STUDY scripting

Task 1

Build a STUDY (via commandline)

Task 2

STUDY structure details

Task 3

Precompute/precluster data measures

Task 4

Choose data measures to cluster

Task 5

Clustering algorithm

Exercise...

Build a STUDY

```
% Faster alternative to building a STUDY manually
% Example STUDY:  15 subjects, 4 conditions

% Define variables:

basedir = 'C:\EEGLAB_WORKSHOP\STUDY\';
setnames = {'attend1_pos1.set','attend1_pos5.set',…
            'attend5_pos5.set','attend5_pos1.set'};
subjs = {'S01','S02','S03','S04','S05','S06','S07',…
         'S08','S09','S10','S11','S12','S13','S14','S15'};
studyname = 'Attention';
taskname = '5-box';
savename = 'attention.study';

% Note: 'EEG' fields 'condition', 'group', and 'session' need to be
% defined in each dataset of every subject before building the STUDY!
```

Build a STUDY

Most important option:

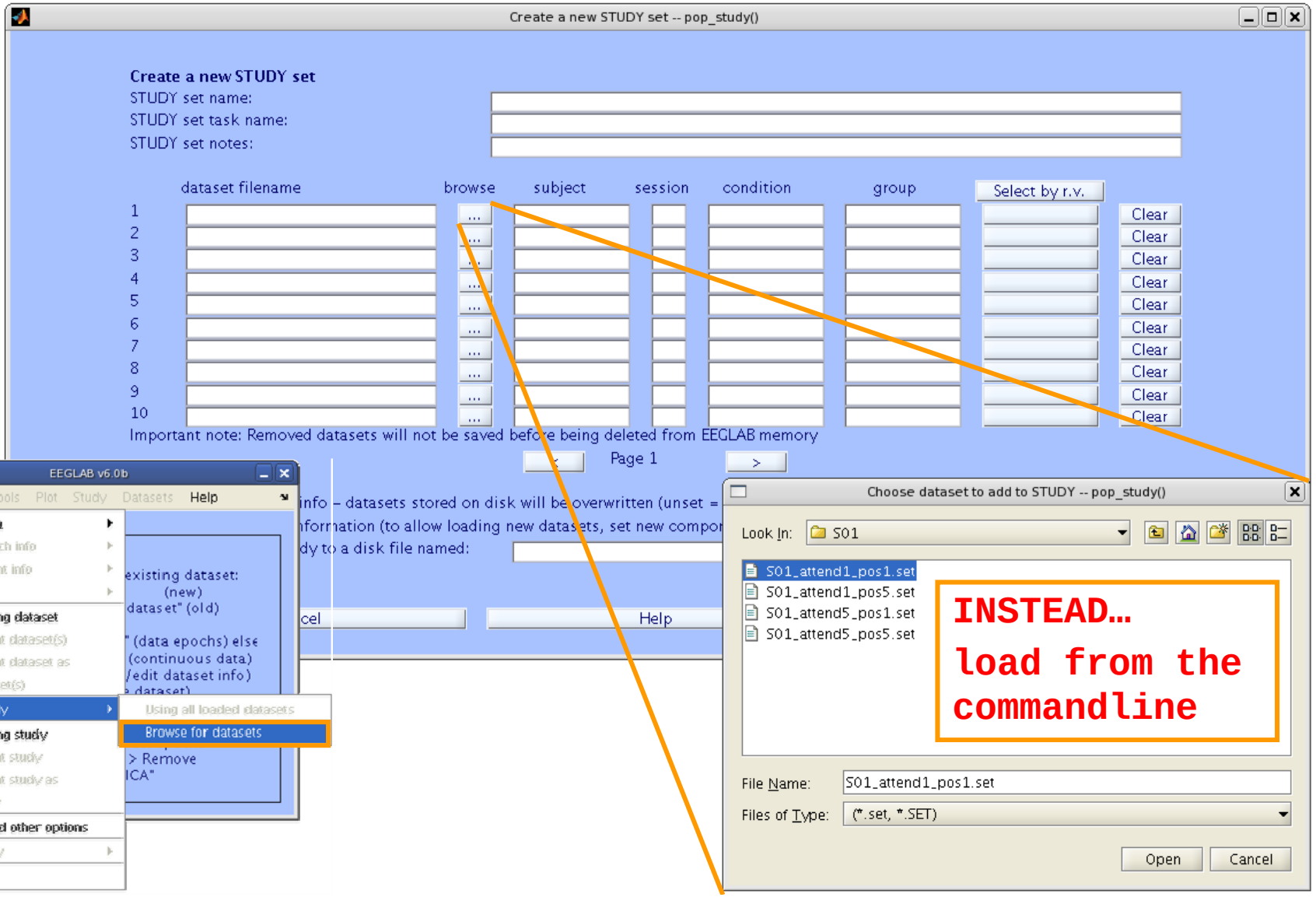
- Allows only one dataset to be loaded at once.
- Most STUDYs are too big to have all data loaded at once.

```
% Open eeglab:
[ALLEEG EEG CURRENTSET ALLCOM] = eeglab;

% Set memory options:
pop_editoptions( 'option_storedisk', 1, 'option_savematlab', 1,…
'option_computeica', 0, 'option_rememberfolder', 1);
% saves a file: 'eeg_options.m' to your current working directory

% Initialize EEGLAB/STUDY variables:
STUDY = []; CURRENTSTUDY = 0; ALLEEG=[]; EEG=[]; CURRENTSET=[];
```

Build a STUDY: GUI (review)



Define variables

```
basedir = 'C:\EEGLAB_WORKSHOP\STUDY\';
setnames = {'attend1_pos1.set','attend1_pos5.set',…
            'attend5_pos5.set','attend5_pos1.set'};
subjs = {'S01','S02','S03','S04','S05','S06','S07',…
         'S08','S09','S10','S11','S12','S13','S14','S15'};

% concatenate string variables:
[] % strings inside brackets will be concatenated
[basedir,subjs{subj},'/',subjs{subj},'_',setnames{cond}];
```

```
C:\EEGLAB_WORKSHOP\STUDY\S01\S01_attend1_pos1.set
```

Load dataset info from commandline

```
% Now loop through subjects and add to the STUDY:
index = 1; % initialize STUDY index
for subj = 1:length(subjs) % for each subject
    for cond = 1:length(setnames) % for each condition
        datset = [basedir,subjs{subj},'/',subjs{subj},…
                  '_',setnames{cond}]; % concatenate strings
        [STUDY ALLEEG] = std_editset( STUDY, ALLEEG,…
                         'name', studyname, 'task', taskname,...
                         'commands',{{'index',index,'load',datset},…
                         {'dipselect',0.15},{'subject',subjs{subj}}},…
                         'inbrain','on',…
                         'updatedat','off', 'savedat', 'off',…
                         'filename', [basedir, savename]);
        index = index + 1;
        CURRENTSTUDY = 1; EEG = ALLEEG; CURRENTSET = [1:length(EEG)];
        [STUDY, ALLEEG] = std_checkset(STUDY, ALLEEG);
    end;
end;
eeglab redraw
```

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Exercise...

Task 2: STUDY structure details

Question:

How do I know which ICs/subjects are in each cluster?

Where in the STUDY structure can I find this information?

Task 2: Understanding STUDY structure

20 = # of clusters

```
>> STUDY.cluster

1x20 struct array with fields:

    name
    parent
    child
    comps
    sets
    algorithm
    centroid
    preclust
    topo
    topox
    topoy
    topoall
    topopol
```

One cluster:

6 = cluster number

```
>> STUDY.cluster(6)
ans =
  name: 'Cls 6'
    parent: {'ParentCluster 1'}
     child: []
     comps: [4 2 22 1 6 15 2 7 2 6 12 15 17 3]
      sets: [4x14 double]
 algorithm: {'Kmeans'  [19]}
  centroid: []
  preclust: [1x1 struct]
      topo: [67x67 double]
      topox: [67x1 double]
      topoy: [67x1 double]
   topoall: {1x14 cell}
   topopol: [-1 -1 -1 1 1 1 -1 -1 1 -1 1 1 1 1]
```

IC indices

4 = # conditions

dataset indices

67 = # of channels

scalp map polarity

Task 2: Understanding STUDY structure

```
>> STUDY.cluster(6)
ans =
  name: 'Cls 6'
        parent: {'ParentCluster 1'}
         child: []
         comps: [4 2 22 1 6 15 2 7 2 6 12 15 17 3]
          sets: [4x14 double]
     algorithm: {'Kmeans'  [19]}
      centroid: []
      preclust: [1x1 struct]
          topo: [67x67 double]
          topox: [67x1 double]
          topoy: [67x1 double]
       topoall: {1x14 cell}
       topopol: [-1 -1 -1 1 1 1 -1 -1 1 -1 1 1 1 1]
```

Which subject?
Which dataset(s)?

