

Robust statistics

EEGLAB workshop, Aspet 2009

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*thanks to Arnaud Delorme and
Guillaume Rousset for most of the slides*

Robust statistics

Parametric & non-parametric statistics: use mean and standard deviation (t-test, ANOVA, ...)

Bootstrap and permutation methods: shuffle/bootstrap data and recompute measure of interest. Use the tail of the distribution to assess significance.

Correction for multiple comparisons: computing statistics on time(/frequency) series requires correction for the number of comparisons performed.

Parametric statistics

Assume gaussian distribution of data

T-test: Compare paired/unpaired Samples for continuous data. In EEGLAB, used for grand-average ERPs.

Paired

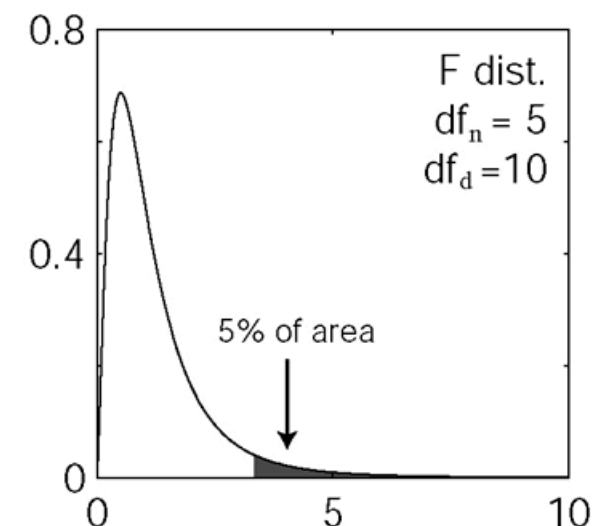
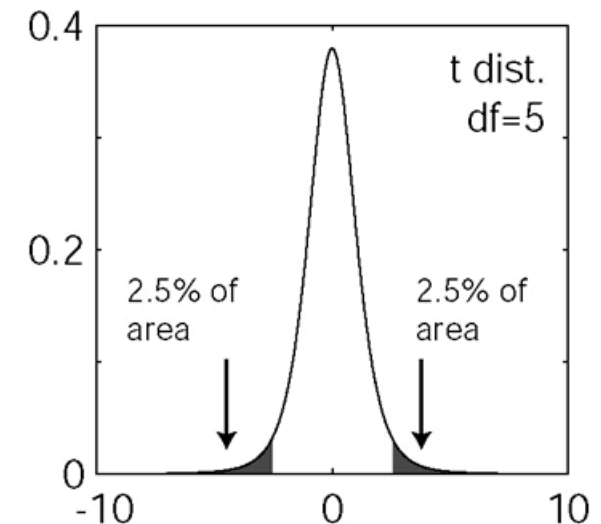
$$t = \frac{\text{Mean_difference}}{\text{Standard_deviation}} \sqrt{N-1}$$

Unpaired

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

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

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

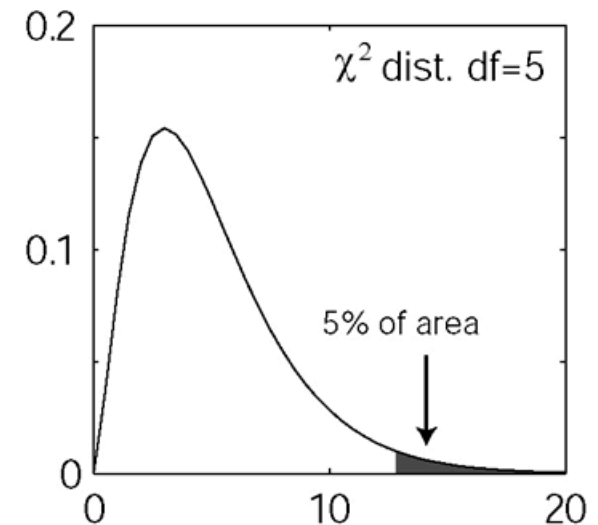
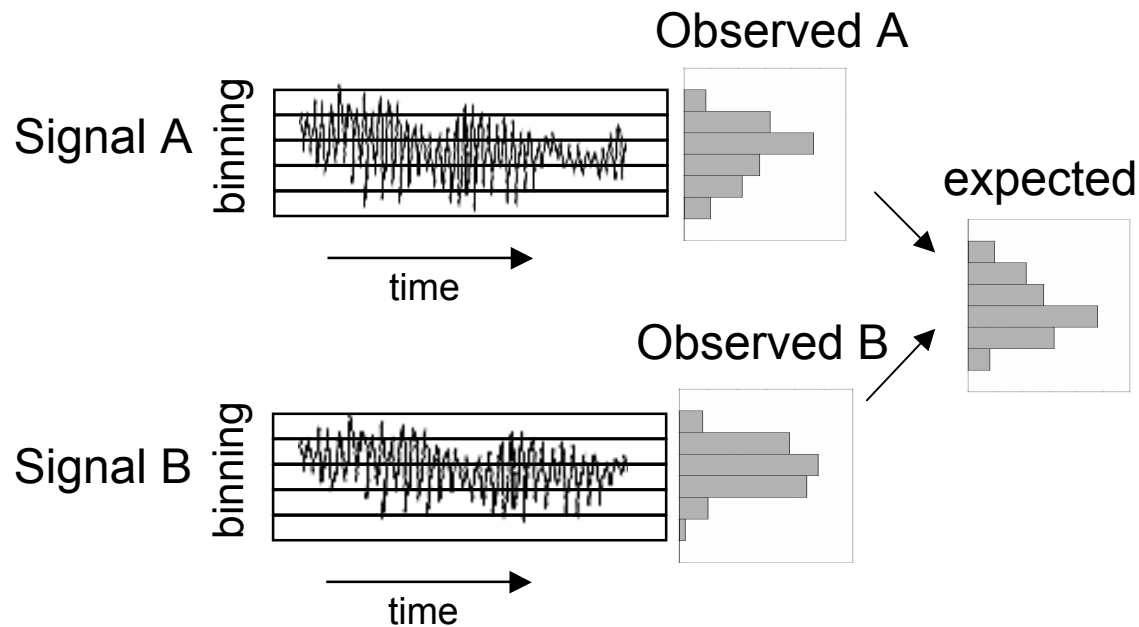


Non-parametric statistics

Do not assume a distribution for the data

χ^2 is used to compare 2 or more unpaired samples

$$\chi^2 = \sum_{i,j} (Observed_{i,j} - expected_{i,j})^2 / expected_{i,j}$$



| Goal | Dataset | | |
|---|---|--|--|
| | Binomial or Discrete | Continuous measurement (from a normal distribution) | Continuous measurement, Rank, or Score (from non- normal distribution) |
| Example of data sample | List of patients recovering or not after a treatment | Readings of heart pressure from several patients | Ranking of several treatment efficiency by one expert |
| Describe one data sample | Proportions | Mean, SD | Median |
| Compare one data sample to a hypothetical distribution | χ^2 or binomial test | One-sample t test | Sign test or Wilcoxon test |
| Compare two paired samples | Sign test | Paired t test | Sign test or Wilcoxon test |
| Compare two unpaired samples | χ^2 square Fisher's exact test | Unpaired t test | Mann-Whitney test |
| Compare three or more unmatched samples | χ^2 test | One-way ANOVA | Kruskal-Wallis test |
| Compare three or more matched samples | Cochrane Q test | Repeated-measures ANOVA | Friedman test |
| Quantify association between two paired samples | Contingency coefficients | Pearson correlation | Spearman correlation |

