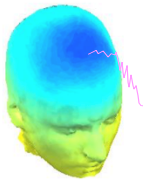
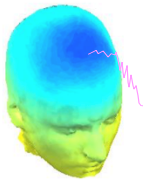


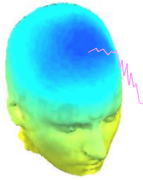
Advanced Scripting in EEGLAB

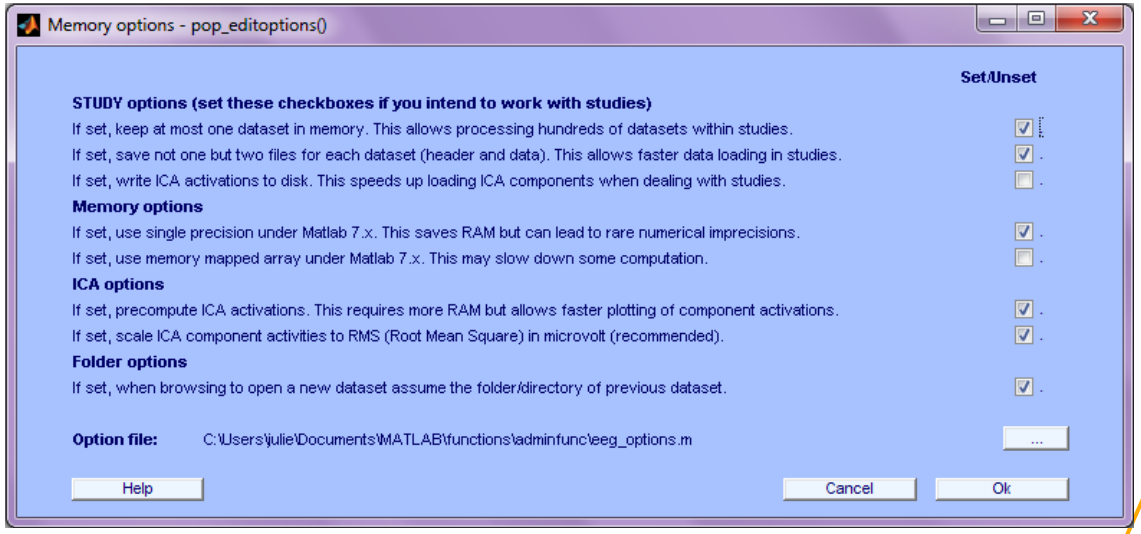


…/eeglab/functions/miscfunc

- compile_eeglab.m
- corrimage.m
- eeg_regepochs.m
- eegmovie.m
- fastregress.m
- fieldtrip2eeglab.m
- fillcurves.m
- tftopo.m
- …

STUDY scripts



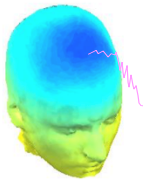


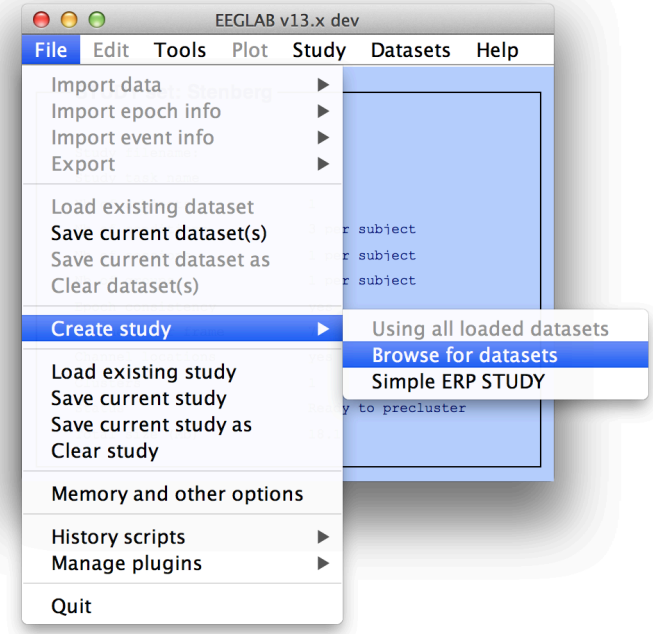
Most important option:

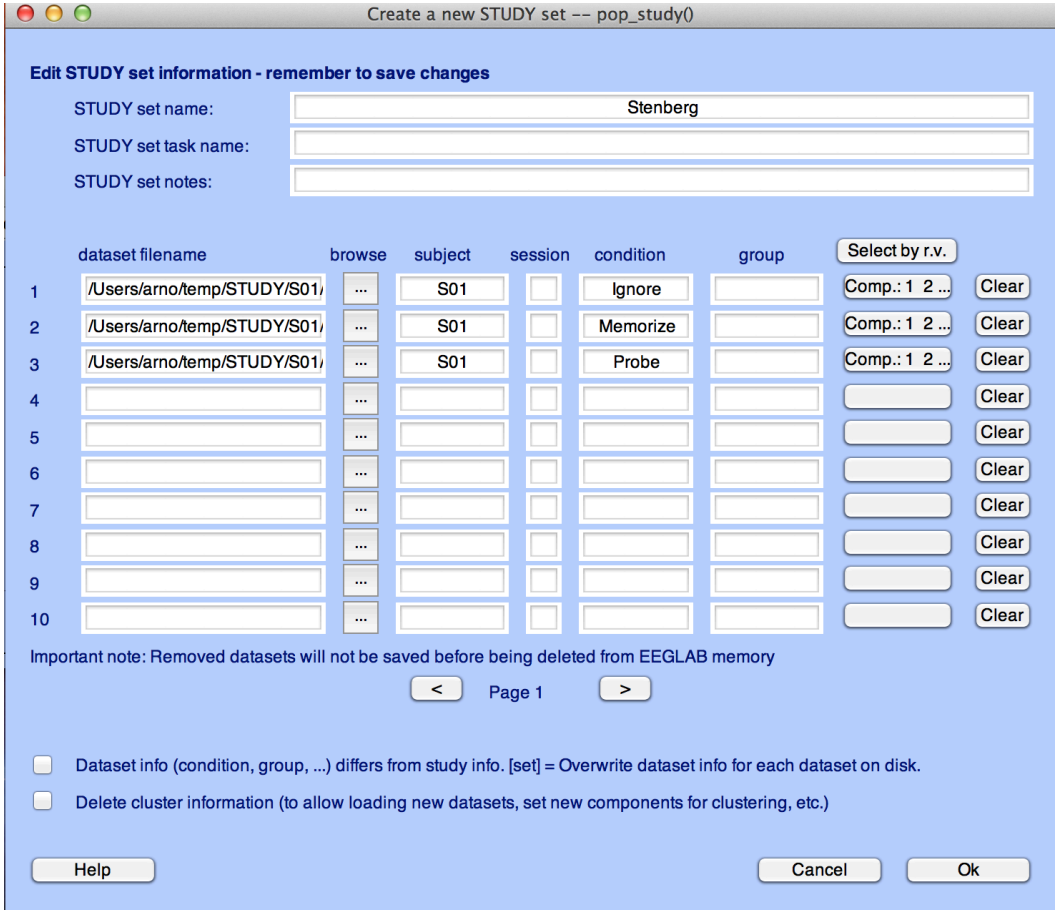
- Allows only one dataset to be loaded at once.
- Most STUDYs are too big to have all data loaded at once.

```
% Set memory options:
pop_editoptions( 'option_storedisk', 1);
```

Edit dataset info

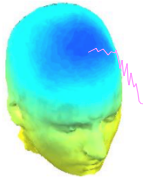


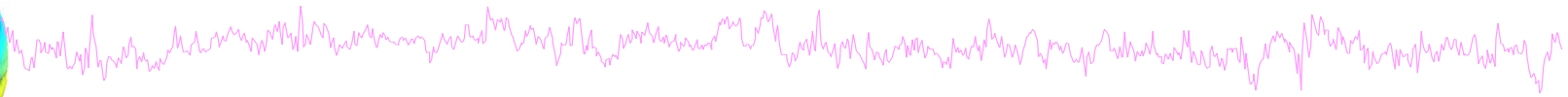





```
[STUDY ALLEEG] = std_editset( STUDY, ALLEEG, 'name','Stenberg','commands',{{'index' 1
'load' '/data/STUDY/S01/Ignore.set'} {'index' 2 'load' '/data/S01/Memorize.set'}
{'index' 3 'load' '/data/S01/Probe.set'} {'index' 1 'subject' 'S01'} {'index' 2
'subject' 'S01'} {'index' 3 'subject' 'S01'} {'index' 1 'condition' 'Ignore'} {'index' 2
'condition' 'Memorize'} {'index' 3 'condition' 'Probe'}},'updatedat','off' );
```

Looking a the function that create STUDY

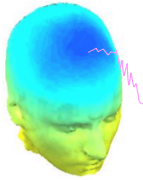


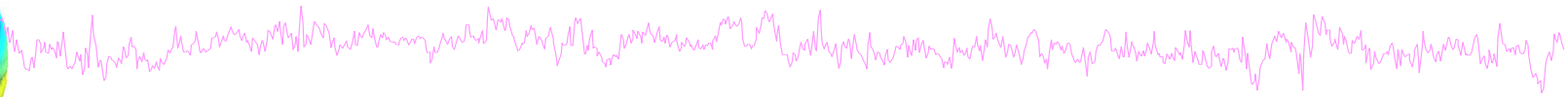


```
[STUDY ALLEEG] = std_editset( STUDY, ALLEEG, 'name','Stenberg','commands',
     {{'index' 1 'load' '/data/STUDY/S01/Ignore.set'} …
     {'index' 2 'load' '/data/S01/Memorize.set'} …
     {'index' 3 'load' '/data/S01/Probe.set'} …
     {'index' 1 'subject' 'S01'} …
     {'index' 2 'subject' 'S01'} …
     {'index' 3 'subject' 'S01'} …
     {'index' 1 'condition' 'Ignore'} …
     {'index' 2 'condition' 'Memorize'} …
     {'index' 3 'condition' 'Probe'}},'updatedat','off' );
```

```
[STUDY ALLEEG] = std_editset( STUDY, ALLEEG, 'name','Stenberg','commands',
     {{'index' 1 'load' '/data/STUDY/S01/Ignore.set' 'subject' 'S01' 'condition' 'Ignore'} …
     {'index' 2 'load' '/data/S01/Memorize.set' 'subject' 'S01' 'condition' 'Memorize'} …
     {'index' 3 'load' '/data/S01/Probe.set' 'subject' 'S01' 'condition' 'Probe'} …
     },'updatedat','off' );
```

