

# Manual for ECoG electrode localization and projection on surface rendering (CTMR package)

Dora Hermes ([d.hermes@umcutrecht.nl](mailto:d.hermes@umcutrecht.nl))

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## Introduction

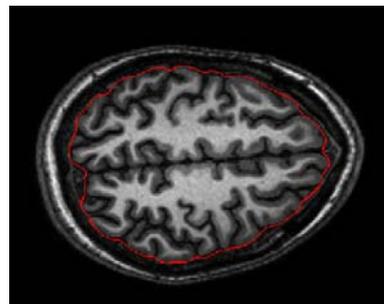
Download the package and put all m-files on one directory. Also make one ‘\data\’ directory to put all the scans. Localizing electrodes and projecting them on the surface consists of 6 steps, also described in master\_ctmr.m with an example for one subject. Open the master\_ctmr.m file, this will run through the scripts stepwise. This master-m-file with the manual will explain the electrode localization, projection and visualization step by step.

Steps:

1. Preprocessing and preparation
  - CT and MRI scans have to be co-registered and a surface is defined to which the electrodes are projected.
2. Localizing electrodes on the CT
3. Houskeeping step 1
  - Since every patient had different grids, electrode XYZ locations need to be numbered and sorted positions and put in a matrix for later reference
4. Projecting the electrodes
  - Every grid is projected to the surface
5. Houskeeping step 2
  - Since every grid is projected separately, they are combined in one matrix for later reference.
6. Visualizing the electrodes on a rendered surface

### 1) Preprocessing and preparation

1. Segment the anatomical MR using SPM5-segment (if this does not work, make sure the anatomical [0 0 0] is on the ac-pc line)
2. Coregister and reslice the CT (source) to the anatomical (reference), the anatomical should stay in the same space.
3. Generate a brain surface
  - `get_mask(subject, degree of smoothing, threshold)`
  - Check whether the mask nicely surrounds the gray matter in MRICron (as in Figure 1)