Non-parametric statistics

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

Values

Ranks

BOTH ASSUME NORMAL DISTRIBUTIONS

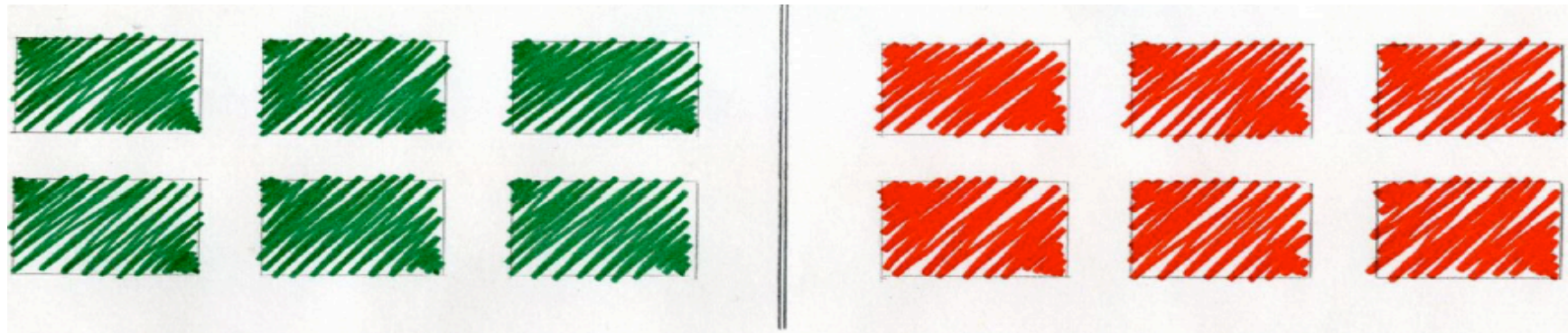
Problems

- 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
-

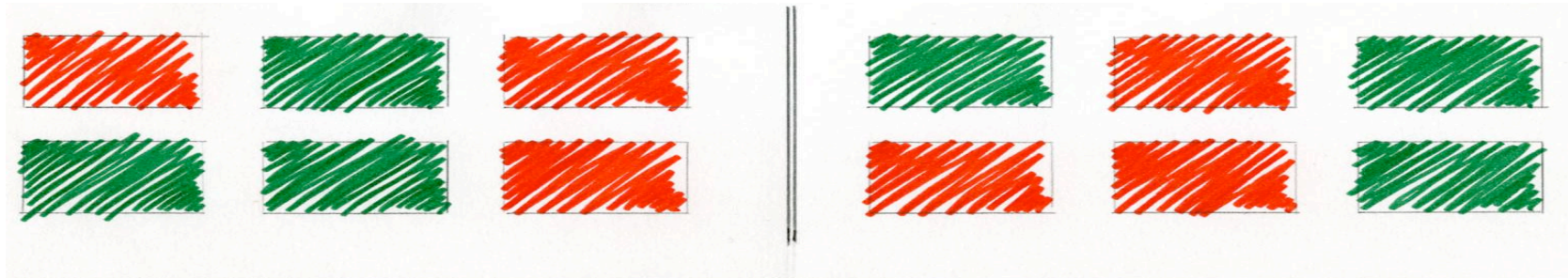
Solutions

1. Randomization approach
2. Bootstrap approach

