

EEG Preprocessing

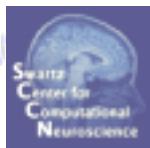
Importing data, rejecting data, and performing ICA decomposition

EEGLAB Workshop XX

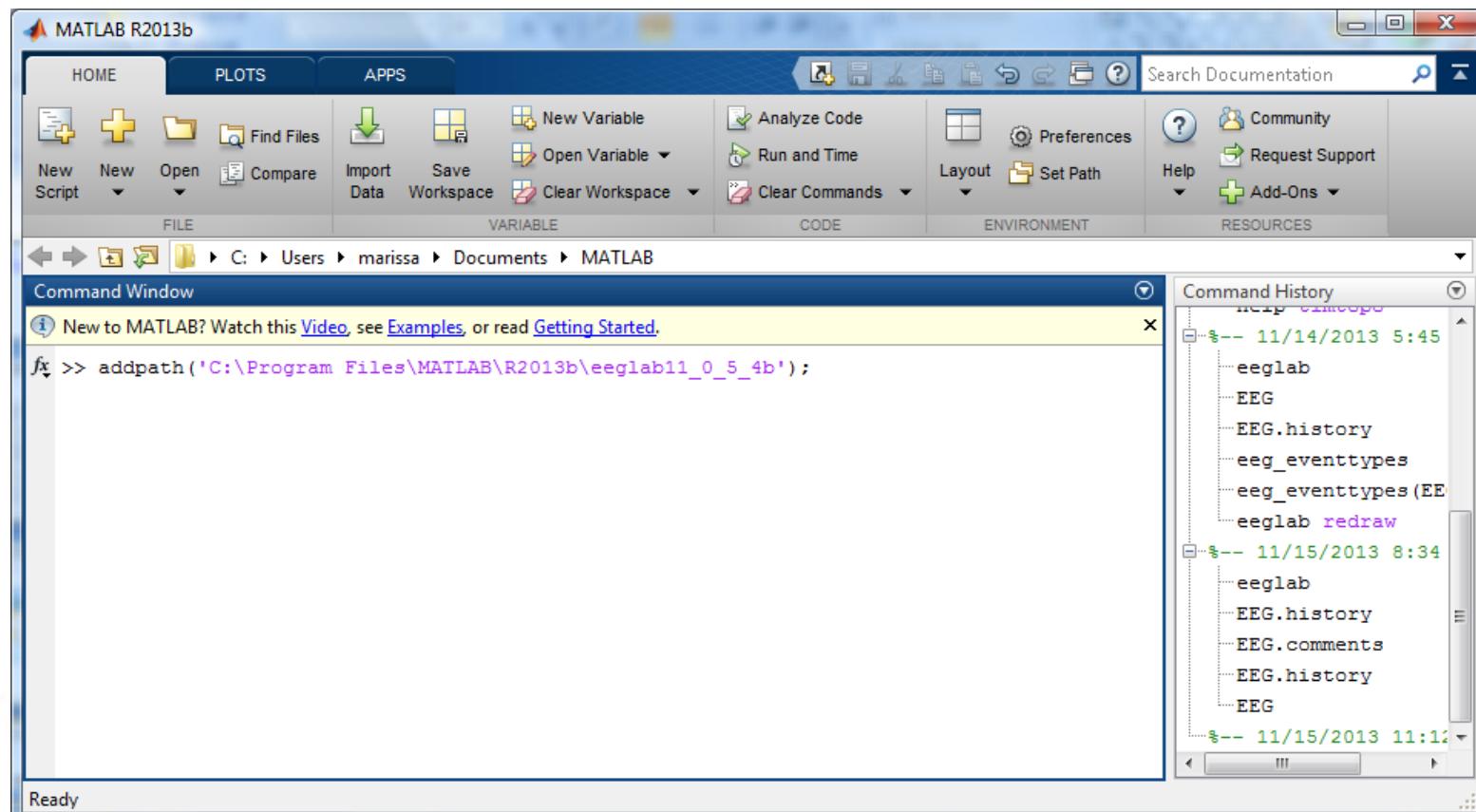
Sheffield, England

Day 1, 14:00-15:30

Installing EEGLAB and data folder



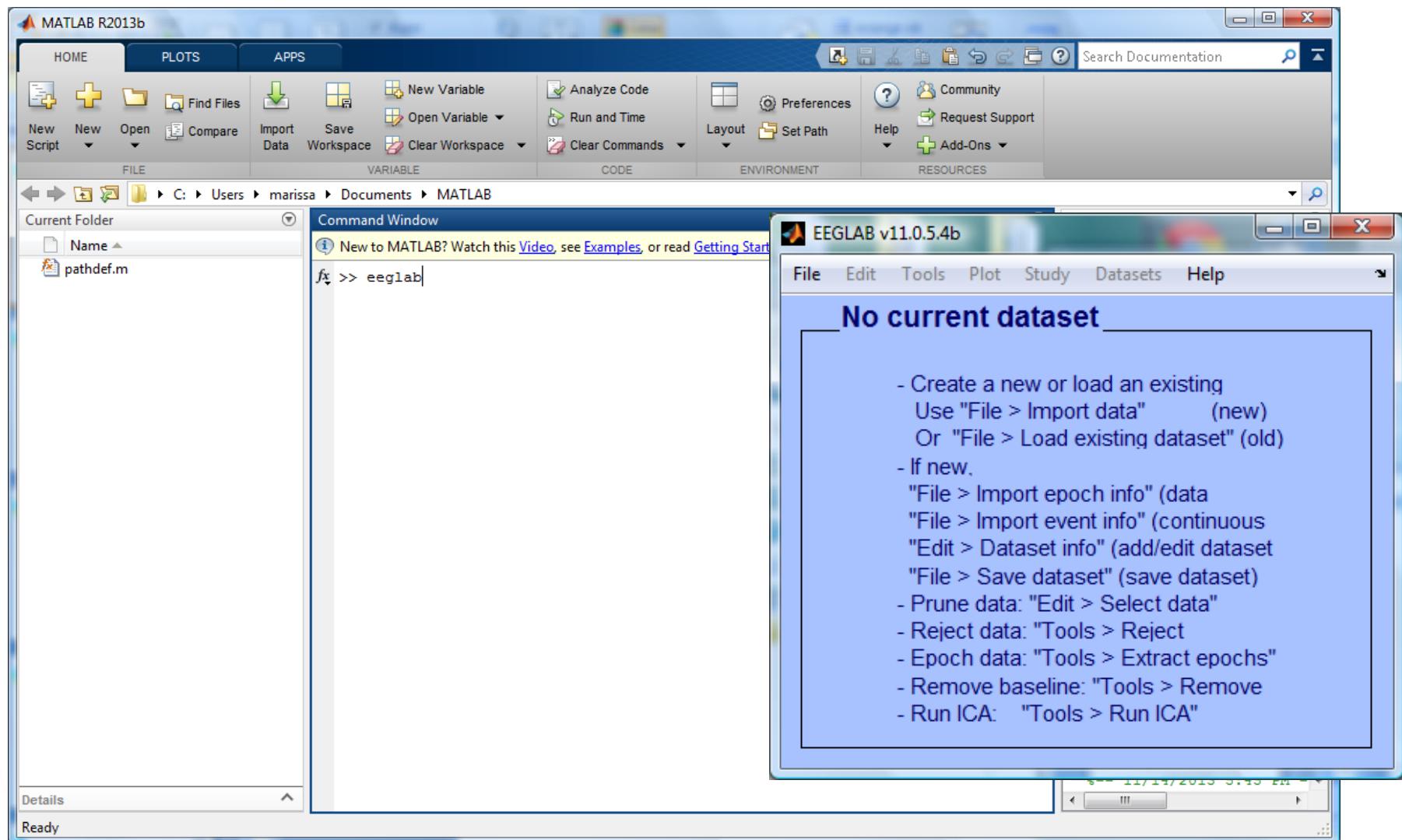
- Start Matlab
- Add the EEGLAB folder to your Matlab path:



The EEGLAB Matlab software



main graphic interface

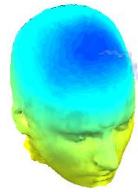


“Secrets” to a good ICA decomposition



- Garbage in... garbage out (it's not magic)
- Remove large, non-stereotyped artifacts
- Do you have enough data? (based mostly on time, not frames)
- High-pass filter to remove slow drifts (no low-pass filter needed)
- Remove bad channels
- Data must be in double precision (not single)

The Goal of Preprocessing



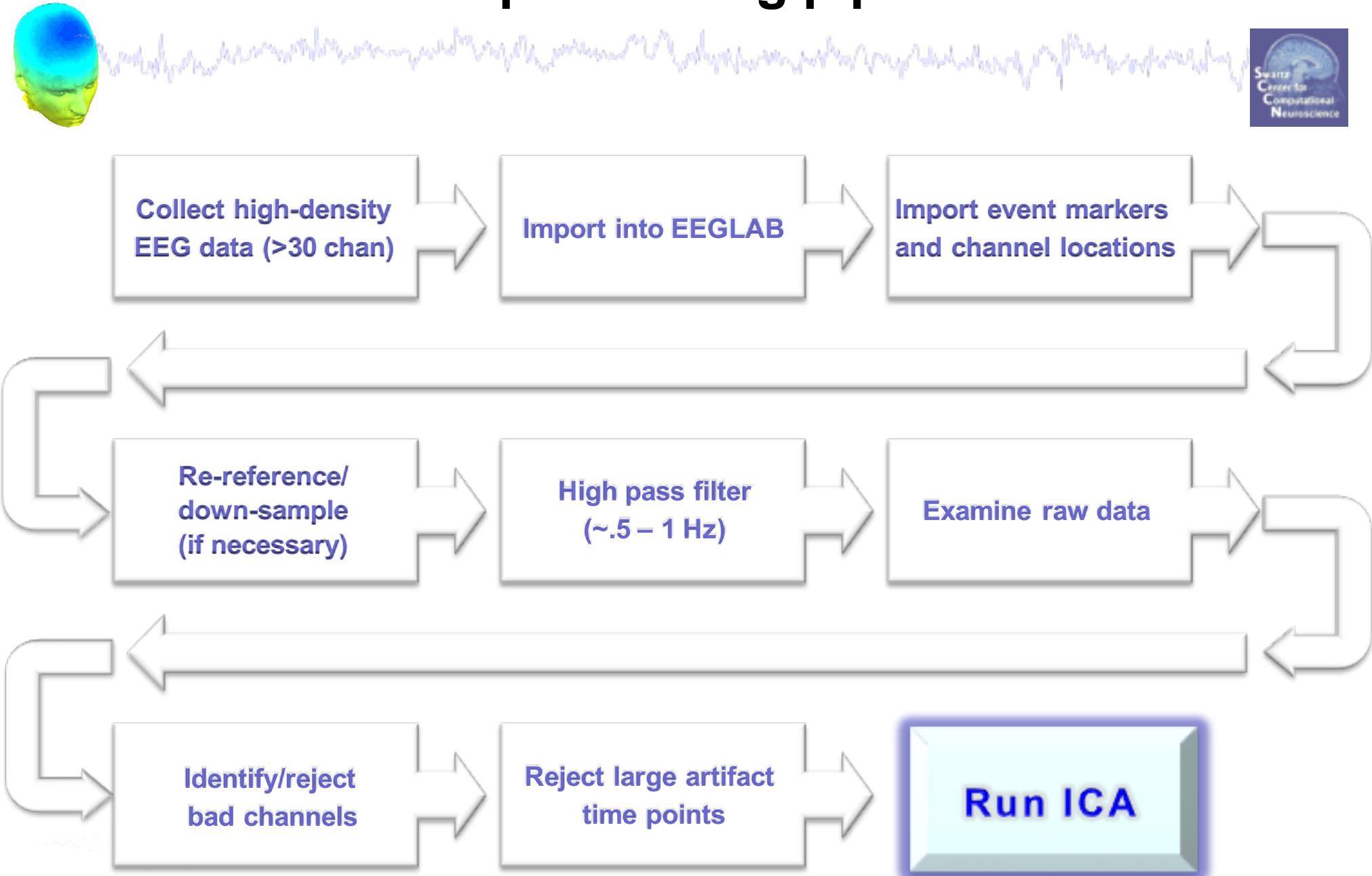
- Create a complete EEG:AB data set with
 - EEG
 - Channel Locations
 - Events
- Preprocess the EEG data to yield optimal ICA decompositions
 - Rereferencing
 - High Pass Filtering
 - Remove bad channels, noisy segments of data
- Run ICA decomposition
 - Then go to my previous lecture...Evaluating ICA Components

Many Preprocessing Variants

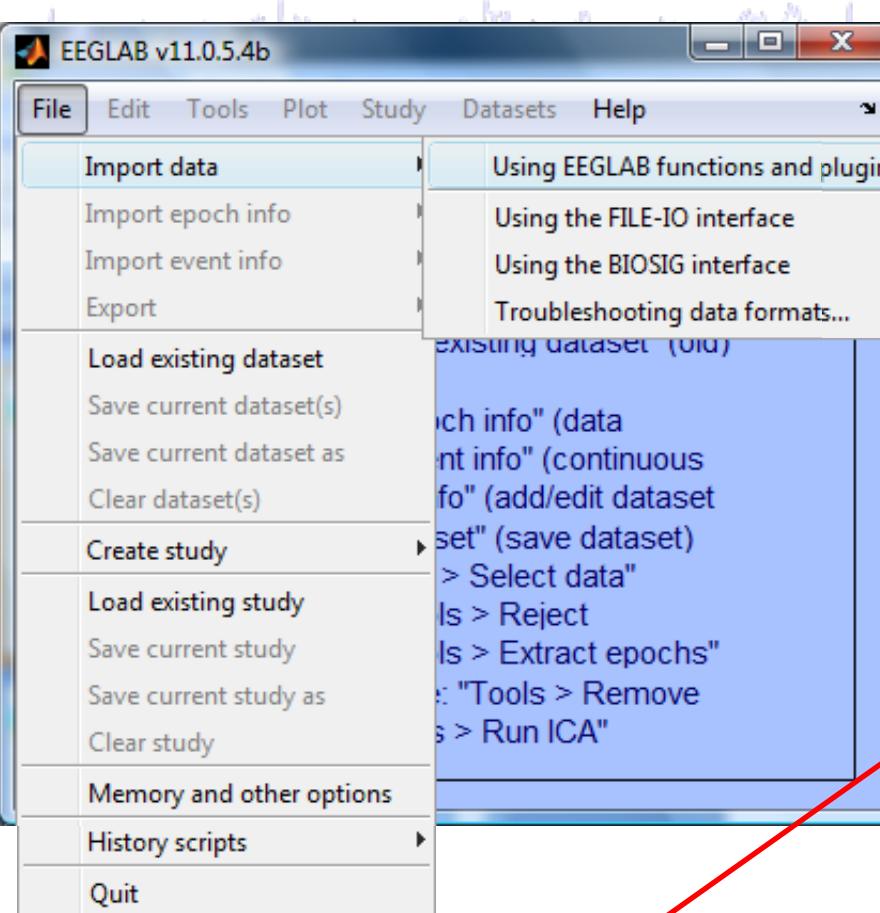


- Resources
 - EEGLAB wiki “Quick Tutorial on Rejection”
 - http://sccn.ucsd.edu/wiki/Quick_Rejection_Tutorial
 - Makoto’s Preprocessing Pipeline
 - http://sccn.ucsd.edu/wiki/Makoto%27s_preprocessing_pipeline
 - Bigdely-Shamlo et al (2015): PREP Pipeline
 - <http://dx.doi.org/10.3389/fninf.2015.00016>
 - EEGLAB Plugins
 - Kothe’s clean_rawdata plugin
 - Miyakoshi’s trimOutlier plugin

Pre-processing pipeline



Importing a dataset



The screenshot shows the EEGLAB v11.0.5.4b software interface. The 'File' menu is open, displaying various options for importing and managing datasets. A red arrow points from a text box at the bottom left to the 'From Biosemi BDF and EDF files (BDF plugin)' option in the 'Import data' submenu.

Tip for Biosemi users:
**Use the 'BDF plugin' version
of the Biosemi BDF/EDF importer**

Import data

- Import epoch info
- Import event info
- Export
- Load existing dataset
- Save current dataset(s)
- Save current dataset as
- Clear dataset(s)
- Create study
- Load existing study
- Save current study
- Save current study as
- Clear study
- Memory and other options
- History scripts
- Quit

Using EEGLAB functions and plugins

- Using the FILE-IO interface
- Using the BIOSIG interface
- Troubleshooting data formats...

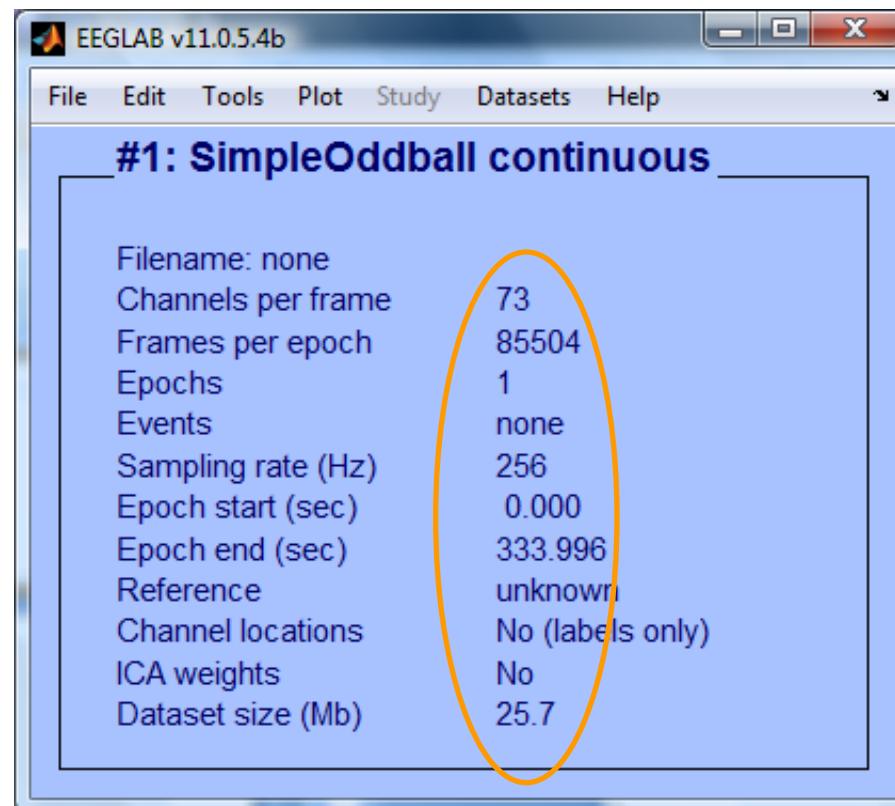
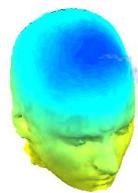
existing dataset (.v10)

- "Epoch info" (data)
- "Event info" (continuous)
- "Dataset" (add/edit dataset)
- "Save dataset"
- > Select data"
- Is > Reject
- Is > Extract epochs"
- : "Tools > Remove
- s > Run ICA"

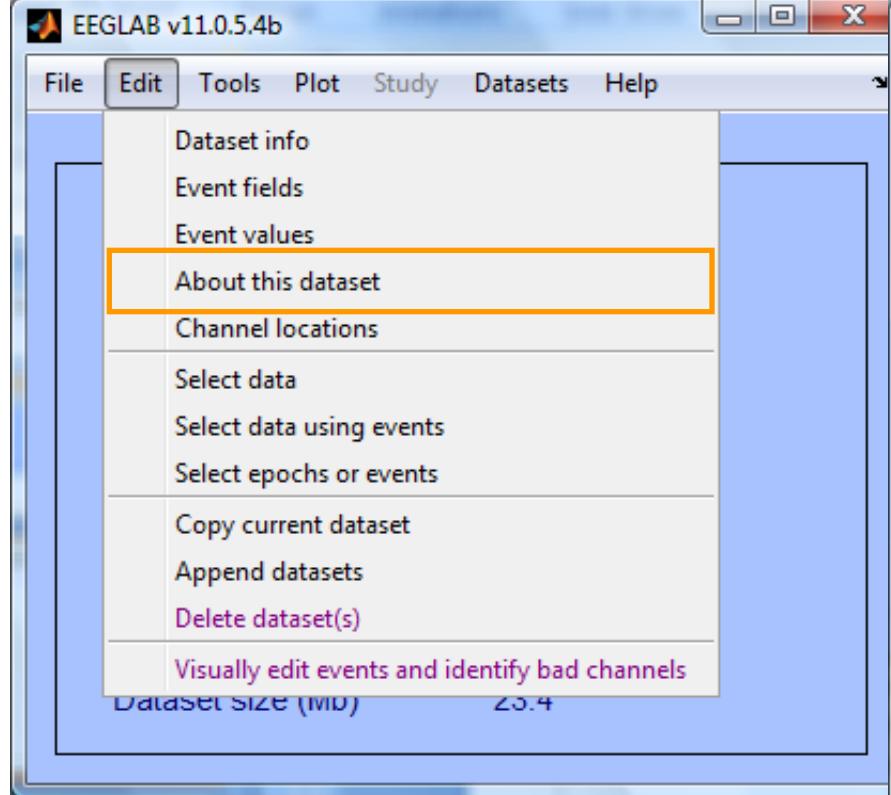
From ASCII/float file or Matlab array

- From Netstation .mff (FILE-IO toolbox)
- From Netstation binary simple file
- From Multiple seg. Netstation files
- From Netstation Matlab files
- From BCI2000 ASCII file
- From Snapmaster .SMA file
- From Neuroscan .CNT file
- From Neuroscan .EEG file
- From Biosemi BDF file (BIOSIG toolbox)
- From Biosemi BDF and EDF files (BDF plugin)**
- From EDF/EDF+/GDF files (BIOSIG toolbox)
- From ANT EEProbe .CNT file
- From ANT EEProbe .AVR file
- From BCI2000 .DAT file
- From BIOPAC MATLAB files
- From Brain Vis. Rec. .vhdr file
- From Brain Vis. Anal. Matlab file
- From CTF folder (MEG)
- From ERPSS .RAW or .RDF file
- From INStep .ASC file
- From 4D .m4d pdf file
- From Procom Infinity Text File

Imported EEG data



Comments and dataset history

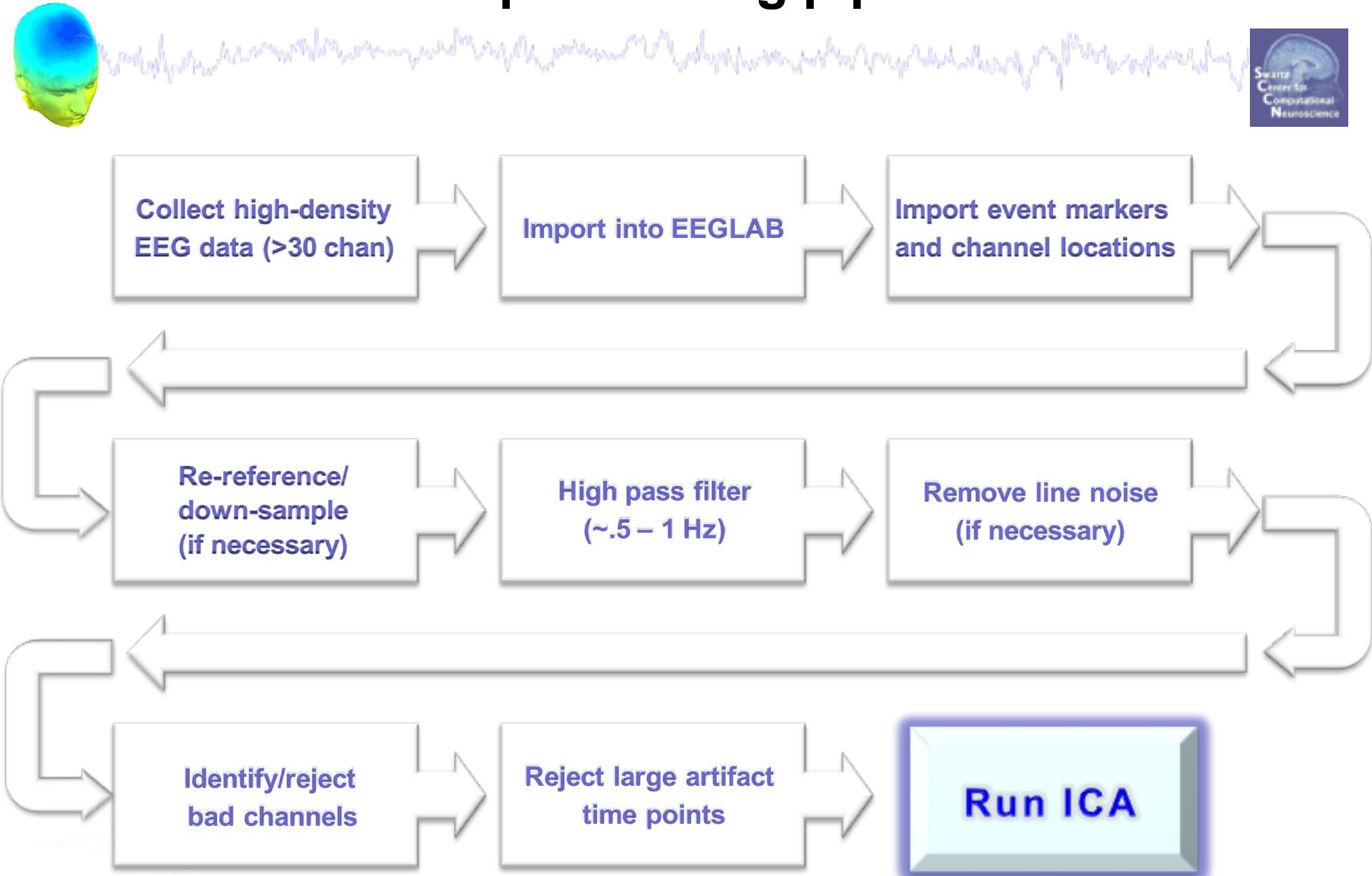


The screenshot shows the EEGLAB v11.0.5.4b software interface. On the left, a vertical menu lists various options: Dataset info, Event fields, Event values, About this dataset (which is highlighted with an orange border), Channel locations, Select data, Select data using events, Select epochs or events, Copy current dataset, Append datasets, Delete dataset(s), and Visually edit events and identify bad channels. Below the menu, it says "Dataset size (IMD) 20.4". On the right, a window titled "Read/Enter comments -- pop_comments()" displays the "About this dataset" section. The text in this section includes details about the recording: "Data recorded by Marissa Westerfield Recording date: Oct. 14, 2011". It also describes the paradigm: "Paradigm: -Participant looked at fixation box in center of screen -Two types of stimuli (outline of a circle, outline of a star) were presented in the fixation box in random order -Participant pressed a button in response to the star". It lists stimulus codes: "Stimulus codes: 1 = circle 2 = star 3 = button press". It provides recording information: "Recording information: -reference electrodes were placed on right and left mastoids (data has already been referenced and the mastoid channels have been removed)". It also lists processing steps: "Processing steps: high-pass filter - 0.5 Hz Cleanline applied to 60, 120 Hz". At the bottom of the window are two buttons: "CANCEL" and "SAVE".

