Fieldtrip - overview

Pros:

1. Flexible in data processing

2. Advanced analysis features

3. Supporting both animal and human data

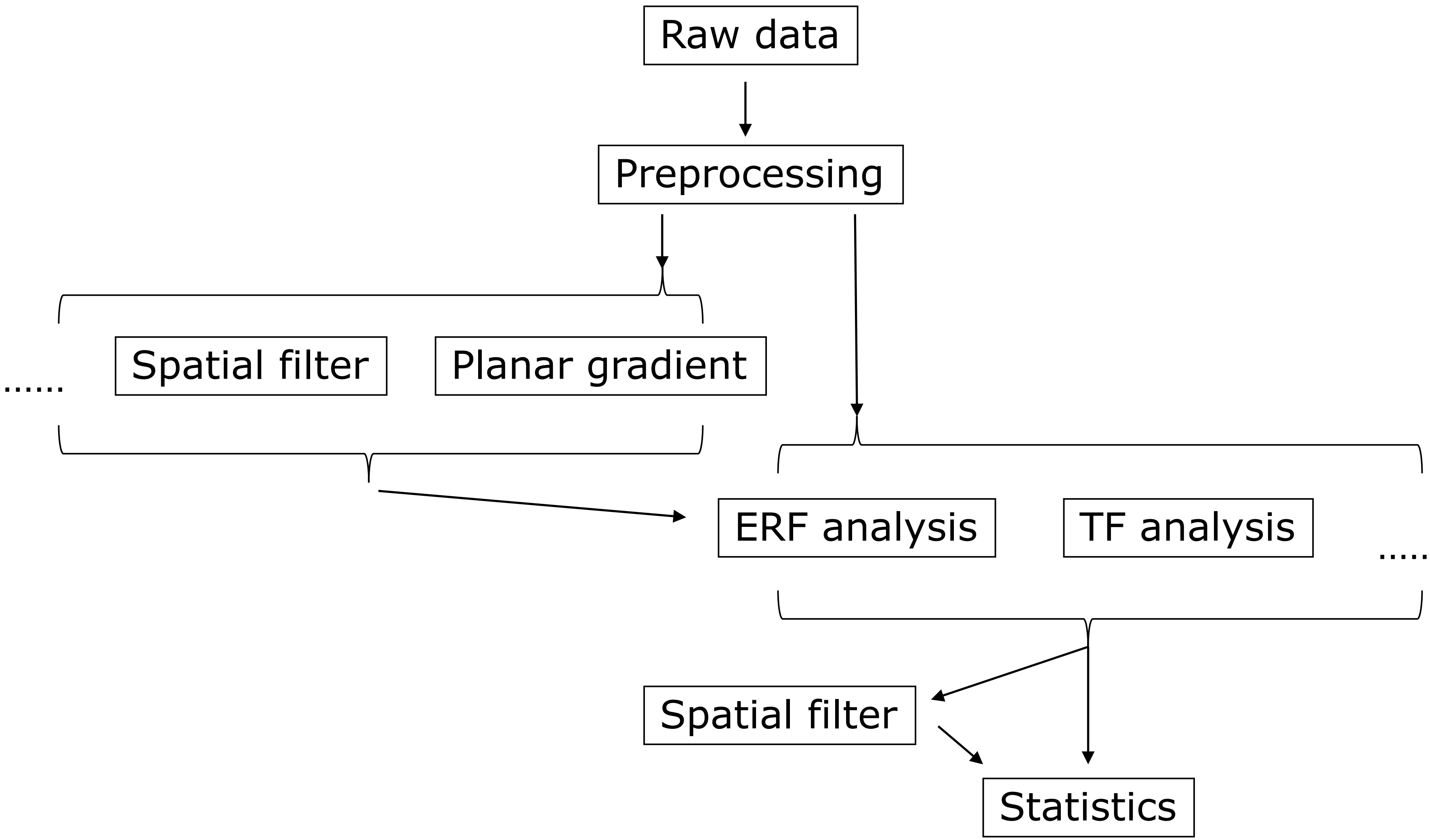
Cons:

1. A matlab toolbox.

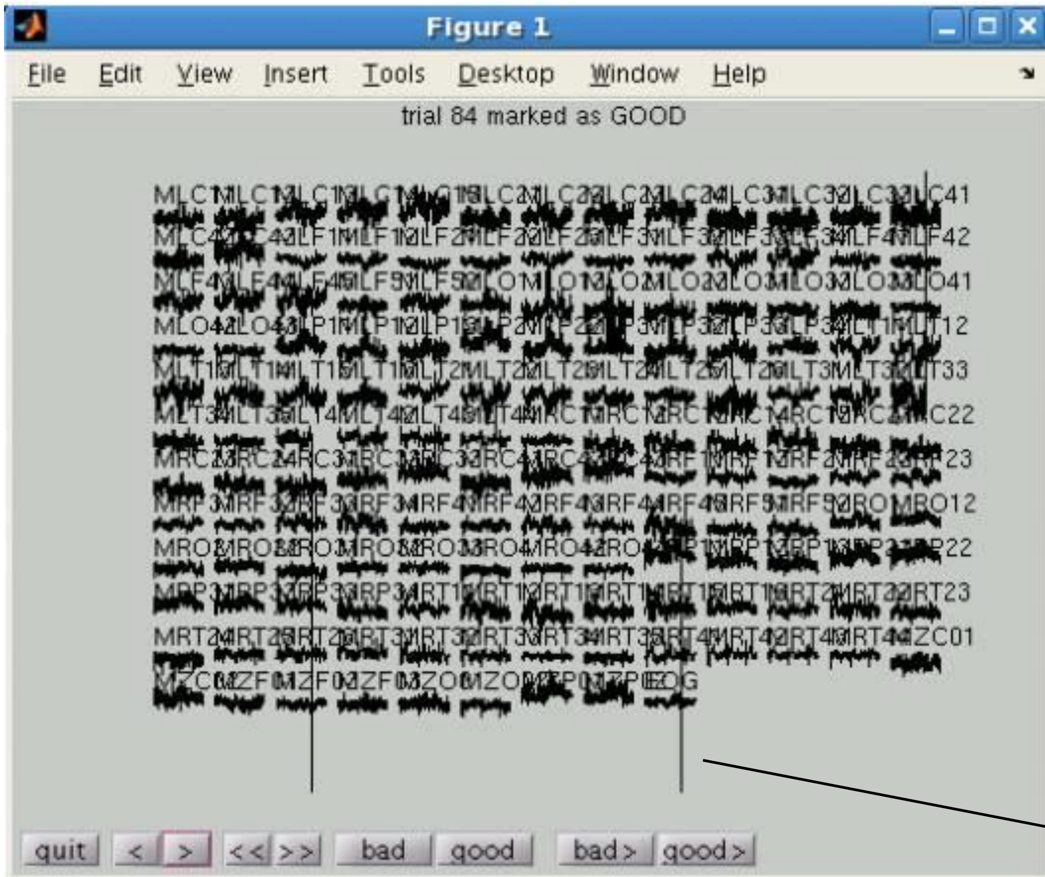
2. No graphic user interface (some experience in script writing)

3. Poor plotting features

Pipeline


Raw data
Preprocessing
......
Spatial filter
Planar gradient
ERF analysis
TF analysis
......
Spatial filter
Statistics

