

STUDY plotting and statistics

STEP 1

Build a STUDY

STEP 2

Build design(s)

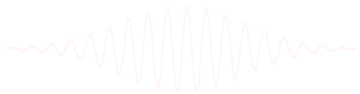
STEP 3

Precompute the data

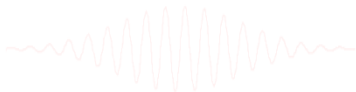
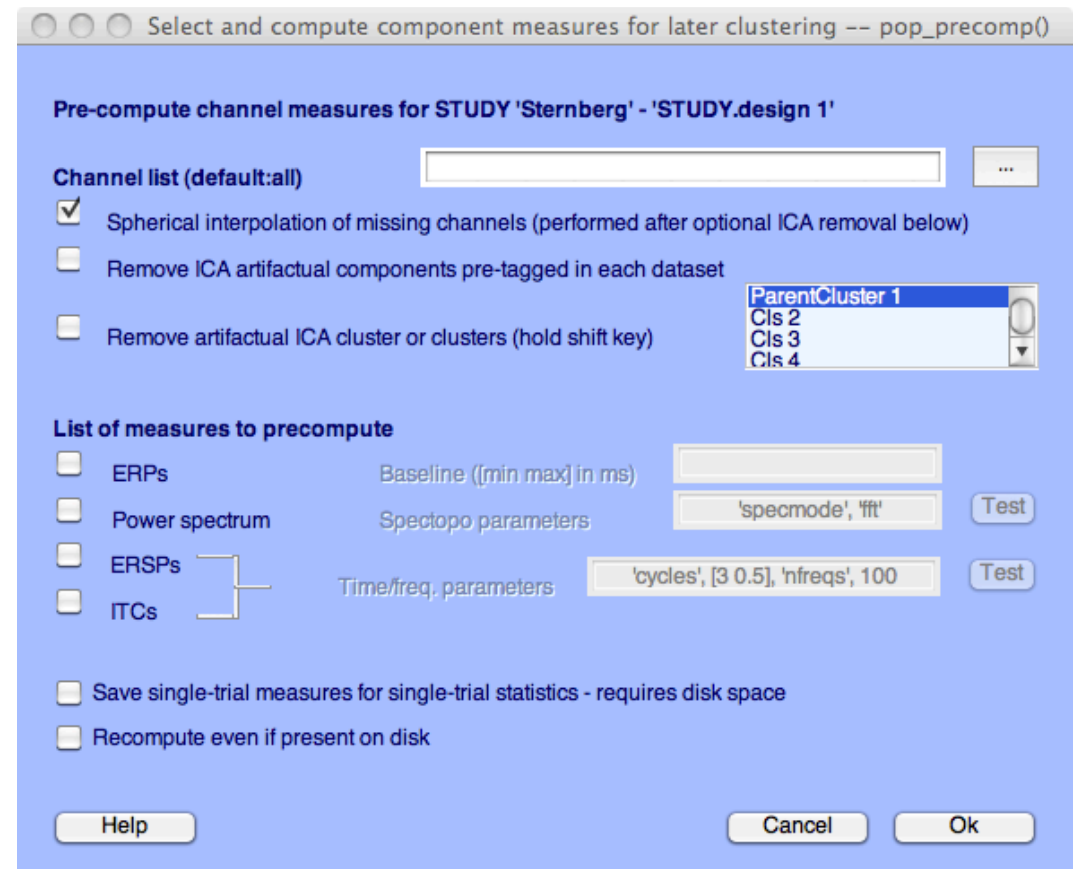
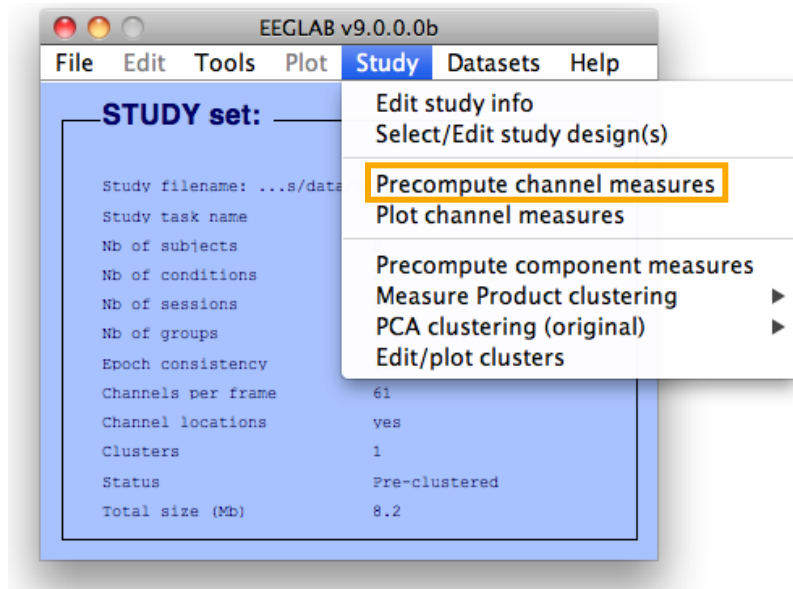
STEP 4

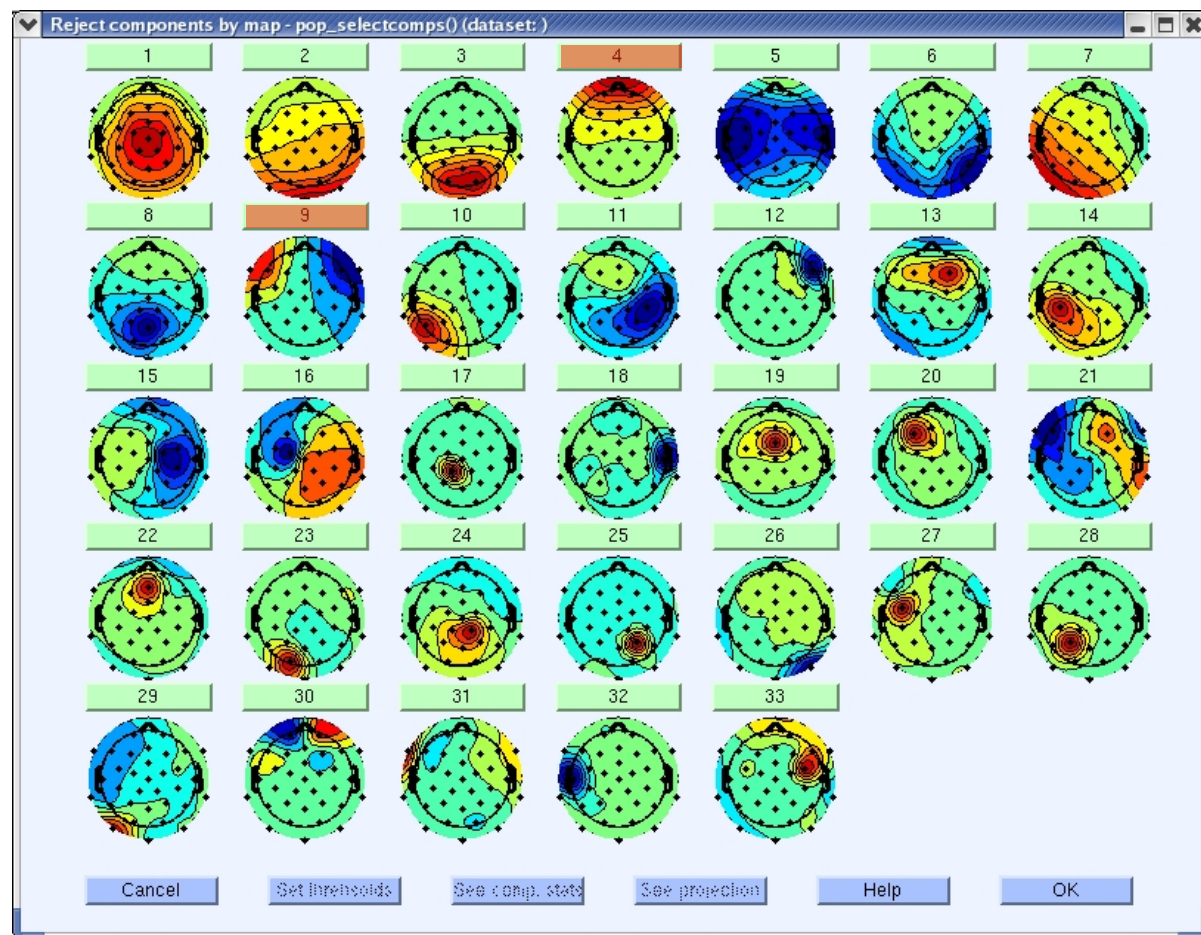
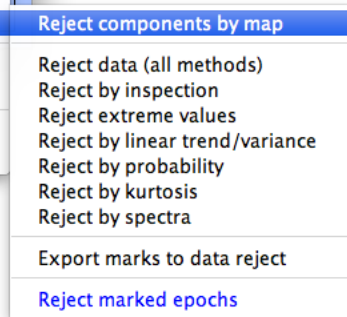
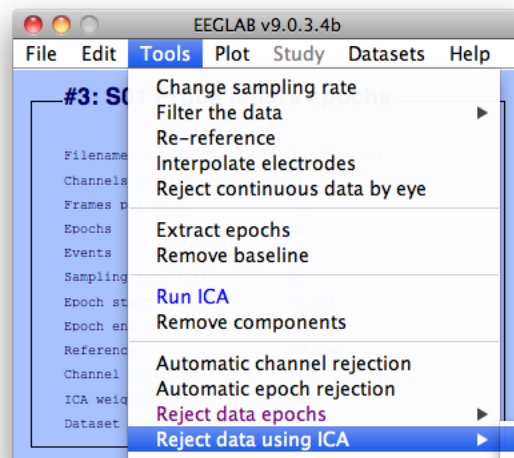
Plot the data

Exercise...



Precompute data measures





Set ERP plotting parameters -- pop_erpparams()

Time range in ms [low high] Plot limits in uV [low high]

Plot scalp map at latency [ms] Display filter in Hz [high]

☒ Plot first variable on the same panel

☐ Plot second variable on the same panel

Statistical method to use Parametric

Statistical threshold (p<)

☐ Compute first variable statistics

☐ Compute second variable statistics

☐ Use single trials (when available)

☐ Use False Discovery Rate to correct for multiple comparisons

Help Cancel Ok

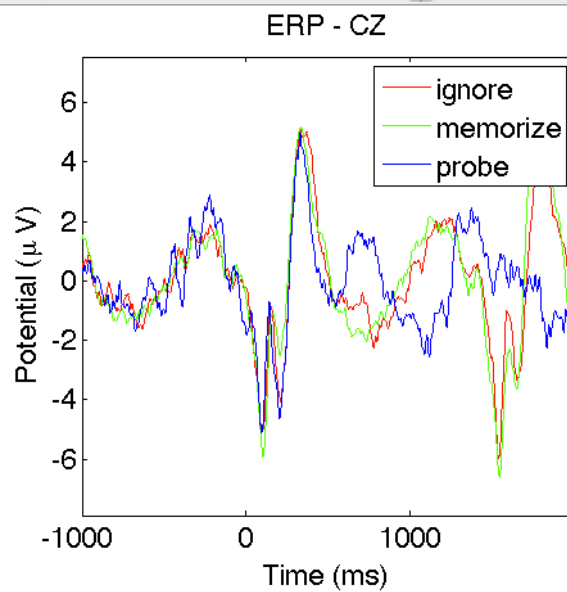
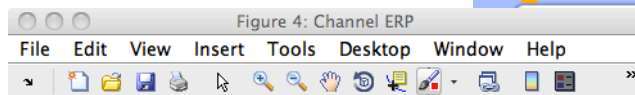
View and edit

STUDY name 'Sternberg' - 'S'

Select channel to plot

All FC8
All FT8
All FT10
All T7
All C5
All C3
All C1
All CZ
All C2
All C4
All C6

S02 CZ
S03 CZ
S04 CZ
S05 CZ
S06 CZ
S07 CZ
S08 CZ
S09 CZ



Set ERP plotting parameters -- pop_erpparams()

Time range in ms [low high] Plot limits in uV [low high]

Plot scalp map at latency [ms] Display filter in Hz [high]

☒ Plot first variable on the same panel
☐ Plot second variable on the same panel

Statistical method to use Parametric

Statistical threshold (p<)

☒ Compute first variable statistics
☐ Compute second variable statistics
☐ Use single trials (when available)
☐ Use False Discovery Rate to correct for multiple comparisons

Help Cancel Ok

View and edit

STUDY name 'Sternberg' - 'S

Select channel to plot

All FC8
All FT8
All FT10
All T7
All C5
All C3
All C1
All C2
All C4
All C6

Plot ERPs

Plot spectra

Plot ERSPs

Params

Params

S02 CZ
S03 CZ
S04 CZ
S05 CZ
S06 CZ
S07 CZ
S08 CZ
S09 CZ

Plot ERP(s)

Plot spectra

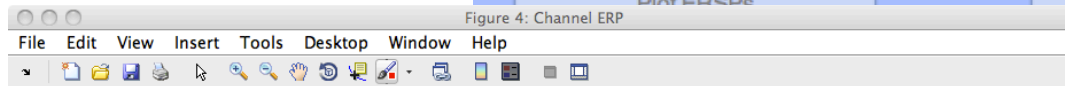
Plot ERSP(s)

Plot ITC(s)

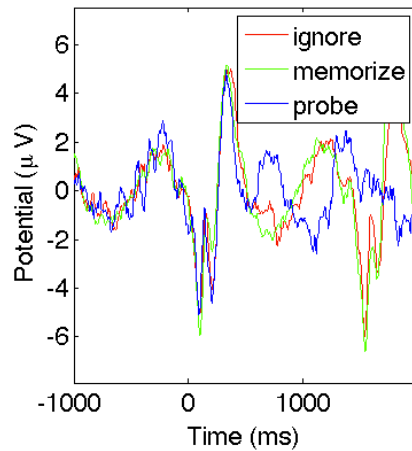
Plot channel properties (soon)

Cancel

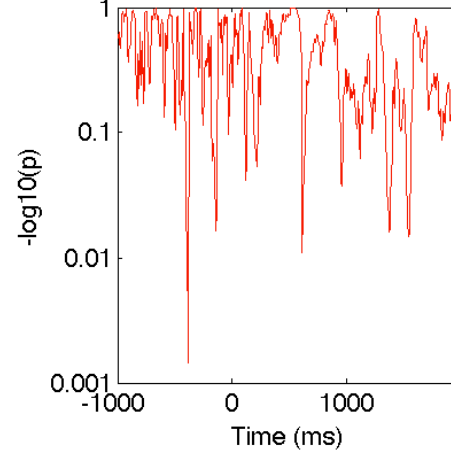
Ok



ERP - CZ



(p-value) param



Set ERP plotting parameters -- pop_erpparams()

Time range in ms [low high] Plot limits in uV [low high]

Plot scalp map at latency [ms] Display filter in Hz [high]

☒ Plot first variable on the same panel
☐ Plot second variable on the same panel

Statistical method to use Parametric Statistical threshold (p<) 0.05

☒ Compute first variable statistics
☐ Compute second variable statistics
☐ Use single trials (when available)
☐ Use False Discovery Rate to correct for multiple comparisons

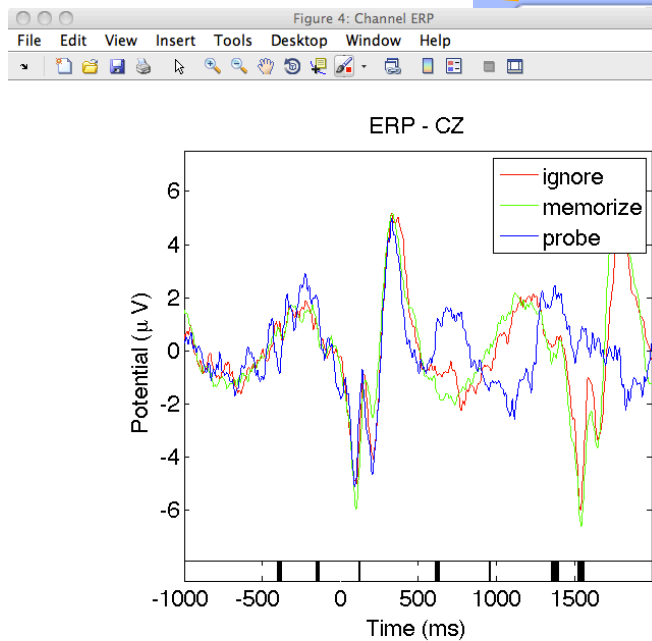
Help Cancel Ok

View and edit

STUDY name 'Sternberg' - 'S

Select channel to plot

All FC8
All FT8
All FT10
All T7
All C5
All C3
All C1
All CZ
All C2
All C4
All C6



S02 CZ
S03 CZ
S04 CZ
S05 CZ
S06 CZ
S07 CZ
S08 CZ
S09 CZ

Ps
Spectra
SPs
Cs
Properties

Params

Plot ERP(s)
Plot spectra
Plot ERSP(s)
Plot ITC(s)
Plot channel properties (soon)

Cancel Ok

Set ERP plotting parameters -- pop_erpparams()

Time range in ms [low high] Plot limits in uV [low high]

Plot scalp map at latency [ms] Display filter in Hz [high]

☒ Plot first variable on the same panel
☐ Plot second variable on the same panel

Statistical method to use Parametric Statistical threshold (p<) 0.05

☒ Compute first variable statistics
☐ Compute second variable statistics
☐ Use single trials (when available)
☒ Use False Discovery Rate to correct for multiple comparisons