Exercice





```
[STUDY ALLEEG] = std_editset( STUDY, ALLEEG, 'name','Stenberg','commands',
     {{'index' 1 'load' '/data/STUDY/S01/Ignore.set' 'subject' 'S01' 'condition' 'Ignore'} …
     {'index' 2 'load' '/data/S01/Memorize.set' 'subject' 'S01' 'condition' 'Memorize'} …
     {'index' 3 'load' '/data/S01/Probe.set' 'subject' 'S01' 'condition' 'Probe'} …
     },'updatedat','off' );
```

1- Start EEGLAB and import the 3 datasets for Subject 1 (Ignore.set, Memorize.set and Probe.set) in a STUDY (menu Tools > Create STUDY > Browse for datasets)

2- Look in the history

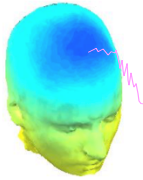
3- Copy to a script, add “eeglab redraw” at the end of your script

4- Restart Matlab, execute the script, look at your STUDY info and design (menu *STUDY* > *Edit STUDY* info and *STUDY* > *Select/Edit STUDY design*)

5- Modify the script to import subject 1 to 4

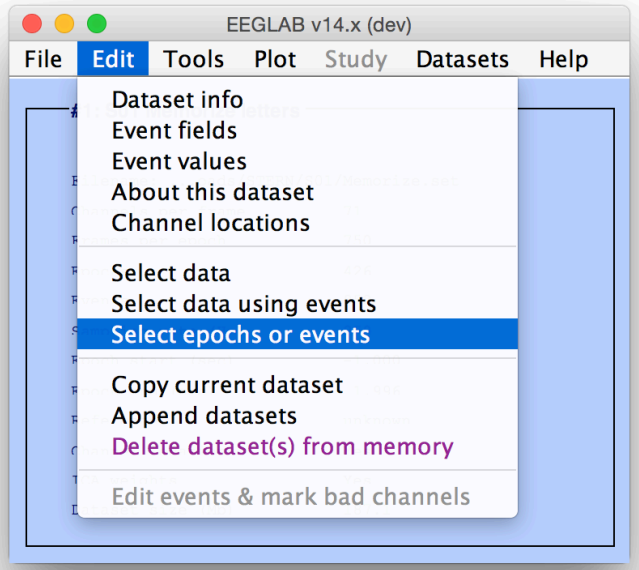
6- Restart Matlab, execute the script, look at your STUDY info and design

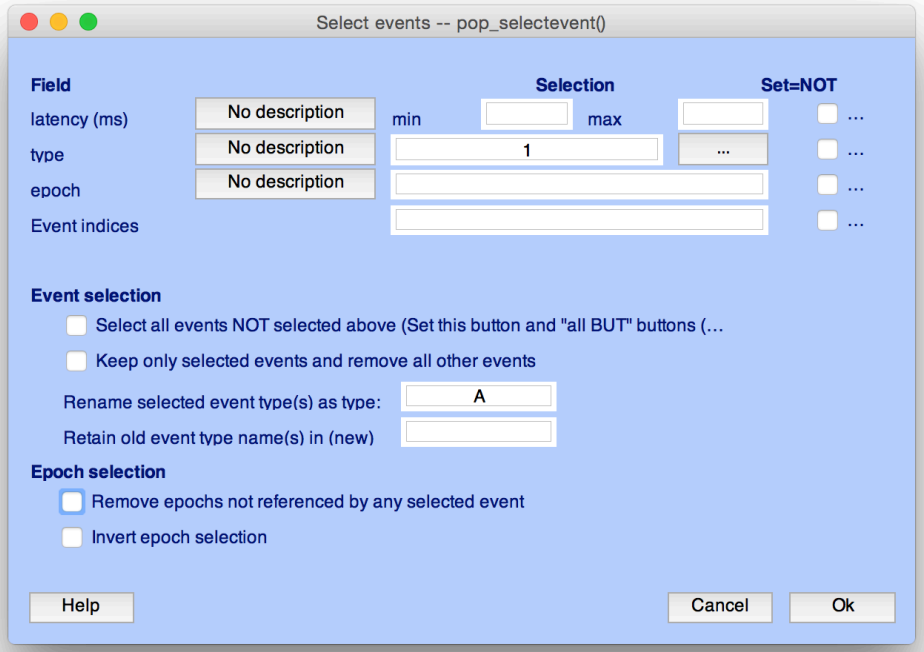
Redefining events



Adjusting latencies

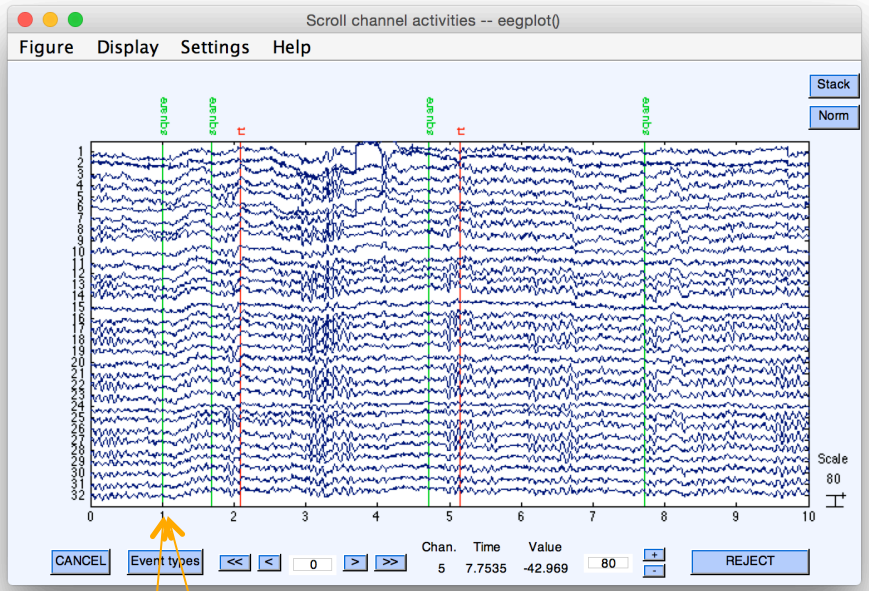
```
for iEvent = 1:length(EEG.event)
    % shift by 16 samples (or 53.3ms at 200Hz) due to filter delay
    EEG.event(iEvent).latency = EEG.event(iEvent).latency + 16;
end;
EEG.saved = 'no';
[ALLEEG EEG CURRENTSET] = eeg_store(ALLEEG, EEG);
eeglab redraw
```

