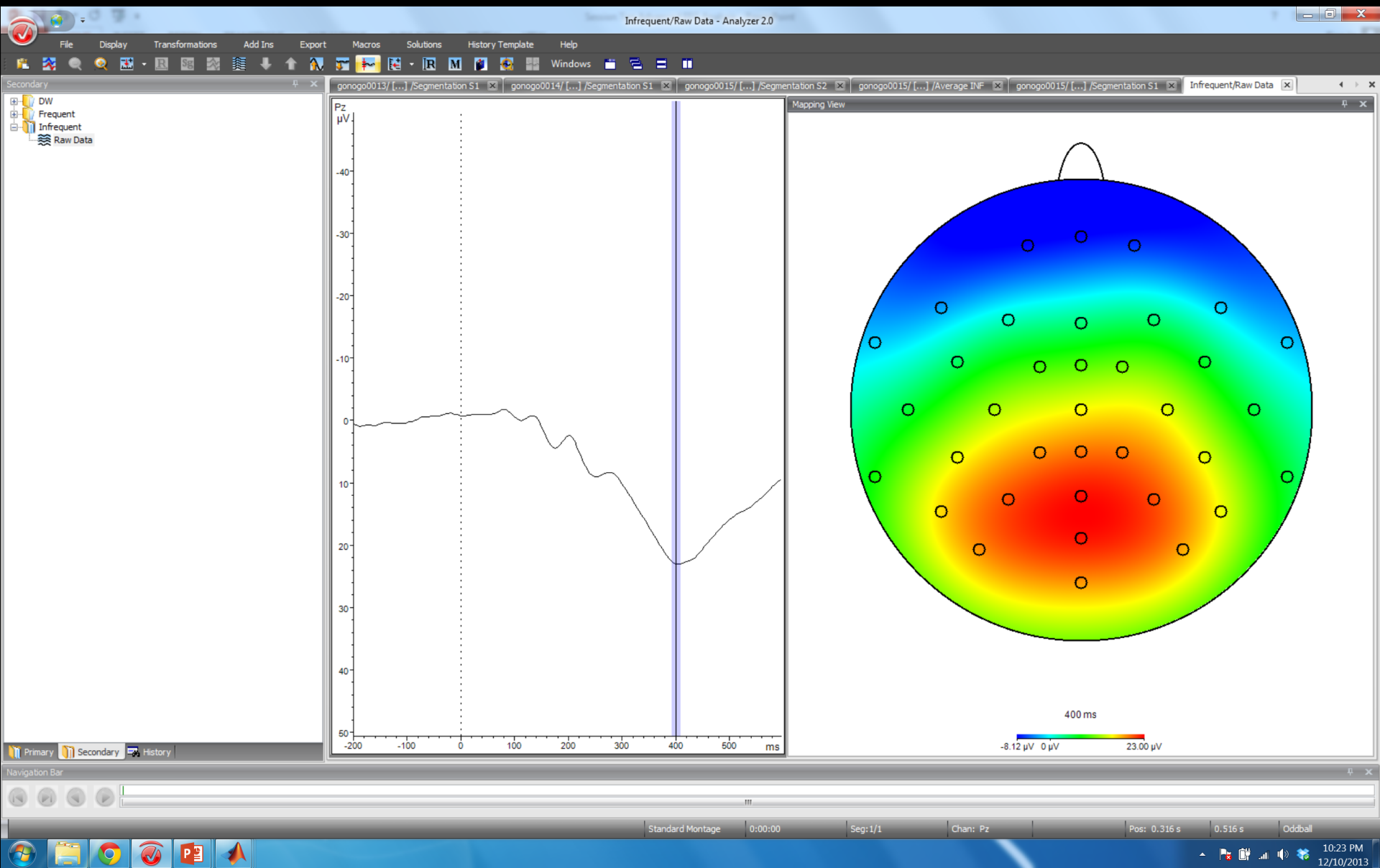


Source Analysis and a Few Other Tricks

Source Analysis



The Inverse Problem

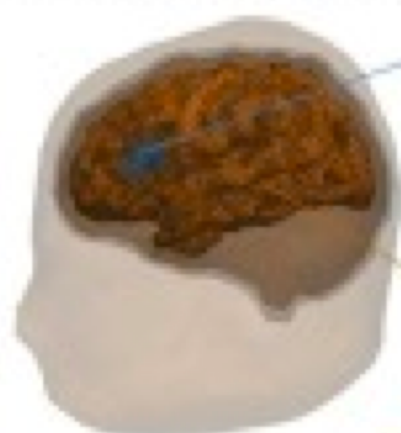
Simply put, because we do not know the number of dipoles at any given point in time, there are an infinite number of potential solutions for a given scalp topography.

Source localization techniques try to get around this by using certain assumptions.