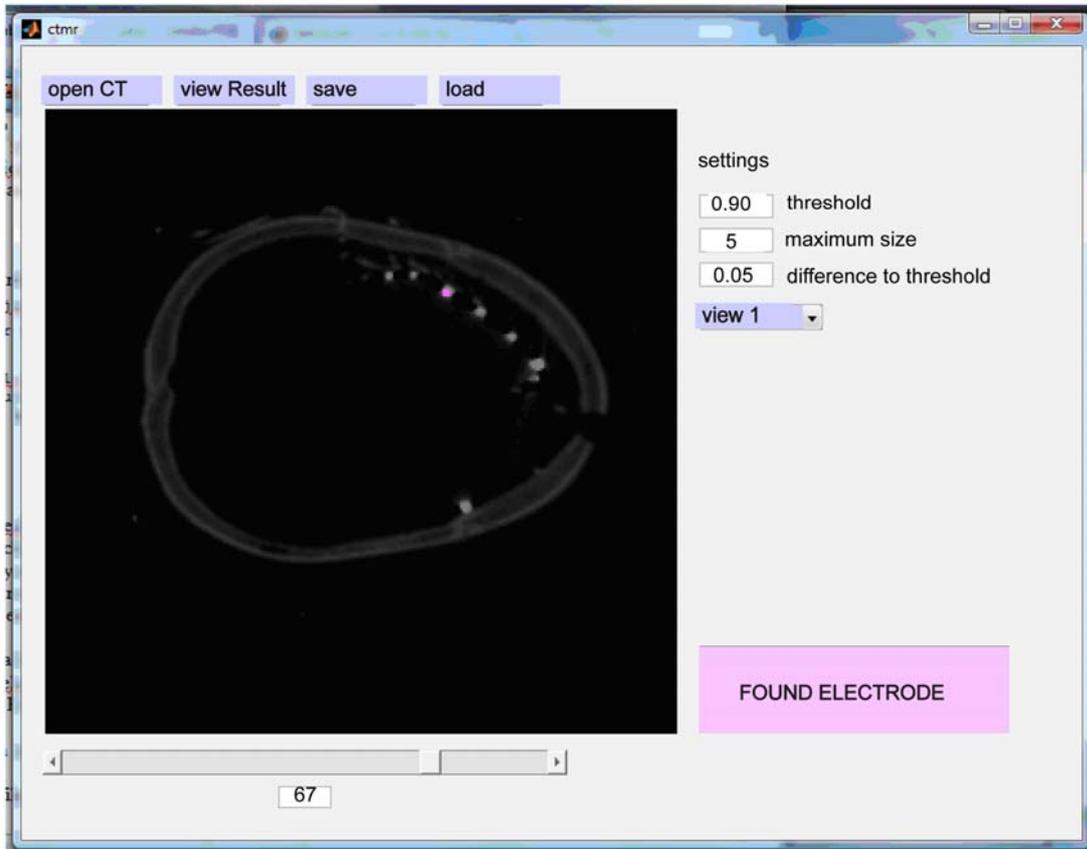


**Figure 1:** anatomical with surface in red.

## 2) Localizing electrodes

CTMR – localize electrodes

Run ctmr.m and the gui in figure 2 will pop up.



**Figure 2:** CTMR gui with one electrode marked in pink

Steps:

- 1) **Open CT** – select resliced CT scan
- 2) *Add an electrode*, by clicking on it in the CT scan with the left mouse button, it fills with pink and 'found electrode' is displayed at the bottom right.
- 3) With **view** (1, 2, 3) you can select axial, sagittal or coronal views
- 4) To *remove an electrode*, click on it and the current electrode and all electrodes that touch this one are removed.
- 5) Press **save** to save electrodesN.img/hdr
- 6) Open CT and **load** Electrode position matrix to load previously made file.

7) **Settings** (see Figure 3):

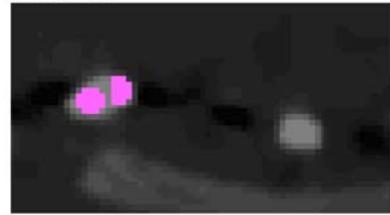
When you click on an electrode, you have to click on a spot where the luminance is above the *threshold*. An electrode is filled up to the *threshold* minus *difference to threshold*, with a *maximum size* of X mm.

Sometimes electrodes are moved on top of each other. If there are 2 adjoining electrodes, so close that the center is detected in the middle of 2 electrodes, reduce the maximum size (e.g. 2).

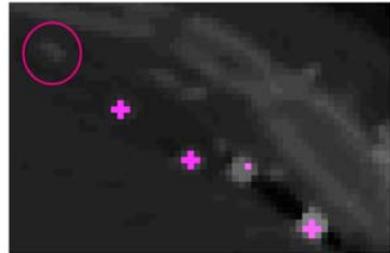
If there is one electrode with reduced luminance, lower the threshold

8) Press **result** to visualize current electrodes in a plot3 to see whether you have all electrodes in a grid.

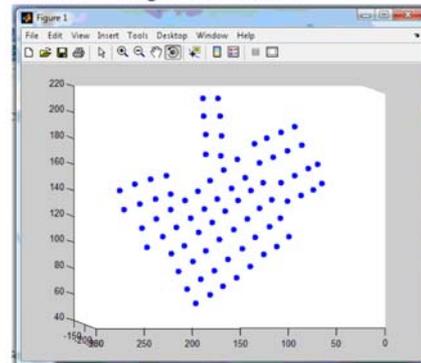
Change maximum size for adjacent electrodes



Change threshold for electrodes with lower luminance



View result to check whether all electrodes in grid are selected



**Figure 3:** CTMR gui settings and result viewing option

### 3) Housekeeping step 1, sort electrodes

Two housekeeping steps are important, the first is assigning numbers to the localized electrodes, so each grid/strip can be projected