Help Cancel Ok

View and edit

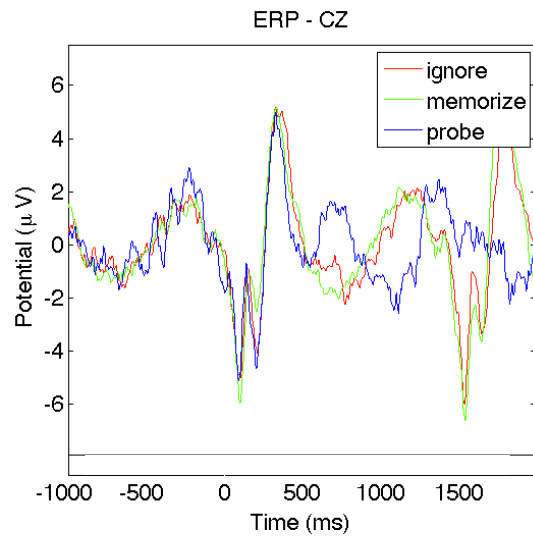
STUDY name 'Sternberg' - 'S

Select channel to plot

All FC8
All FT8
All FT10
All T7
All C5
All C3
All C1
All CZ
All C2
All C4
All C6

Figure 4: Channel ERP

File Edit View Insert Tools Desktop Window Help



S02 CZ
S03 CZ
S04 CZ
S05 CZ
S06 CZ
S07 CZ
S08 CZ
S09 CZ

Ps
Spectra
SPs
Cs
Properties

Params
Params
Params

Plot ERP(s)
Plot spectra
Plot ERSP(s)
Plot ITC(s)
Plot channel properties (soon)

Cancel Ok

Set ERP plotting parameters -- pop_erpparams()

Time range in ms [low high] Plot limits in uV [low high]

Plot scalp map at latency [ms] ☐ Plot first variable on the same panel
☐ Plot second variable on the same panel

Statistical method to use Parametric Statistical threshold (p<)

☐ Compute first variable statistics
☐ Compute second variable statistics
☐ Use single trials (when available)
☐ Use False Discovery Rate to correct for multiple comparisons

Help Cancel Ok

View and edit

STUDY name 'Sternberg' - 'S'

Select channel to plot

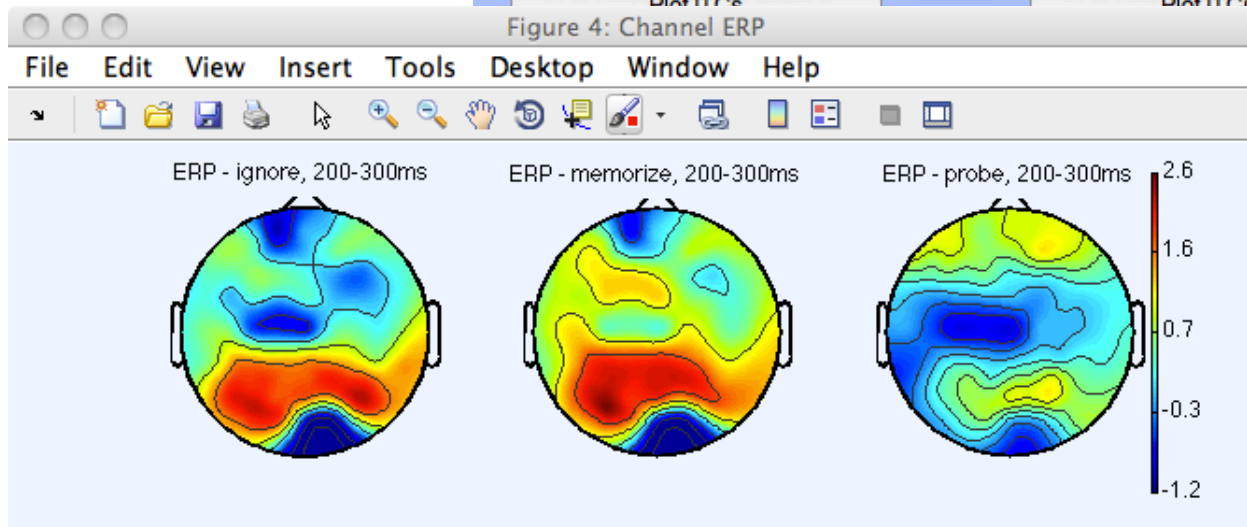
All P6
 All P8
 All PO9
 All PO7
 All PO3
 All POZ
 All PO4
 All PO8
 All PO10
 All O1

Plot ERPs
 Plot spectra
 Plot ERSPs
 Plot ITCs

Params
 Params
 Params

Plot ERP(s)
 Plot spectra
 Plot ERSP(s)
 Plot ITC(s)

S03 All
 S04 All
 S05 All
 S06 All
 S07 All
 S08 All
 S09 All



Set ERP plotting parameters -- pop_erpparams()

Time range in ms [low high]

Plot scalp map at latency [ms]

Plot limits in uV [low high]

Display filter in Hz [high]

☒ Plot first variable on the same panel

☐ Plot second variable on the same panel

Statistical method to use

Statistical threshold (p<)

☒ Compute first variable statistics

☐ Compute second variable statistics

☐ Use single trials (when available)

☒ Use False Discovery Rate to correct for multiple comparisons

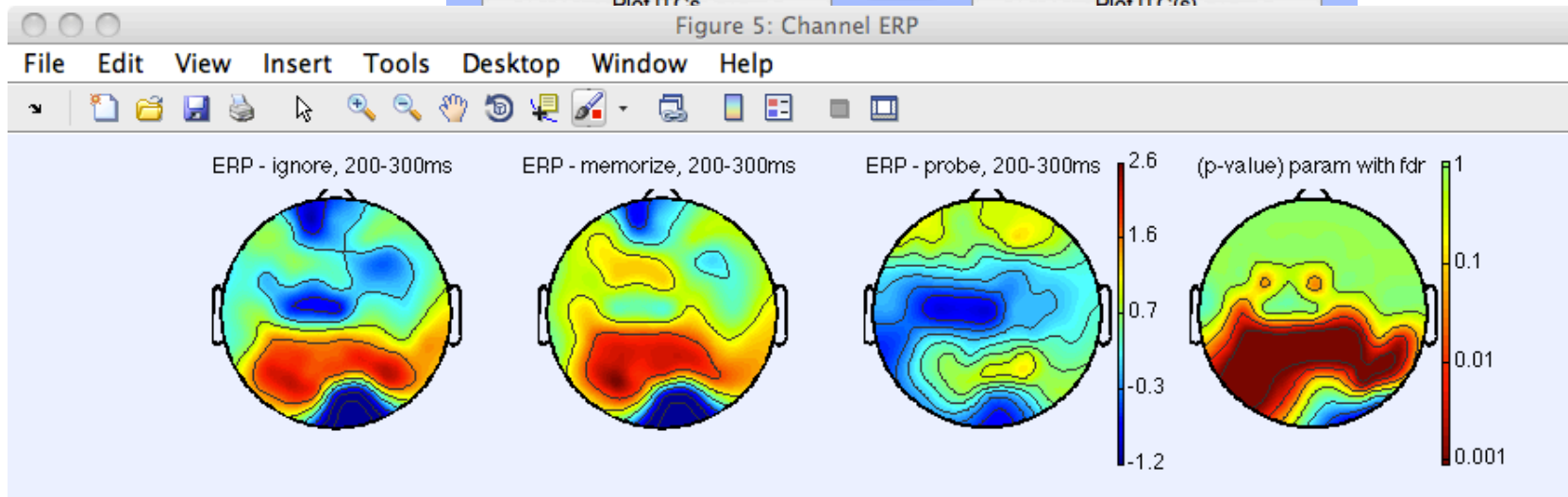
View and edit

STUDY name 'Sternberg' - 'S'

Select channel to plot

All P6
All P8
All PO9
All PO7
All PO3
All POZ
All PO4
All PO8
All PO10
All O1

Figure 5: Channel ERP



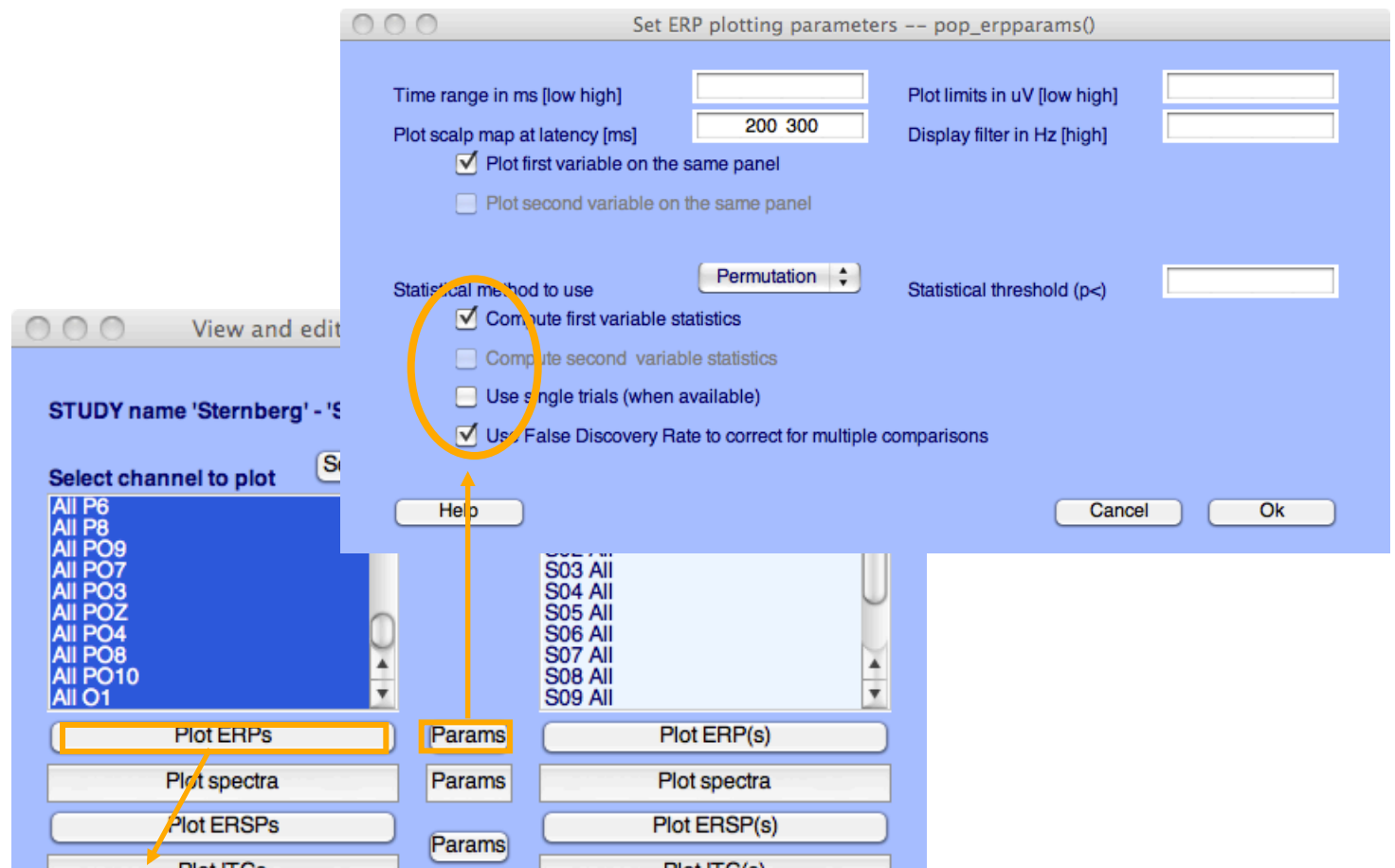
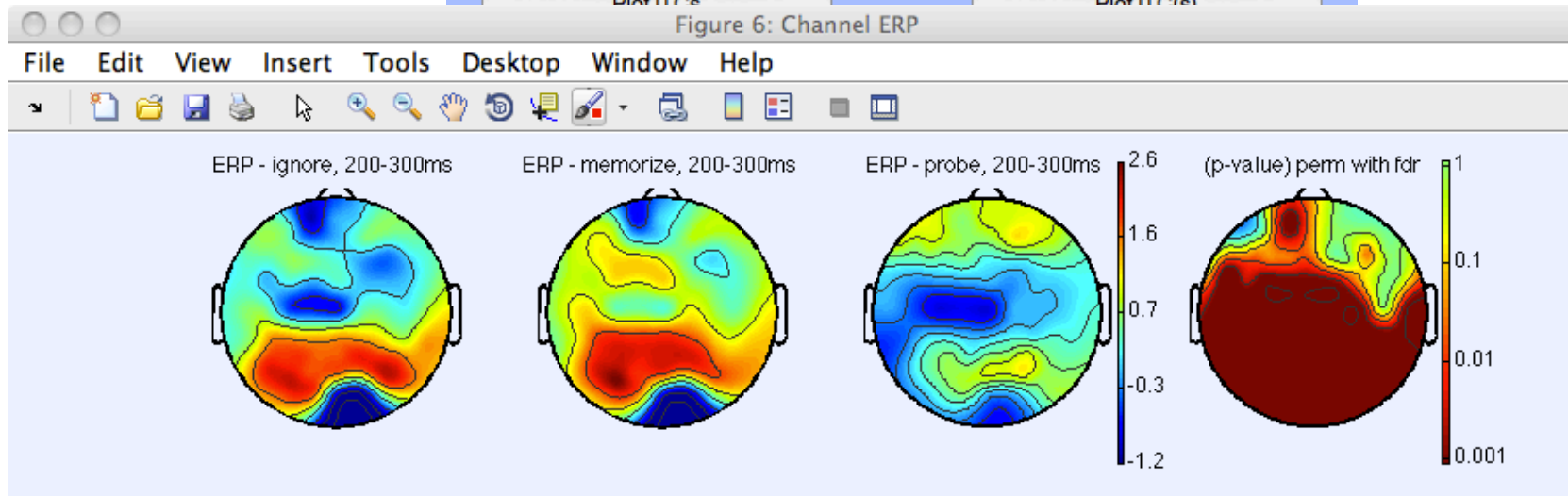


Figure 6: Channel ERP



Computing Spectrum

Select and compute component measures for later clustering -- pop_precomp()

Pre-compute channel measures for STUDY 'Sternberg' - 'STUDY.design 1'

Channel list (default:all) ...

☒ Spherical interpolation of missing channels (performed after optional ICA removal below)

☐ Remove ICA artifactual components pre-tagged in each dataset

☐ Remove artifactual ICA cluster or clusters (hold shift key)

ParentCluster 1
Cls 2
Cls 3
Cls 4

List of measures to precompute

☐ ERPs Baseline ([min max] in ms)