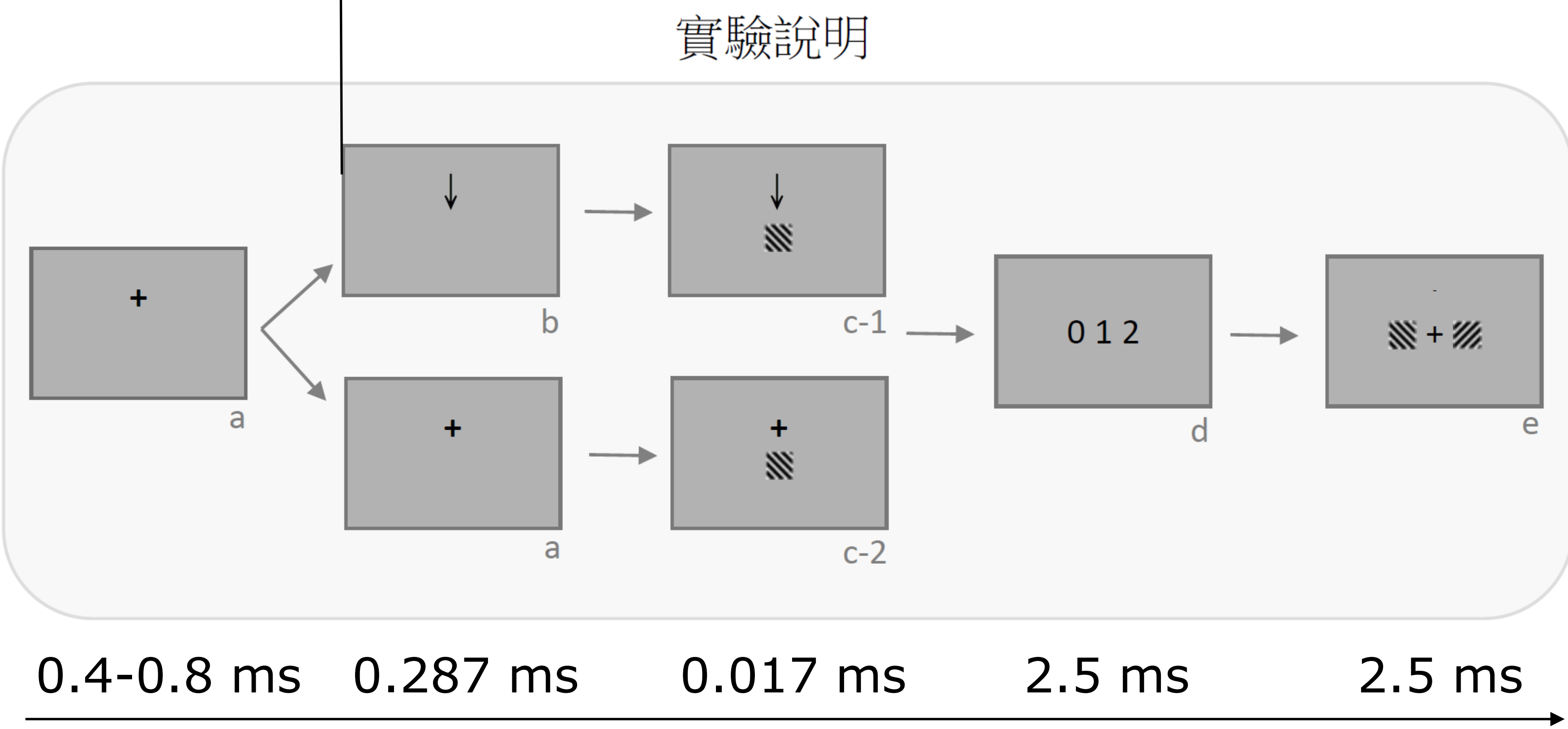
Preprocessing – quality check



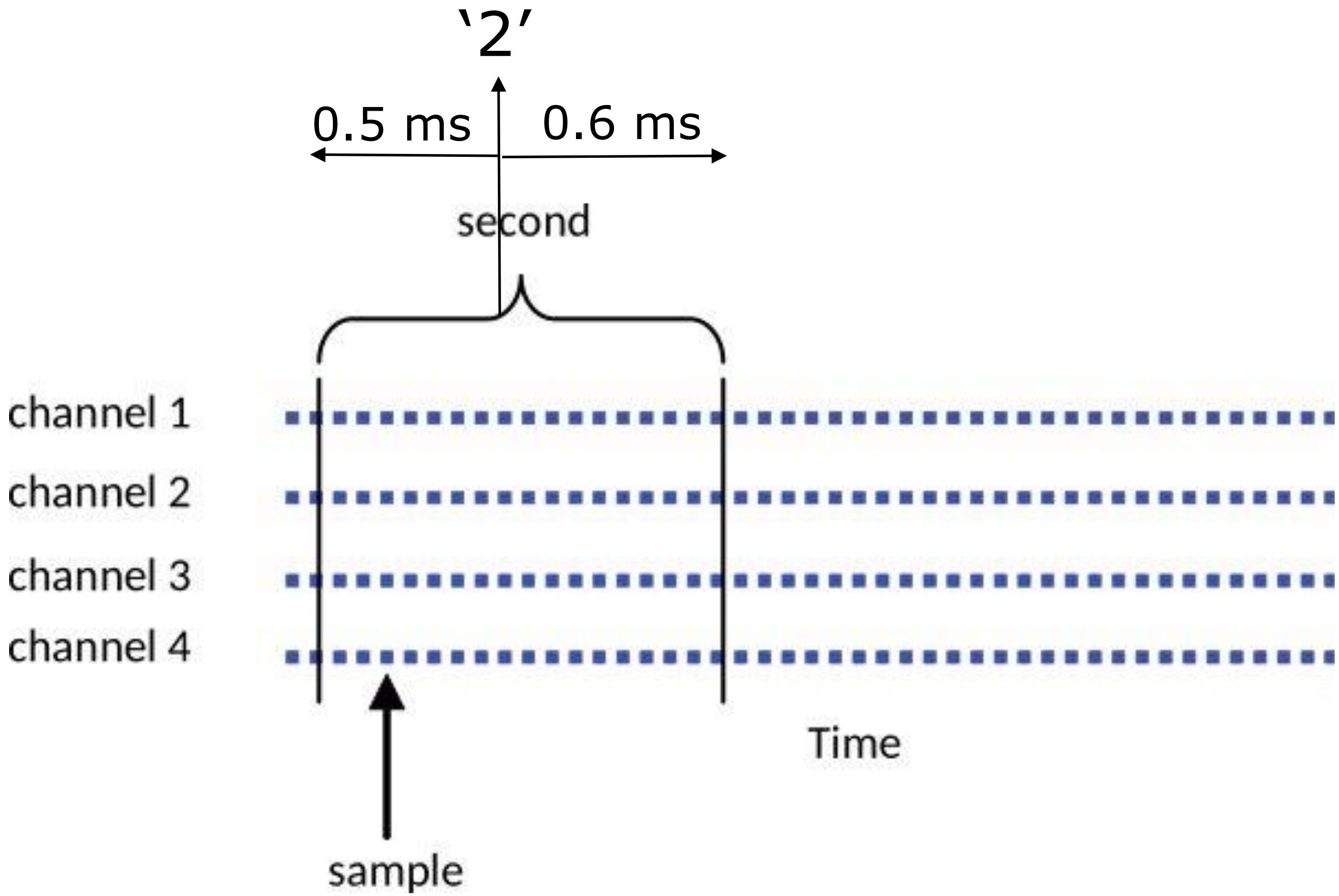
SQUID jumps

Preprocessing - importing data and defining trials