Forward problem: data generation

$$\mathbf{X} = \mathbf{G} \cdot \mathbf{S}$$

head model
lead field matrix: \mathbf{G}



source signals
signal matrix: \mathbf{S}

activity of interest

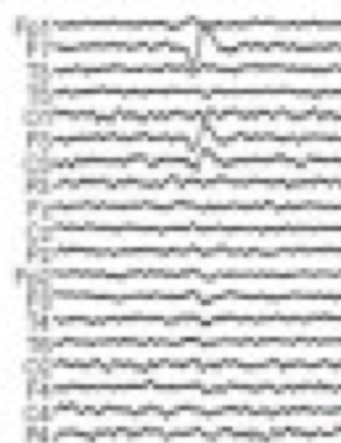


background activity



EEG

data matrix: $\mathbf{X} \in \mathbb{R}^{N \times K}$



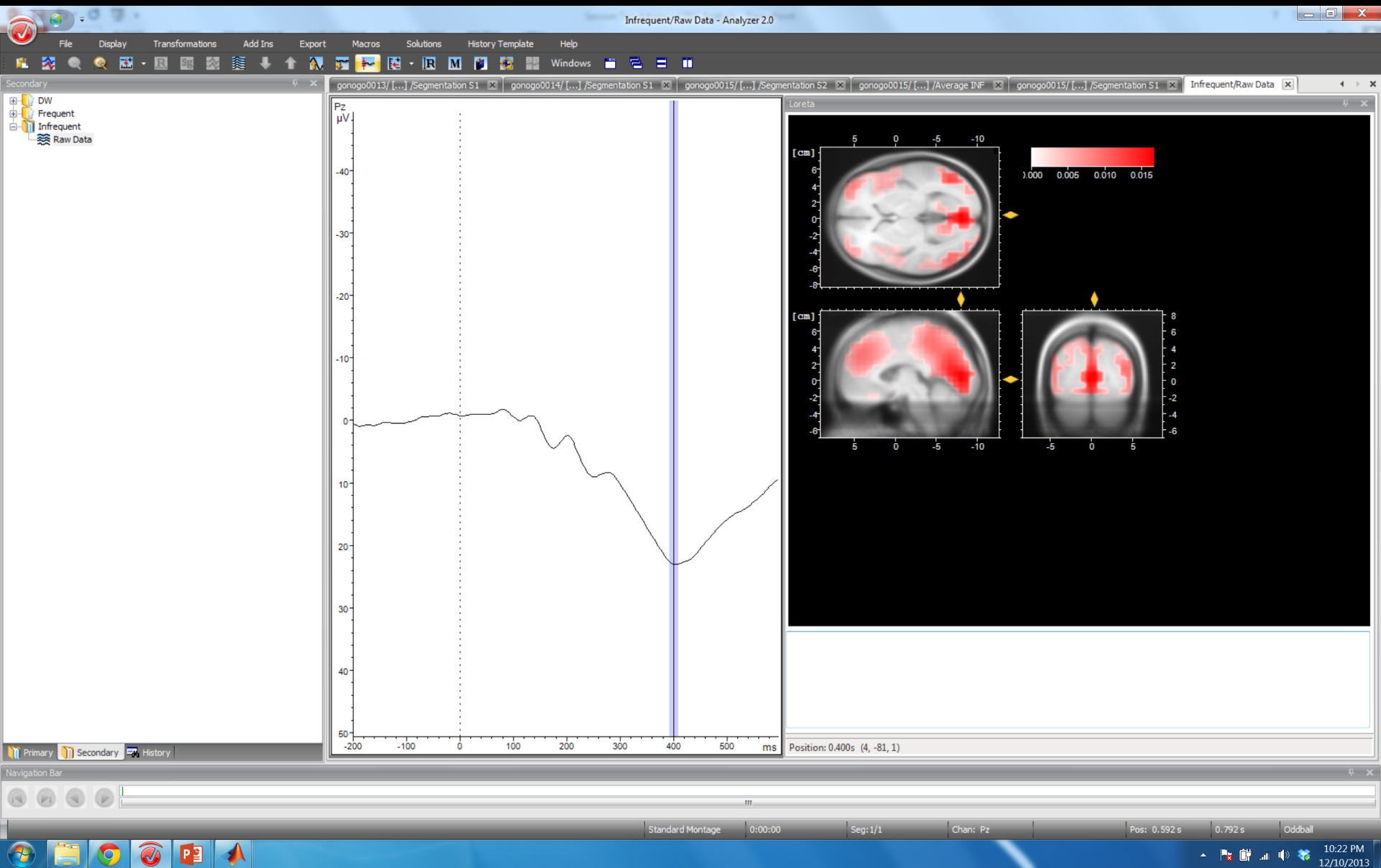
$$\mathbf{S} = ?$$

Inverse problem: source imaging

Discrete vs Distributed Source Solutions

Discrete source solutions focus on dipoles.

Distributed source solutions use dipoles but “consider” whole brain activity.



Loreta

The mathematics behind these techniques is beyond the scope of what we are covering here.

In a nutshell, Loreta divides the brain into a number of voxels each containing three perpendicular dipoles (X, Y, Z) and then varies the parameters of these dipoles for each voxel to obtain the observed scalp topography.

Loreta

There are still multiple solutions. So, the determined solution is the one that has the best smoothness – contiguous voxels should have gradual changes in dipole strength.

There are additional constraints such as perpendicular dipoles only, minimum overall source magnitudes, and more...

Be careful...

Loreta has a strong bias towards the midline and towards the cortical surface.

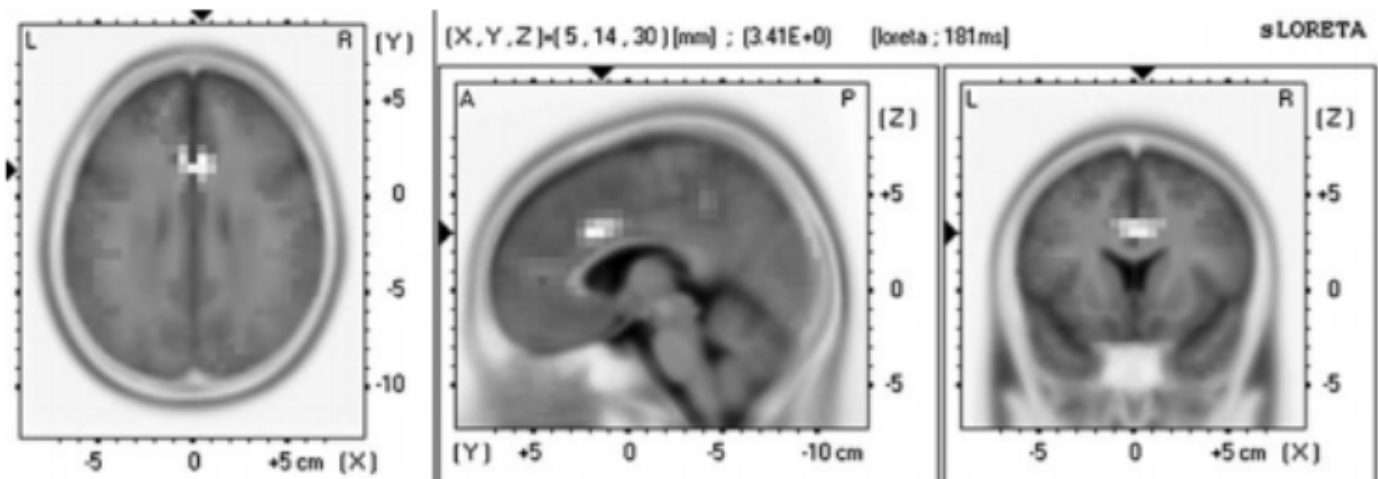
When using a source technique, do not use it like fMRI. At best, it is a confirmation of something we already know from other lines of research.