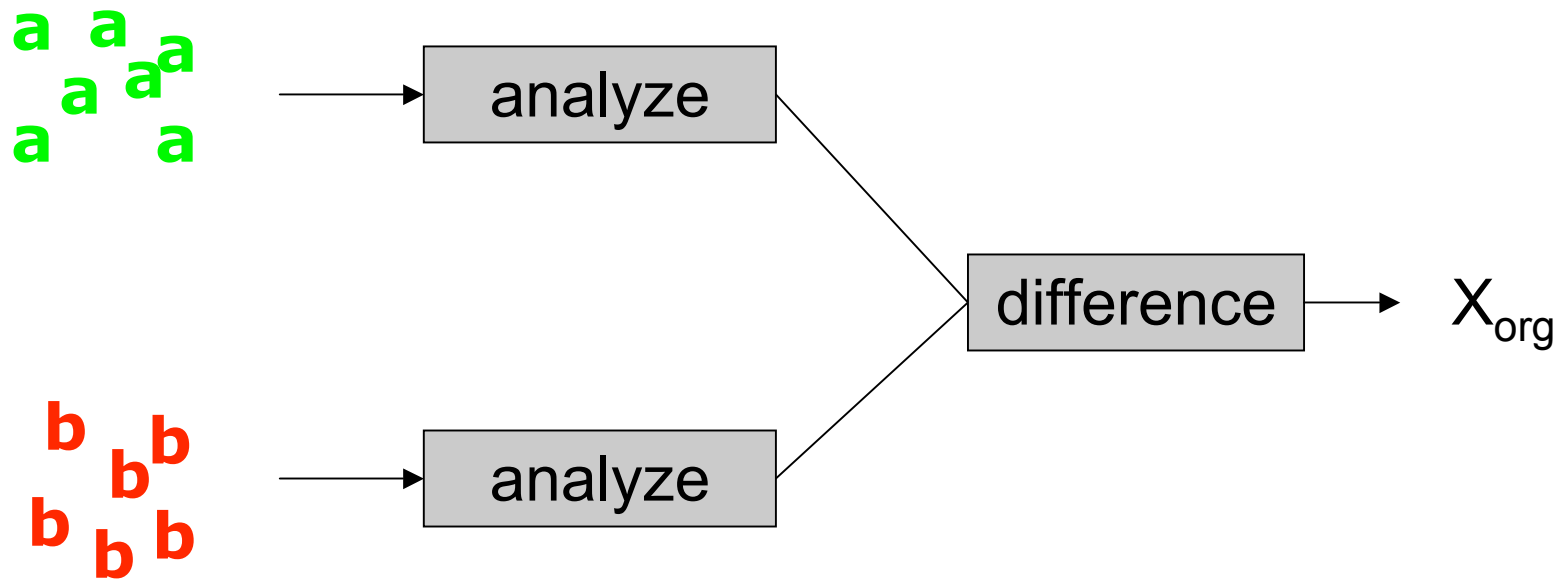
Randomization approach



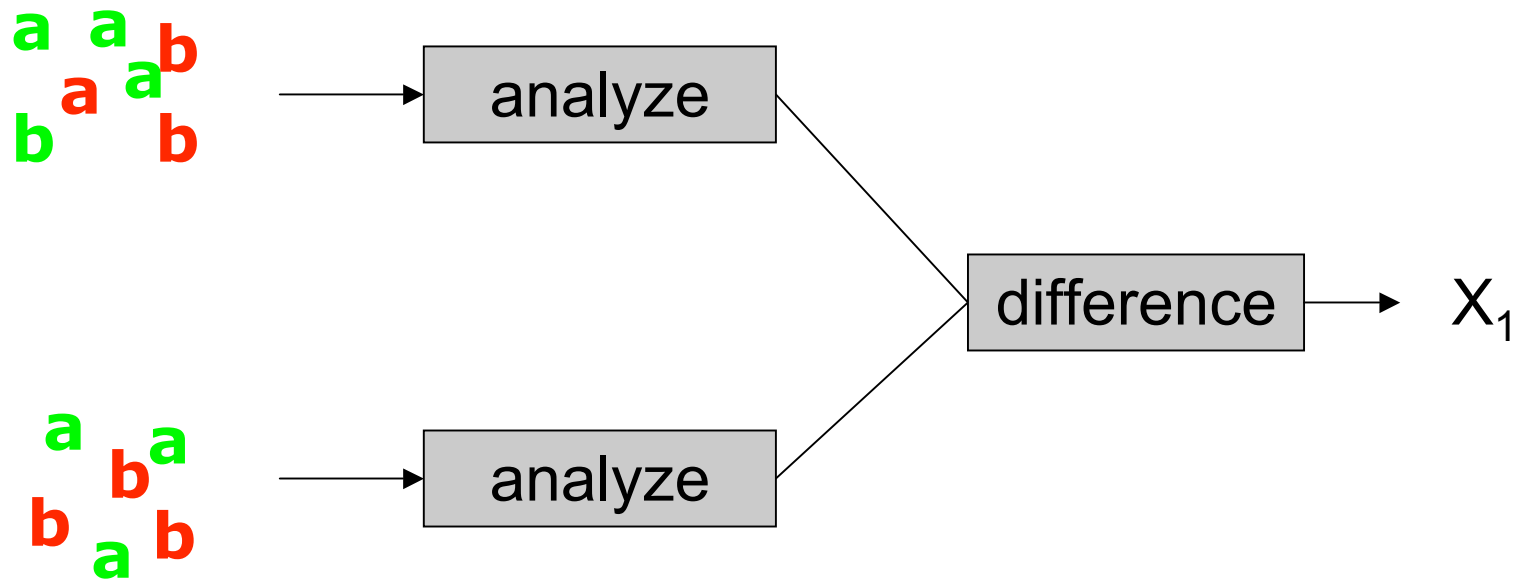
Randomization approach



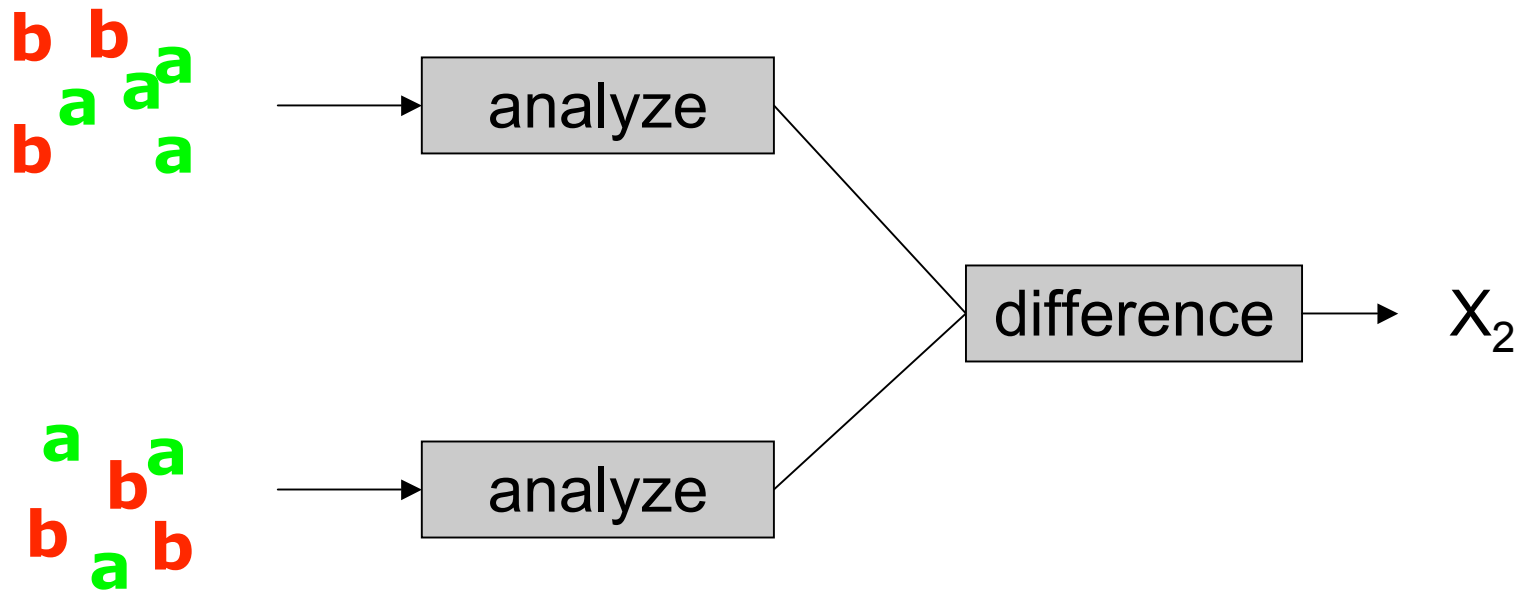
Randomization approach



Randomization approach



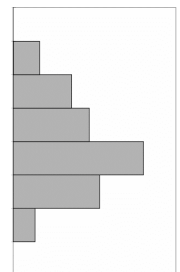
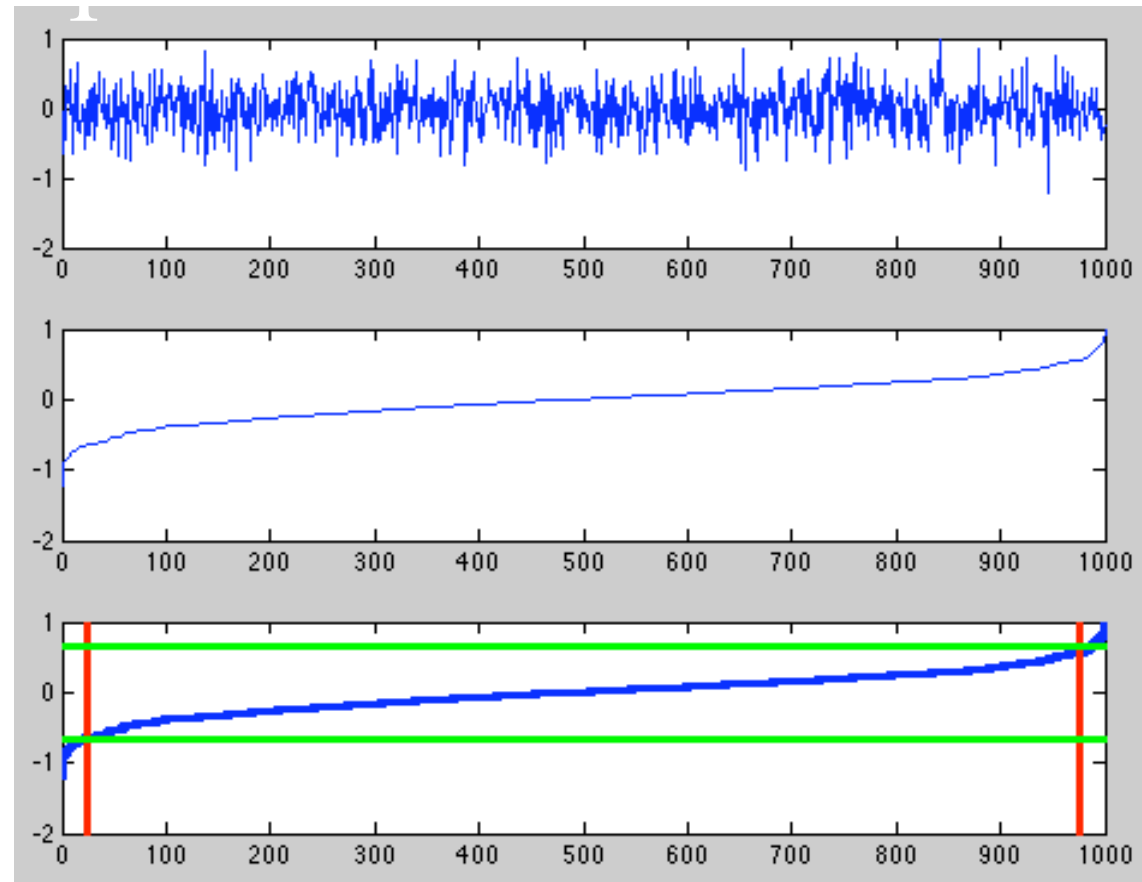
Randomization approach