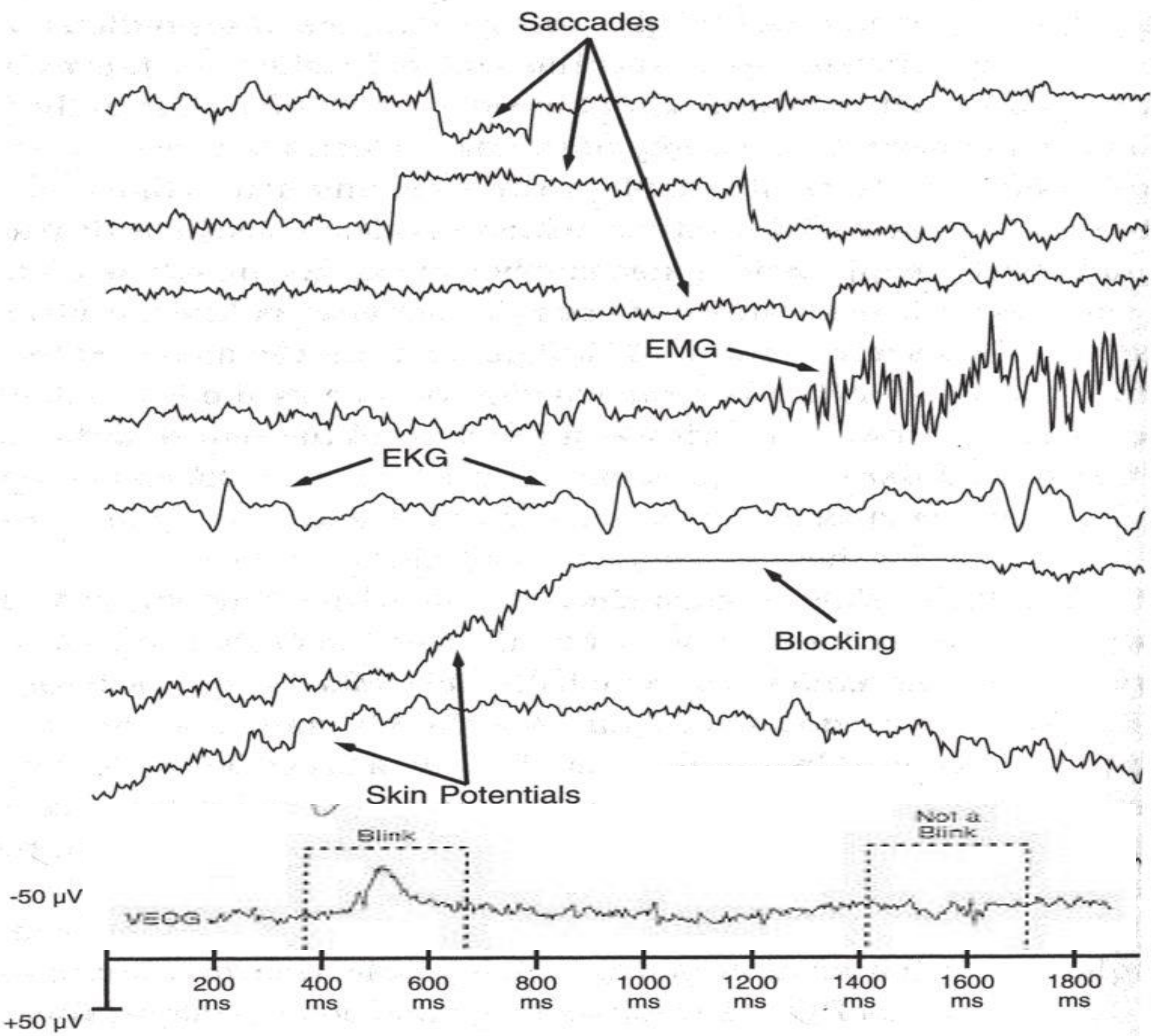
Condition b: Trigger = 2



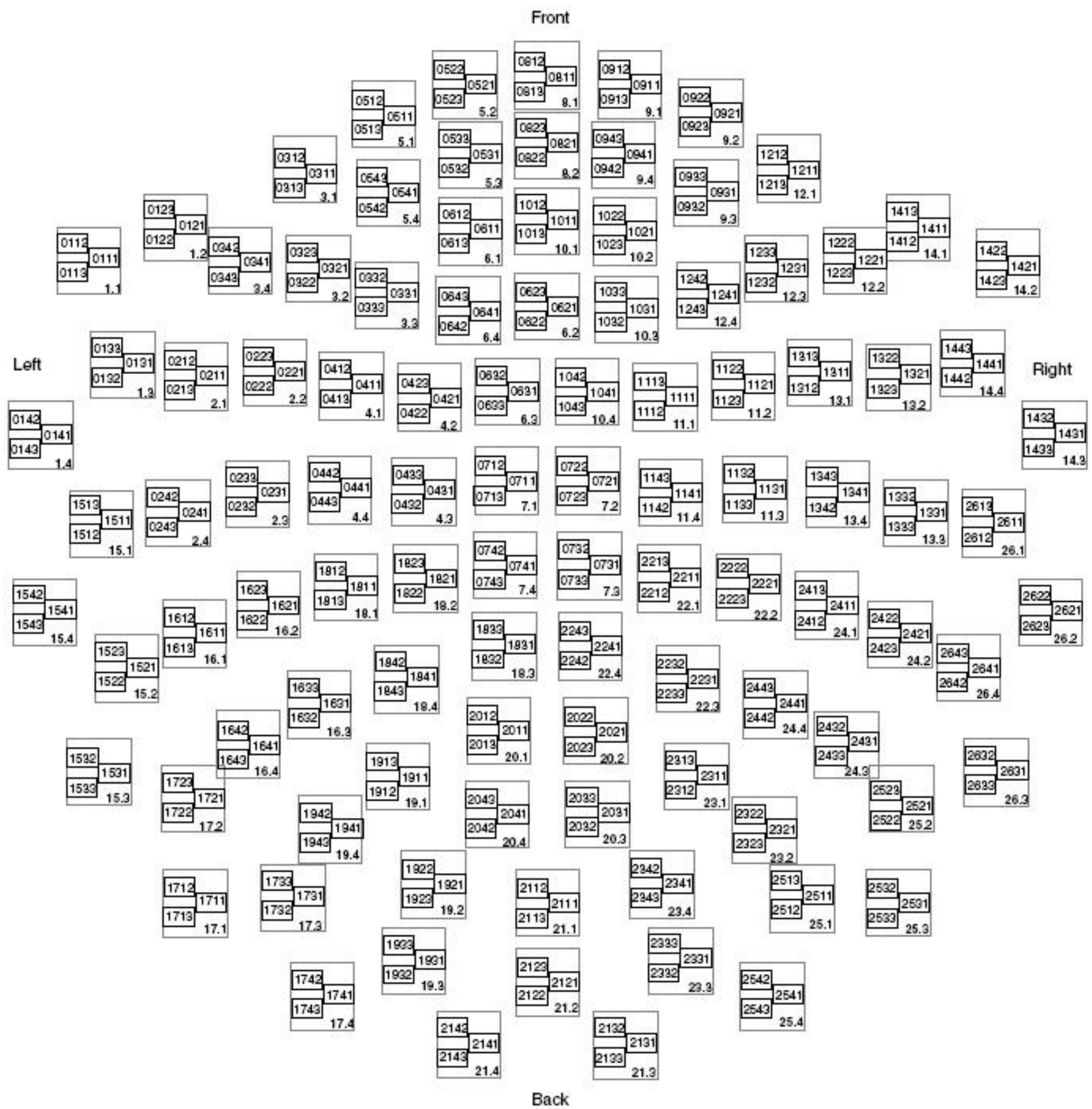
Preprocessing - importing data and defining trials