sLoreta and eLoreta

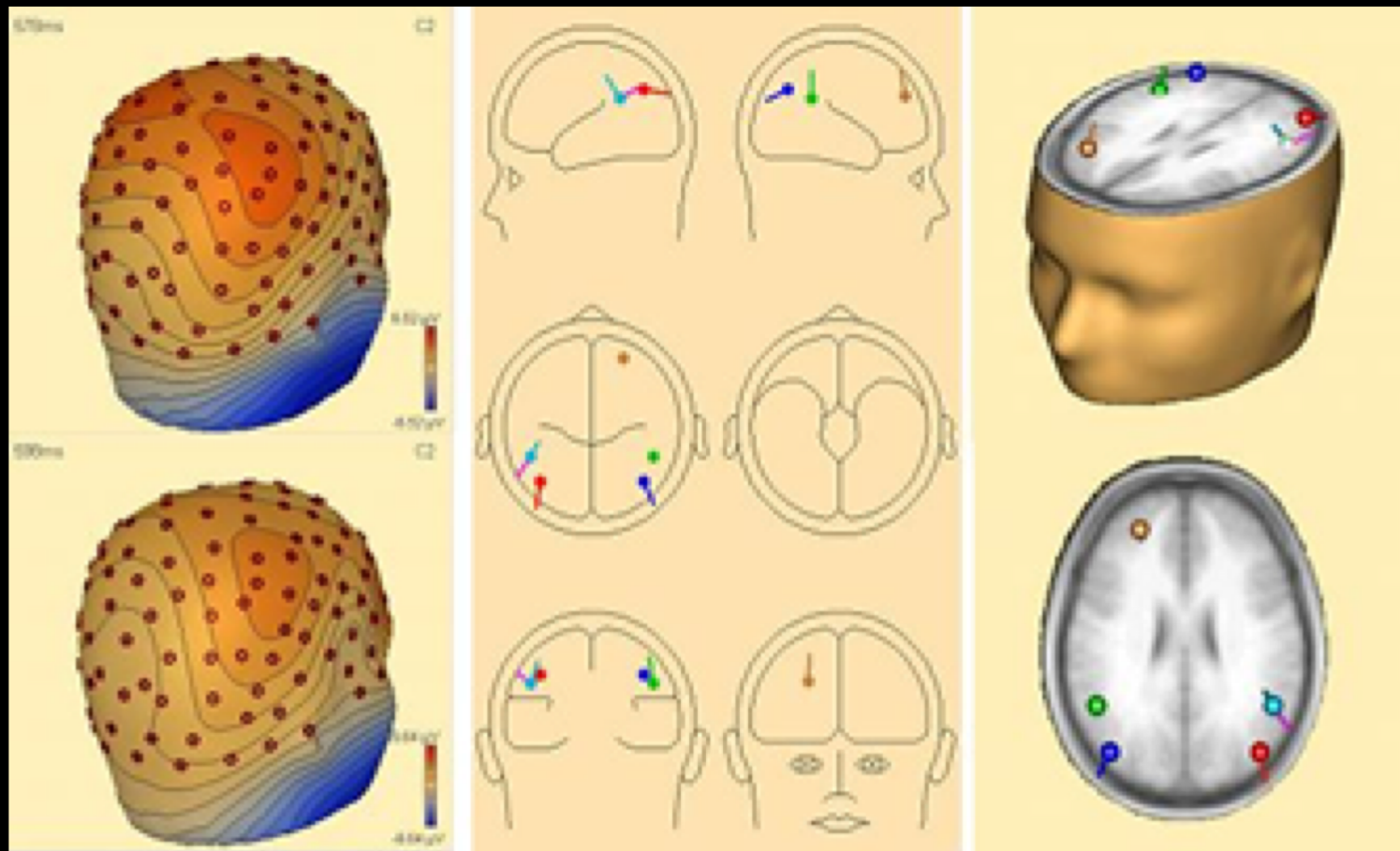
<http://www.uzh.ch/keyinst/loreta.htm>

Reporting Source Data

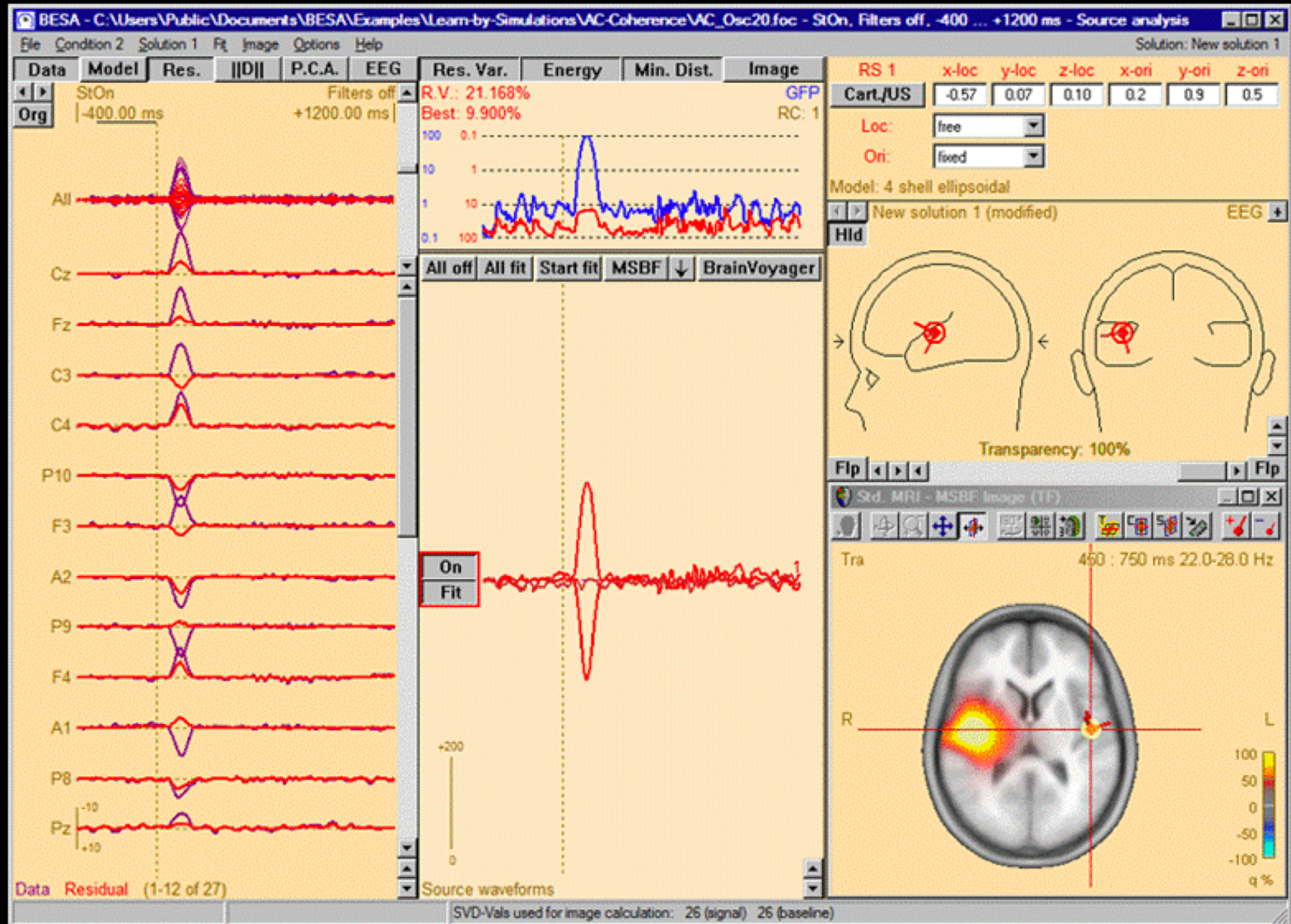
Fig. 4 sLORETA source analysis of self-ownership, as compared with other-ownership, cues at 190–240 ms post-cue-onset. Statistical non-parametric mapping (SnPM) at a significance level of .05 revealed differences localized in Brodmann area 24 (sLORETA value = 34.1) within the cingulate gyrus