Dataset indices

```
>> STUDY.cluster(6).sets

ans =
```

Second IC = second column

2	6	22 …
4	8	24 …
1	5	21 …
3	7	23 …

Condition 4

```
>> STUDY.datasetinfo(7) % access dataset 7
ans =
     filepath: 'C:\EEGLAB_WORKSHOP\STUDY\S02'
     filename: 'S02_attend5_pos5.set'
      subject: 'S02'
      session: 1
    condition: 'TargAttnR'
        group: 'normals'
        index: 7
        comps: [1 2 3 4 5 6 7 10 11 13 14 15 16 19 22]
```

Subject 2

Condition 4

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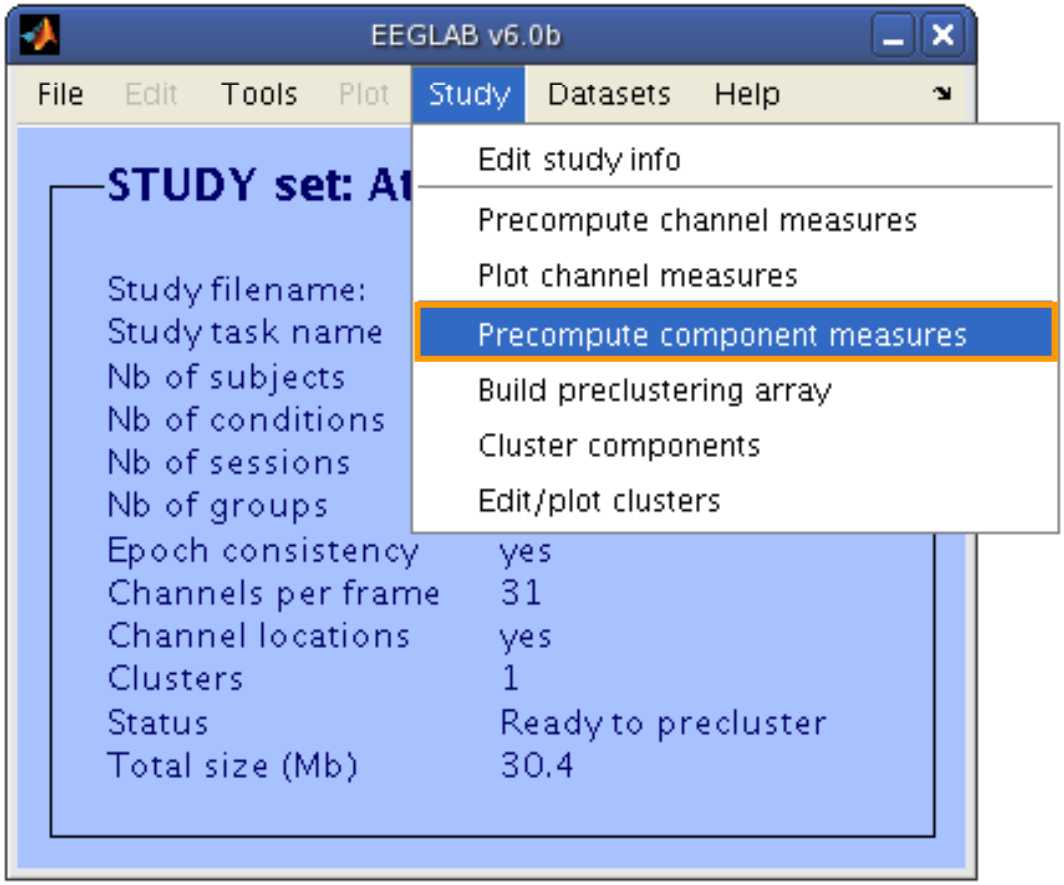
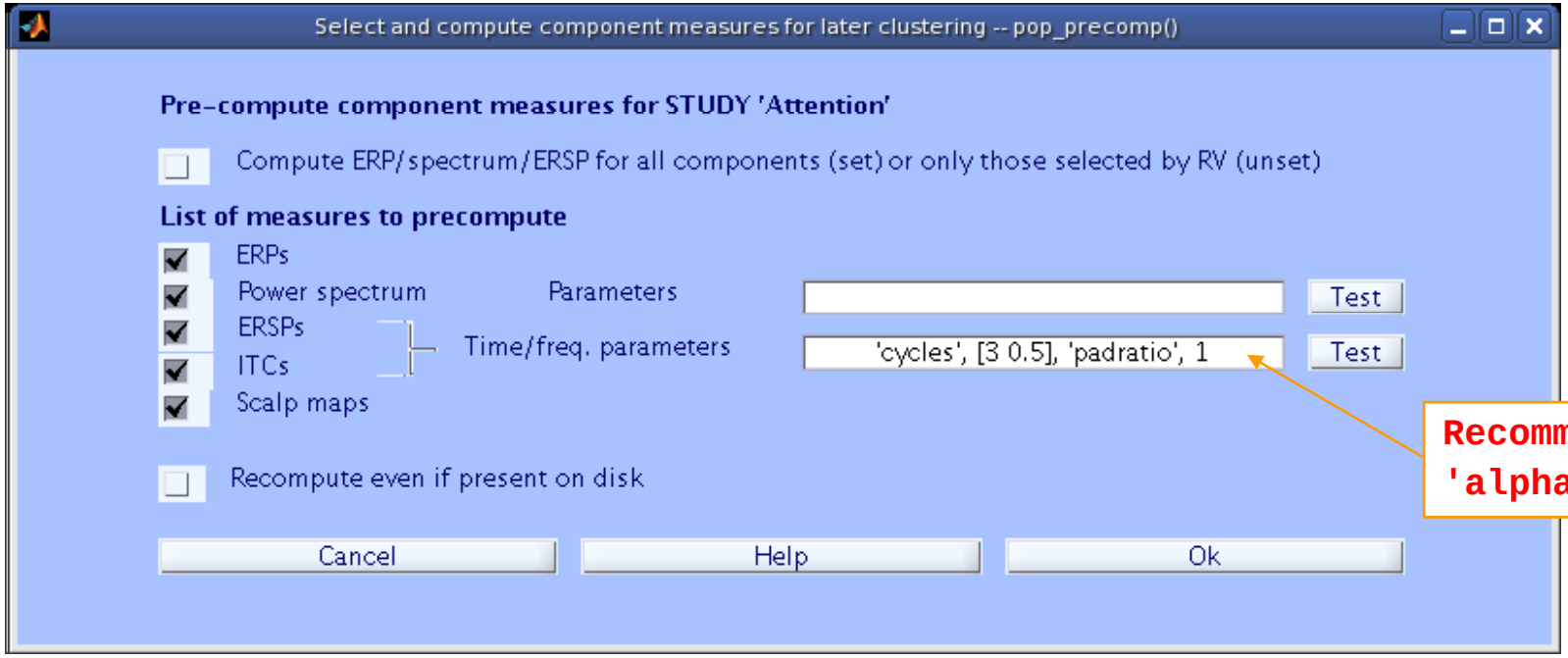
Exercise...