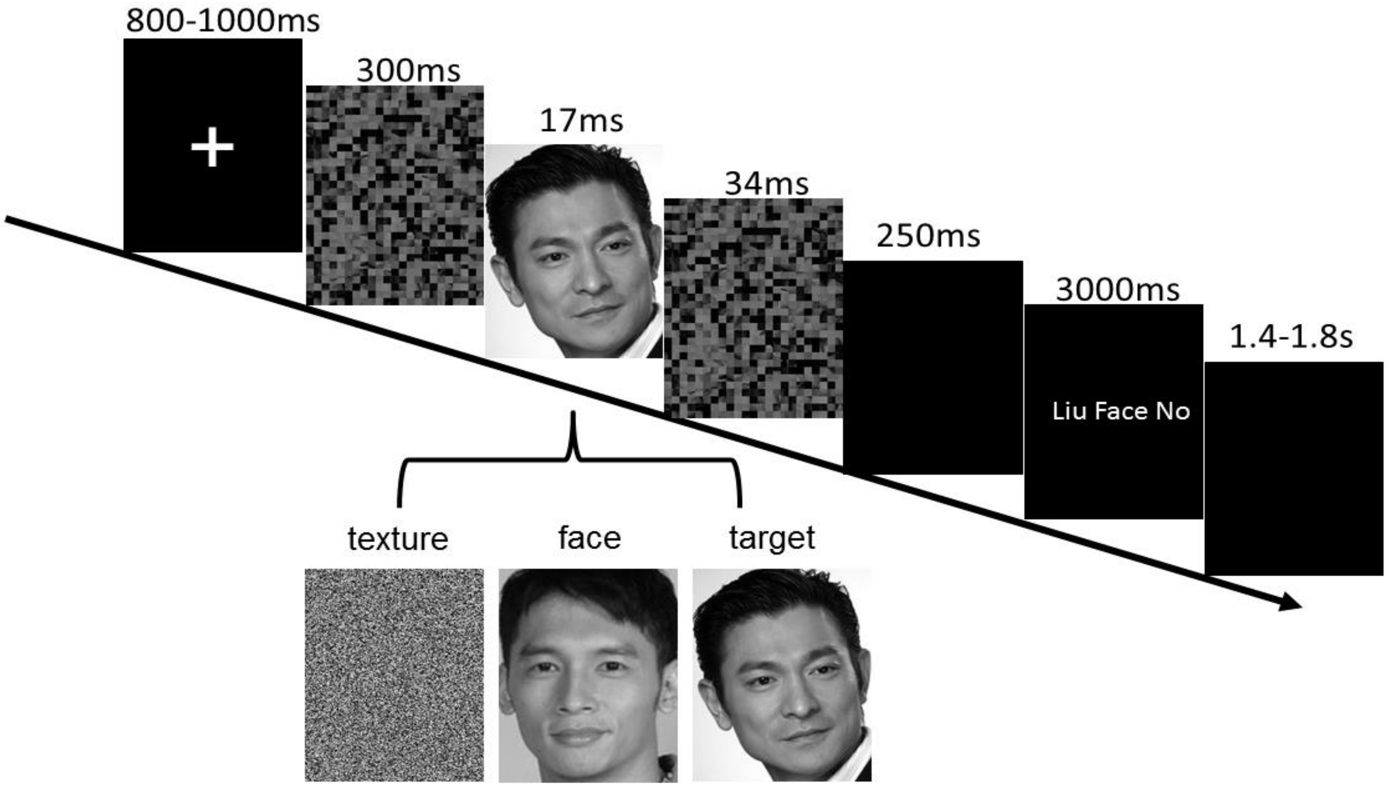
Preprocessing – artifact



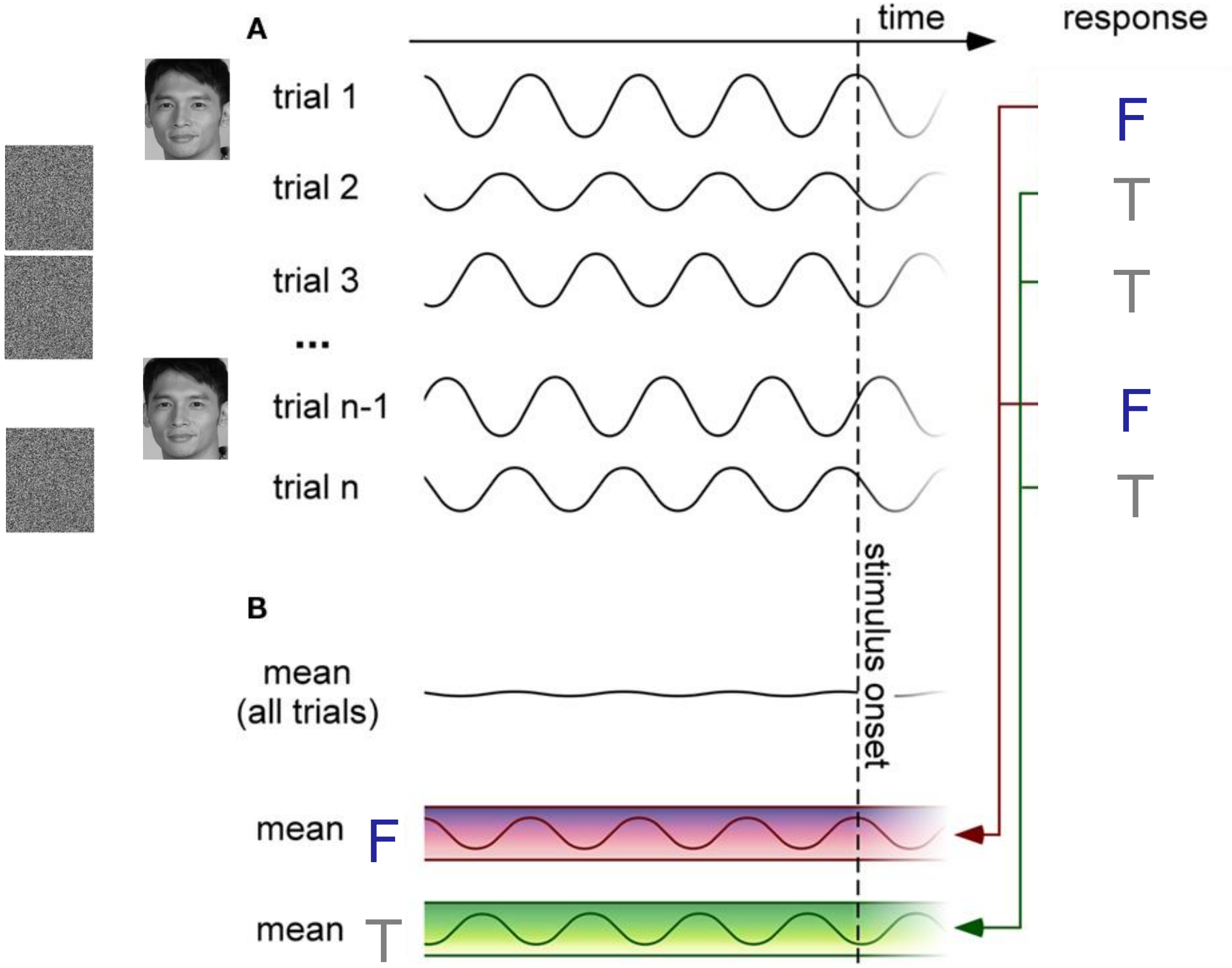
Preprocessing – artifact



Event-related field – example dataset

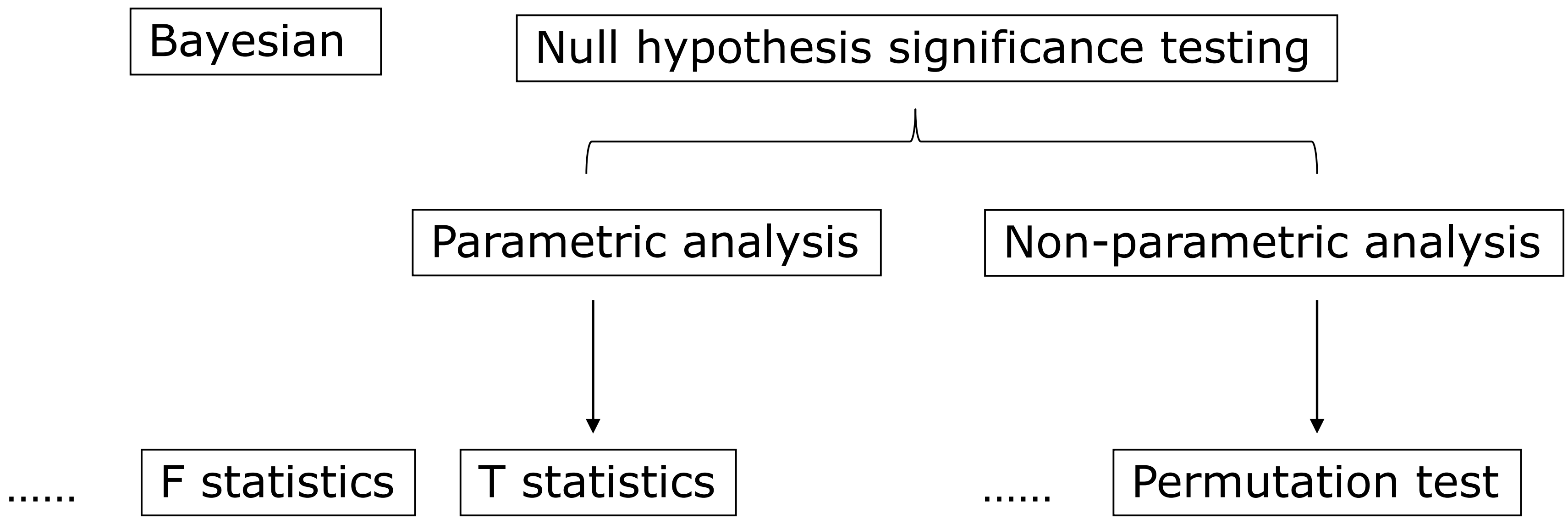


Event-related field



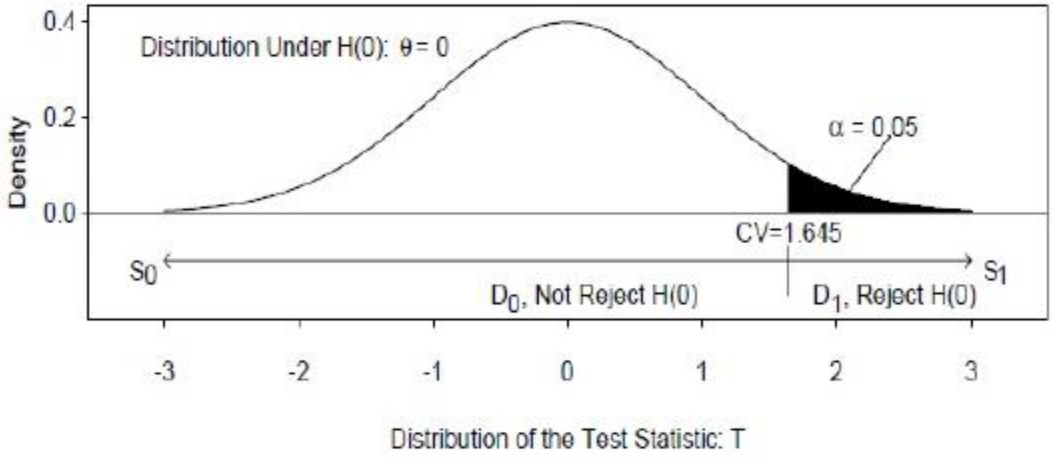
Cluster-based permutation test

2^{nd}-level inferential statistics:
testing whether the effect is consistent over subjects



NHST

1. Begin with a research hypothesis.
2. Set up a null hypothesis.
3. Construct the sampling distribution of the particular statistic on the assumption that H0 is true.
4. Collect some data.
5. Compare the sample statistic to that distribution.
6. Reject or retain H0, depending on the probability, under H0, of a sample statistic as extreme as the one we have obtained.