Permutation
/bootstrap

Sorted values

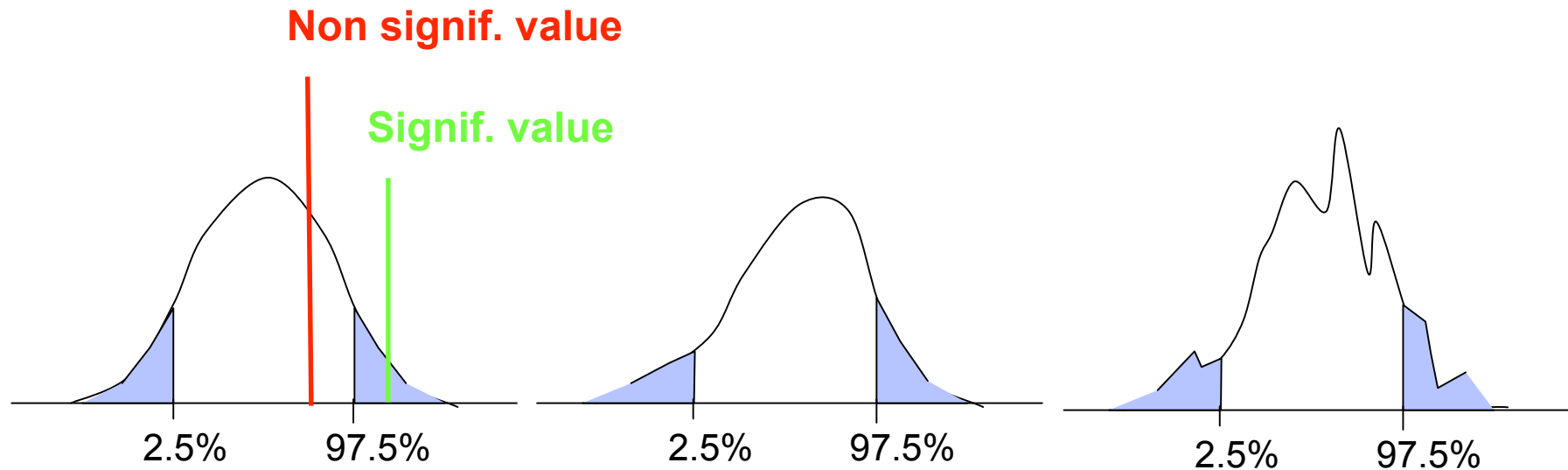
Thresholds



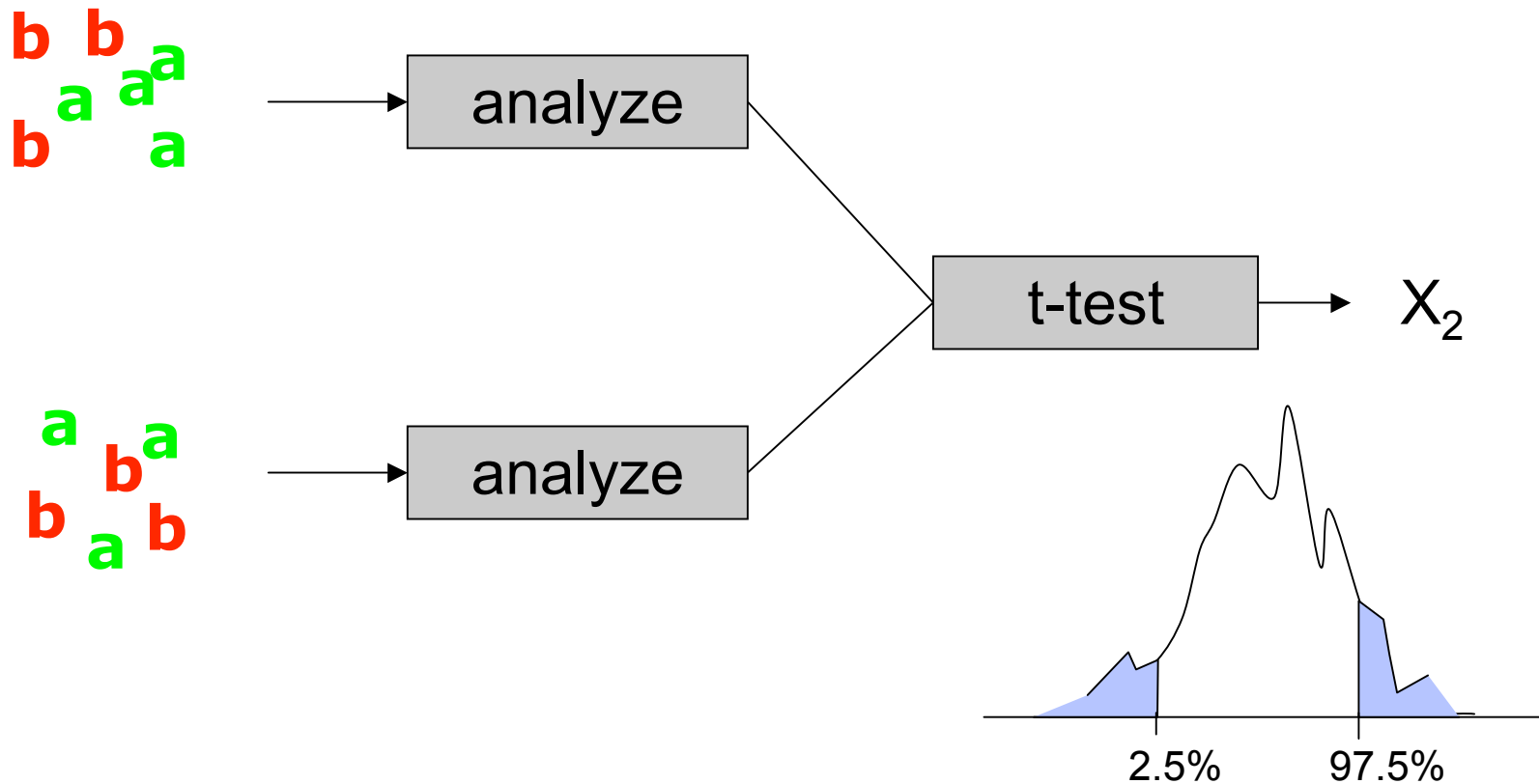
2.5%

97.5%

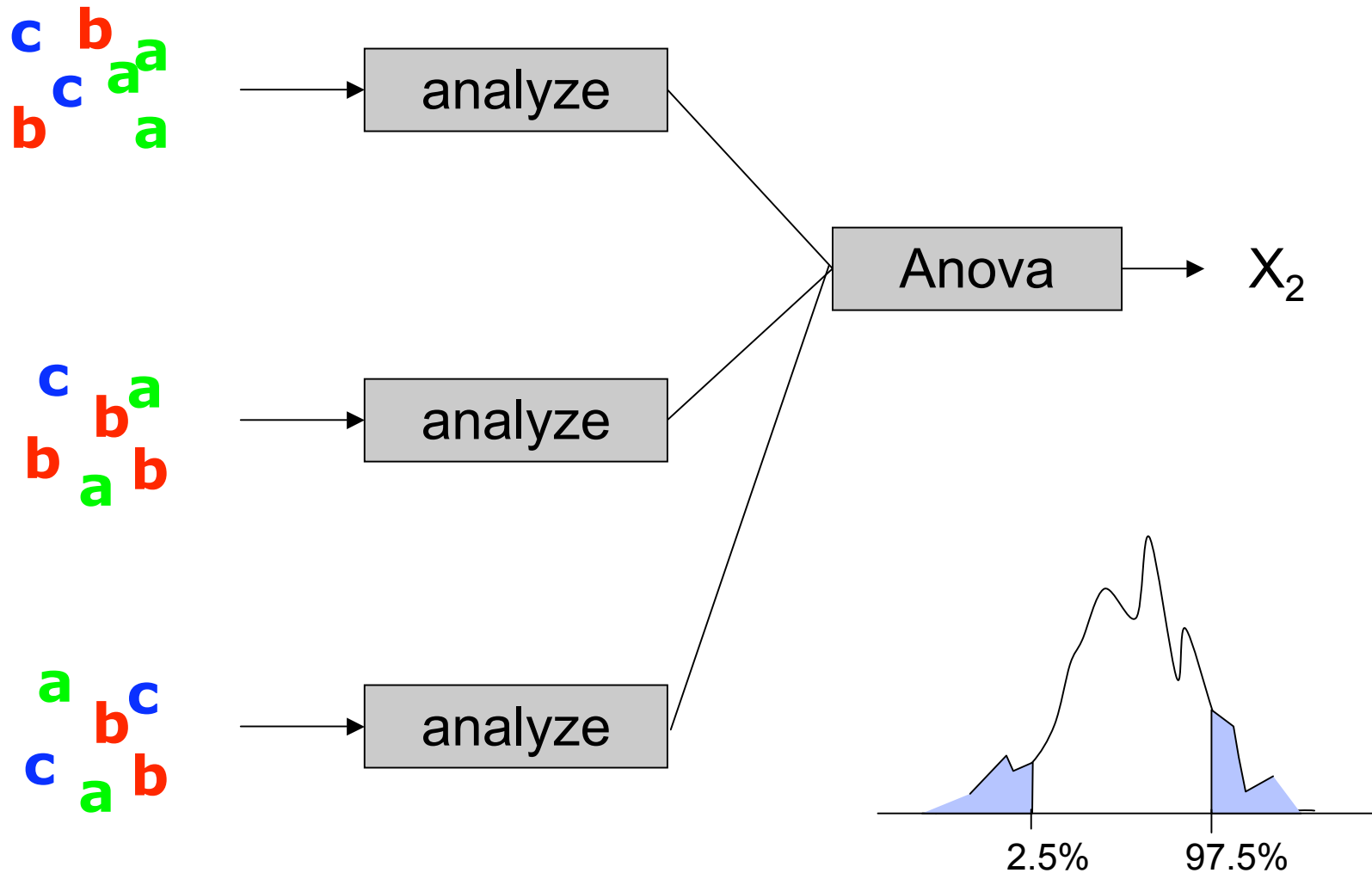
Distribution can take any shape



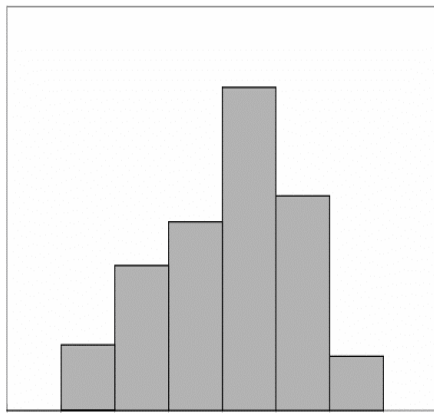
Randomization approach



Randomization approach



Sample and population



Sample



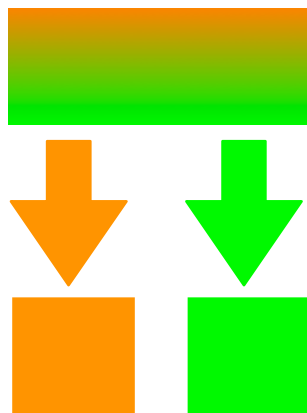
Population

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

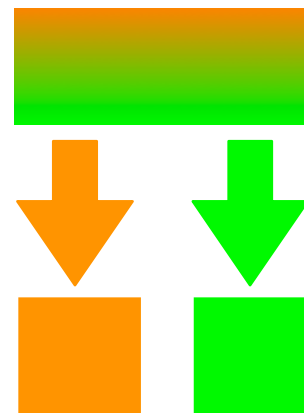


each element only
get picked once

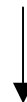


