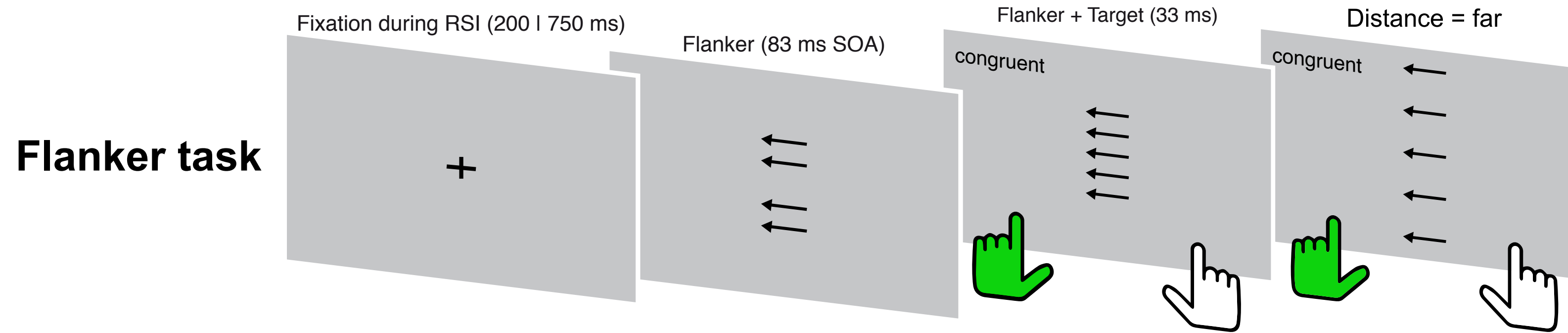


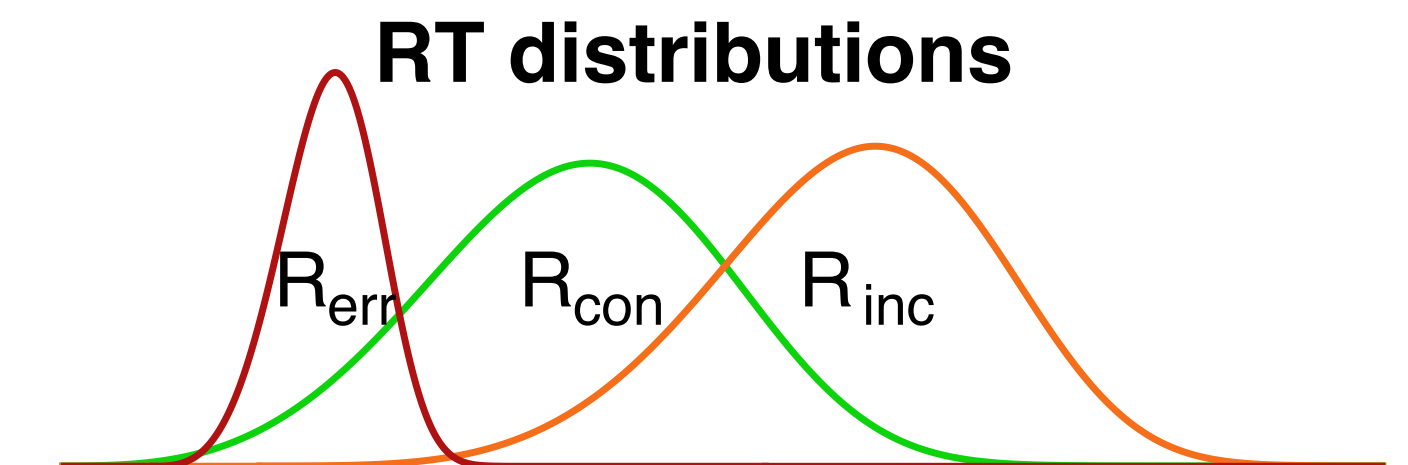
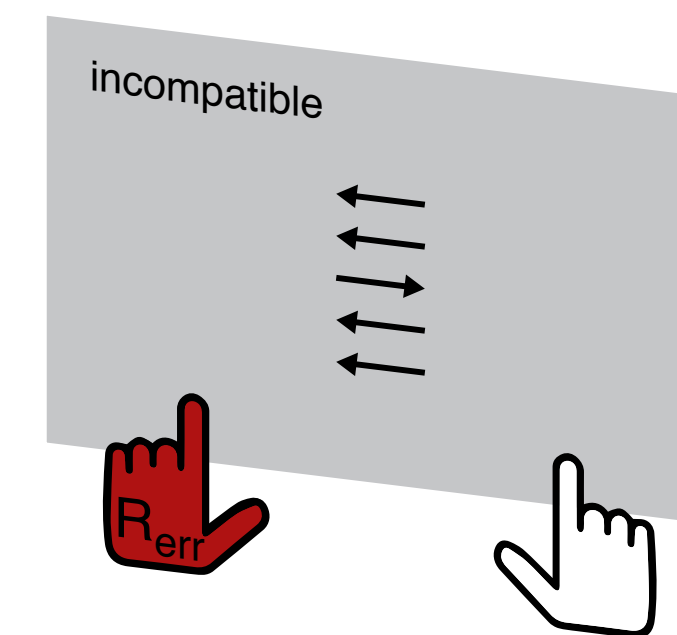
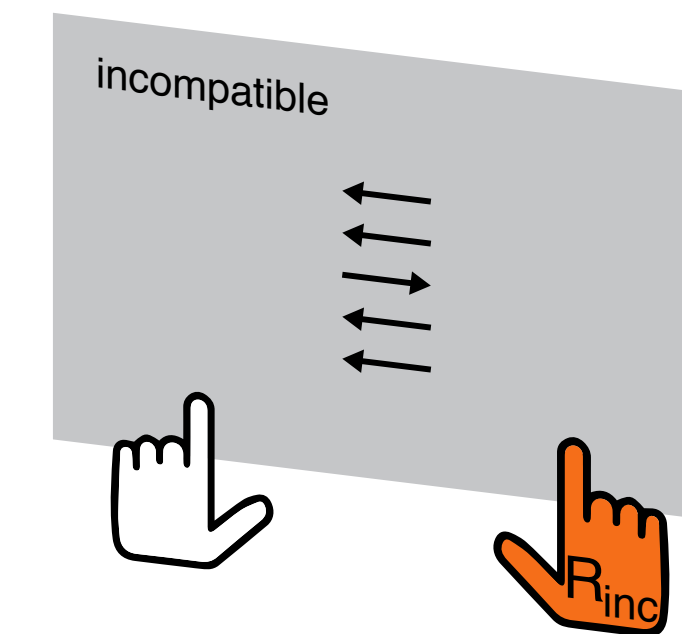
- Session 1 - Why single-trial EEG analyses?
- Session 2 - Pre-processing, introduction to ICA
 - **Example session I: Setting-up your data and running a single-trial regression analysis with the *STA-TB***
- Session 3 - ICA as a tool to increase SNR in EEG data
 - Example session II: COMPASS to select ICs
 - Example session III: EEG regression with independent component activity
- Session 4 - Within-subject to across-subject analyses
 - Example session IV: Combine data across participants
- Session 5 - Time-frequency decomposition and single-trial analyses
 - Example session V: Run a TF decomposition and GLM analysis
- End and Discussion



- **Experimental manipulations**

- ▶ stimulus congruence (con, inc)
- ▶ RSI (short, long)
- ▶ flanker distance (close, far)

➔ Flanker-target distance: far 6.5° and 4° and close 3.5° and 1.75°



- **Data description**

- ▶ 1080 trials per subject
- ▶ 50% congruent, 50% incongruent
- ▶ 50% short, 50% long RSI
- ▶ 50% close, 50% far
- ▶ 50% left, 50% right responses
- ▶ average n error trials = 142

- **Recording settings**

- ▶ 500 Hz
- ▶ 64 Ag/Cl electrodes
- ▶ BrainAmp MR plus amplifiers

- **Sample description**

- ▶ n = 863
- ▶ age 18 - 40 (mean = 24)
- ▶ 438 female, 436 male

```
>> EEG.epoch(1).eventtype{5}
```

ans =

Stim	C	Inc	L	700	LH	cor
------	---	-----	---	-----	----	-----

Stim or Resp
(stimulus or response)

F or C
(flankers
were Far or
Close)

Com or Inc
(congruent
or
incongruent)

L or R
(target
direction)

250 or 700
or bbb
(RSI; bbb =
previous
trial was
break or
this trial
is the first
in exp.)

or mul
(error or
correct or
multiple
responses)

LH or RH or
MISS
(left or
right hand
resp. or
miss)

Behavioral data in a structure

```
>> D

D =

1x995 struct array with fields:

    distance
    congr
    stime
    resp
    reqresp
    rt
    posterr
    postinc
    postfar
    postinfo
    RSI
    error
    rt_follow
    rt_previous
    congr_follow
    dist_follow
    RSI_follow
    RSI_previous
    trnr
    prev_congr
    prev_dist
    prev_resp
    hand_repeat
    congr_repeat
    dist_repeat
    MissInEEG
    Nresponses
    ResponseAfterFlanker
    CorrectionResponse
    NewRT
```

Why behavior separate?

- ▶ easy to use
 - ▶ select trials:
`trials = [D.rt] > 90 & [D.congr] == 2 & [D.posterr] == 1`
 - ▶ creates a logical index
 - ▶ `find(trials)`
 - ▶ returns the trials' positions

```
>> find(trials)

ans =

Columns 1 through 19
    41    62    69   217   227   231   262   267   292   297   304   318   328   356   382   405   423   451   475

Columns 20 through 38
   485   548   575   584   618   686   698   711   723   729   791   797   799   800   878   893   938   946   966

Columns 39 through 40
   975   990
```

- ▶ in most cases, it is very easy to add information to a behavioral file (e.g., of a computational model)
- ▶ adds another layer of safety (EEG and behavior have to match!)

1. EEG Preparation

short
overview
of
behavior

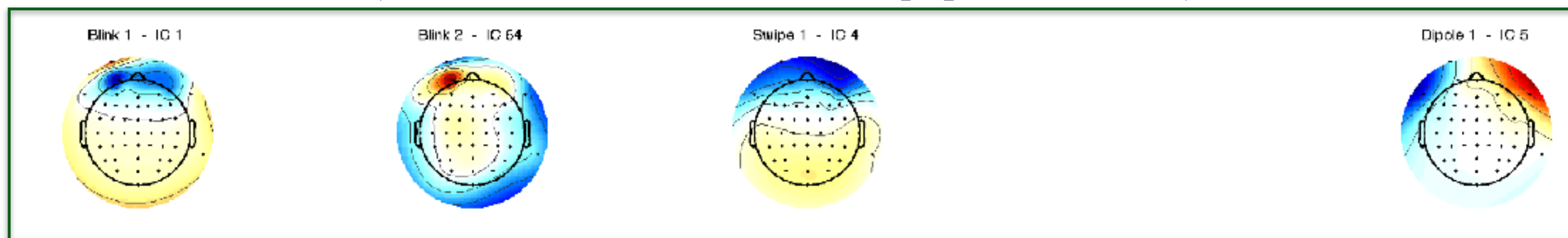
Miss outlier: no
Too few trials? no

n Error All: 123
n Error Incom: 110
n Error Close: 71
n Error Far: 39

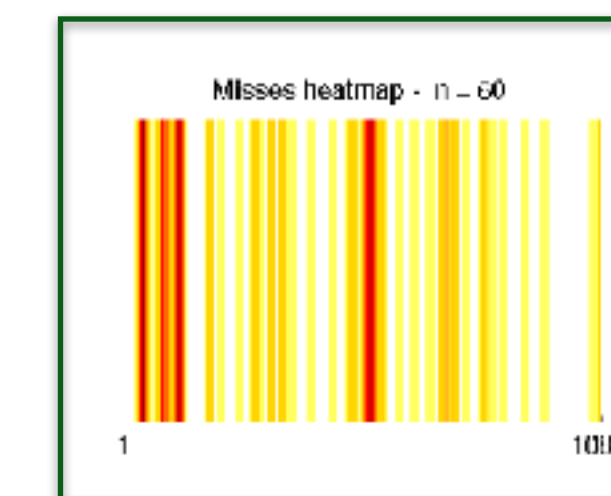
Highest ERN RMS @ Cz = -1.9953
ERN = -10.3596 @ 52 ms
p-value = 0
t-value = -13.1737
U3-value = 0.93496
RT match deviation all = 0 ms
Deviation Incompatible ~ = -105.4 ms
p-value close inc = 4.1329e-26
p-value far inc = 1.7483e-25
Best U3-value = 0.93496 @ Cz

Factor Far vs Close = 1.1564
ERN Far = -15.096 @ 40 ms
ERN Close = -13.0544 @ 54 ms

automatic artifact component selection
(Viola et al., *Clin Neurophysiol*, 2009)