Permutation test

Univariate

Null hypothesis

Data (1,1)

	1		2		3		4		5		6		7		8	
	A	B	A	B	A	B	A	B	A	B	A	B	A	B	A	B
Sub1	8	5	8	5	8	5	8	5	5	8	5	8	5	8	5	8
Sub2	4	3	4	3	3	4	3	4	4	3	4	3	3	4	3	4
Sub3	6	4	4	6	6	4	4	6	6	4	4	6	6	4	4	6
t value	3.46		0.46		1.11		0.0		0.0		−1.11		−0.46		−3.46	

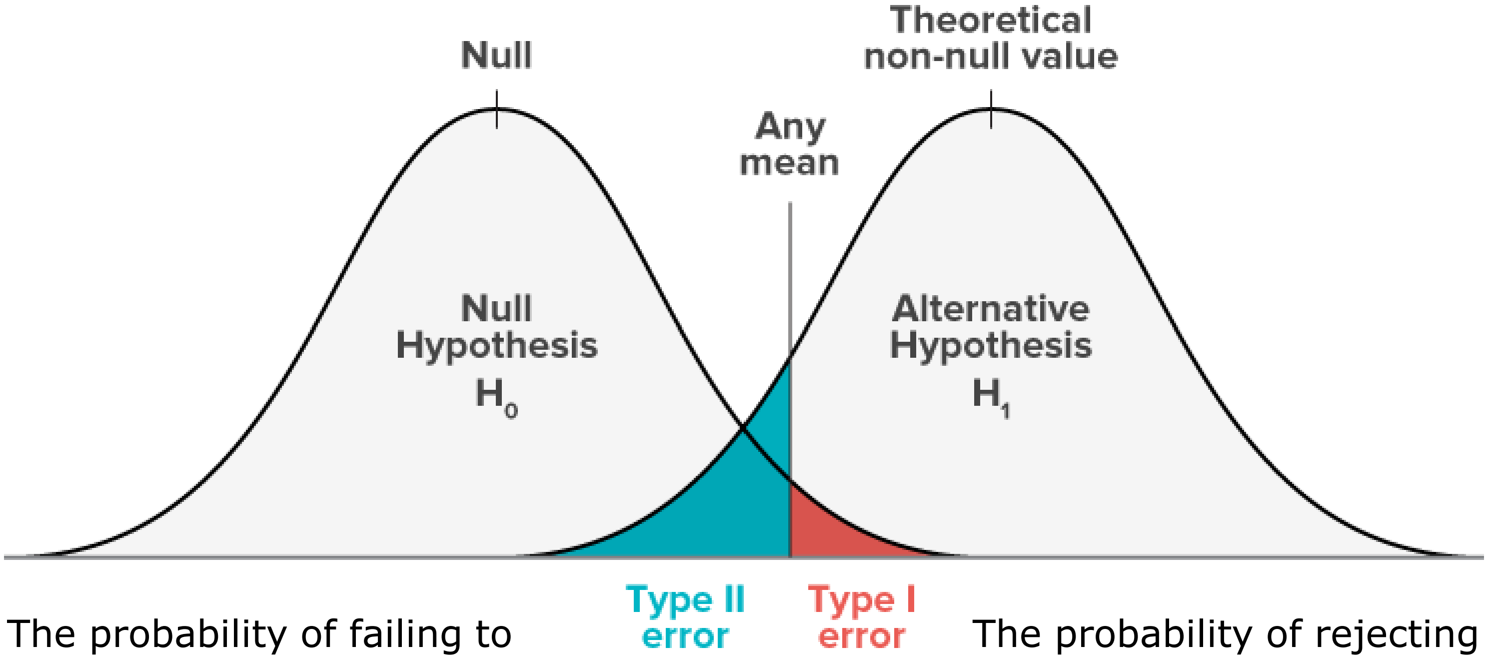
Mass univariate

Data (1,1:2)

	1		2		3		4		5		6		7		8	
	A	B	A	B	A	B	A	B	A	B	A	B	A	B	A	B
	8, 6	5, 2	8, 6	5, 2	8, 6	5, 2	8, 6	5, 2	5, 2	8, 6	5, 2	8, 6	5, 2	8, 6	5, 2	8, 6
	4, 3	3, 1	4, 3	3, 1	3, 1	4, 3	3, 1	4, 3	4, 3	3, 1	4, 3	3, 1	3, 1	4, 3	3, 1	4, 3
	6, 7	4, 4	4, 4	6, 7	6, 7	4, 4	4, 4	6, 7	6, 7	4, 4	4, 4	6, 7	6, 7	4, 4	4, 4	6, 7
t values	(3.46; 5.20)		(0.46; 0.48)		(1.11; 0.90)		(0.0; −0.15)		(0.0; 0.15)		(−1.11; −0.90)		(−0.46; −0.48)		(−3.46; −5.20)	
t_{sum}	8.66		0.94		2.01		−0.15		0.15		−2.01		−0.94		−8.66	
$t_{\|sum\|}$	8.66		0.94		2.01		0.15		0.15		2.01		0.94		8.66	
t_{max}	5.20		0.48		1.11		−0.15		0.15		−1.11		−0.48		−5.20	

Multiple comparison problems

The more comparisons we conduct, the more Type I errors we will make when the Null Hypothesis is true.
* Must consider Familywise (vs. per-comparison) Error Rate



The probability of failing to reject H0 given that it is false

The probability of rejecting H0 given that it is true

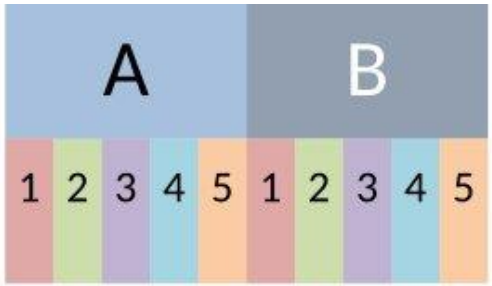
Cluster-based test

1. For every sample (a (channel,time)-pair or a (channel,frequency,time)-triplet) the experimental conditions are compared by means of a t-value or some other number that quantifies the effect at this sample.
2. All samples are selected whose t-value is larger than some threshold as specified in cfg.clusteralpha. If cfg.clusteralpha is equal to 0.05, the t-values are thresholded at the 95-th quantile for a one-sided t-test, and at the 2.5-th and the 97.5-th quantiles for a two-sided t-test (cfg.clustertail = 0).
3. Selected samples are clustered in connected sets on the basis of temporal, spatial and spectral adjacency (cfg.minnbchan = 2).
4. Cluster-level statistics are calculated by taking the sum of the t-values within every cluster.
5. The maximum of the cluster-level statistics is taken (cfg.clusterstatistic = 'maxsum‘).