☒ Power spectrum Spectopo parameters

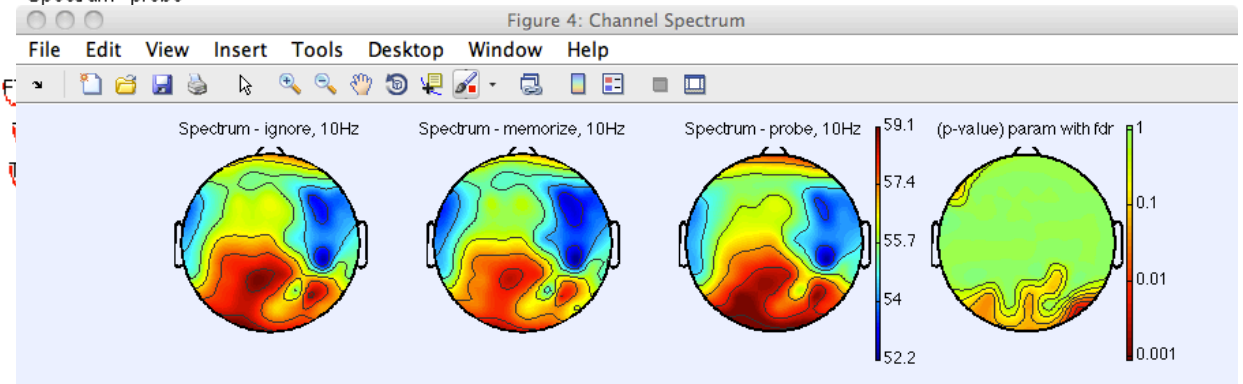
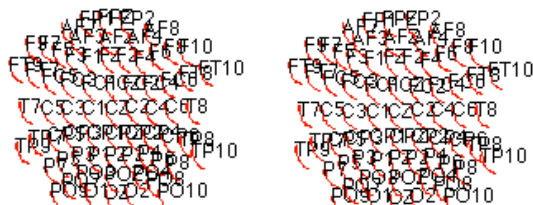
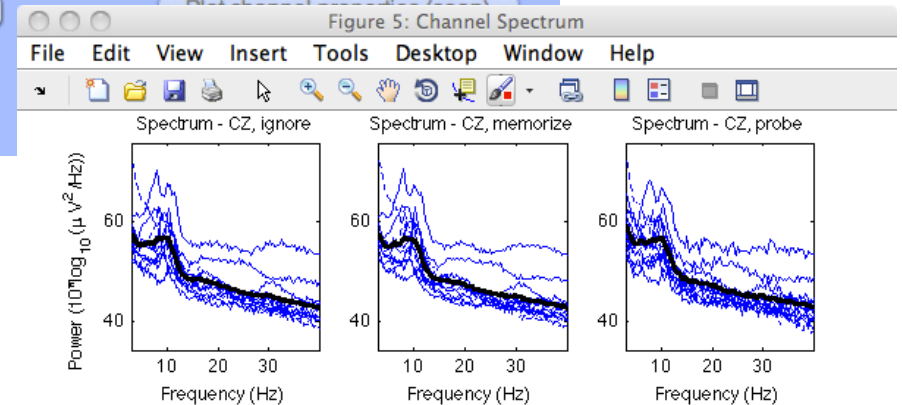
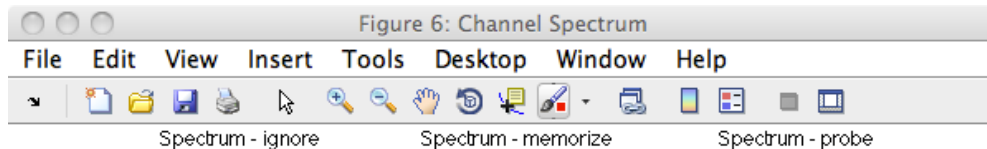
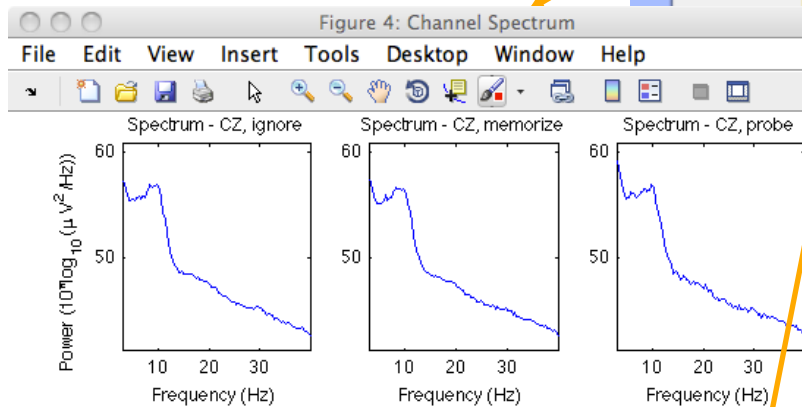
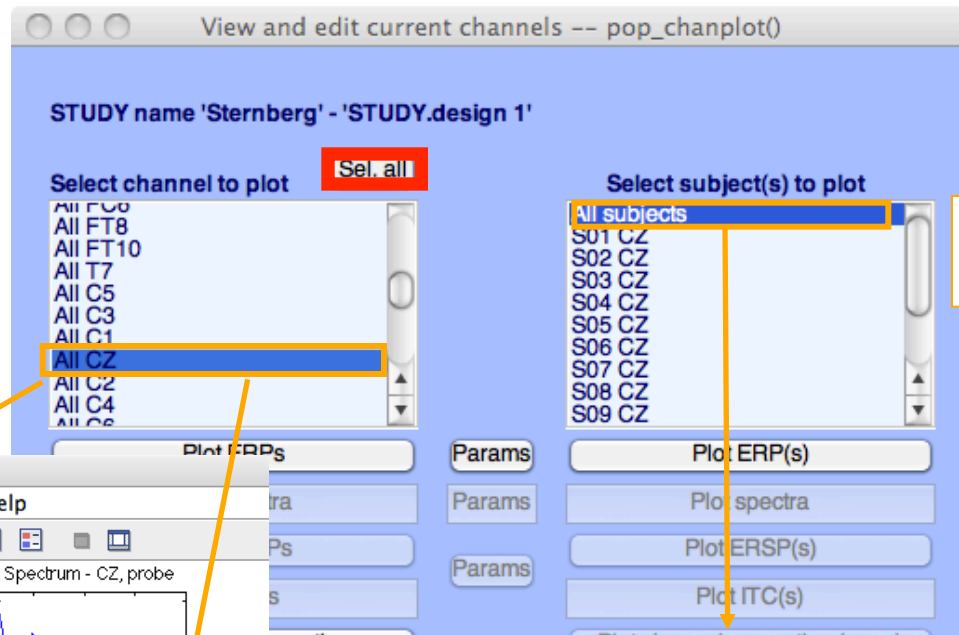
☐ ERSPs

☐ ITCs

☐ Save single-trial measures for single-trial statistics - requires disk space

☐ Recompute even if present on disk

Use 'timerange' option
to select time range,
see "help std_spec"



Computing ERSP

'cycles', [3 0.8], 'nfreqs', 50, 'ntimesout', 100

Select and compute component measures for later clustering -- pop_precomp()

Pre-compute channel measures for STUDY 'Sternberg' - 'Design 2'

Channel list (default:all) ...

☒ Spherical interpolation of missing channels (performed after optional ICA removal below)

☐ Remove ICA artifactual components pre-tagged in each dataset

☐ Remove artifactual ICA cluster or clusters (hold shift key)

ParentCluster 1
Cls 2
Cls 3
Cls 4

List of measures to precompute

☐ ERPs Baseline ([min max] in ms)

☐ Power spectrum Spectopo parameters Test

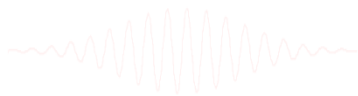
☒ ERSPs Time/req. parameters Test

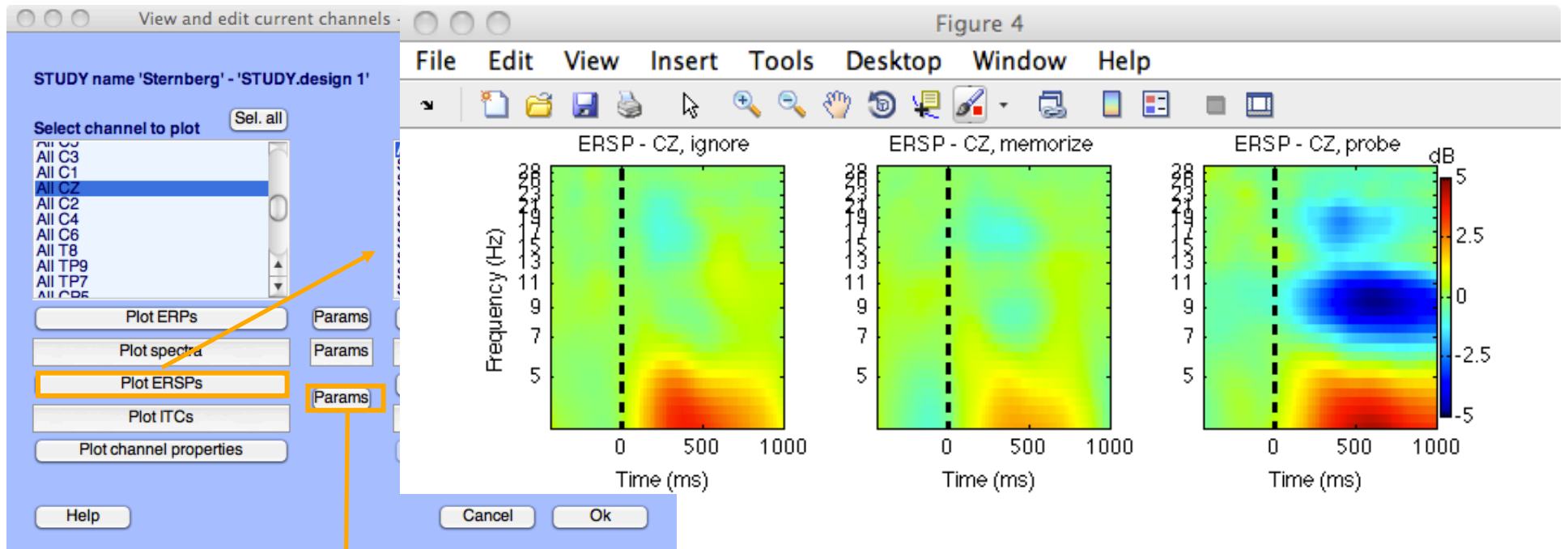
☐ ITCs

☐ Save single-trial measures for single-trial statistics - requires disk space

☐ Recompute even if present on disk

Help Cancel Ok





Set ERSP/ITC plotting parameters -- pop_erspparams()

Time range in ms [Low High] **-500 1000** Plot scalp map at time [ms]

Freq. range in Hz [Low High] **3 30** Plot scalp map at freq. [Hz]

Power limits in dB [Low High] ITC limit (0-1) [High]

☒ Compute common ERSP baseline (assumes additive baseline)

Statistical method to use **Permutation** Statistical threshold (p<)

☒ Compute first variable statistics

☐ Compute second variable statistics

☐ Use single trials (when available)

☒ Use False Discovery Rate to correct for multiple comparisons

Help Cancel Ok

Set ERSP|ITC plotting parameters -- pop_erspparams()

Time range in ms [Low High] Plot scalp map at time [ms]

Freq. range in Hz [Low High] Plot scalp map at freq. [Hz]

Power limits in dB [Low High] ITC limit (0-1) [High]

☒ Compute common ERSP baseline (assumes additive baseline)

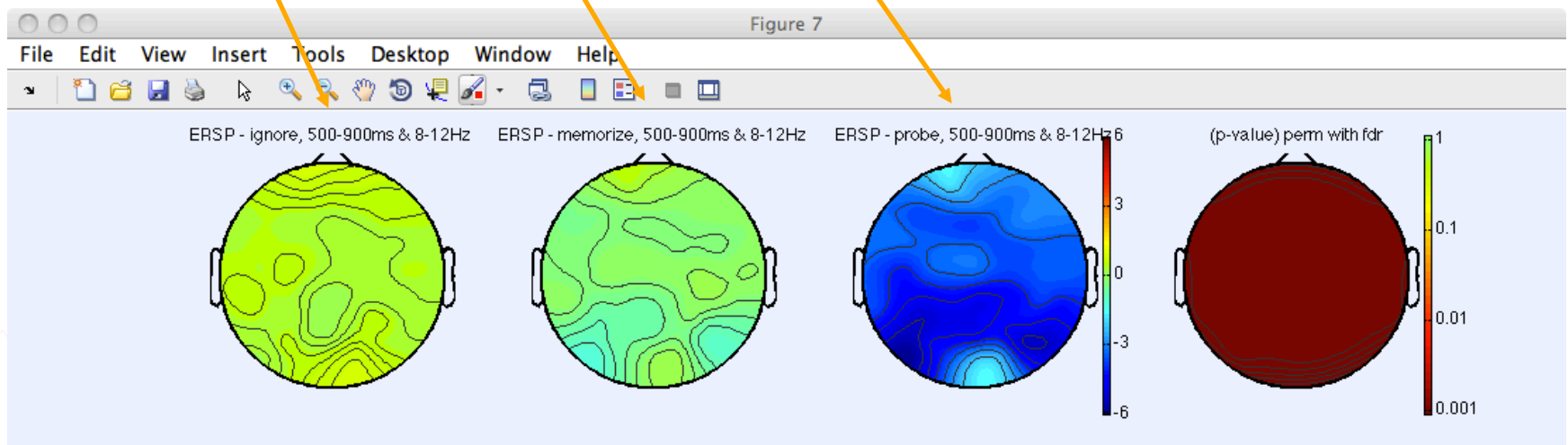
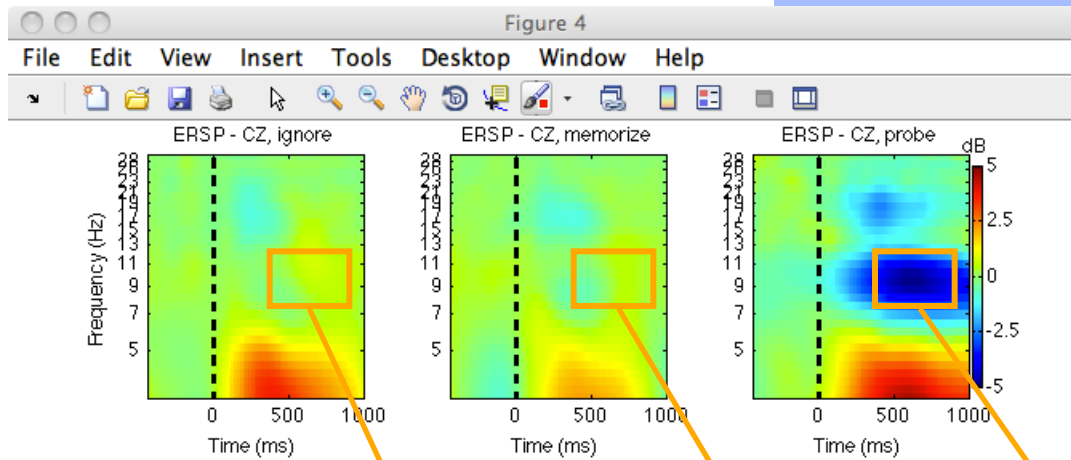
Statistical method to use Statistical threshold (p<)

☒ Compute first variable statistics

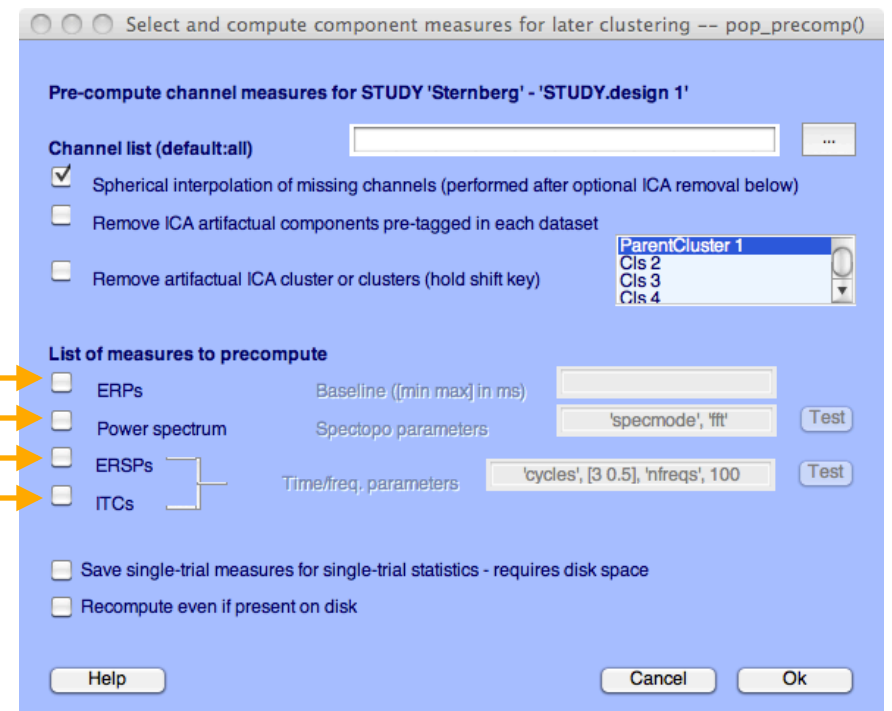
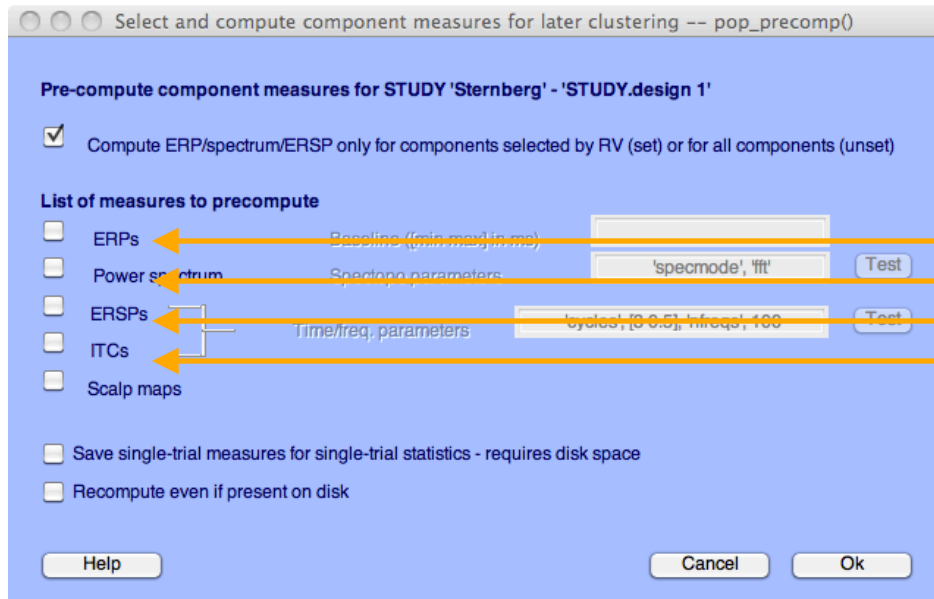
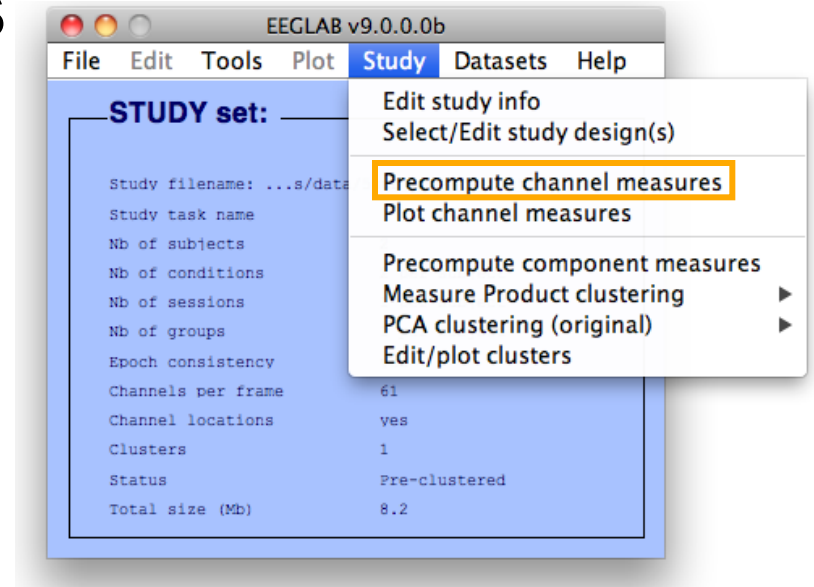
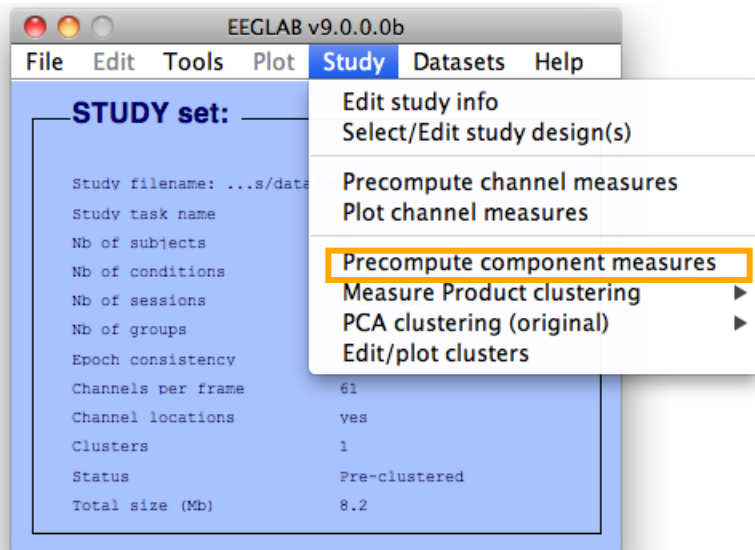
variable statistics

when available)