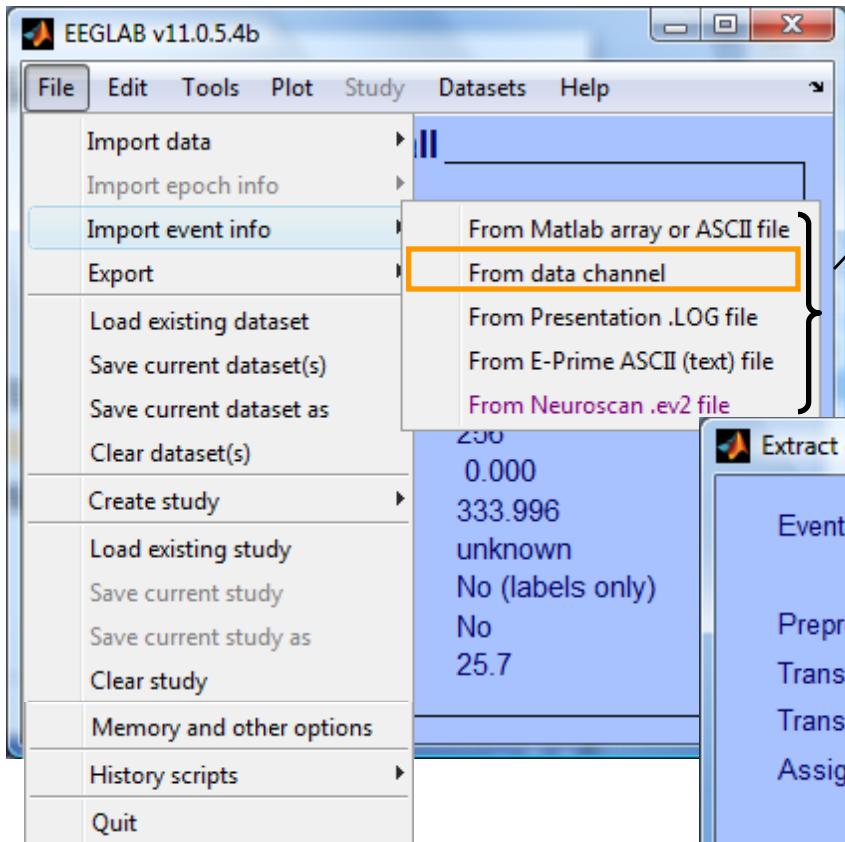
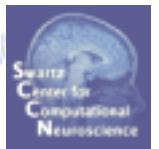
Also:
>> EEG.comments

and
>> EEG.history

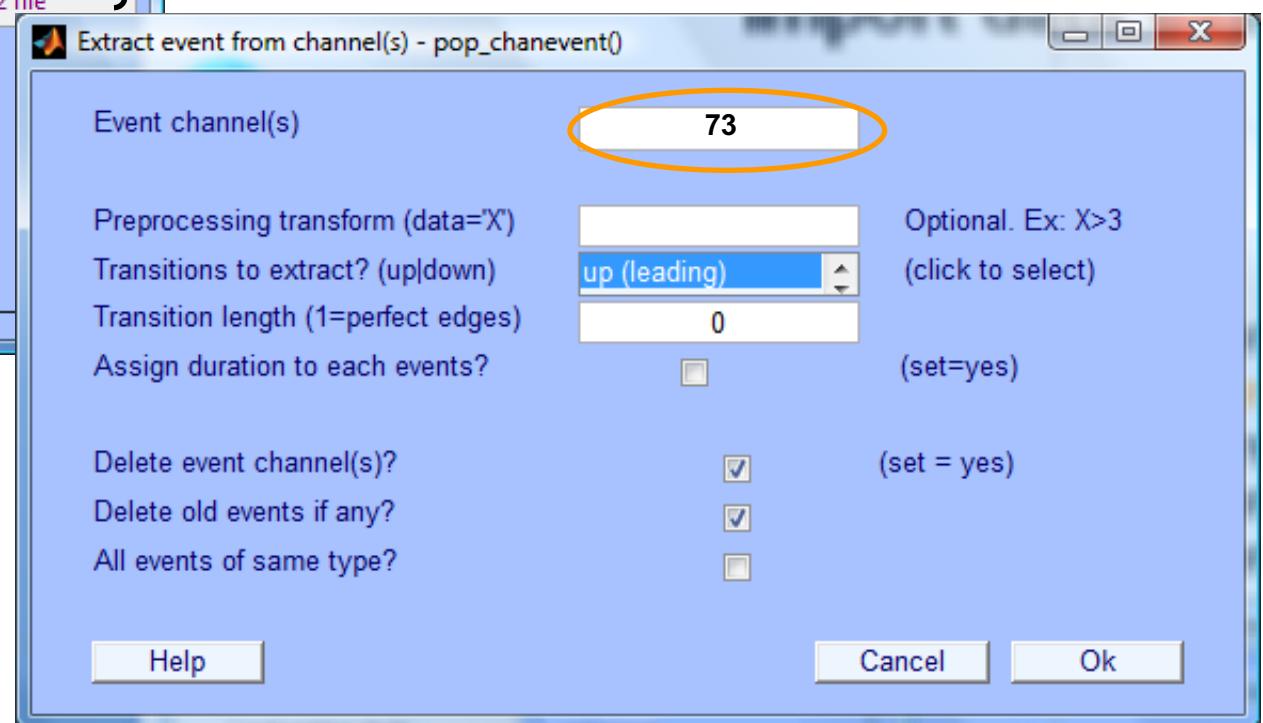
Pre-processing pipeline



Import data events



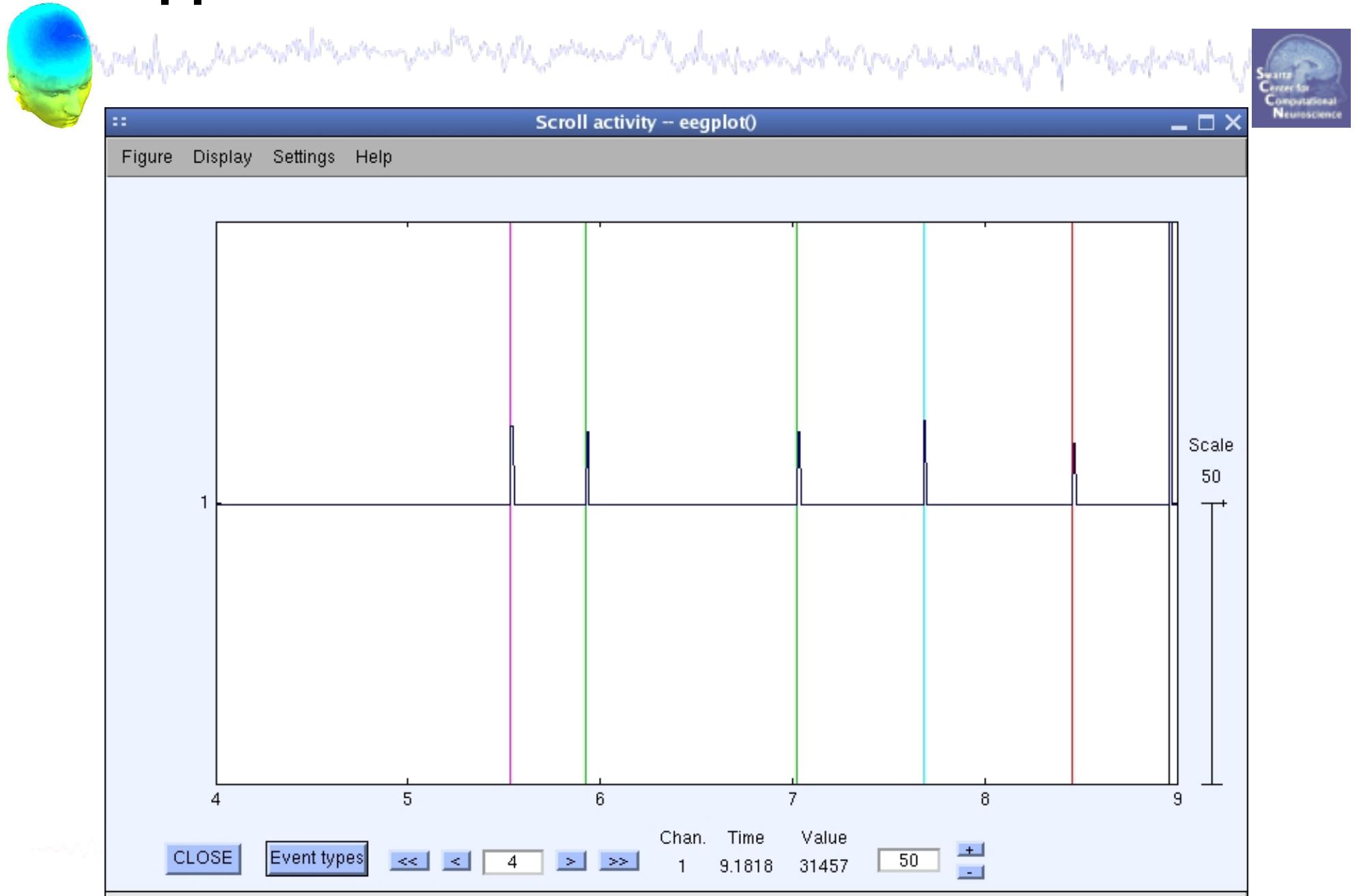
- Import events from Matlab array or ASCII file
- Import events from data channel
- Import from Presentation event file
- Import events from E-Prime event file
- Import events from Neuroscan event file



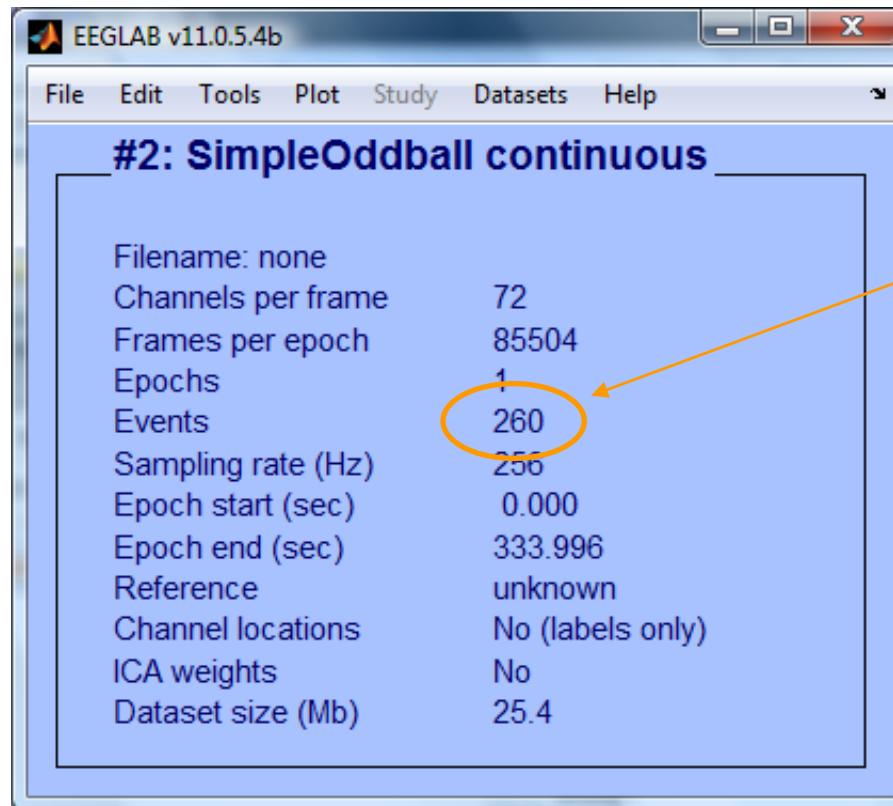
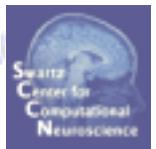
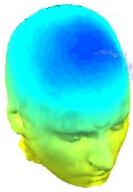
(Often imported automatically

— during data import)

Appearance of an event channel in raw data



Imported data events



If event import was
successful,
you will see an
appropriate
number here

Sample data: basic P300 paradigm



File

SimpleOddball.set

Data

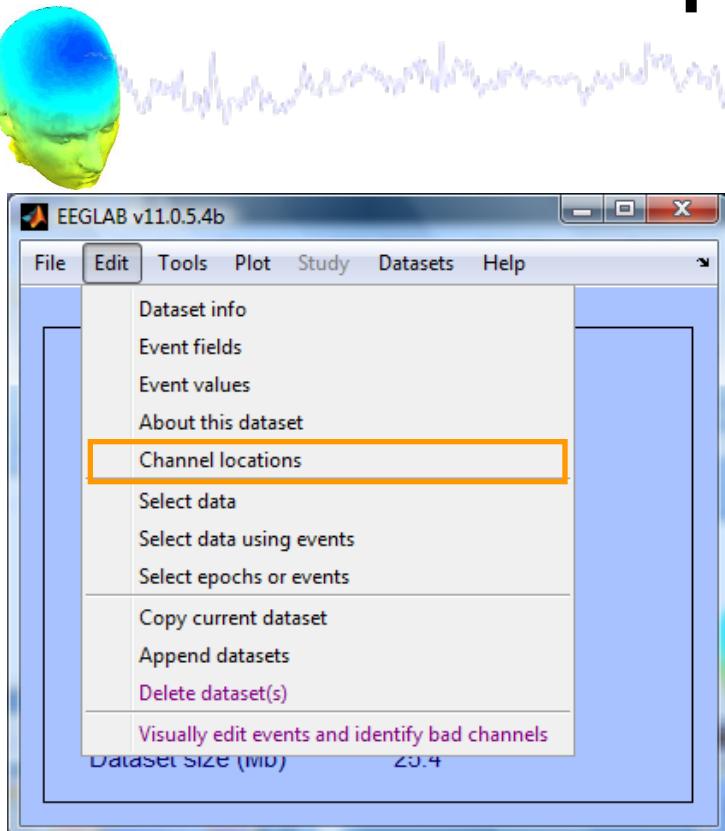
68 channel EEG, 256 Hz sampling rate, Biosemi system, re-referenced during import to averaged left and right mastoid electrodes

Task

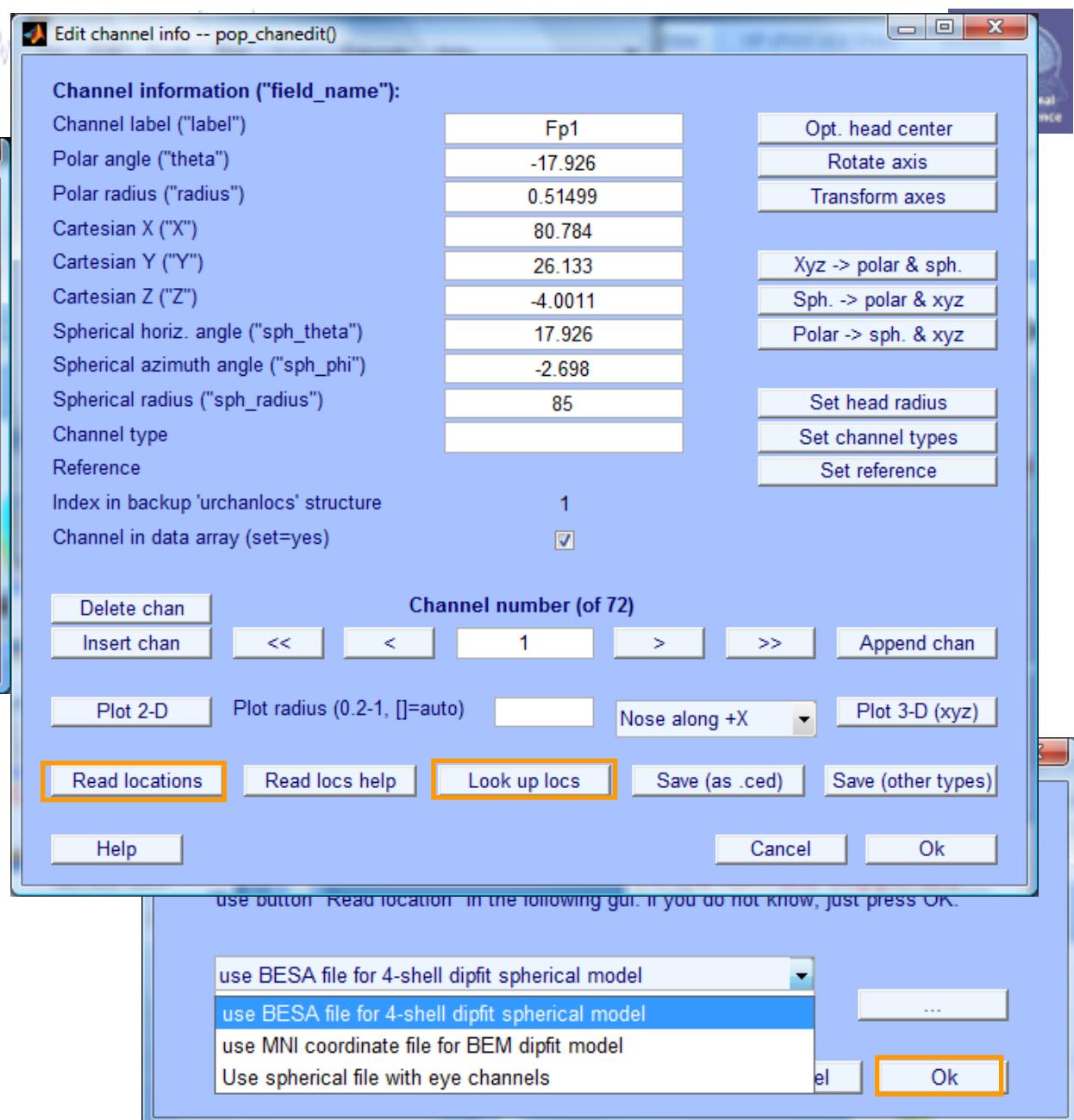
speeded button press response to star shape (no response to circle shape), 100 ms presentation duration, 200 trials



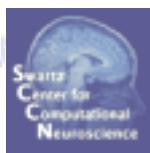
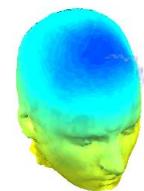
Import channel locations



7 file formats supported
(Polhemus, BESA, ...)



Import channel locations



Edit channel info -- pop_chanedit()

Channel information ("field_name"):

Channel label ("label")	LEYE
Polar angle ("theta")	-45.1543
Polar radius ("radius")	0.54374
Cartesian X ("X")	0.79487
Cartesian Y ("Y")	0.79917
Cartesian Z ("Z")	-0.15585
Spherical horiz. angle ("sph_theta")	45.1543
Spherical azimuth angle ("sph_phi")	-7.8725
Spherical radius ("sph_radius")	1.1379
Channel type	EEG
Reference	

Index in backup 'urchanlocs' structure

Channel in data array (set=yes)

Channel number (of 71)

Delete chan Insert chan << < 1 > >> Append chan

Plot 2-D Plot radius (0.2-1, []=auto) Nose along +X Plot 3-D (xyz)

Read locations Read locs help Look up locs Save (as .ced) Save (other types)

Help Cancel Ok

Convert channel locations -- pop_chancenter()

Optimize center location or specify center 0 0 0

Channel indices to ignore for best-sphere matching Browse

Help Cancel Ok

Force electrode location -- forcelocs()

X/Y value Coordinate Electrode list

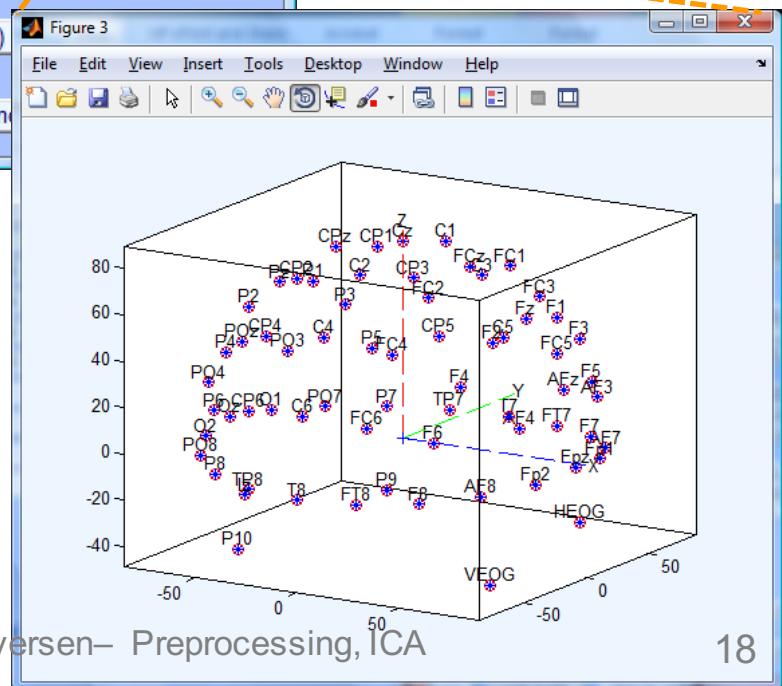
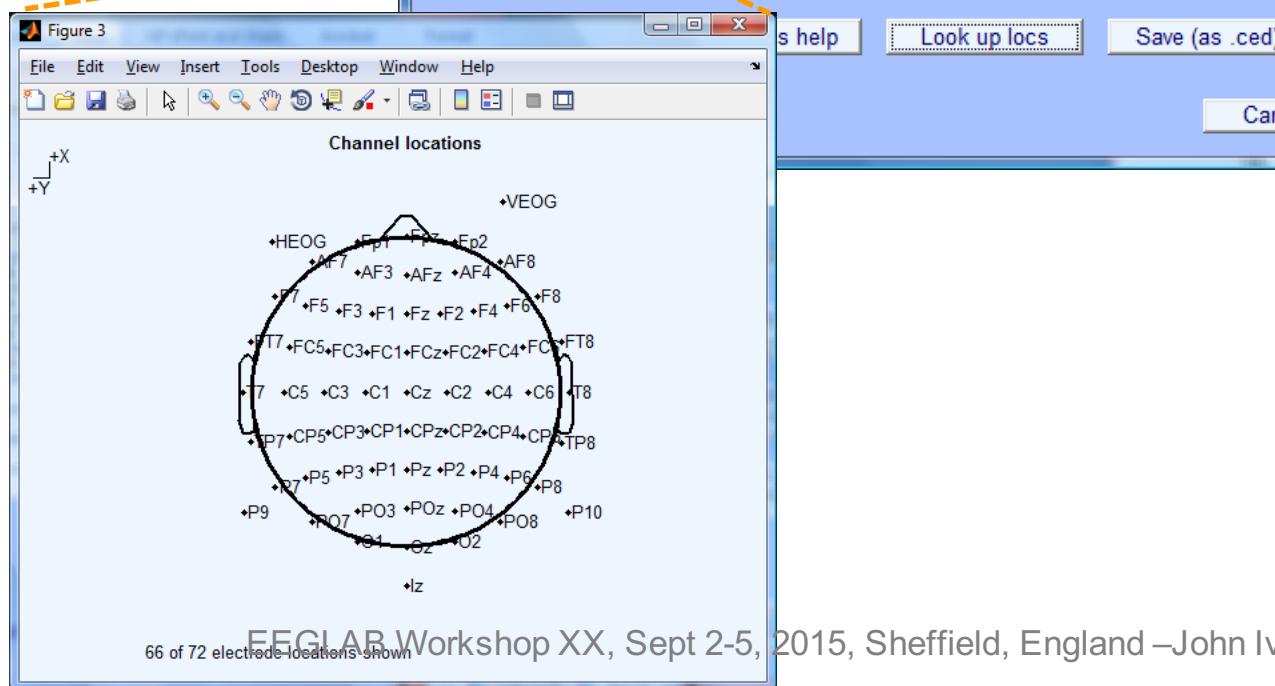
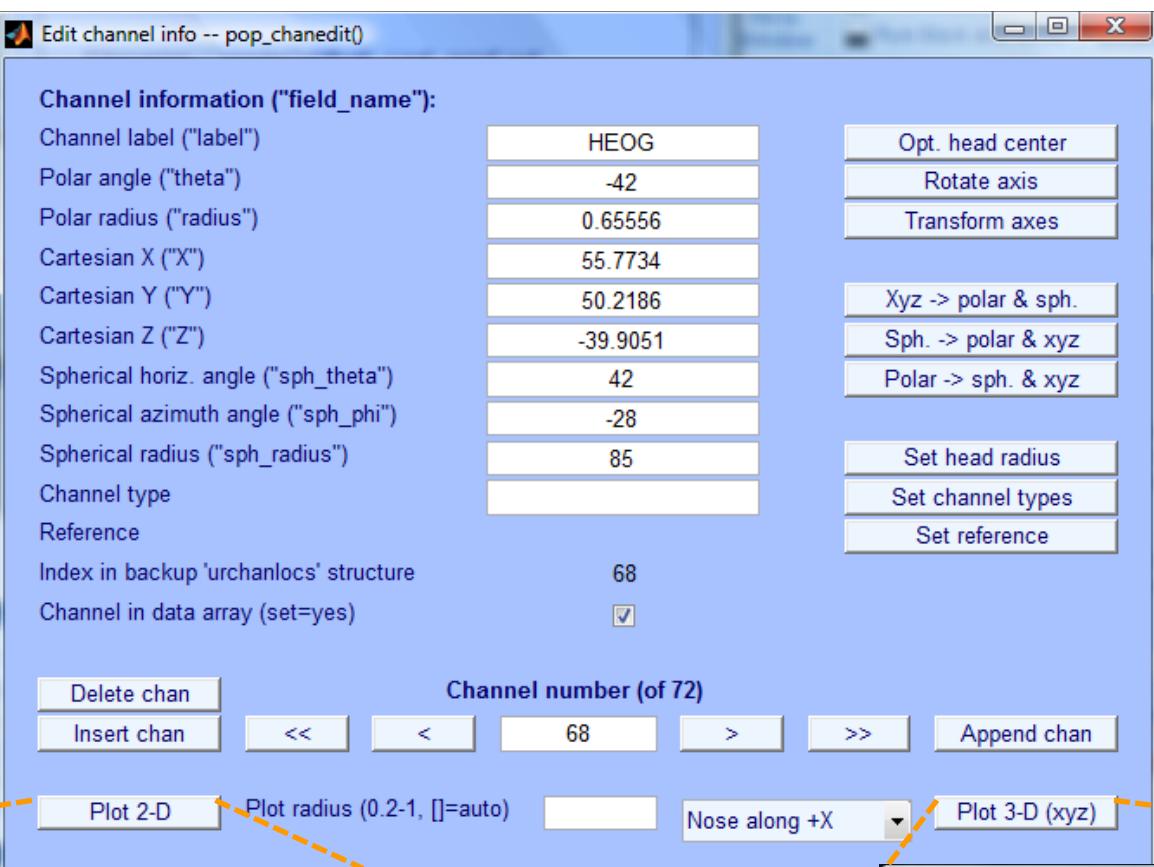
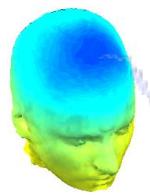
0 X (rotate X-Z plane) Cz Pick