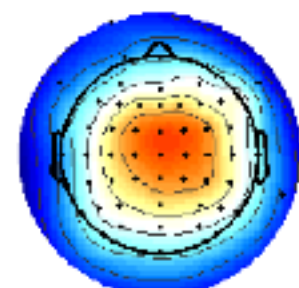


missed trial
heatmap

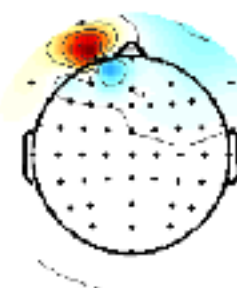


additional manual component selection

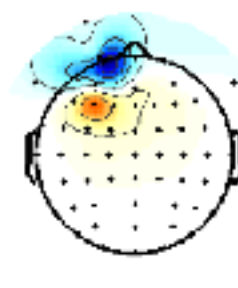
No Rem - IC 2



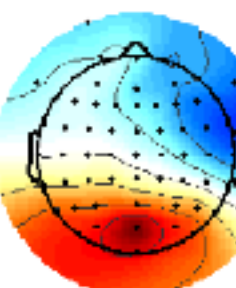
No Rem - IC 3



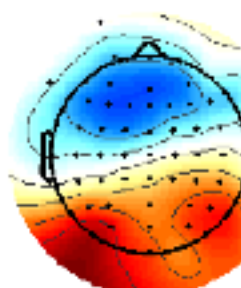
No Rem - IC 6



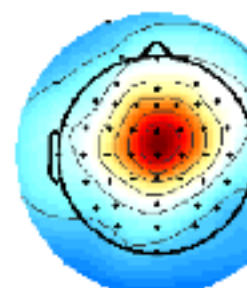
No Rem - IC 7



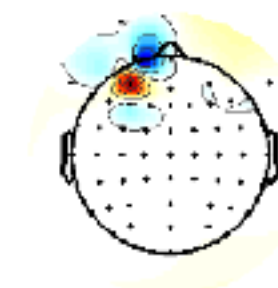
No Rem - IC 8



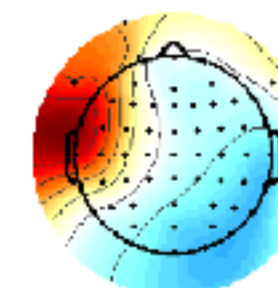
No Rem - IC 9



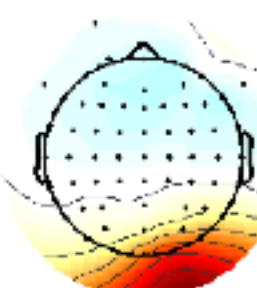
No Rem - IC 10



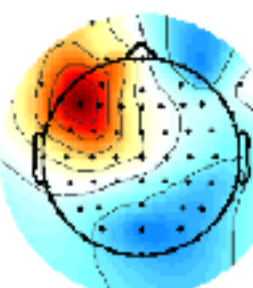
No Rem - IC 11



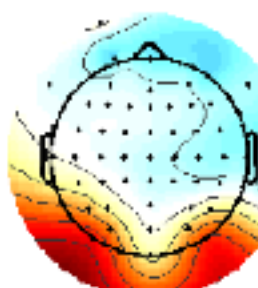
No Rem - IC 12



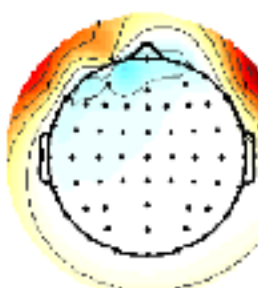
No Rem - IC 13



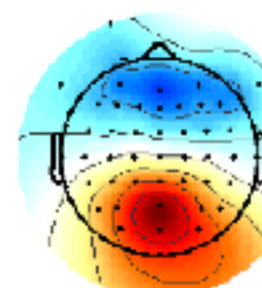
No Rem - IC 14



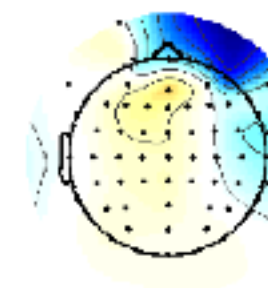
No Rem - IC 15



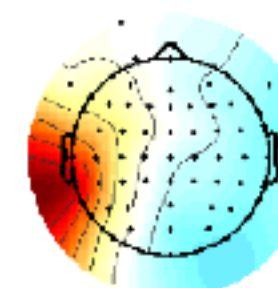
No Rem - IC 16



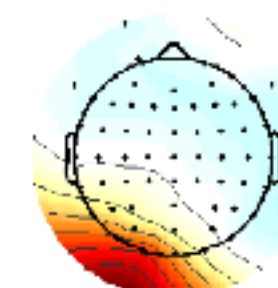
No Rem - IC 17



No Rem - IC 18

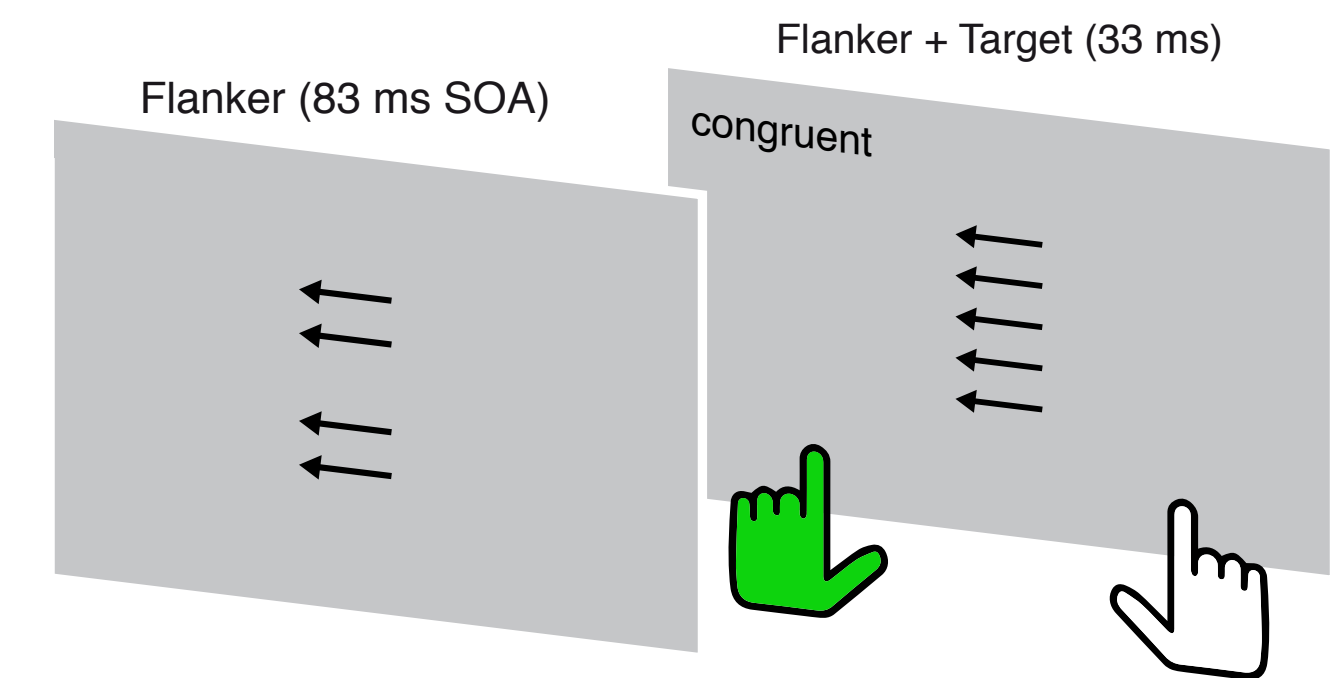
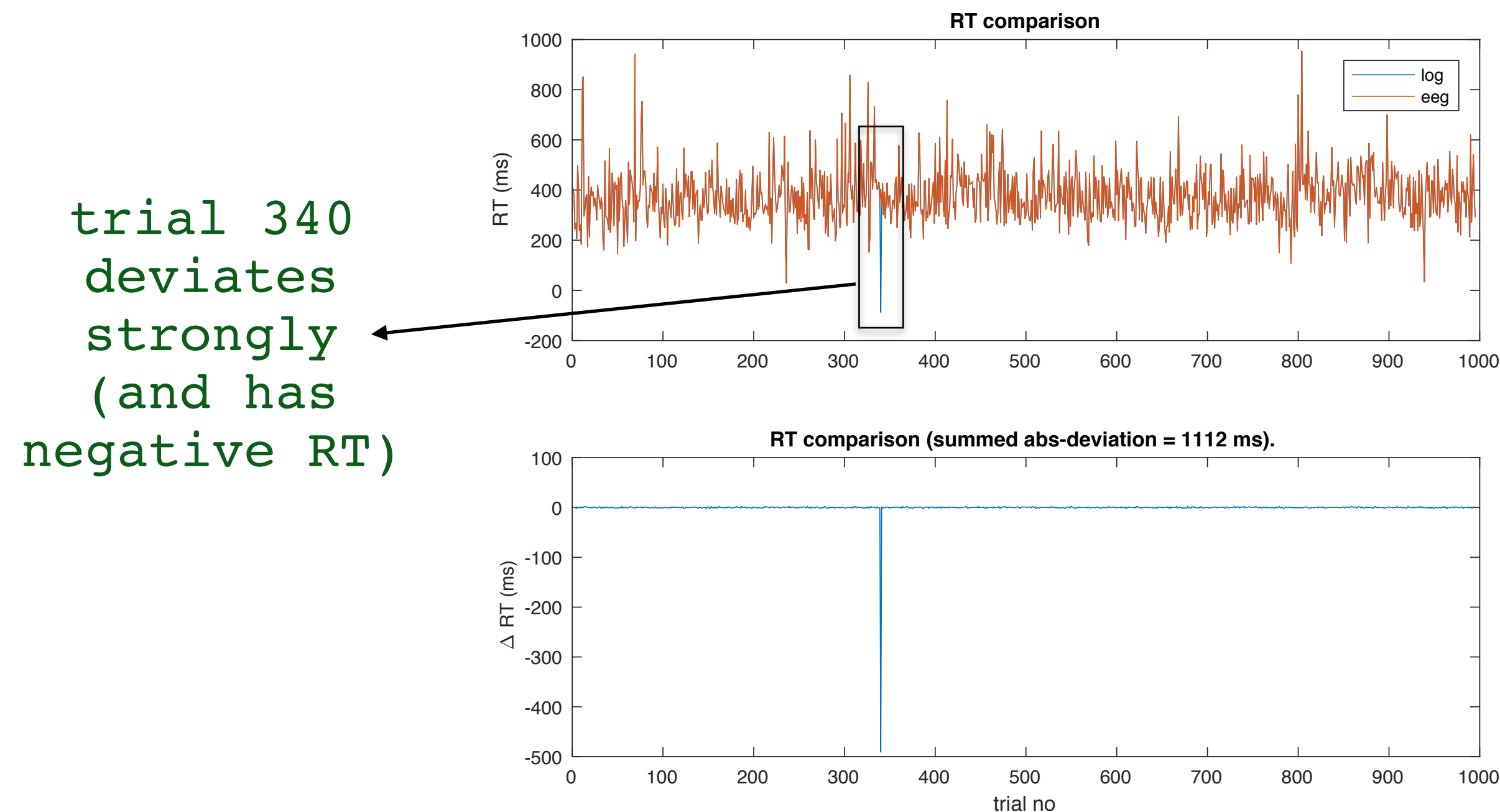


No Rem - IC 19



2. Re-epoch EEG

- EEG is stimulus-locked, we want response-locked data
- Additionally, we want to be sure that EEG and behavioral trials are identical (e.g., after artifact removal in EEG during pre-processing)
 - ▶ we just loop through all epochs, check the event type after latency = 0 (always a stimulus)
 - ▶ if it is a response, we include it and note the latency (for comparison with the RT in the logfile)



- We already removed trials with strong amplitude deviations before running the IC analysis
 - ▶ now, we have much cleaner data (no blinks!) and in many cases it is a good idea to remove those outlier trials that remain (artifacts that are non-stereotypical and therefore are not found by ICA)
 - ▶ additionally, it can be tricky to find the right value (in SD) that defines an artifact for each participant (some have overall very noisy data)
 - ▶ finally, SNR may not be the same in conditions and SD to detect outliers in one condition, might remove too many trials in the other
 - ➡ for example, single-trial ERN can have very large amplitudes ($> 60 \mu V$!)
- Solution: run repeated variance based trial rejection for conditions (correct, error) separately and remove *at least 1* trial, but here not more than 5%
 - ➡ *depends on your task, data, etc.*

3. Post-ICA Artifact Rejection

```
S.max_p = 5;  
S.min_n = 1;  
S.StartSD = 8;  
S.EpLimit = [-0.5 1];
```

```
% remove no more than 5% of trials...  
% but find a threshold that removes at least one trial(s)  
% start at high threshold (conservative, do not remove too many trials!)  
% sometimes, you may have longer epochs, but artifacts far away from the  
% event of interest do not matter. Just limit the  
% time to look for artifacts here
```

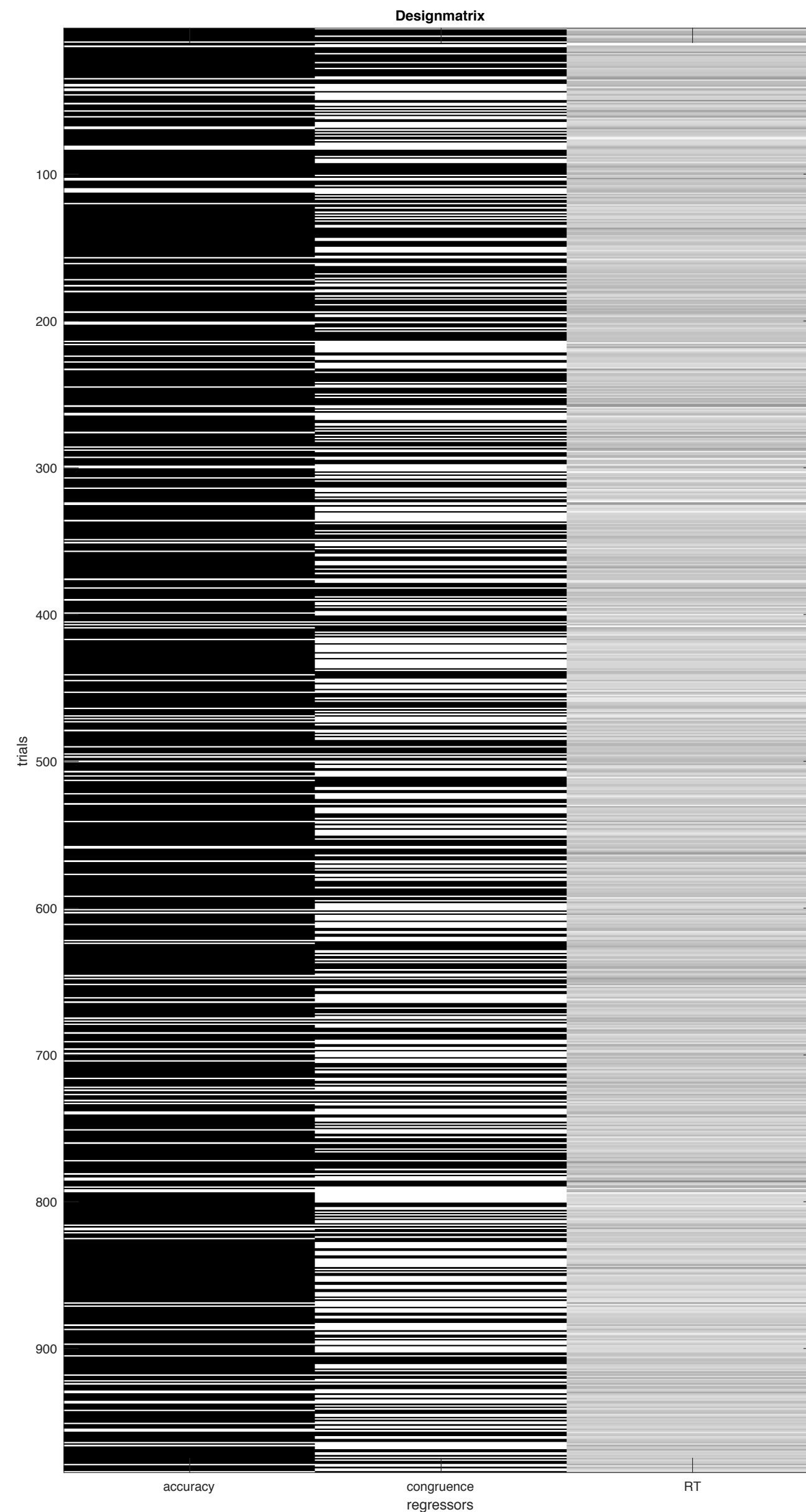
```
RemoveErrors = STA_adaptive_artifact(RESP, [D.error]==1, S)
```

EEG data structure
locked to responses

logic index to
error trials

settings for
the function

4. Setup the design matrix



- For this model, we just use 3 regressors:

- ▶ accuracy (error, correct)
- ▶ congruence (congruent, incongruent)
- ▶ RT (log-scaled)

- We run the regression at fewer electrodes:

```
Electrodes = structfind(ESP.chanlocs,'labels',{'Fz' 'FCz' 'Cz' 'C3' 'C4' 'F5' 'F6'})
```

- ▶ *finds all elements in a field of a structure corresponding to all elements in the input cell array*

5. Call the regression

```
select_trials = find([D.posterr]==0); % we only want trials that are not preceded by an error, i.e., C-C or C-E trials only.  
This also removes trials after pauses!
```

```
Predictors = {R_error(select_trials)    R_incongr(select_trials)    R_logRT(select_trials) };  
Reg2Name    = {'Accuracy'                'Congruence'                'RT'                        };  
RegLables   = [{'cor' 'err'};            {'con' 'inc'};              {'low' 'high'}              ];
```

Regression call 1

output data
information about
the regression

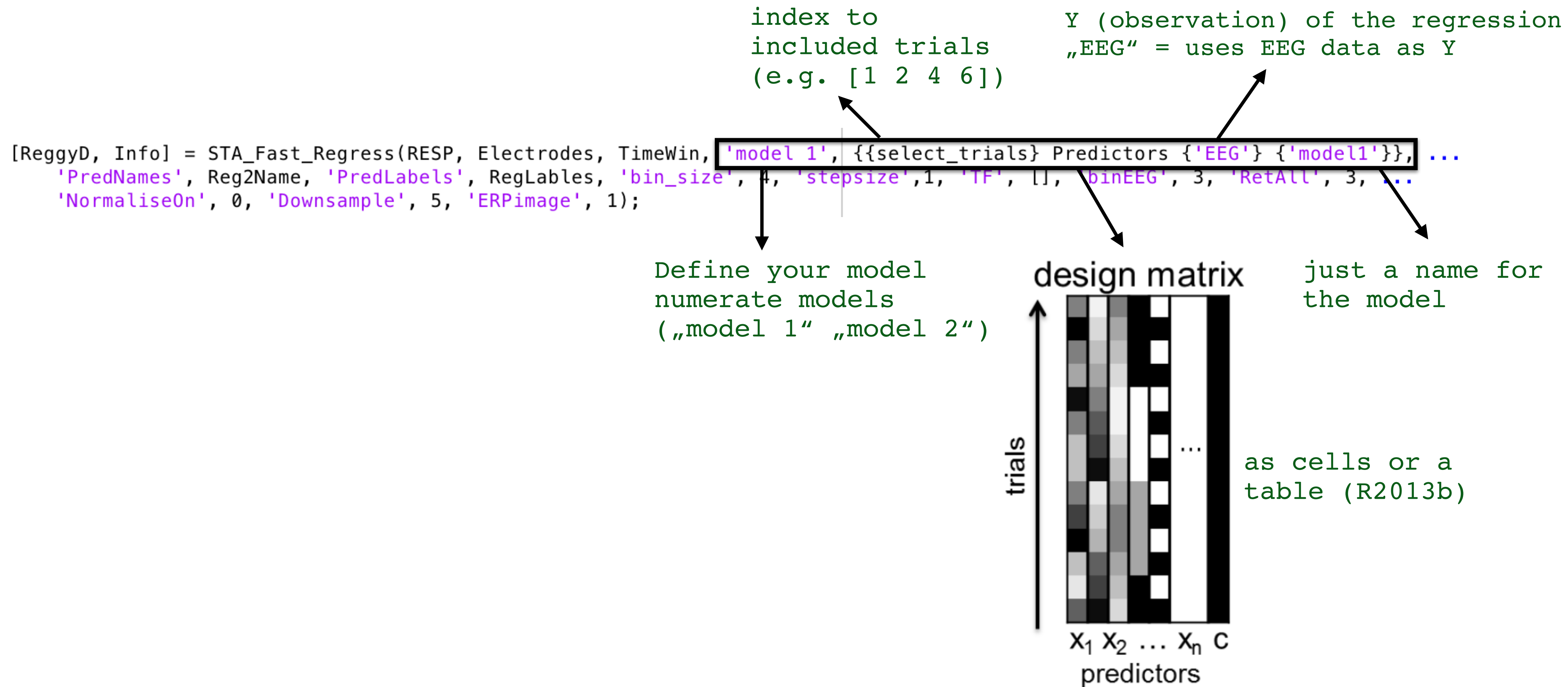
eeglab EEG structure → **indata**
at least fields: *times*, *chanlocs*, *data*
optional: *srate*, *icaact*, *icawinv*, *filename*

```
[ReggyD, Info] = STA_Fast_Regress(Resp, Electrodes, TimeWin, 'model 1', {{select_trials} Predictors {'EEG'} {'model1'}} , ...  
    'PredNames', Reg2Name, 'PredLabels', RegLables, 'bin_size', 4, 'stepsize', 1, 'TF', [], 'binEEG', 3, 'RetAll', 3, ...  
    'NormaliseOn', 0, 'Downsample', 5, 'ERPimage', 1);
```

electrodes: numbers [3 12 22 30]
or labels as cell {',FCz' ,Cz'}

time window in ms: [-500 800]
(indata.times used for indexing)