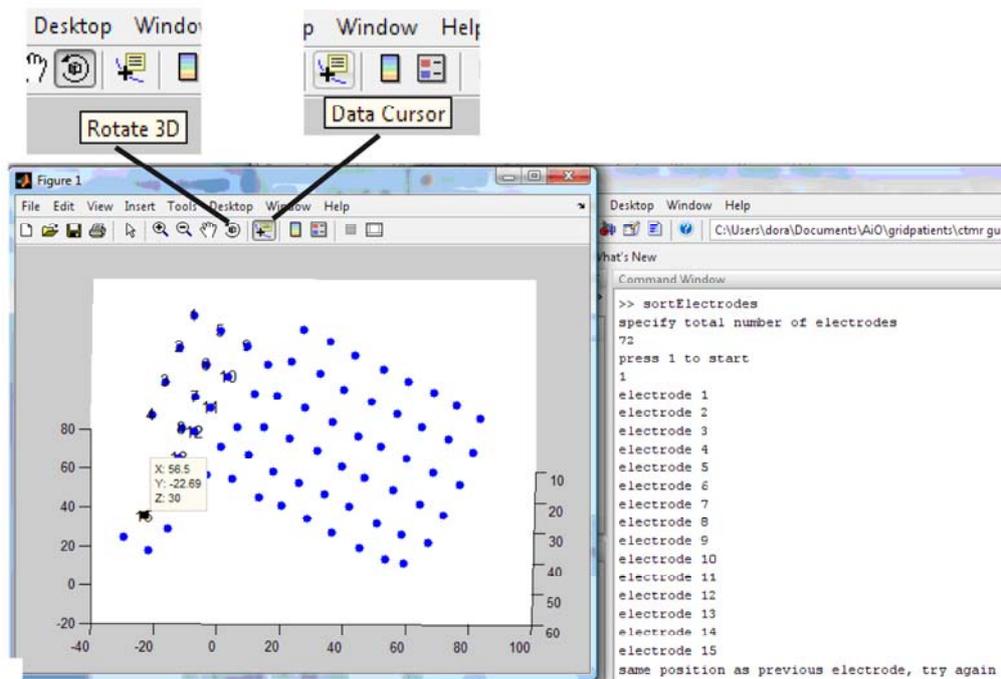
#### *Sort electrodes – assign numbers*

Run sortElectrodes.m

1. Select an electrodesX.img, output from ctrmr
2. Rotate the grid so all electrodes are visible
3. In matlab specify total number of electrodes you want to number
4. Select the datacursor and press 1 to start clicking on electrodes
5. After clicking, the number will appear on the selected electrode.
6. You can not click twice on the same electrode
7. If the datacursor is displayed on top of the next electrode, just drag and drop it out of the way.
8. After clicking the specified number of electrodes, the program asks for an output directory, the output will be saved as electrodes\_locX.mat, where X is the number, so previous files are not overwritten.

#### *Add all electrodes in one mat-file*

```
% load electrode files
elec1=load('./data/electrodes_loc1.mat');
elec2=load('./data/electrodes_loc2.mat');
% put in the correct order in one matrix
elecmatrix=[elec1.elecmatrix(1:48,:);...
            elec2.elecmatrix(1:end,:)];
% save matrix
save('./data/electrodes_loc_all.mat','elecmatrix');
```



**Figure 4:** Sort electrodes display

## 4) Project electrodes

*Project electrodes to the surface:*

Electrodes2surf

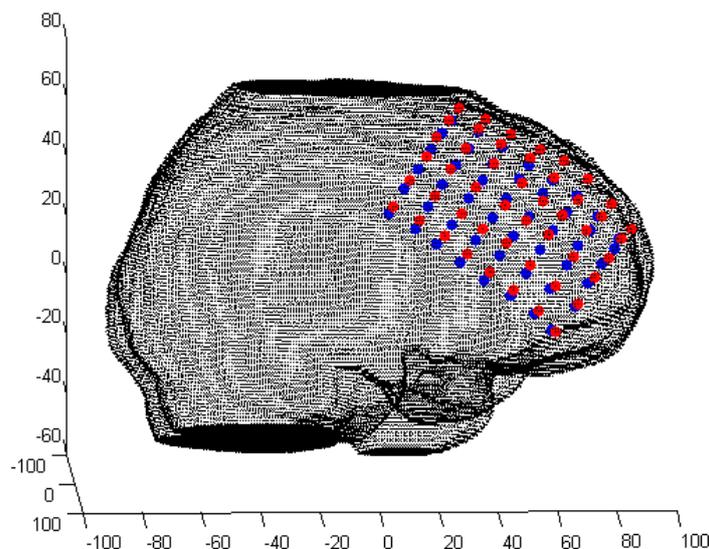
For grids with size  $n \times m$

- grid size ( $n > 2, m > 2$ )
  - 5 adjacent electrodes are used to estimate local norm
  - `electrodes2surf(patient,5,1,electrode numbers in file,electrodes.mat-file,surface,anat)`
- grid size ( $n=2, m \geq 2$ ):
  - 4 adjacent electrodes are used to estimate local norm
  - `electrodes2surf(patient,4,1,electrode numbers in file, electrodes.mat-file,surface,anat)`
- strips: grid size ( $n=1, m \geq 1$ ):
  - electrodes are projected to the nearest point on the surface
  - `electrodes2surf(patient,0,2,electrode numbers in file, electrodes.mat-file,surface,anat)`