Precompute data measures

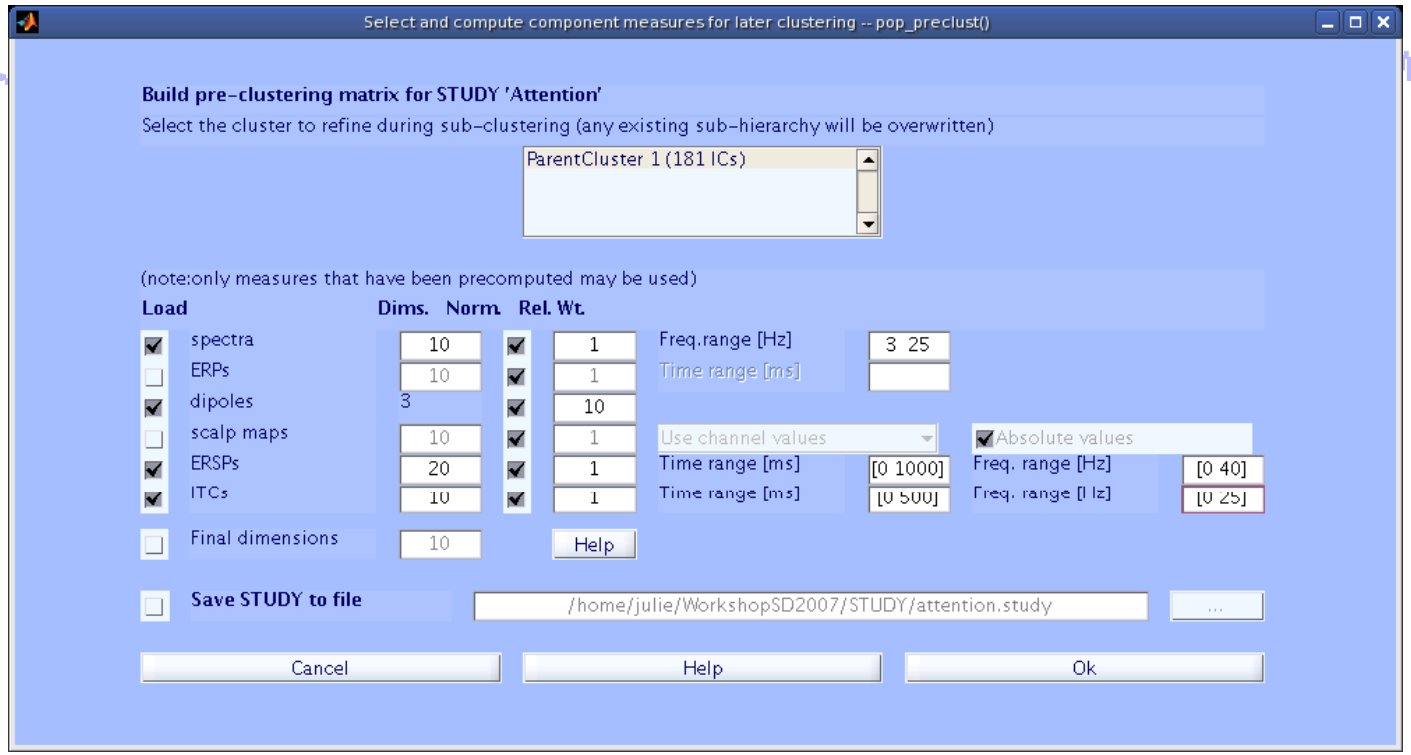


Precompute data measures




```
[STUDY ALLEEG] = std_precomp( STUDY, ALLEEG,'components',…
'erp','on', 'spec','on', 'scalp','on', 'allcomps','off',…
'itc','on', 'ersp','on', 'recompute','off', …
'erspparams',{'cycles',[3 0.5],'padratio',1,'alpha',0.01});
```

Precluster data measures




```
parentclust = 1; % cluster 1 is always full parent cluster
[STUDY ALLEEG] = std_preclust( STUDY, ALLEEG, parentclust,…
{'spec','npca',10,'norm',1,'weight',1,'freqrange',[3 25]},…
{'dipoles','norm',1,'weight',10},…
{'ersp','npca',20,'norm',1,'weight',1,'freqrange',[3 40],…
'timewindow',[0 1500]},…
{'itc', 'npca',10,'norm',1,'weight',1,'freqrange',[3 30],…
'timewindow',[0 600]});
```

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Exercise...

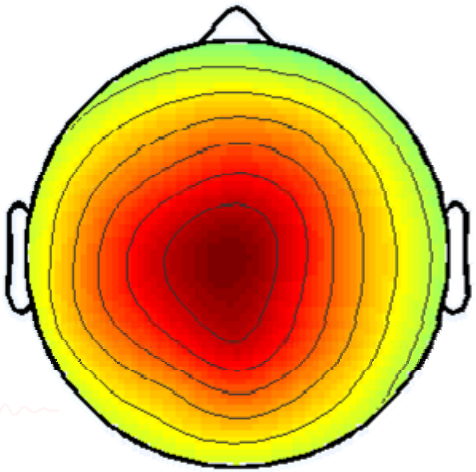
Choosing data measures

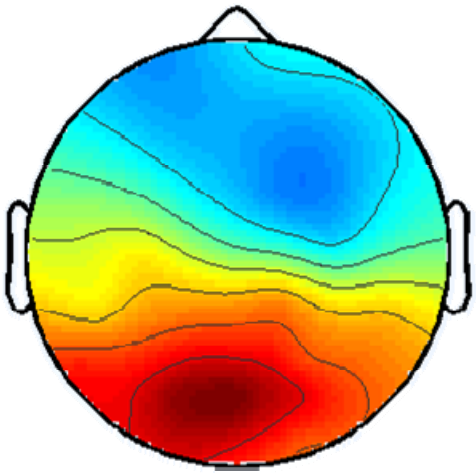
What measure(s) should you use?

- It depends on your final cluster criteria…
  - If for example, your priority is dipoles, then cluster only based on dipole location…

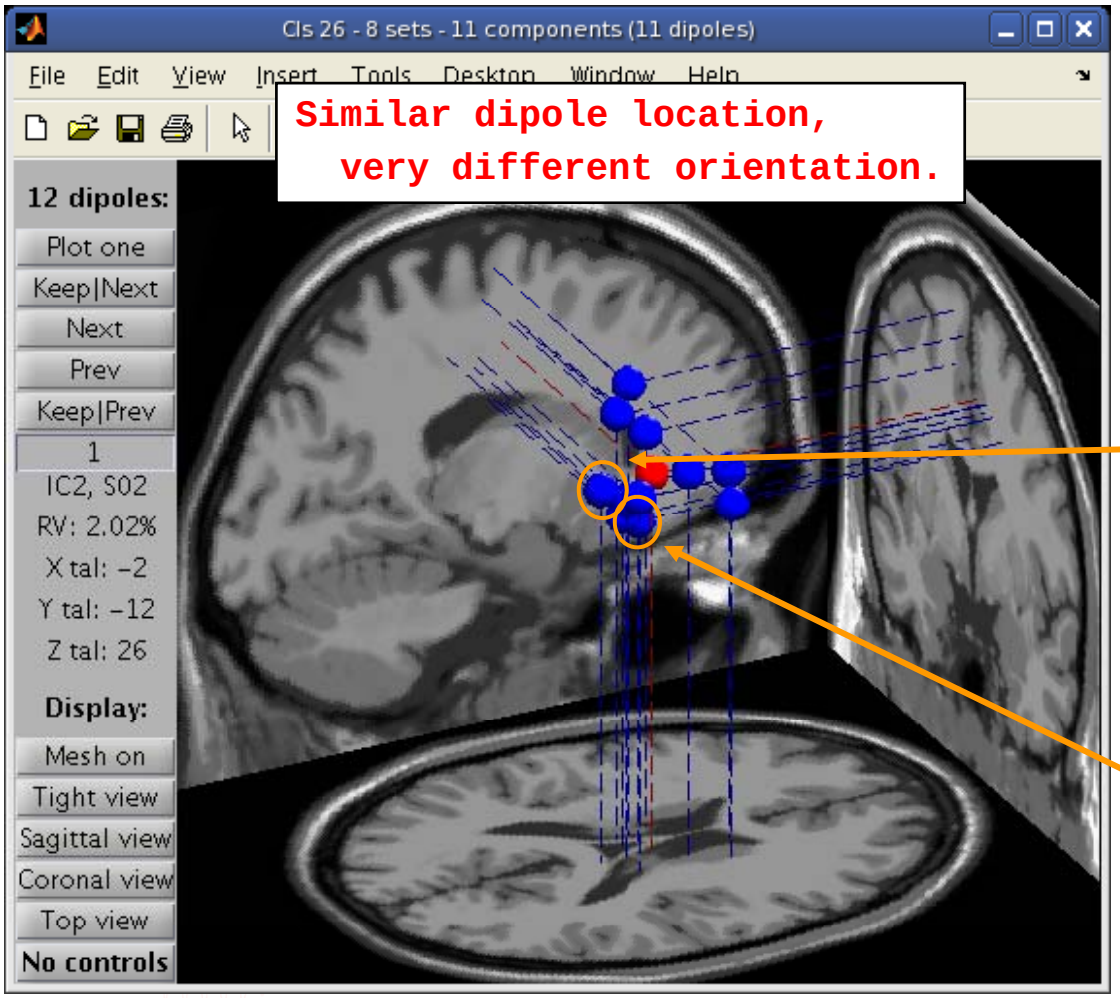
But consider:

- What is the difference between these two components?



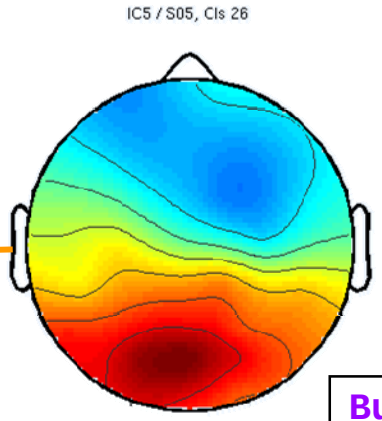


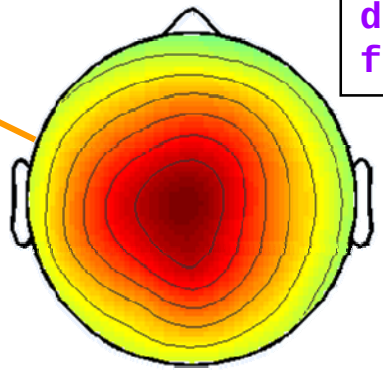
Choosing data measures



Similar dipole location, very different orientation.