BESA



BESA



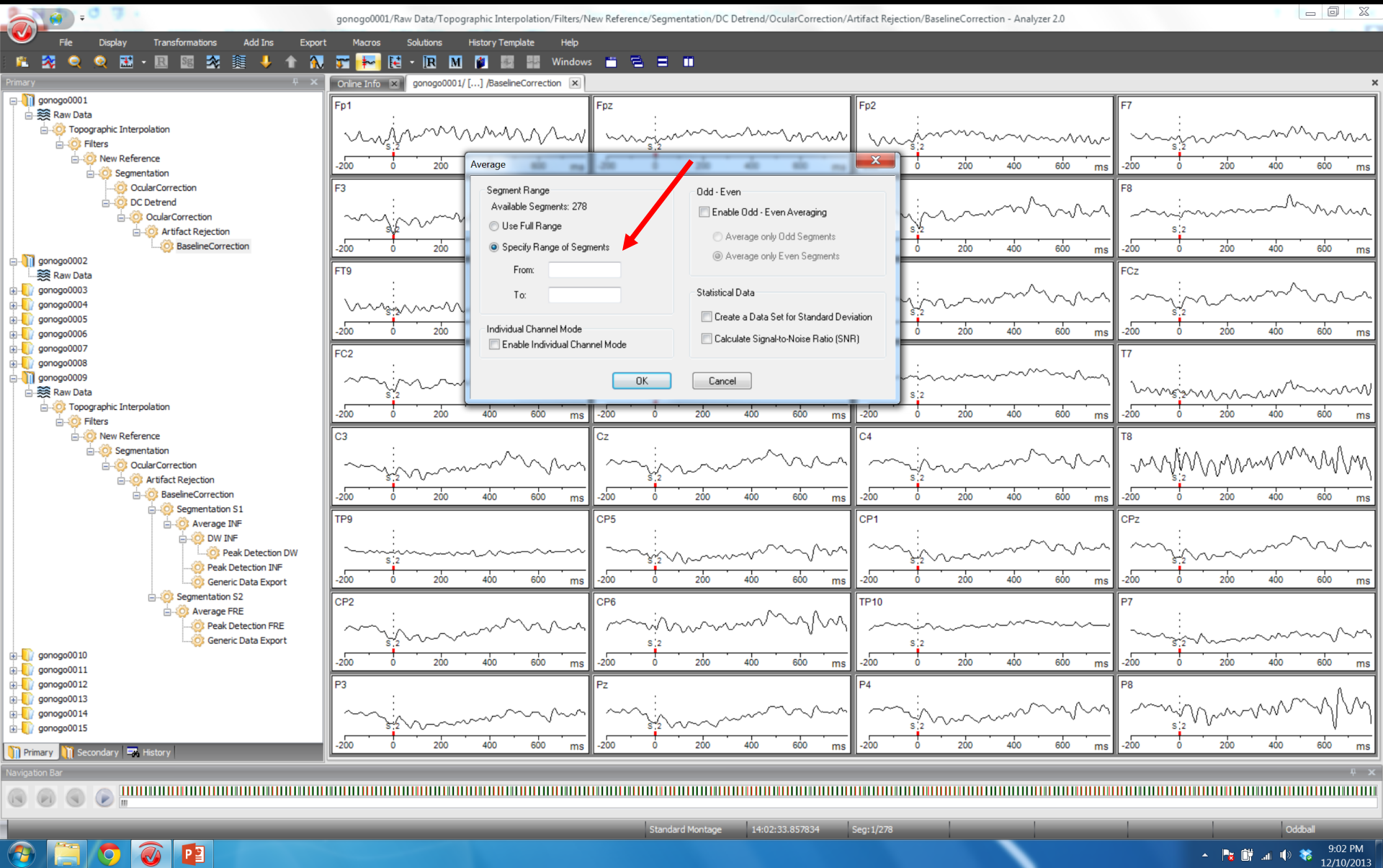
What to do?

Bins and Running Averages

Bins

You do not always have to collapse all of your markers across an entire experiment.

You may want to look at learning effects for instance.



The Oddball Data

For instance, you have 60 infrequent markers, so:

Bin 1 = Segments 1 to 30, Bin 2 = 31 to 60

In a like manner, for the 240 frequent markers:

Bin 1 = Segments 1 to 120, Bin 2 = 121 to 240

You could then do your peak detection to compare the first half of the experiment.

Obviously, the same logic could be applied to any other break down of the average.

Running Averages

The principle behind a running average is somewhat similar to bins, but somewhat more “smooth”.

As opposed to creating 2 bins (or more bins) you create a series of bins.