Help Cancel Ok

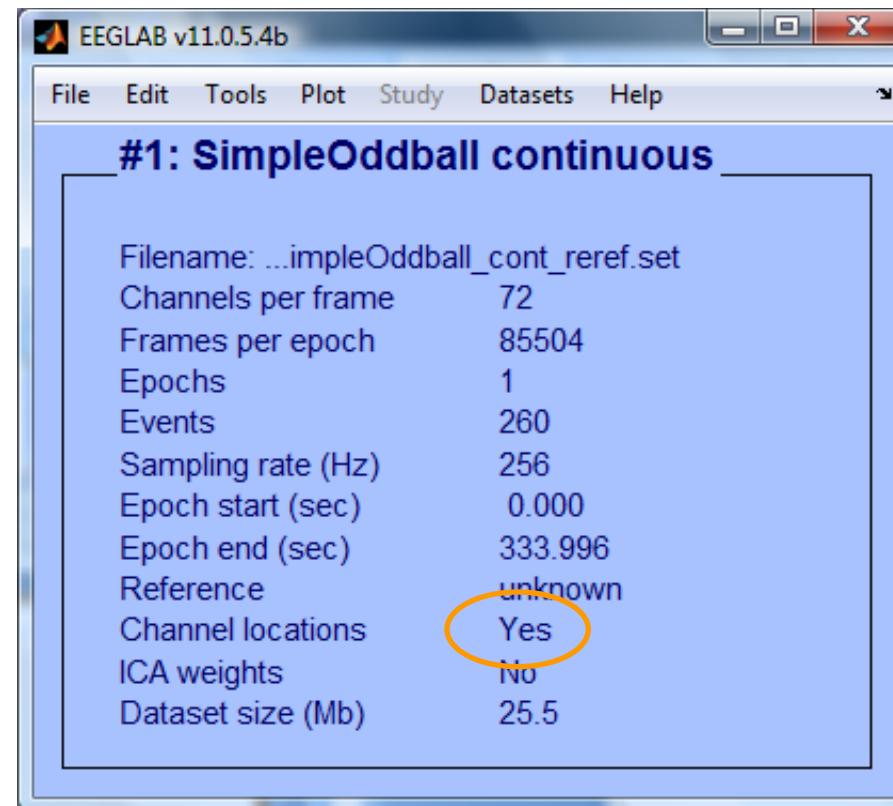
Set channel ...

Channel indices 1:71 Type (e.g. EEG) EEG

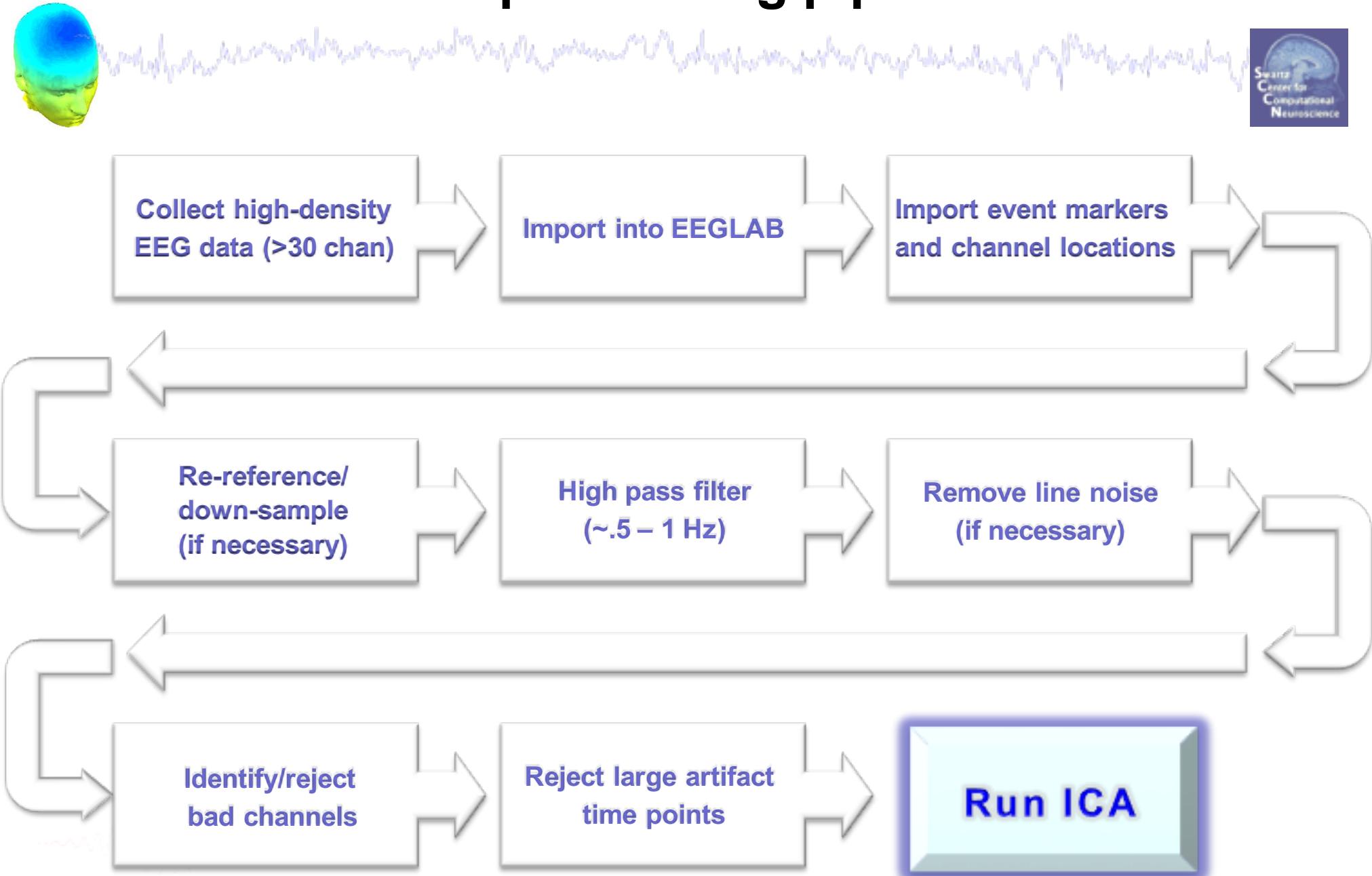
Help Cancel Ok



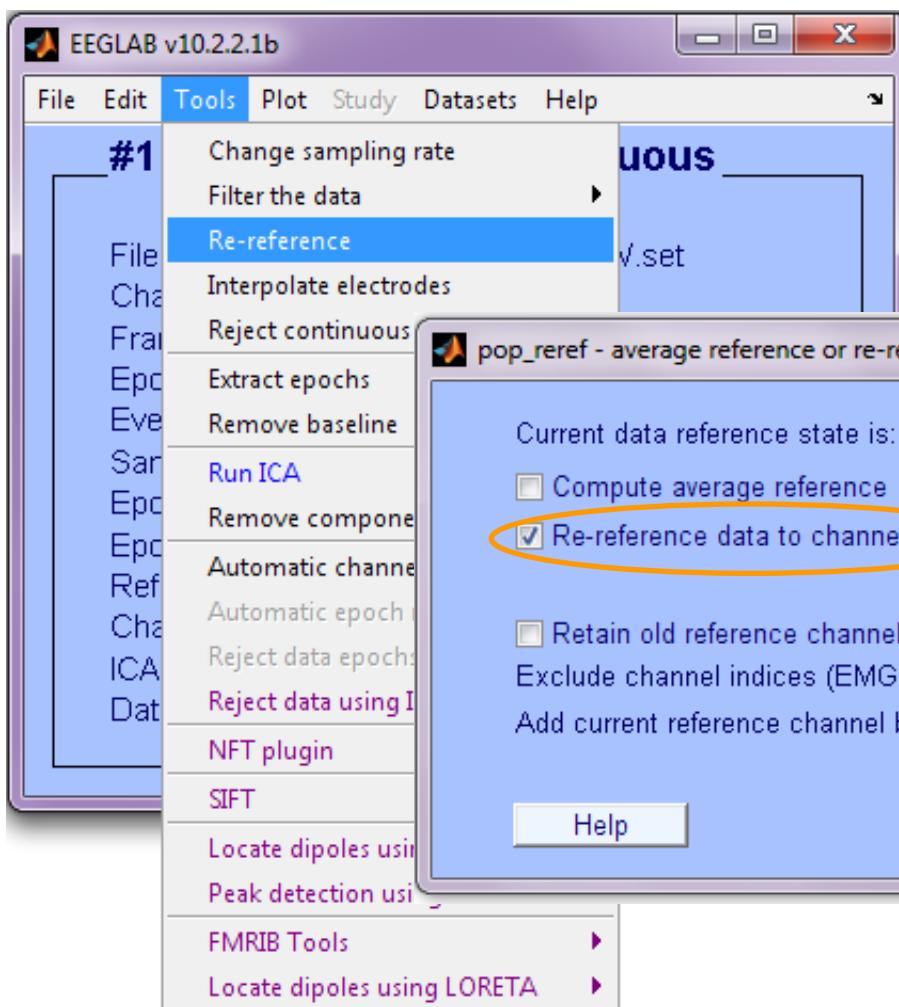
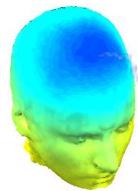
Imported channel locations



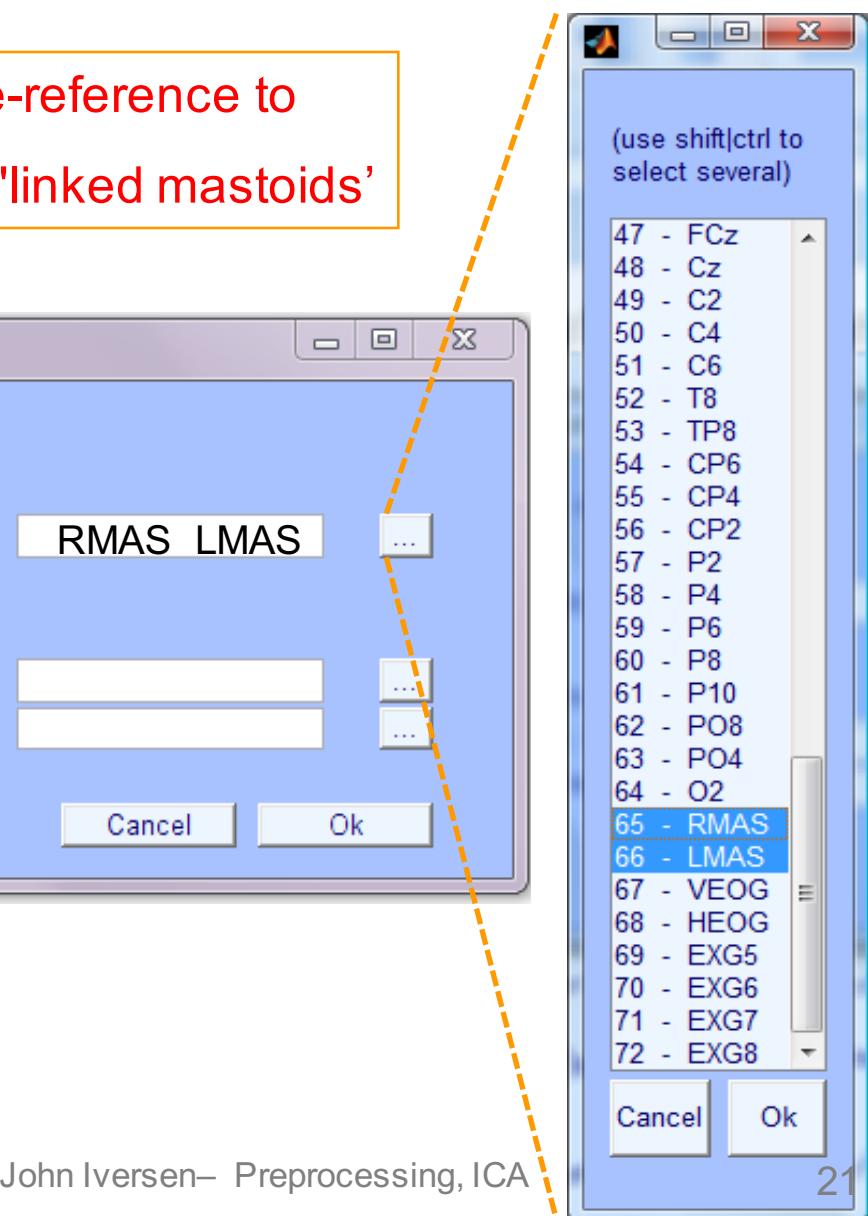
Pre-processing pipeline



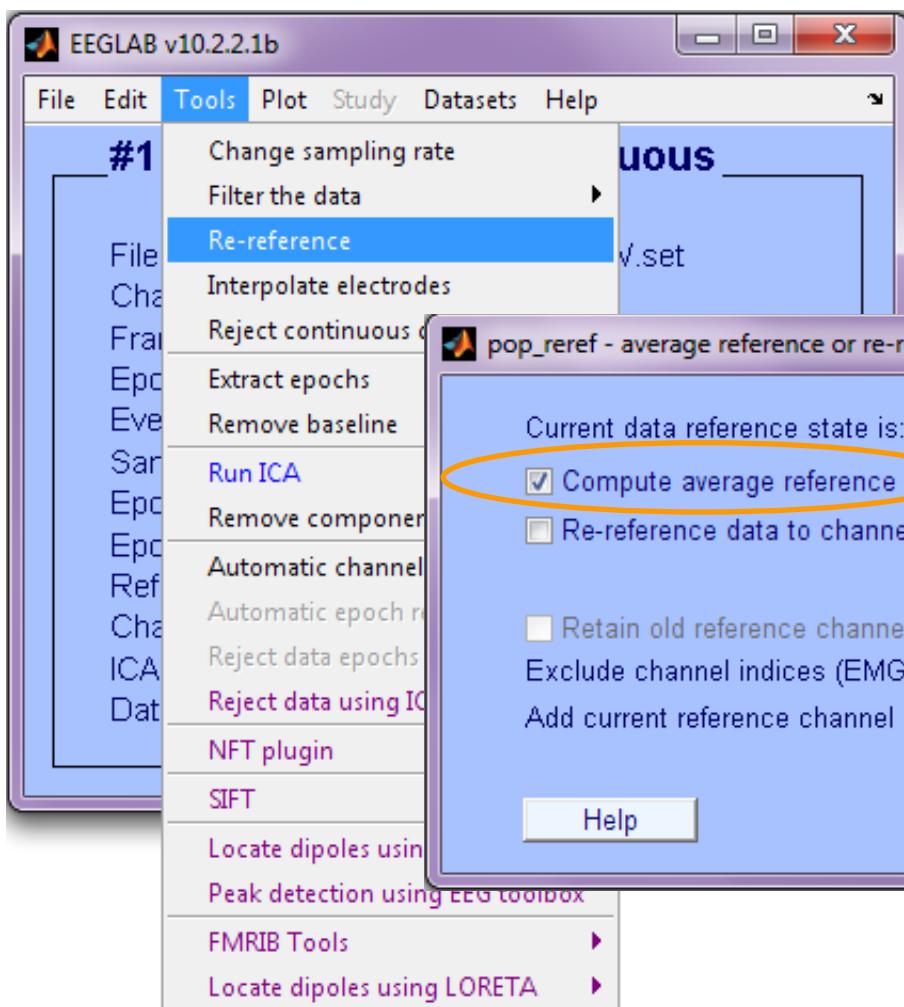
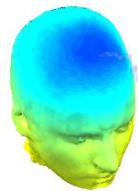
Re-reference data (if necessary/desired)



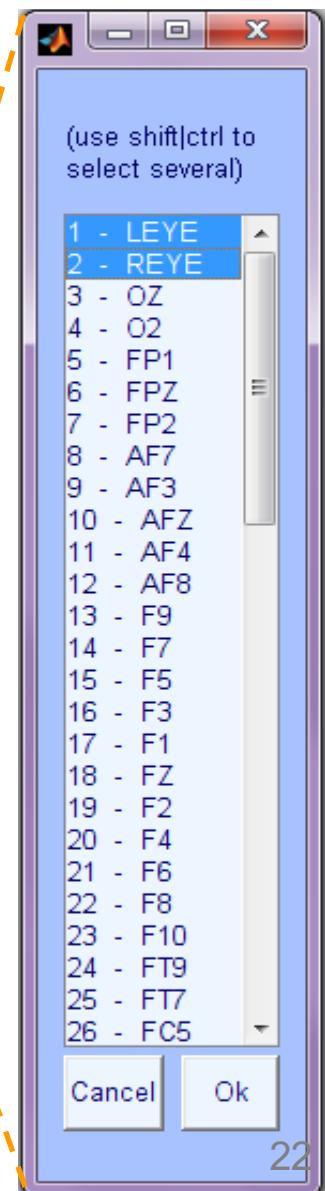
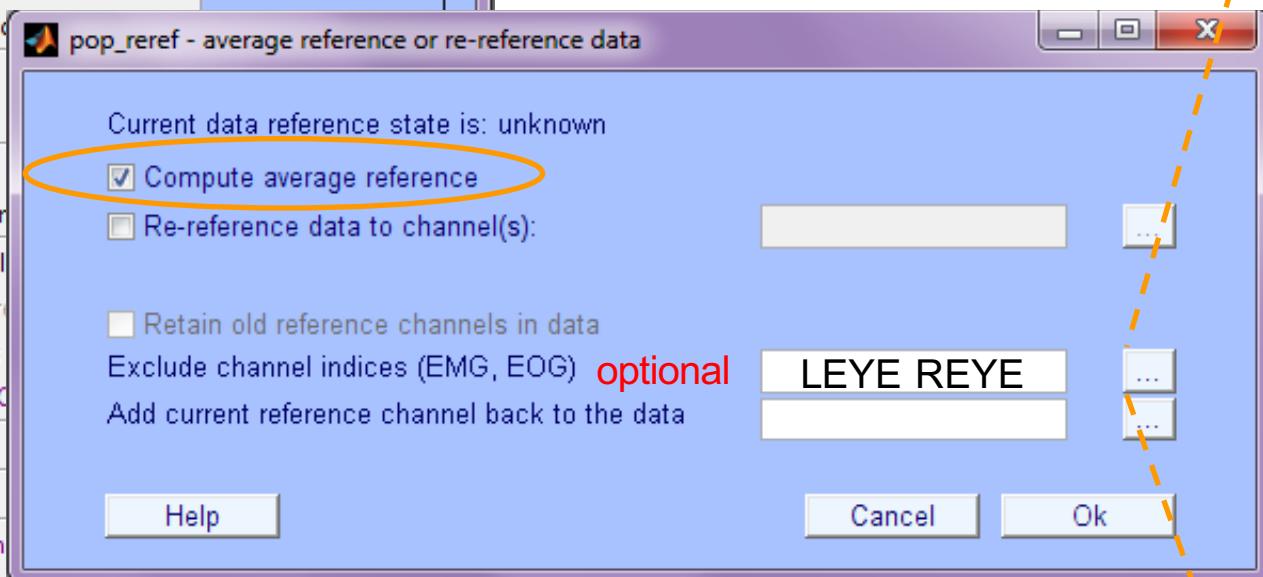
Re-reference to
(e.g.) 'linked mastoids'



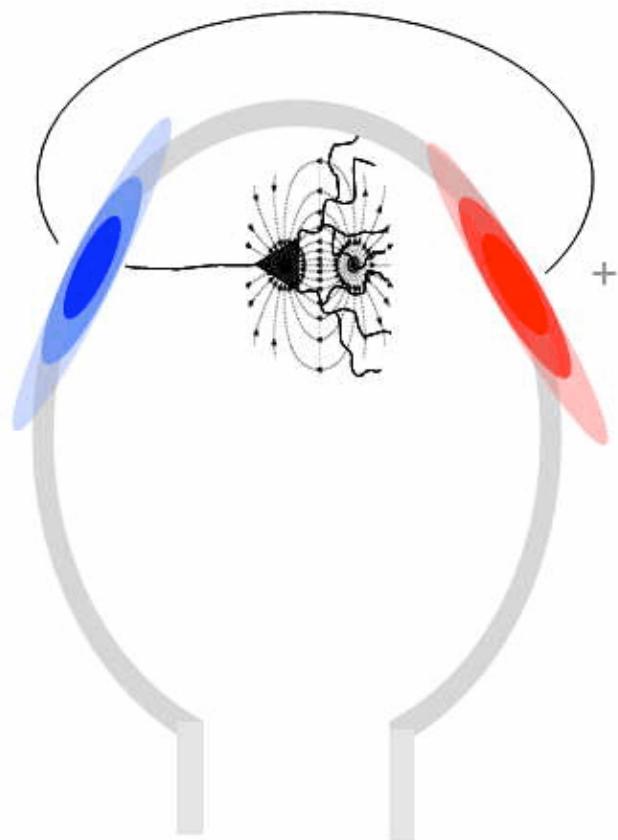
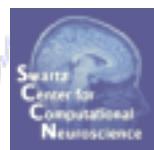
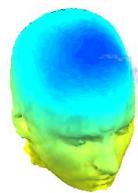
Re-reference data (if necessary/desired)



Or,
average reference



On Average Referencing

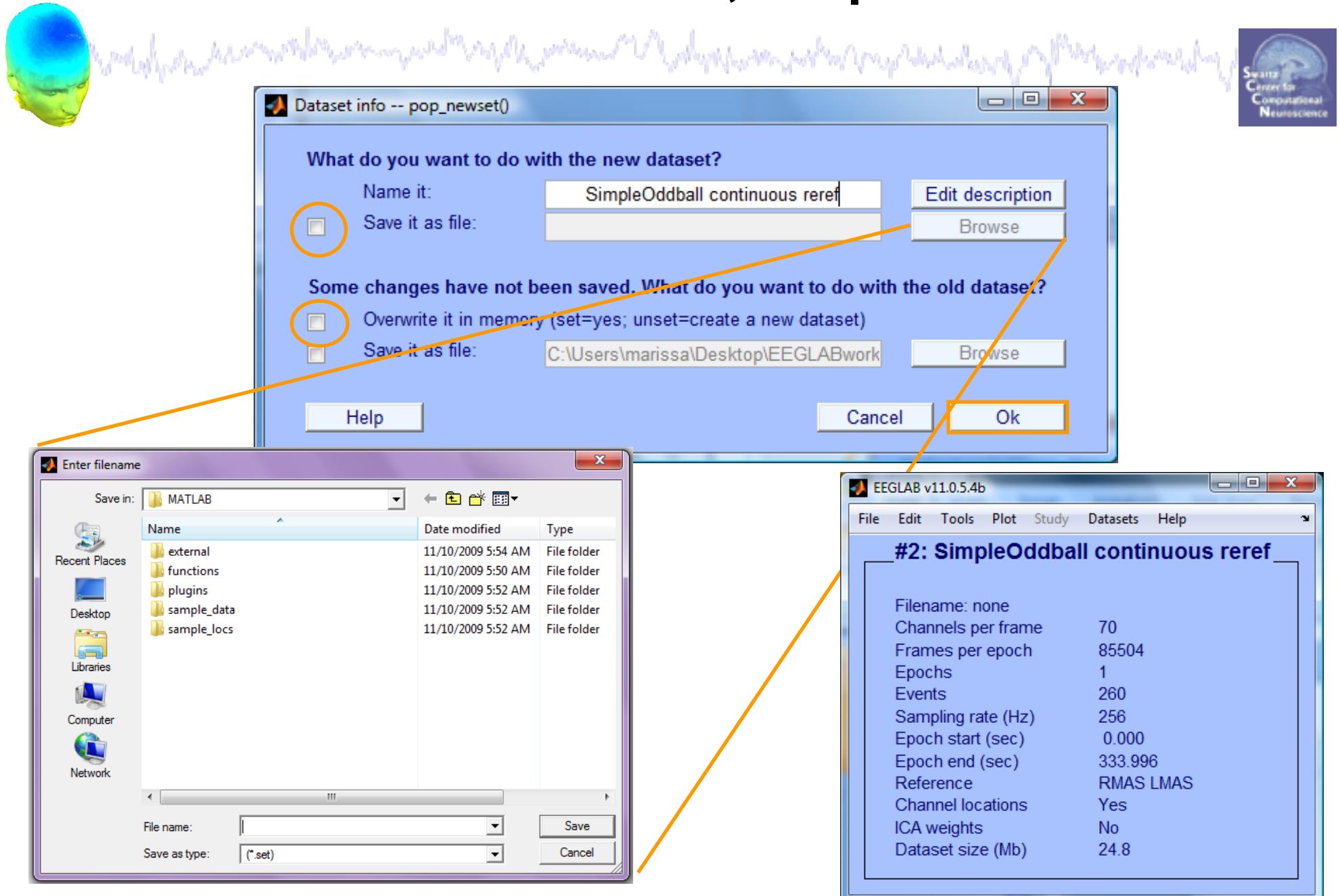


In theory, positive and negative current across entire head should balance—no net current source or sink: Average referencing enforces this.