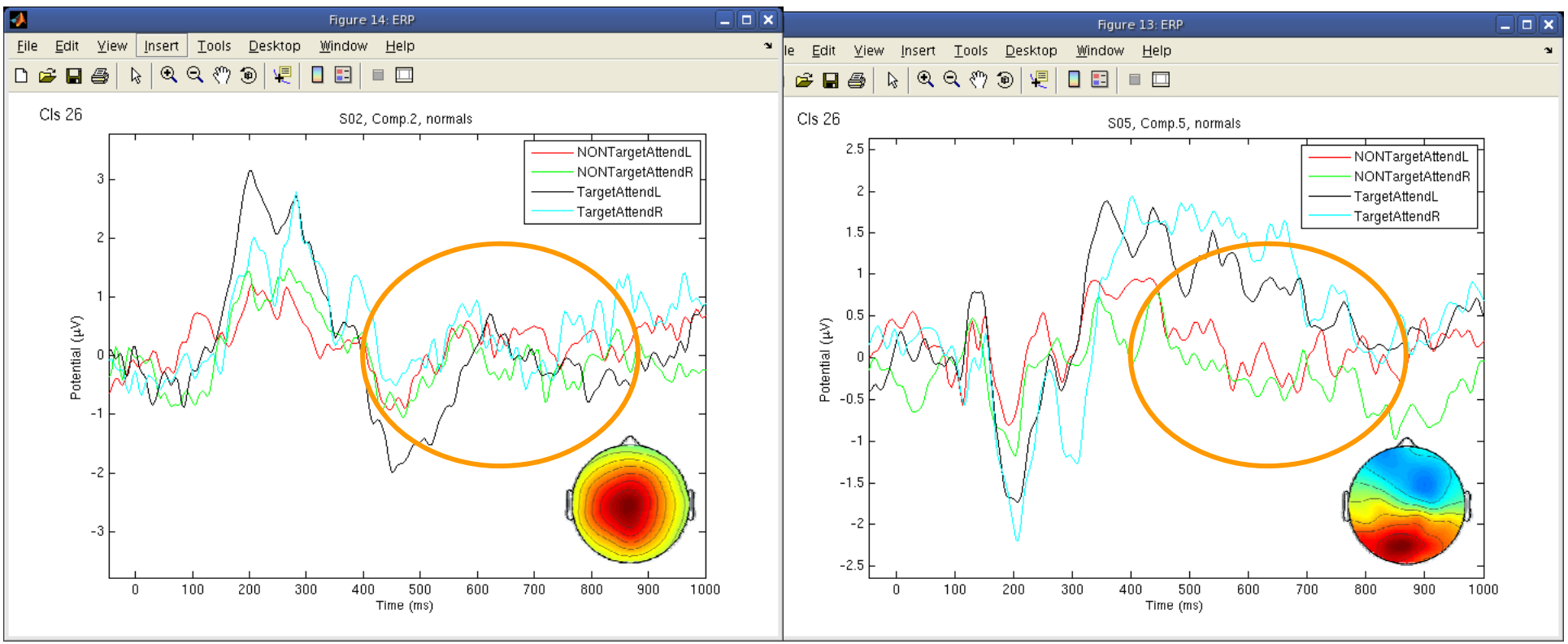
Obvious dramatic effect on scalp map topography:





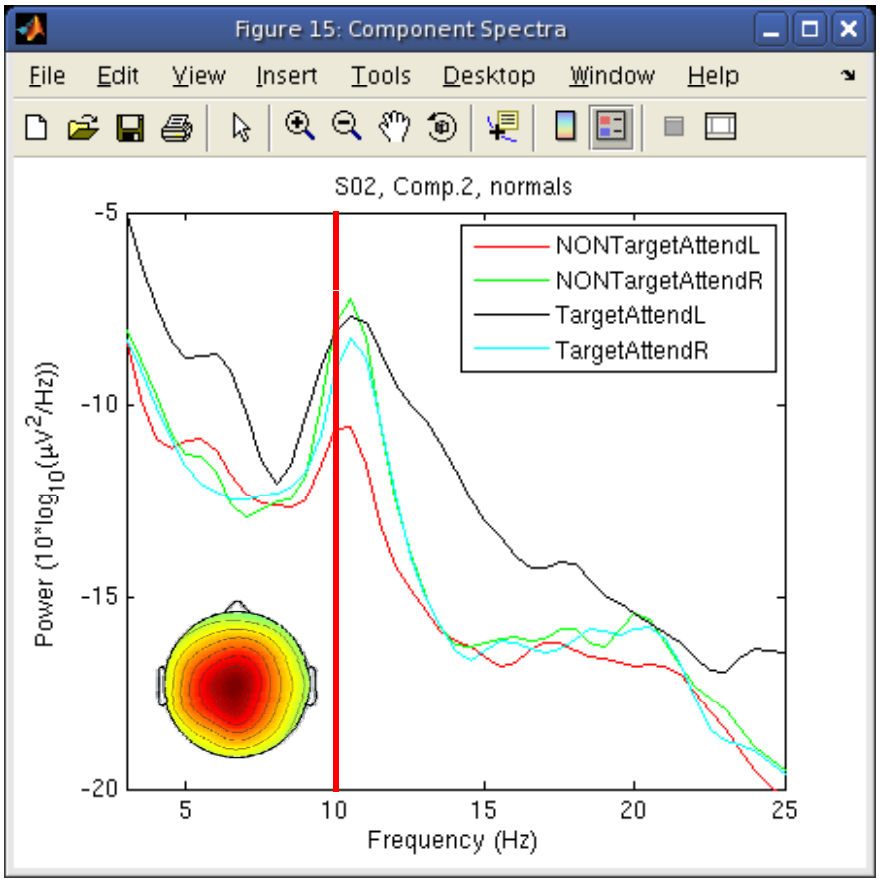
But, does this indicate a difference in function?