Draws are dependent of each others

Bootstrap



each element can
get picked several
times



Draws are independent of each others

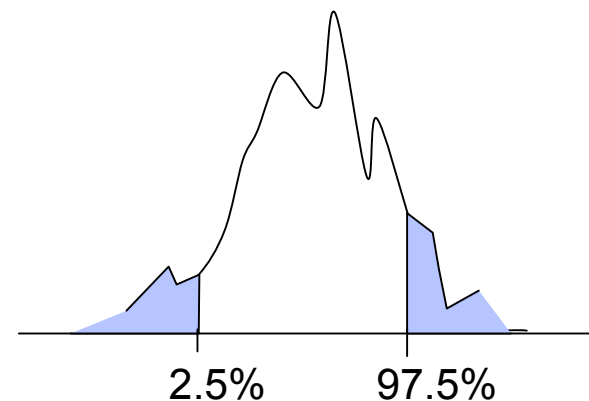
Bootstrap is better!

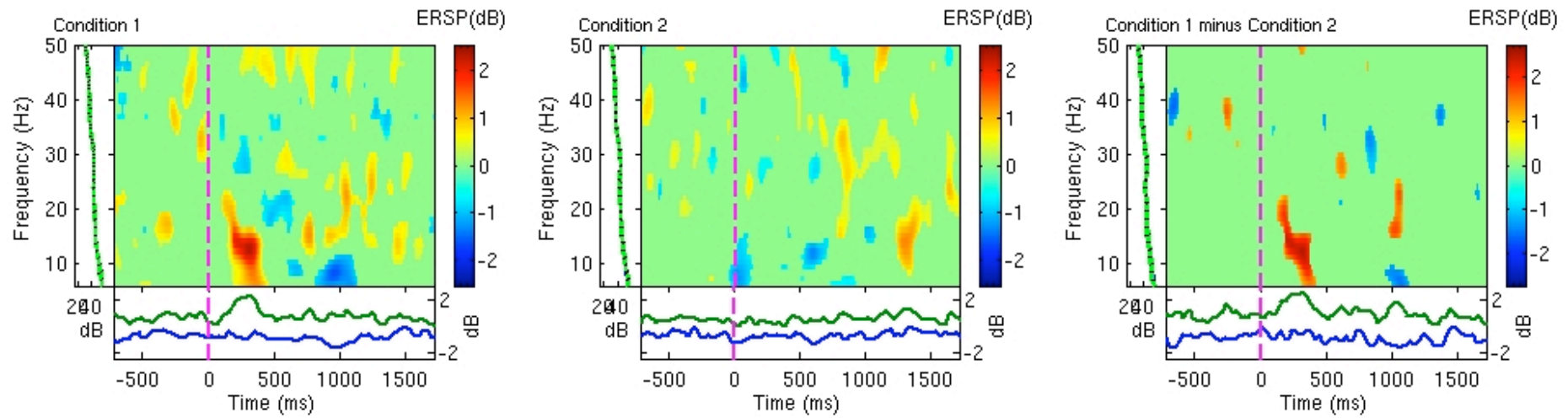
| Husband | Wifes |
|---------|-------|
| 22 | 25 |
| 32 | 25 |
| 50 | 51 |
| 25 | 25 |
| 33 | 38 |
| 27 | 30 |
| 45 | 60 |
| 47 | 54 |
| 30 | 31 |
| 44 | 54 |
| 23 | 23 |
| 39 | 34 |
| 24 | 25 |
| 22 | 23 |
| 16 | 19 |
| 73 | 71 |
| 27 | 26 |
| 36 | 31 |
| 24 | 26 |
| 60 | 62 |
| 26 | 29 |
| 23 | 31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