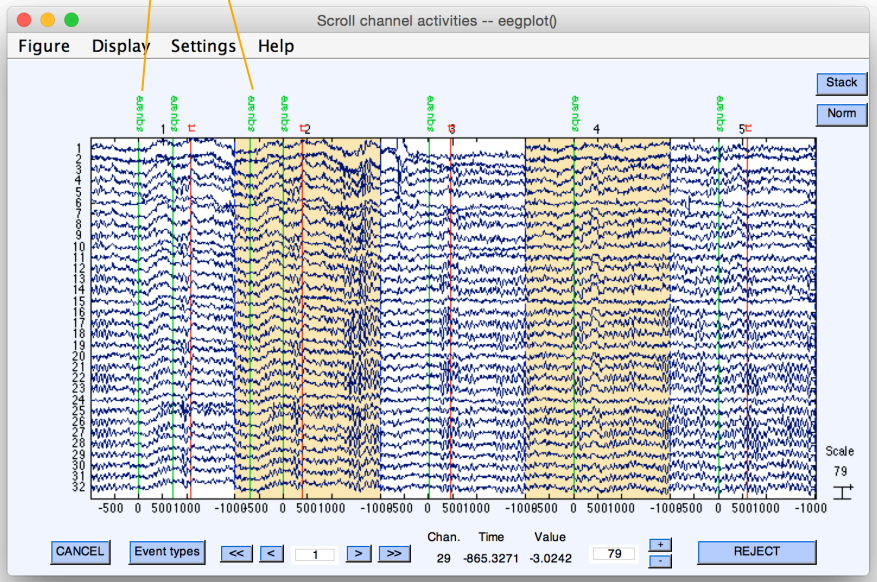




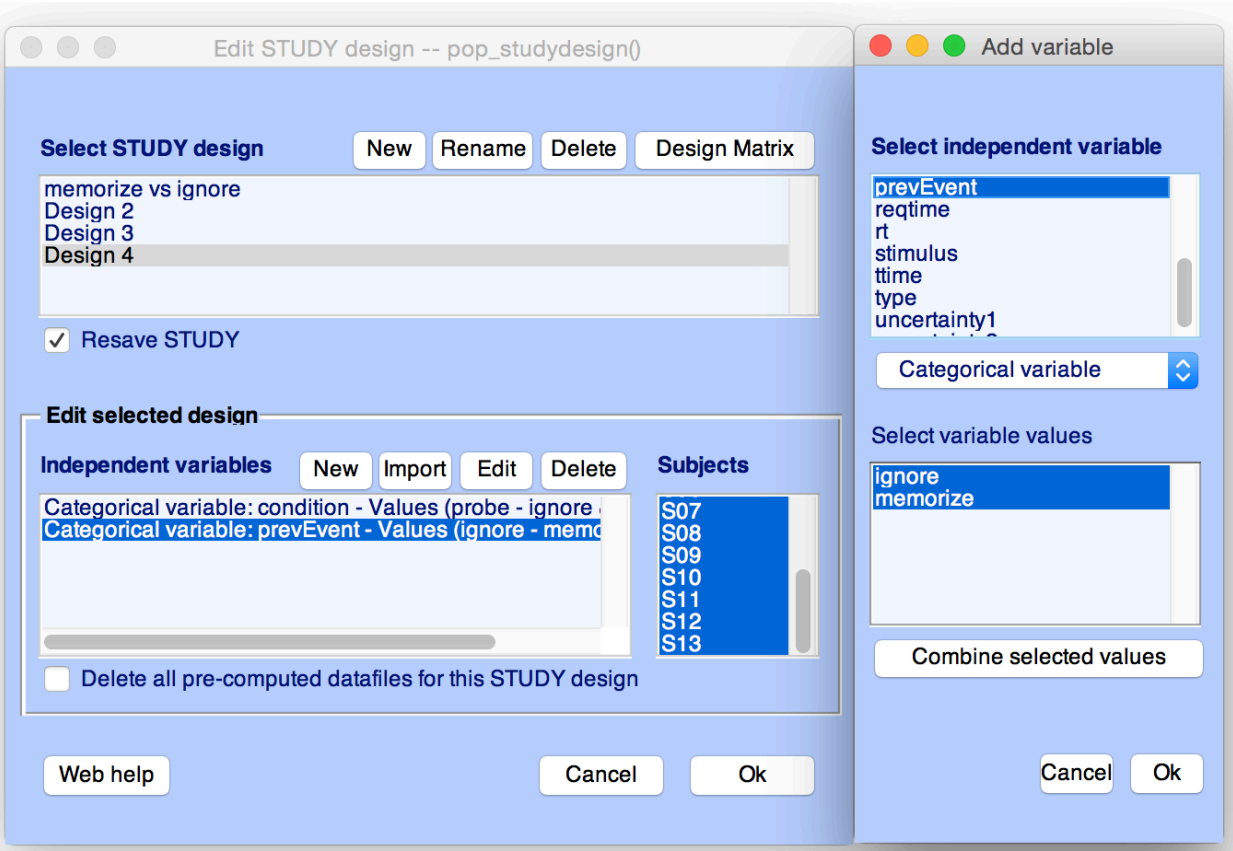
Renaming events

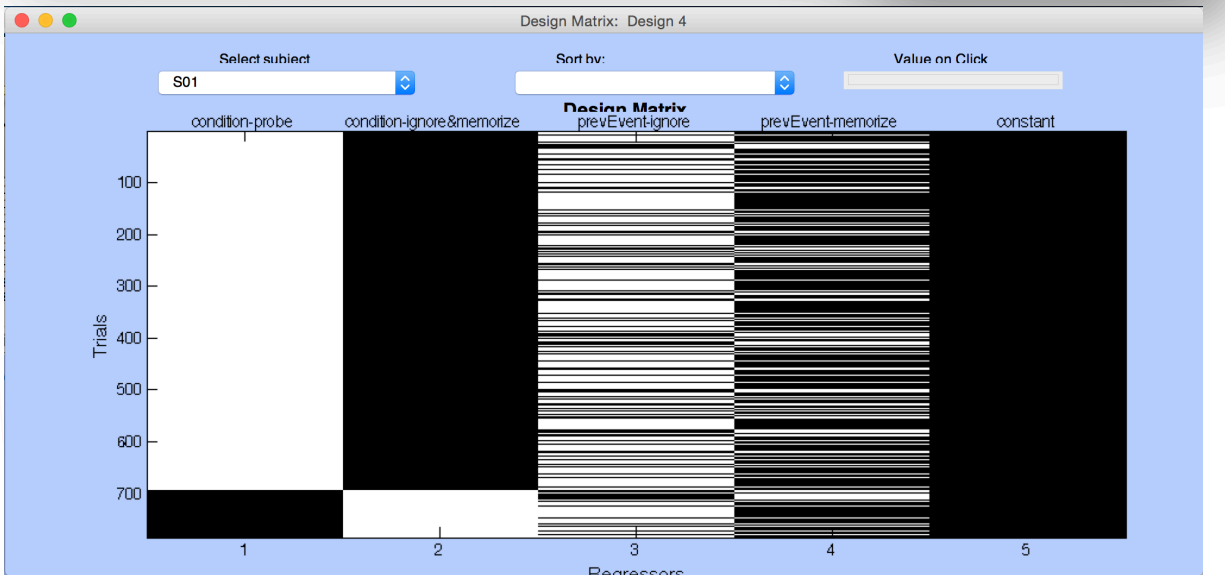
```
for iEvent = 1:length(EEG.event)
    % rename events
    EEG = pop_selectevent( EEG, 'type',1,'renametype','A','deleteevents','off');
    EEG = pop_selectevent( EEG, 'type',2,'renametype','B','deleteevents','off');
    EEG = pop_selectevent( EEG, 'type',3,'renametype','C','deleteevents','off');
    EEG = pop_selectevent( EEG, 'type',4,'renametype','D','deleteevents','off');
    EEG = pop_selectevent( EEG, 'type',8,'renametype','rt','deleteevents','off');
end;
EEG.saved = 'no';
[ALLEEG EEG CURRENTSET] = eeg_store(ALLEEG, EEG);
eeglab redraw
```



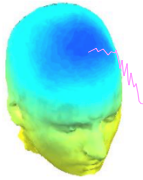



```
EEG.event(4)
        type: 'square'
    position: 2
     latency: 424
     urevent: 1
       epoch: 2

EEG.event(1)
        type: 'square'
    position: 2
     latency: 129
     urevent: 1
       epoch: 1

EEG.urevent(1)
        type: 'square'
    position: 2
     latency: 129
```


Edit STUDY design -- pop_studydesign()
Select STUDY design
New
Rename
Delete
Design Matrix
memorize vs ignore
Design 2
Design 3
Design 4
Resave STUDY
Edit selected design
Independent variables
New
Import
Edit
Delete
Categorical variable: condition - Values (probe - ignore
Categorical variable: prevEvent - Values (ignore - memo
Subjects
S07
S08
S09
S10
S11
S12
S13
Delete all pre-computed datafiles for this STUDY design
Web help
Cancel
Ok
Add variable
Select independent variable
prevEvent
reqtime
rt
stimulus
ttime
type
uncertainty1
Categorical variable
Select variable values
ignore
memorize
Combine selected values
Cancel
Ok


Design Matrix: Design 4
Select subject
S01
Sort by:
Value on Click
Design Matrix
condition-probe
condition-ignore&memorize
prevEvent-ignore
prevEvent-memorize
constant
Trials
100
200
300
400
500
600
700
1
2
3
4
5
Regressors

Exercice - Redefining events

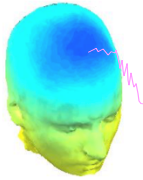


```
for iDat = 1:length(ALLEEG)
    TMPEEG = eeg_checkset(ALLEEG(iDat), 'loaddata'); % load data

    % 'B'  'C'  'D'  'F'  'G'  'H'  'J'  'K'  'L' ... -> Memorize
    % 'gB' 'gC' 'gD' 'gF' 'gG' 'gH' 'gJ' 'gK' 'gL' ... -> Ignore
    for iEvent = 1:length(TMPEEG.event)
          ... prevEvent = TMPEEG.event(iEvent).urevent-2;
        if ...  prevEvent > 2 && TMPEEG.urevent(prevEvent).type(1) == 'g'
             TMPEEG.event(iEvent).prevEvent = 'ignore';
        else TMPEEG.event(iEvent).prevEvent = 'memorize';
        end;
    end;

    TMPEEG.saved = 'no'; % tag as not saved
    pop_saveset(TMPEEG, 'savemode', 'resave'); % resave data
end;

STUDY = std_maketrialinfo(STUDY, ALLEEG); % update STUDY
STUDY.saved = 'no';
[STUDY EEG] = pop_savestudy( STUDY, EEG, 'savemode', 'resave'); % resave STUDY
```

This is the correct way to do it! Editing the single trial information in *STUDY.datasetinfo(x).trialinfo* breaks the consistency with datasets.

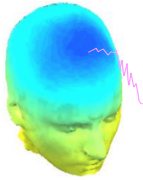
Precomputed files need to be recomputed after changing events.

Load dataset info from commandline



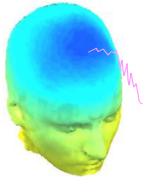
```
% Create Stern STUDY
[ALLEEG EEG CURRENTSET ALLCOM] = eeglab;
pop_editoptions( 'option_storedisk', 1);
subjects = {'S01' 'S02' 'S03' 'S04' 'S05' 'S06' 'S07' 'S08' 'S09' 'S10' 'S11' 'S12'};
filepath = '/Users/arno/temp/STUDY'; % XXXXX Change path here XXXXX
if ~exist(filepath), error('You need to change the path to the STUDY'); end;
commands = {}; % initialize STUDY dataset list

% Loop through all of the subjects in the study to create the dataset
for loopnum = 1:length(subjects) %for each subject
    IgnoreFile   = fullfile(filepath, subjects{loopnum}, 'Ignore.set');
    MemorizeFile = fullfile(filepath, subjects{loopnum}, 'Memorize.set');
    ProbeFile    = fullfile(filepath, subjects{loopnum}, 'Probe.set');
    commands = {commands{:} ...
        {'index' 3*loopnum-2 'load' IgnoreFile   'subject' subjects{loopnum} 'condition' 'Ignore'} ...
        {'index' 3*loopnum-1 'load' MemorizeFile 'subject' subjects{loopnum} 'condition' 'Memorize'} ...
        {'index' 3*loopnum   'load' ProbeFile    'subject' subjects{loopnum} 'condition' 'Probe'}};
end;
% Uncomment the line below to select ICA components with less than 15% residual variance
% commands = {commands{:} {'dipselect', 0.15}};
[STUDY, ALLEEG] = std_editset(STUDY, ALLEEG, 'name','Sternberg','commands',commands,'updatedat','on');

% Update workspace variables and redraw EEGLAB
CURRENTSTUDY = 1; EEG = ALLEEG; CURRENTSET = [1:length(EEG)];
[STUDY, ALLEEG] = std_checkset(STUDY, ALLEEG);
eeglab redraw
```

STUDY structure



```
STUDY =
            name: 'Sternberg'
            task: 'Sternberg'
     datasetinfo: [1x39 struct]
           notes: ''
        filename: 'stern.study'
        filepath: 'C:\Users\julie\Documents\Workshops\Finland\STUDY'
         history: [1x7332 char]
         subject: {1x13 cell}
           group: {''}
         session: []
       condition: {'ignore'  'memorize'  'probe'}
          setind: [3x13 double]
             etc: [1x1 struct]
        preclust: [1x1 struct]
         cluster: [1x1 struct]
         changrp: [1x71 struct]
           saved: 'yes'
```