If you have 100 segments, you create the following bins:

Average 1 = Segments 1 to 50

Average 2 = Segments 2 to 51

Average 3 = Segments 3 to 52

etc

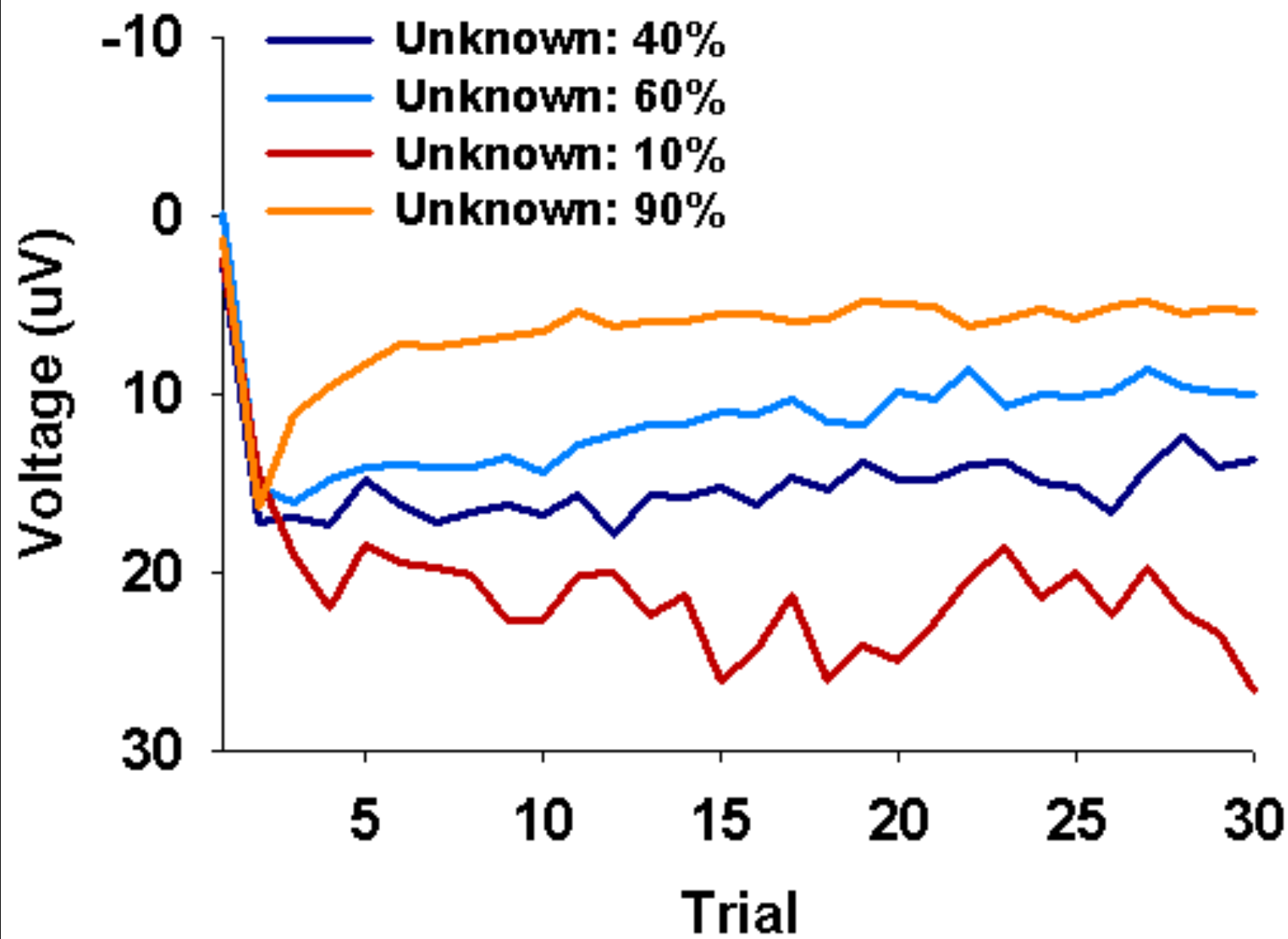
Running Averages

To be able to do this, you need to work with MATLAB.

But, its not as hard as you think.

Analyzer has a MATLAB interface so you can export directly to MATLAB and then bring the data back in.

Single Trial Analysis



So how do you do it?

Strategy One

Focus on the P300 – its large and easy to see.

Similar to Running Averages, calculate the a peak voltage - the mean – but do this for every trial and not on the average of a subset of trials.

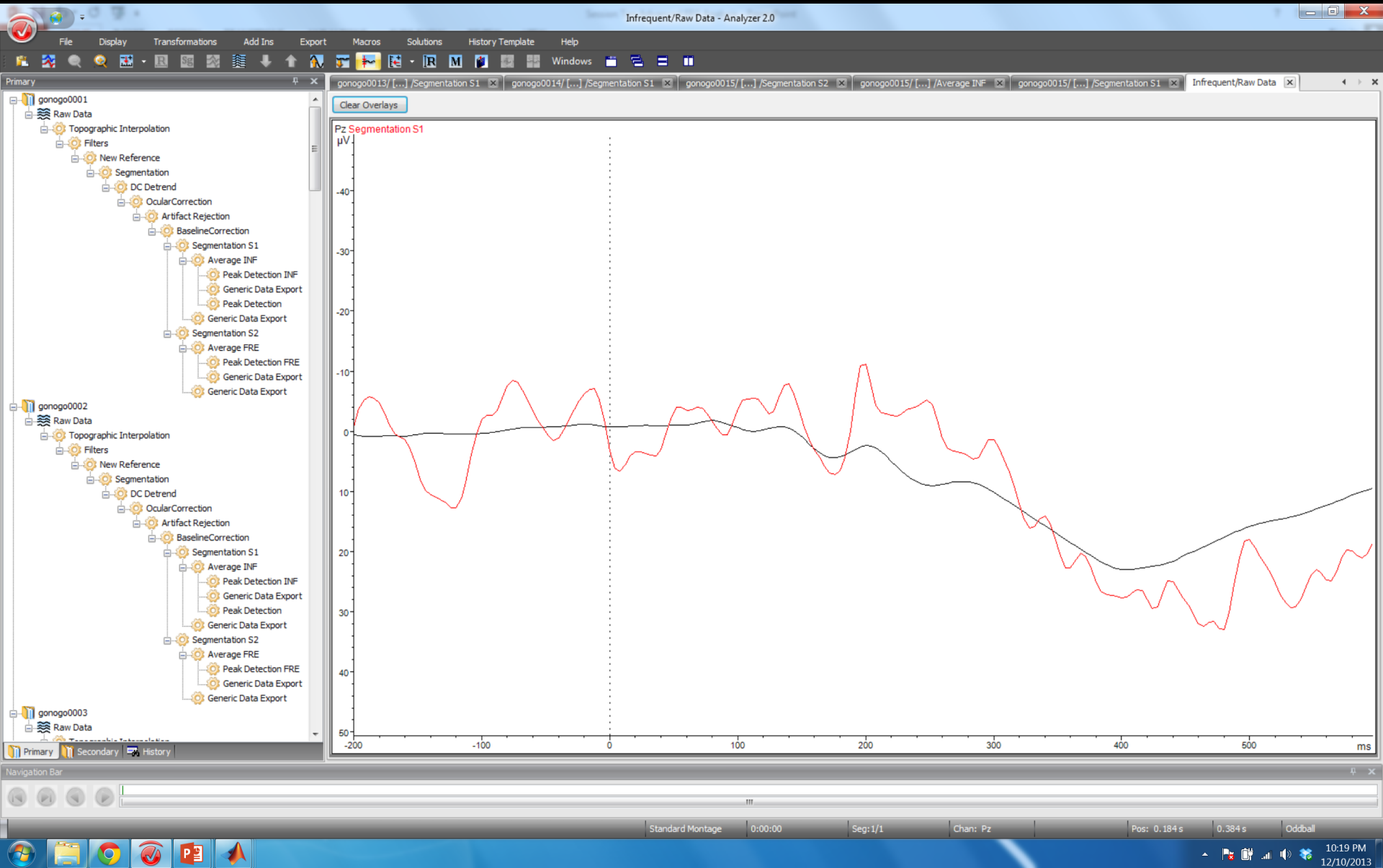
You can then plot this as a function of time.

