for example)
7. Base resolution = 42
8. Bandwidth = 3970 Hz/px
9. Reference Scan box unchecked

To achieve higher scan number, please use "Averages" option

10. Averages = 1,2,3,.....

    For example: total 20 min = 20*60 / (0.1sec) = 12000 scans

    set "Measurements = 2000" and "Averages = 6",

    let "Measurements" * "Averages" = total scan

Reconstruction (matlab code files are in dir: “*recon*”):

Using matlab toolbox that we provide

```
>> [ ref, acc ] = MBrecon ( 'meas_ref.dat','meas _acc.dat', 0.0001 );
```