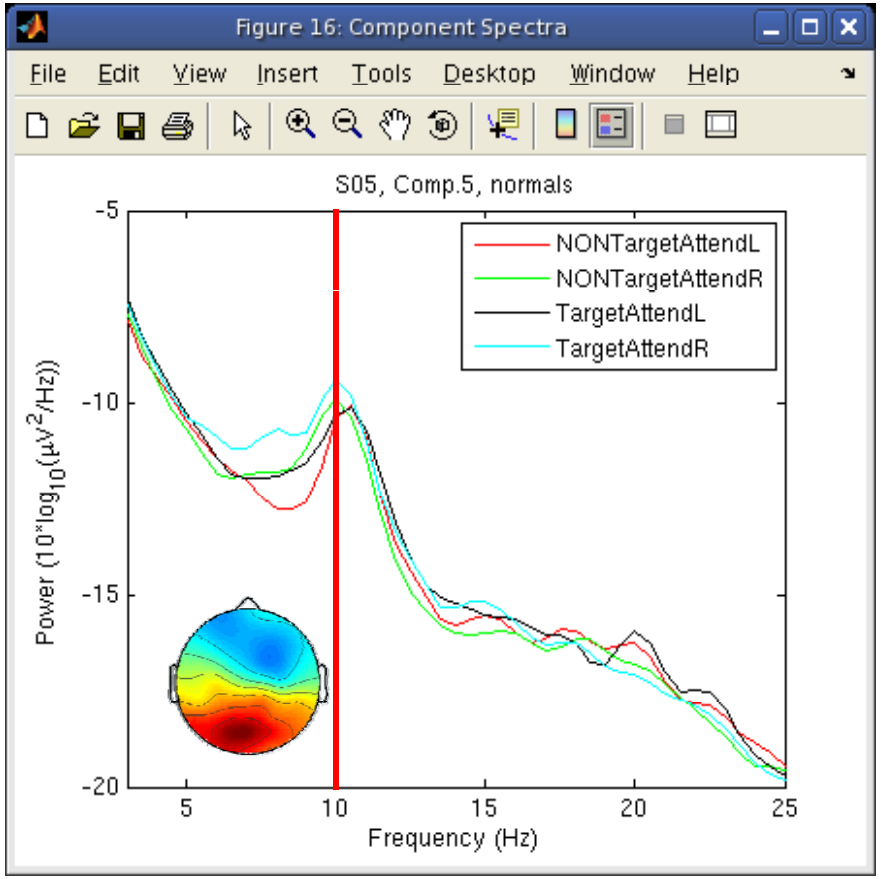
Choosing data measures



ERPs seem different…

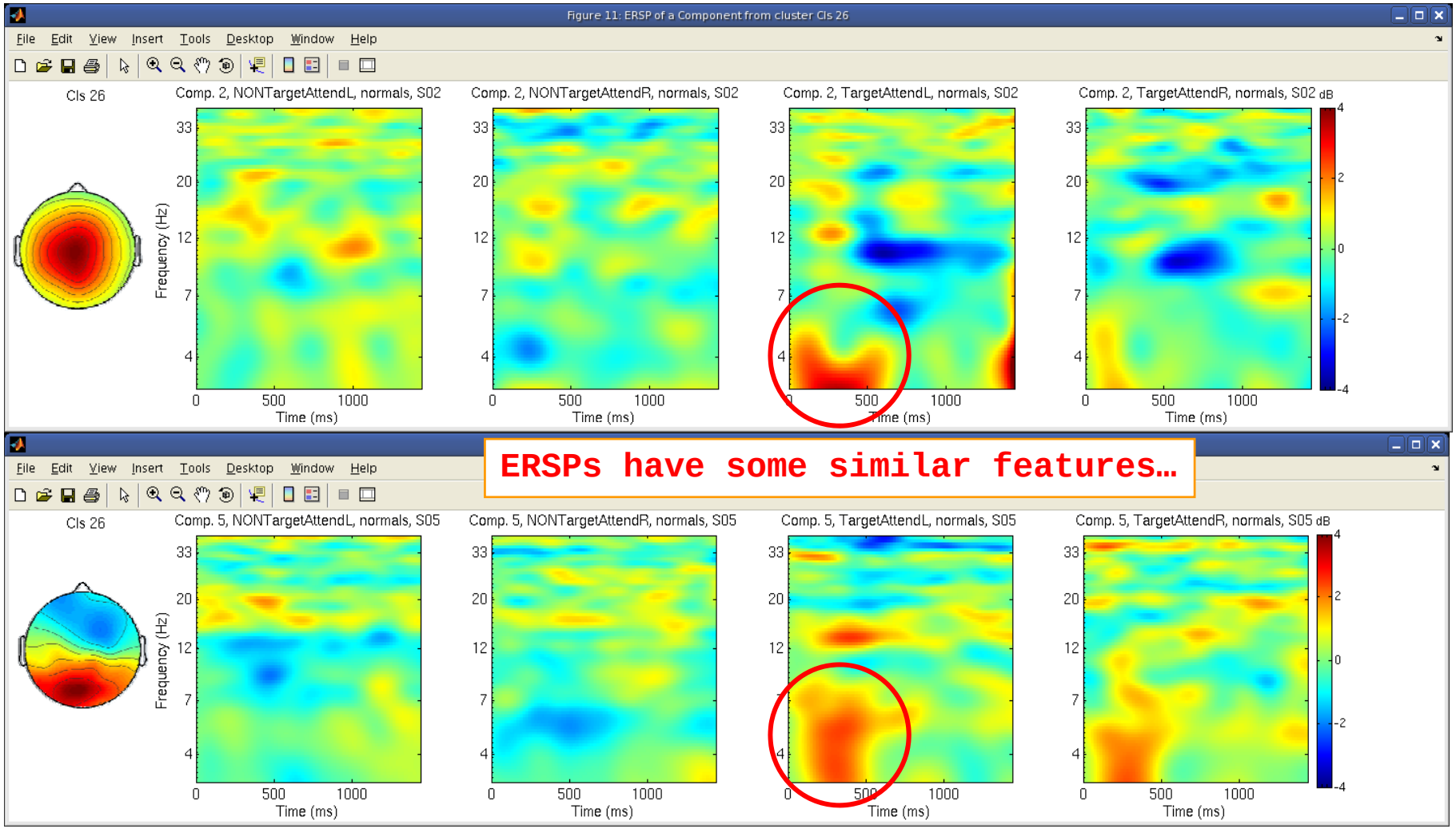
Choosing data measures



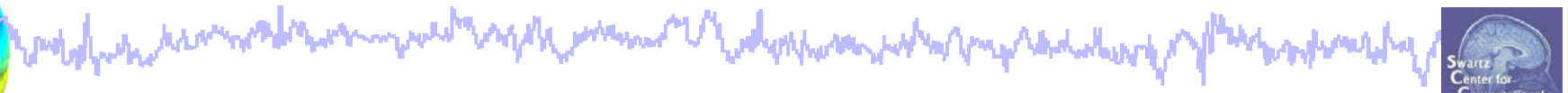


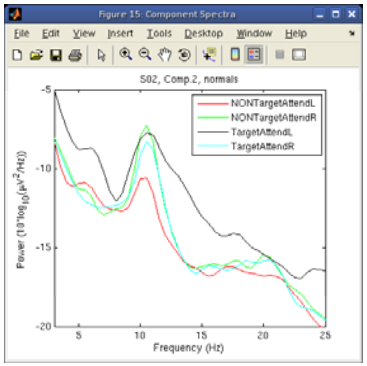
Spectra are similar,
though different condition effects…

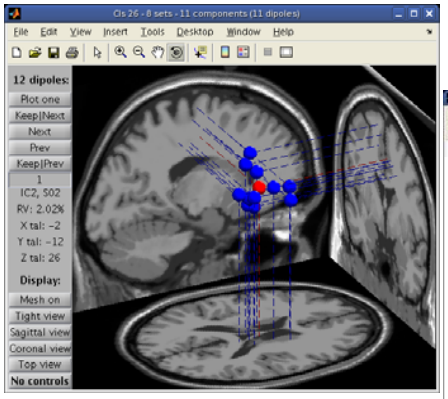
Choosing data measures

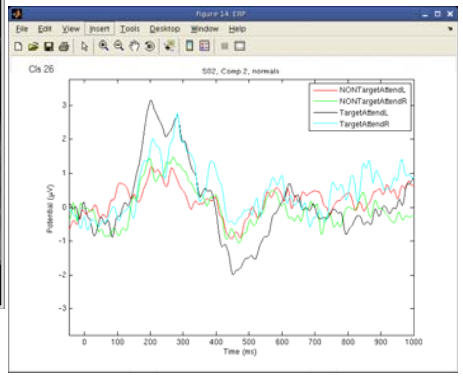


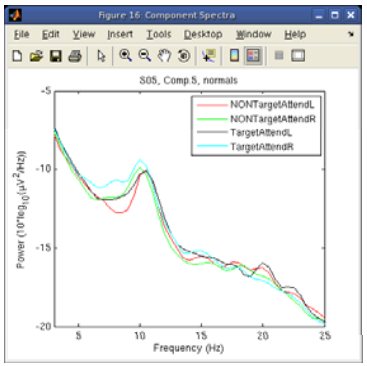
Choosing data measures







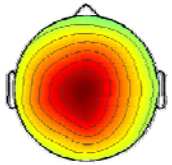




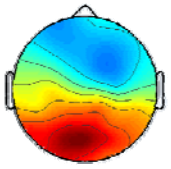
What data measures should you use?

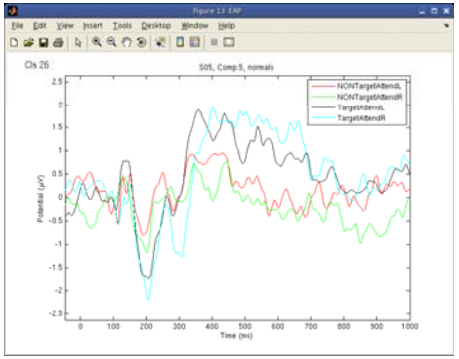
It depends…

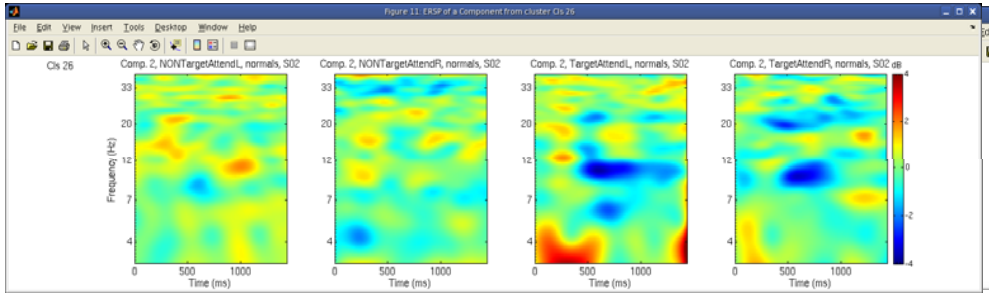
- **broadly-matched ICs:** use many/all of the measures.

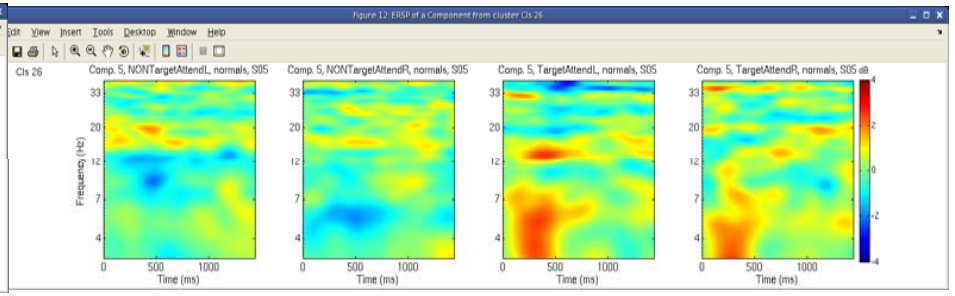


- **specifically-matched ICs:** use one/few of the measures.