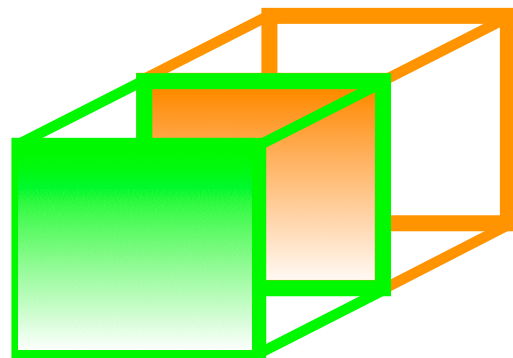
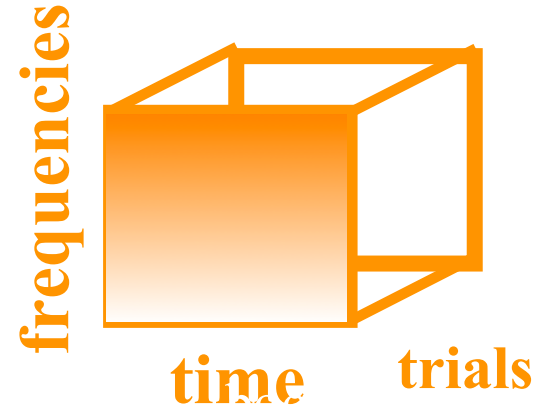
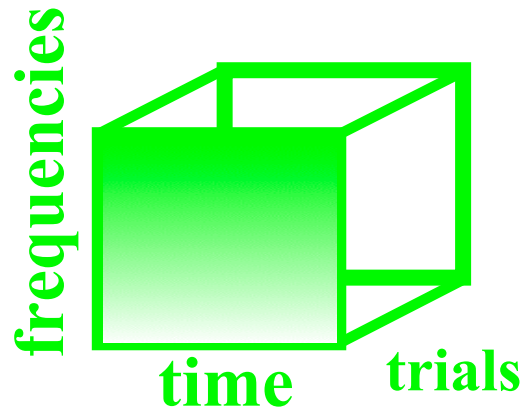
Are husbands older than wives: that's a paired test. Compute difference between the two and change sign to bootstrap.





EEG1

EEG2



list

1

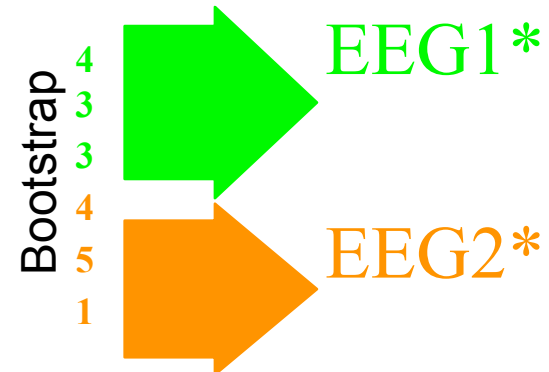
2

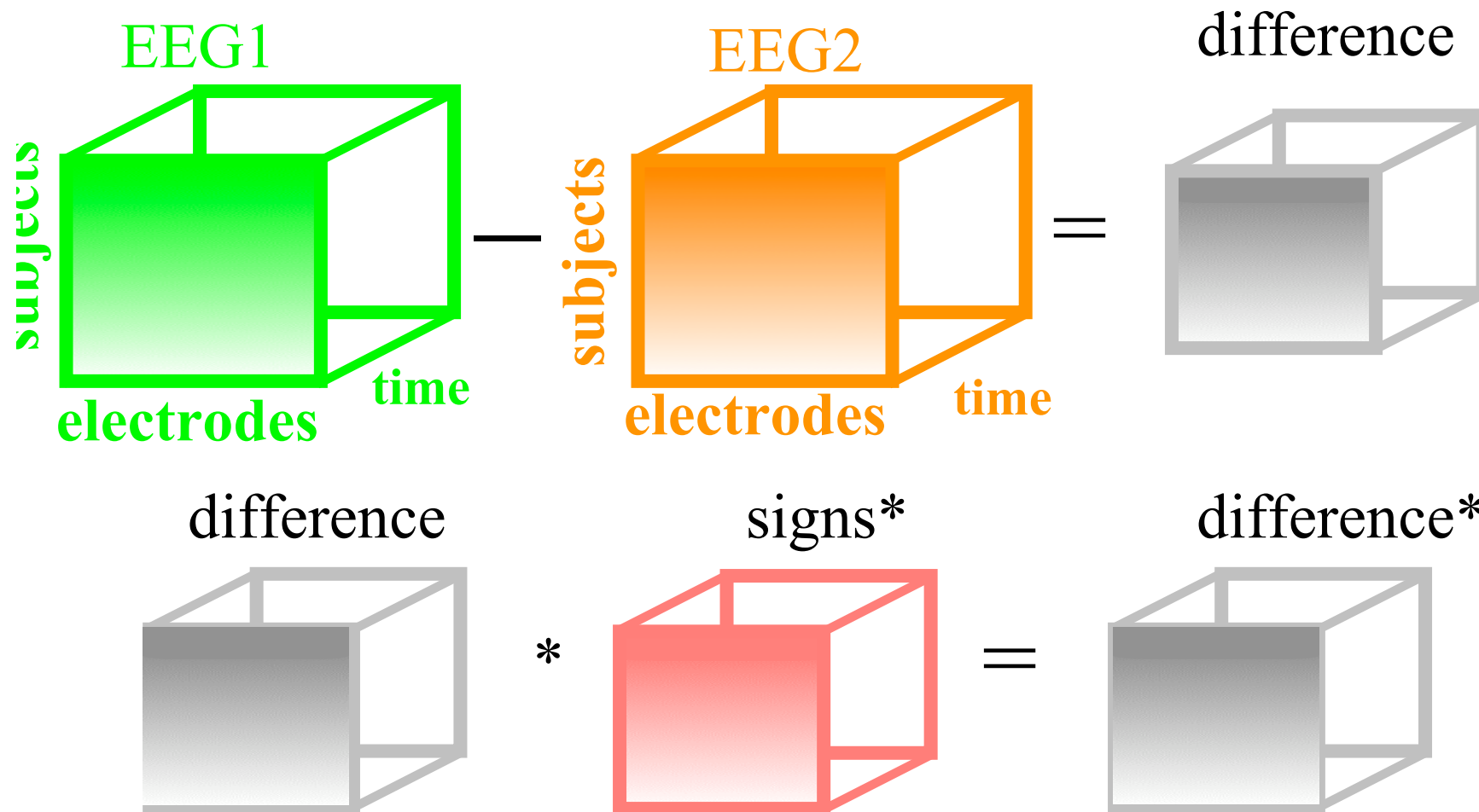
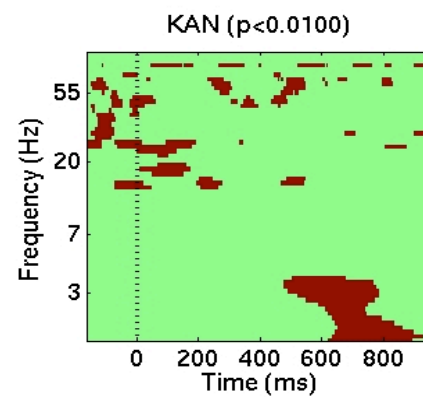
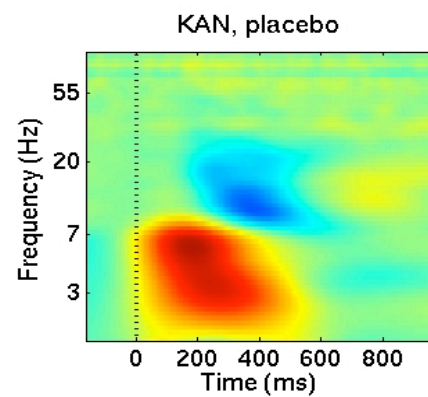
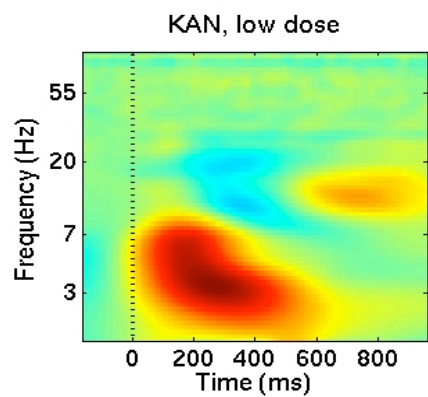
3