Regression call 1



Regression call 1

optional cell
with a name for
each predictor

optional cell (size = predictors x 2)
for non-categorical predictors, or more than 2 categories
just use {'low' ,high'} for example

```
[ReggyD, Info] = STA_Fast_Regress(RESP, Electrodes, TimeWin, 'model 1', {{select_trials} Predictors {'EEG'} {'model1'}}), ...  
'PredNames', Reg2Name, 'PredLabels', RegLables, 'bin_size', 4, 'stepsize',1, 'TF', [], 'binEEG', 3, 'RetAll', 3, ...  
'NormaliseOn', 0, 'Downsample', 5, 'ERPimage', 1);
```

Reg2Name =
'Accuracy' 'Congruence' 'RT'

RegLables =
'cor' 'err'
'con' 'inc'
'low' 'high'

Regression call 1

```
[ReggyD, Info] = STA_Fast_Regress(RESP, Electrodes, TimeWin, 'model 1', {{select trials} Predictors {'EEG'} {'model1'}}}, ...  
  'PredNames', Reg2Name, 'PredLabels', RegLables, 'bin_size', 4, 'stepsize', 1, 'TF', [], 'binEEG', 3, 'RetAll', 3, ...  
  'NormaliseOn', 0, 'Downsample', 5, 'ERPimage', 1);
```

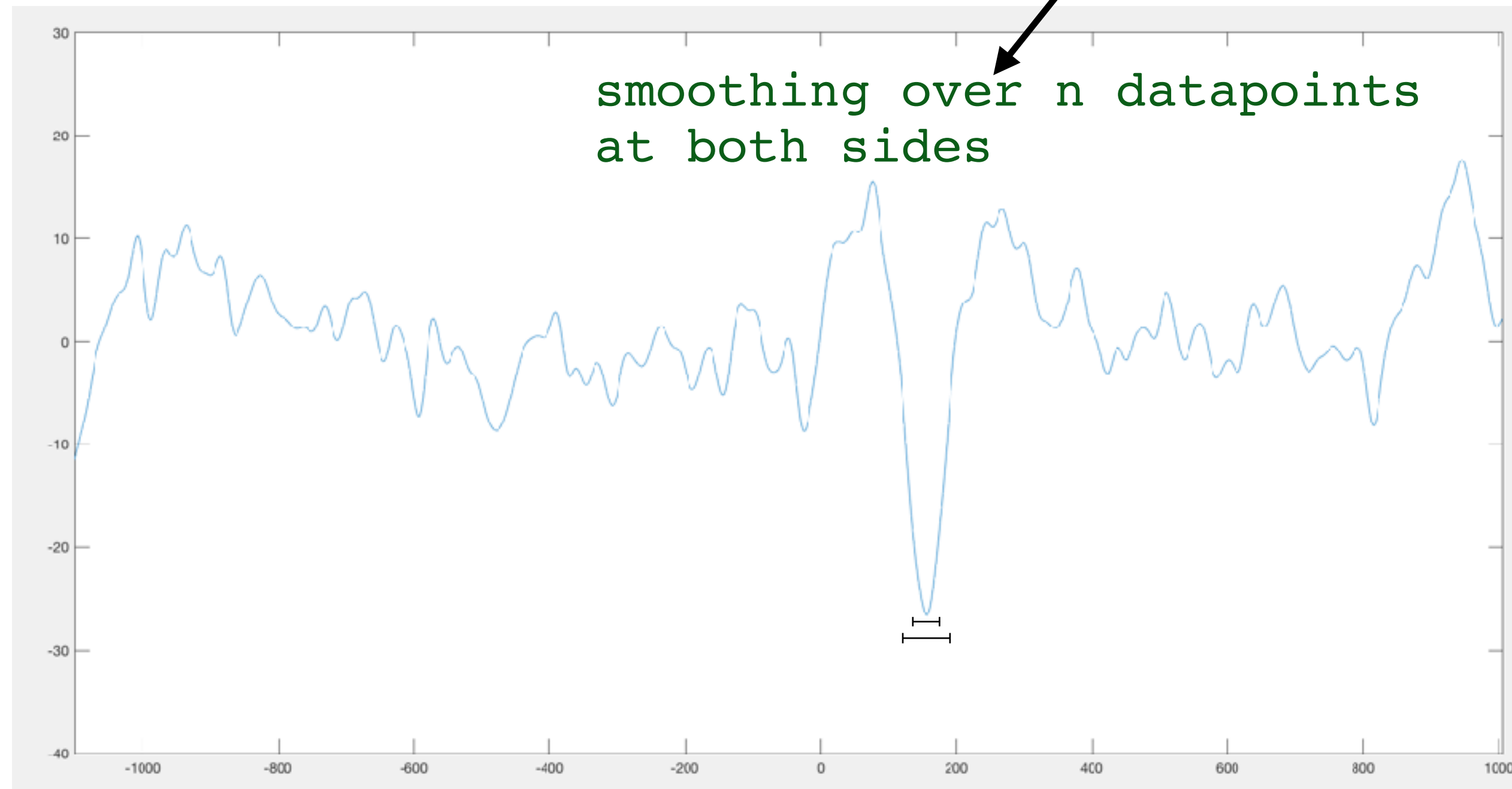
separate settings for
TF decomposition

also returns regular ERP data
binned by ,binEEG' categories
(if scalar predictor)

how far to „jump“ per
regression step

smoothing over n datapoints
at both sides

return more details from the regression
0 = only returns b- and t-values
1 = returns pseudo R2 additionally
2 = returns R2 for each Regressor
3 = also returns p-value time-course



Regression call 1

down-sample the data by
this factor after
regression (500 Hz data,
5 = 100 Hz)

```
[ReggyD, Info] = STA_Fast_Regress(Resp, Electrodes, TimeWin, 'model 1', {{select_trials} Predictors {'EEG'} {'model1'}}, ...  
    'PredNames', Reg2Name, 'PredLabels', RegLabels, 'bin_size', 4, 'stepsize', 1, 'TF', [], 'binEEG', 3, 'RetAll', 3, ...  
    'NormaliseOn', 0, 'Downsample', 5, 'ERPimage', 1);
```

If (1) will normalise
(demean, std = 1)
predictor matrix before
regression

use eeglab function „ERPimage“
and return an image of single-
trial signals

Note: ,ERPimageDim' sets the
maximum dimension (for all
participants). If participants
have fewer trials, the STA plot
function will use gridded
interpolation to allow averaging
across participants.

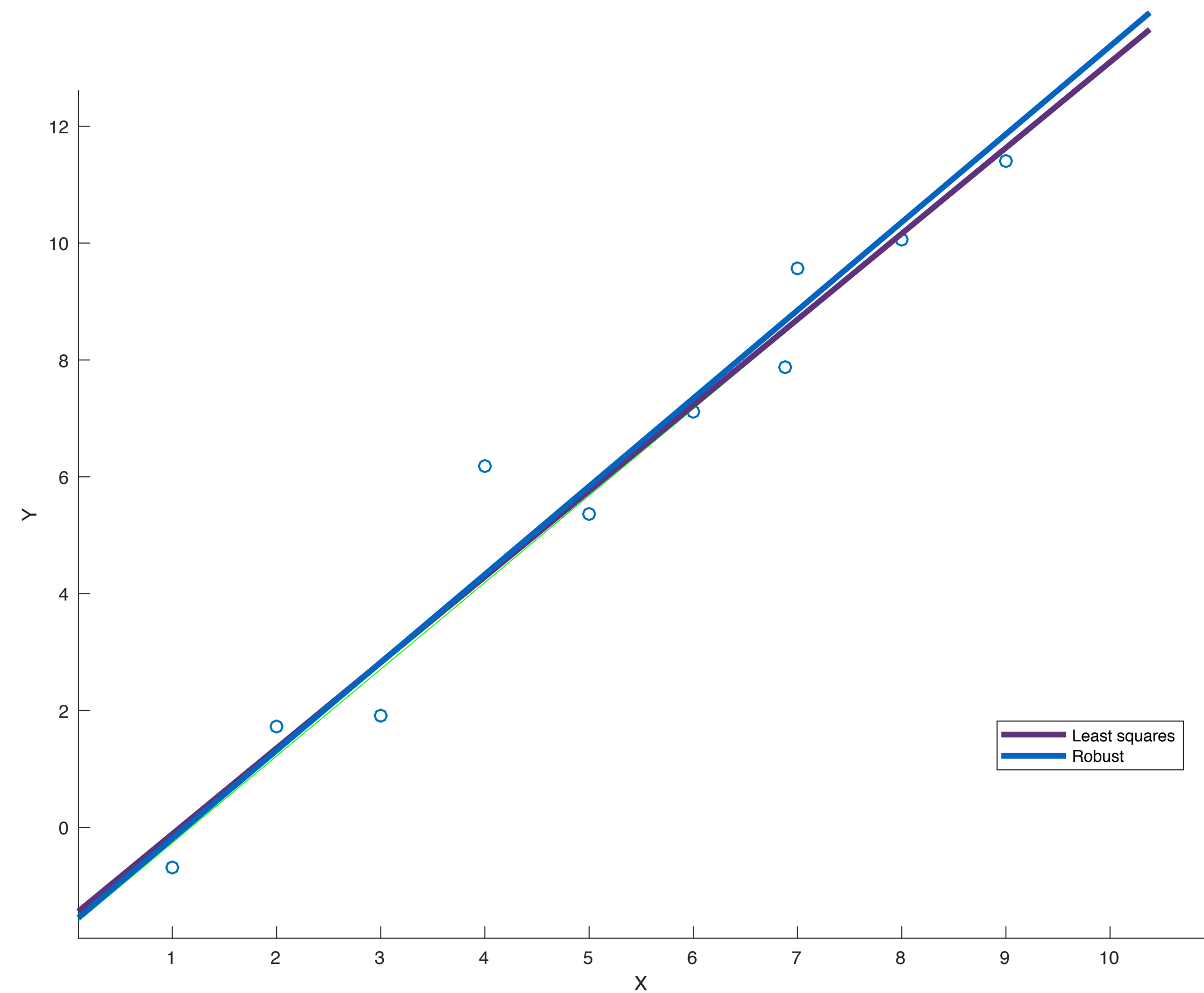
Note2: ERP images can be very large and
cause memory problems. If this is the
case, plot function uses cumulative
averaging instead of loading all
participant data first (slower). To
avoid, do not use all electrodes for
ERP image calculation.

- Other optional arguments:

- **'RegMode'** – arguments 'Robust' uses matlab robustfit (slower), 'ols' uses ols regression.

- ➡ *default: robust regression*

Robust regression



Least squares:

$$Y = -1.58743 + 1.47242 \cdot X$$

RMS error = 0.886135

Robust:

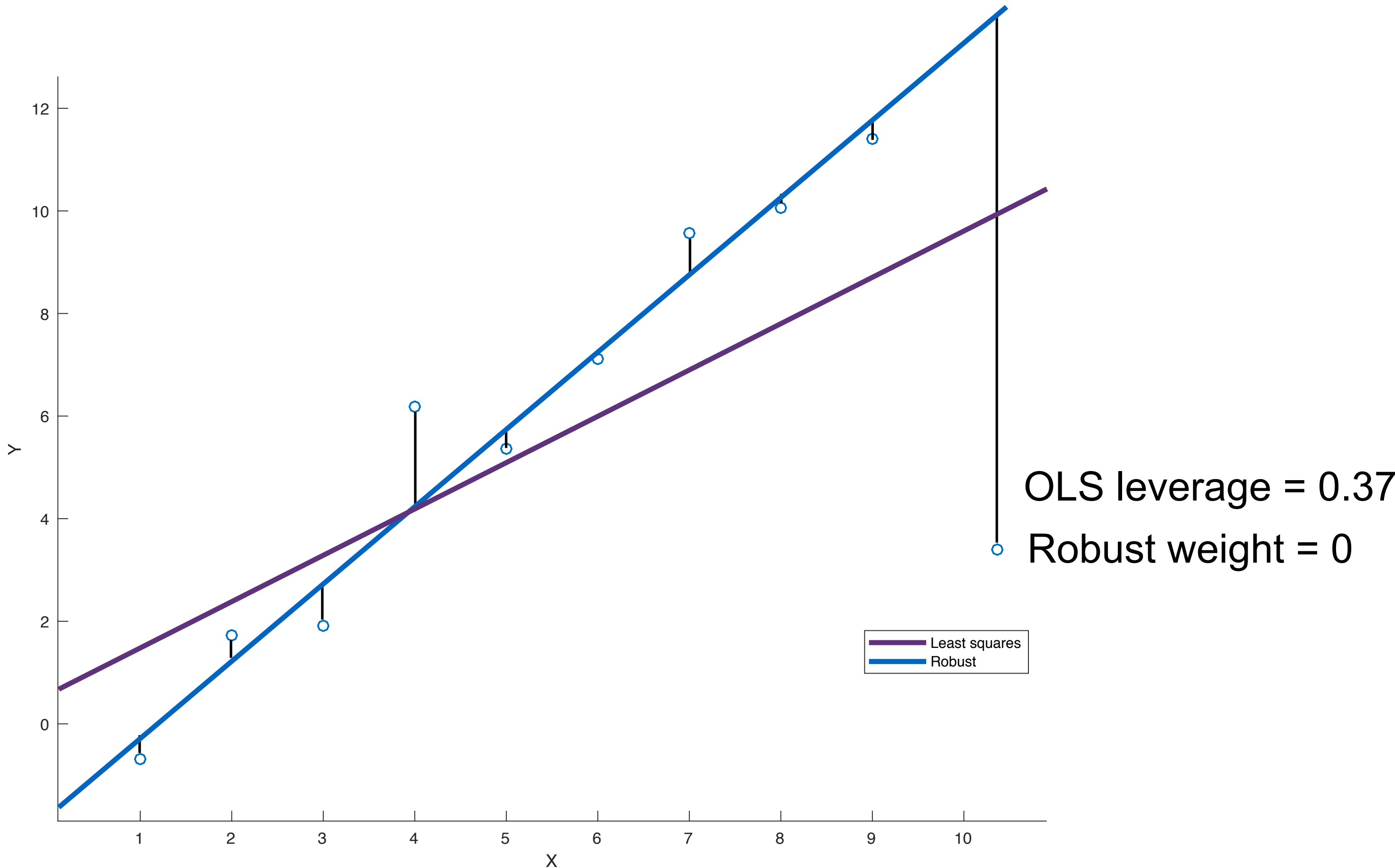
$$Y = -1.74917 + 1.48546 \cdot X$$

RMS error = 0.872908

MAD
|

$$k = 4.685\sigma$$

Essentially, mild outliers are down-weighted, and extreme outliers ($>k$) receive a weight of 0 (*they do not affect the result at all*)



Least squares:

$$Y = 0.591737 + 0.905309 \cdot X$$

RMS error = 3.05328

Robust:

$$Y = -1.77328 + 1.50419 \cdot X$$

RMS error = 1.82386

6. Output

```
>> Info
```

```
Info =
```

```
        Bin_size_ms: 8
        Step_size_ms: 2
Scale_2_Baseline_Percent: 0
        EEG_is_predictor: 0
        ICA_Used: 0
        ICs_Included: []
        ChannelLocations: [1x64 struct]
        Output_Electrodes: [13 22 31 29 33 10 16]
        Output_Labels: {'Fz' 'FCz' 'Cz' 'C3' 'C4' 'F5' 'F6'}
Individual_Trial_Baseline: NaN
        TotalTrials: 833
        RegNames: {'Accuracy' 'Congruence' 'RT'}
        RegLables: {3x2 cell}
        RegValues: {[2x1 double] [2x1 double] [5.6082 5.8902 6.1516]}
        RegNumbers: {[712 121] [420 413] [278 274 281]}
        NaNsRemoved: 0
        IncluReg: [1 2 3]
        Return_Timewindow_ms: [1x141 double]
        srate_Hz: 100
        TF: 'Time Domain'
        AutocorrMatrix: [3x3 double]
        Warnings: {}
```


6. Output

```
>> ReggyD
```

```
ReggyD =
```

```
      EEG_Values: {[2x1 double]  [2x1 double]  [5.7751  6.0162]}
      EEG_per_regressor: [4-D double]
      EEG_SD_per_regressor: [4-D double]
      ERP_Image: [4-D single]
      ERP_Image_TV: [98x3 double]
      t_values: [7x3x141 double]
      b_values: [7x3x141 double]
      Normalization: [7x1x2 double]
      PseudoR2: [7x4x141 double]
      UniqueR2: [7x4x141 double]
      Robust_p: [7x3x141 double]
      Intercept: [7x141 double]
```

We save this output...