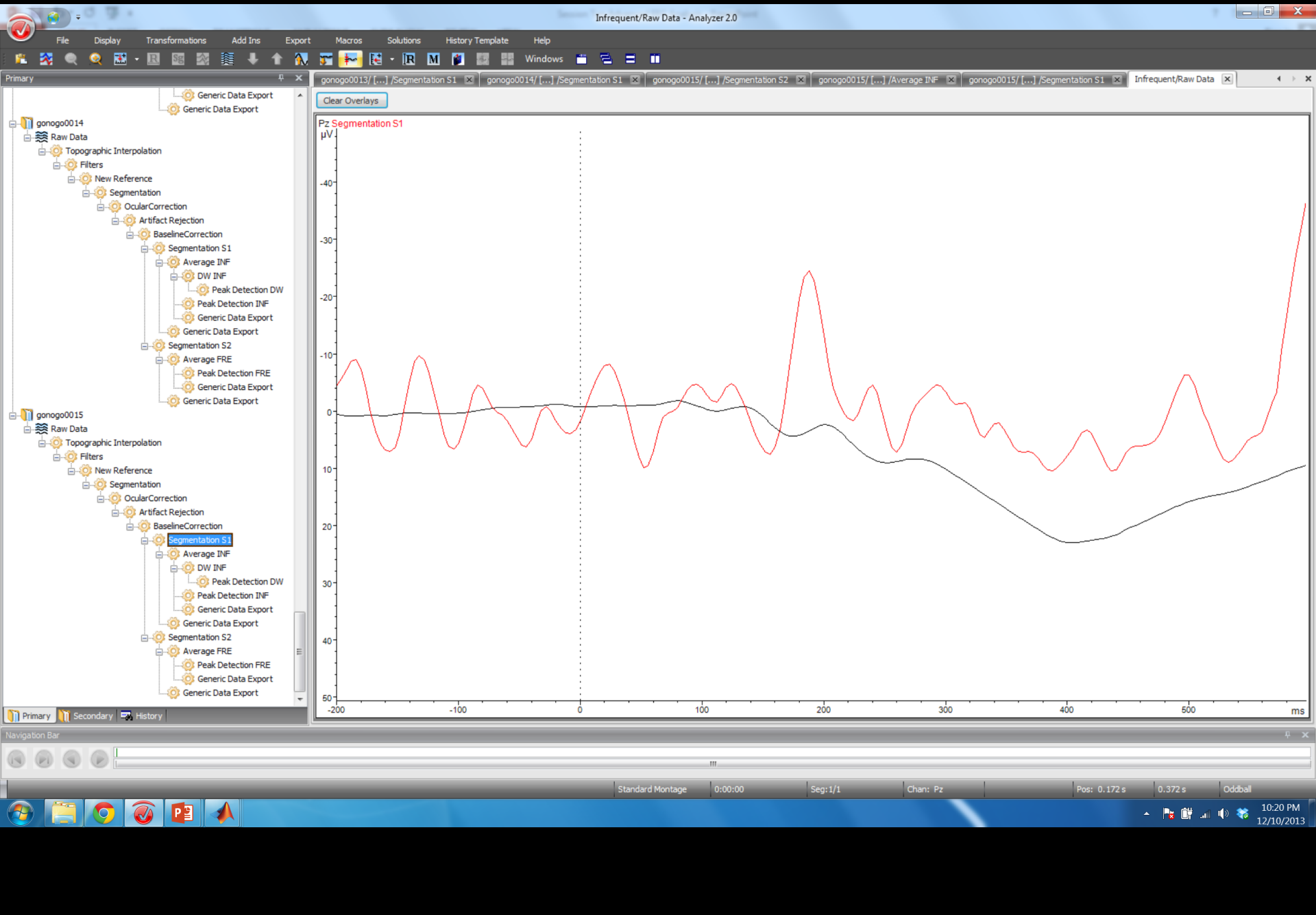
So how do you do it?

Strategy Two

Fit a function to the component of interest on the grand average.

Estimate the quality of fit for each individual trial.





Component Latency and Onset Analysis

Component Latency

It is relatively easy to do a component latency analysis.

All you need to do is use a maxima / minima peak detection approach and get a latency value for the peak for each subject for each condition.

Following that, traditional null hypothesis testing can be used.