4

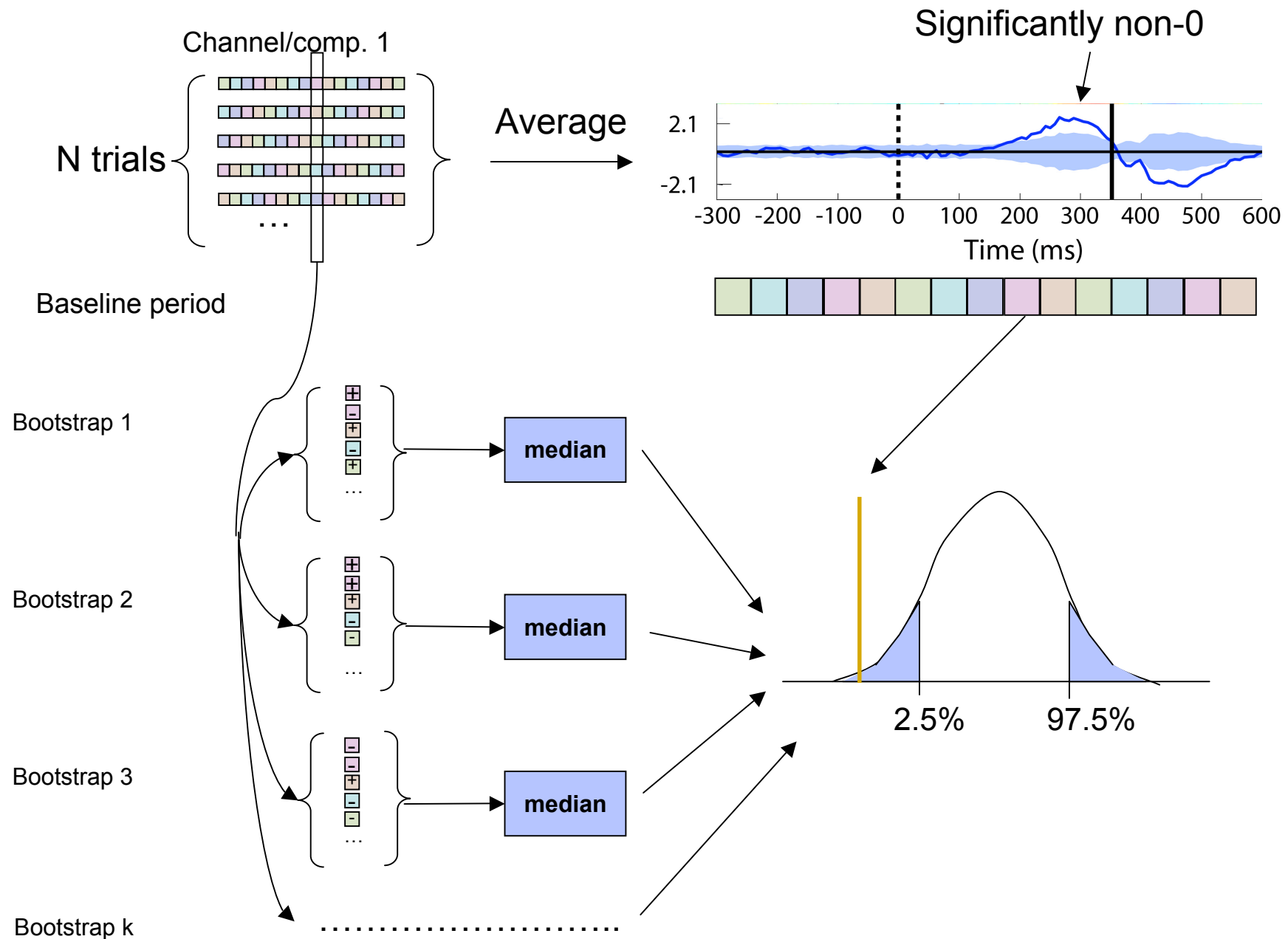
5

6

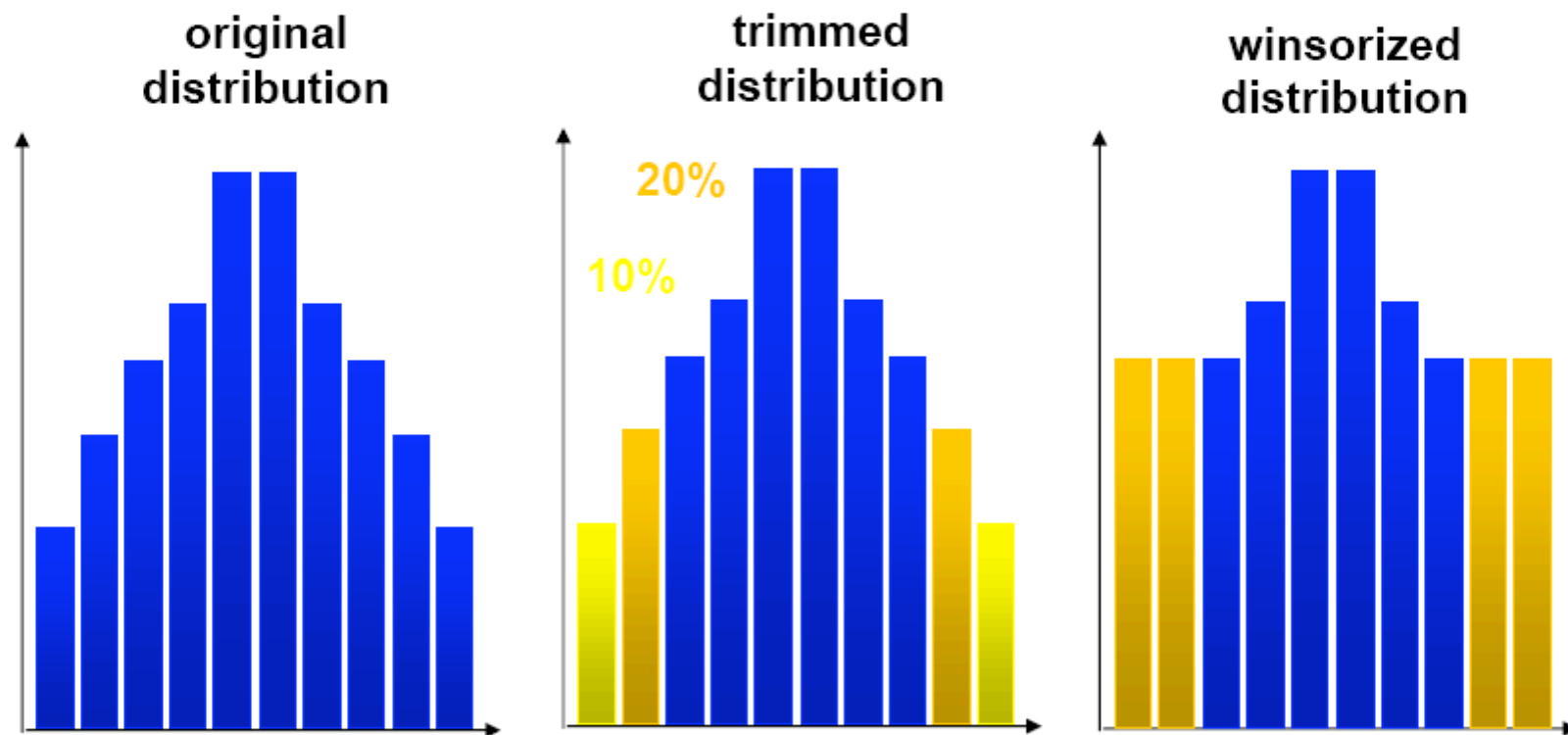




Bootstrap for ERPs and time-frequency



Measures of central tendency

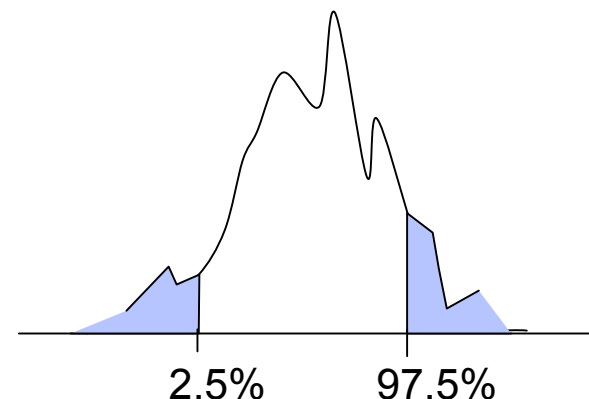


Correcting for multiple comparisons

- 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:

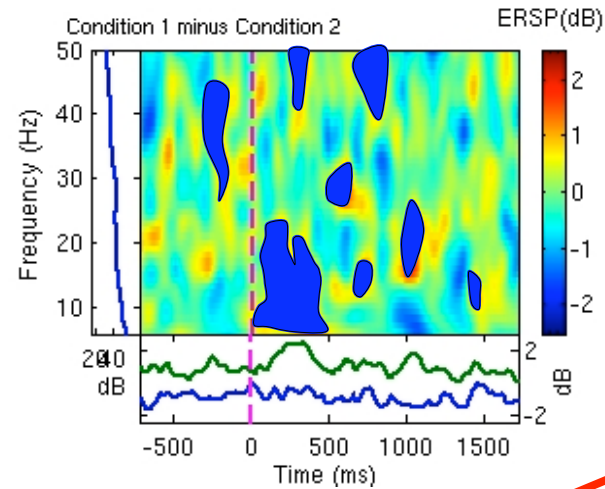
- Sort all p values (column C1)
C3
- Create column C2 by computing $j*\alpha/N$
- Subtract column C1 from C2 to build
column C3
- Find the highest negative index in C3
and
find the corresponding p-value in C1
(p_{fdr})
- Reject all null hypothesis whose p-value
are less than or equal to p_{fdr}

| | C1 | C2 | 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 |

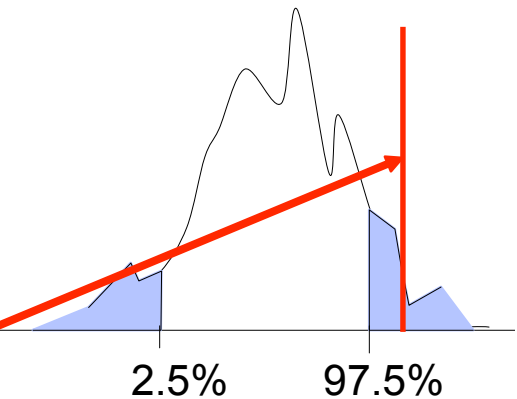


Cluster correction for multiple comparison

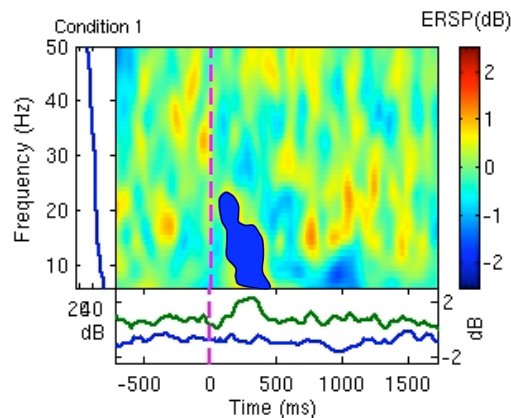
Original difference



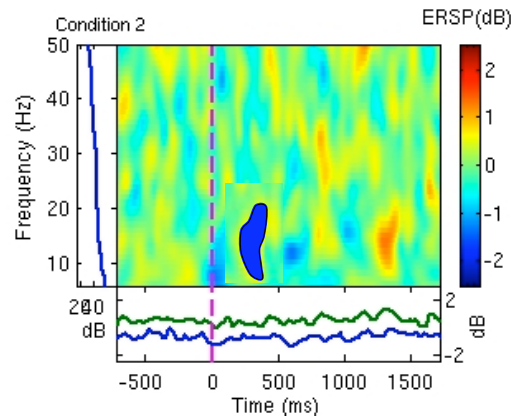
44 pixels



