DIPFIT and model co-registration

1. Co-register electrodes with model
2. Autofit, plot dipoles, fine fit
3. 3D headplot co-registration
Finding dipole locations using DIPFIT in EEGLAB
Co-register to model

Note: For EEG, check that the channel locations are on the surface of the head model (To do this: ‘Set head radius’ to about 85 in the channel editor).
Alternatively, warp to standard montage

Check to see that electrodes are correctly matched

stats toolbox required for warping
Check coregistration with model
Confirm electrode transformation

Head model (click to select)
- Spherical Four-Shell (BESA)
- Boundary Element Model (MNI)
- CTF MEG
- Custom model files

Head model file:
- lab/plugins/dipfit2.2/standard_BEM/standard_vol.mat

Output coordinates:
- lab/plugins/dipfit2.2/standard_BEM/standard_mm.mat

MRI file:
- plugins/dipfit2.2/standard_BEM/standard_mm.mat

Model template channel locations file:
- plugins/dipfit2.2/standard_BEM/samples/standard_1005.mnc

Co-register chan. locs. with head model:
- 0 -1.570796 108 30 93.05485

Channels to omit from dipole fitting:
- List

Note: For EEG, check that the channel locations are on the surface of the head model.
(To do this: 'Set head radius' to about 85 in the channel editor.)
Co-register to model, cont'd
Perform translation of electrode positions

- $\pi/2$
Perform translation of electrode positions

Requires a shift toward back of the head
AND
an expansion along the X-axis

shift backward
Perform translation of electrode positions

- Shift left
- Resize
EEG.dipfit structure

>> EEG.dipfit
ans =

    hdmfile: [1x76 char]
    mrifile: [1x71 char]
    chanfile: [1x83 char]
    chansel: [1x33 double]
    coordformat: 'spherical'
    model: [1x33 struct]
    current: 32
    vol: [1x1 struct]

    coord_transform: [0 0 -1.570796 100 76 90.87264 1 1 1]

From head model transformations
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Autofit equivalent dipoles
Plot dipoles
Scroll through dipoles
Fine fit options in DIPFIT
Fine fit menu

Component to fit: 6
Plot map
Residual variance = 3.21%

| dipole | fit | position     | moment       | Flip (in|cut)       |
|--------|-----|--------------|--------------|--------------|
| #1     | ☑   | 28.222  -2.401  37.331   | 2.380 475942.653 3819304.288        |               |
| #2     | ☐   | 0.000     0.000  0.000     | 0.000 0.000 0.000            | Flip (in|cut)      |

Symmetry constrain for dipole ...

Fit dipole(s)' position & moment  Or fit only dipole(s)' moment  Plot dipole(s)

Cancel  Help  Ok
Bilateral dipoles

Bilateral

Ambiguous

Manual dipole fit – pop_dipfit_nonlinear()

Component to fit: 6

Plot map

Residual variance = 1.23%

dipole  fit  position  moment
#1  ✓  -35.066 -32.492 -4.684  32721.382 46141.284 5880.224  Flip (in|out)
#2  ✓  -35.066 32.492 -4.684  005.419 -38050.427 14094.824  Flip (in|out)

Symmetry constrain for dipole ...

Fit dipola(s)' position & moment  Or fit only dipola(s)' moment  Plot dipola(s)

Cancel  Help  Ok
EEG.dipfit structure

>> EEG.dipfit.model
ans =

1x33 struct array with fields:
    posxyz
    momxyz
    rv
    active
    select

>> EEG.dipfit.model(1)
ans =
   X        Y        Z
    14.9791  -86.0094  47.9448

    posxyz: [1x3 double]
    momxyz: [1x3 double]
    rv: 0.0288
    active: 1
    select: 1
Localization of activity using Loreta
DIPFIT and model co-registration

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Plot scalp maps in 3D
Headplot co-registration

Go through co-registration in the same way as with dipfit co-registration.
Confirm headplot co-registration
Spline file in EEG structure

2D scalp map for IC 12

3D scalp map for IC 12
Exercise

• **Novice / Intermediate**
  – Load ‘stern_125.set’
  – Practice co-registering electrodes with **BEM** model (choose 'Erase' because this dataset has co-registration done already)
  – Autofit IC dipoles
  – Fine fit dipoles
  – Plot dipoles from the GUI; scroll through components individually
  – Co-register the head model for 3D scalp map plotting. Then plot some ICs in 3D

• **Advanced**
  - In the Finefit menu, try fitting a bilateral dipole, what happens to the residual variance?
  - Try plotting a subset of dipoles in 'summary mode'
  - Try purposely misaligning electrodes with model, how far off are the resulting dipoles from the original locations?