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7. Plot within subjects effects

```
settings.plotsteps      = [-200 -100 0 50 100 150 200 300 400 500]; %define time points of topo plots  
settings.plotelect      = 'Cz'; %define electrode to plot time course (if empty, uses electrode with maximum effect)  
settings.ERP_Im_plot    = 1; %plot an ERP image  
settings.PlotPval       = 1; %plot a time course for the p-values  
settings.AddString      = [' ' P_name]; %we add the participants name to the output file
```

```
STA_Plot_Regression( [pathOut ModelName '/' ] , [pathPic ModelName] , settings )
```

folder where we saved the data

folder where we save
the plots

R2 and general information

Overall R2
n subjects: 1
n Regressors 3
Min 0
Max 0.383 at 60 ms

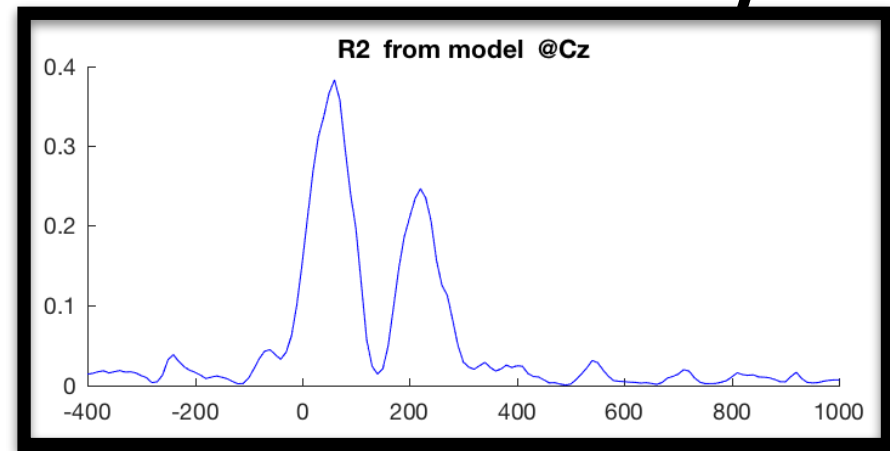
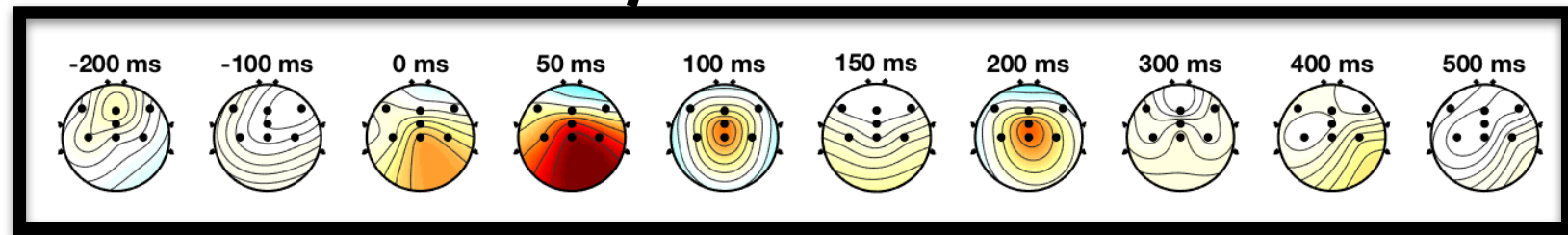
Regressor: Accuracy
-1 = cor
1 = err
Maplimits -21.19 21.19
Maplimits -21.19 21.19
Crit p = 0.05
Max 13.85 at 220 ms
Min -21.85 at 60 ms
p max = 2.11×10^{-39}
p min = 6.36×10^{-84}

Regressor: Congruence
-1 = con
1 = inc
Maplimits -4.88 4.88
Maplimits -4.88 4.88
Crit p = 0.05
Max 5.81 at 30 ms
Min -3.81 at -70 ms
p max = 8.95×10^{-9}
p min = 0.00014779

Regressor: RT
5.6082 = low
6.1516 = high
Maplimits -4.95 4.95
Maplimits -4.95 4.95
Crit p = 0.05
Max 6.27 at -60 ms
Min -5.5 at 60 ms
p max = 5.67×10^{-10}
p min = 5.14×10^{-8}

topographies of R2 plot
(where can we explain
variance at all?)

Overview at Cz for Simple Error Model VP0005 t

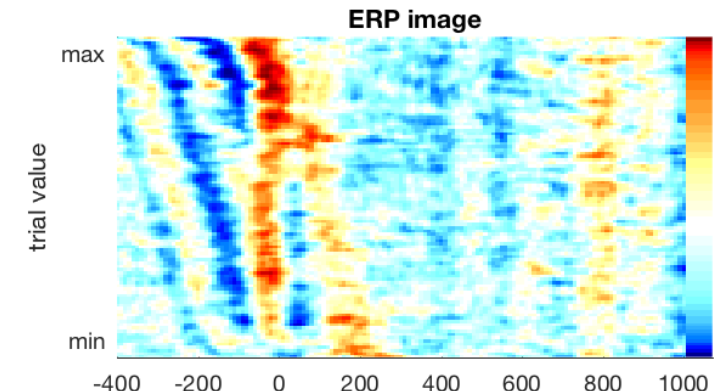
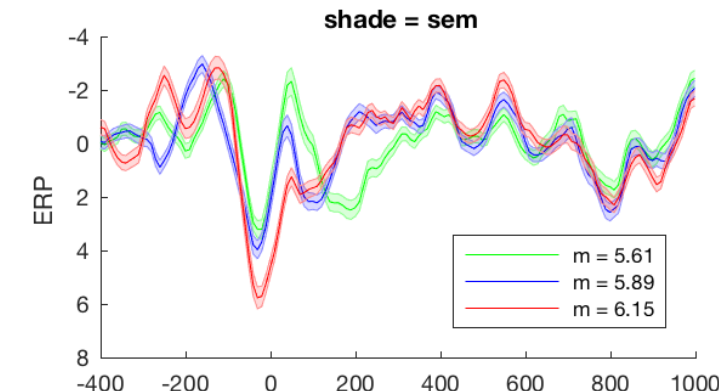
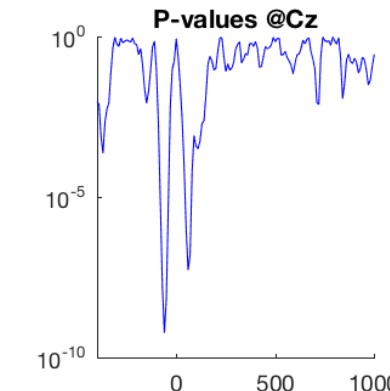
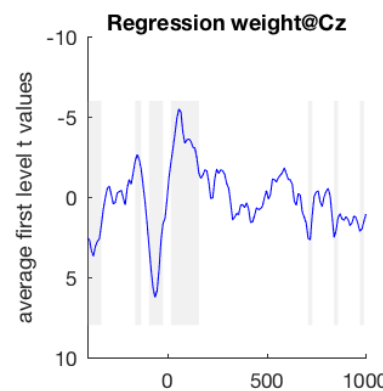
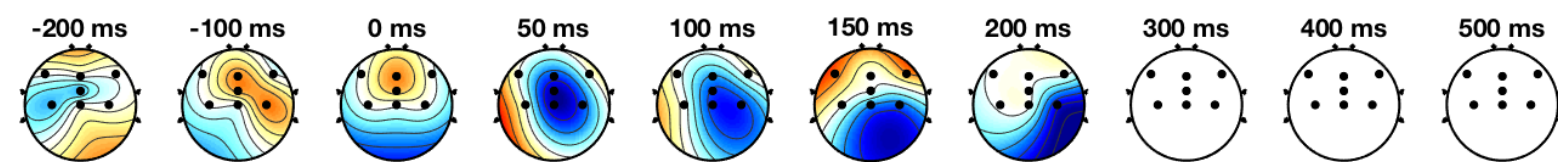
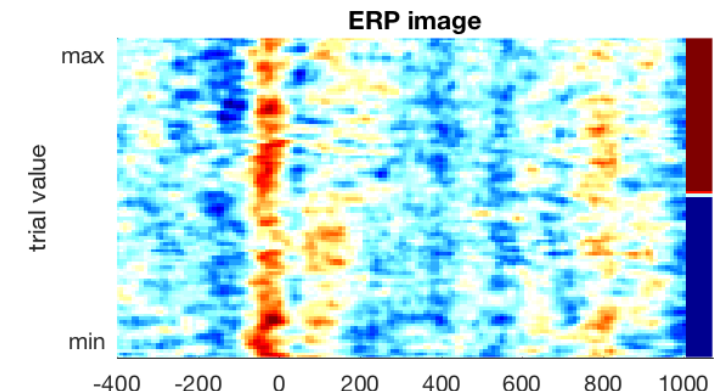
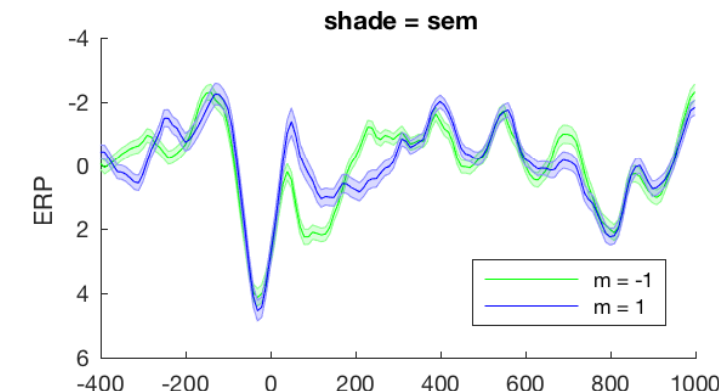
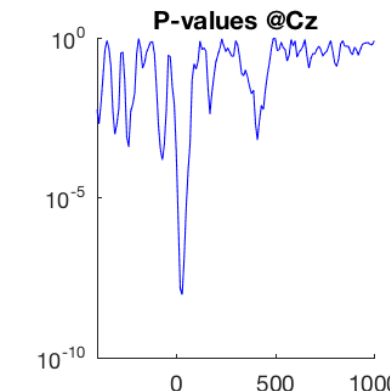
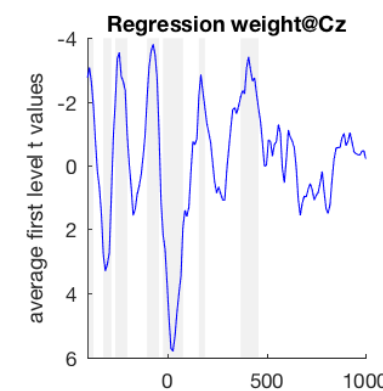
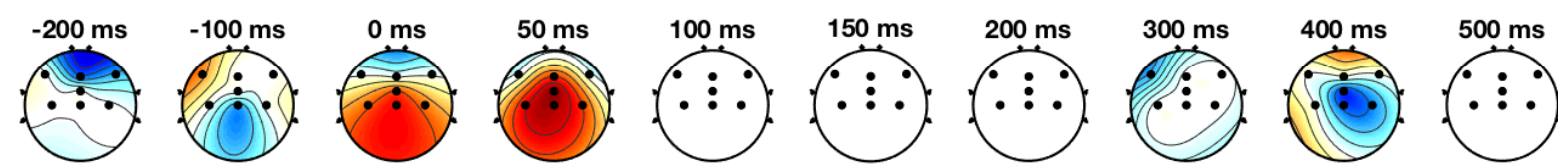
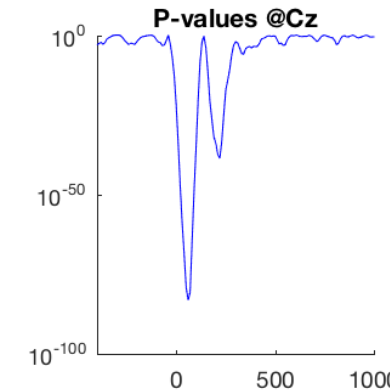
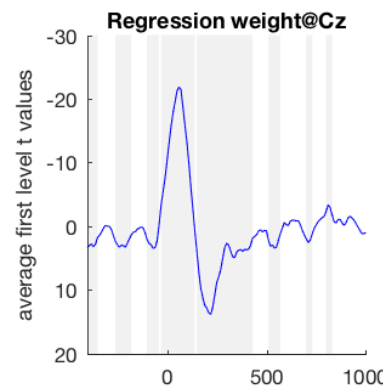
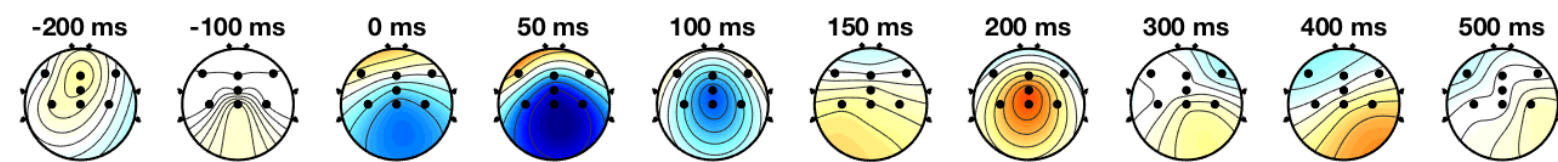


precise R2
time course
at plotted electrode

Note: robust regression
does not maximize
R2 primarily!