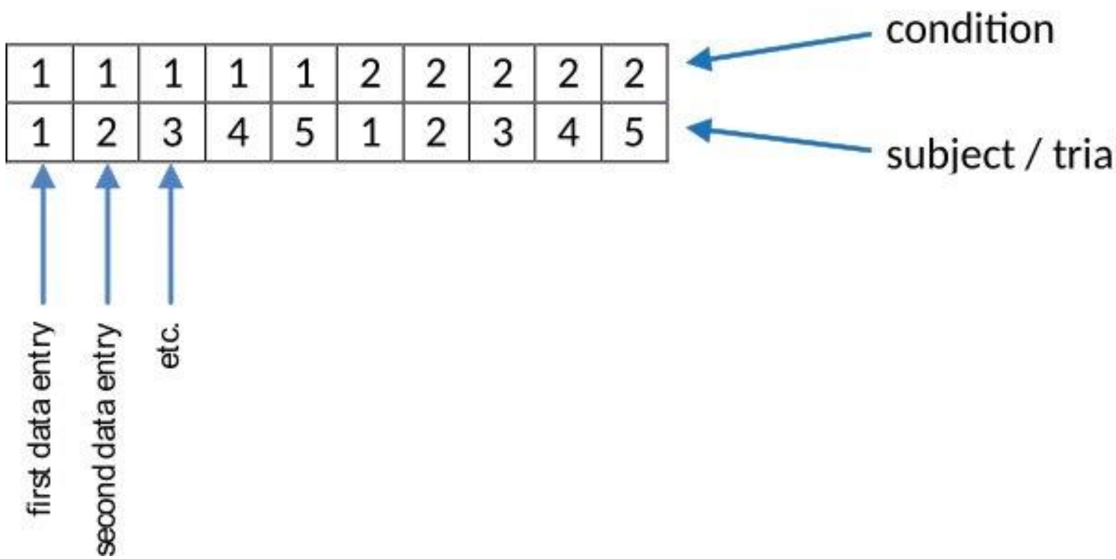
Cluster-based permutation test

1. Collect the trials of the different experimental conditions in a single set.
2. Randomly draw as many subjects from this combined data set as there were subjects in condition 1 and place them into subset 1. The remaining subjects are placed in subset 2.
3. Calculate the test statistic (i.e., the maximum of the cluster-level summed t-values) on this random partition.
4. Repeat steps 2 and 3 a large number of times and construct a histogram of the test statistics. The computation of this Monte Carlo approximation involves a user-specified number of random draws (specified in cfg.numrandomization).
5. From the test statistic that was actually observed and the histogram in step 4, calculate the proportion of random partitions that resulted in a larger test statistic than the observed one. This proportion is the Monte Carlo significance probability, which is also called a p-value.

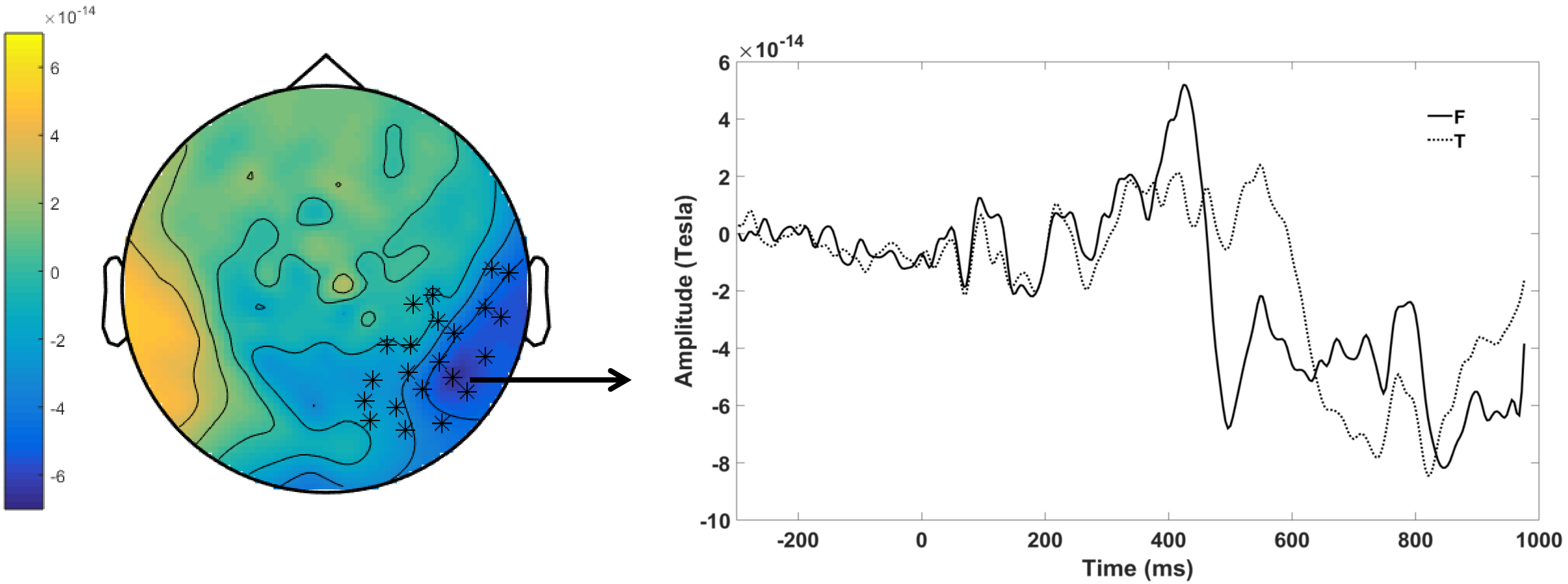
Design matrix



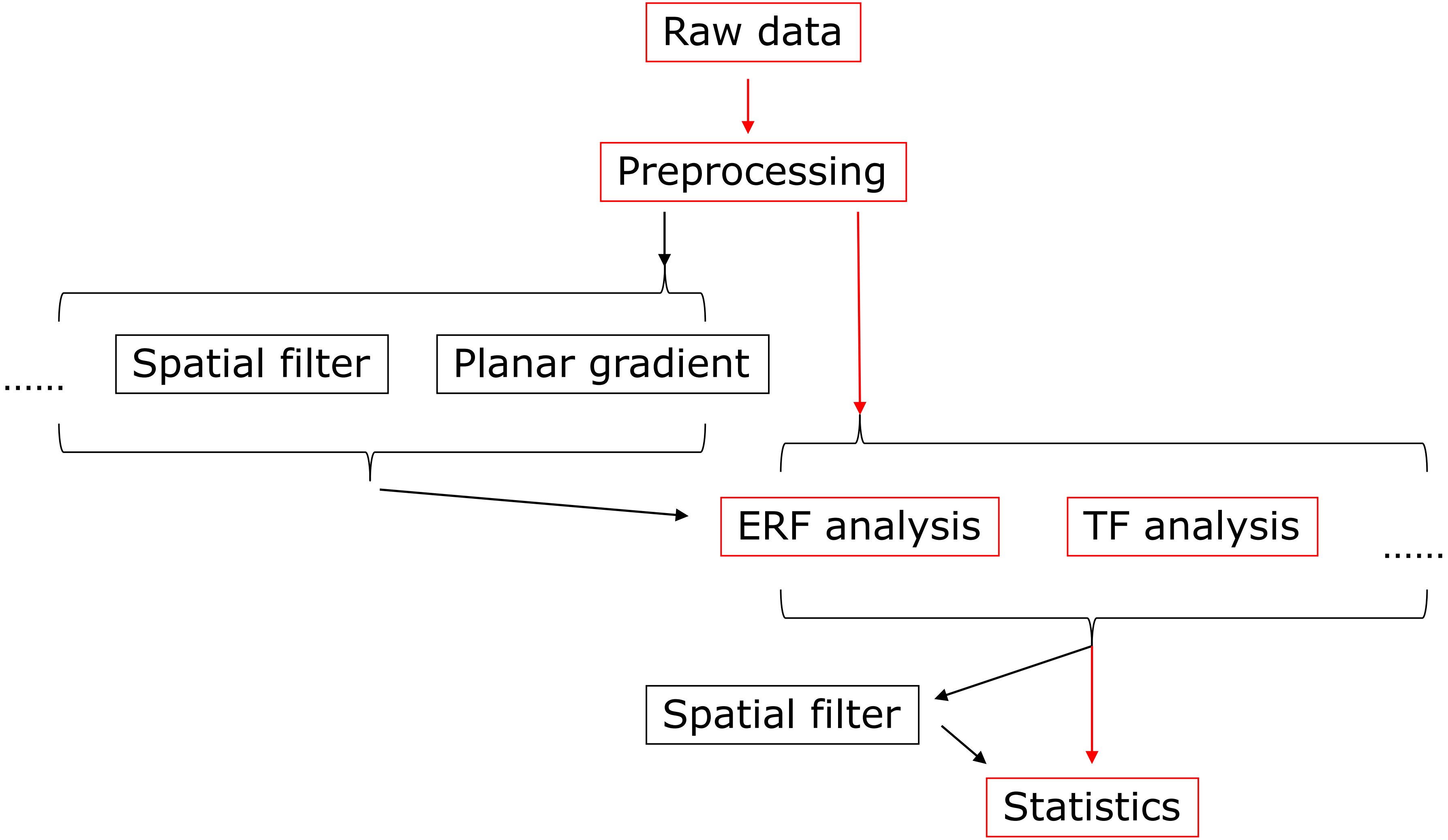

```
cfg.design = [ ones(1,5)  ones(1,5)*2; 1:5 1:5 ];
cfg.ivar = 1;
cfg.uvar = 2;
```