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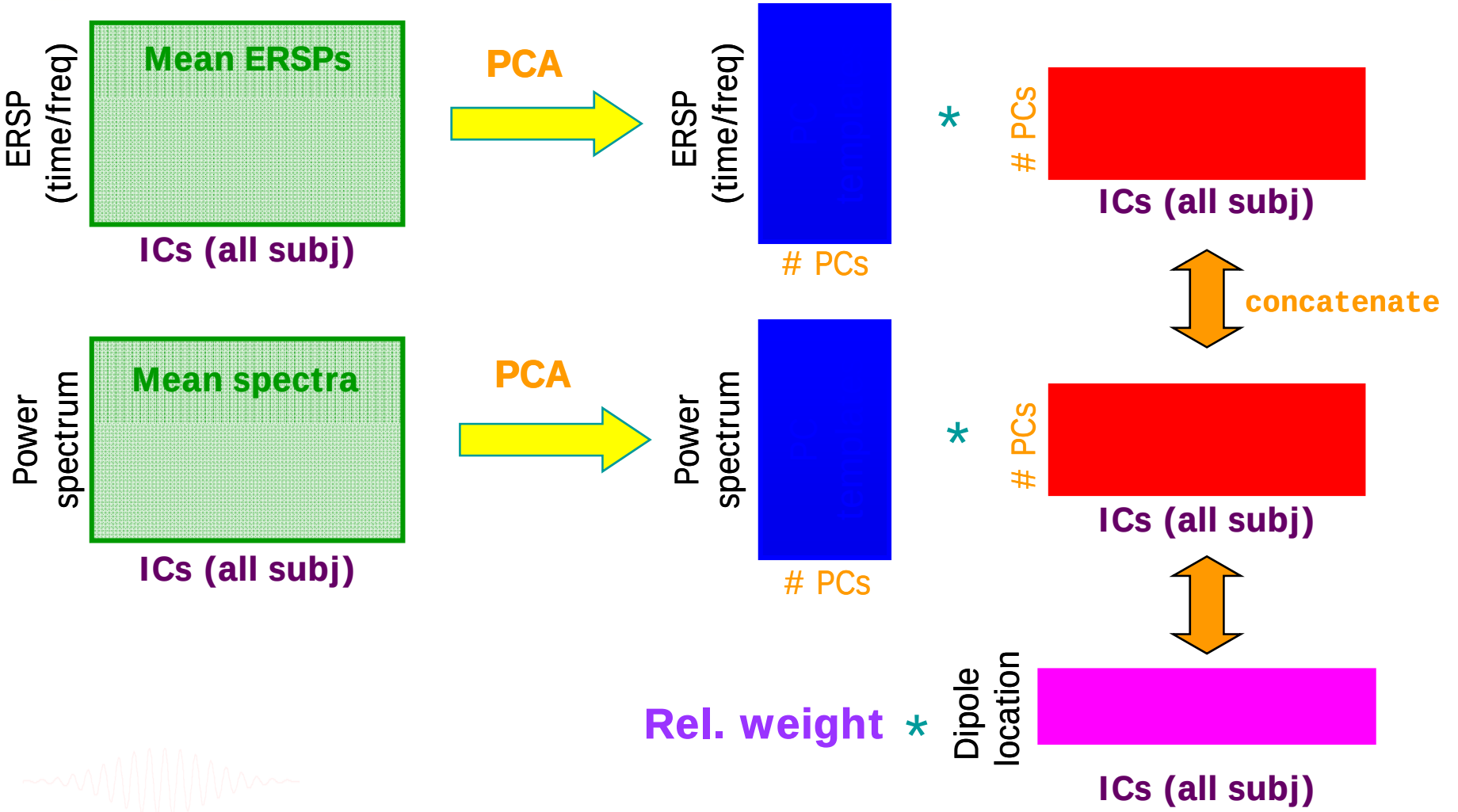
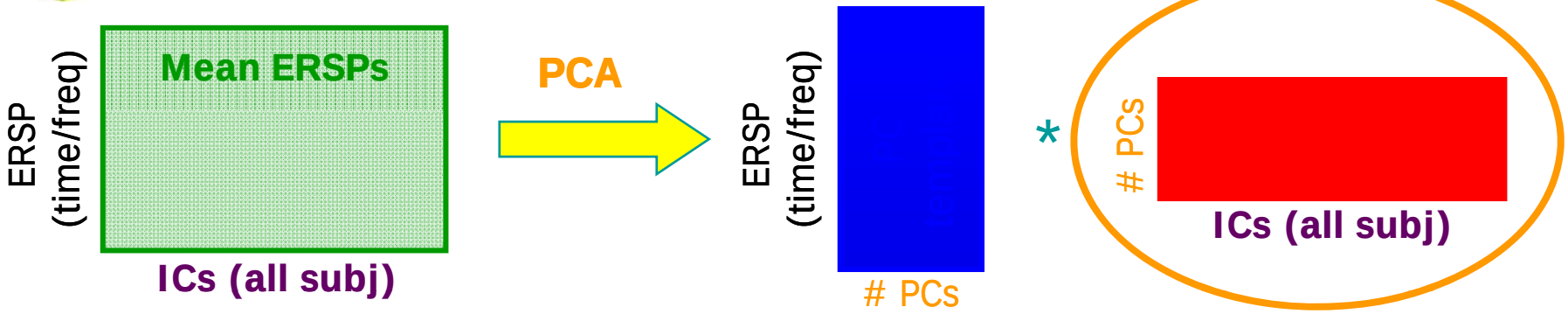
Exercise...

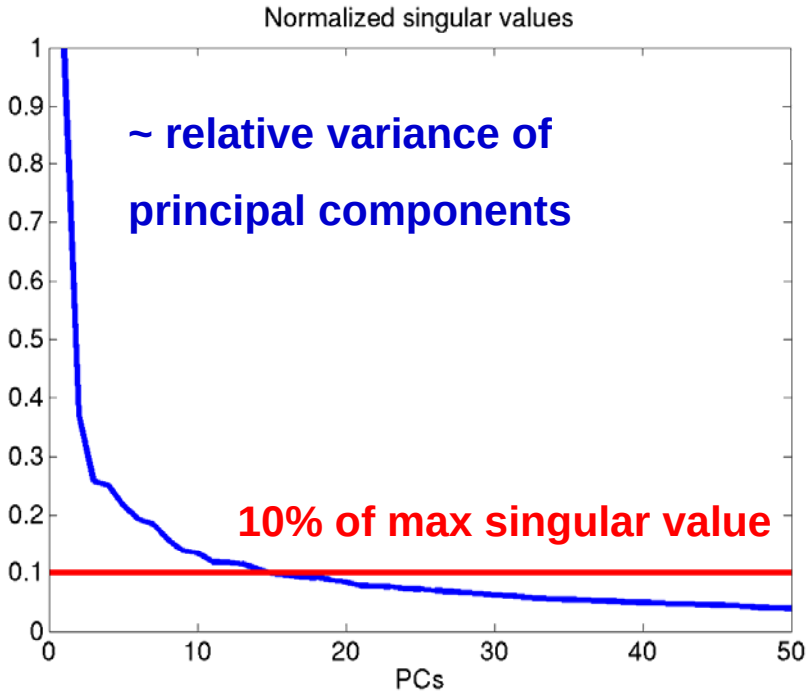
Precluster schematic



Precluster: Use singular values from PCA




```
%% Do it yourself:
%% Load all ERSP data
%% decompose with PCA
%% plot singular values
(See code in 'practicum_10.m')
```



Clustering: K-means

The **k-means algorithm** is an algorithm to cluster objects into *k* partitions.