Note 2: This is a pseudo /
empirical

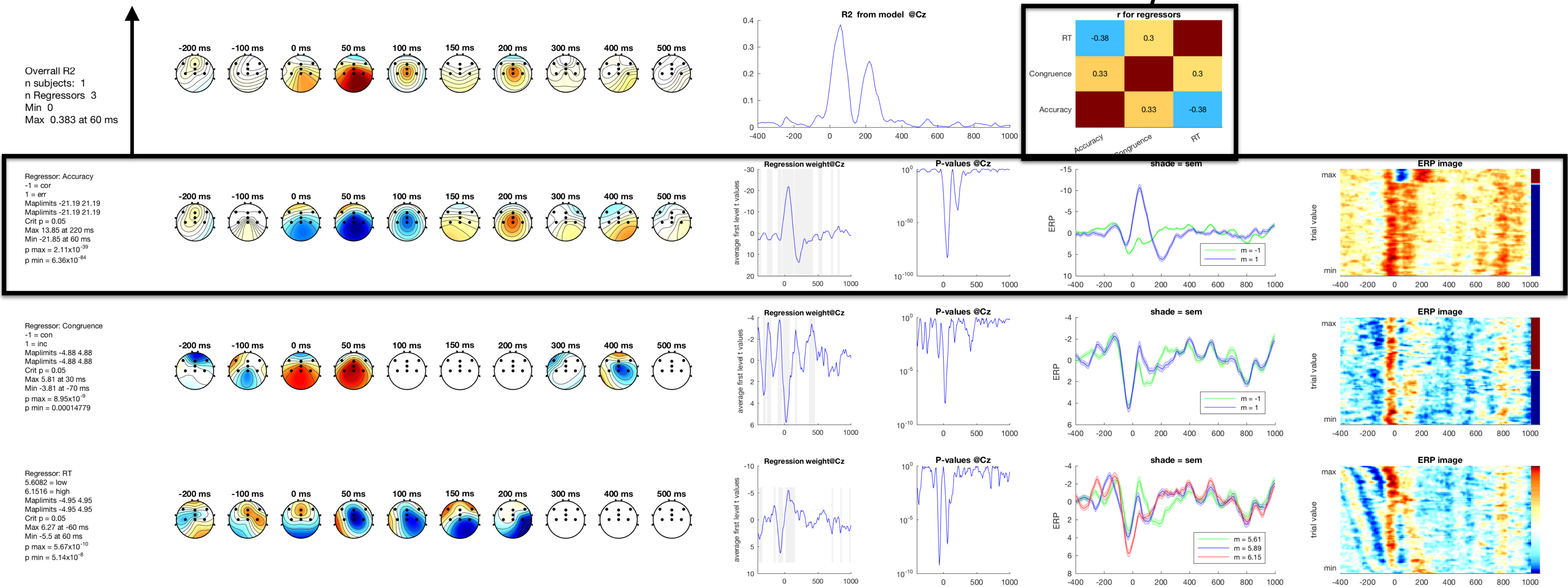
R2 (squared correlation
between model prediction
on every trial, and observed data)



correlation matrix
between regressors

one row for each regressor

Overview at Cz for Simple Error Model VP0005 t

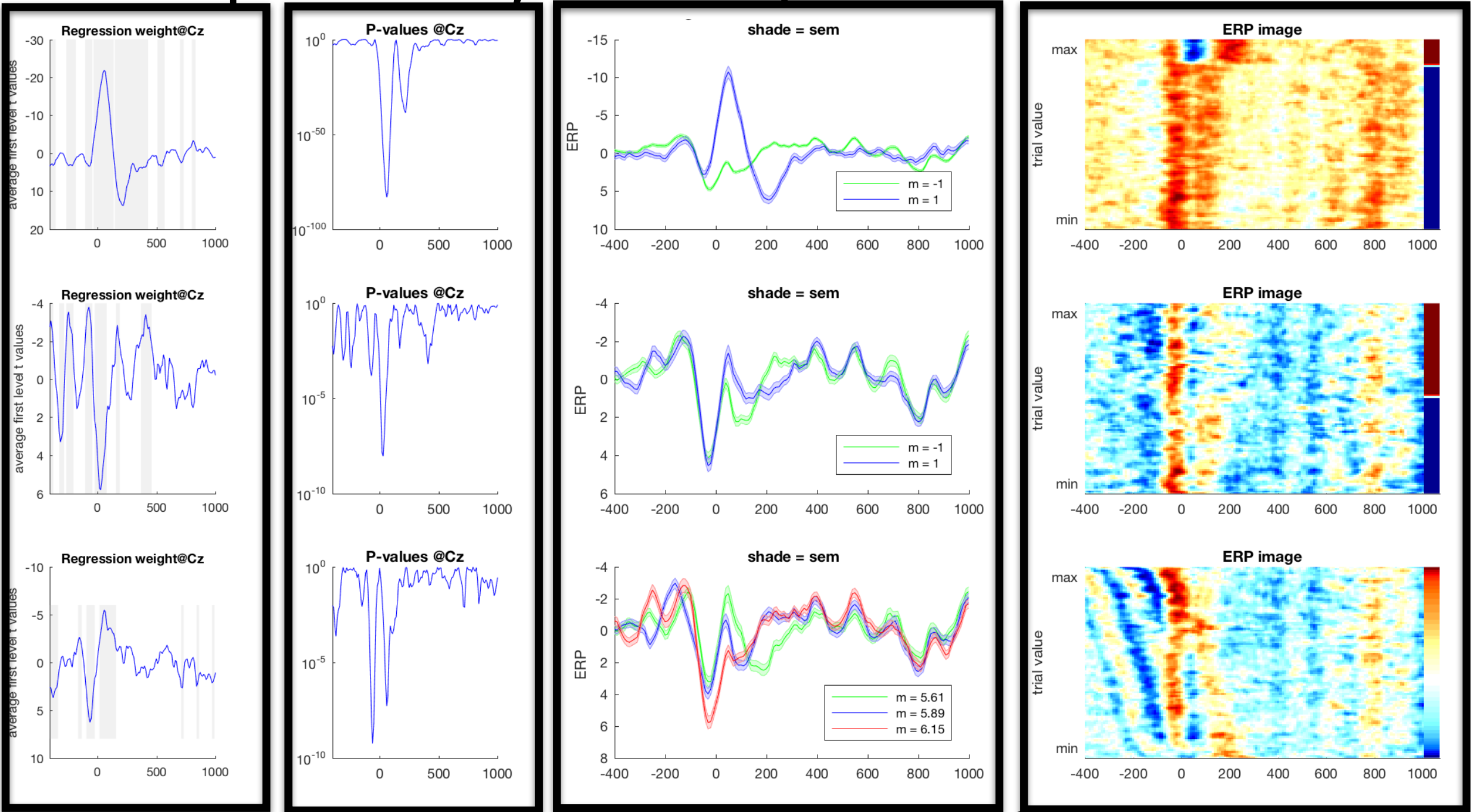
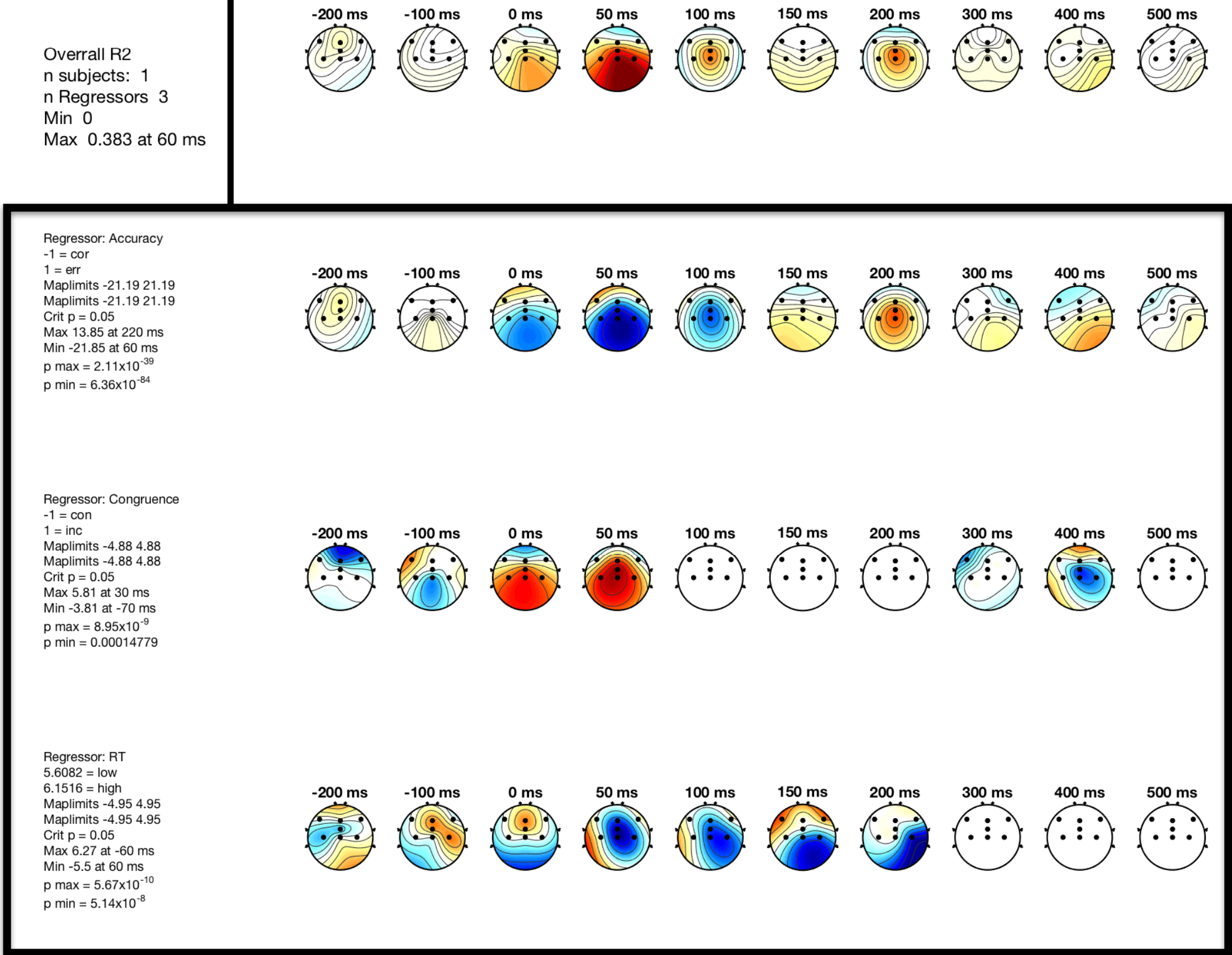


scalp topography plots

regression weight time courses
(either b- or t-values)

individual regressor p-values
(from regression output)

the standard ERP
(i.e., the signal when variance
by other factors,
is not accounted for)



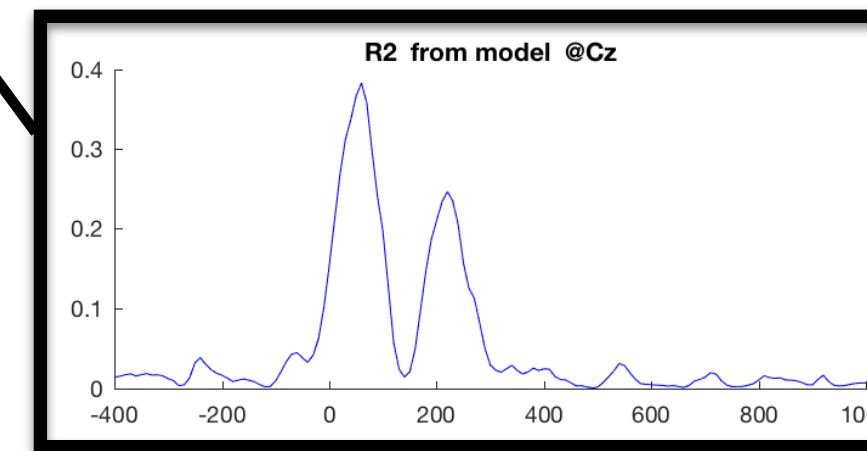
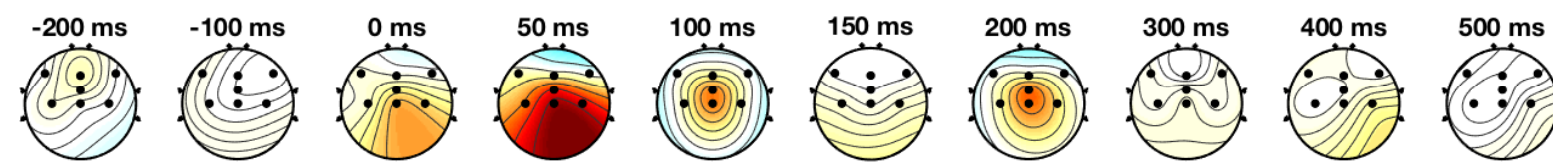
ERP image (right inlay = regressor value)

Interpretation

can be used to assess pre-processing,
 can also be used to exclude participants
 (if you we can not explain variance in the EEG signal,
 probably all following interpretations are meaningless)

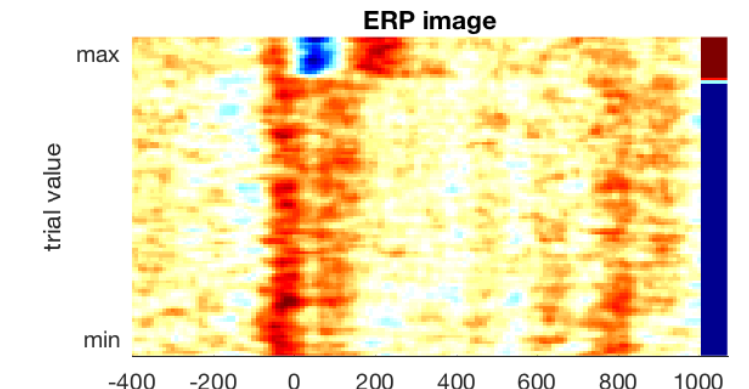
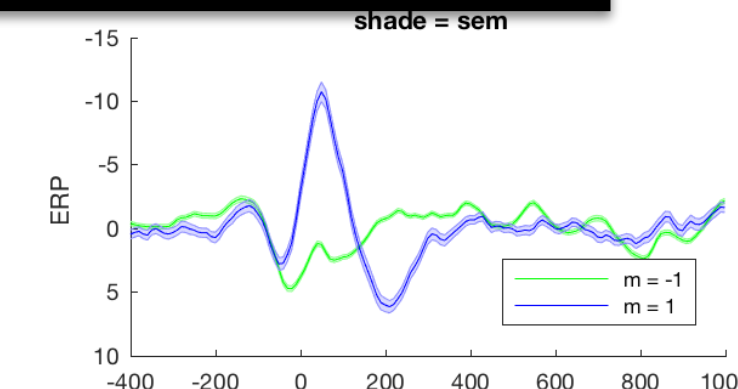
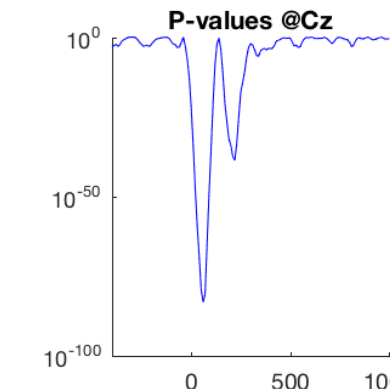
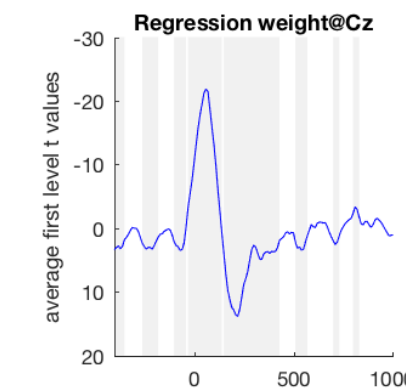
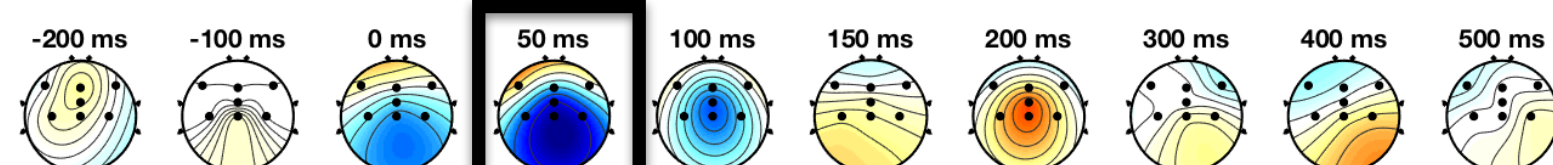
there is some co-variance
 between regressors present

Overall R2
 n subjects: 1
 n Regressors 3
 Min 0
 Max 0.383 at 60 ms

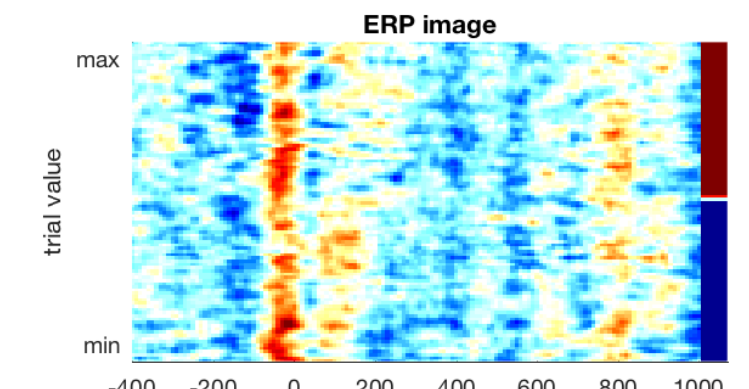
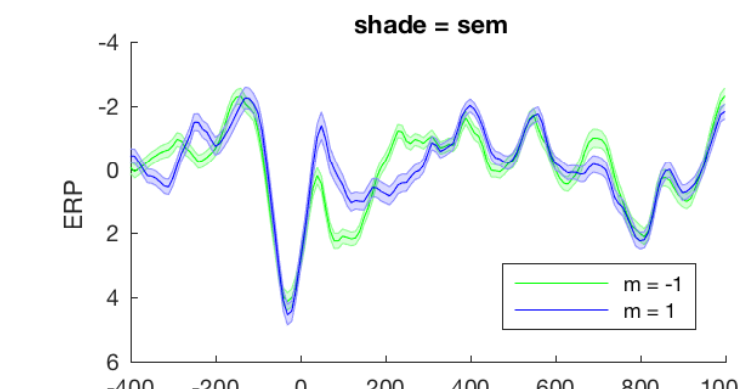
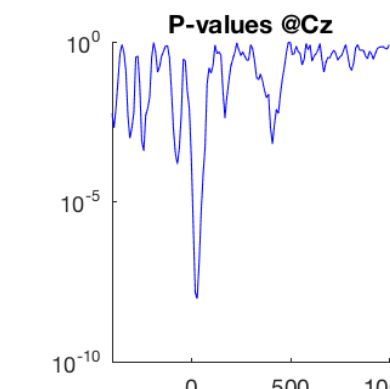
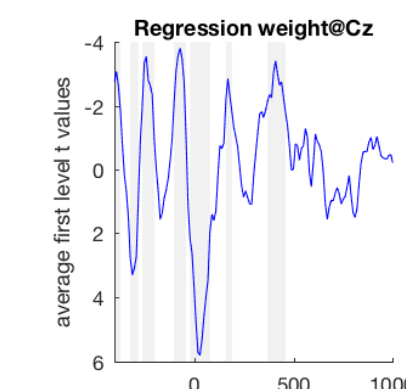
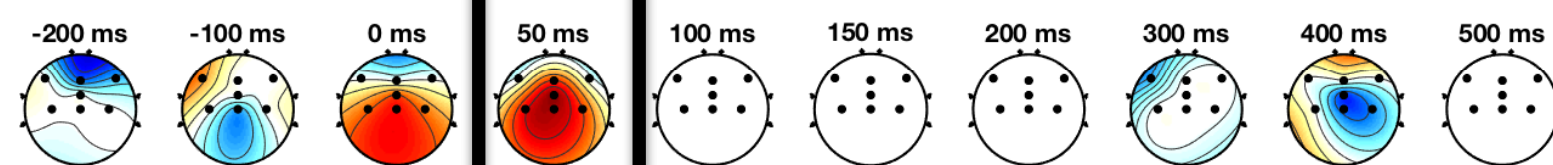


	r for regressors		
RT	-0.38	0.3	
Congruence	0.33		0.3
Accuracy		0.33	-0.38
	Accuracy	Congruence	RT