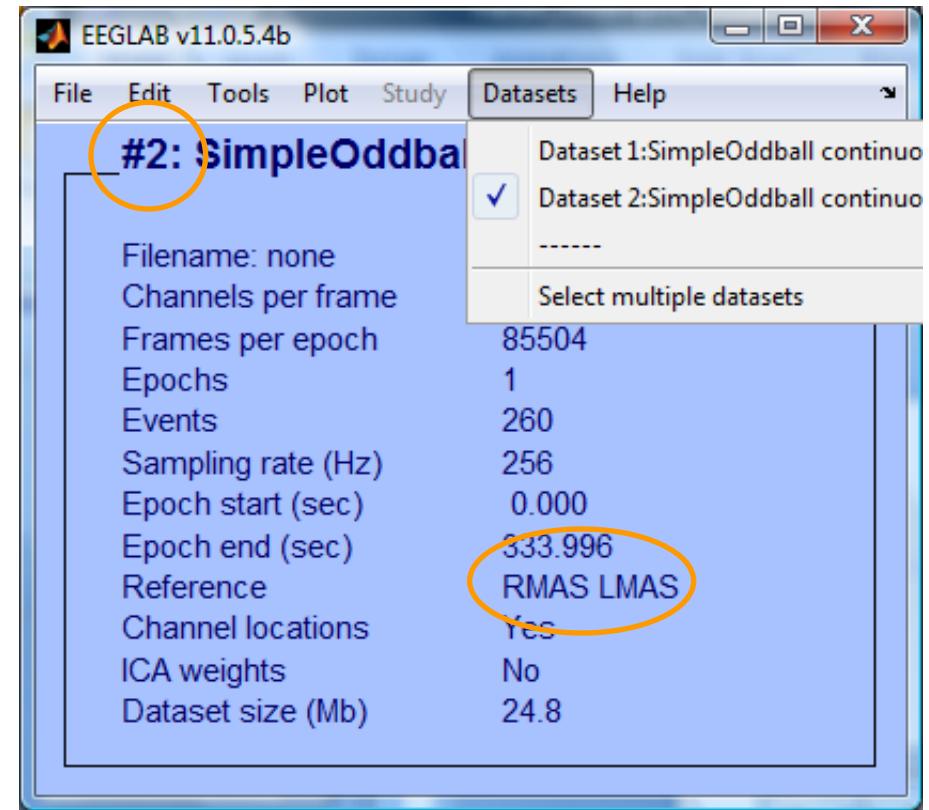
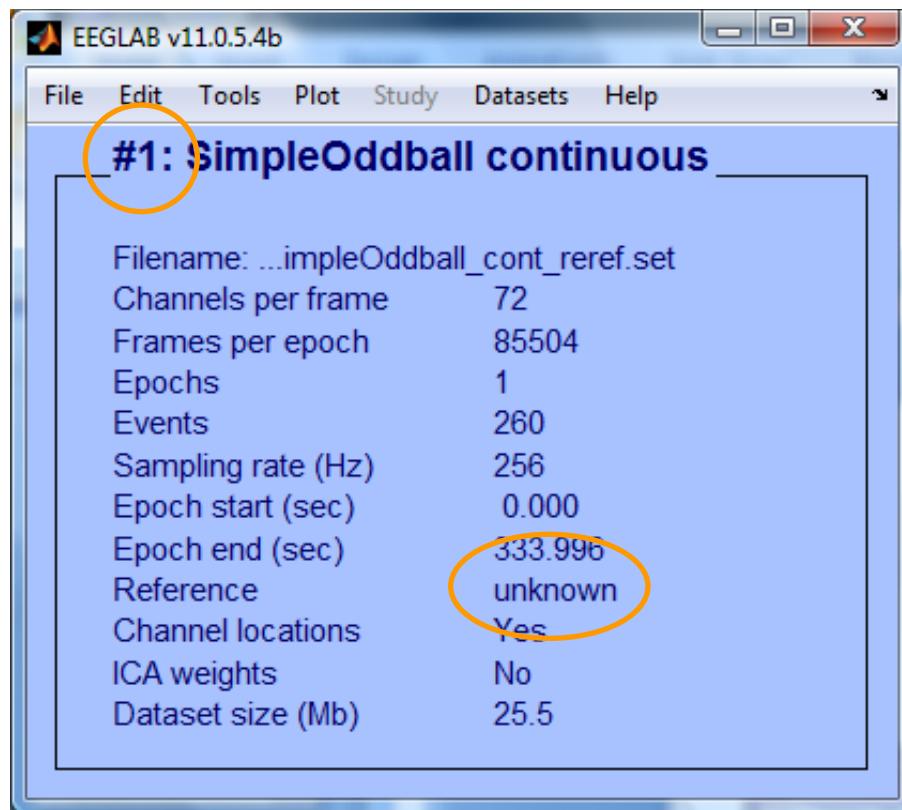
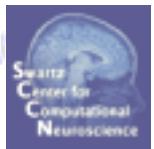
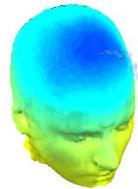
In practice, depends on distribution of electrodes.

Average referencing reduces data rank by 1, so you must remove one channel (Cz often)

Save new dataset, keep old one



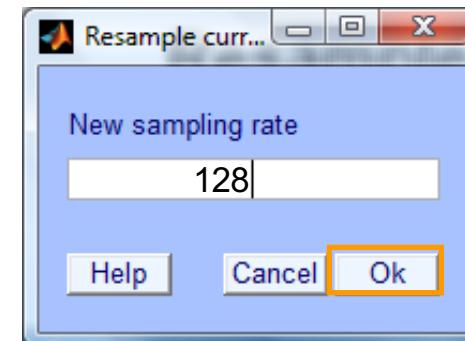
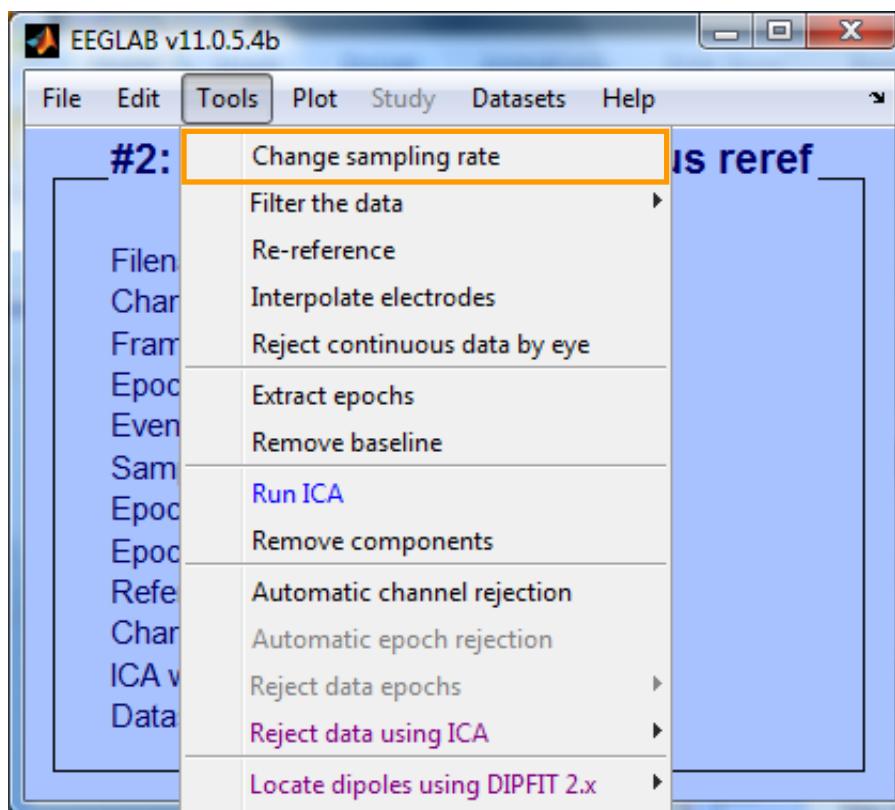
Multiple active datasets (ALLEEG)



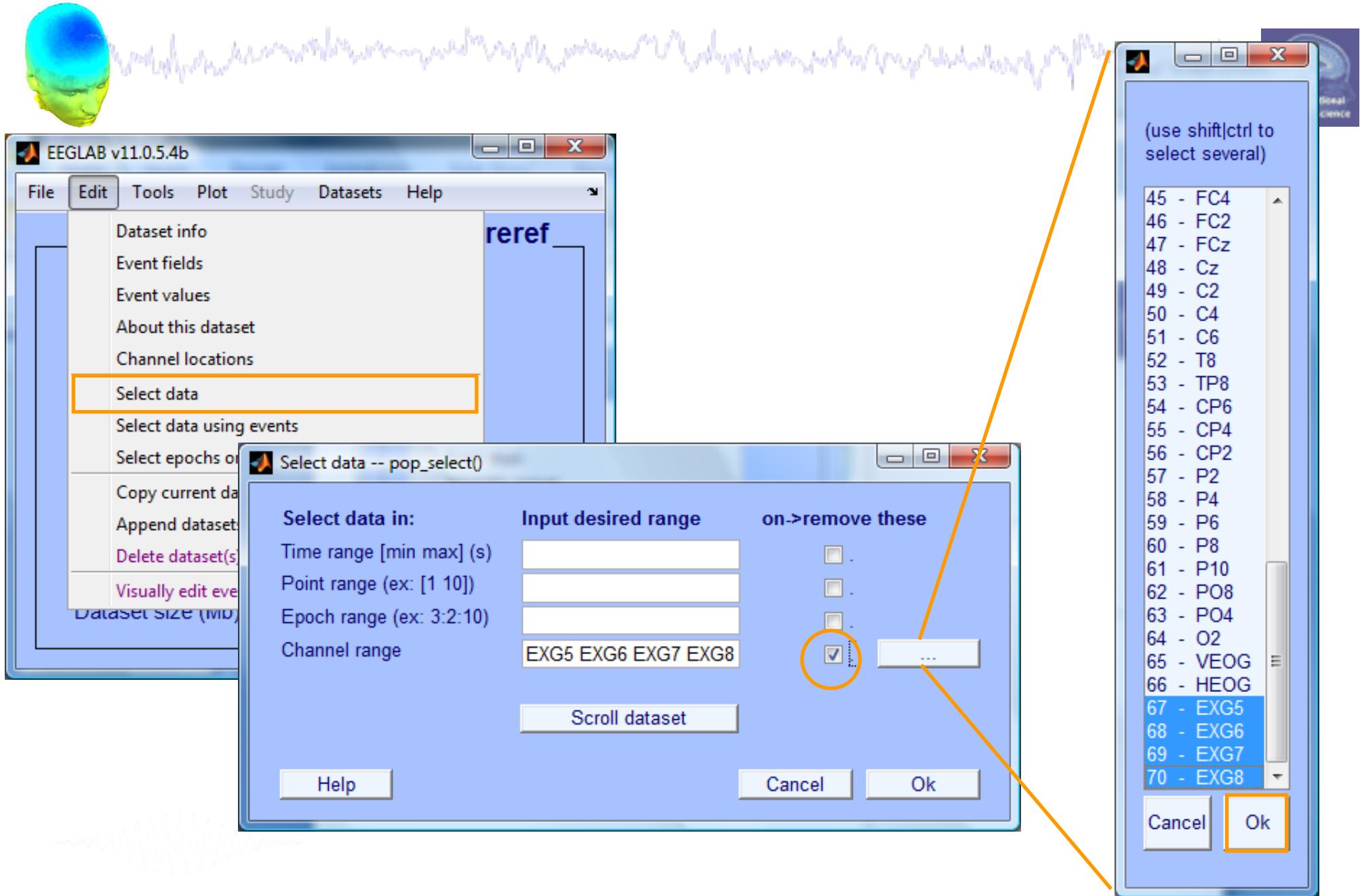
Resample data (if desired)



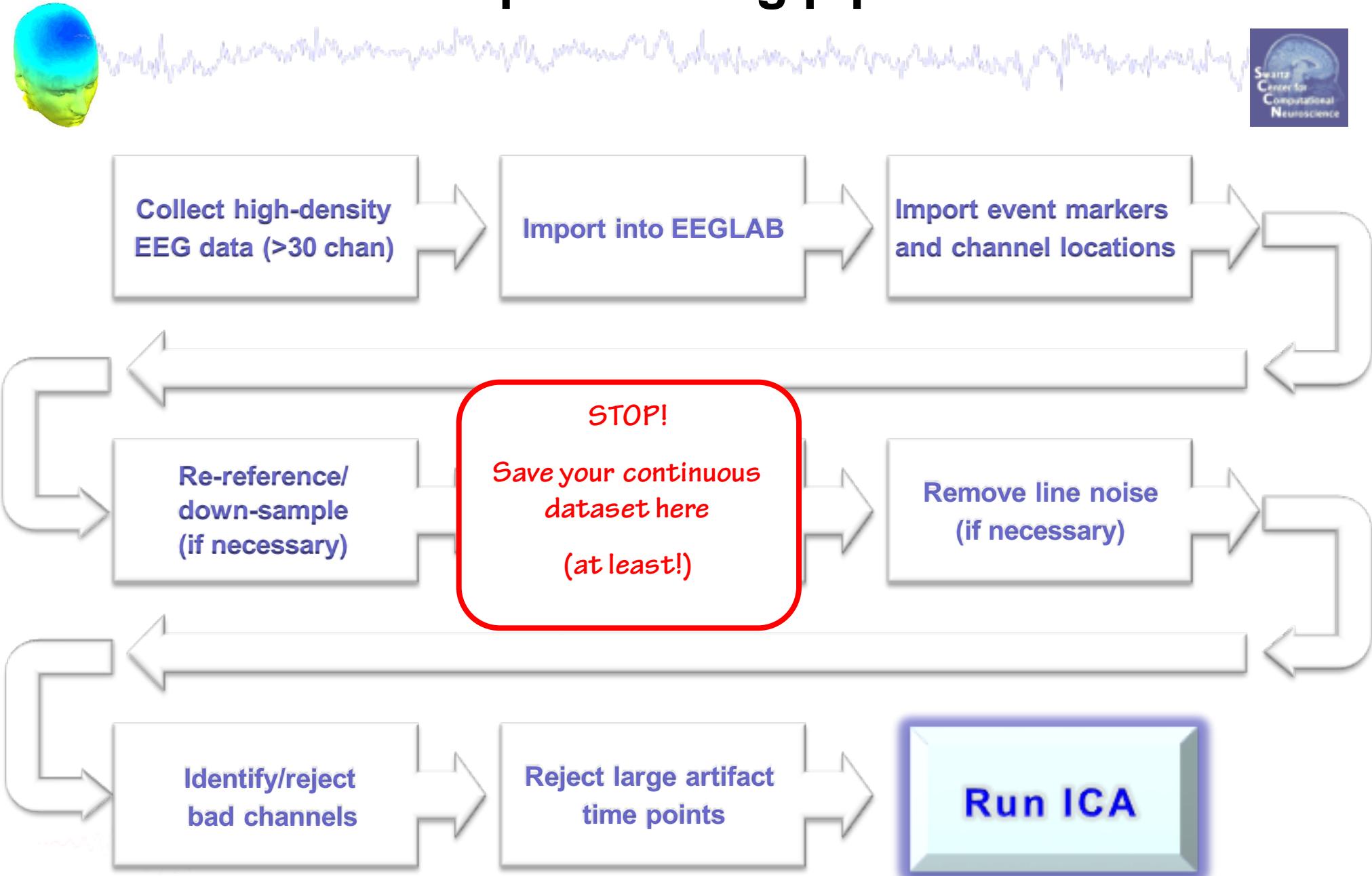
Reason: Reduce space, time. But keep nyquist and ICA data length requirements in mind...



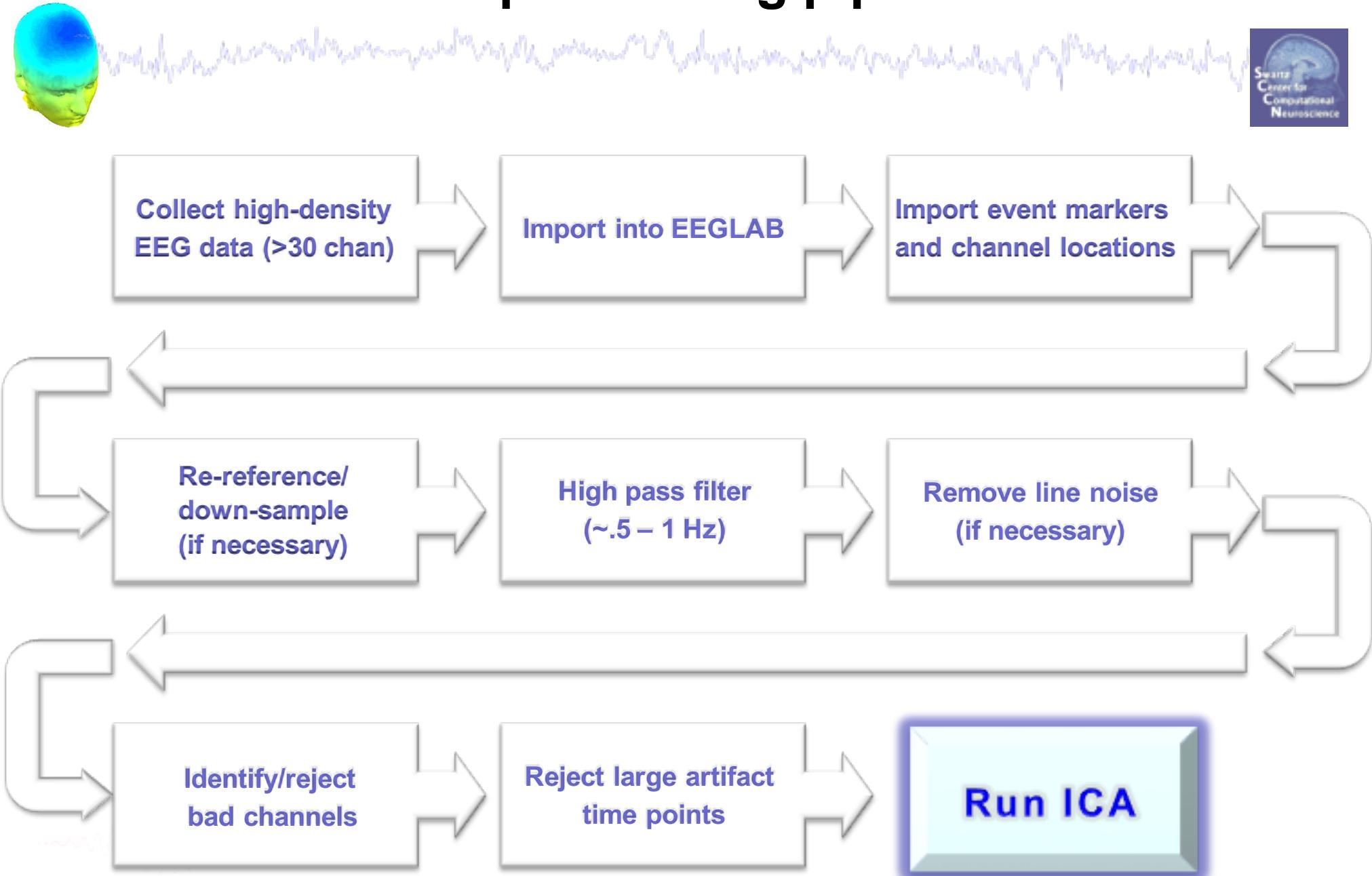
Remove unwanted channels



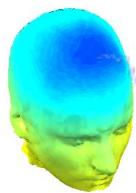
Pre-processing pipeline



Pre-processing pipeline



High-Pass Filter the data



Reason: remove slow, possibly large amplitude, drift

EEGLAB v11.0.5.4b

File Edit Tools Plot Study Datasets Help

#1:

- Change sampling rate
- Filter the data
- Re-reference
- Interpolate electrodes
- Reject continuous data by eye
- Extract epochs
- Remove baseline
- Run ICA
- Remove components
- Automatic channel rejection
- Automatic epoch rejection
- Reject data epochs
- Reject data using ICA
- Locate dipoles using DIPFIT 2.x
- Peak detection using EEG toolbox
- FMRIB Tools
- Locate dipoles using LORETA
- CleanLine

Filter the data -- pop_eegfilt()

Lower edge of the frequency pass band (Hz)
Higher edge of the frequency pass band (Hz)
FIR Filter order (default is automatic)

Notch filter the data instead of pass band
 Use (sharper) FFT linear filter instead of FIR filtering
(Use the option above if you do not have the Signal Pro
 Use causal filter (useful when performing causal ana
 Plot the filter frequency response
 Use fir1 (check, recommended) or firls (uncheck, leg
Help Cancel Ok

Dataset info -- pop_newset()

What do you want to do with the new dataset?
Name it: SimpleOddball hipass0.5 Edit description
 Save it as file: Browse