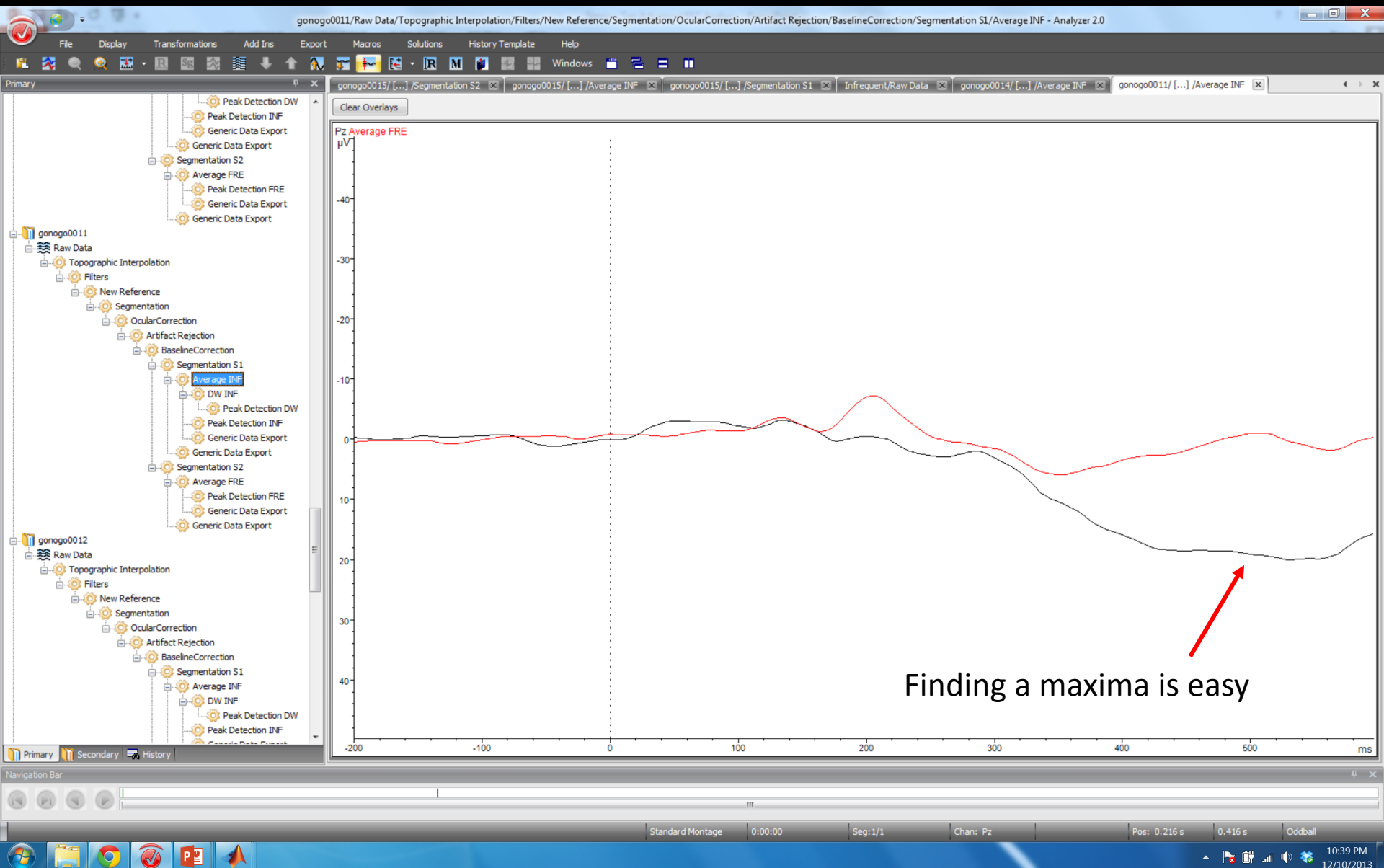
Condition A			Condition B	
12.4 μV	324 ms		11.3 μV	378 ms
9.8 μV	333 ms		10.4 μV	402 ms
10.3 μV	356 ms		8.8 μV	444 ms
4.2 μV	401 ms		7.6 μV	424ms
7.8 μV	367 ms		6.4 μV	401 ms