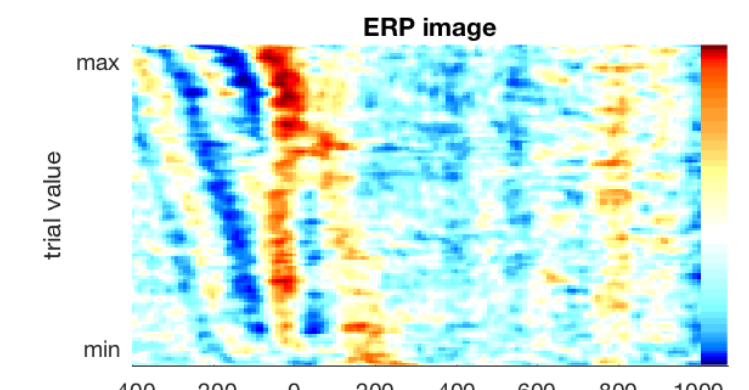
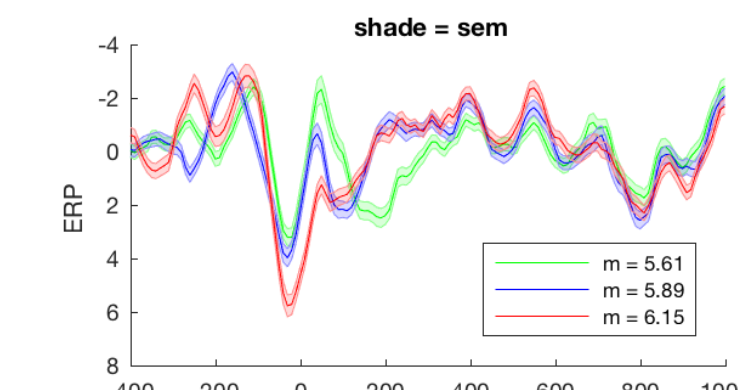
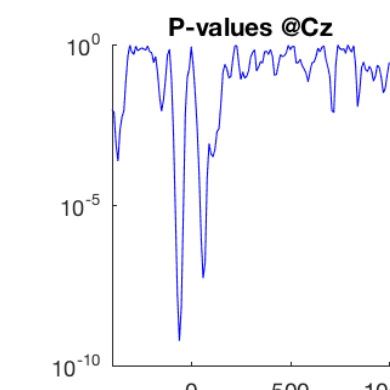
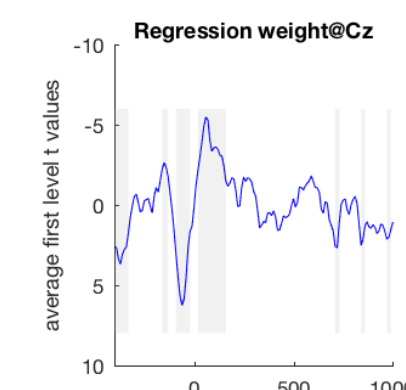
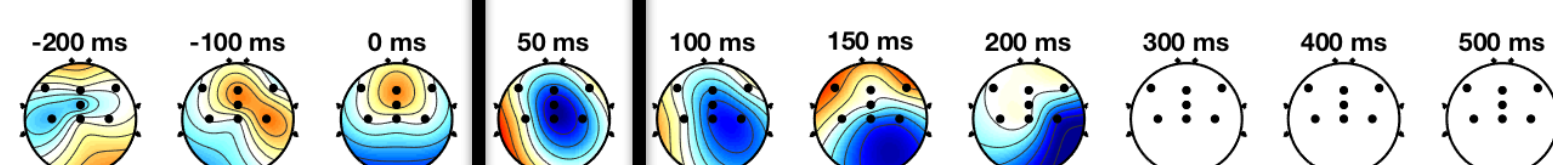
Regressor: Accuracy
 -1 = cor
 1 = err
 Maplimits -21.19 21.19
 Maplimits -21.19 21.19
 Crit p = 0.05
 Max 13.85 at 220 ms
 Min -21.85 at 60 ms
 p max = 2.11×10^{-39}
 p min = 6.36×10^{-84}



Regressor: Congruence
 -1 = con
 1 = inc
 Maplimits -4.88 4.88
 Maplimits -4.88 4.88
 Crit p = 0.05
 Max 5.81 at 30 ms
 Min -3.81 at -70 ms
 p max = 8.95×10^{-9}
 p min = 0.00014779



Regressor: RT
 5.6082 = low
 6.1516 = high
 Maplimits -4.95 4.95
 Maplimits -4.95 4.95
 Crit p = 0.05
 Max 6.27 at -60 ms
 Min -5.5 at 60 ms
 p max = 5.67×10^{-10}
 p min = 5.14×10^{-8}



especially at the time of the ERN,
 all regressors have a significant effect
 note: white data-points are masked ($p > 0.05$)

Add an interaction

many people like to center (demean) variables before calculating the dotproduct

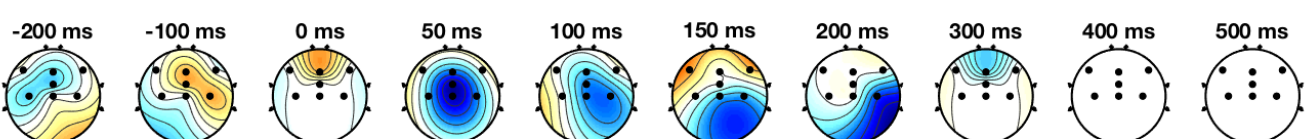
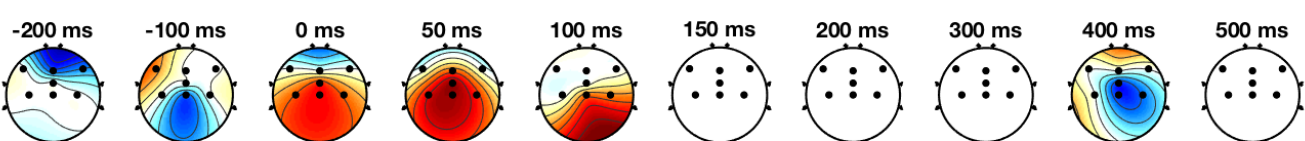
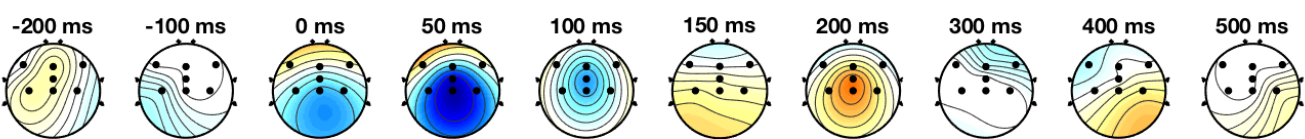
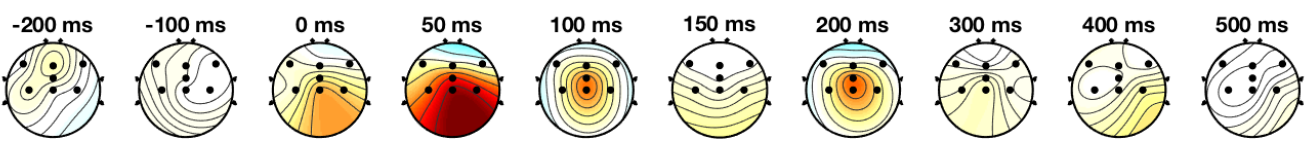
```
Predictors = {R_error(select_trials)  R_incongr(select_trials)  R_logRT(select_trials)  demean(R_logRT(select_trials)).*demean(R_error(select_trials))};
Reg2Name    = {'Accuracy'              'Congruence'          'RT'              'Acc_X_RT'};
RegLabels   = [{'cor' 'err'};          {'con' 'inc'};        {'low' 'high'};   {'low' 'high'}];
```

Overview at Cz for Simple Error Model Interact VP0005 t

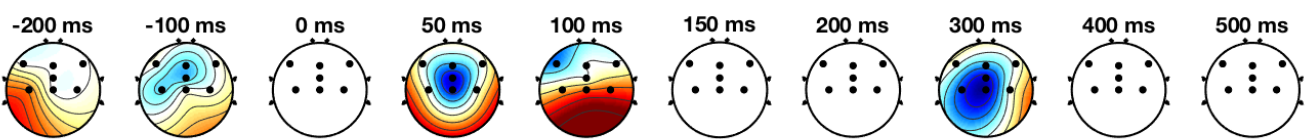
not much change in R²...

Overall R2
n subjects: 1
n Regressors 4
Max 0.384 t 60 ms

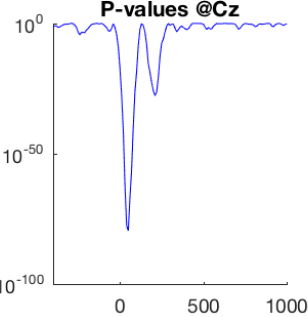
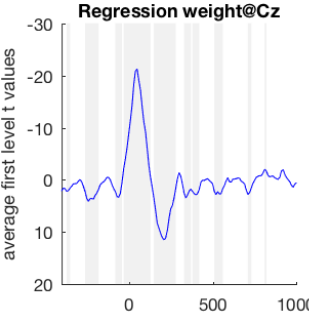
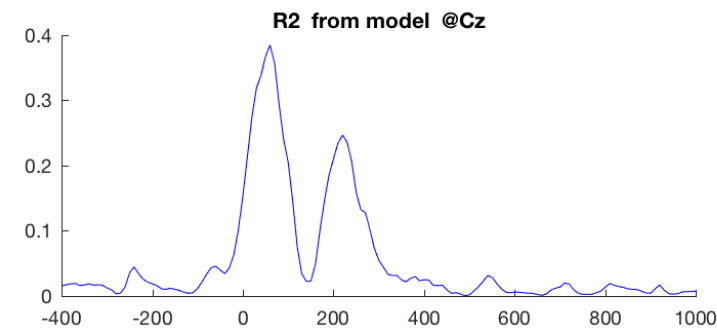
Regressor: Accuracy
-1 = cor
1 = err
Maplimits -21.24 21.24
Maplimits -21.24 21.24
Crit p = 0.05
Max 11.48 at 210 ms
Min -21.24 at 50 ms
p max = 2.01x10⁻²⁸
p min = 2.90x10⁻⁸⁰



Regressor: Acc X RT
-0.23966 = low
0.064051 = high
Maplimits -5.71 5.71
Maplimits -5.71 5.71
Crit p = 0.05
Max 4.12 at 120 ms
Min -5.71 at 300 ms
p max = 4.19x10⁻⁵
p min = 1.57x10⁻⁸

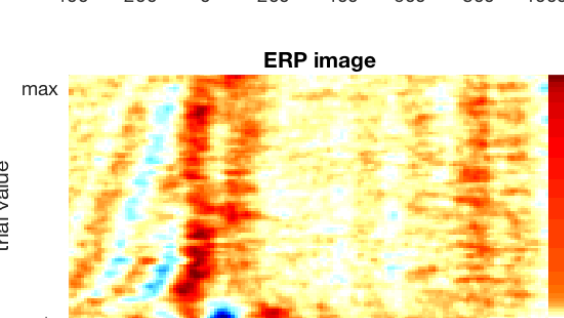
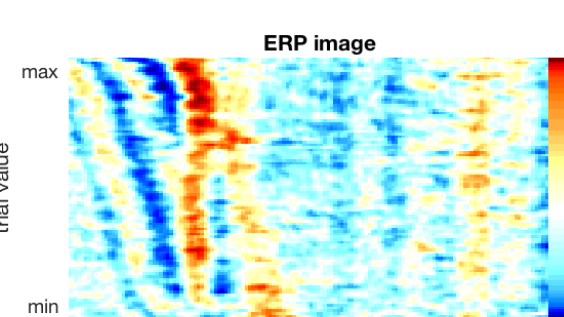
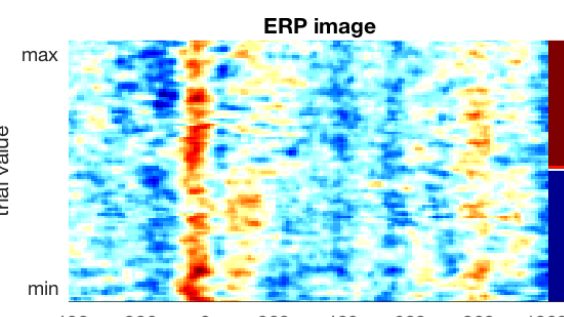
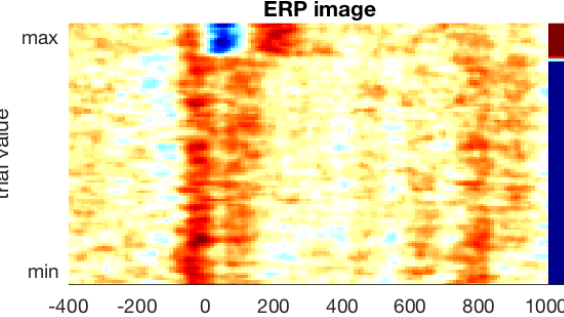
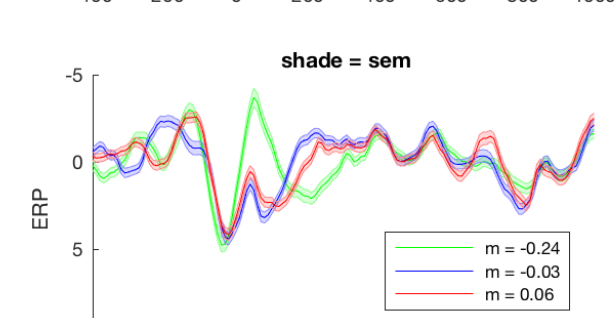
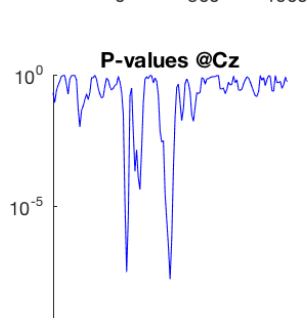
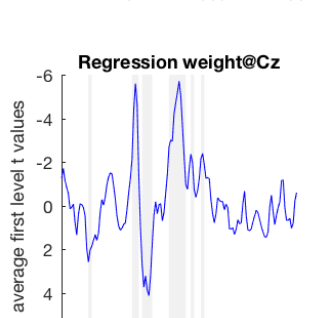
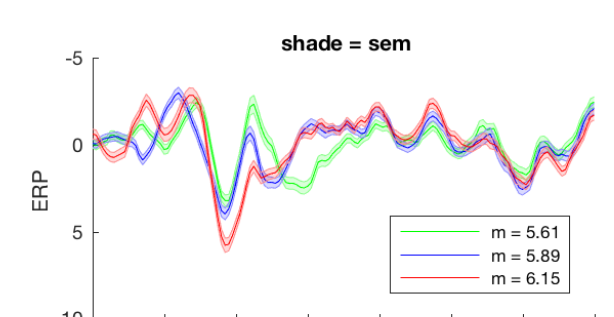
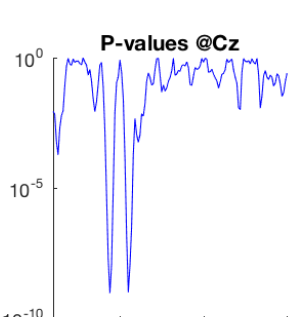
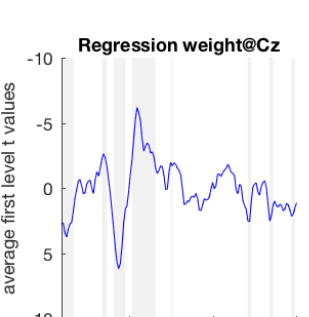
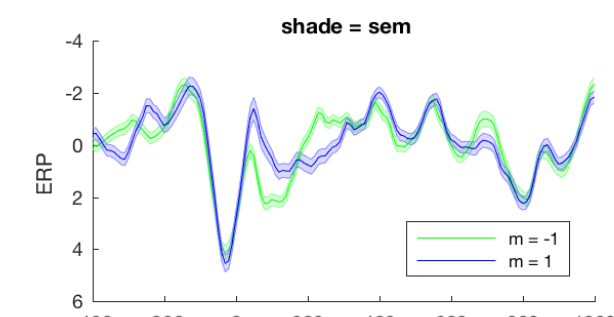
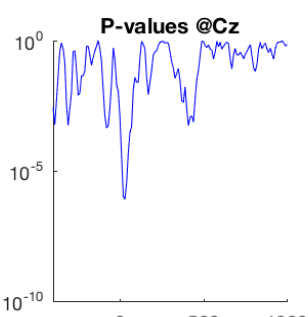
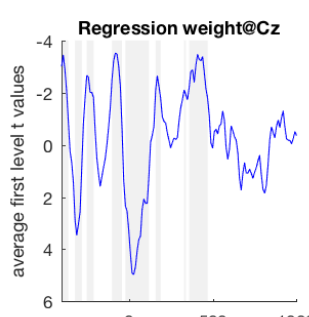
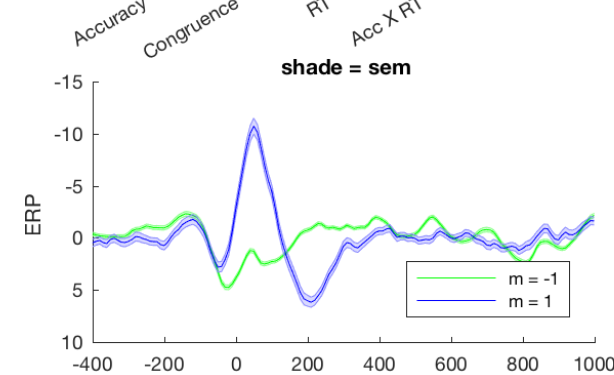