Event-related field – example dataset



Pipeline



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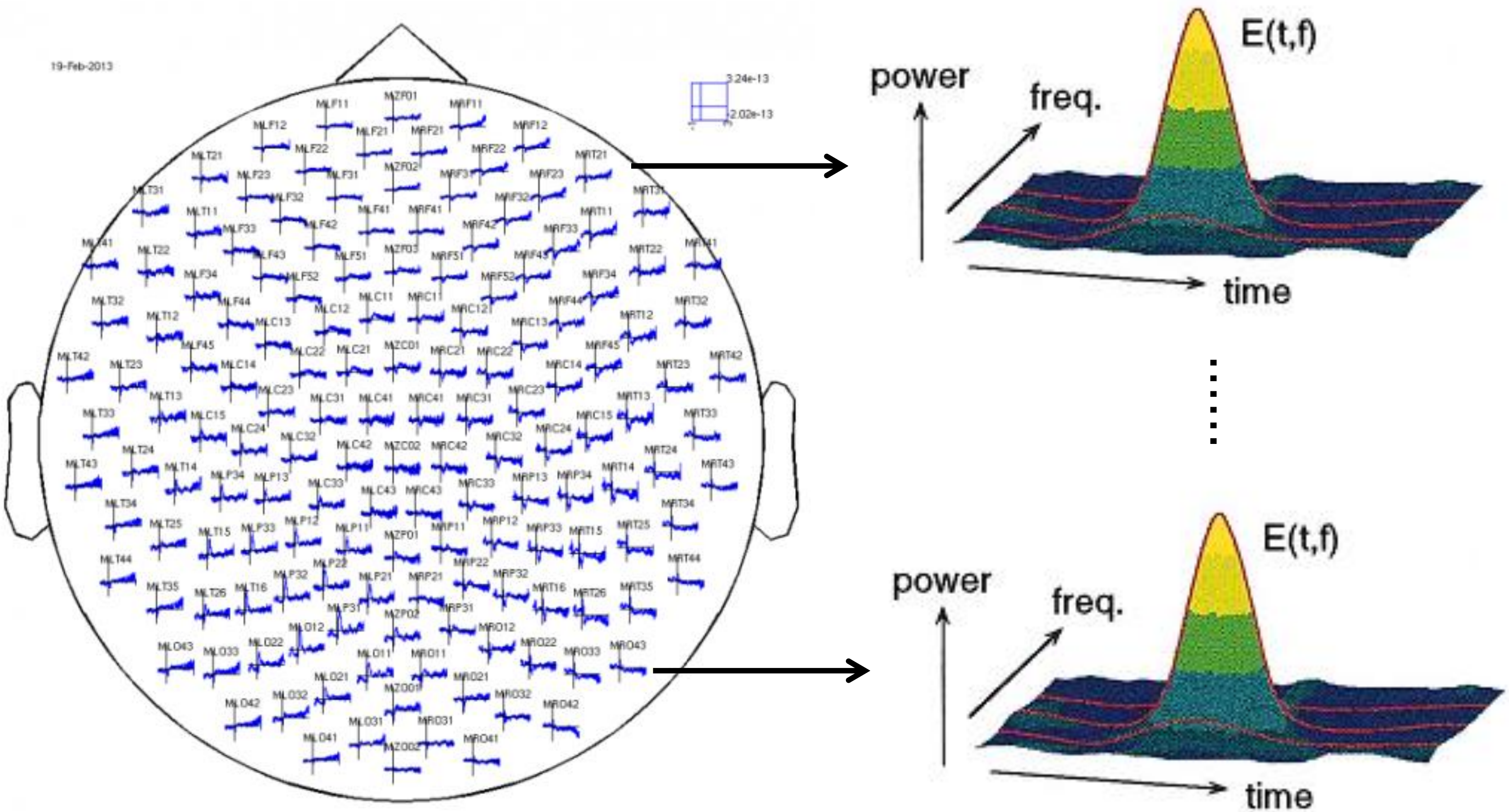
Time frequency analysis – power



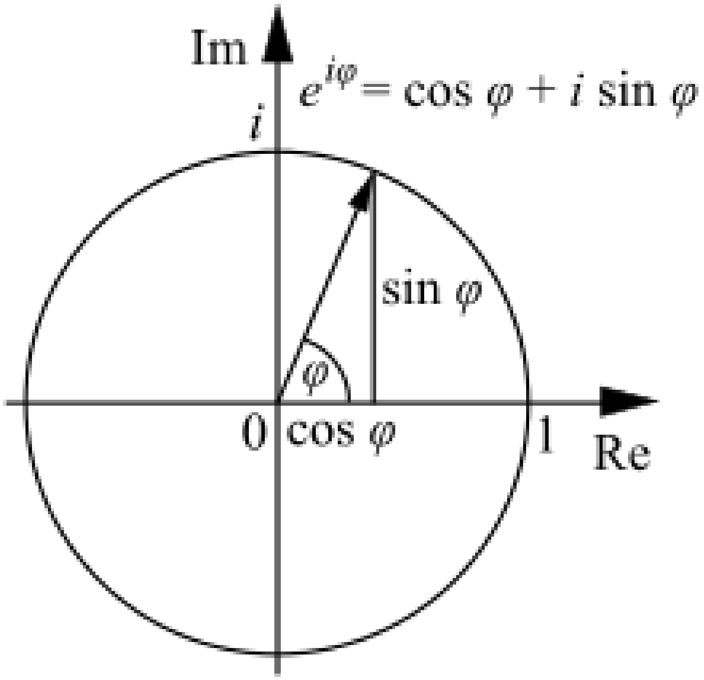
Frequency and power

Band	Frequency (Hz)
Delta	<4
Theta	4-7
Alpha	8-12
Beta	13-30
Gamma	>30

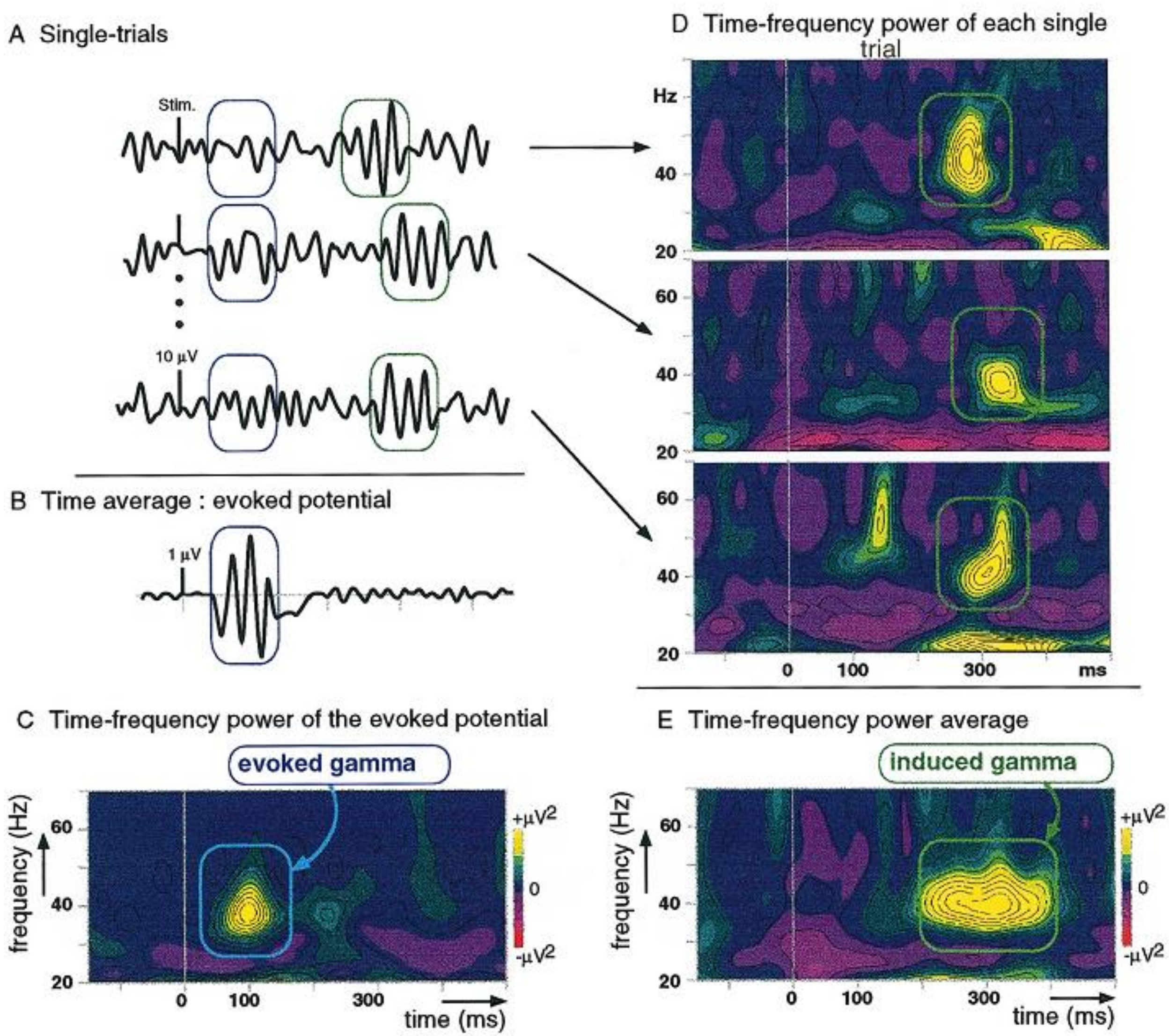
Power

$$z = x + iy = |z|(\cos\varphi + i\sin\varphi) = re^{i\varphi}$$

x = Re z, the real part
y = Im z, the imaginary part
r = |z| = √x2 + y2, the magnitude of z
φ = arg z = atan2(y, x)