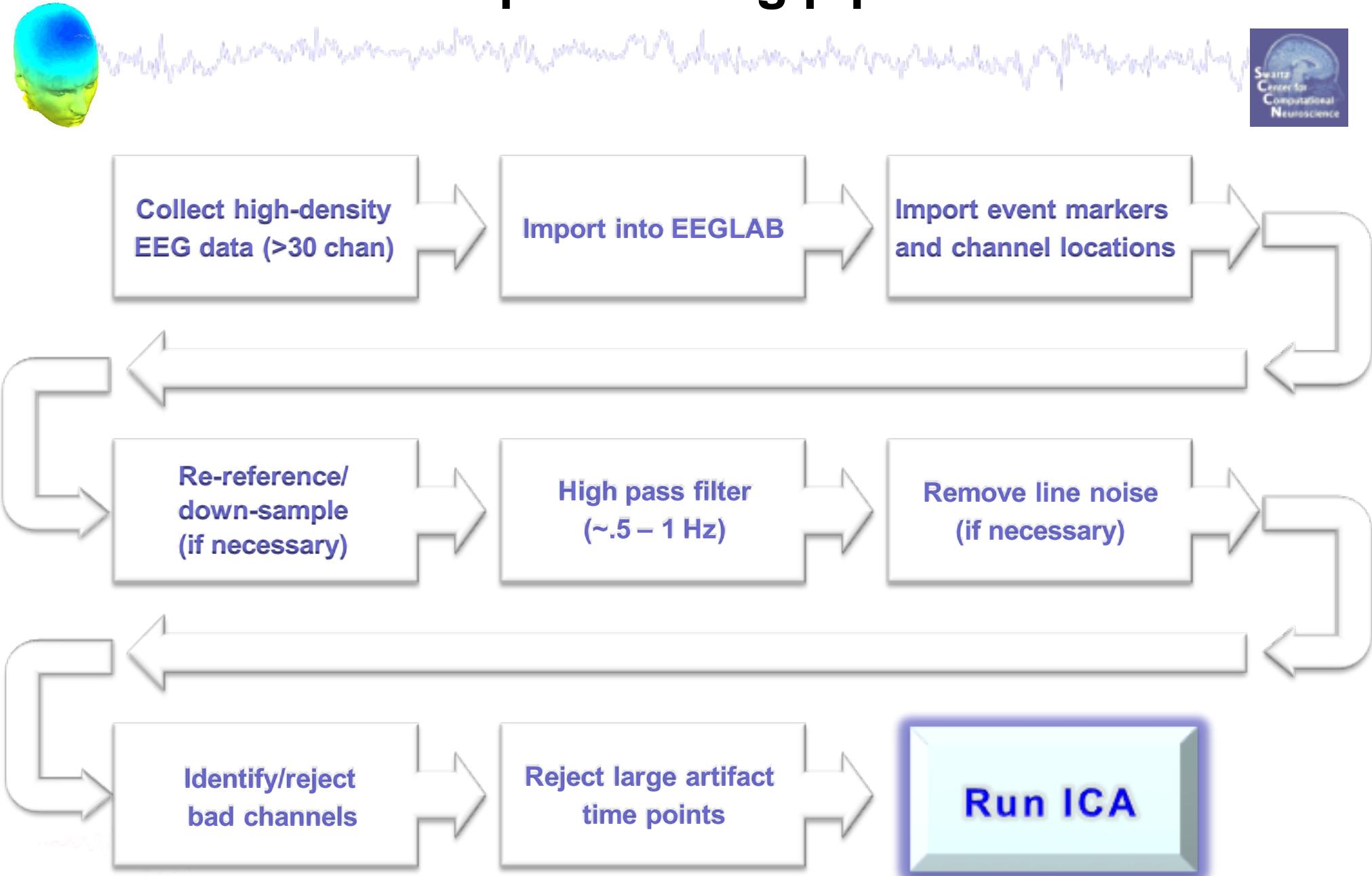
What do you want to do with the old dataset (not modified since last saved)?
 Overwrite it in memory (set=yes; unset=create a new dataset)

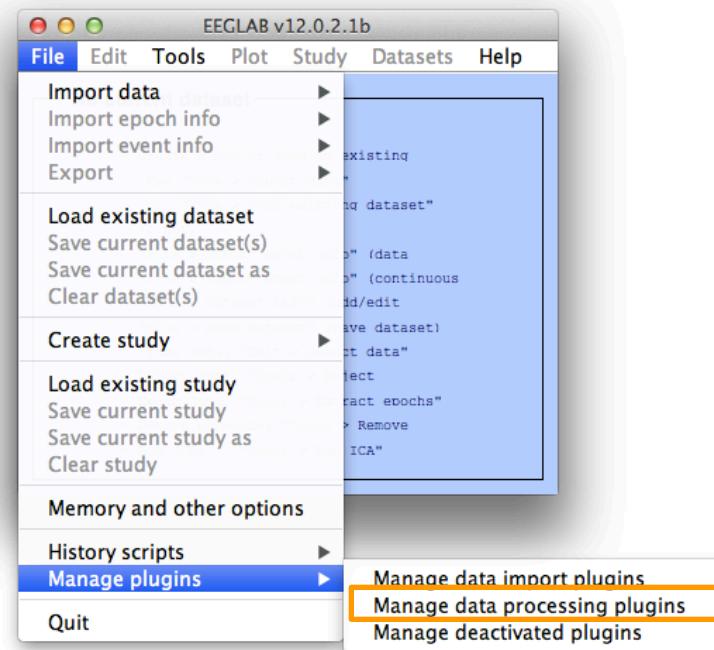
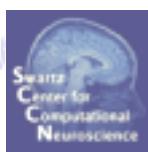
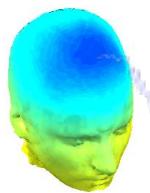
Help Cancel Ok

EEGLAB Workshop XX, Sept 2-5, 2015, Sheffield, England –John Iversen– Preprocessing, ICA

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Pre-processing pipeline





Plutings available for install on the internet

Install	Plugin	Version	Description	Doc
<input type="checkbox"/>	ERPLABfilters	1.00	Interface ERPLAB filters (requires separate ERPLAB installation)	<input type="button" value="Doc"/>
<input checked="" type="checkbox"/>	Cleanline	1.21	Automatic artifact rejection	<input type="button" value="Doc"/>
<input type="checkbox"/>	BERGEN	1.1	Removal of fMRI-related gradient artifacts from simultaneous...	<input type="button" value="Doc"/>

Update Deactivate

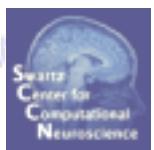
Installed plutings

Plugin	Version	Description	Doc
brainmovie	0.1	Brainmovies (command line only)	<input type="button" value="Doc"/>
corrmap	2.00	New version 1.03 available. Click update to install.	<input type="button" value="Doc"/>
eeg_toolbox	1.0	Interface EEG toolbox functions for ERP peak detection	<input type="button" value="Doc"/>
fMRIb	1.21	Remove fMRI artifacts from EEG	<input type="button" value="Doc"/>
MP_clustering	1.00	Measure projection clustering of ICA components	<input type="button" value="Doc"/>
MutualInfoClustering	1.00	Mutual information clustering	<input type="button" value="Doc"/>
StudyEnvtopo	0.9	Add envtopo capabilities to STUDY	<input type="button" value="Doc"/>
VisEd	1.05	New version 1.04 available. Click update to install.	<input type="button" value="Doc"/>
iirfilt	1.02	Non linear filtering	<input type="button" value="Doc"/>
loreta	1.1	New version 1.0 available. Click update to install.	<input type="button" value="Doc"/>

EEGLAB Workshop XX, Sept 2-5, 2015, Sheffield, England –John Iverson—Preprocessing, ICA

Cancel Ok

Remove line noise (Cleanline)

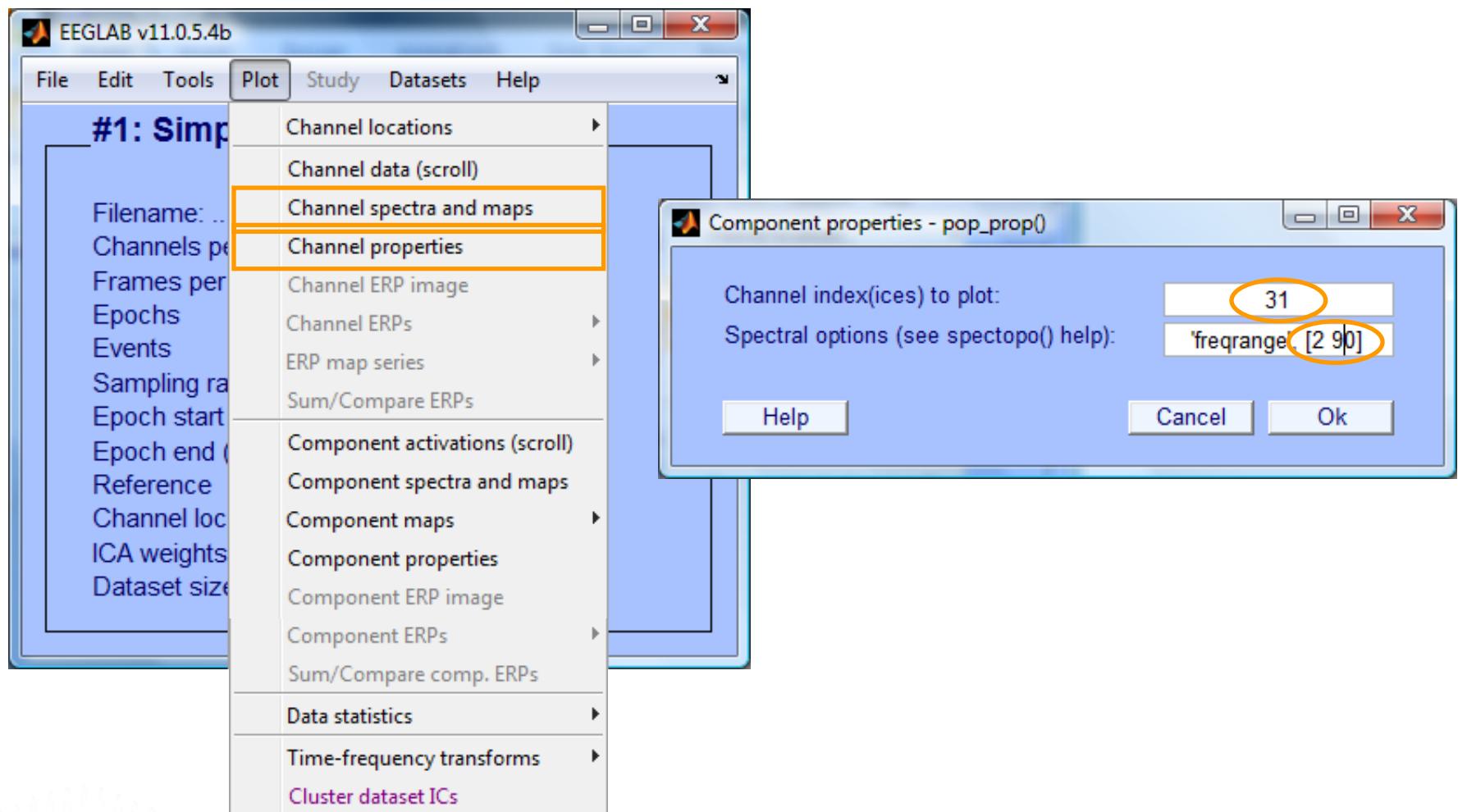
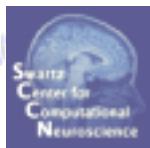


The screenshot shows the EEGLAB software interface. The main window title is "EEGLAB v11.0.5.4b". The "Tools" menu is open, and the "CleanLine" option is highlighted with a yellow box. A second window titled "CleanLine Options" is overlaid on the main window. This dialog box contains various parameters for signal cleaning:

- Line noise frequencies to remove: [60 120] (circled in orange)
- Scan for line noise: (set)
- p-value for detection of significant sinusoid: 0.01
- Bandwidth (Hz): 2
- Channels: '1:66' (dropdown menu)
- Type of signal to clean: 4 (circled in orange)
- Indices of Channels/Components to clean: 2 (circled in orange)
- Sliding window length (sec): 100
- Sliding window step size (sec): 2
- Window overlap smoothing factor: 2
- FFT padding factor: 4
- Visualize Original and Cleaned Spectra: (set) (with a red arrow pointing to it from a "check" box)
- Normalize log spectrum by detrending: (set)
- Produce verbose output: (set)
- Plot Individual Figures: (set)

At the bottom of the dialog box are "Help", "Cancel", and "Ok" buttons.

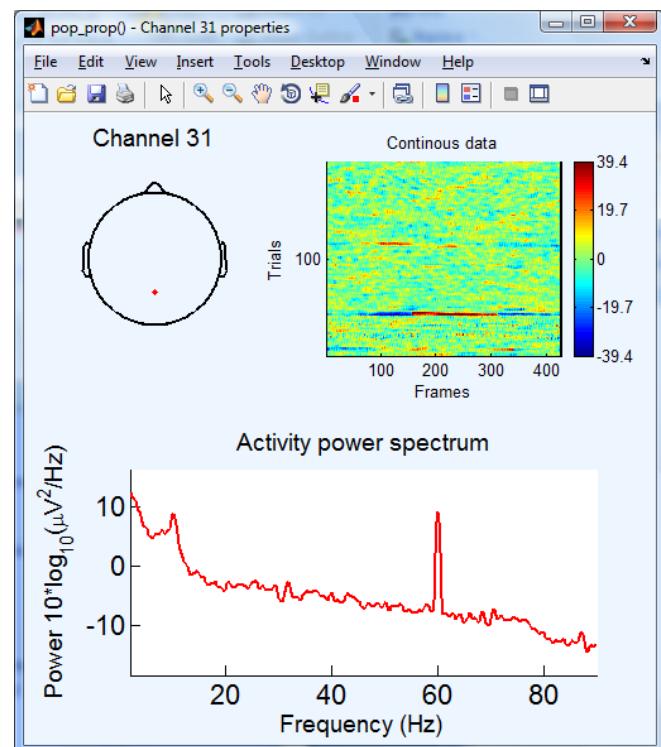
Plot channel spectra



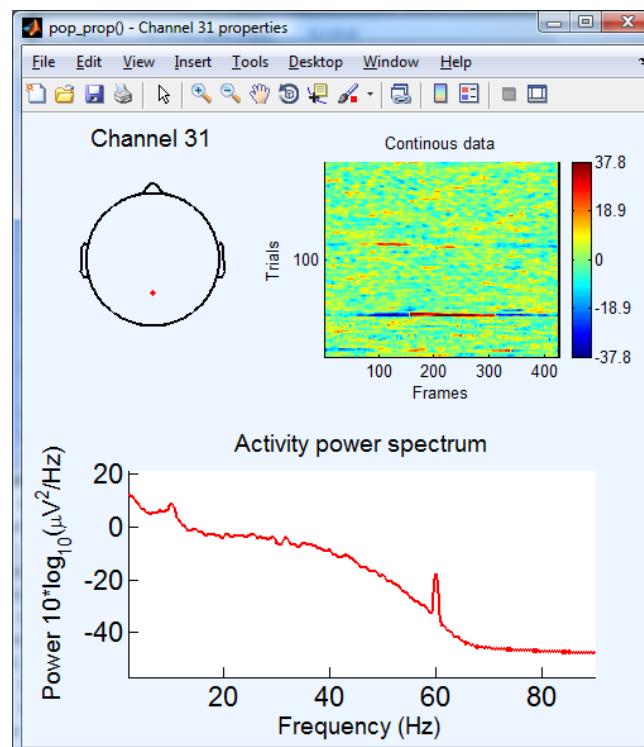
Filter comparisons



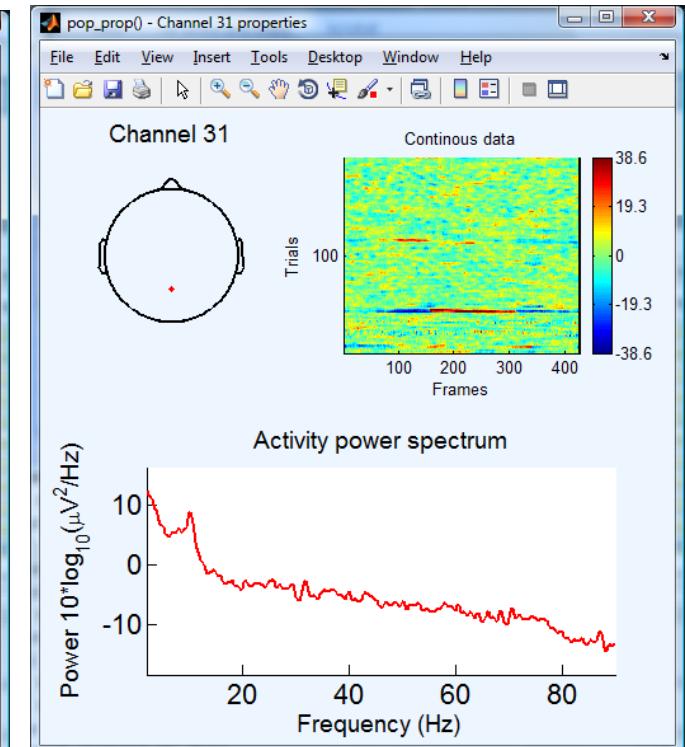
0.5 Hz high-pass filter



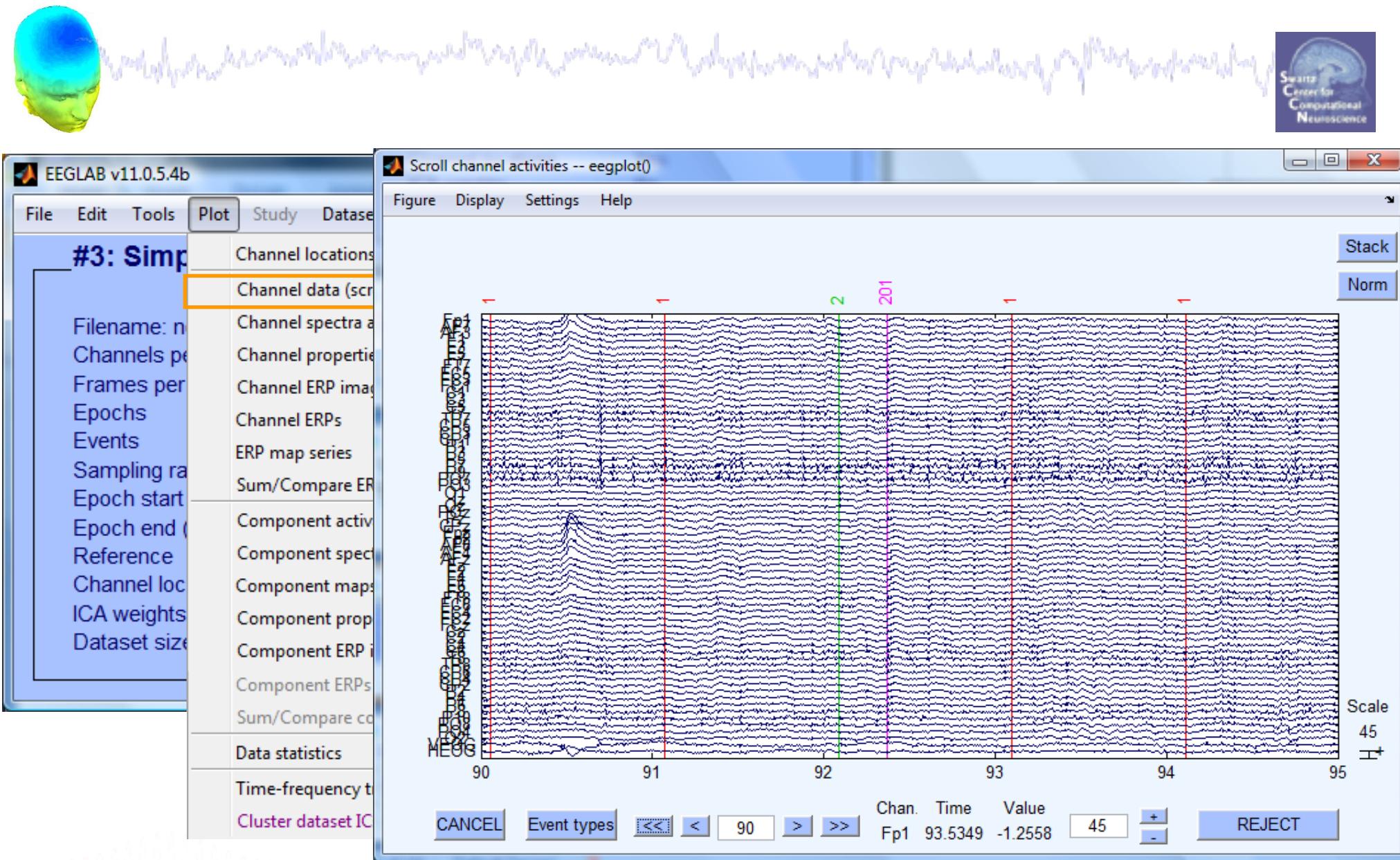
0.5 Hz high-pass filter
50 Hz low-pass filter