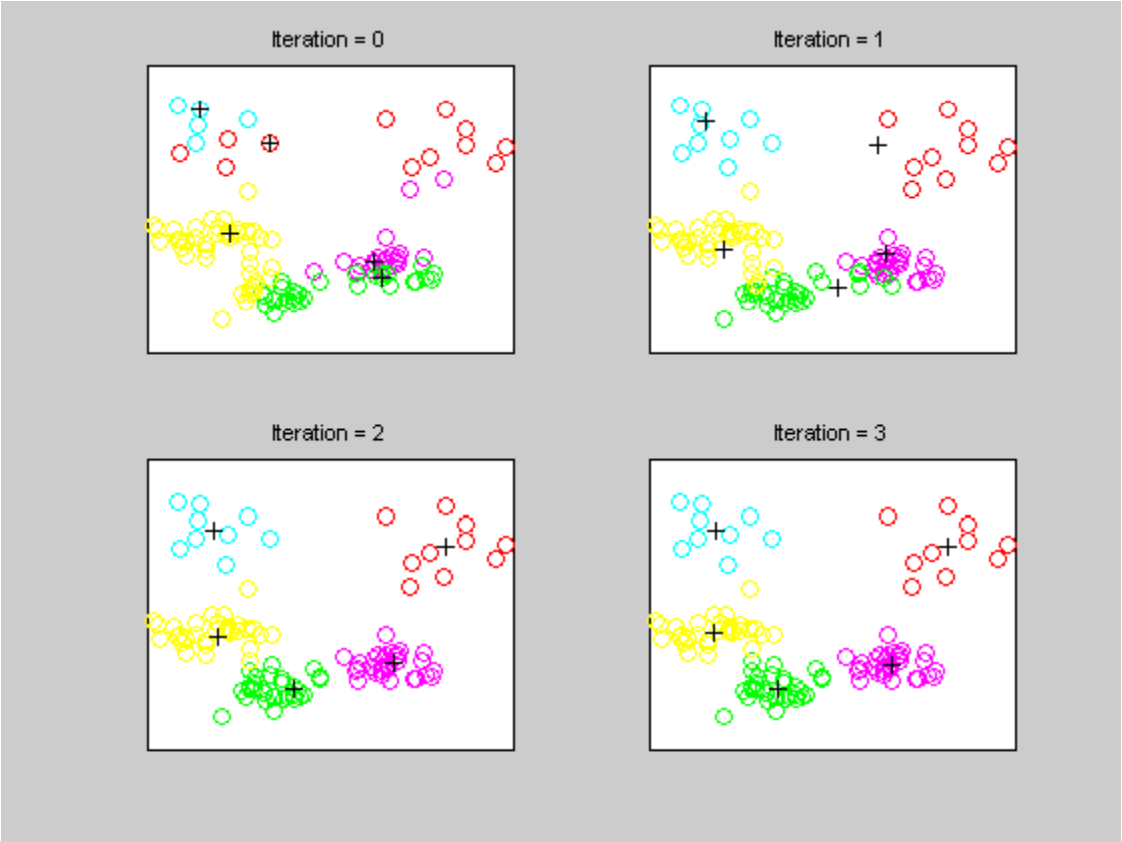
• It attempts to find the centers of **natural clusters** in the data by minimizing the total **intra-cluster variance**, or the squared error function:

$$V = \sum_{i=1}^{k} \sum_{x_j \in S_i} | x_j - u_i |^2$$

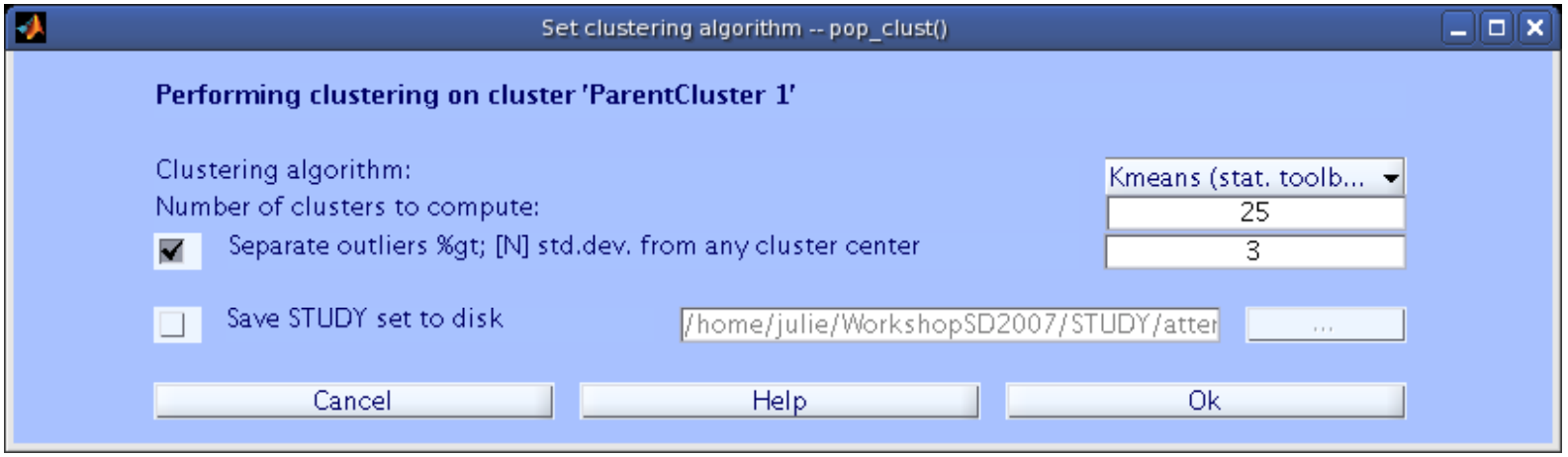
where there are k clusters S_i, i = 1,2,...,k and u_i is the **centroid** or mean of all the points.

•A drawback of the algorithm is that it has to be told the number of clusters (i.e. k) to find.

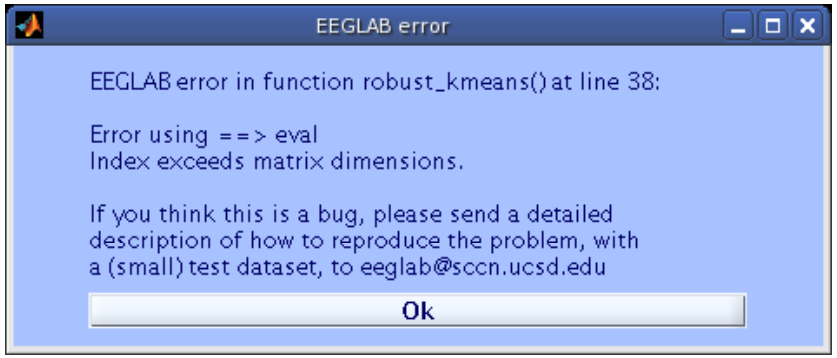
•If the data is not naturally clustered, you get some strange results.