or anywhere else...



r for regressors

Acc X RT	-0.68	-0.45	0.18	
RT	-0.38	0.3		0.18
Congruence	0.33		0.3	-0.45
Accuracy		0.33	-0.38	-0.68



Perfect collinearity

$$\begin{bmatrix} 1 & 2 & 0 \\ 1 & 2 & 0 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \end{bmatrix} : c_2 = 2c_1$$

second row perfectly correlated with first
first row perfectly anti-correlated with third

$$\begin{bmatrix} 1 & 0 & 2 \\ 1 & 0 & 2 \\ 0 & 1 & 4 \\ 0 & 1 & 4 \end{bmatrix} : c_3 = 2c_1 + 4c_2$$

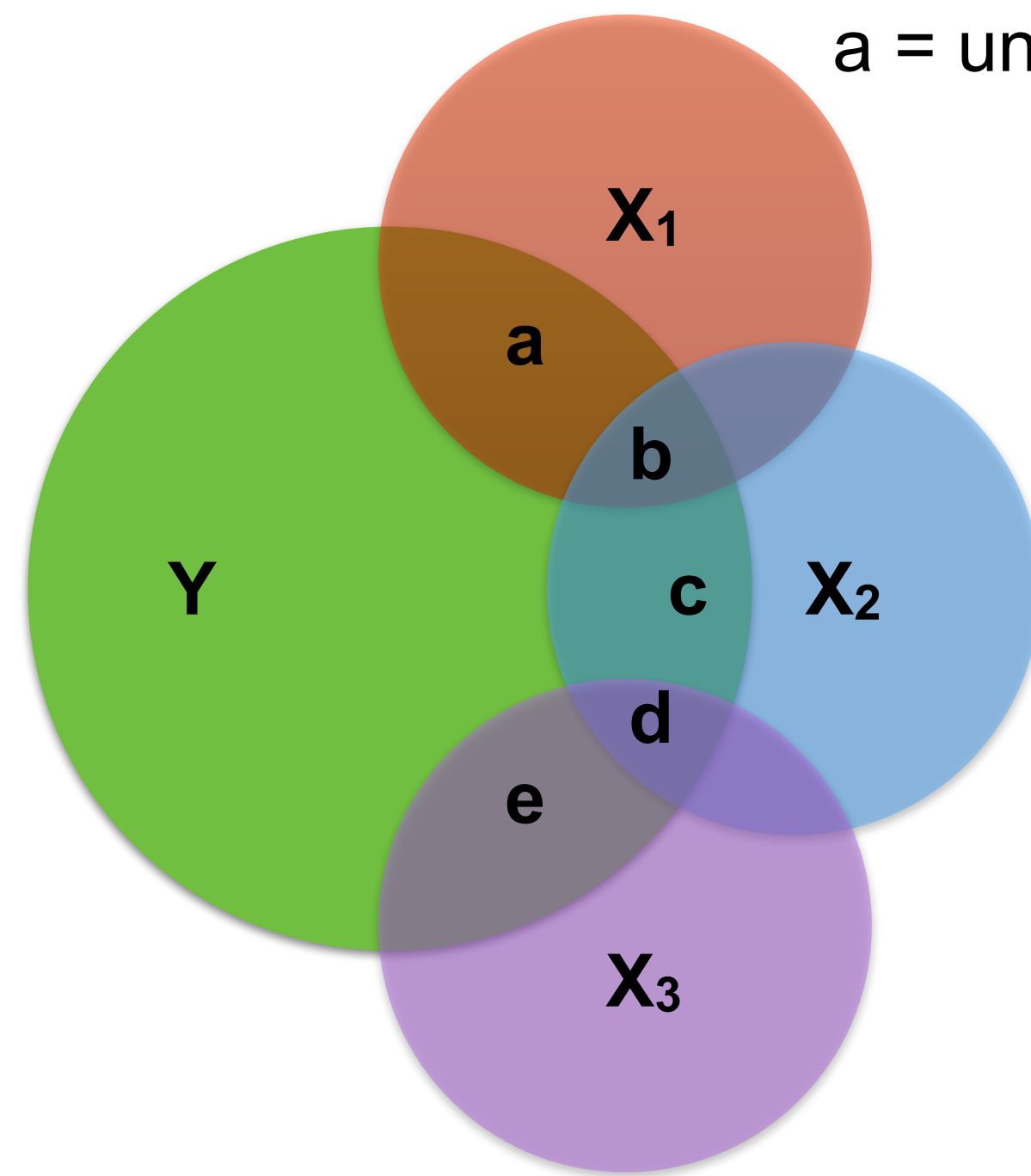
third row = linear combination of first and second row

in both cases, the model has an infinite amount of solutions
(matlab tells you, the matrix is rank deficient)

collinearity can be due to bad study design, or unavoidable because of systematic participant behaviour (e.g., errors are more common in incongruent trials, and errors are faster in many conflict tasks)

Where is the variance?

$R^2 = \text{sum}(a - e) \rightarrow$ independent from degree of covariance between X_{1-3}

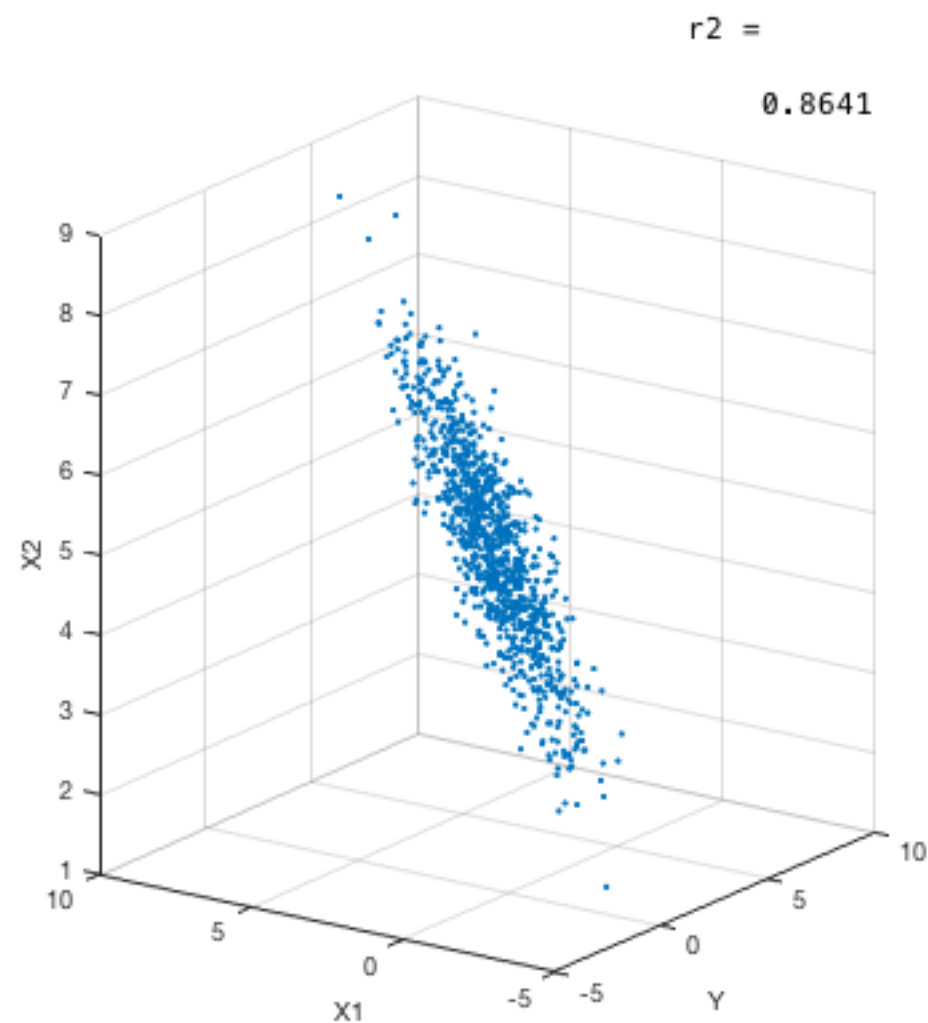


a = unique variance explained by X_1

„In order to be sure that the signal in the ventral striatum represents a reward prediction error, we must therefore subject the data to a further, more difficult, test. We must allow the three potential regressors (Reward magnitude, expectation of reward magnitude and rewarding outcome) to **compete for variance** in the fMRI data.“
(Behrens et al., *Nature*, 2008)

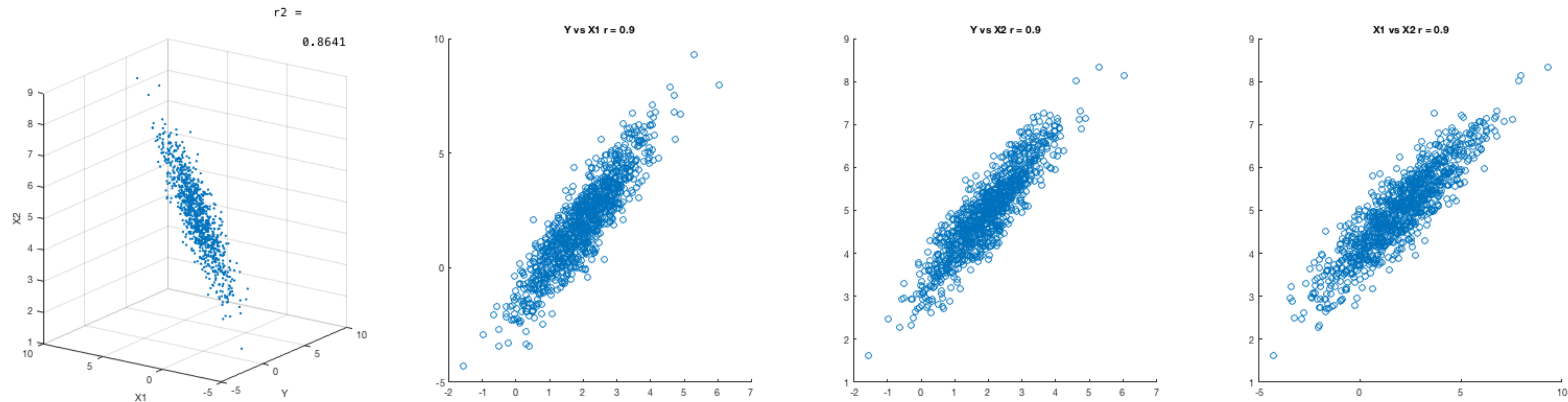
„We did not orthogonalize the regressors because, in linear regression, variance shared by different regressors is automatically **not attributed to any of the regressors**.“
(Leon et al., *Neuron*, 2017)

Where is the variance?



	<u>separate models</u>		<u>one model</u>		
	X1 vs Y	X2 vs Y	X1 vs Y	X1 vs Y	
beta for models:	0.5	0.9			b ~half
se for models:	0.006	0.014			se ~double
t for models:	69.6	65.7			4

Where is the variance?



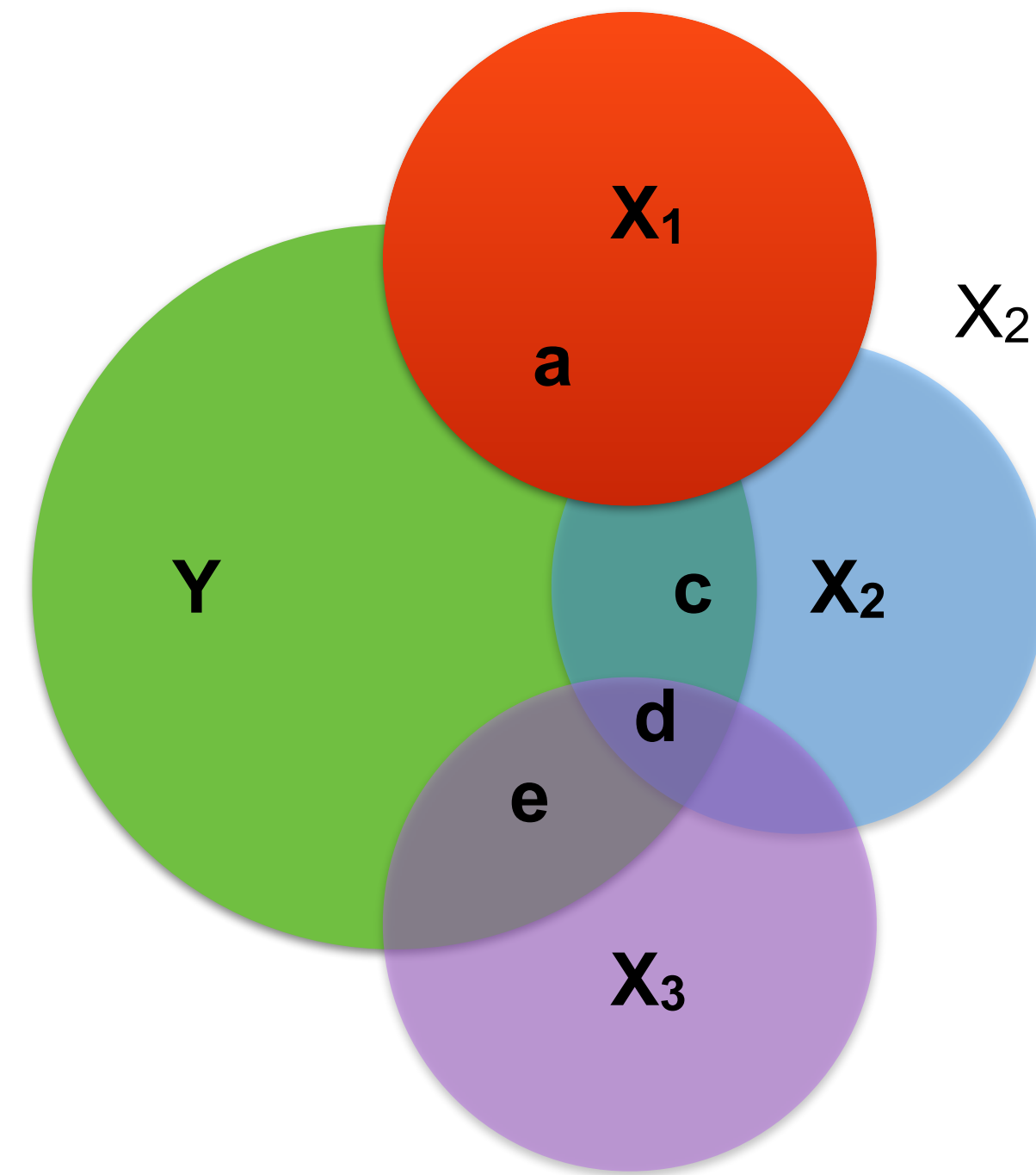
1. residualize Y wrt to X_1 (regress X_1 against Y and keep the residuals)
2. residualize X_2 wrt to X_1 (regress X_1 against X_2 and keep the residuals)
3. regress $\text{resid}(X_2)$ against $\text{resid}(Y)$

$$b = 0.4$$

$$se = 0.027$$

$$t = 16$$

same as when both are in one model



shared variance between X_1 and X_2 is attributed to X_1 alone
(*the effect of X_2 is no longer controlled for*)