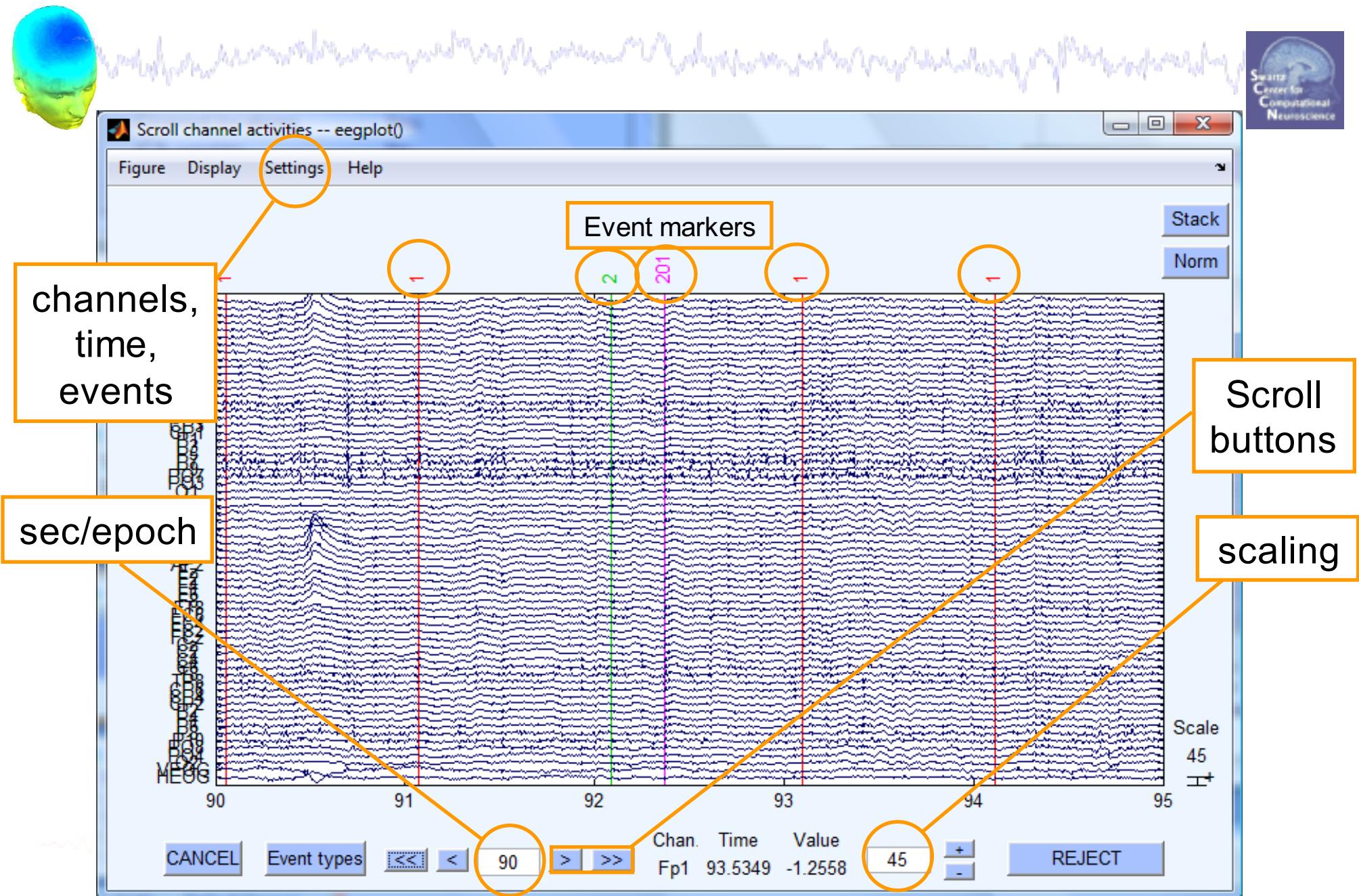
0.5 Hz high-pass filter
Cleanline



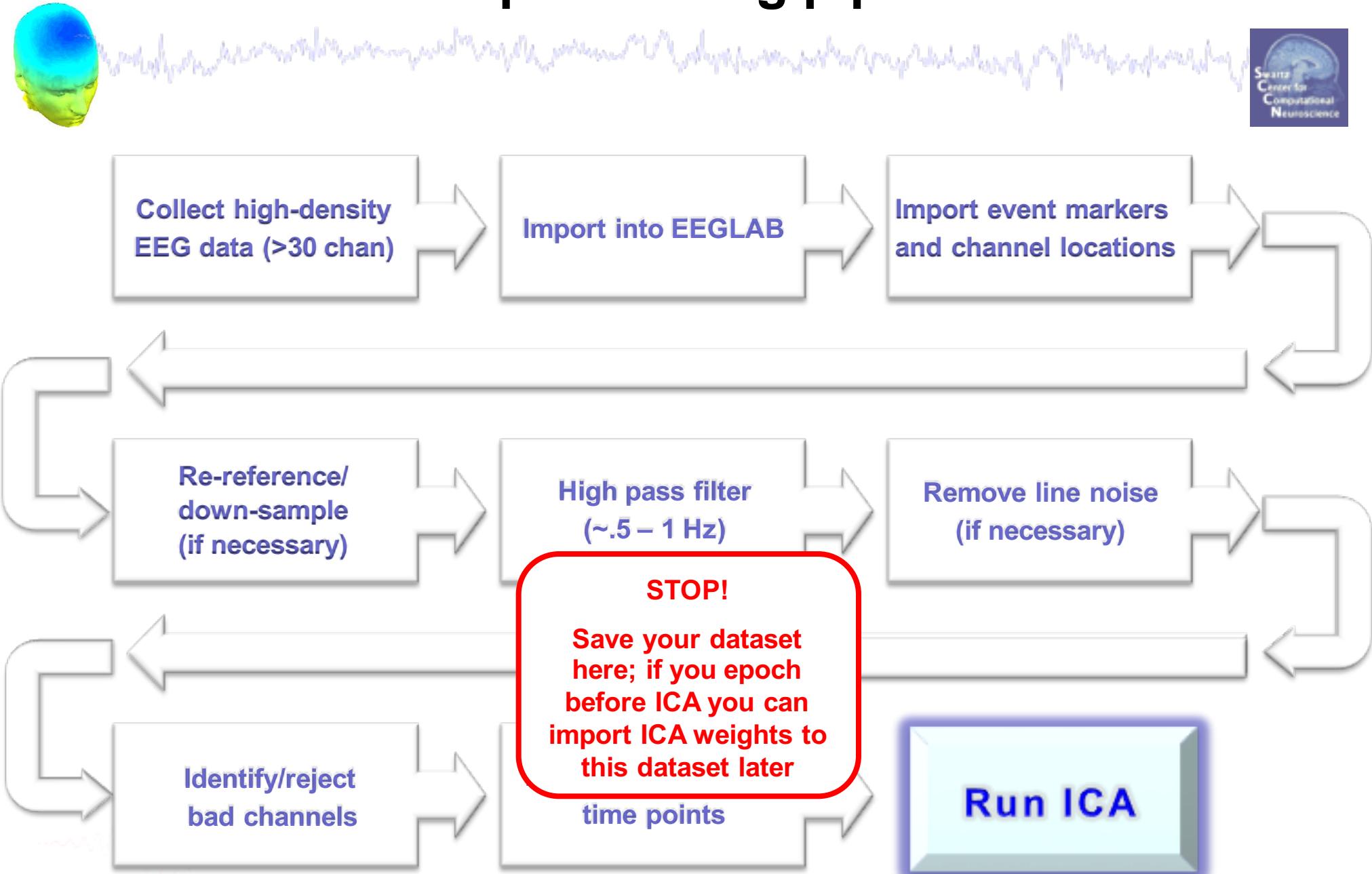
Scroll channel data

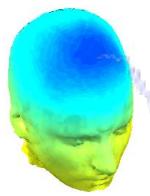


Scroll channel data



Pre-processing pipeline

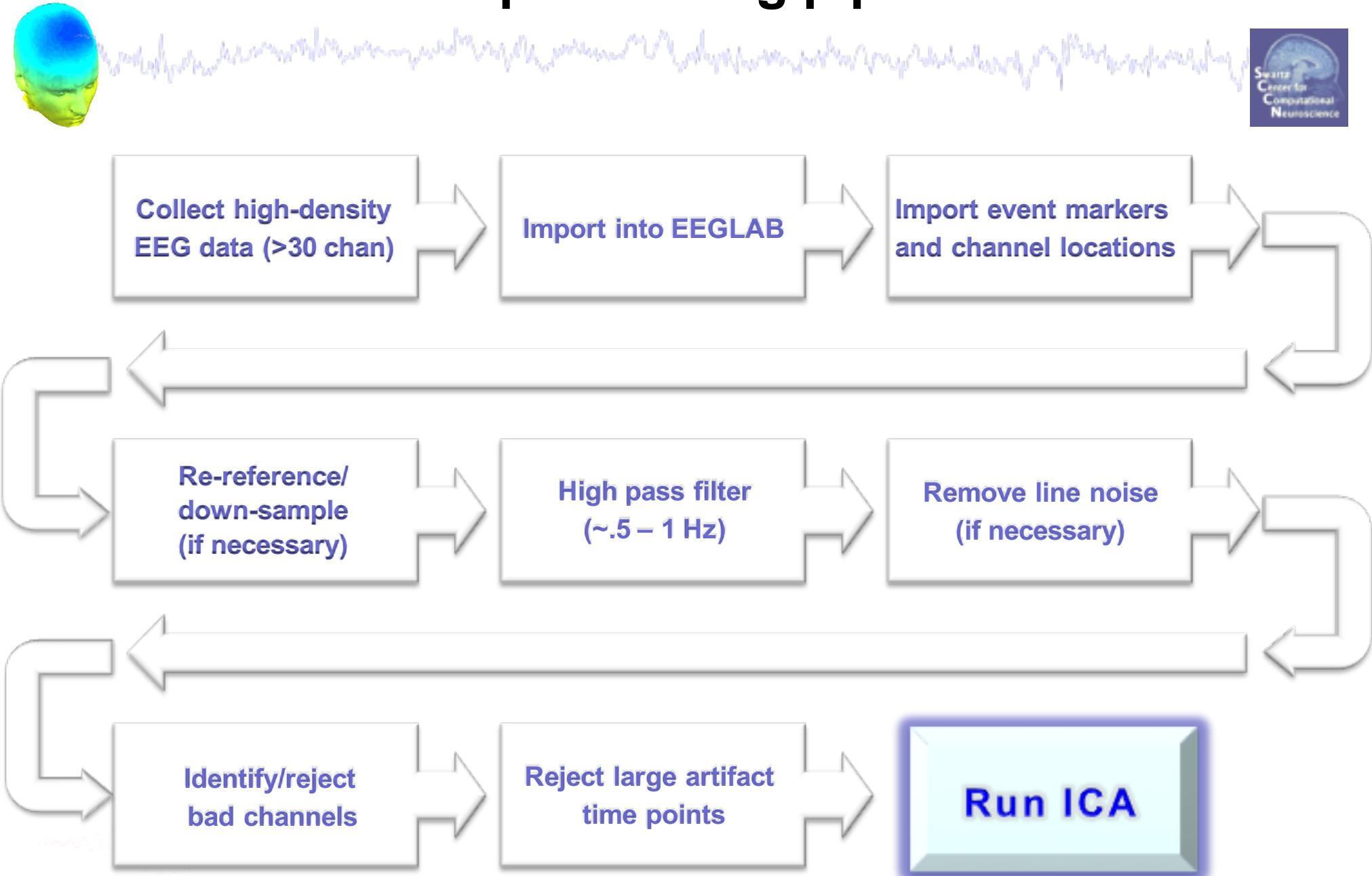




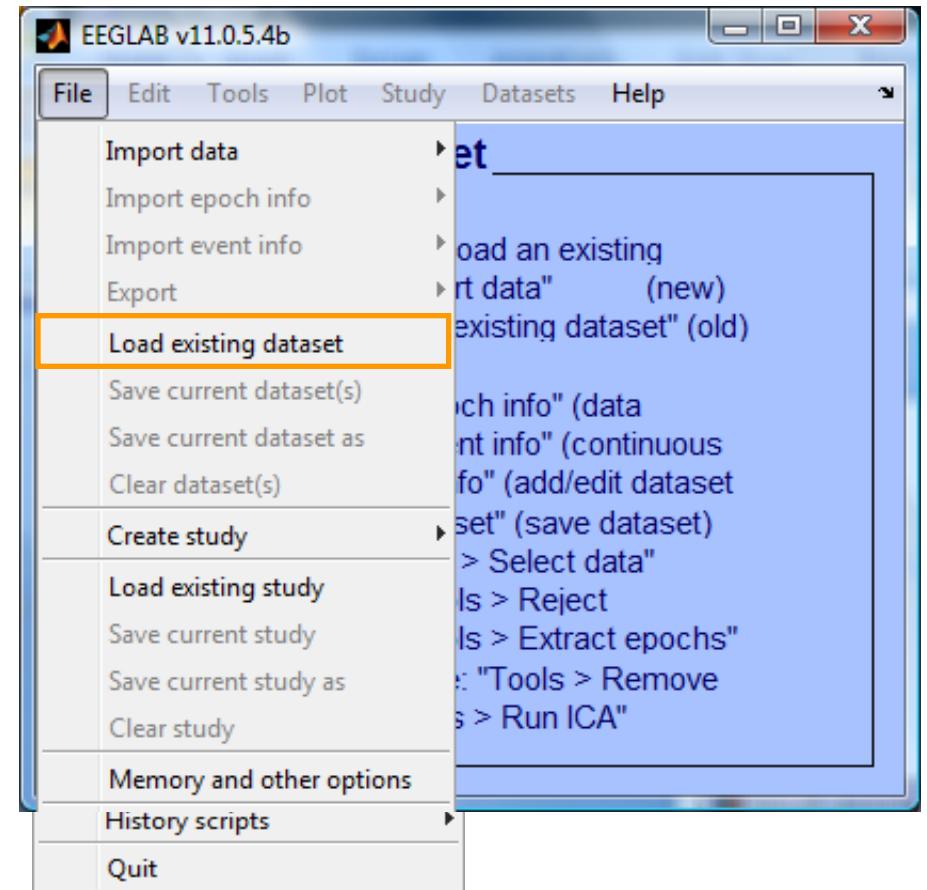
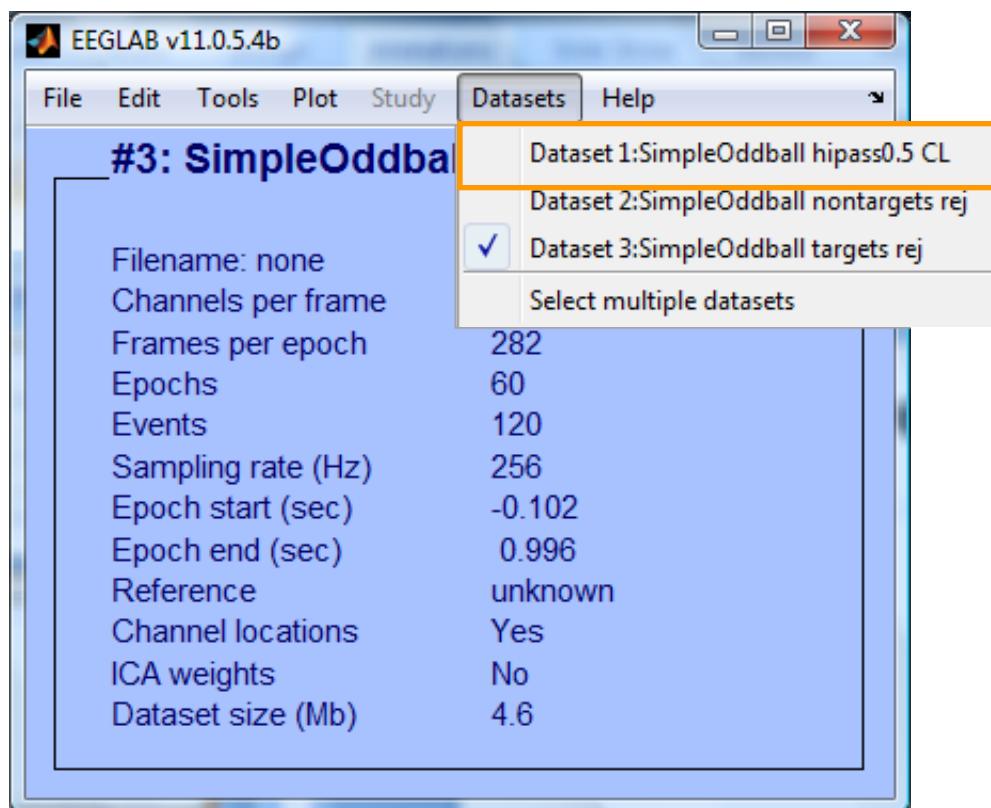
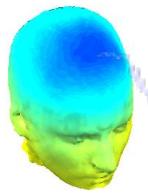
Data Cleaning for ICA

Variant 1: Continuous Data

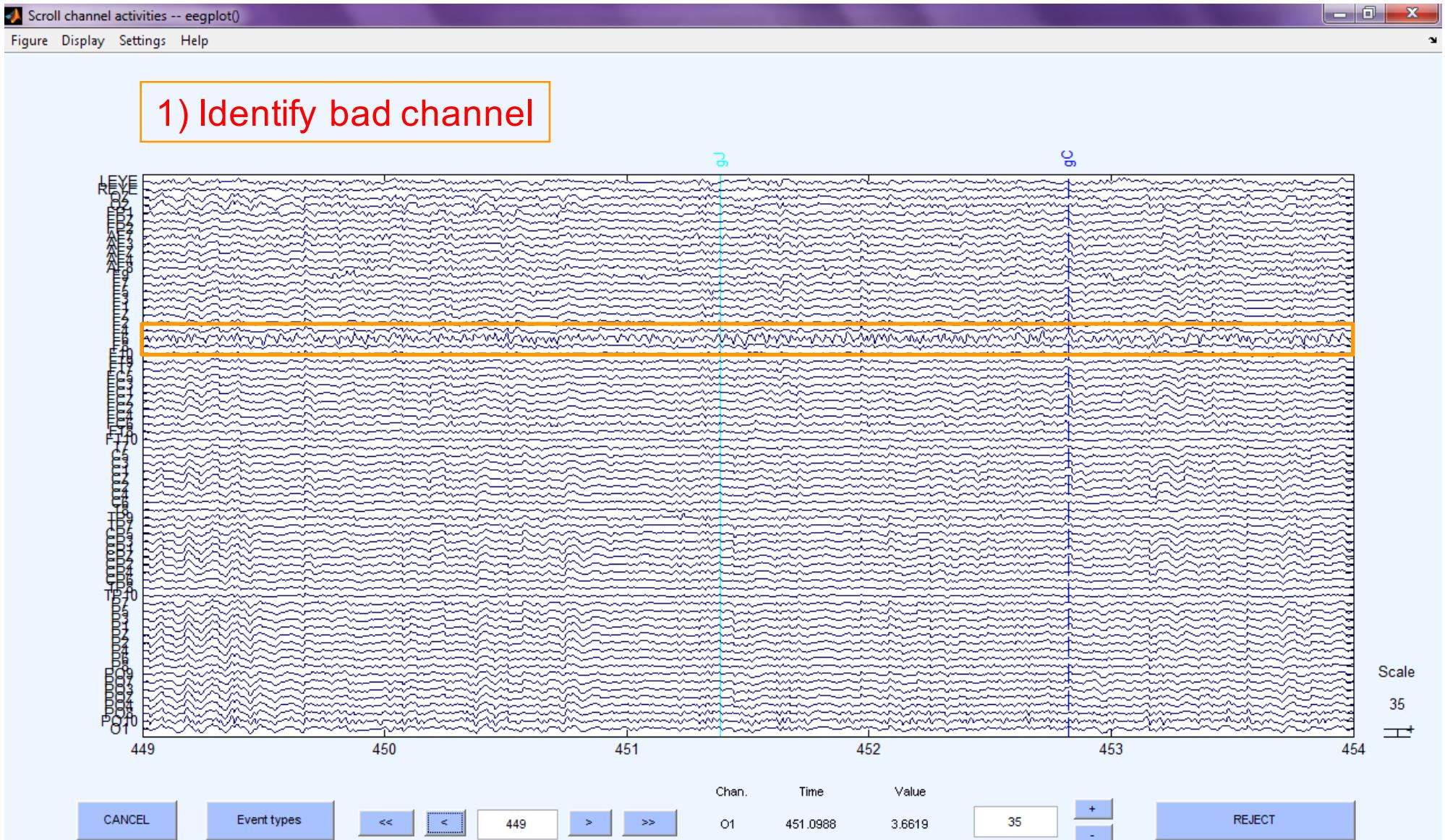
Pre-processing pipeline



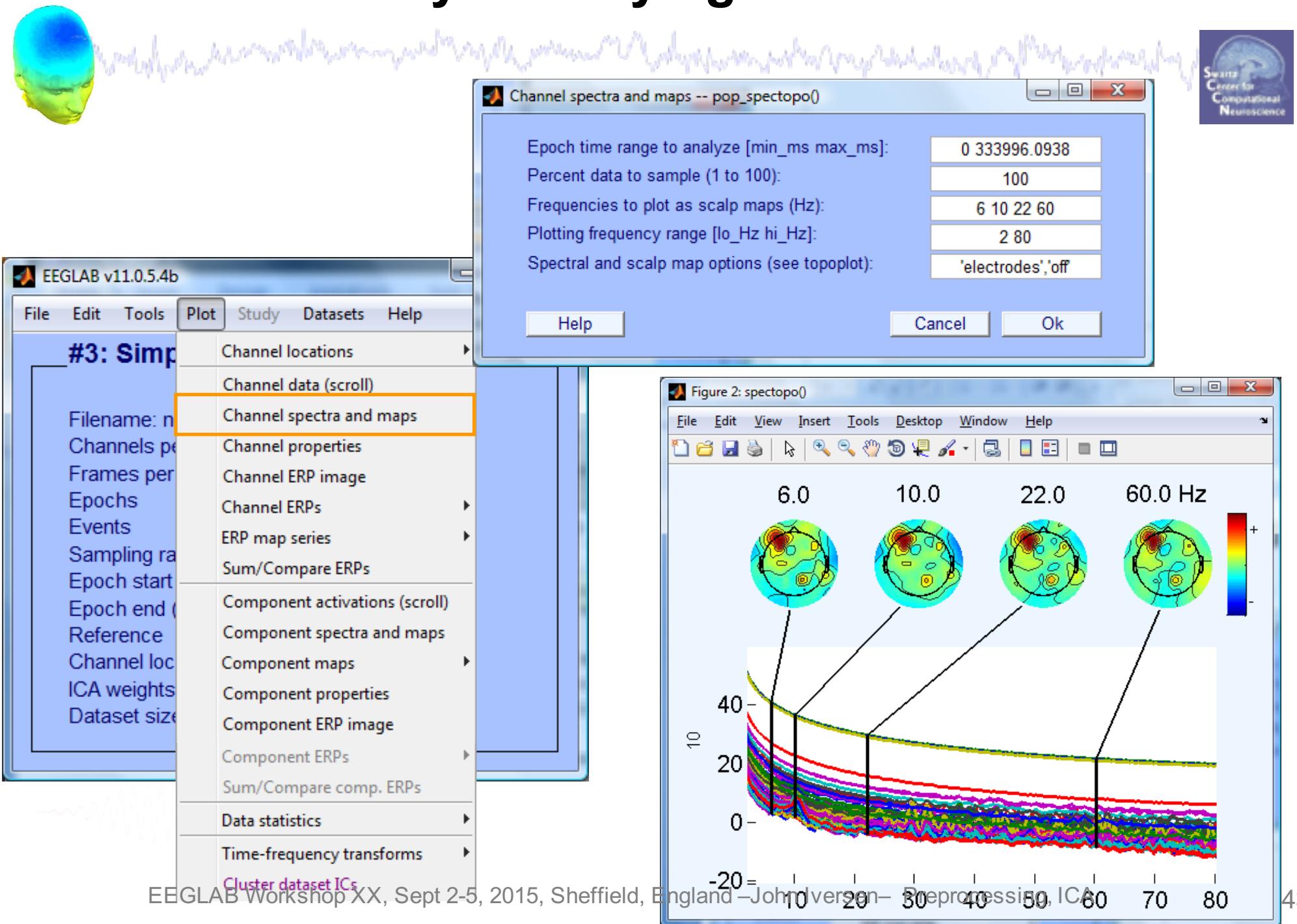
Retrieve or reload continuous EEG dataset



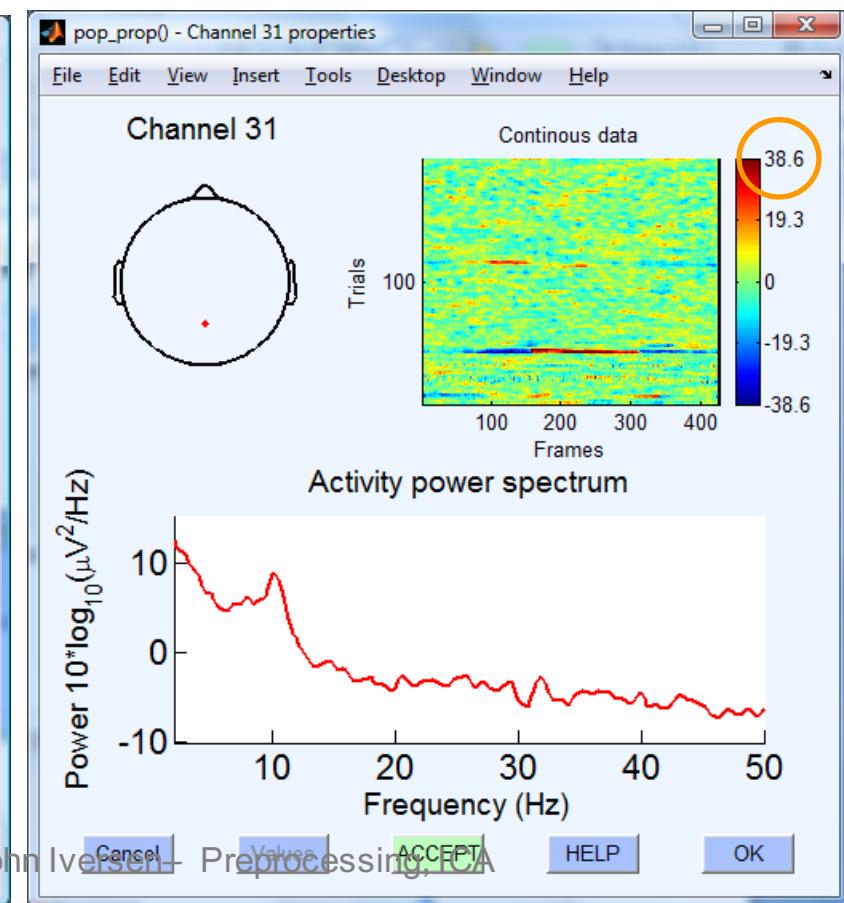
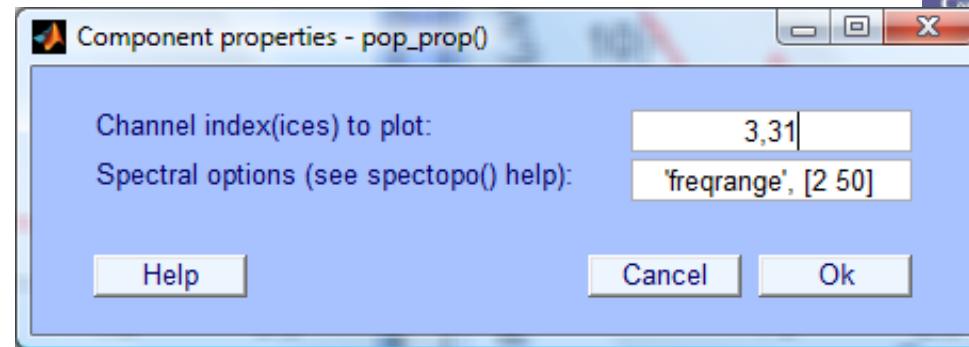
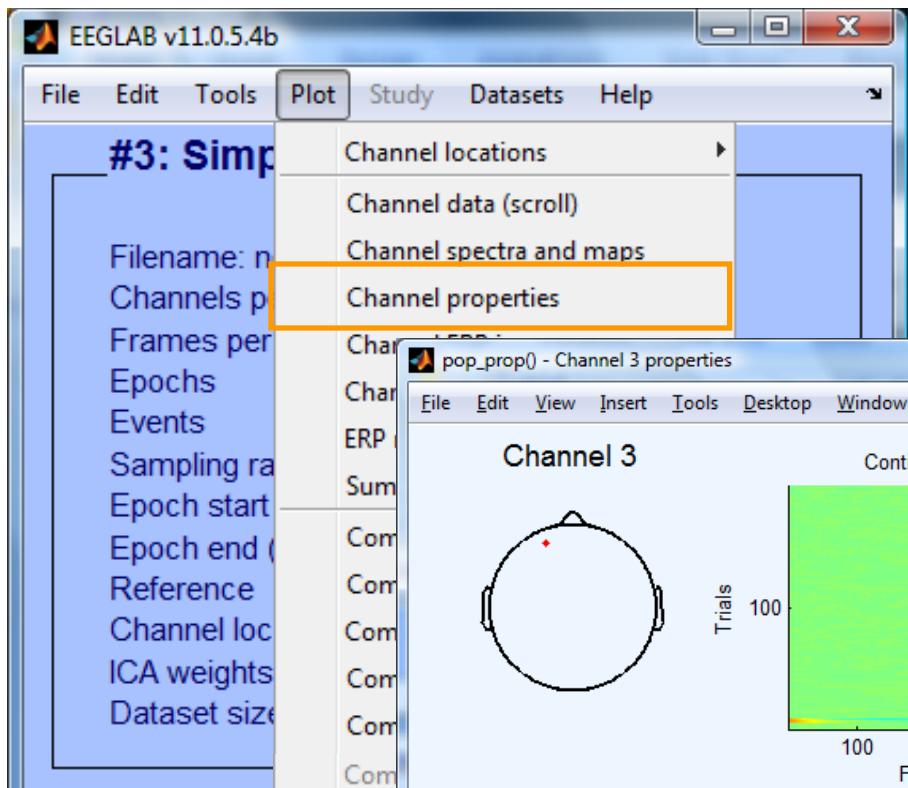
Manually identifying bad channels