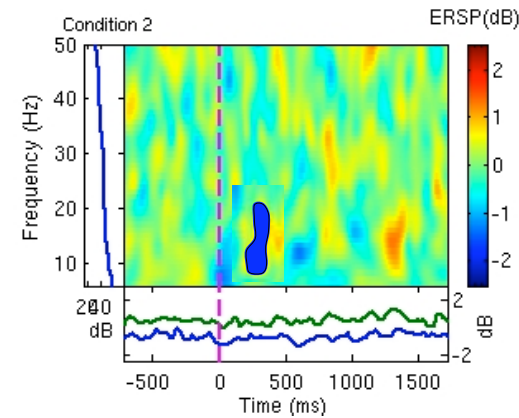
Difference bootstrap 1



Difference bootstrap 2



Difference bootstrap 3



...

References

Delorme, A. 2006. Statistical methods. *Encyclopedia of Medical Device and Instrumentation*, vol 6, pp 240-264. Wiley interscience.

Genovese et al. 2002. Thresholding of statistical maps in functional neuroimaging using the false discovery rate. *NeuroImage*, 15: 870-878

Nichols & Hayasaka, 2003. Controlling the familywise error rate in functional neuroimaging: a comparative review. *Statistical Methods in Medical Research*, 12:419-446

Maris, 2004. Randomization tests for ERP topographies and whole spatiotemporal data matrices. *Psychophysiology*, 41: 142-151

Maris et al. 2007. Nonparametric statistical testing of coherence differences. *Journal of Neuroscience Methods*, 163: 161-175

Thanks to G. Rousselet

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
```