*Example*

For example, electrodes, in correct order are in `electrodes_loc_all.mat` and there are 3 grids of sizes  $4 \times 8$ ,  $2 \times 4$  and  $1 \times 8$ . Electrodes [1:32] are in grid 1, electrodes [33:40] are in grid 2 and electrodes [41:48] are in grid 3.

```
electrodes2surf('name',5,1,[1:32], './data/electrodes_loc_all.mat',...  
    './data/name_surfacel_6_01.img', './data/anat.img');  
electrodes2surf('name',4,1,[33:40], './data/electrodes_loc_all.mat',...  
    './data/name_surfacel_6_01.img', './data/anat.img');  
electrodes2surf('name',0,2,[41:48], './data/electrodes_loc_all.mat',...  
    './data/name_surfacel_6_01.img', './data/anat.img');
```



**Figure 5:** After projecting the electrodes to quickly visualize the results a figure is produced with original positions (blue) and projected electrodes (red) on the surface (black). Note that in this subject the top part of the brain was not scanned.

## 5) Housekeeping step 2, put all electrodes in 1 file

Put projected electrodes in one file and generate nifti image

```
% load all projected electrodes:
% electrodes are saved as out_els
load('./data/name_electrodesOnsurface1_5.mat');
elecmatrix=out_els;
load('./data/name_electrodesOnsurface1_2.mat');
elecmatrix=[elecmatrix;out_els];
load('./data/spoo_electrodesOnsurface1_0.mat');
elecmatrix=[elecmatrix;out_els];
save('./data/spoo_electrodes_surface_loc_all.mat','elecmatrix');

% make a nifti image with electrodes on surface
% use function position2reslicedimage(electrodematrix,anat.nii) to add
% electrodes in one nifti image file
[output,els,els_ind,outputStruct]=position2reslicedImage2(elecmatrix,'./data/anat.img');
outputStruct.fname=['./data/name_electrodes_surface_all'
int2str(filenummer) '.img' ];
spm_write_vol(outputStruct,output);
```

## 6) Visualize projected electrodes

Generate a cortex

```
gen_cortex_click('name',ip_parameter,sm_par);
```

- 'name' string with subject name
- ip\_parameter reflects amount of atrophy 0.2/0.4 is generally ok
- sm\_par reflects the amount of smoothing, 1 or 2 is nice.

Visualize electrodes

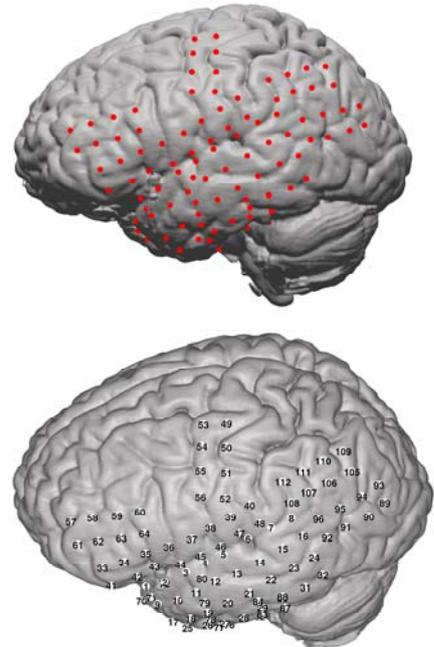
```
%load electrodes and surface
load(['./data/' subject '_cortex.mat']);
load(['./data/' subject
'_electrodes_surface_loc_all.mat']);
```

```
% make a surface rendering
ctmr_gauss_plot(cortex,[0 0 0],0)
```

```
% add electrodes in red, size 20
el_add(elecmatrix,'r',20);
```

```
% add electrode numbers
label_add(elecmatrix)
```

```
% loc_view to rotate brain
Loc_view(90,0) % left
Loc_view(270,0) % right
```



**Figure 6:** rendering with red electrodes (top) and numbers (bottom).

## 7) Copyright

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## 8) Content

ctmr.fig  
ctmr.m  
ctmr\_gauss\_plot.m  
el\_add.m  
electrodes2surf.m  
gen\_cortex\_click.m  
get\_mask.m  
hollow\_brain.m  
label\_add.m  
loc\_colormap.mat  
loc\_view.m  
manual ctmr gui.pdf  
master\_CTMR.m  
p\_zoom.m  
positiob2reslicedImage2.m  
sm\_filt.m  
sortElectrodes.m  
tripatch.m