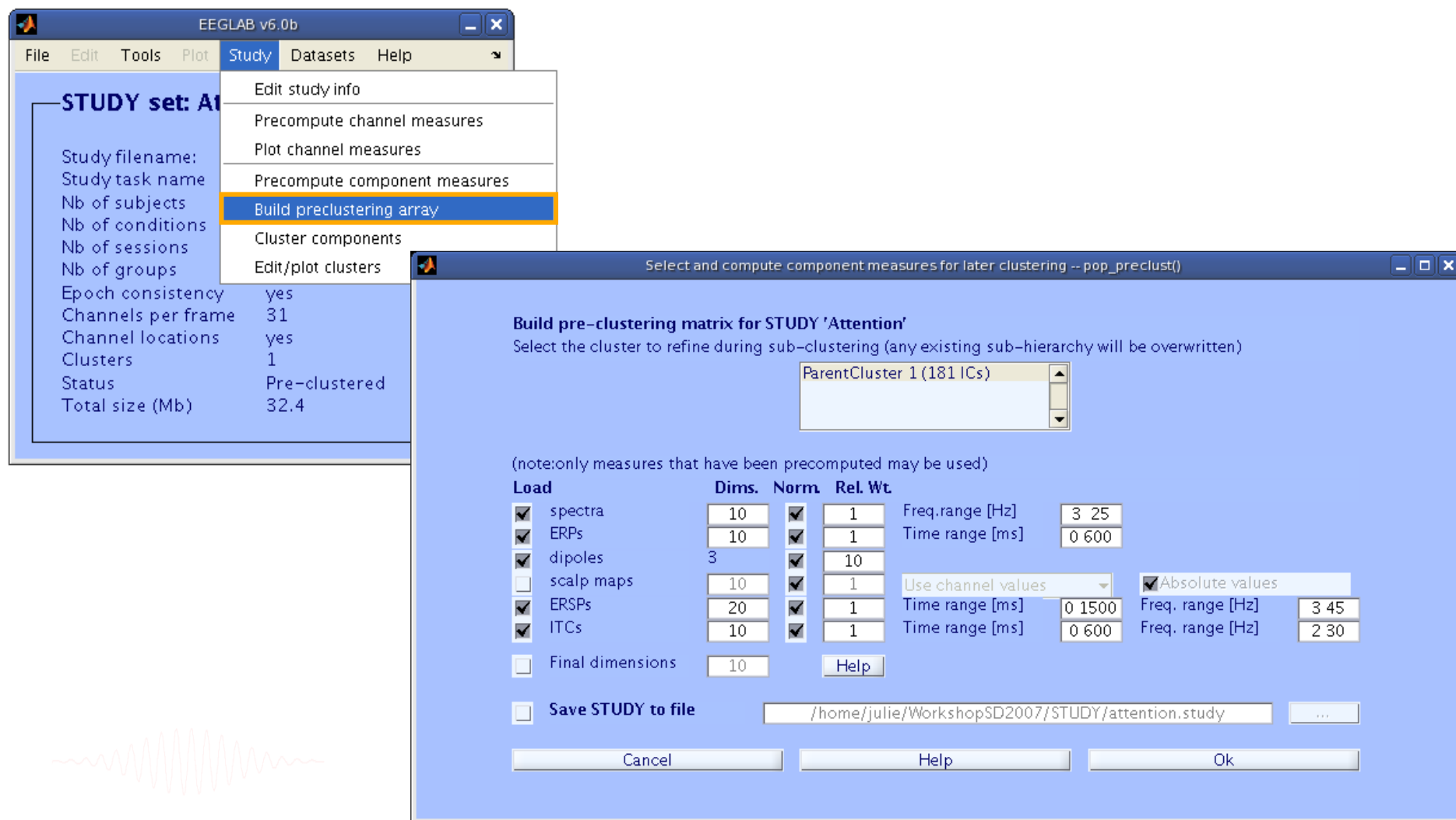
very Rate to correct for multiple comparisons



2. Pre-compute measures



3. Cluster components



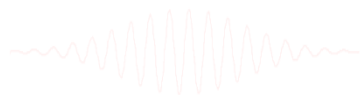
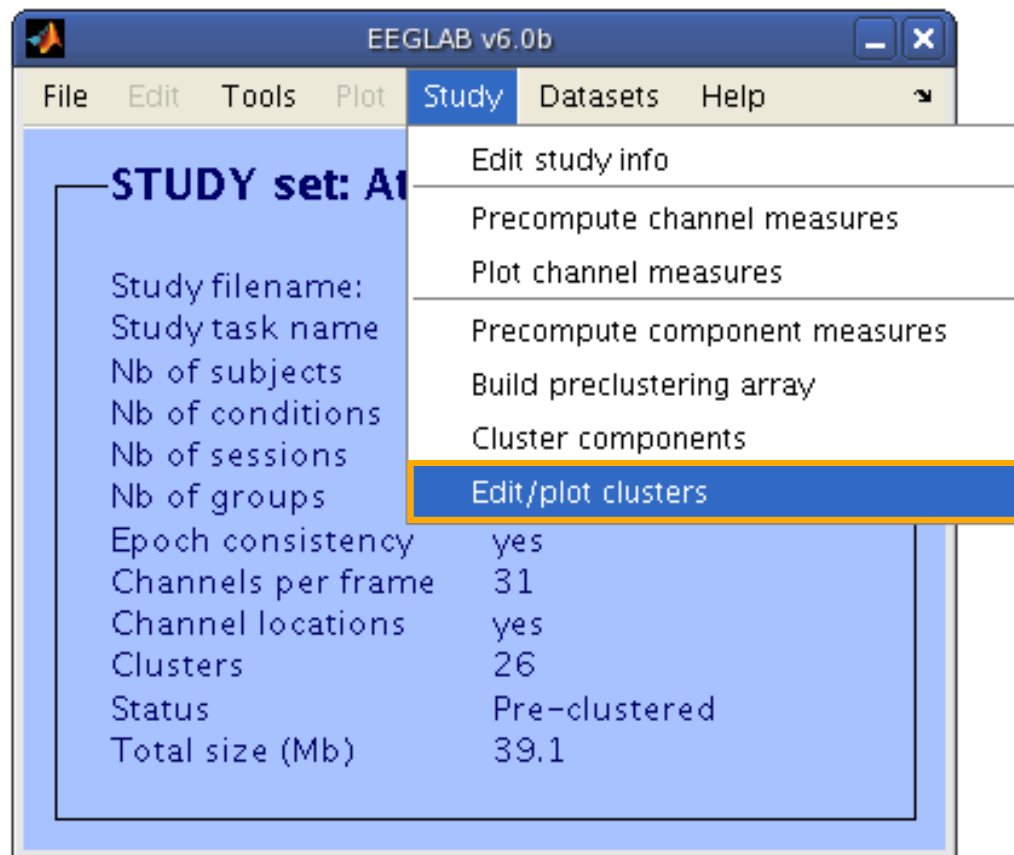
The image displays the EEGLAB v6.0b software interface. The 'Study' menu is open, showing options like 'Edit study info', 'Precompute channel measures', 'Plot channel measures', 'Precompute component measures', 'Build preclustering array' (highlighted), 'Cluster components', and 'Edit/plot clusters'. The 'STUDY set: Attention' panel shows study details: filename, task name, 31 subjects, 1 condition, 1 session, 1 group, epoch consistency, 31 channels, 1 cluster, pre-clustered status, and 32.4 Mb size.

The 'Select and compute component measures for later clustering -- pop_preclust()' dialog box is open, titled 'Build pre-clustering matrix for STUDY 'Attention''. It allows selecting a cluster to refine (ParentCluster 1 (181 ICs)). A note states: '(note: only measures that have been precomputed may be used)'. The 'Load' section includes checkboxes for 'spectra', 'ERPs', 'dipoles', 'scalp maps', 'ERSPs', and 'ITCs', each with 'Dims.', 'Norm.', and 'Rel. Wt.' fields. The 'Final dimensions' checkbox is also present. The 'Save STUDY to file' section shows the file path: '/home/julie/WorkshopSD2007/STUDY/attention.study'. The 'Absolute values' checkbox is checked. The 'Freq. range [Hz]' and 'Time range [ms]' fields are set for 'spectra' and 'ERPs'. The 'Help' button is visible.

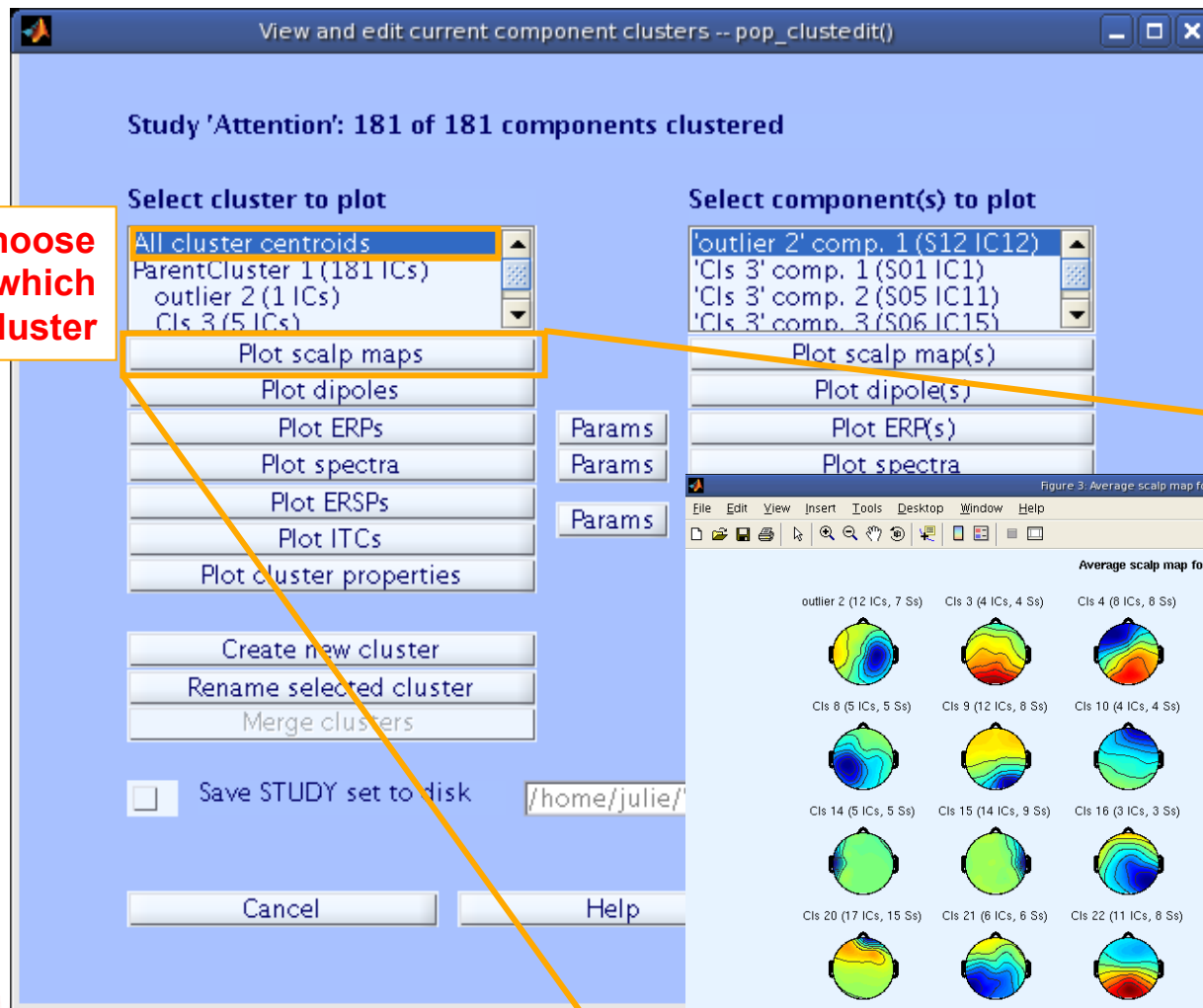
Load	Dims.	Norm.	Rel. Wt.
<input checked="" type="checkbox"/> spectra	10	<input checked="" type="checkbox"/>	1
<input checked="" type="checkbox"/> ERPs	10	<input checked="" type="checkbox"/>	1
<input checked="" type="checkbox"/> dipoles	3	<input checked="" type="checkbox"/>	10
<input type="checkbox"/> scalp maps	10	<input checked="" type="checkbox"/>	1
<input checked="" type="checkbox"/> ERSPs	20	<input checked="" type="checkbox"/>	1
<input checked="" type="checkbox"/> ITCs	10	<input checked="" type="checkbox"/>	1
<input type="checkbox"/> Final dimensions	10		

Buttons: Cancel, Help, Ok

View and edit clusters



Plot cluster data



Choose
which
cluster

Select component(s) to plot

'outlier 2' comp. 1 (S12 IC12)

'Cls 3' comp. 1 (S01 IC1)

'Cls 3' comp. 2 (S05 IC11)

'Cls 3' comp. 3 (S06 IC15)

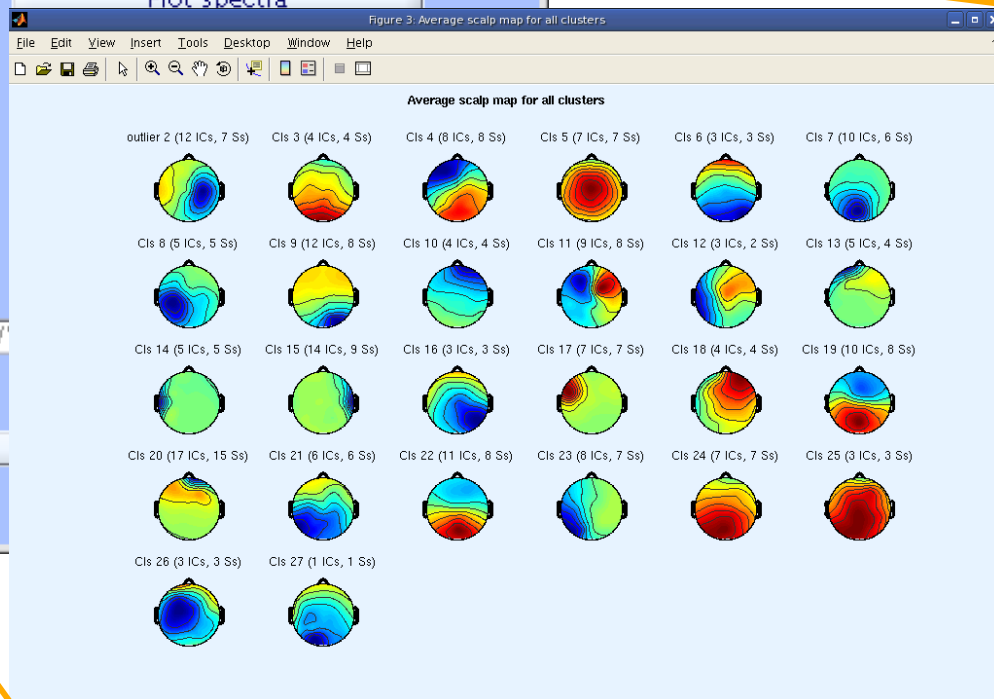
Plot scalp map(s)

Plot dipole(s)