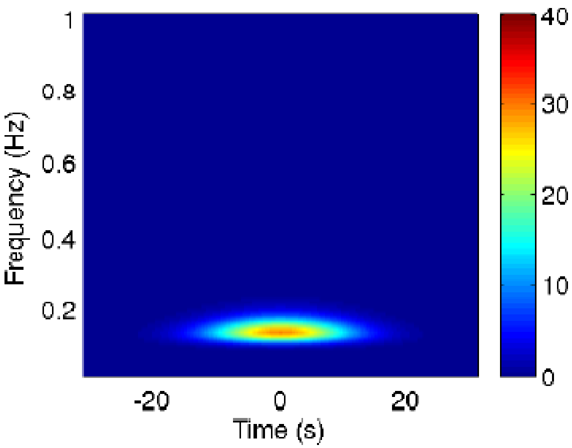


Evoked vs Induced activity

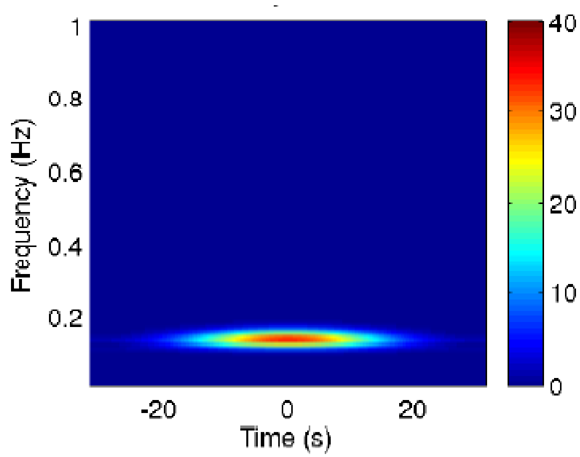


Wavelet

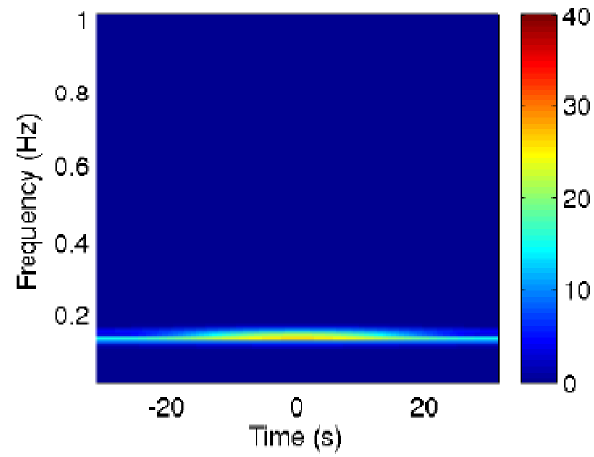
M = 5



M = 10



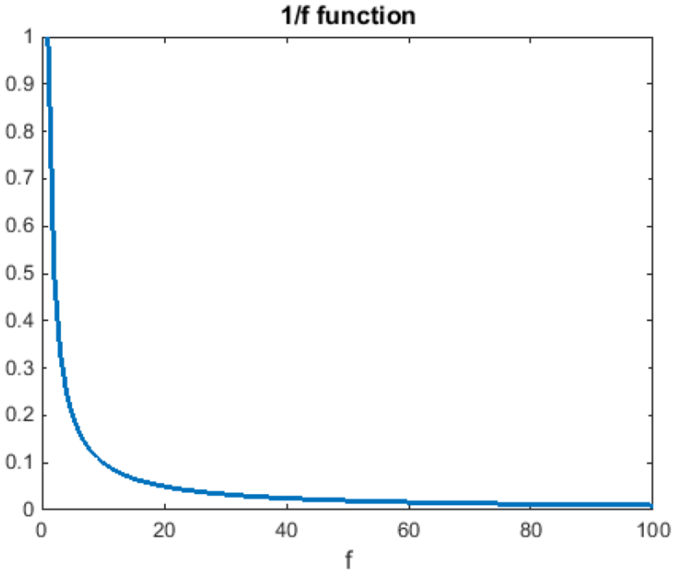
M = 20

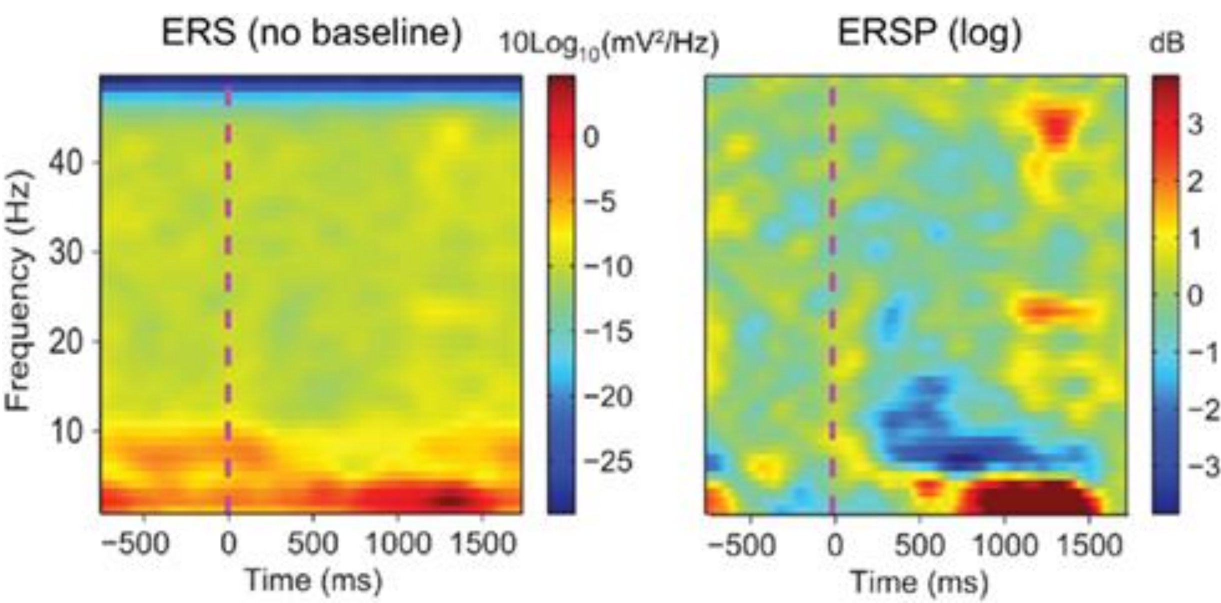


Frequency resolution at frequency f: $$\sigma_f = \frac{f}{m}$$

Temporal resolution at frequency f: $$\sigma_t = \frac{m}{2*\pi*\sigma_f}$$

Power – baseline normalization





Power – baseline normalization

Additive model

$$\mathrm{ERSP}_z(f,t) = \left(\frac{\mathrm{ERS}(f,t) - \mu_B(f)}{\sigma_B(f)}\right)$$

Gain model

$$\mathrm{ERSP}_{\%}(f,t) = \frac{\mathrm{ERS}(f,t)}{\mu_B(f)}$$

$$\mathrm{ERSP}_{\log}(f,t) = 10\log_{10}\left(\mathrm{ERSP}_{\%}(f,t)\right)$$

Others ......

Further reading

- General: Gross et al. (2013) Good practice for conducting and reporting MEG research, Neuroimage.
- ERF analysis: Steven J Luck, An Introduction to the Event-Related Potential Technique
- TF analysis: Mike X. Cohen, Analyzing Neural Time Series Data: Theory and Practice.