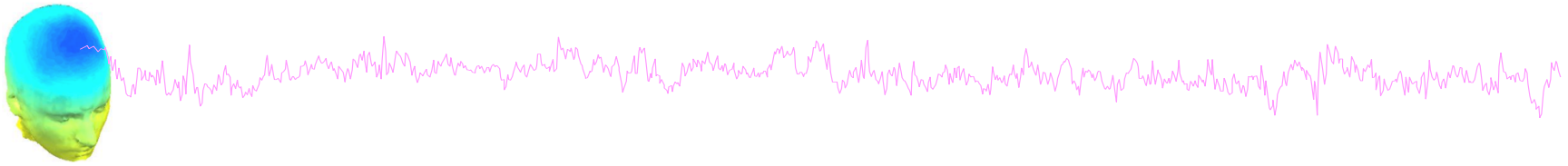
Understanding STUDY structure

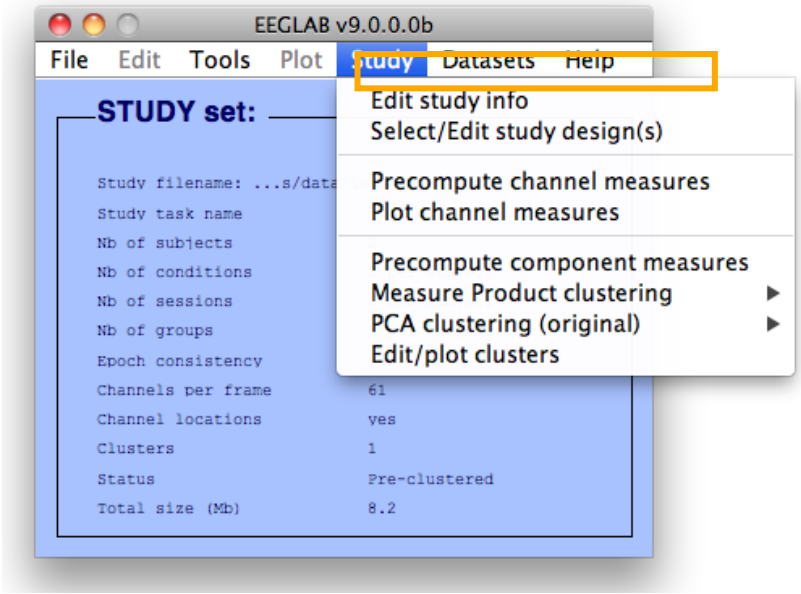


```
>> STUDY.datasetinfo(11) % access dataset 11
ans =
       filepath: [1x61 char]
      filename: 'S04.set'
       subject: 'S04'
       session: []
     condition: ''
         group: ''
     trialinfo: 1x350 struct
         index: 11
         comps: [1x24 double]
```

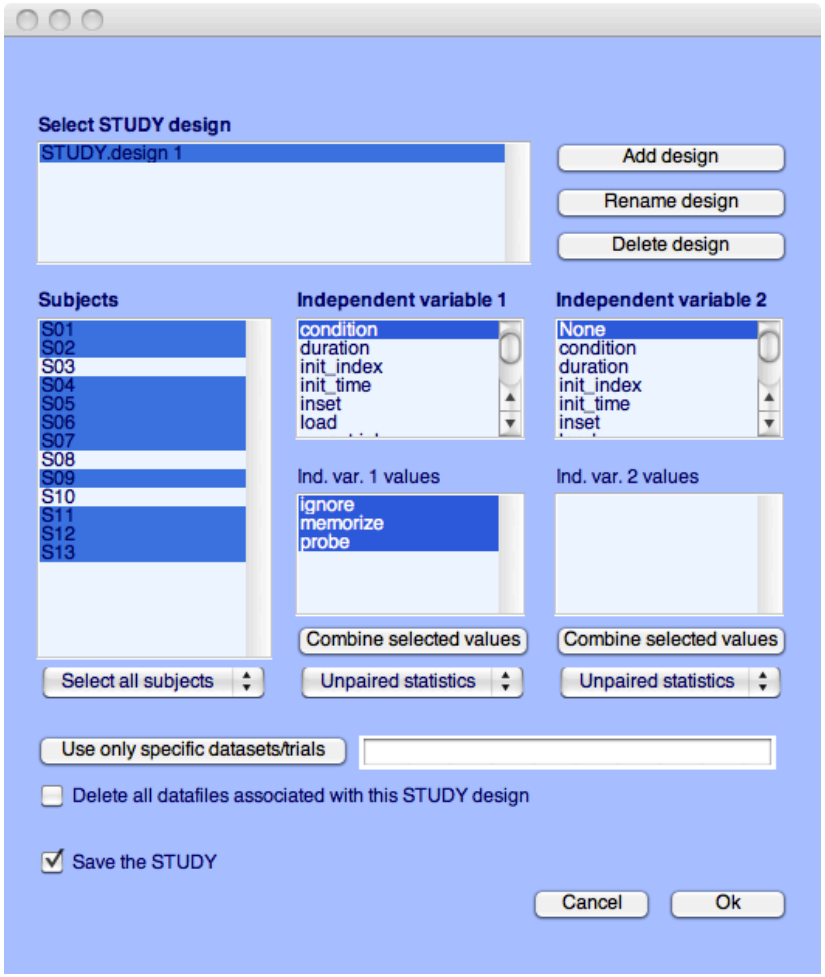
Subject 4!

```
>> trialinfo(163) % access trial 163
ans =
       stimtype: 'Memorize'
        latency: 13201
       duration: 0
       ...
```



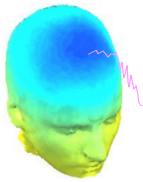


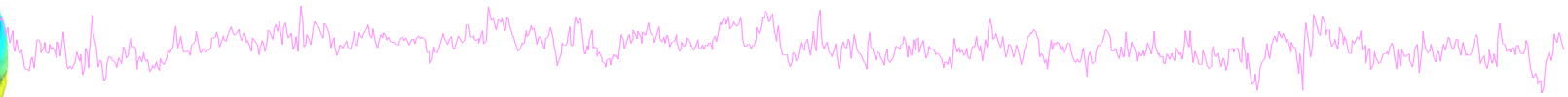
Select subjects




```
STUDY = std_makedesign(STUDY, ALLEEG, 3,
'variable1','condition',
'variable2','',
'name','Design 3',
'values1',{'ignore' 'memorize' 'probe'},
'subjselect',{'S02' 'S03'},
'dataselect',{'condition' {'probe'}});
```

STUDY design structure



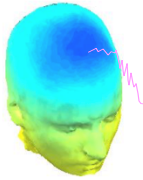


```
STUDY.design(1)

ans =

           name: 'Design 1 - compare letter types'
       variable: [1x2 struct]
          cases: [1x1 struct]
        include: {}
          cells: [1x39 struct]
```

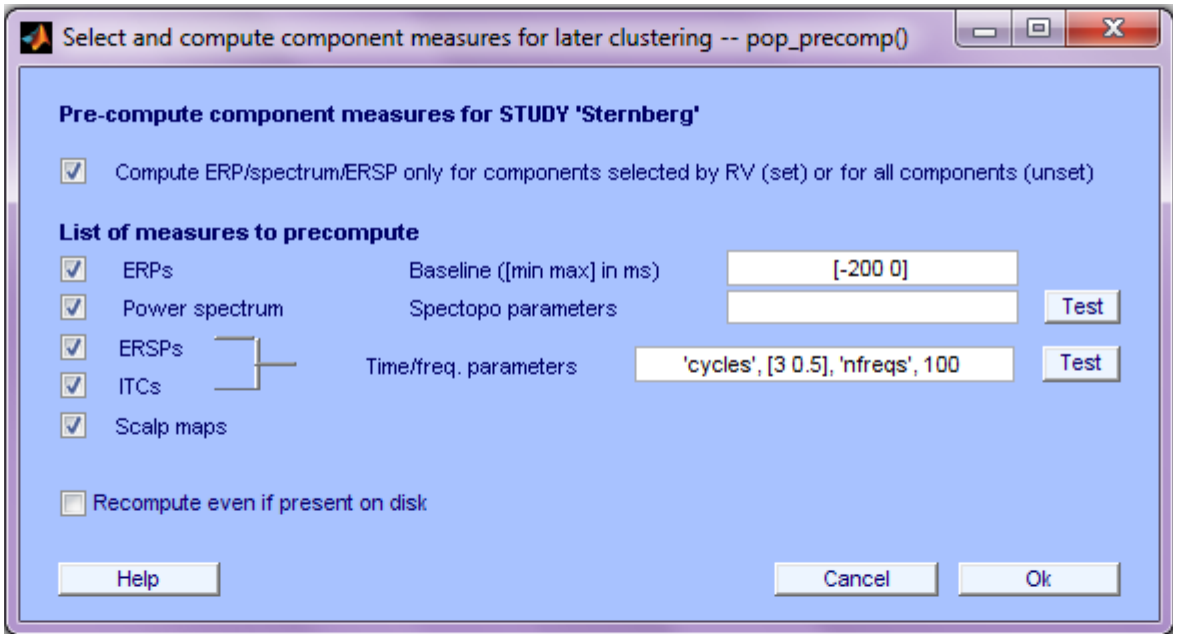
Exploding the contents of each of these sub-structures, we obtain

```
           name: 'Design 1 - light and audio all subjects'

       variable: [1x2 struct]
            (1).label   : 'condition'
            (1).pairing: 'on'
            (1).value   : {'ignore'  'memorize'  'probe'}
            (2).label   : ''
            (2).pairing: 'off'
            (2).value   : {}

         cases: [1x1 struct]
            label: 'subject'
            value: {'S01'  'S02'  'S03'  'S04'  'S05'  'S06' }
```