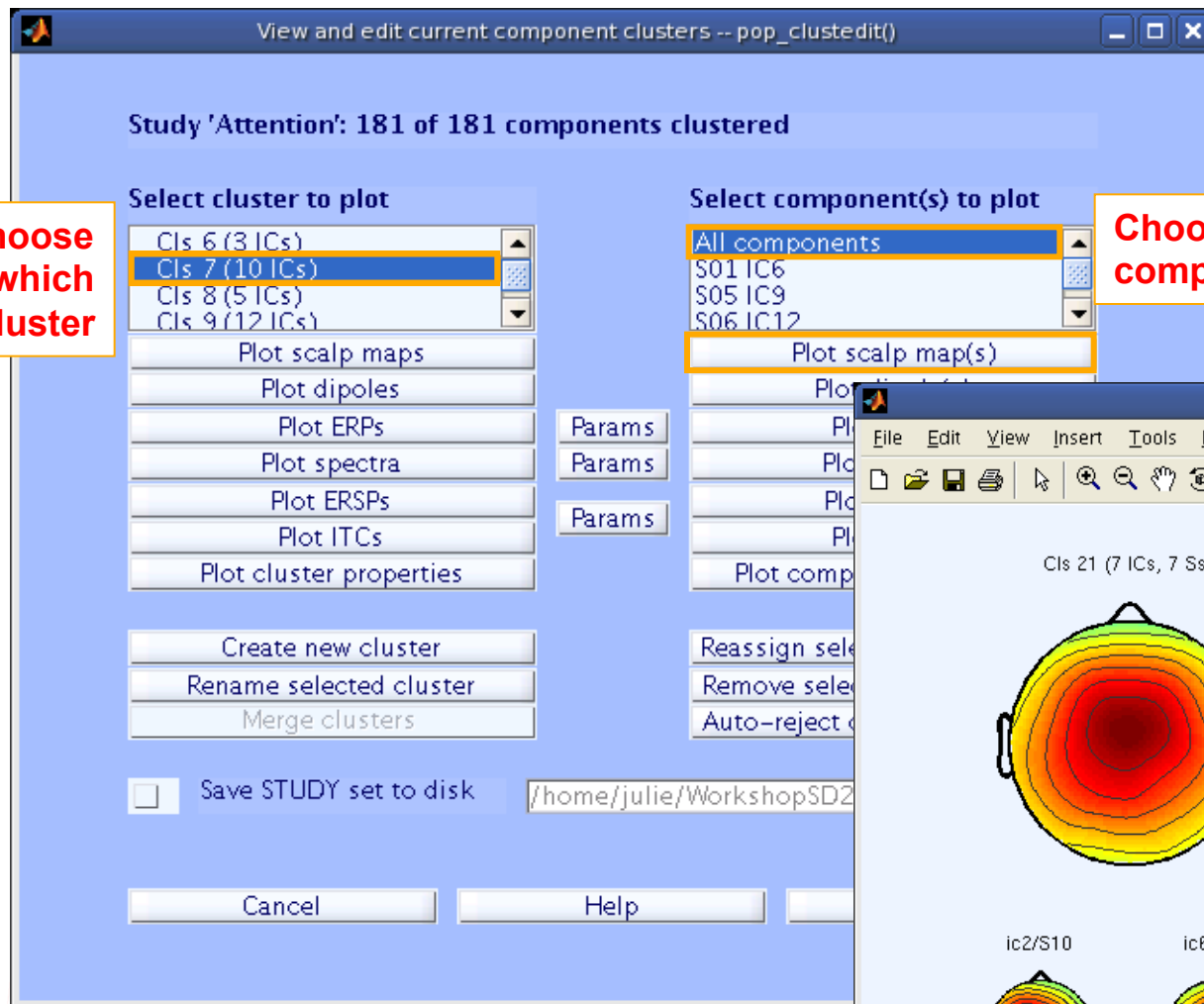
Plot ERP(s)

Plot spectra

Plot mean scalp
maps for easy
reference

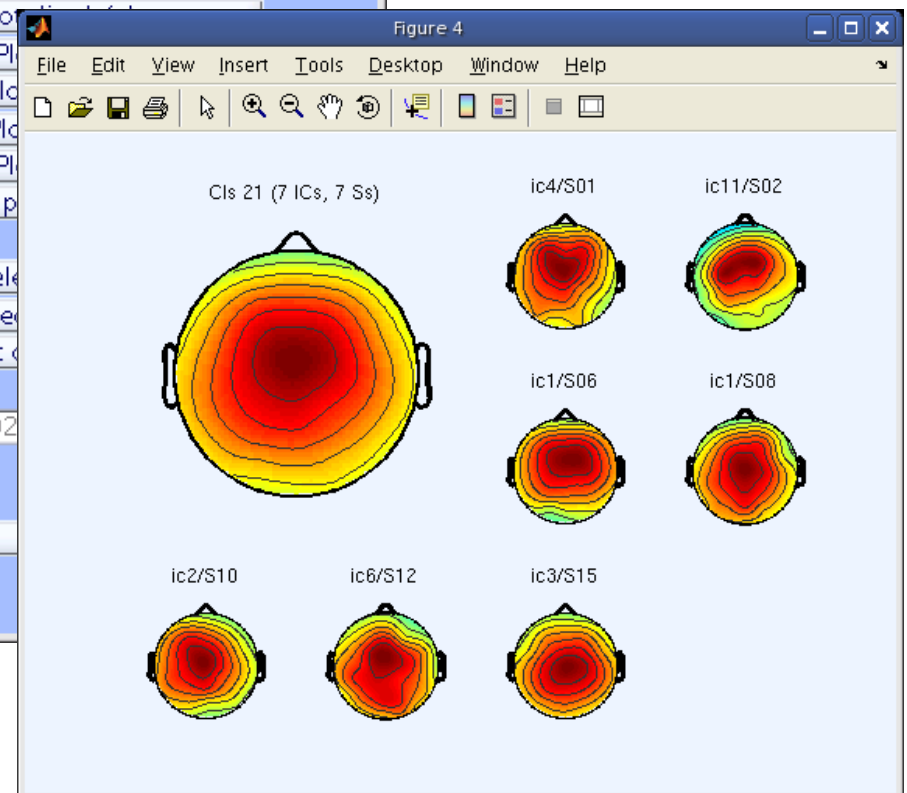


Plot cluster data

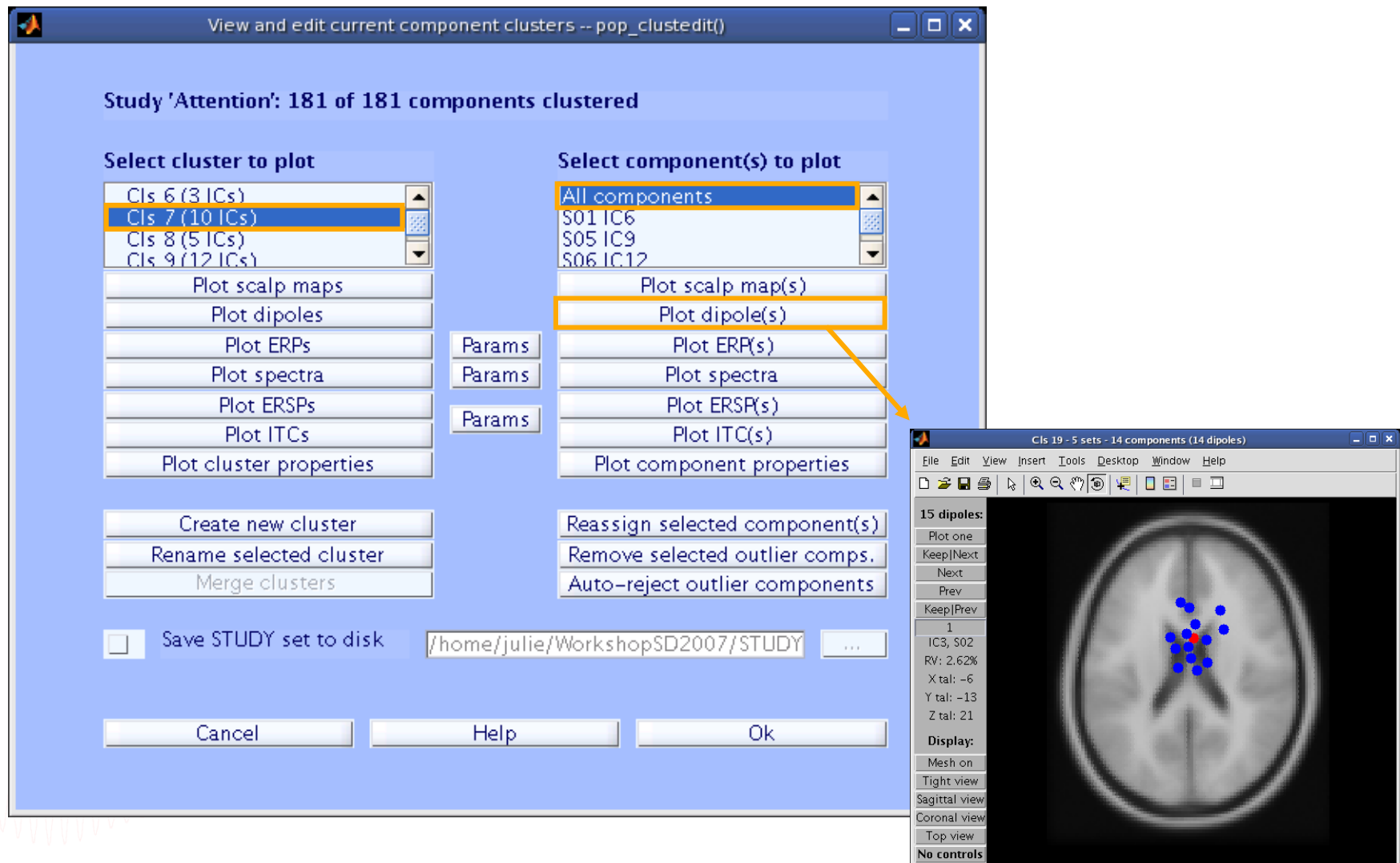


Choose which cluster

Choose which components



Plot cluster data



Parametric statistics

Assume gaussian distribution of data

T-test: Compare paired/
unpaired

Samples for continuous
data. In EEGLAB, used for
grand-average ERPs.

ANOVA: compare several
groups (can test interaction
between two factors for the
repeated measure ANOVA)

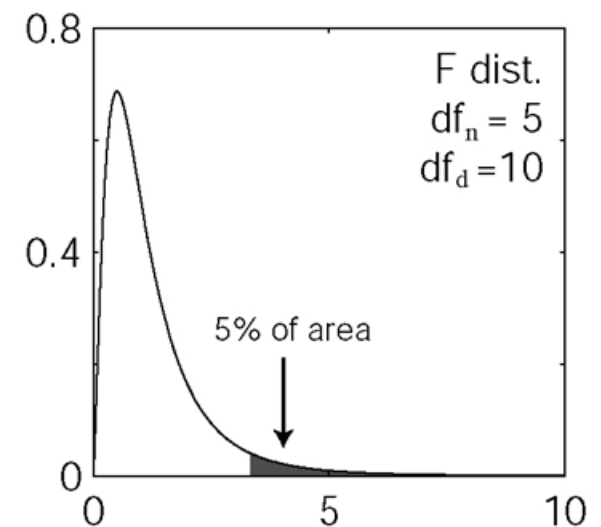
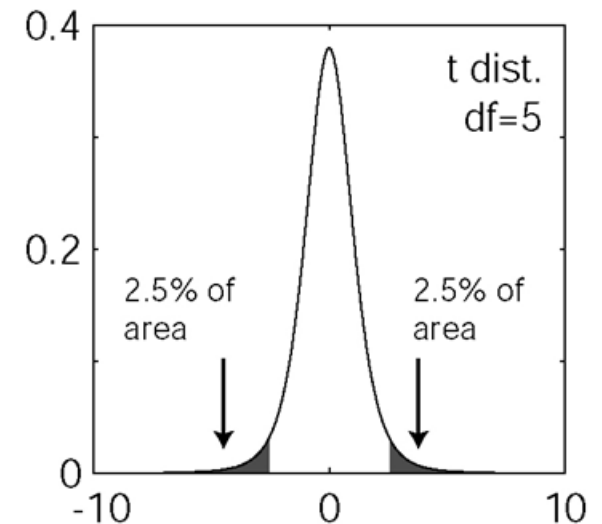
Paired

$$t = \frac{\text{Mean_difference}}{\text{Standard_deviation}} \sqrt{N-1}$$

Unpaired

$$t = \sqrt{N} \frac{\text{Mean}_A - \text{Mean}_B}{\sqrt{(\text{SD}_A)^2 + (\text{SD}_B)^2}}$$

$$F = \frac{\text{Variance}_{\text{interGroup}} / N_{\text{Group}} - 1}{\text{Variance}_{\text{WithinGroup}} / N - N_{\text{Group}}}$$



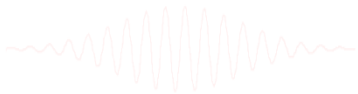
Non-parametric statistics

Paired t-test	—————→	Wilcoxon
Unpaired t-test	—————→	Mann-Whitney
One way ANOVA	—————→	Kruskal Wallis

Values

Ranks

BOTH ASSUME NORMAL DISTRIBUTIONS

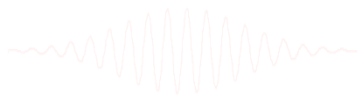


Problems

- Not resistant against outliers
- For ANOVA and t-test non-normality is an issue when distributions differ or when variances are not equal.
- Slight departure from normality can have serious consequences