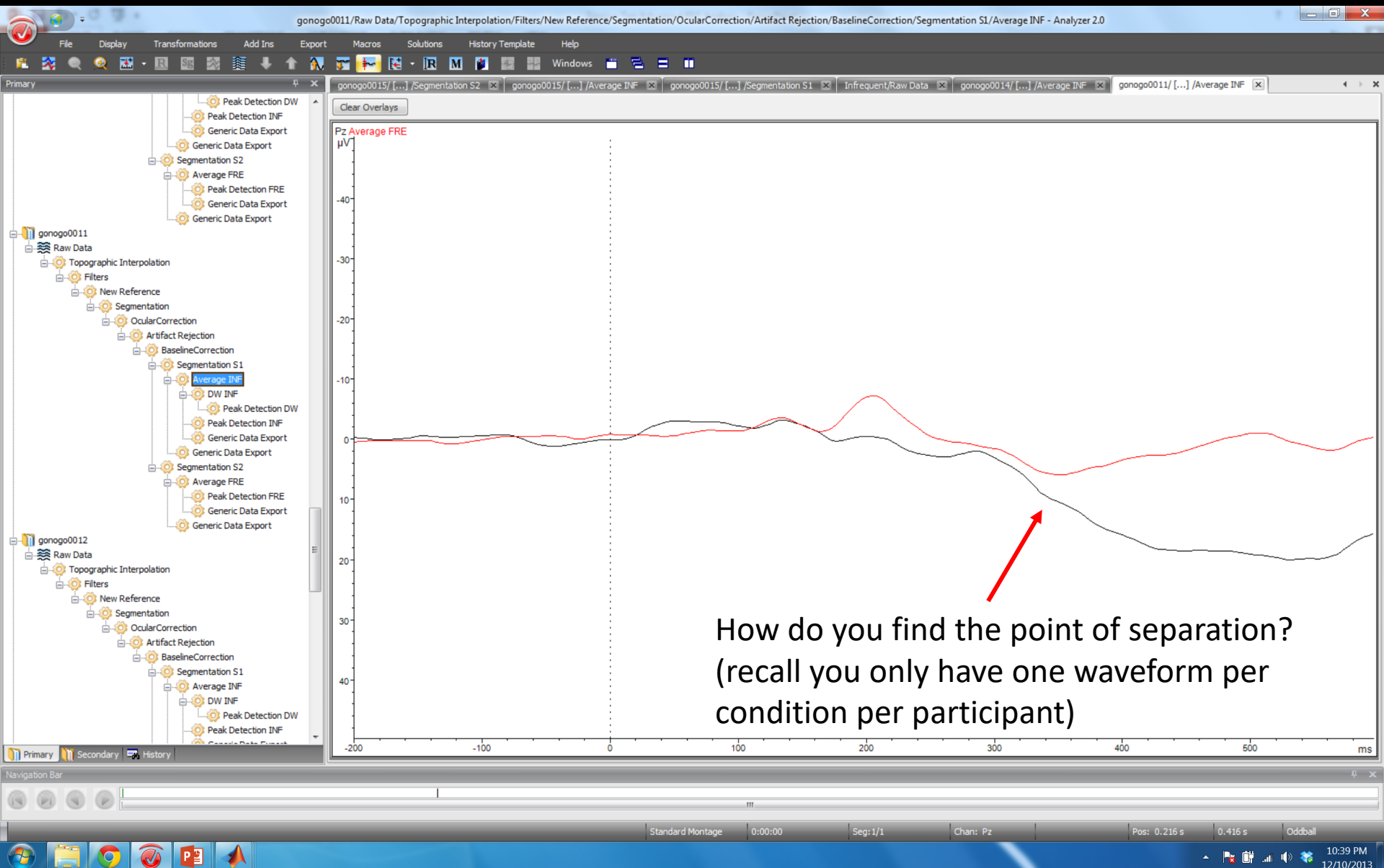
Component Onset

Component onset is a bit trickier.

Why?

Because we cannot do single trial analysis very effectively, we cannot get an onset value for each subject based on their own data. Why is that?





One Solution

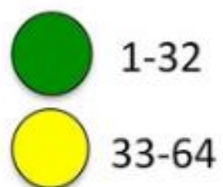
Rodrigues – Fornells

1. Get the average waveform for each participant for the channel of interest for each condition.
2. Use a running average to smooth these, say ± 5 time points on either side.
3. Sequentially t-test every point of the smoothed waveforms till there is a significant difference using a stricter alpha (0.001)

The Problem

This approach will tell you when two conditions diverge, it does not allow you to compare the difference of onset between A and B with the difference in onset between C and D.

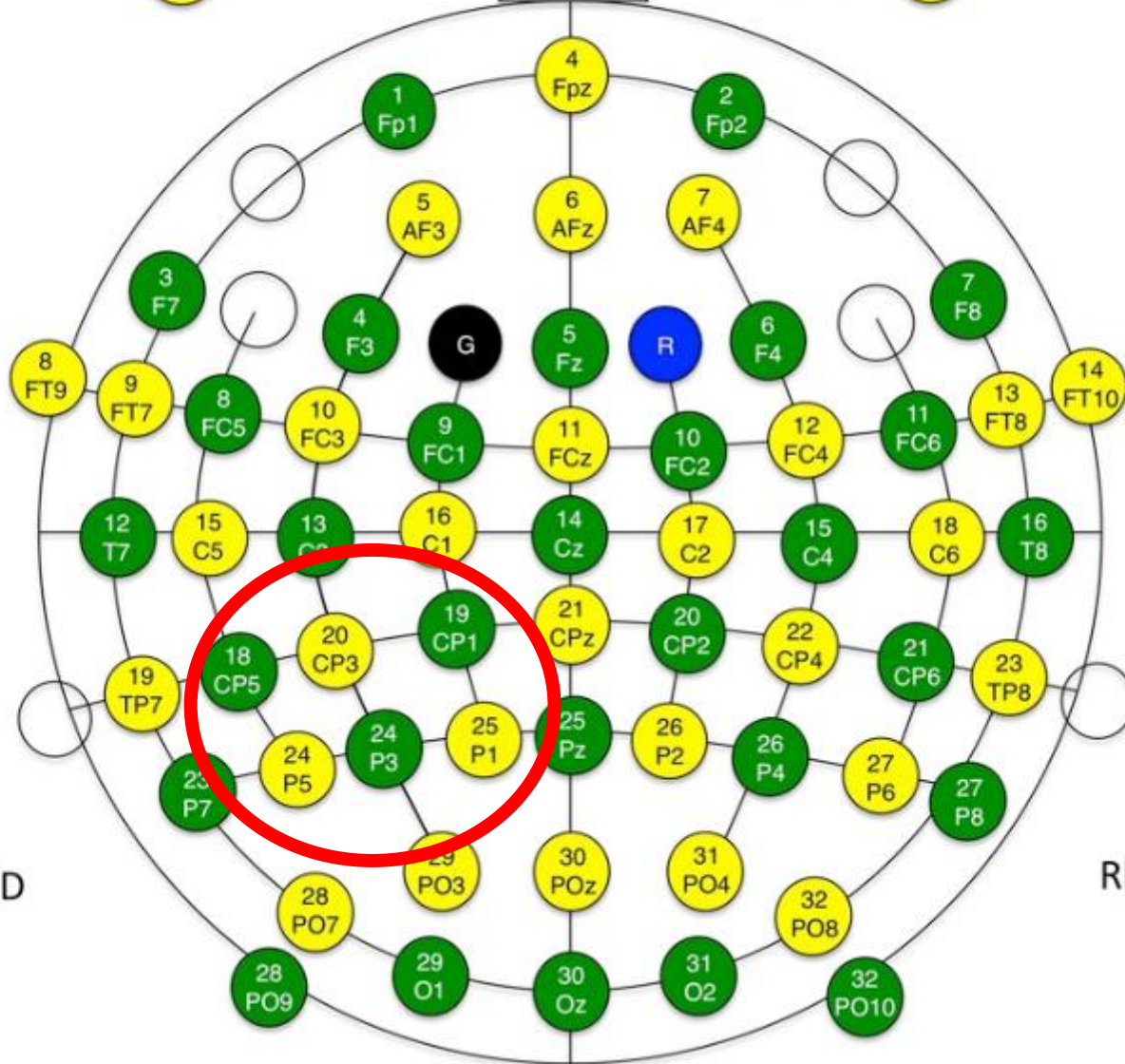
Pooling Electrodes



BELOW RIGHT EYE 1 VEOG

2 LEFT EYE LEOG

RIGHT EYE 3 REOG



LEFT MASTOID

RIGHT MASTOID