Precompute data measures

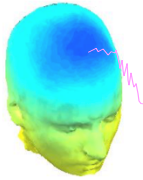


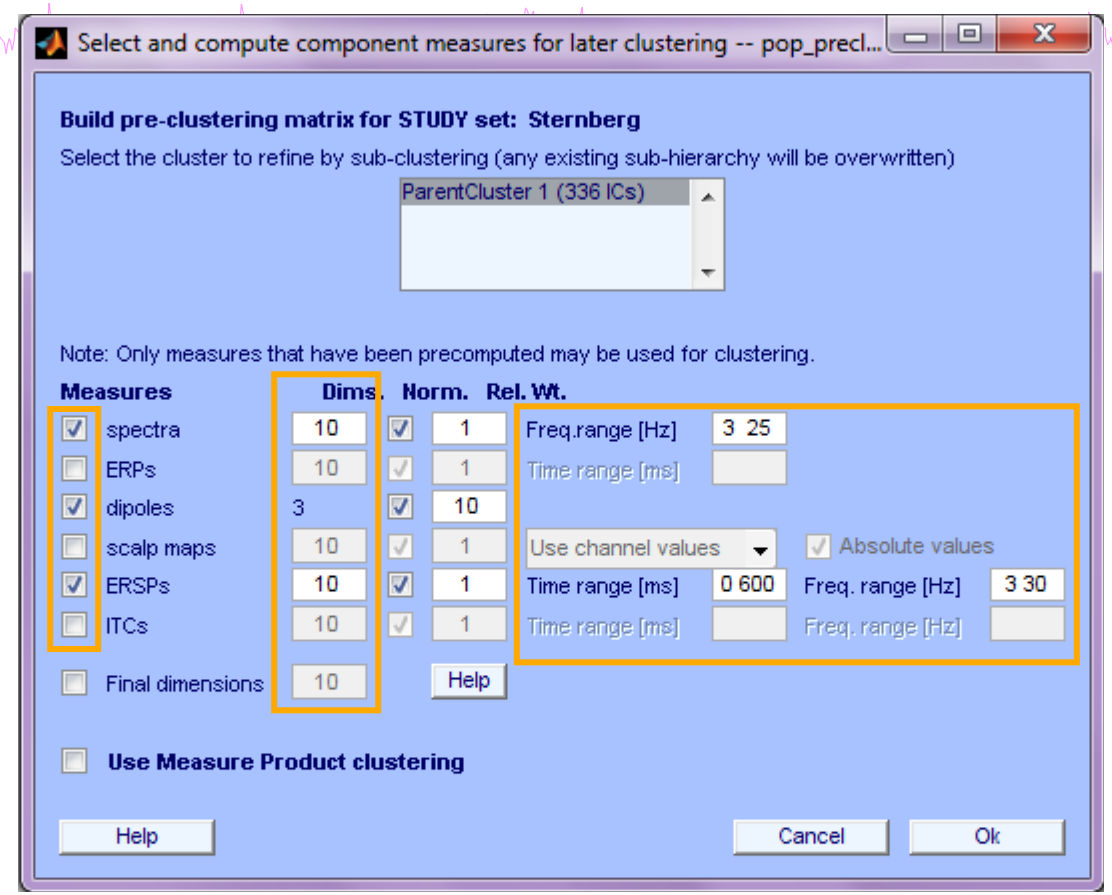
TIP: Compute all measures so you can test different combinations for clustering




```
[STUDY ALLEEG] = std_precomp(STUDY, ALLEEG, 'components', 'erp', ...
'on', 'rmbase',[-200 0] , 'scalp', 'on', 'spec', 'on', ...
'specparams',{}, 'ersp', 'on', 'erspparams', {'cycles' [3 0.5] ...
'nfreqs',100, 'freqs',[3 70] }, 'itc', 'on');
```

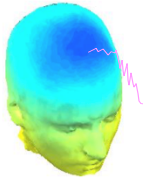
Precluster the data

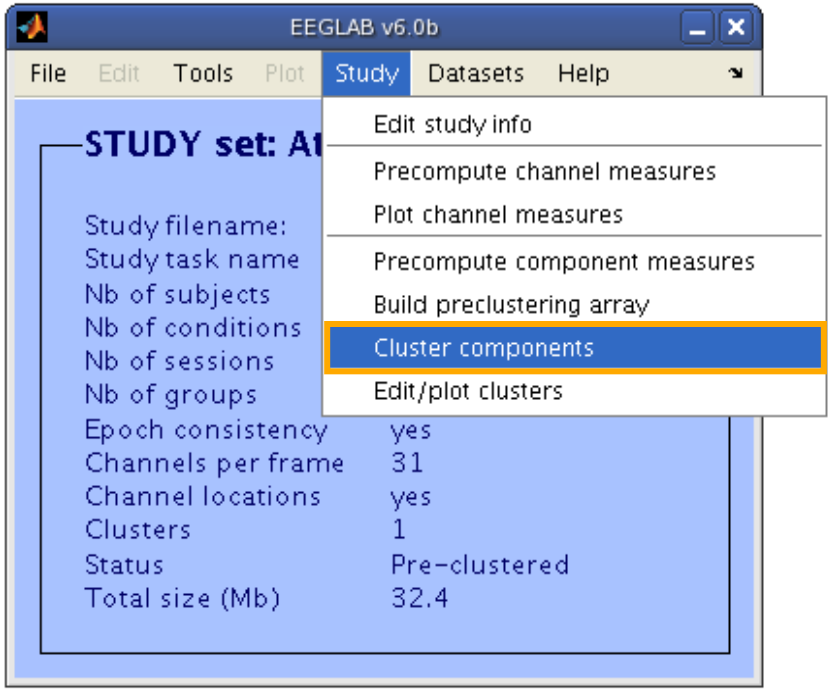


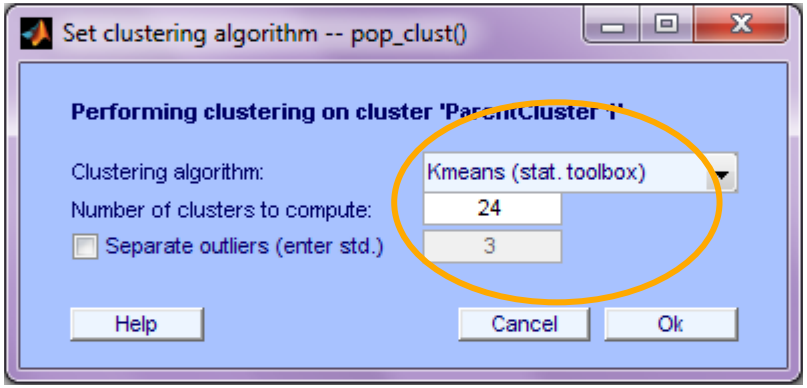



```
parentclust = 1;
[STUDY ALLEEG] = std_preclust(STUDY, ALLEEG, parentclust,{'spec','npca',5,…
   'norm',1,'weight',1,'freqrange',[3 25]},{'erp','npca',6,'norm',1,…
   'weight',1, 'timewindow',[0 400]},{'scalp','npca',10,'norm',1,'weight',1,…
   'abso',1},{'dipoles','norm',1,'weight',10},{'ersp','npca',20,…
   'freqrange',[3 30] ,'timewindow',[0 600],'norm',1,'weight',1},{'itc',…
   'npca',6,'freqrange',[3 30],'timewindow',[0 400] , 'norm',1, 'weight',1});
```

Cluster components

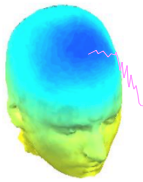


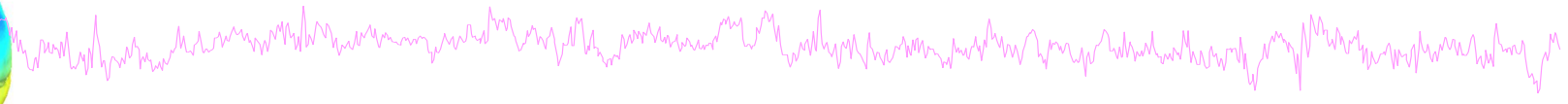





```
nclusts = 24; % choose # of clusters to create
[STUDY] = pop_clust(STUDY, ALLEEG,'algorithm','kmeans','clus_num',nclusts);
```

Understanding STUDY structure





26 = # of clusters

```
>> STUDY.cluster
1x26 struct array with fields:
    parent
    name
    child
    comps
    sets
    algorithm
    preclust
    dipole
    allinds
    setinds
```

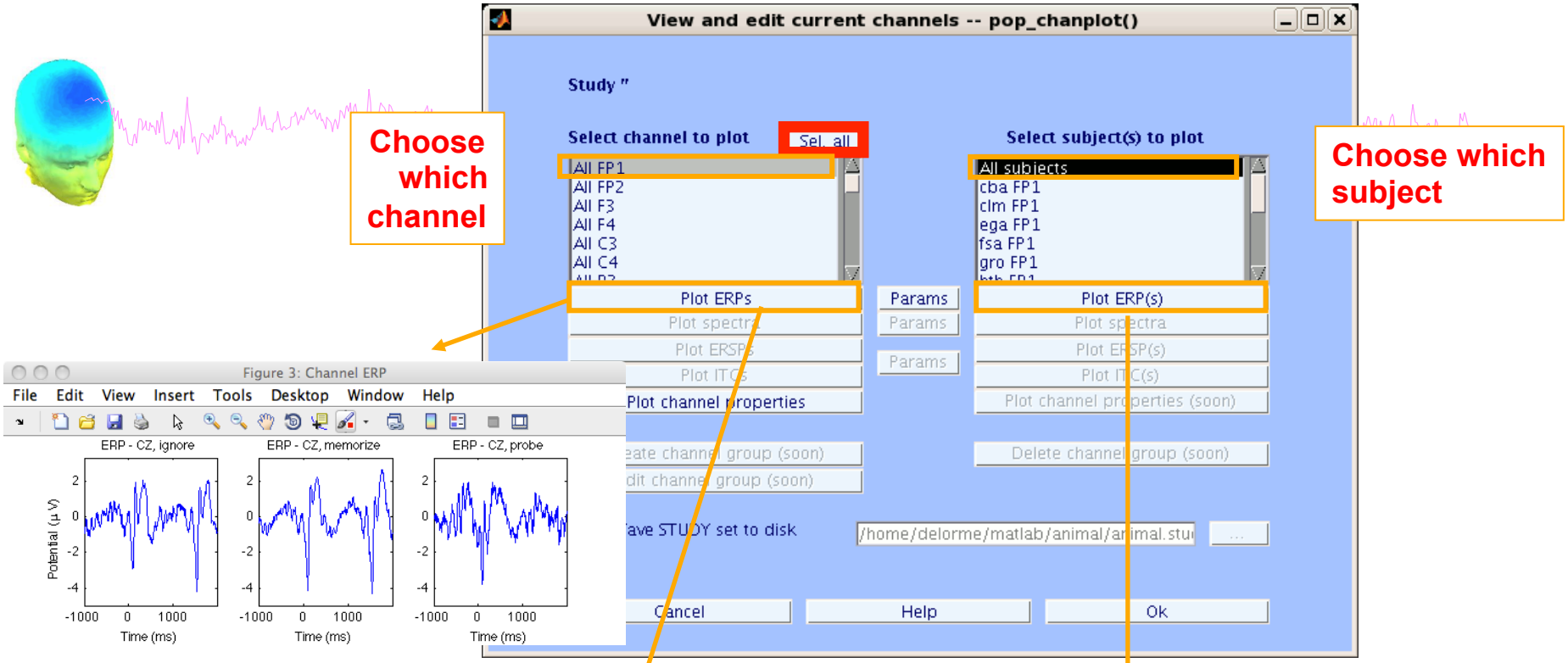
One cluster:

```
>> STUDY.cluster(6)
ans =
       parent: {'ParentCluster 1'}
         name: 'Cls 6'
        child: []
        comps: [35 7 12 35 10 23 7 30 4 …]
         sets: [1 2 3 4 5 6 7 8 9 10 1 2 …]
    algorithm: {'Kmeans'  [24]}
     preclust: [1x1 struct]
       dipole: [1x1 struct]
```