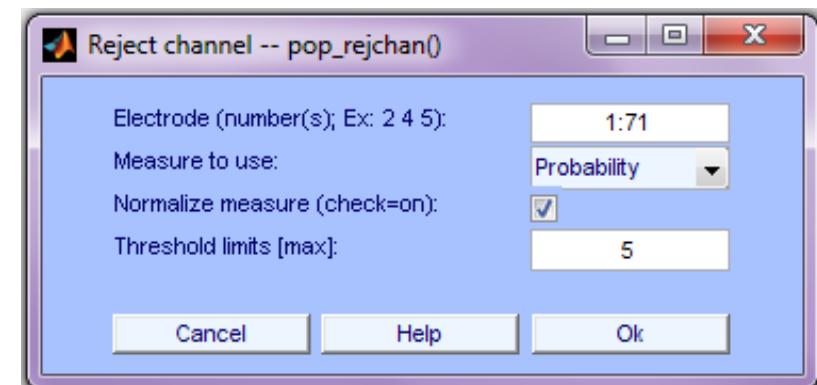
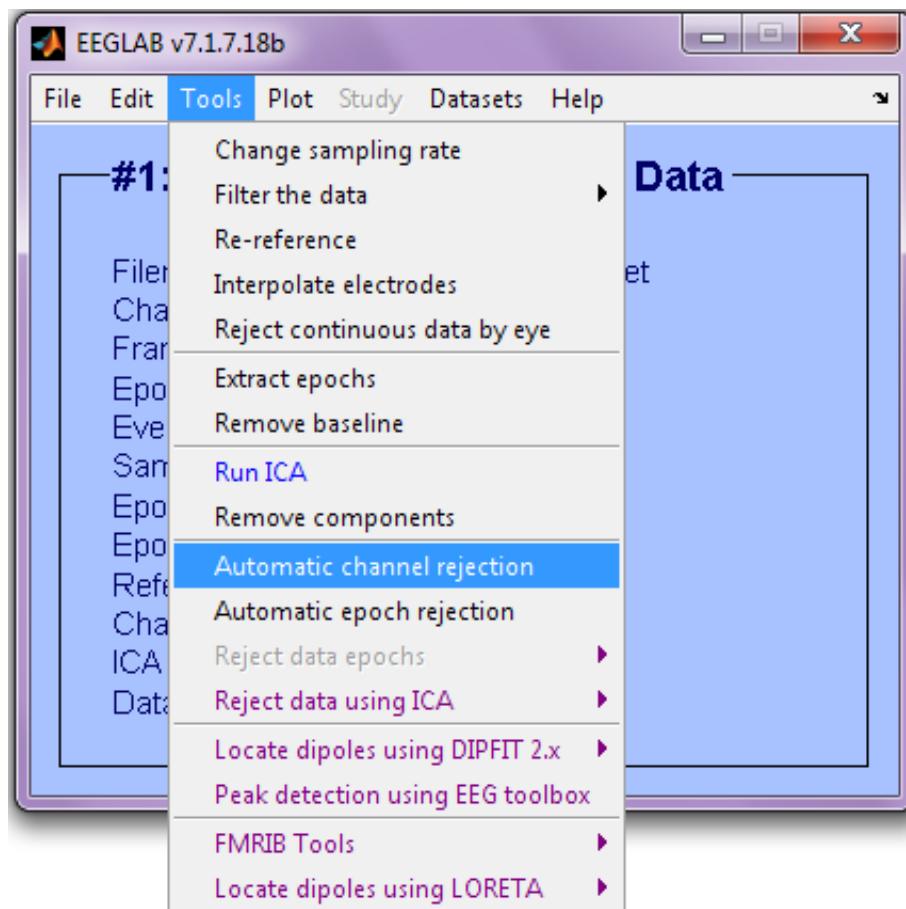
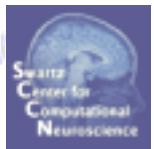
Manually identifying bad channels



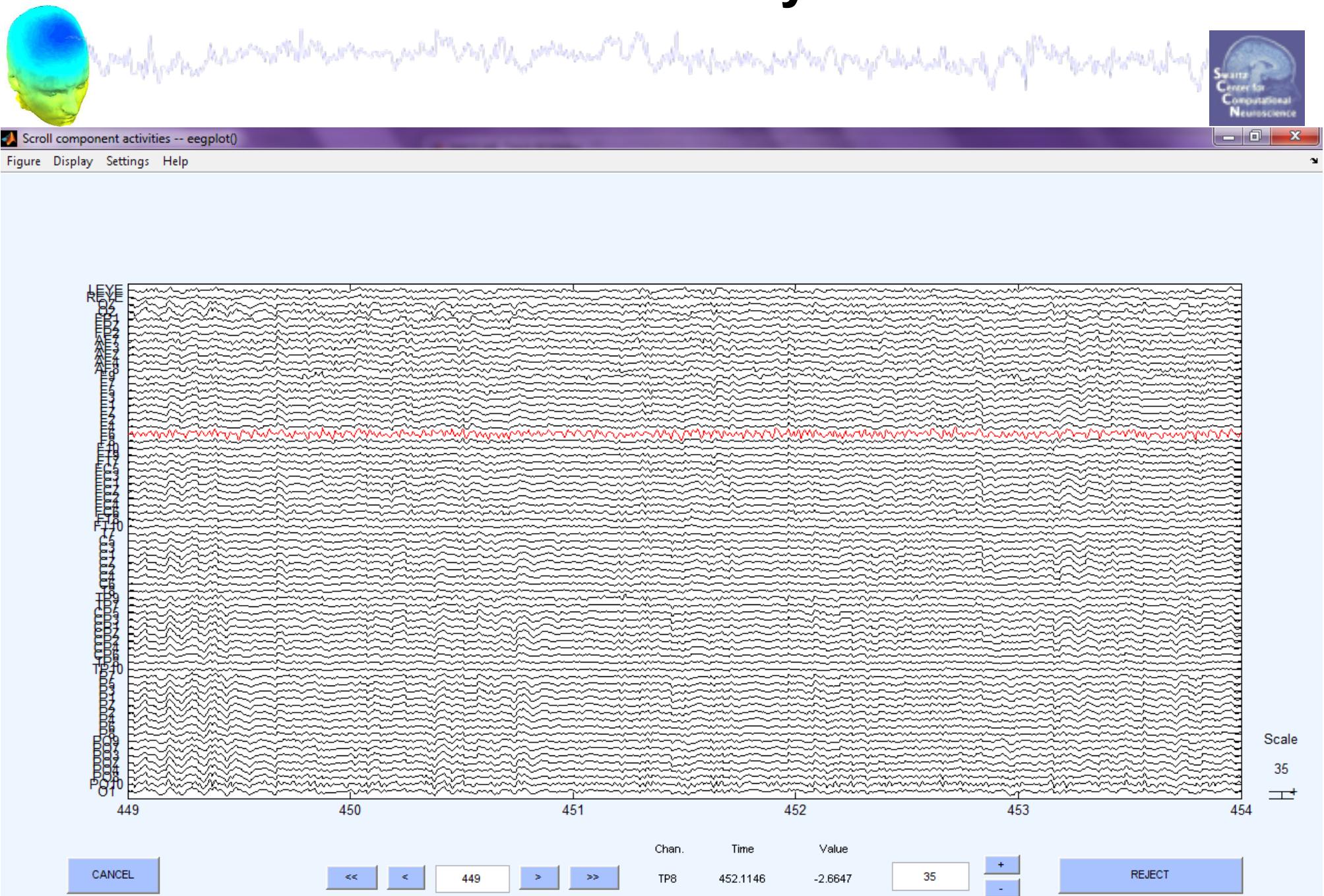
Manually identifying bad channels



Auto-detection of noisy channels



Auto-detected noisy channel



Removing channel(s)



EEGLAB v11.0.5.4b

File Edit Tools Plot Study Datasets Help

Dataset info Event fields Event values About this dataset Channel locations

Select data Select data using ev Select epochs or ev

Copy current dataset Append datasets Delete dataset(s)

Visually edit events

Dataset size (MB)

Select data -- pop_select()

Select data in:

- Time range [min max] (s)
- Point range (ex: [1 10])
- Epoch range (ex: 3:2:10)
- Channel range

Input desired range

on->remove th

F6

...
...
...
 ...
...

Scroll dataset

Cancel

If not checked, will result in dataset with one channel

Dataset info -- pop_newset()

What do you want to do with the new dataset?

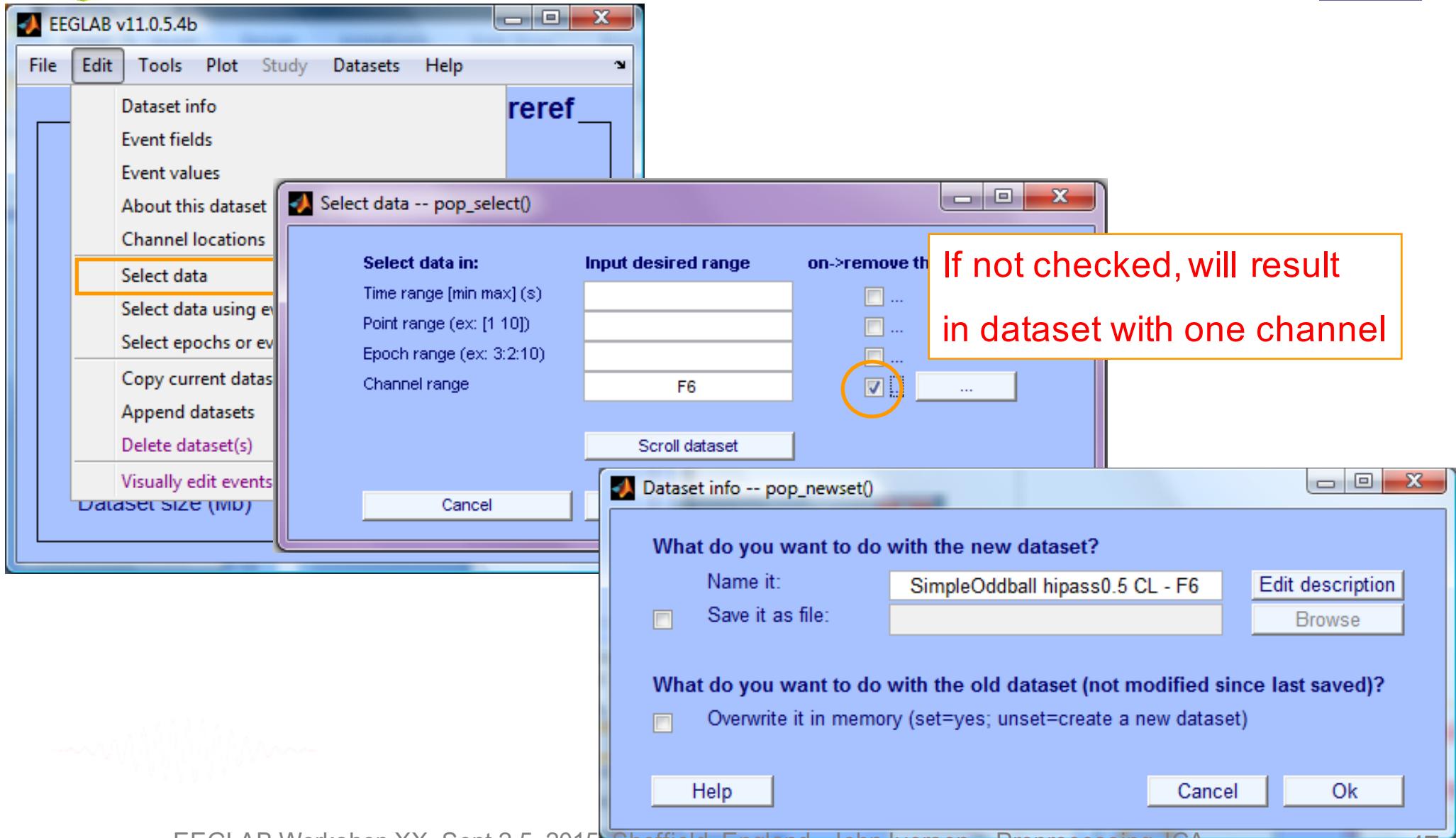
Name it: SimpleOddball hipass0.5 CL - F6 Edit description

Save it as file: Browse

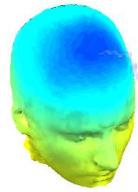
What do you want to do with the old dataset (not modified since last saved)?

Overwrite it in memory (set=yes; unset=create a new dataset)

Help Cancel Ok



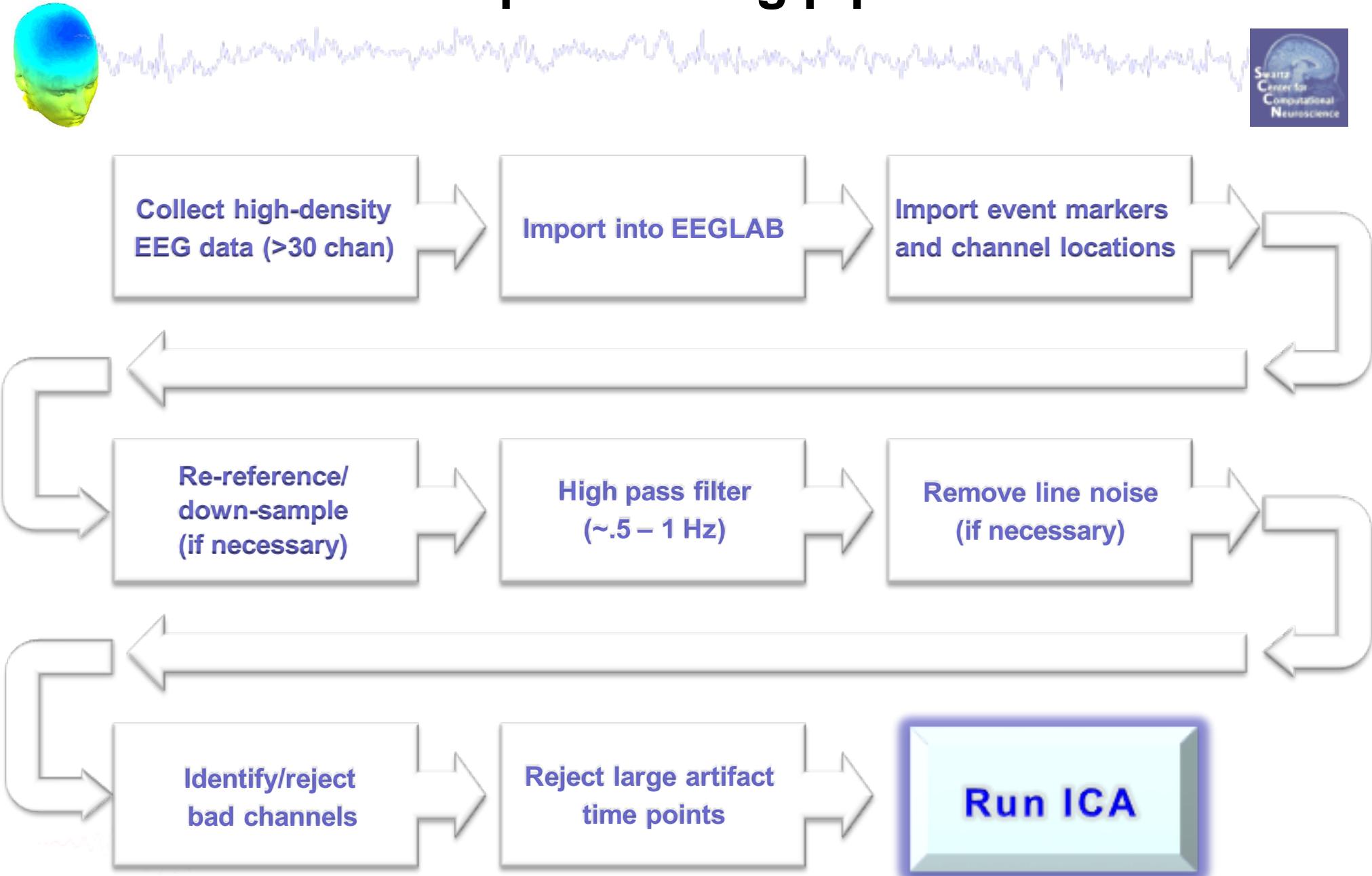
Removing channel(s)



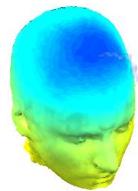
- You may prefer to interpolate bad channels rather than remove them altogether
- The loss in dimensionality will affect the ICA decomposition
- Usual solution:
 - Delete the bad channels before running ICA
 - STUDY tools will do much of this automatically (interpolate missing channels, etc)



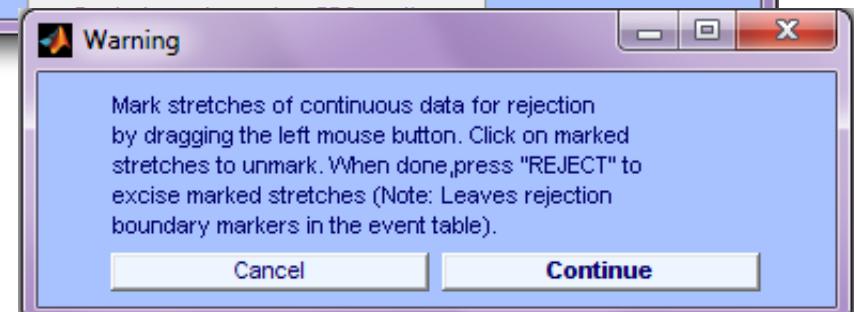
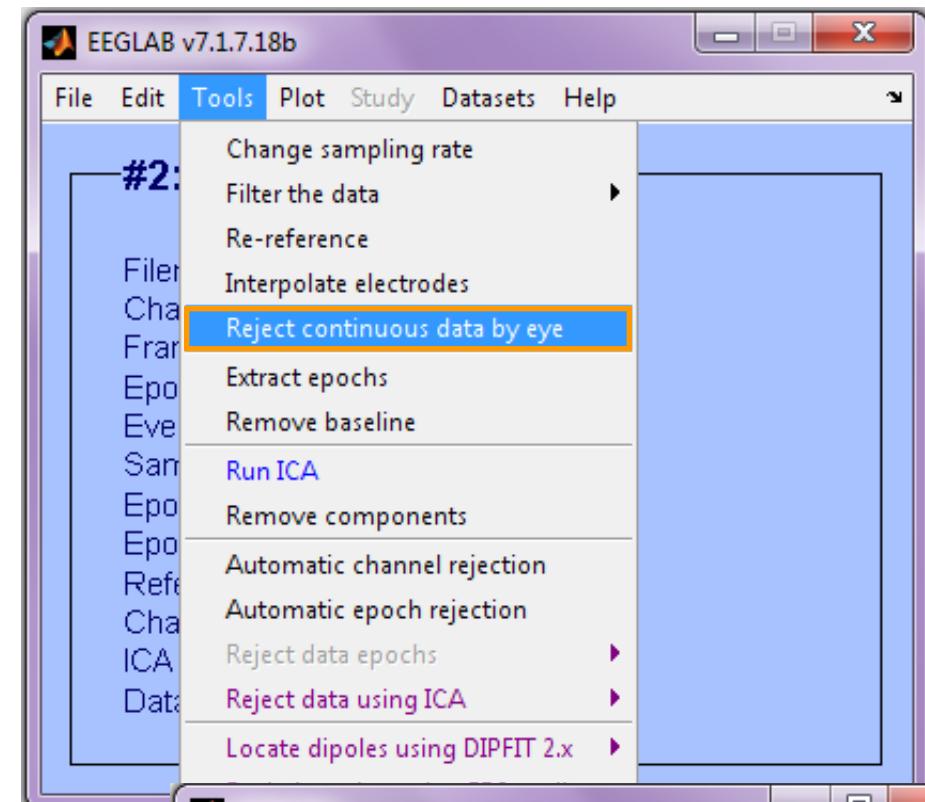
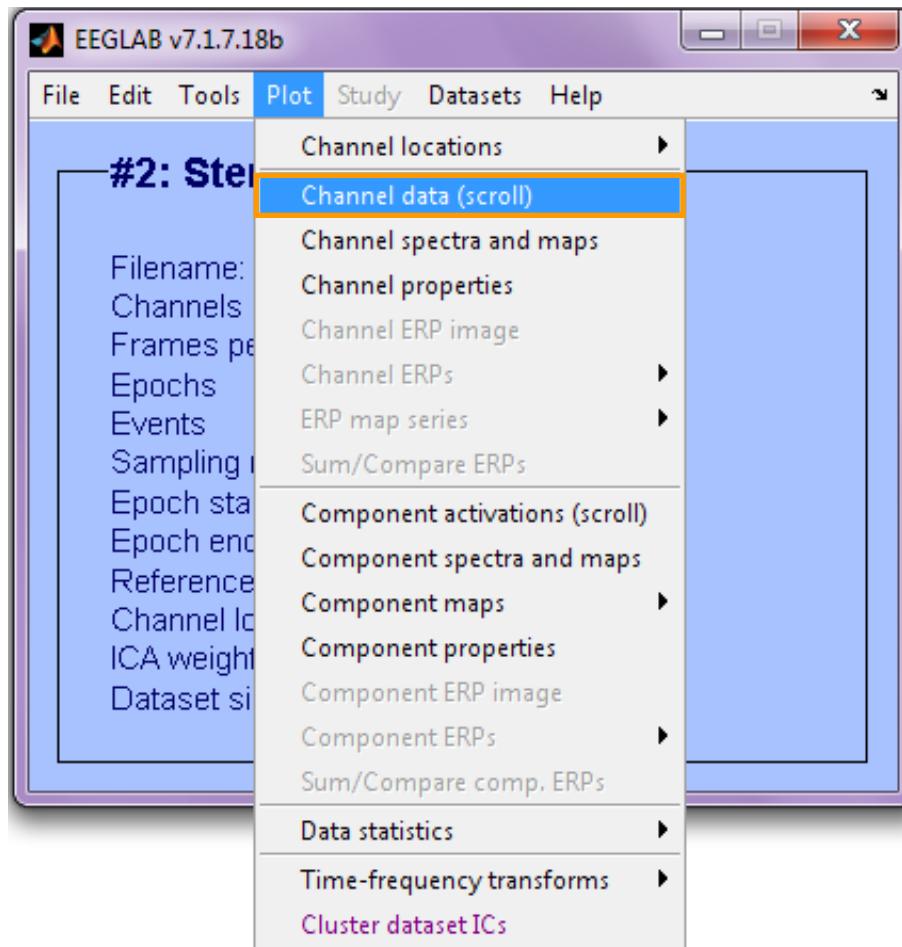
Pre-processing pipeline



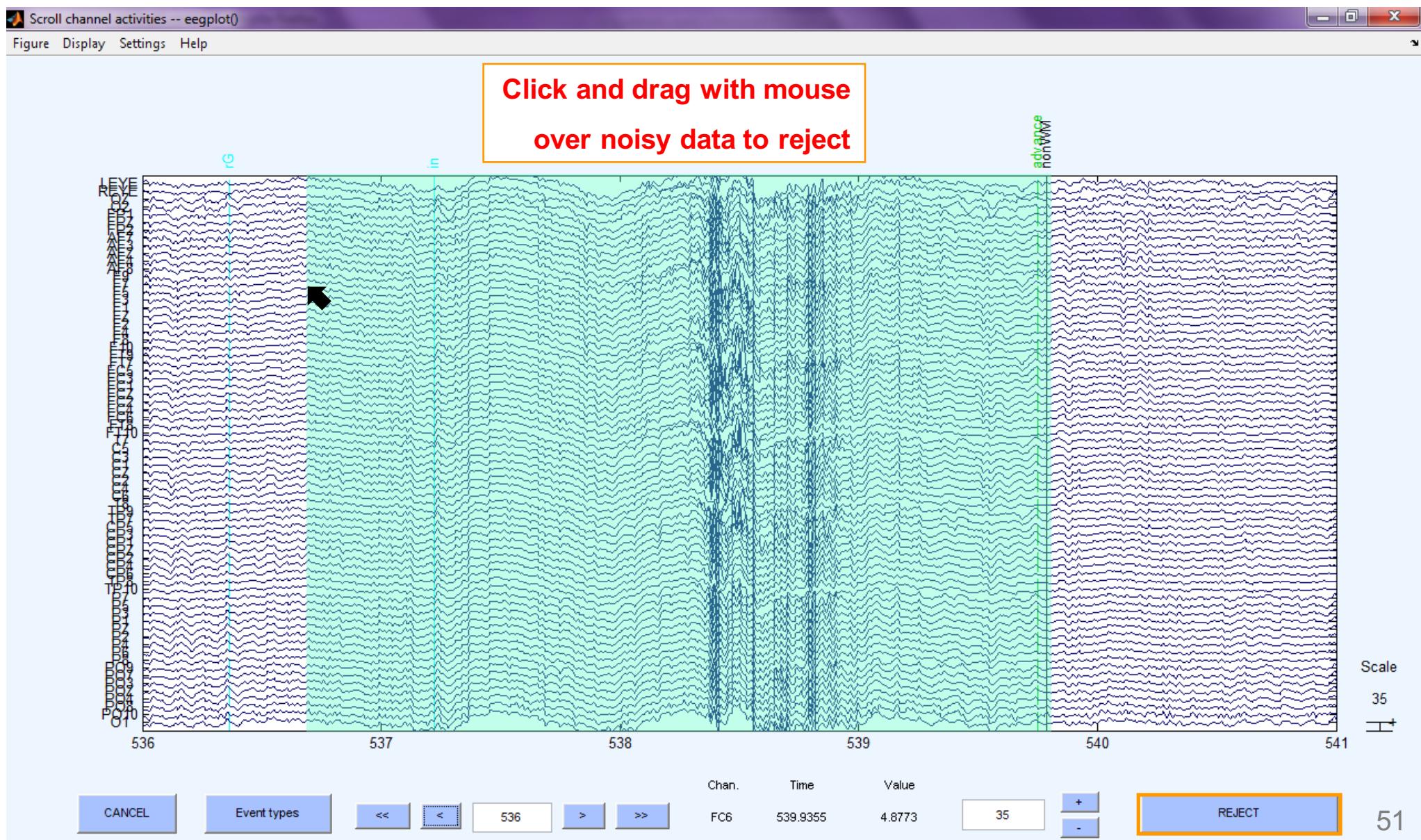
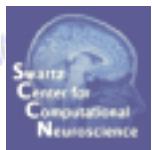
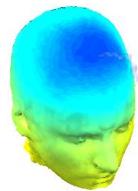
Reject continuous data