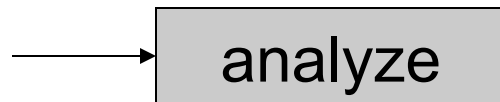
Solutions

1. Randomization approach
2. Bootstrap approach

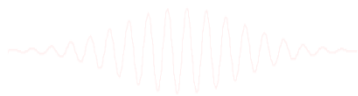


Randomization approach

a a a
a a a

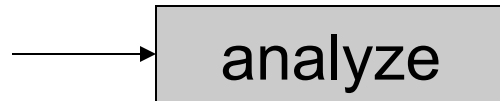


b b b
b b b

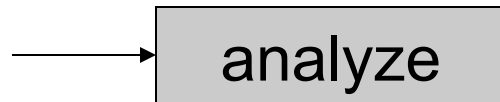


Randomization approach

a a b
b a b

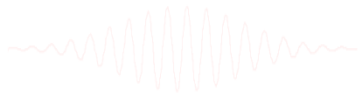


a b a
b a b

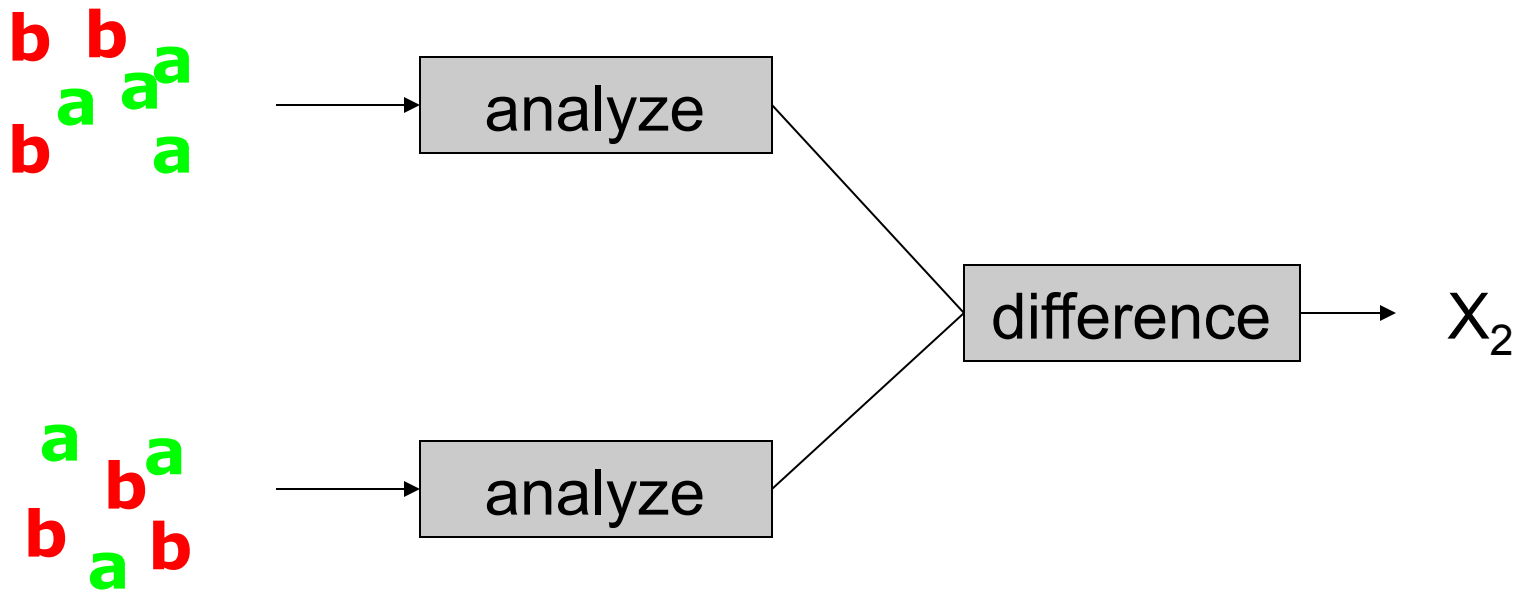


difference

X_1

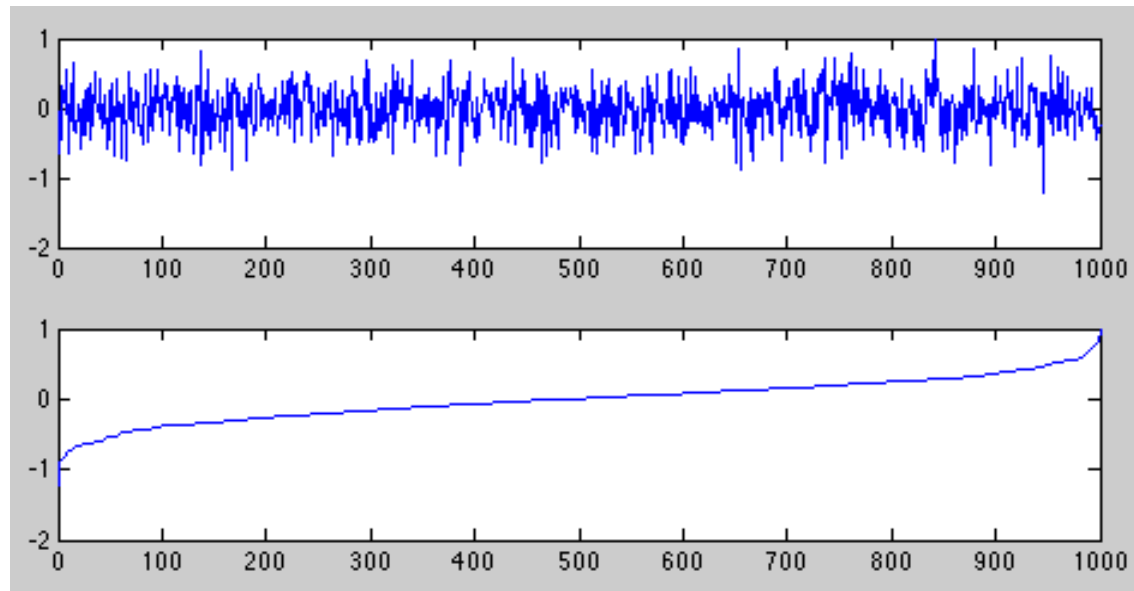


Randomization approach



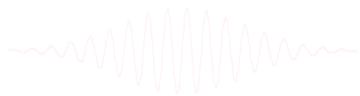
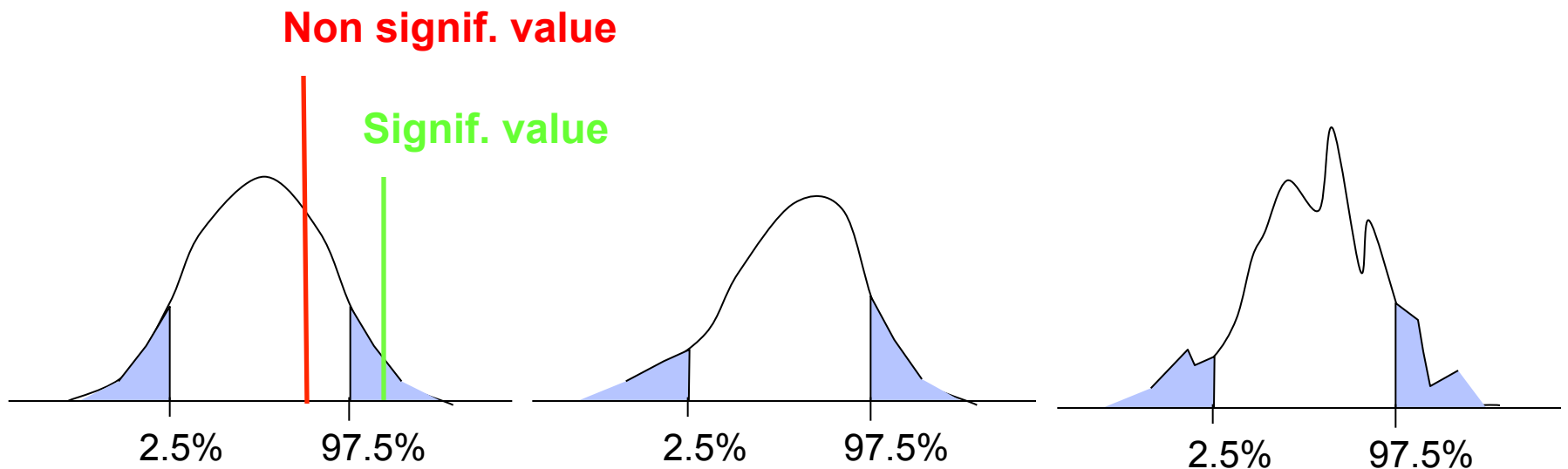
Inferences based on percentile bootstrap method

Permutation
/bootstrap

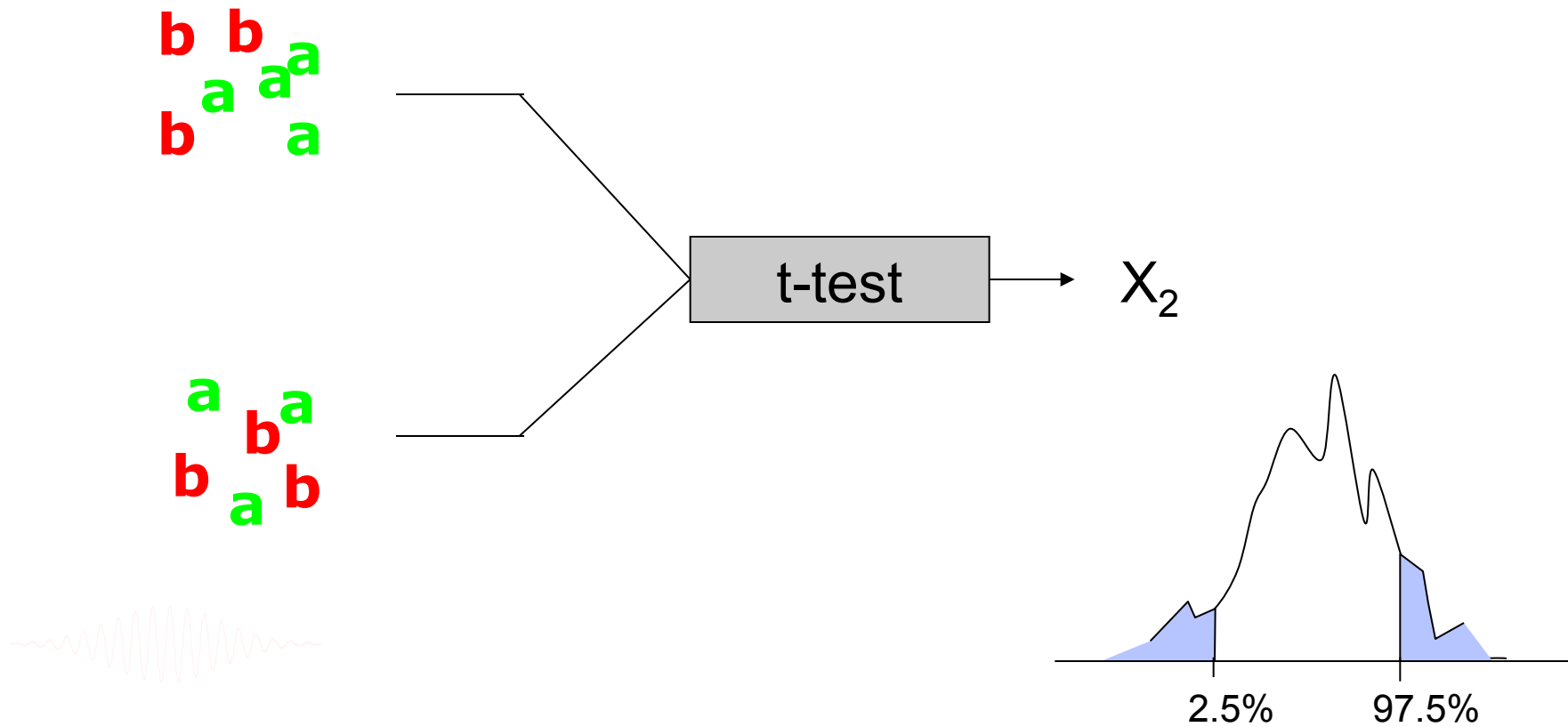


Sorted values

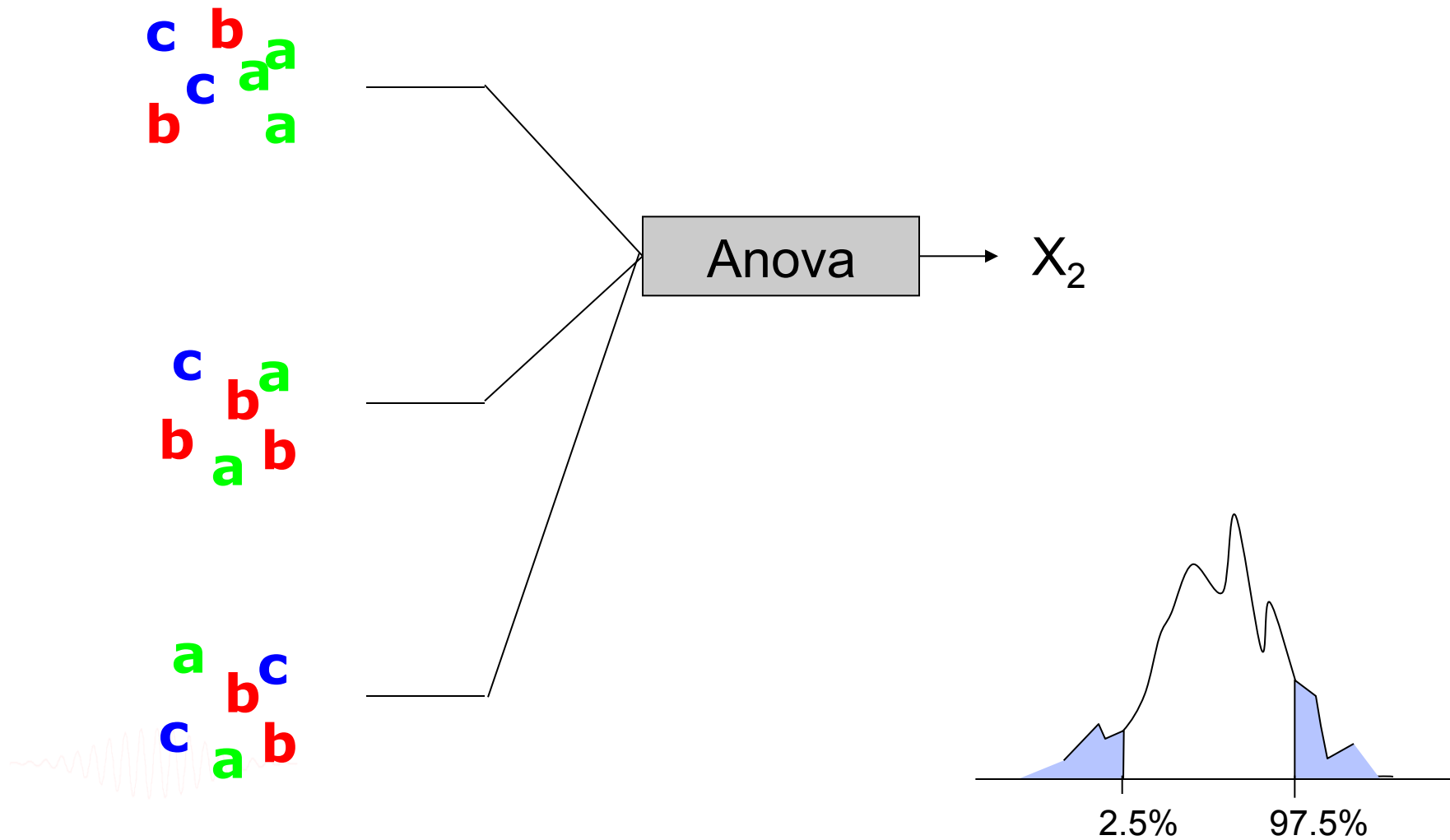
Distribution can take any shape



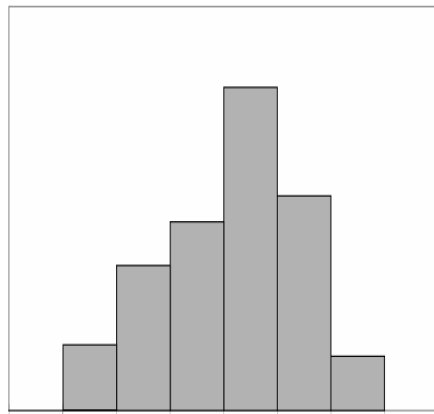
Randomization approach



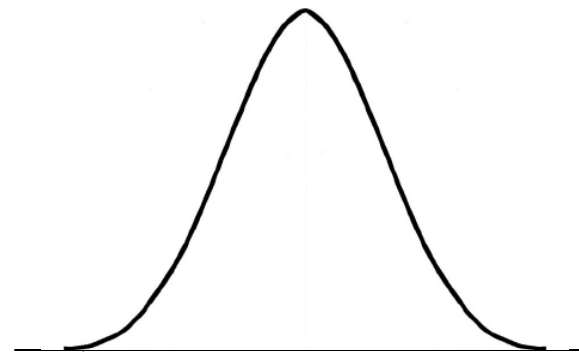
Randomization approach



Sample and population



Sample



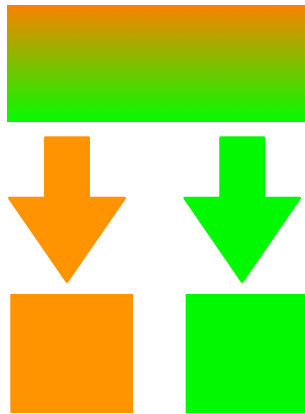
Population

given that we have no other information about the population, the sample is our best single estimate of the population

H0: the mean is not 0 for the population

Bootstrap versus permutation

Permutation

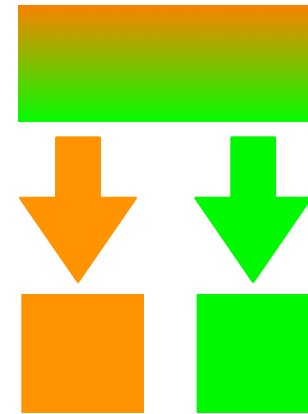


each element only
get picked once



Draws are dependent of each others

Bootstrap



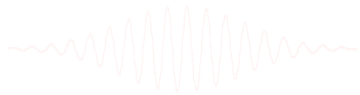
each element can
get picked several
times

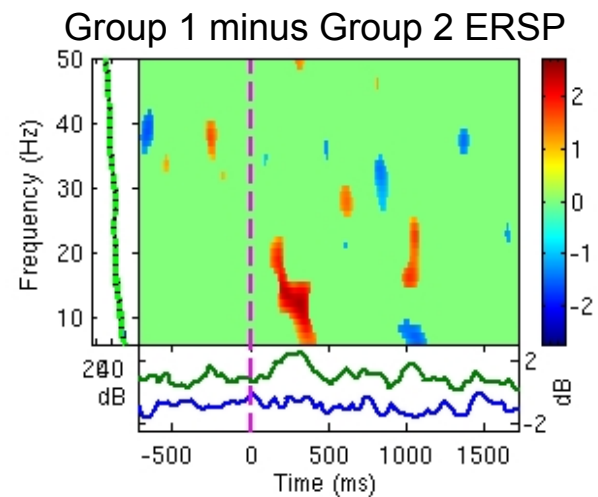
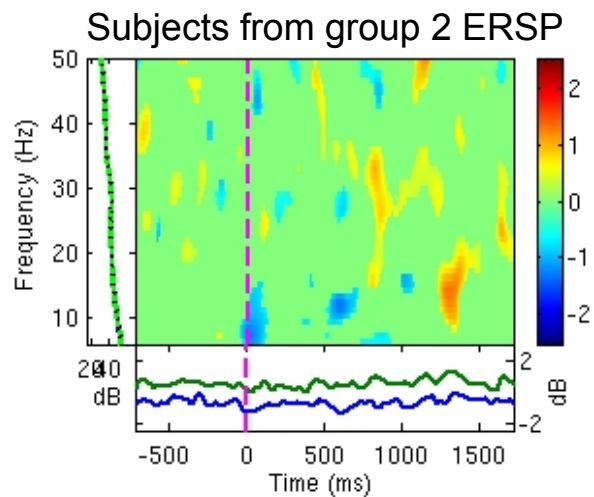
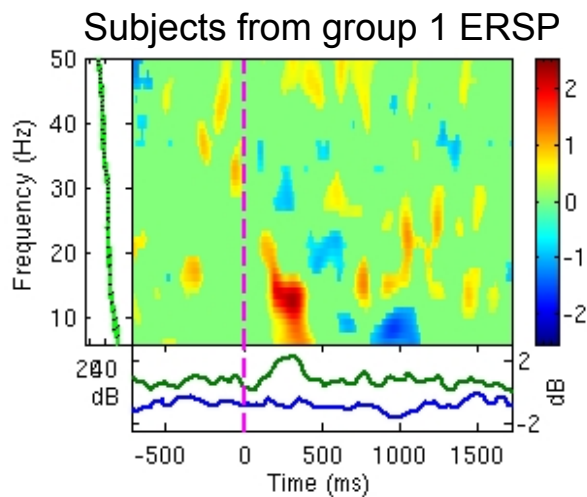


Draws are independent of each others

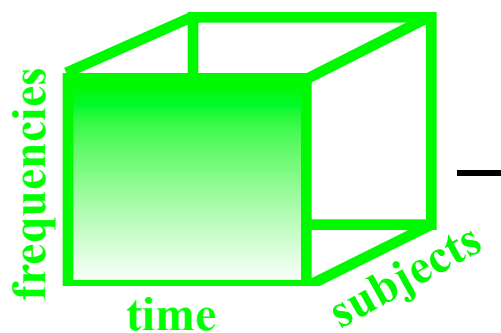
Bootstrap is more rigorous!