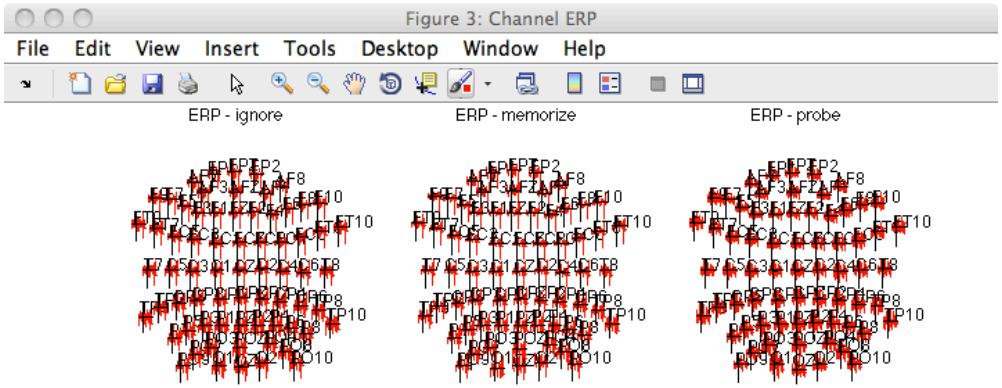
6 = cluster index

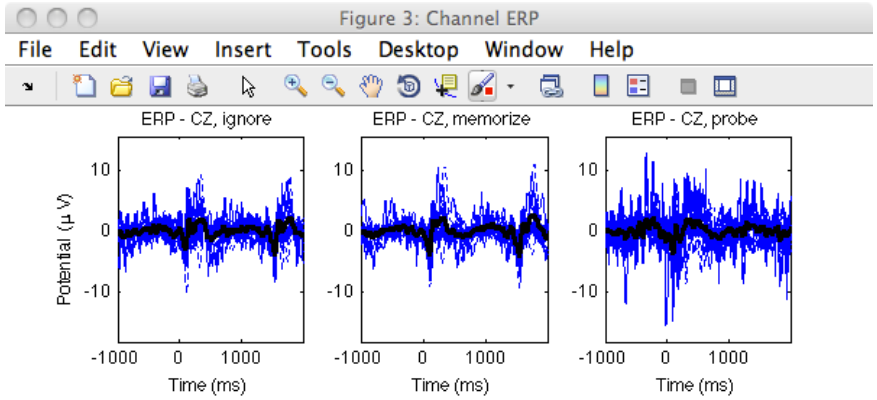
IC indices

dataset indices for ICs



STUDY = std_erpplot(STUDY,ALLEEG,'channels',{'FP1'});



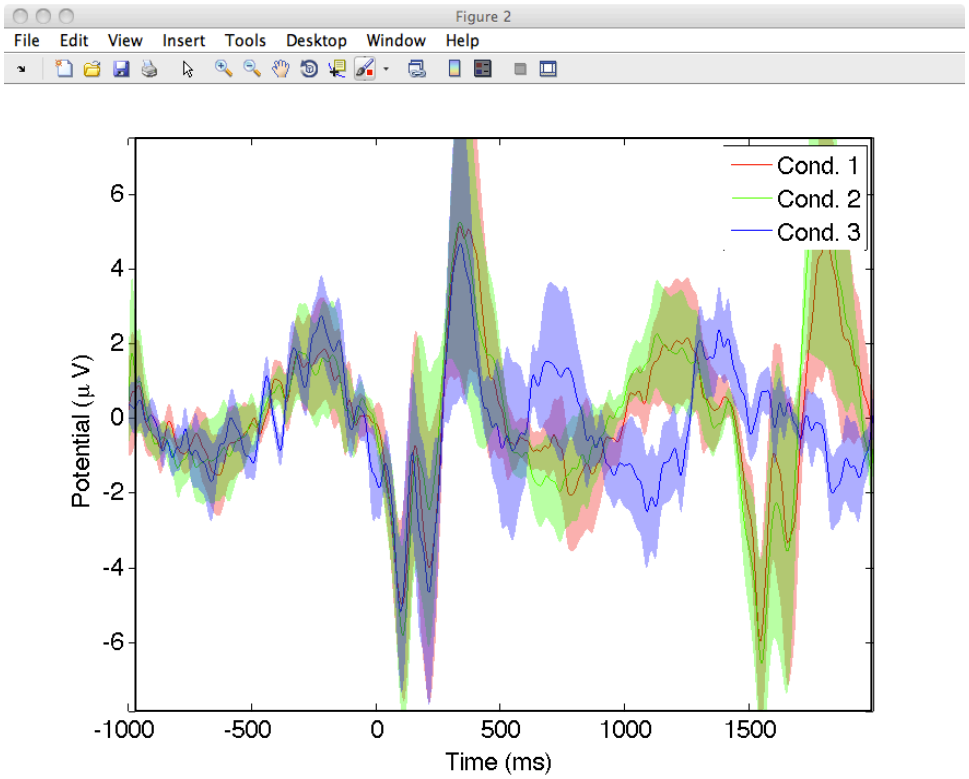


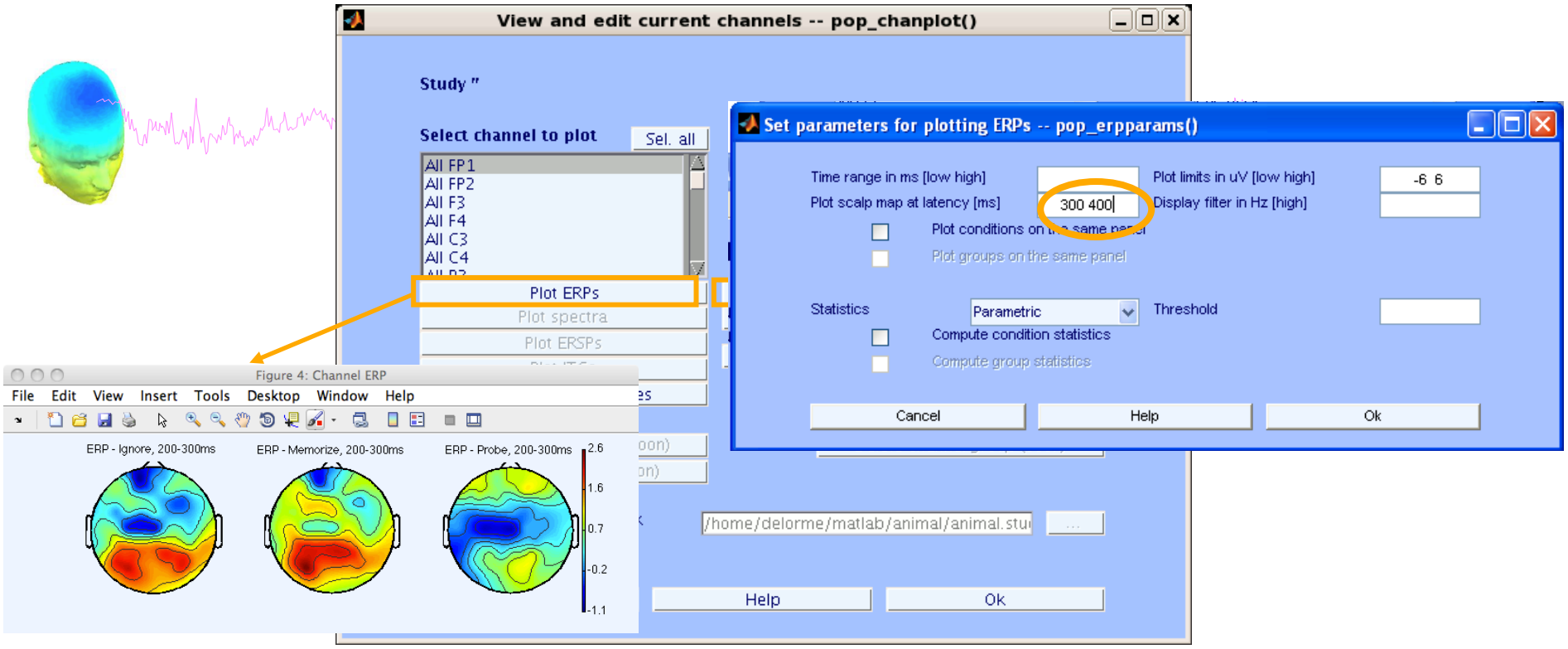
STUDY = std_erpplot(STUDY,ALLEEG,'channels',{'FP1' … });

STUDY = std_erpplot(STUDY,ALLEEG,'channels',{'FP1'}, 'plotsubjects', 'on');

Advanced plotting features

```
STUDY = std_erpplot(STUDY,ALLEEG,'channels',{'CZ'});
std_plotcurve(STUDY.changrp(39).erptimes,
   STUDY.changrp(39).erpdata,  'plotconditions',
   'together', 'plotstderr', 'on', 'filter', 30);
```