8.2 Orthogonalize regressors

Y = RT needs ones for intercept add the accuracy regressor

```
%orthogonalize RT wrt accuracy --> all shared variance as ascribed to accuracy!  
[~,~,RT_resid] = regress(R_logRT(select_trials),[ones(length(select_trials),1) R_error(select_trials)]);
```

Predictors = {R_error(select_trials) R_incongr(select_trials) RT_resid};
Reg2Name = {'Accuracy' 'Congruence' 'RT_Ort' };
RegLables = [{'cor' 'err'}; {'con' 'inc'}; {'fast' 'slow'}];

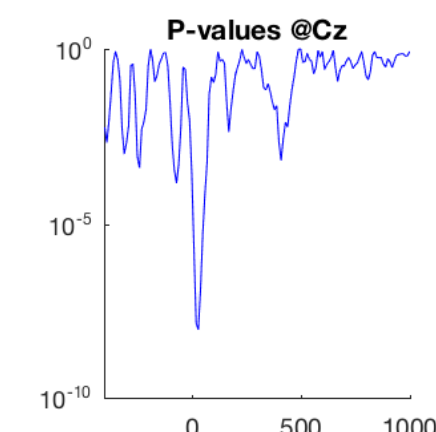
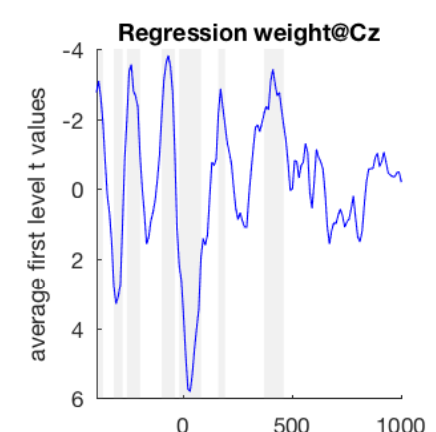
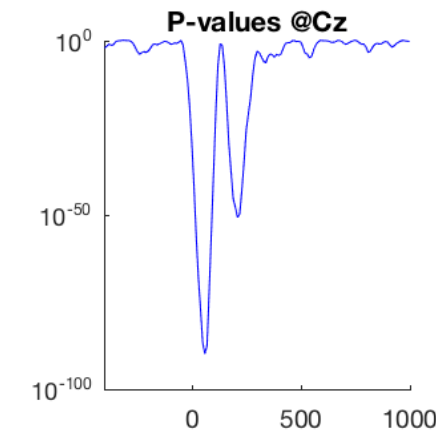
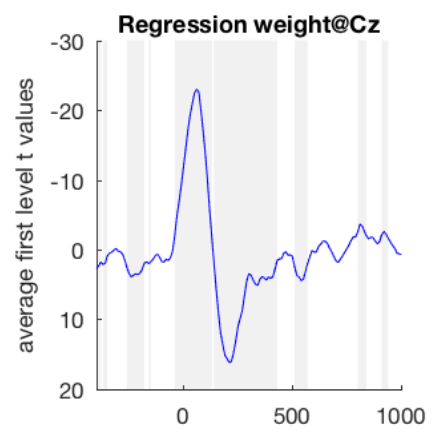
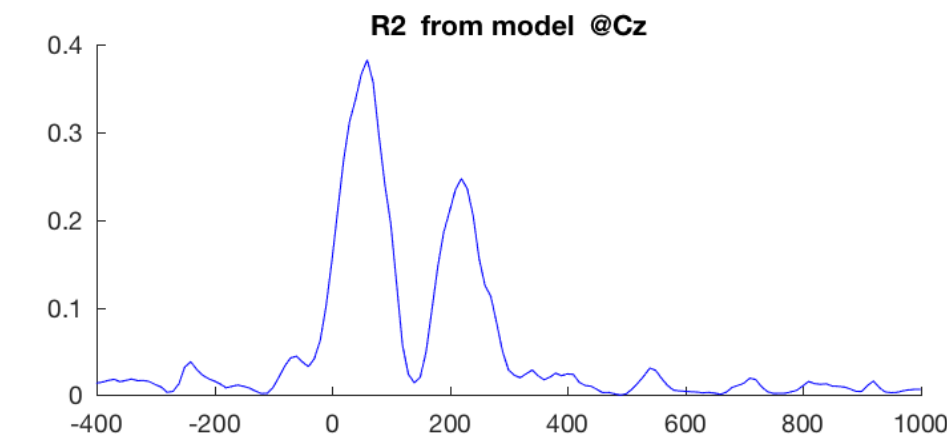
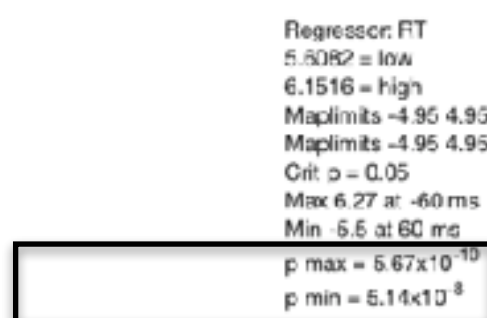
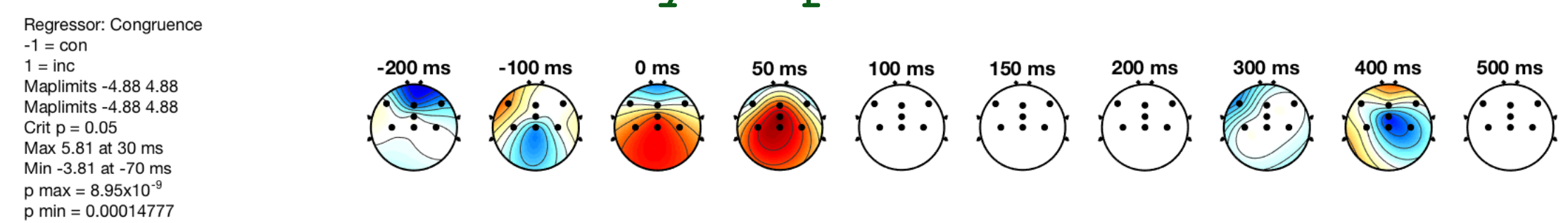
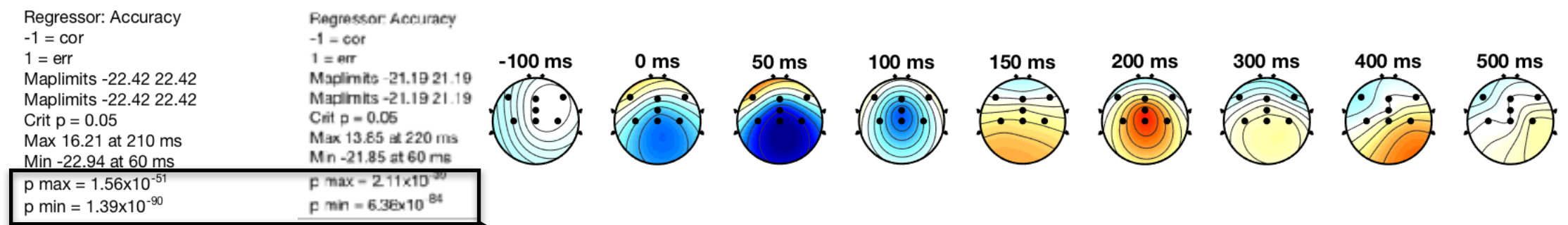
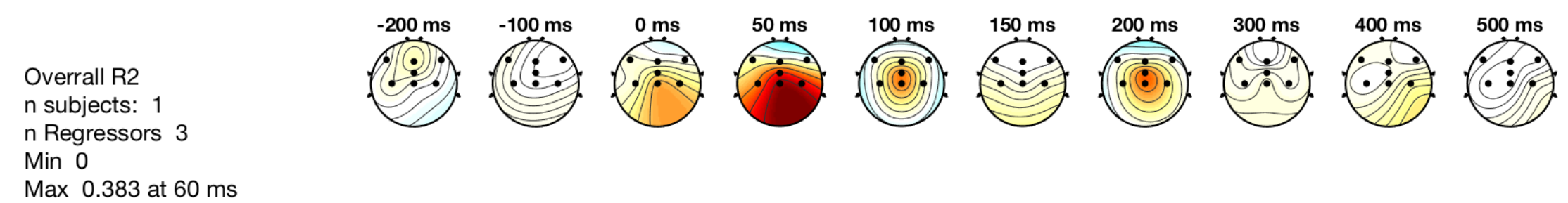
add residuals instead of RT

call the same regression

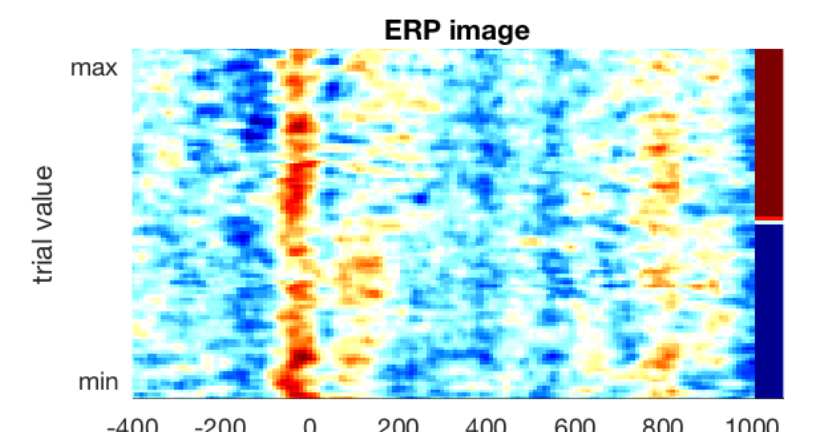
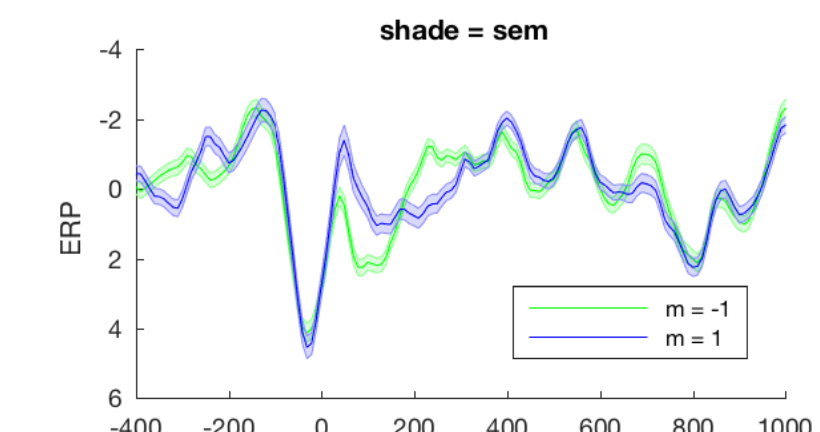
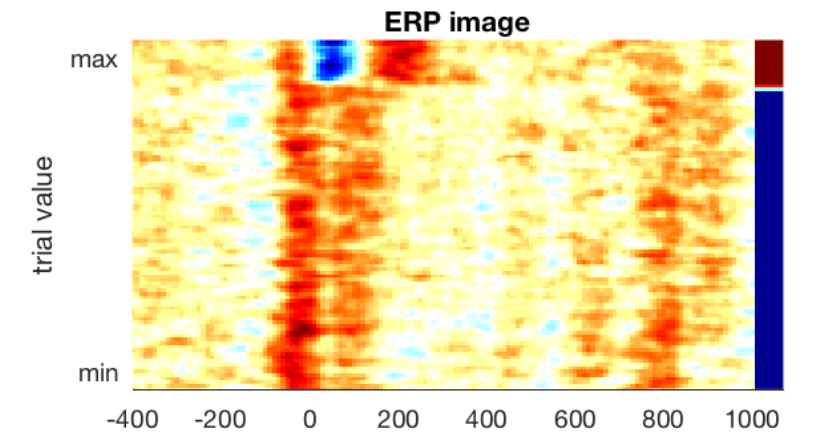
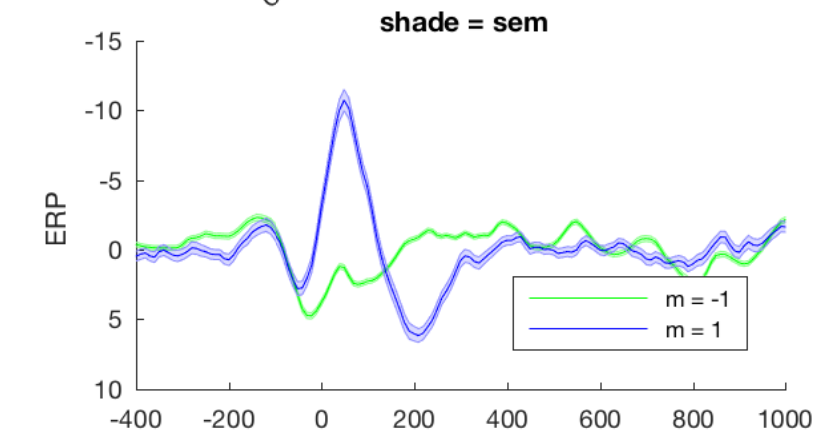
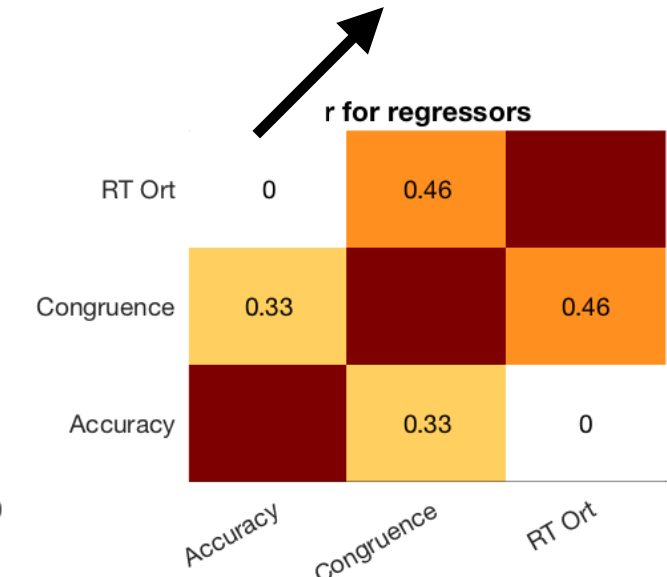
```
[ReggyD, Info] = STA_Fast_Regress RESP, Electrodes, TimeWin, 'model 1', {{select_trials} Predictors {'EEG'} {'model1'}}, ...  
  'PredNames', Reg2Name, 'PredLabels', RegLables, 'bin_size', 4, 'stepsize',1, 'TF', [], 'binEEG', 3, 'RetAll', 3, ...  
  'NormaliseOn', 0, 'Downsample', 5, 'ERPimage', 1);
```


8.2 Orthogonalize regressors

Overview at Cz for Simple Error Model Orthogonal VP0005 t



de-correlated



accuracy explains more variance

what happens with RT regressor?

completely unchanged

- Running a single-trial robust regression analysis allows to...
 - account for outlier data (very large outliers are removed, small outliers down-weighted)
 - assess goodness of fit of your model
 - ➡ SNR in your data per participant
 - ➡ very useful if you test different pre-processing pipelines, etc.
 - easily combine parametric and categorical experimental factors
 - control for possible confounds, if wanted (many reviewers will! :))
 - ➡ already on a within-subject level
- and is easy to handle and change at any time