Clustering: K-means

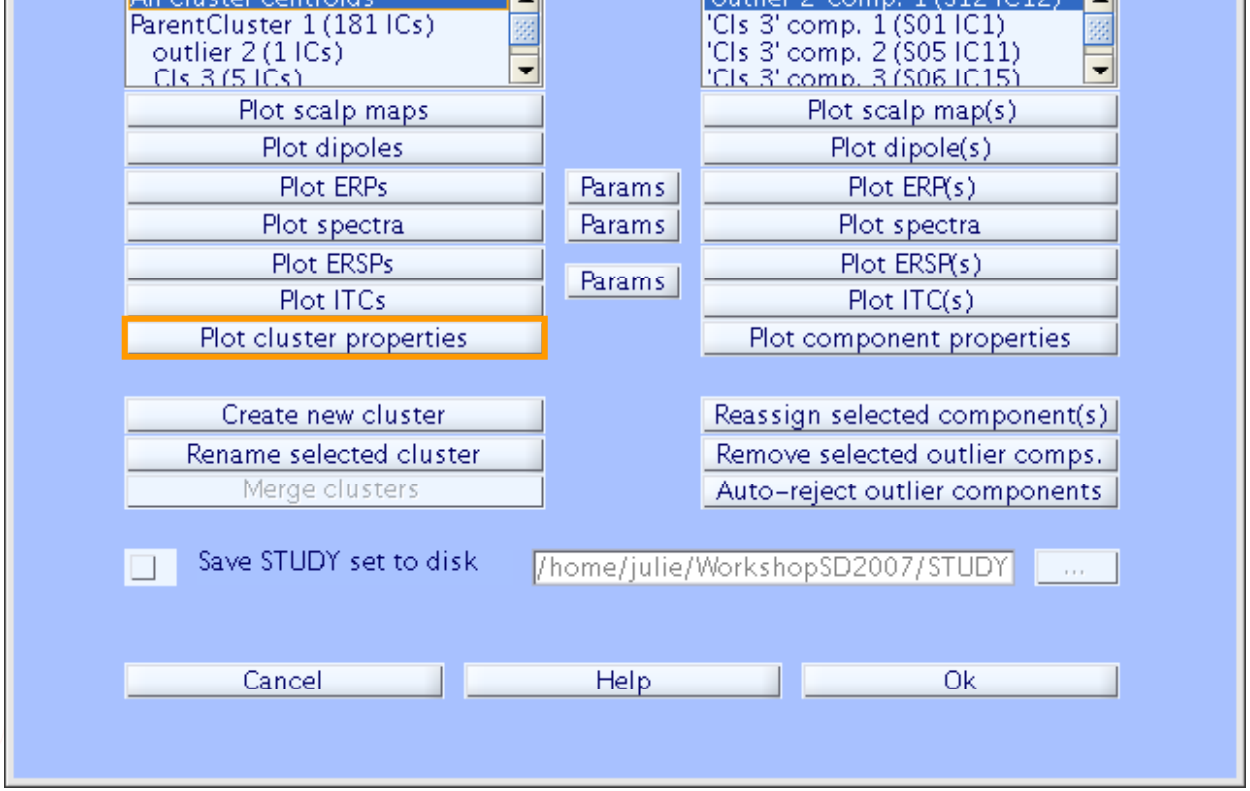


Note: If too many clusters were requested, you may get this error →

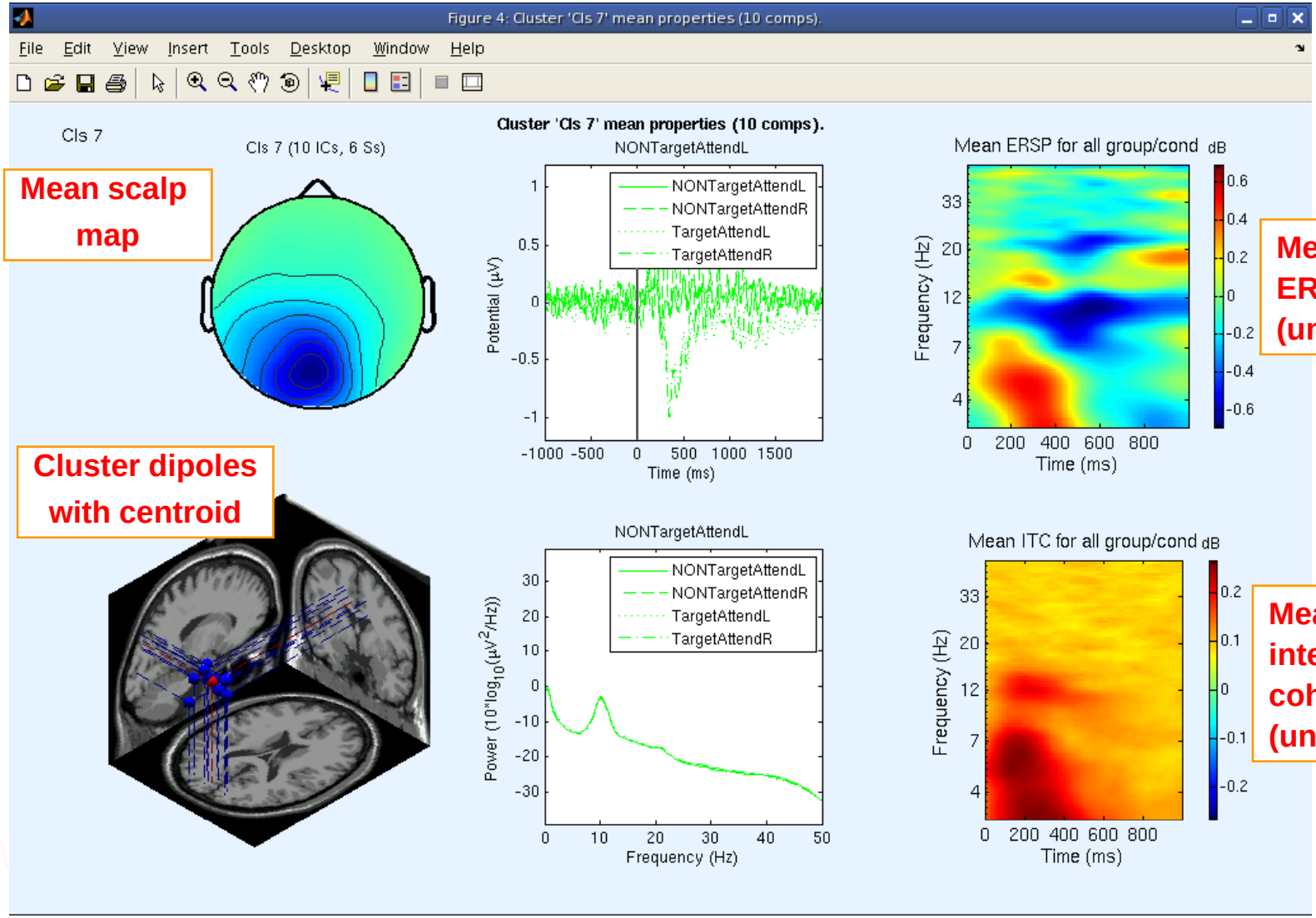



```
nclusts = 25; % choose # of clusters to create
[STUDY] = pop_clust(STUDY, ALLEEG,'algorithm','kmeans','clus_num',nclusts);
```

Successful clustering



Cluster properties



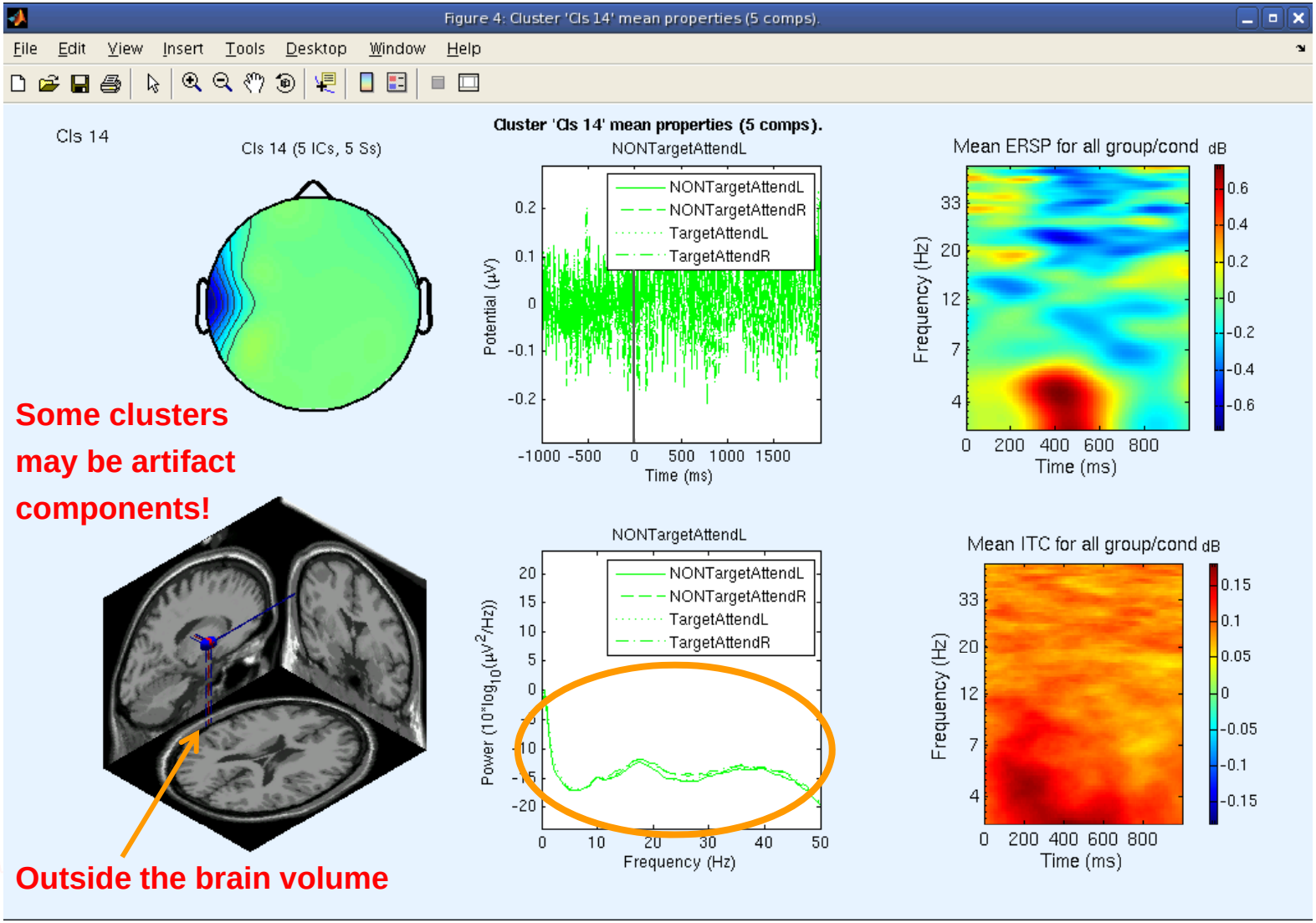
Mean scalp map

Cluster dipoles with centroid

Mean ERSP (un-masked)

Mean inter-trial coherence (un-masked)

Cluster properties



Exercise

- **Novice**
  - Use the GUI to build a STUDY (for practice, try just a few subjects).
  - Choose 'precompute' options (but do not recalculate for the sake of time).
  - Choose 'precluster' options and cluster.

- **Intermediate**
  - Script a loop to build a STUDY from the commandline
  - Precluster (pre-computation already done) and cluster components using measures of your choice.

- **Advanced**
  - Load raw data measures and run PCA to determine the relative size of PCA dimensions for each data measure.
  - Try preclustering/clustering based on your observations

** All scripts for Intermediate/Advanced exercises can be found in …/EEGLAB_WORKSHOP/Scripts/practicum_10.m