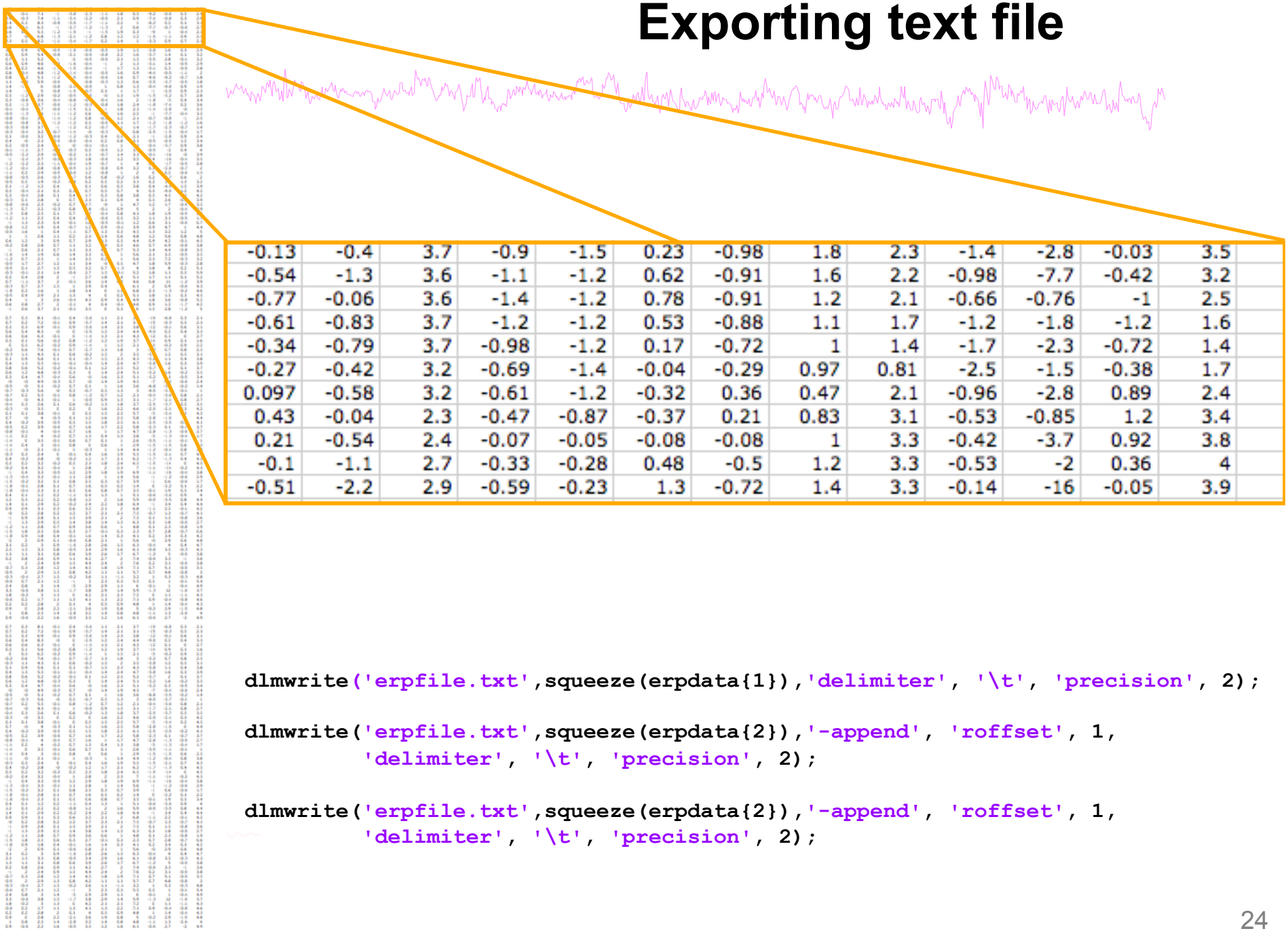

```
STUDY = std_erpplot(STUDY,ALLEEG, 'topotime',[200 300] , 'channels',{'OZ' 'O2' 'FP1' 'FPZ' 'FP2'});
[STUDY erpdata ] = std_erpplot(STUDY,ALLEEG, , 'topotime',[200 300] , 'channels',{'OZ' 'O2'});
```

Exporting to excell file

```
[1x67x13 double]
[1x67x13 double]
[1x67x13 double]
```

```
xlswrite('myxlsfile',squeeze(erpdata{1}),1);
xlswrite('myxlsfile',squeeze(erpdata{2}),2);
xlswrite('myxlsfile',squeeze(erpdata{3}),3);
```

Exporting text file



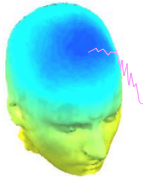
-0.13	-0.4	3.7	-0.9	-1.5	0.23	-0.98	1.8	2.3	-1.4	-2.8	-0.03	3.5
-0.54	-1.3	3.6	-1.1	-1.2	0.62	-0.91	1.6	2.2	-0.98	-7.7	-0.42	3.2
-0.77	-0.06	3.6	-1.4	-1.2	0.78	-0.91	1.2	2.1	-0.66	-0.76	-1	2.5
-0.61	-0.83	3.7	-1.2	-1.2	0.53	-0.88	1.1	1.7	-1.2	-1.8	-1.2	1.6
-0.34	-0.79	3.7	-0.98	-1.2	0.17	-0.72	1	1.4	-1.7	-2.3	-0.72	1.4
-0.27	-0.42	3.2	-0.69	-1.4	-0.04	-0.29	0.97	0.81	-2.5	-1.5	-0.38	1.7
0.097	-0.58	3.2	-0.61	-1.2	-0.32	0.36	0.47	2.1	-0.96	-2.8	0.89	2.4
0.43	-0.04	2.3	-0.47	-0.87	-0.37	0.21	0.83	3.1	-0.53	-0.85	1.2	3.4
0.21	-0.54	2.4	-0.07	-0.05	-0.08	-0.08	1	3.3	-0.42	-3.7	0.92	3.8
-0.1	-1.1	2.7	-0.33	-0.28	0.48	-0.5	1.2	3.3	-0.53	-2	0.36	4
-0.51	-2.2	2.9	-0.59	-0.23	1.3	-0.72	1.4	3.3	-0.14	-16	-0.05	3.9

```
dlmwrite('erpfile.txt',squeeze(erpdata{1}),'delimiter', '\t', 'precision', 2);

dlmwrite('erpfile.txt',squeeze(erpdata{2}),'-append', 'roffset', 1,
         'delimiter', '\t', 'precision', 2);

dlmwrite('erpfile.txt',squeeze(erpdata{2}),'-append', 'roffset', 1,
         'delimiter', '\t', 'precision', 2);
```

STUDY Script

```
% Create Stern STUDY
[ALLEEG EEG CURRENTSET ALLCOM] = eeglab;
pop_editoptions( 'option_storedisk', 1);
subjects = {'S01' 'S02' 'S03' 'S04' 'S05' 'S06' 'S07' 'S08' 'S09' 'S10' 'S11' 'S12'};
filepath = '/Users/arno/temp/STUDY'; % XXXXX Change path here XXXXX
if ~exist(filepath), error('You need to change the path to the STUDY'); end;
commands = {}; % initialize STUDY dataset list

% Loop through all of the subjects in the study to create the dataset
for loopnum = 1:length(subjects) %for each subject
    IgnoreFile   = fullfile(filepath, subjects{loopnum}, 'Ignore.set');
    MemorizeFile = fullfile(filepath, subjects{loopnum}, 'Memorize.set');
    ProbeFile    = fullfile(filepath, subjects{loopnum}, 'Probe.set');
    commands = {commands{:} ...
        {'index' 3*loopnum-2 'load' IgnoreFile   'subject' subjects{loopnum} 'condition' 'Ignore'} ...
        {'index' 3*loopnum-1 'load' MemorizeFile 'subject' subjects{loopnum} 'condition' 'Memorize'} ...
        {'index' 3*loopnum   'load' ProbeFile    'subject' subjects{loopnum} 'condition' 'Probe'}};
end;
% Uncomment the line below to select ICA components with less than 15% residual variance
% commands = {commands{:} {'dipselect', 0.15}};
[STUDY, ALLEEG] = std_editset(STUDY, ALLEEG, 'name','Sternberg','commands',commands,'updatedat','on');

% Update workspace variables and redraw EEGLAB
CURRENTSTUDY = 1; EEG = ALLEEG; CURRENTSET = [1:length(EEG)];
[STUDY, ALLEEG] = std_checkset(STUDY, ALLEEG);
eeglab redraw

[STUDY ALLEEG] = std_precomp(STUDY, ALLEEG, {},'rmicacomps','on','interp','on','recompute','on','erp','on');
STUDY = pop_erpparams(STUDY, 'topotime',[200 300] );
[STUDY erpdata] = std_erpplot(STUDY,ALLEEG,'channels',{'LEYE' 'REYE' 'OZ' 'O2' 'FP1' 'FPZ' 'FP2' 'AF7' ...
            'AF3' 'AFZ' 'AF4' 'AF8' 'F9' 'F7' 'F5' 'F3' 'F1' 'FZ' 'F2' 'F4' 'F6' 'F8' 'F10' 'FT9' ...
            'FT7' 'FC5' 'FC3' 'FC1' 'FCZ' 'FC2' 'FC4' 'FC6' 'FT8' 'FT10' 'T7' 'C5' 'C3' 'C1' 'CZ' ...
            'C2' 'C4' 'C6' 'T8' 'TP9' 'TP7' 'CP5' 'CP3' 'CP1' 'CPZ' 'CP2' 'CP4' 'CP6' 'TP8' 'TP10' ...
            'P7' 'P5' 'P3' 'P1' 'PZ' 'P2' 'P4' 'P6' 'P8' 'PO9' 'PO7' 'PO3' 'POZ' 'PO4' 'PO8' 'PO10' 'O1'});

dlmwrite('erpfile.txt',squeeze(erpdata{1}),'delimiter', '\t', 'precision', 2);
dlmwrite('erpfile.txt',squeeze(erpdata{2}),'-append', 'roffset', 1, 'delimiter', '\t', 'precision', 2);
dlmwrite('erpfile.txt',squeeze(erpdata{2}),'-append', 'roffset', 1, 'delimiter', '\t', 'precision', 2);
```

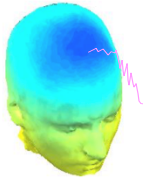
STUDY datafiles



- *design1_S01_ignore.daterp (ERPs)*
- *design1_S01_ignore.datspec (power spectra)*
- *design1_S01_ignore.dattimef (time-freq.)*

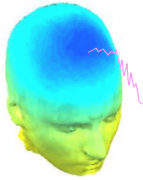
- *design1_S01_ignore.icaerp (ERPs)*
- *design1_S01_ignore.icaspec (power spectra)*
- *design1_S01_ignore.icatopo (scalp maps)*
- *design1_S01_ignore.icatimef (time-freq.)*

STUDY datafiles



```
tmp = load('-mat', 'design1_S01_ignore.daterp');
>> tmp

tmp =

          chan1:   [1x750 double]
          chan2:   [1x750 double]
          chan3:   [1x750 double]
          chan4:   [1x750 double]
          chan5:   [1x750 double]
          chan6:   [1x750 double]
          chan7:   [1x750 double]
            …
         chan69:  [1x750 double]
         chan70:  [1x750 double]
         chan71:  [1x750 double]
         labels:  {1x71 cell}
          times:  [1x750 double]
       datatype:  'ERP'
     parameters:  {'rmcomps'  {1x1 cell}  'interp'  [1x71 struct]}
       datafile:  '/Volumes/donnees/data/STUDYstern/S01/Ignore.set'
```