UNPAIRED STATISTICS IN EEGLAB

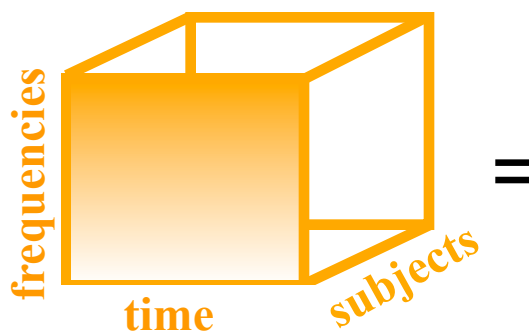




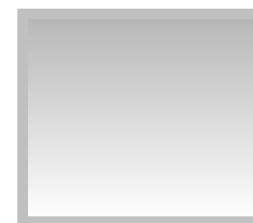
EEG1 (group 1)



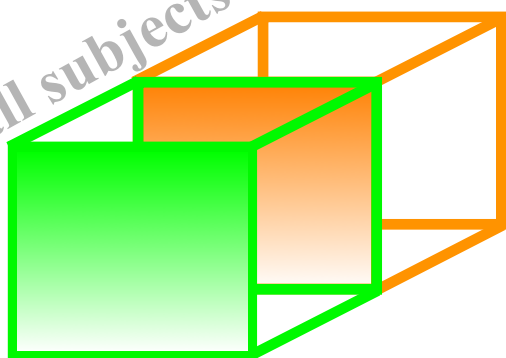
EEG2 (group 2)



Difference

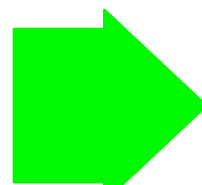


all subjects



Subject's list
1
2
3
4
5
6

Bootstrap 1
4
3
3
4
5
1



EEG1*



EEG2*



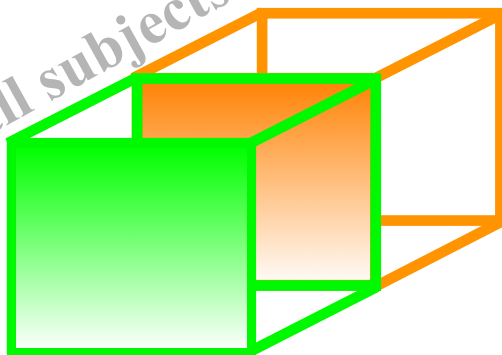
Difference 1

-

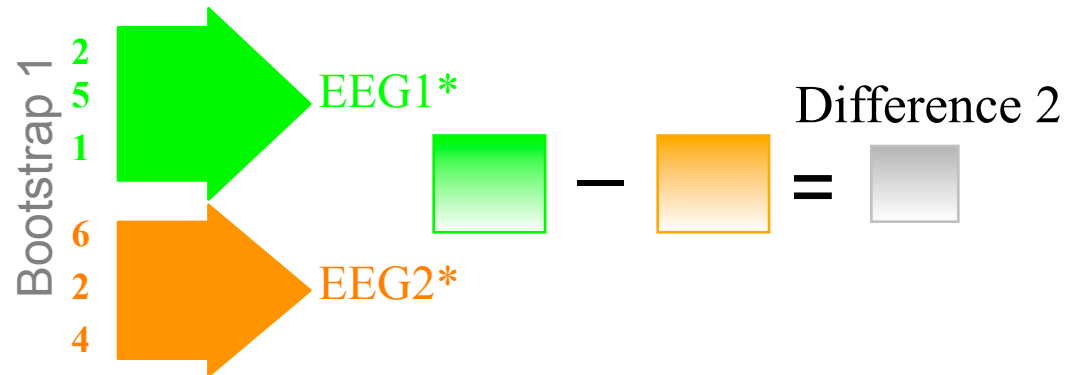
=



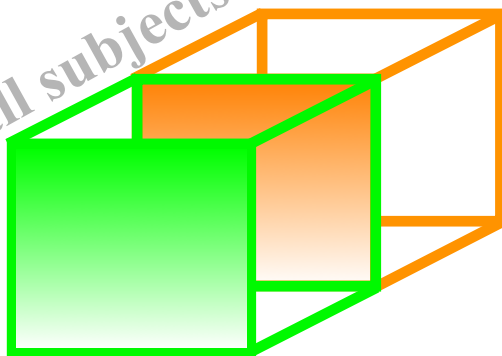
all subjects



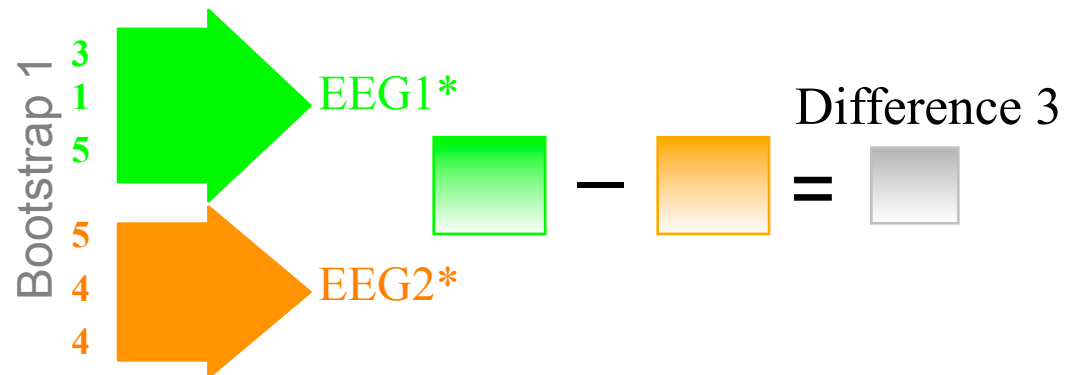
Subject's list
1
2
3
4
5
6



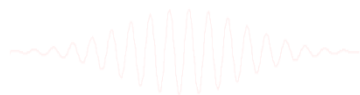
all subjects



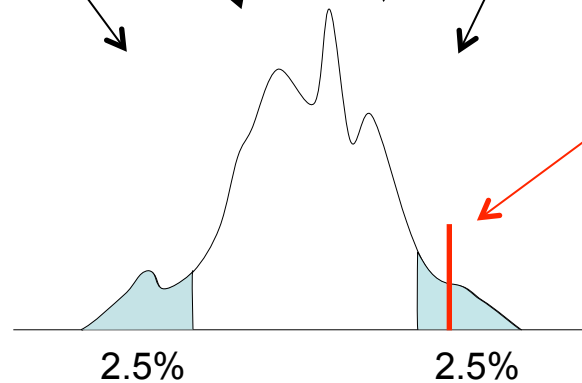
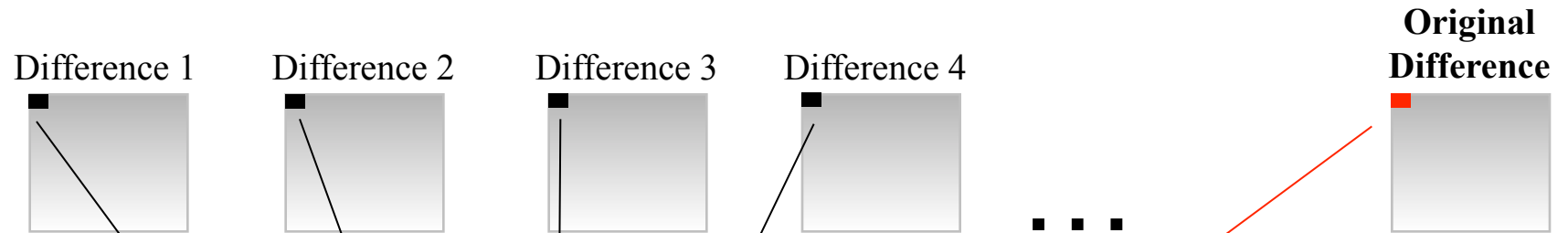
Subject's list
1
2
3
4
5
6



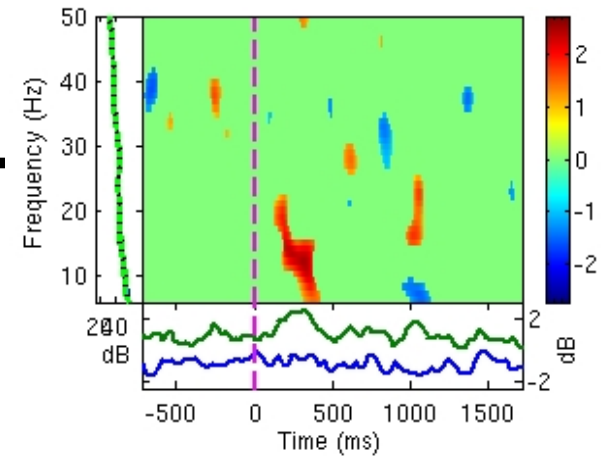
...



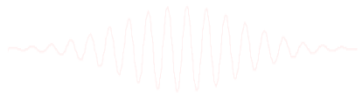
Assessing significance



Difference mask at $p < 0.05$



PAIRED STATISTICS IN EEGLAB

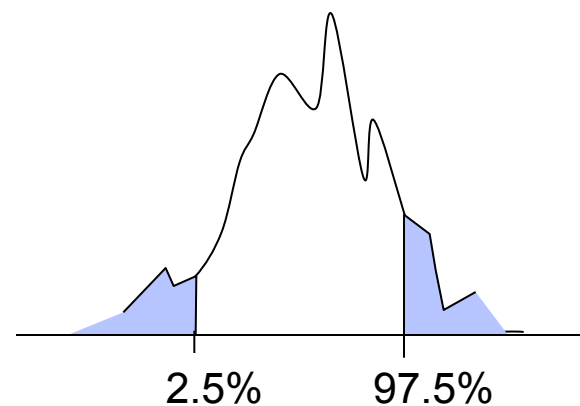


Husband	Wifes
22	25
32	25
50	51
25	25
33	38
27	30
45	60
47	54
30	31
44	54
23	23
39	34
24	25
22	23
16	19
73	71
27	26
36	31
24	26
60	62
26	29
23	31
28	29
36	35

Median

Are the two groups different: that's an unpaired test (comparing the median of husband and the median of wife)

Are husbands older than wives: that's a paired test. Compute difference between the two and change sign to bootstrap.



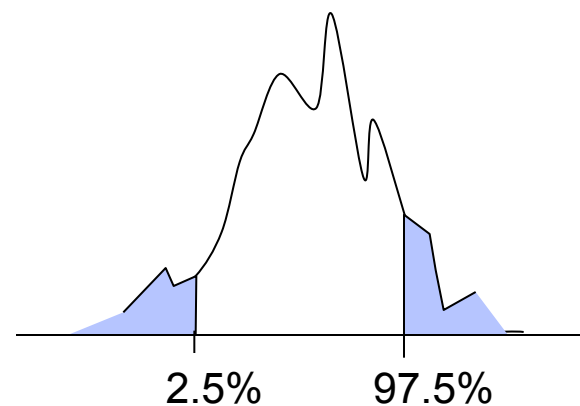
Husband	Wifes	Difference
22	25	-3
32	25	7
50	51	-1
25	25	0
33	38	-5
27	30	-3
45	60	-15
47	54	-7
30	31	-1
44	54	-10
23	23	0
39	34	5
24	25	-1
22	23	-1
16	19	-3
73	71	2
27	26	1
36	31	5
24	26	-2
60	62	-2
26	29	-3
23	31	-8
28	29	-1
36	35	1

Median

-1

Are the two groups different: that's an unpaired test (comparing the median of husband and the median of wife)

Are husbands older than wives: that's a paired test. Compute difference between the two and change sign to bootstrap.

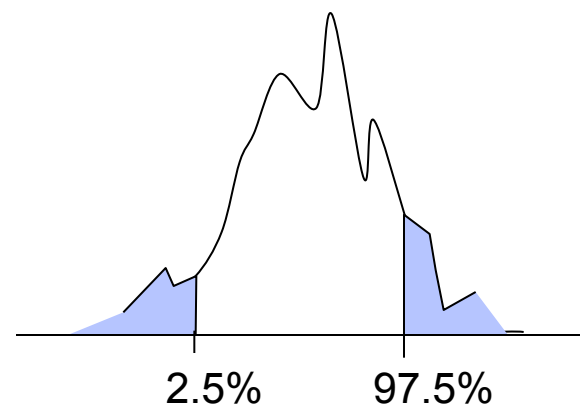


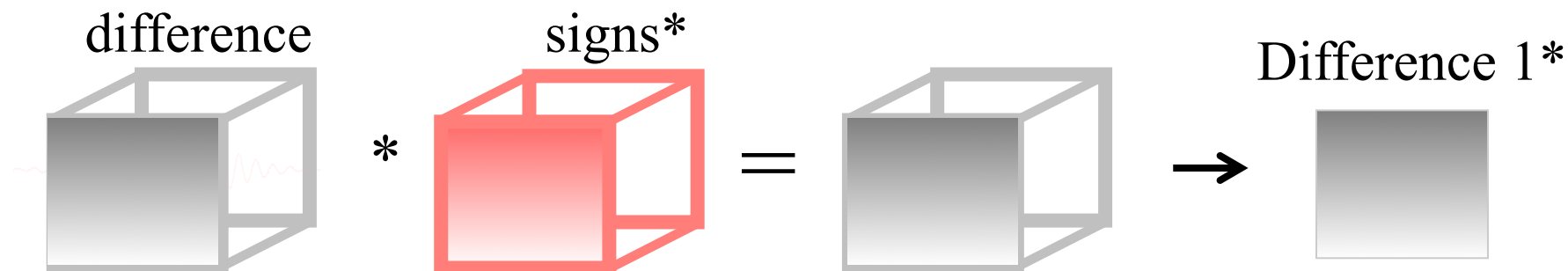
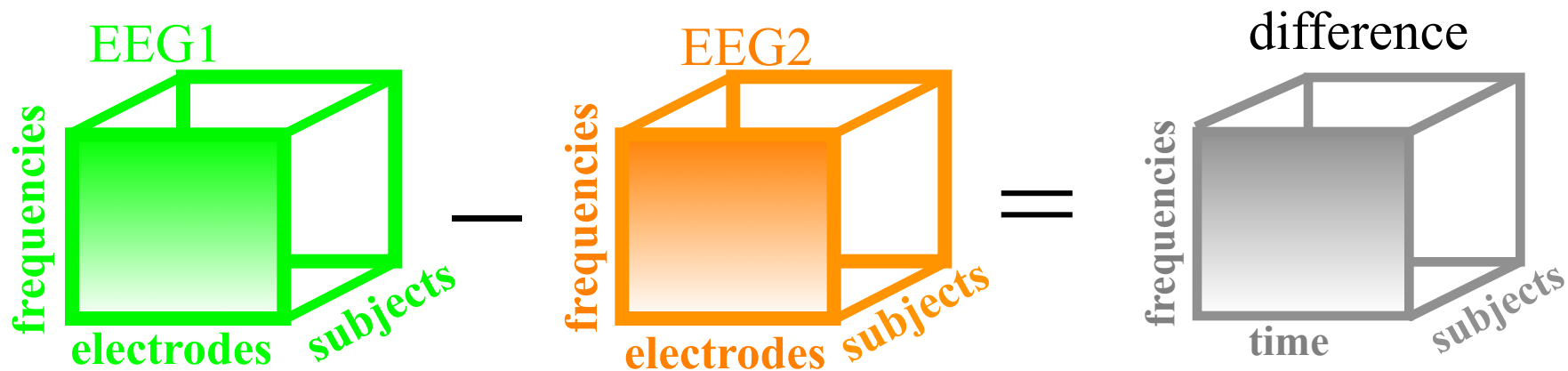
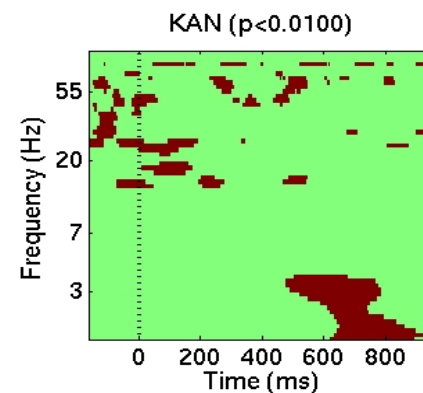
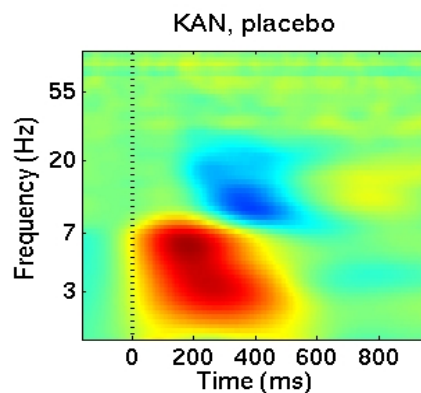
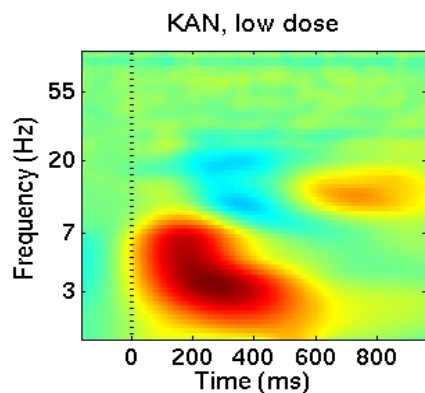
Husband	Wifes	Difference	Sign boot.	Sign boot.	Sign boot.
22	25	-3	3	3	-3
32	25	7	-7	7	7
50	51	-1	-1	-1	1
25	25	0	0	0	0
33	38	-5	5	5	5
27	30	-3	3	3	3
45	60	-15	15	15	15
47	54	-7	-7	7	7
30	31	-1	-1	1	-1
44	54	-10	-10	-10	-10
23	23	0	0	0	0
39	34	5	5	5	-5
24	25	-1	1	1	-1
22	23	-1	1	-1	1
16	19	-3	-3	3	3
73	71	2	-2	-2	-2
27	26	1	-1	1	1
36	31	5	5	5	-5
24	26	-2	-2	2	2
60	62	-2	-2	2	-2
26	29	-3	-3	3	3
23	31	-8	8	-8	8
28	29	-1	1	1	1
36	35	1	-1	-1	-1

