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## Channel locations and anatomical labelling for iEEG data

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To: Lionel Barnett <l.c.barnett@sussex.ac.uk>

Cc: Guillaume Corlouer <G.Corlouer@sussex.ac.uk>

Dear Lionel and Guillaume,

The coordinates that appear in the EEGLAB dataset are in MNI (to be more accurate, they are Talairach coordinates that were converted to MNI using the Jack Lancaster's transform (tal2icbm\_fsl.m). This conversion is not the most accurate one (so you can expect errors of up to ~10 mm).

The visualization tools in EEGLAB cannot deal with intracranial electrodes... they were developed for scalp EEG - and this is why you get this weird electrode location map.

Visualizing intracranial electrodes on top of the cortical surface is not so simple. There are many different ways to do it.

I use the method described [here](#), which is very similar, in principle, to the method described in the [iElvis toolbox](#) (except that we use SUMA to resample the cortical surface to the same number of vertices, thereby allowing us to establish node-to-node correspondence across brains of different subjects).

To make things much more simple for you guys - I can upload to the FTP the reconstructed (and re-sampled) [FreeSurfer](#) brains (stroke in struct array), and you can plot them in MATLAB using custom-developed routines that I'll send you (the code is pretty straightforward, mostly involving the surf.m function).

The location of each electrode after projection to the nearest site on the surface, is stored in another variable called "electrodes.mat". These locations are X,Y,Z coordinates reflecting the electrode position within the native MRI space of each patient (i.e. without any transformation, extracted directly from co-registered CT and MRI scans) - so it's much more accurate than MNI. You can also find there the electrodes'

anatomical labels taken from the [Desikan-Killiany atlas](#) (under the field [SUMAprojectedElectrodes.aparcaseg.elecByLabelMinDist.labels](#), the corresponding electrode names are stored in [SUMAprojectedElectrodes.elecNames](#)).

Since all brains were re-sampled to same number of vertices - any given site on one brain correspond to the exact same site on another brain (adhering to its location in relation to individual gyri and sulci). Thus, you can plot the electrodes from different patients on one brain serving as a template ("[fsaverage](#)"; uploaded to FTP)

Everything will be much clearer after you'll play a little with the data. If you need further explanations we can set a WhatsApp meeting.

For starters, I uploaded a representative example (AnRa's brain) and a basic visualization code (in the folder "plot\_brain\_example\_code"). The main script is: "plot\_FS\_basic\_call\_script\_example\_code.m" (but you will need to add the relevant path)  
Let me know if you have any questions.

Regarding your second question - the answer is no, the resting state was with eyes closed.

Best  
Itzik