Exercises



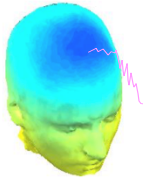
Suggestion for exercise

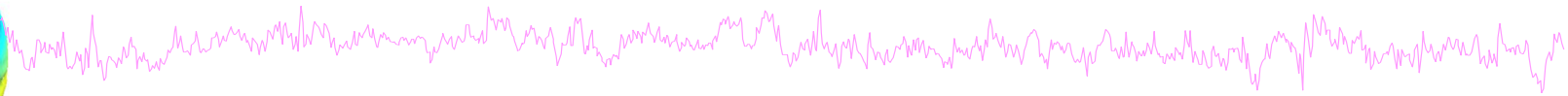
1. Load stern.study in STUDY folder
2. Choose a cluster to investigate and plot ERP
3. Get command line call for plotting ERP
4. Modify the script to plot spectrum instead of ERP
5. Export output to text file
6. Visualize output text file in another software

---

7. Copy and paste the script from the PDF

Advanced scripting: EEG pipeline





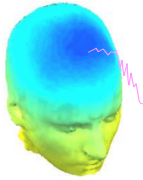
```
sInfo = [];
sInfo(end+1).file = 'rawdata/S01.raw';
sInfo(end).name = 'S01';
sInfo(end).bad_channels = { 'E1' };
```

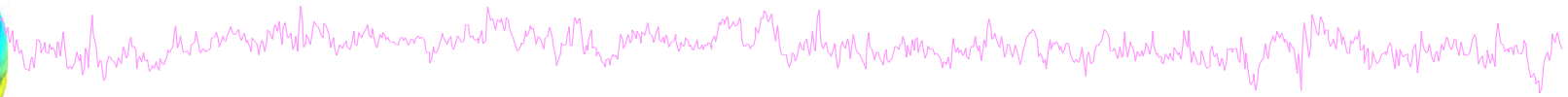
Raw data file

Subject name

Subject name

Advanced scripting: EEG pipeline





```
sInfo = [];
sInfo(end+1).file = 'rawdata/S01.raw';
sInfo(end).name = 'S01';
sInfo(end).bad_channels = { 'E1' };
sInfo(end).bad_data  = [726 1495;6098 6831;13245 14057;15715 16399;22756 2445
```

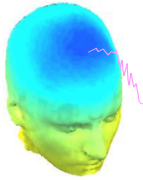
Raw data file

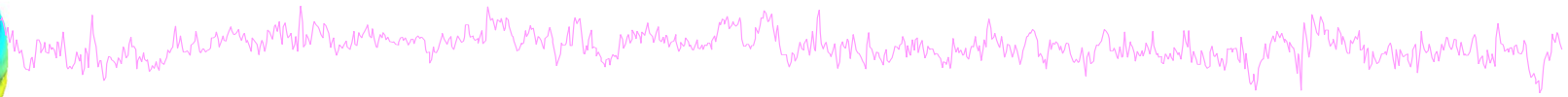
Subject name

Subject name

Copy the output from the eeg_eegrej function in the history

Advanced scripting: EEG pipeline





```
sInfo = [];
sInfo(end+1).file = 'rawdata/S01.raw';
sInfo(end).name = 'S01';
sInfo(end).bad_channels = { 'E1' };
sInfo(end).bad_data  = [726 1495;6098 6831;13245 14057;15715 16399;22756 2445
sInfo(end).bad_comps = [1.6681  1.9870 0.3979 0.4444 -0.2274 -0.1433 -0.2626
                        1.1917 -1.4838 0.7469 -1.1599 0.4773 -0.3257  0.3074
```

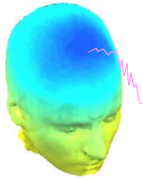
Raw data file

Subject name

Subject name

Copy transposed columns of the inverse weight matrix
EEG.icawinv for your selected artifact components

Advanced scripting: EEG pipeline

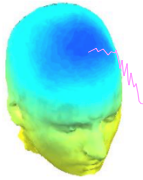


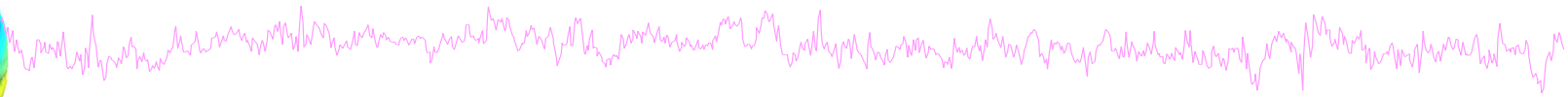
datainfo.m file

```
sInfo = [];
sInfo(end+1).file = 'rawdata/S01.raw';
sInfo(end).name = 'S01';
sInfo(end).bad_channels = { 'E1' };
sInfo(end).bad_data  = [726 1495;6098 6831;13245 14057;15715 16399;22756 2445
sInfo(end).bad_comps = [1.6681  1.9870 0.3979 0.4444 -0.2274 -0.1433 -0.2626
                        1.1917 -1.4838 0.7469 -1.1599 0.4773 -0.3257  0.3074

sInfo(end+1).file = 'rawdata/S02.raw';
sInfo(end).name = 'S02';
sInfo(end).bad_channels = { };
sInfo(end).bad_data  = [41661 43713;24000 24833;44878 46501;48706 49210;51190
sInfo(end).bad_comps = [0.6960 -0.8637  0.9087 -0.8028  0.4873 -0.2142  0.273
                       -0.0875 -0.4056 -0.0287 -0.3870  0.0600 -0.3716  0.342
                        2.1928  1.5712  0.8622  0.3215 -0.0357 -0.3125 -0.226

sInfo(end+1).file = 'rawdata/S03.raw';
sInfo(end).name = 'S03';
sInfo(end).bad_channels = { 'E10' 'E19' 'E20' 'E29' };
sInfo(end).bad_data  = [1 10449;19808 21815;25678 27254;29257 30010;34023 360
sInfo(end).bad_comps = [ 1.8583  2.0468 -0.0516  0.3159 -0.4256 -0.2770 -0.36
                         1.2189 -0.7385  1.2464 -0.8913  0.5475 -0.3971  0.29
                        -0.1248 -0.1358 -0.1954 -0.2533 -0.1555 -0.2313 -0.03
```

```
datainfo;
pop_editoptions( 'option_storedisk', 1);
Folder = 'ds_eeg_preprocessed_data';
if ~exist(outputfolder), mkdir(outputfolder); end;

for iSubject = 1:length(sInfo)

    % load dataset
    EEG = pop_biosig( sInfo(iSubject).file);
    EEG.setname = sInfo(iSubject).name;

    % proprocess data
    EEG = pop_iirfilt( EEG, 0.5, 0, [], 0, 0); % high pass filtering
    EEG = pop_iirfilt( EEG, 0, 55, [], 0, 0); % low pass filtering
    EEG = pop_select(EEG, 'nochannel', sInfo(iSubject).bad_channels); % remove bad channels
    EEG = pop_reref( EEG, []); % average reference (optional)
    EEG = eeg_eegrej( EEG, sInfo(iSubject).bad_data); % remove bad portions of data

    % run ICA
    EEG = pop_runica(EEG, 'pca', EEG.nbchan-1);

    % tag bad components
    if ~isempty(sInfo(iSubject).bad_comps)
        [corr,indx,indy] = matcorr(EEG.icawinv', sInfo(iSubject).bad_comps);
        if ~all(abs(corr(1:size(sInfo(iSubject).bad_comps,1))) > 0.92),
              error('Correlation too low'); end;
        EEG.reject.gcompreject(indx(1:size(sInfo(iSubject).bad_comps,1))) = 1;
    end;

    % extract data epochs
    EEG = pop_epoch(EEG, { 'S1' 'S2' });

    % save dataset
    EEG.saved = 'no';
    EEG = pop_saveset( EEG, 'filepath', folder, 'filename', [ sInfo(iSubject).name '.set' ]);
end;
```

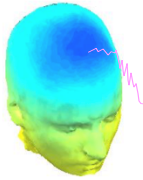
Create STUDY





```
datainfo;
pop_editoptions( 'option_storedisk', 1);
outputEEGFolder = 'preprocessed_data';
studyCommand    = {};

% generate STUDY commands
for iSubject = 1:length(sInfo)
    fileName  = fullfile(outputEEGFolder, [ sInfo(iSubject).name '.set' ]);
    studyCommand = [ studyCommand { 'index' iSubject 'load' fileName 'subject' ...
           sInfo(iSubject).name } ];
end;

% create data
[STUDY ALLEEG] = std_editset( [], [], 'name', 'test', 'commands', studyCommand, ...
         'updatedat','off', 'filename', 'test.study', 'resave', 'on');
STUDY = std_makedesign(STUDY, ALLEEG, 1, 'variable1','','variable2','','name', 'Design 1', ...
    'pairing1','on','pairing2','on','delfiles','off','defaultdesign','off','subjselect', ...
    {sInfo.name},'filepath','studyfiles');

% update workspace variables and redraw EEGLAB
CURRENTSTUDY = 1; EEG = ALLEEG; CURRENTSET = [1:length(EEG)];
[STUDY, ALLEEG] = std_checkset(STUDY, ALLEEG);
eeglab redraw

% precompute and plot data
[STUDY ALLEEG] = std_precomp(STUDY, ALLEEG, {},'interp','on','recompute','on','erp', 'on', ...
     'topotime',[200 300]);
[STUDY erp] = std_erpplot(STUDY,ALLEEG, 'channels',{allchanlocs.labels}, );
```

Exercice: build your own pipeline



Suggestion for exercise

1. Load SimpleOddball.set dataset
2. High pass filter at 1Hz (menu Tools > Filter)
3. Reject bad portion of data by hand (menu Tools > Reject continuous…)
4. Re-reference to average ref. (optional) (menu Tools > Re-reference)
5. Build your *datainfo.m* file using EEGLAB history (see scripting lecture)
6. Run ICA (use PCA if necessary); select bad ICA components
7. Epoch data on Oddball (type 2) and Standard (type 1) – save dataset
8. Add components to you *datainfo.m* file

9. Create a STUDY with this single file
10. Compare the ERP for Oddball (type 2) and Standard (type 1) and use single-trial statistics with cluster correction for multiple comparisons
11. Build a script that creates the STUDY and perform the same analysis
12. Save the figure at the end of the script in eps or jpg format (“print –deps file” command or “print –djpg file” command).
13. Run the full pipeline (dataset processing and STUDY processing)
14. Change the filtering in the pipeline (step 2) and observe effects