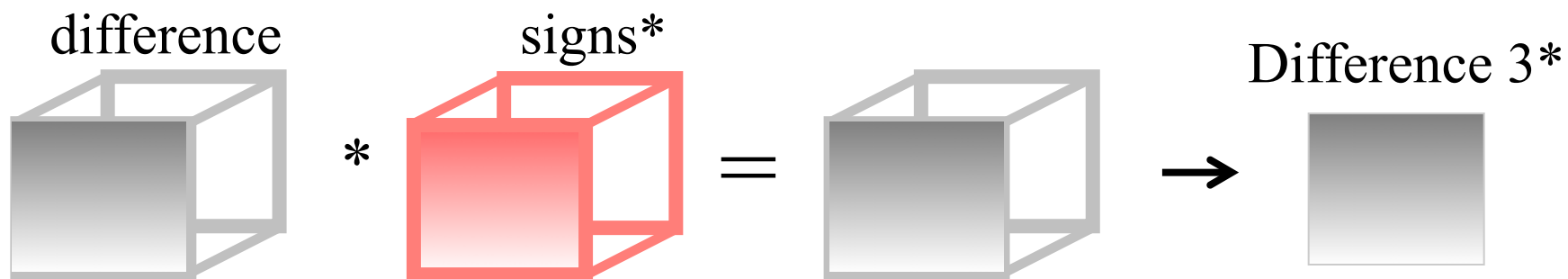
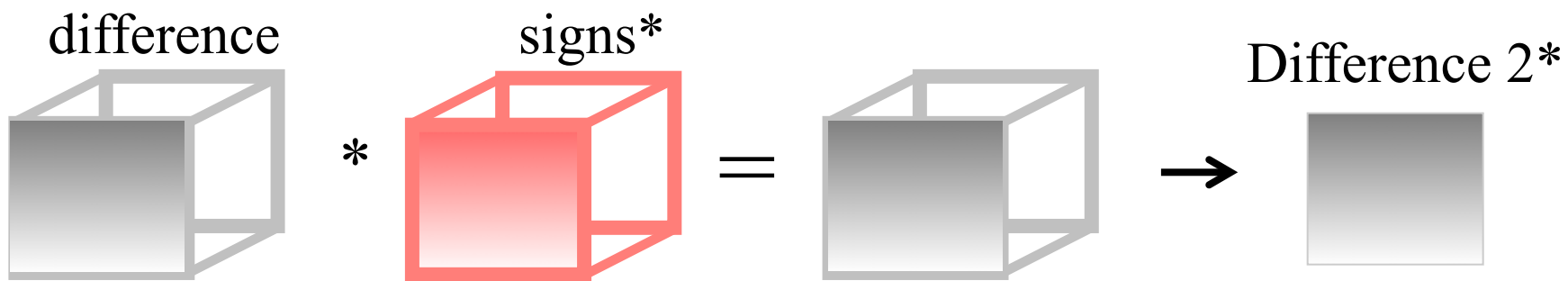
Median -1 -0.5 1.5 1

Are the two groups different: that's an unpaired test (comparing the median of husband and the median of wife)

Are husbands older than wives: that's a paired test. Compute difference between the two and change sign to bootstrap.

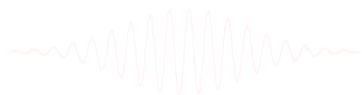




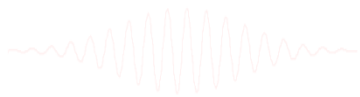
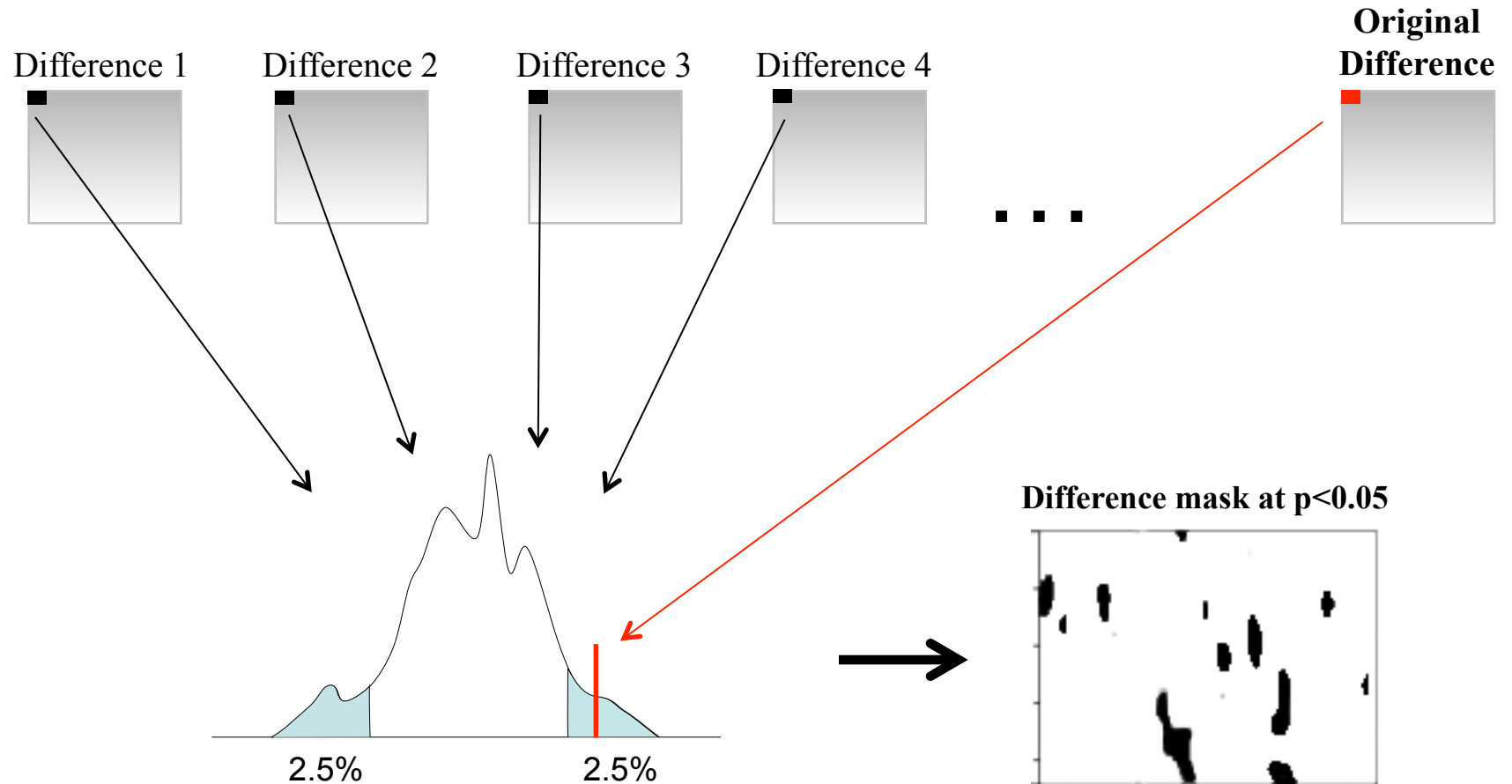


...

Simply invert polarity at random location
in the 3-D difference matrix



Assessing significance

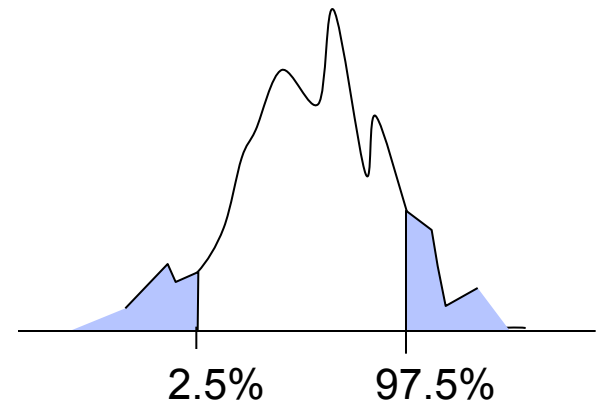
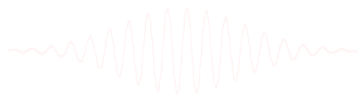


Correcting for multiple comparisons

- Bonferroni correction: divide by the number of comparisons (Bonferroni CE. Sulle medie multiple di potenze. Bollettino dell'Unione Matematica Italiana, 5 third series, 1950; 267-70.)
- Holms correction: sort all p values. Test the first one against α/N , the second one against $\alpha/(N-1)$
- Max method
- False detection rate
- Clusters

Max procedure

- for each permutation or bootstrap loop, simply take the MAX of the absolute value of your estimator (e.g. mean difference) across electrodes and/or time frames and/or temporal frequencies.
- compare absolute original difference to this distribution



FDR procedure

Procedure:

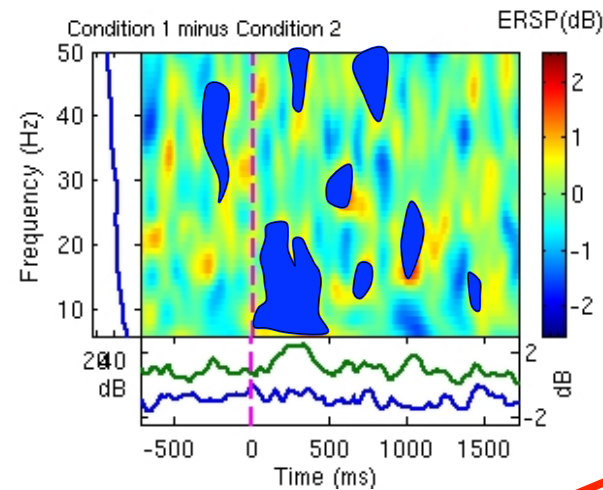
- Sort all p values (column C1)
C3
- Create column C2 by computing $j * \alpha / N$
- Subtract column C1 from C2 to build
column C3
- Find the highest negative index in C3
and
find the corresponding p-value in C1
(p_{fdr})
- Reject all null hypothesis whose p-value
are less than or equal to p_{fdr}

	C1	C2	Bonferoni C3
Index "j"	Actual	$j * 0.05 / 10$	C2-C1
1	0.001	0.005	-0.004
2	0.002	0.01	-0.008
3	0.01	0.015	-0.005
4	0.03	0.02	0.01
5	0.04	0.025	0.015
6	0.045	0.03	0.015
7	0.05	0.035	0.015
8	0.1	0.04	0.06
9	0.2	0.045	0.155
10	0.6	0.05	0.55

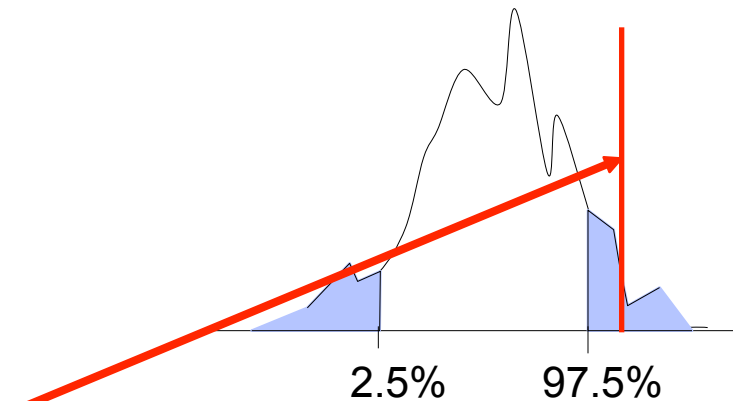
Holms (points to index 1)
FDR (points to index 3)
Uncorrected (points to index 10)

Cluster correction for multiple comparisons

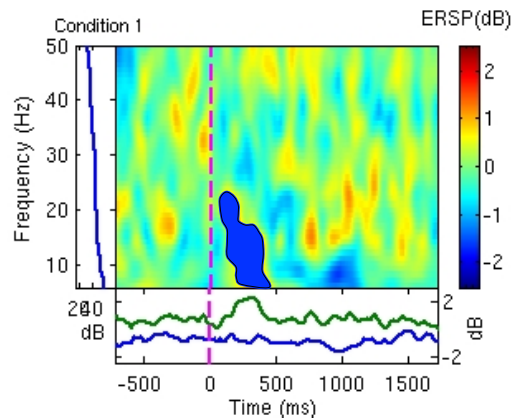
**Original
difference**



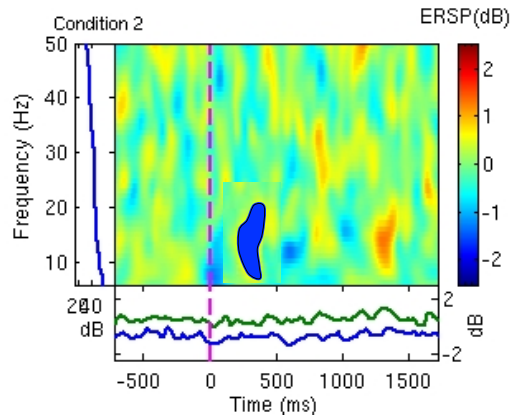
44 pixels



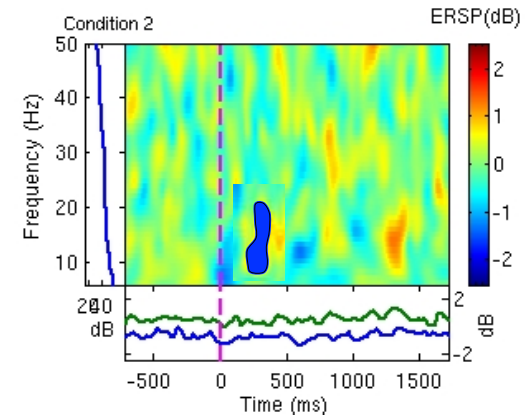
Difference bootstrap 1



Difference bootstrap 2



Difference bootstrap 3



....

statcond function in EEGLAB

```
a = { rand(1,10) rand(1,10)+0.5 }; % pseudo 'paired' data vectors
```

```
[t df pvals] = statcond(a , 'mode', 'perm'); % perform paired t-test  
pvals = 5.2807e-04 % standard t-test probability value
```

```
% Note: for different rand() outputs, results will differ.
```

```
[t df pvals surog] = statcond(a, 'mode', 'perm', 'naccu', 2000);  
pvals = 0.0065 % nonparametric t-test using 2000 permuted data sets
```

```
a = { rand(2,11) rand(2,10) rand(2,12)+0.5 };
```

```
[F df pvals] = statcond(a , 'mode', 'perm'); % perform an unpaired ANOVA
```

```
pvals =
```

```
0.00025 % p-values for difference between columns
```

```
0.00002 % for each data row
```

statcond function in EEGLAB

```
a = { rand(3,4,10) rand(3,4,10) rand(3,4,10); ...  
      rand(3,4,10) rand(3,4,10) rand(3,4,10)+0.5 };
```

```
% pseudo (2,3)-condition data array, each entry containing  
% ten (3,4) data matrices
```

```
[F df pvals] = statcond(a , 'mode', 'perm');  
                % paired 2-way ANOVA
```

```
% Output:
```

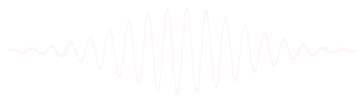
```
pvals{1} % a (3,4) matrix of p-values; effects across columns
```

```
pvals{2} % a (3,4) matrix of p-values; effects across rows
```

```
pvals{3} % a (3,4) matrix of p-values; interaction effects across  
          rows and columns
```

Exercise

- Experiment with the statcond function
 - Create 2 random vectors of values
 - Add “signal” to one of the variable
 - Use statcond and compare permutation and parametric results
 - Repeat 100 times and plot the histogram of p-values
- Experiment with STUDY statistics
 - Load the Stern STUDY
 - Look at significant difference between probe and memorize in component clusters (time-frequency plot, ERSP)



Exercises

Suggestion for exercises:

Load stern.study in STUDY folder

From the GUI, plot grand average ERP for all channels.
Experiment with statistics.

Build a STUDY design to compare Ignore letter grouped with Memorize letter with Probe letters. Recompute spectrum and plot spectrum for electrode Fz using statistics. Do the same for the frontal midline component cluster (cluster 19).