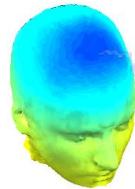
Equivalent



Reject continuous data



Rejecting data for ICA



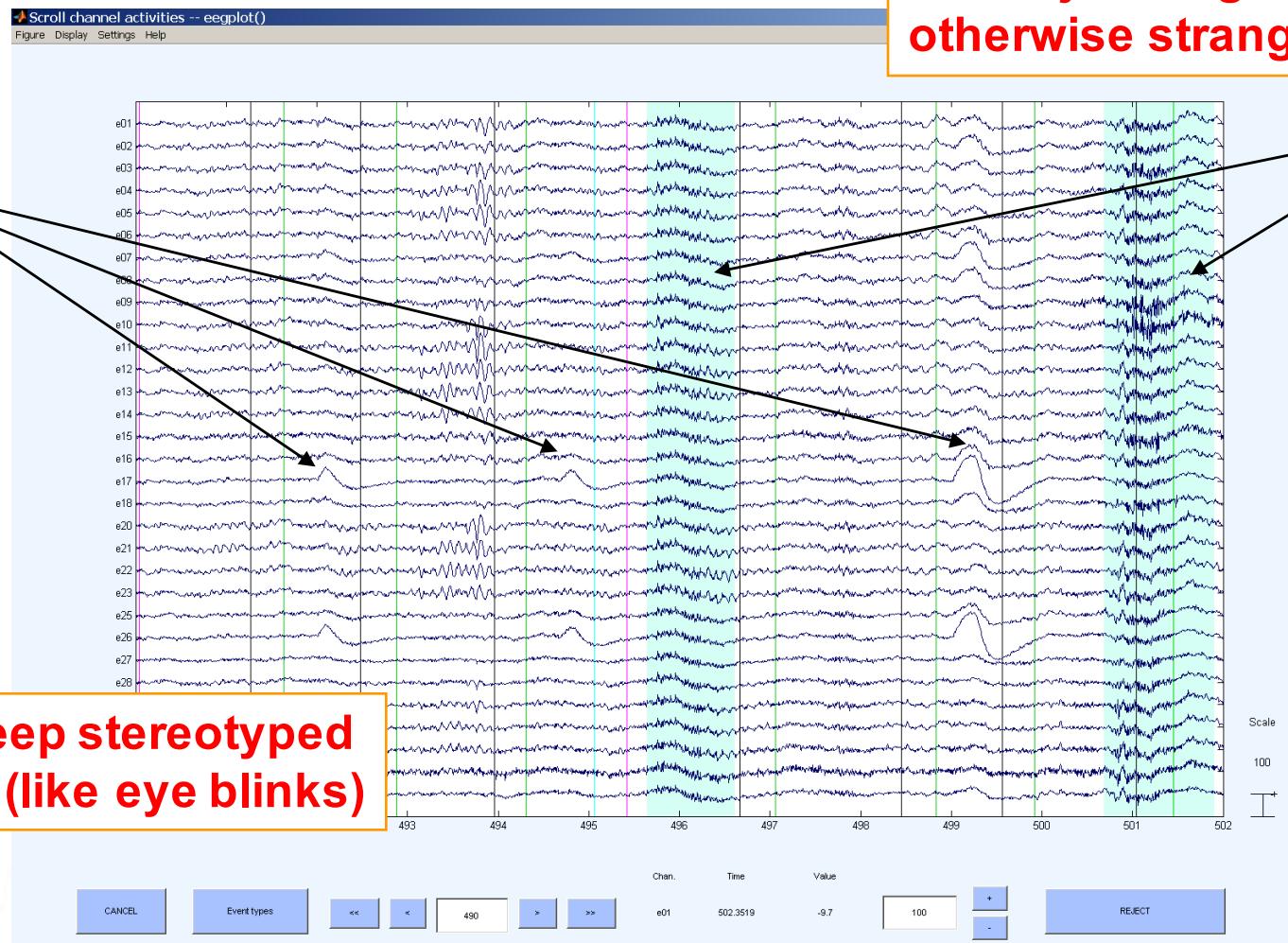
To prepare data for ICA:

Reject large muscle or
otherwise strange events...

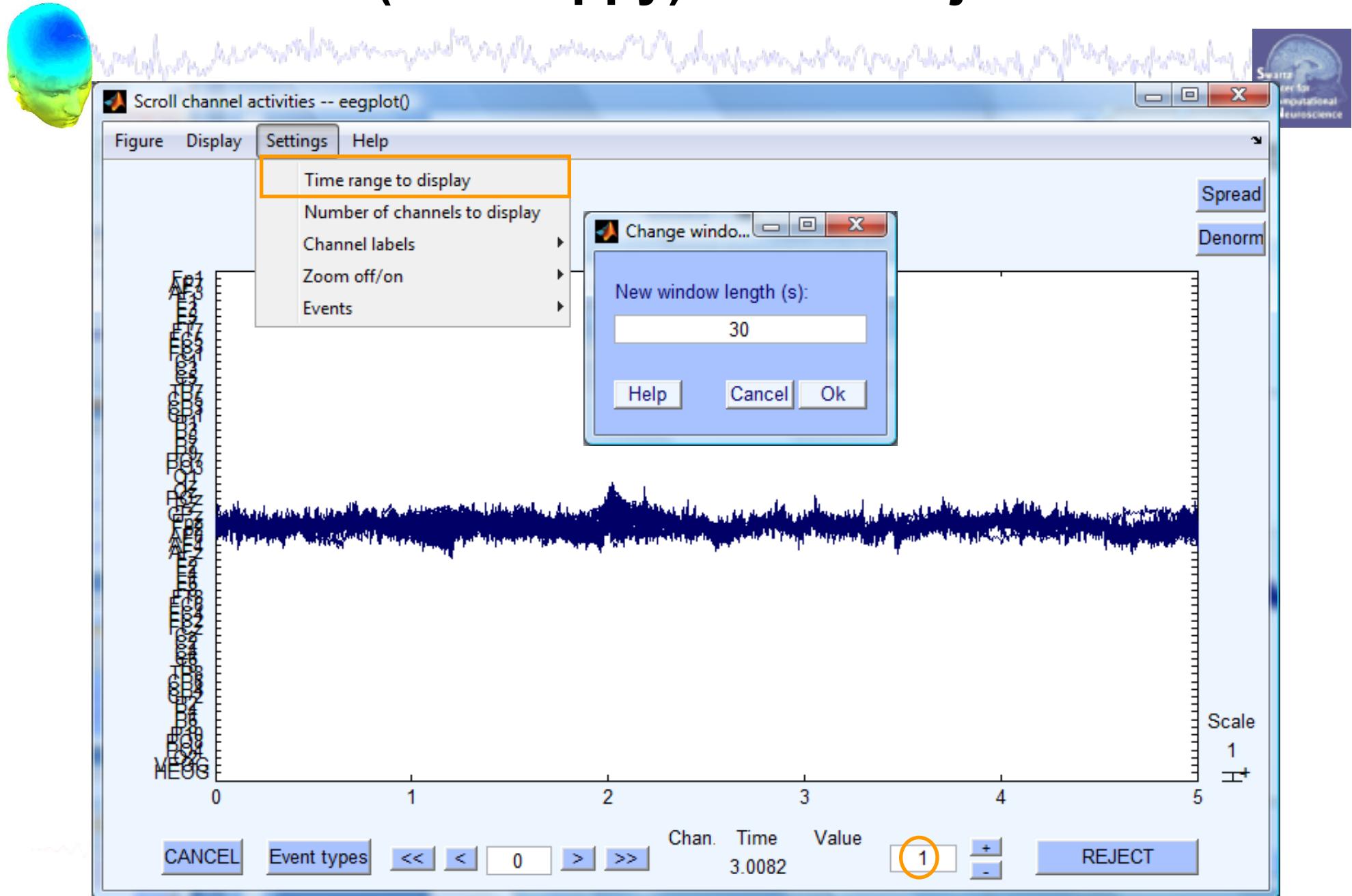
Keep

Reject

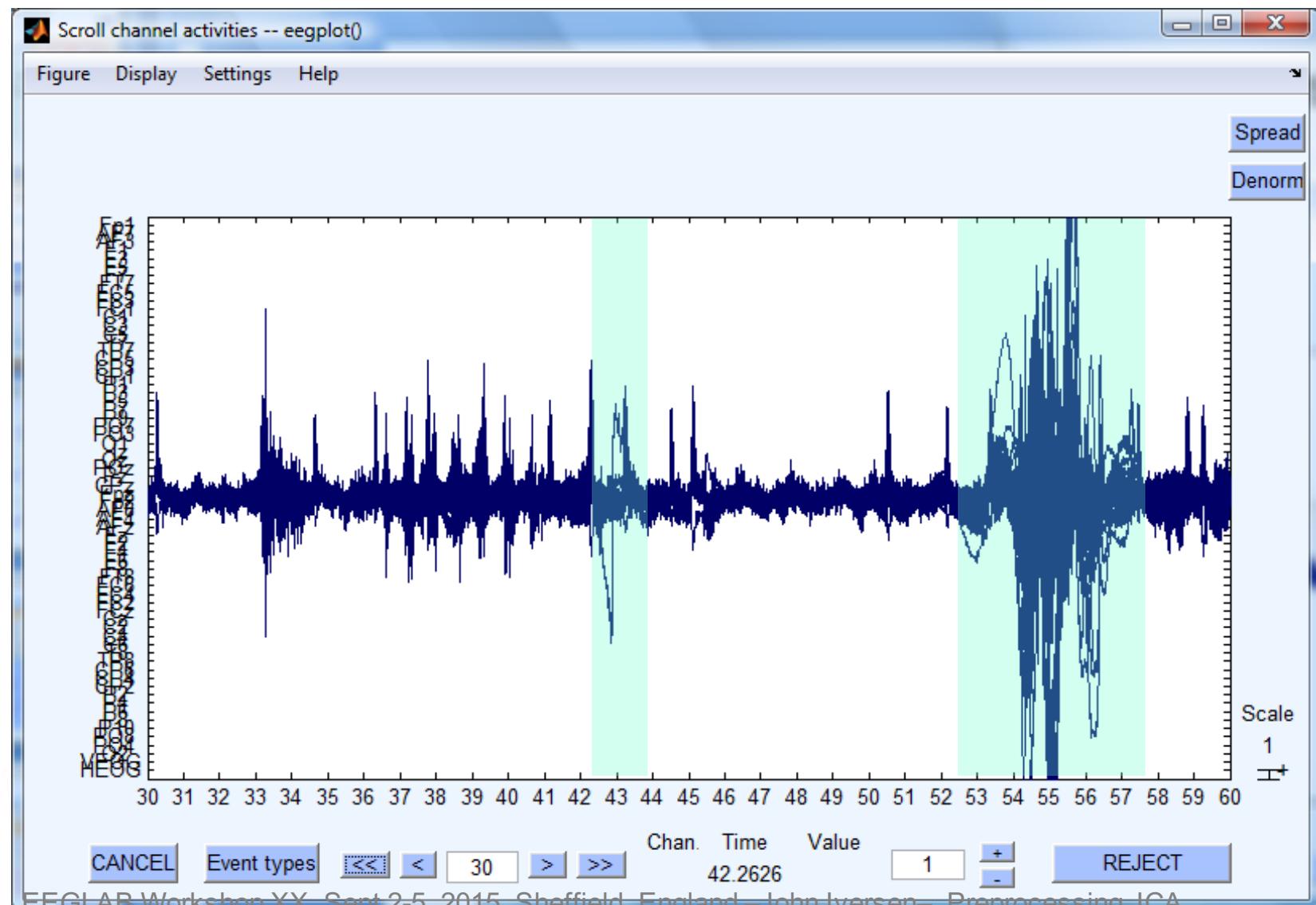
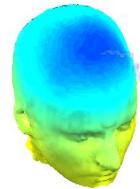
... but keep stereotyped
artifacts (like eye blinks)

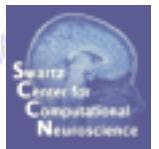
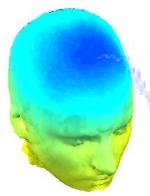


Fast (but sloppy) artifact rejection



Fast (but sloppy) artifact rejection





Data Cleaning for ICA

Variant 2: Epocched Data

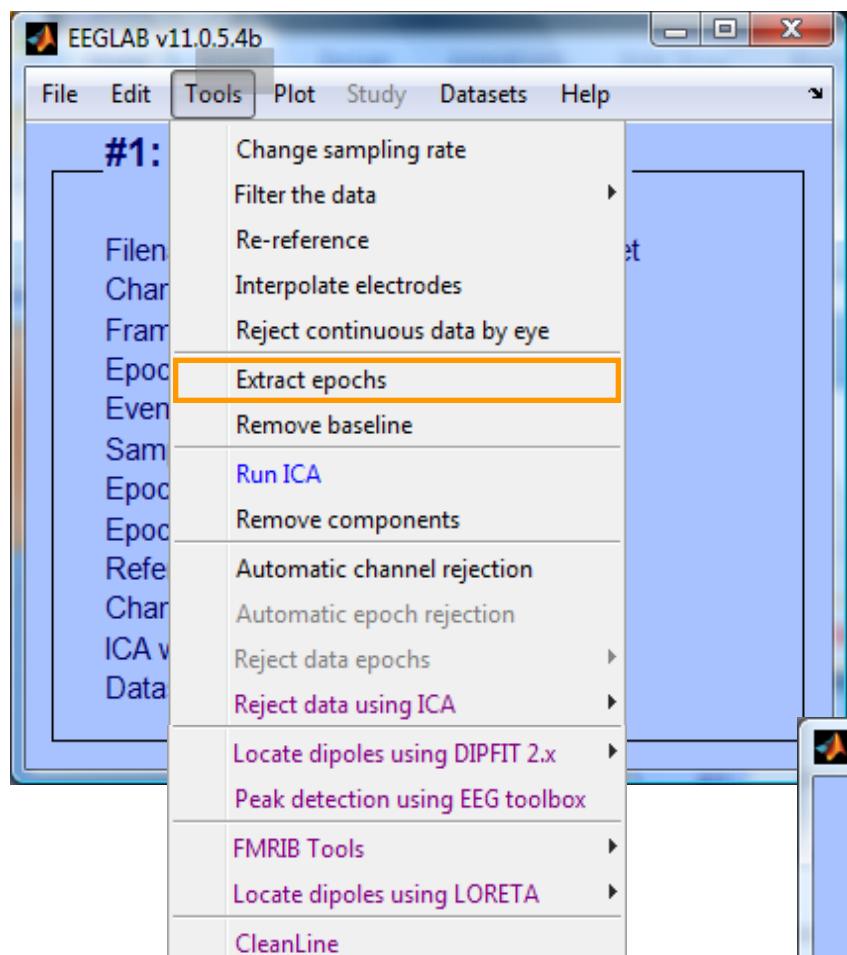
Visualizing ERPs



- Epoch data according to different event types
- Reject epochs containing artifact
- Various plot types (channel and scalp topography)

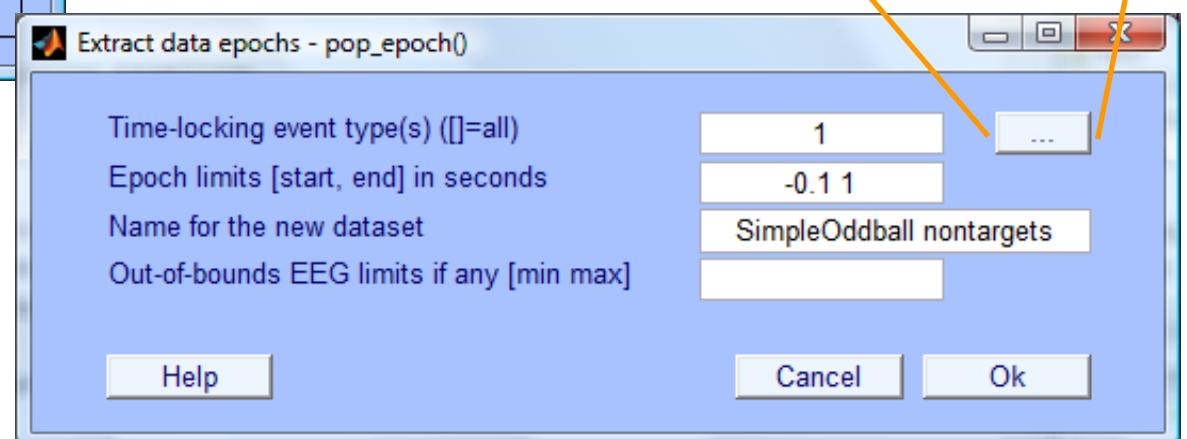
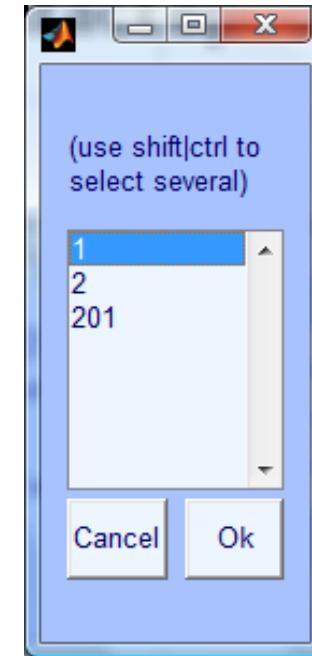


Extract epochs

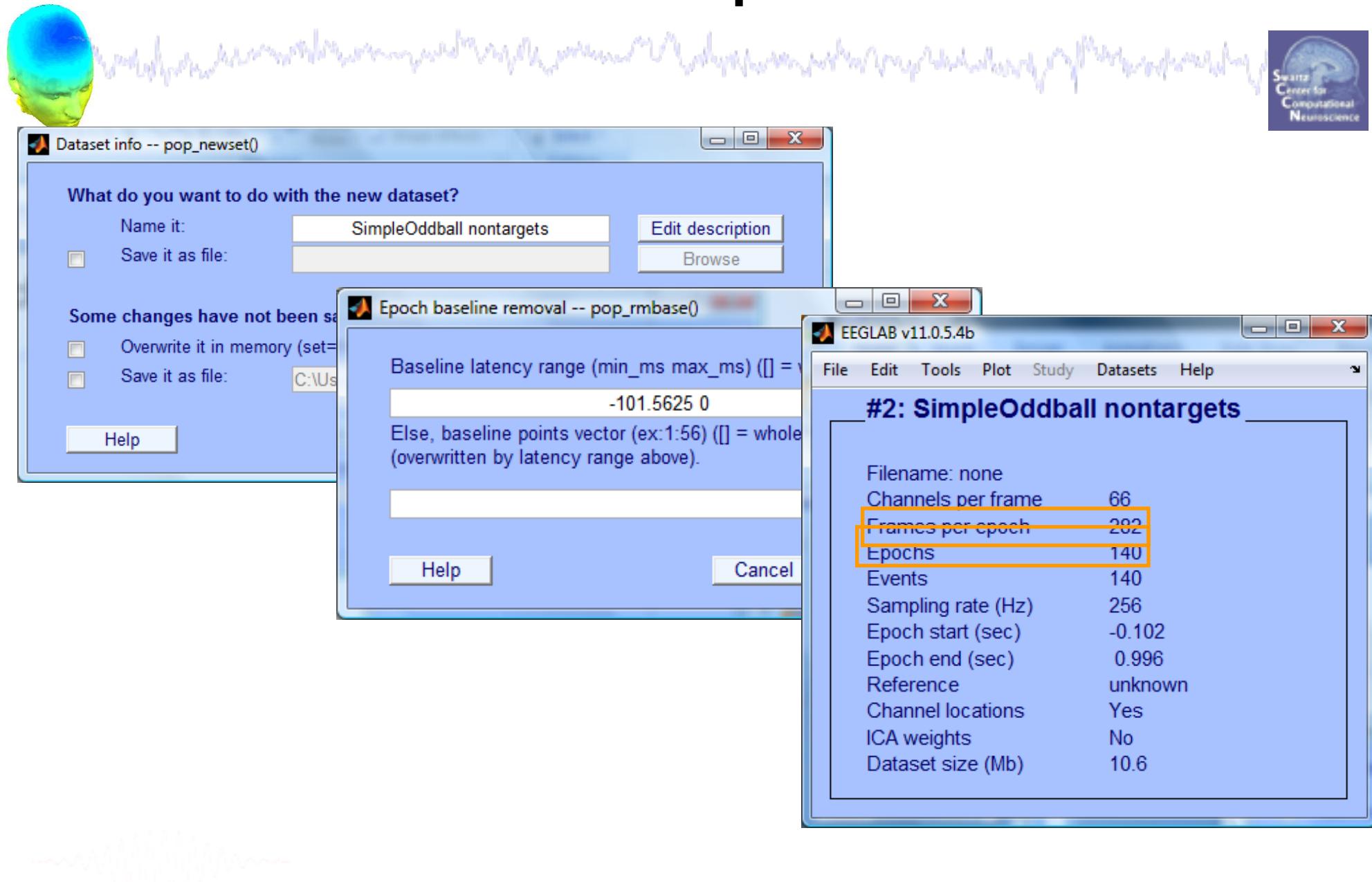


```
>> eeg_eventtypes (EEG)
```

1	140
2	60
201	60



Extract epochs



Select a subset of epochs

The screenshot shows the EEGLAB software interface. A red box highlights the 'Edit' menu, and another red box highlights the 'Select epochs or events' option under the 'Edit' menu. A callout box with a red border and yellow arrow points from the text '0' because the subject did not miss any targets' to the 'Confirmation' dialog box. The 'Confirmation' dialog box contains the text 'Warning: delete 0 (out of 60) un-referenced epochs ?' with 'Cancel' and 'Ok' buttons. The main window is titled 'Select events -- pop_selectevent()' and includes sections for 'Field', 'Selection', and 'Set=NOT THESE'. In the 'Selection' section, the 'min' field is set to '201' and has a yellow circle around it. The 'Event selection' section contains several checkboxes and dropdowns. The 'Epoch selection' section contains two checkboxes: 'Remove epochs not referenced by any selected event' (which is checked) and 'Invert epoch selection'. At the bottom are 'Help', 'Cancel', and 'Ok' buttons.

'0' because the subject did not miss any targets

EEGLAB v11.0.5.4b

File Edit Tools Plot Study Datasets Help

Dataset info Event fields Event values About this dataset Channel locations Select data Select data using events Select epochs or events Copy current dataset Append datasets Delete... Visual... Datasets

Confirmation

Warning: delete 0 (out of 60) un-referenced epochs ?

Cancel Ok

Select events -- pop_selectevent()

Field Selection Set=NOT THESE

latency (ms) No description min max

type No description

epoch No description

Event indices

Event selection

Select all events NOT selected above (Set this button and "all BUT" buttons (above) for logical OR)

Keep only selected events and remove all other events

Rename selected event type(s) as type:

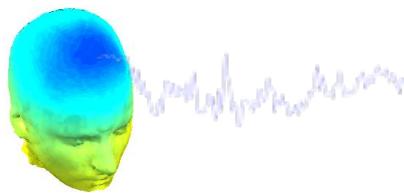
Retain old event type name(s) in (new) field named:

Epoch selection

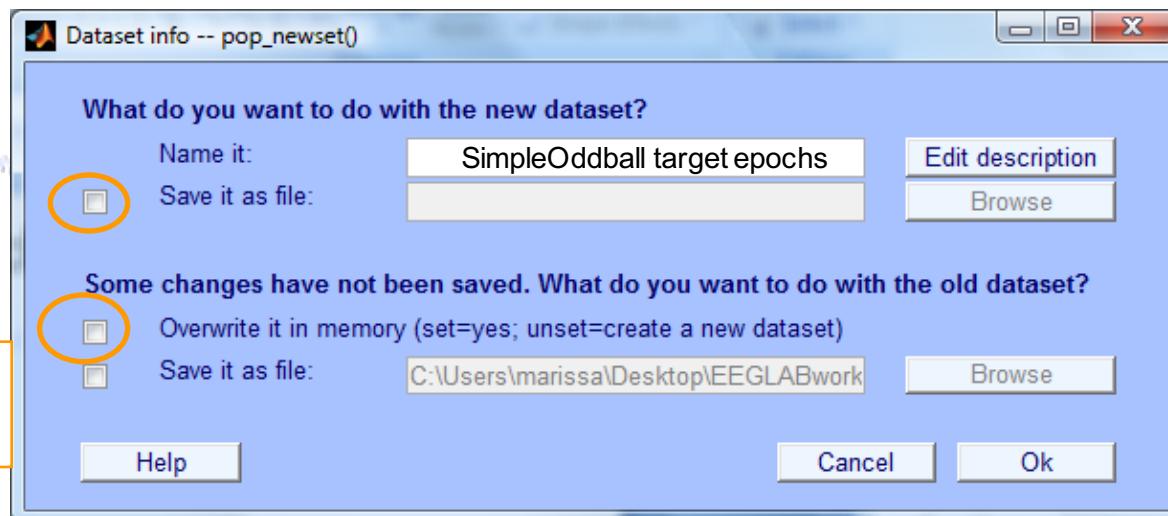
Remove epochs not referenced by any selected event

Invert epoch selection

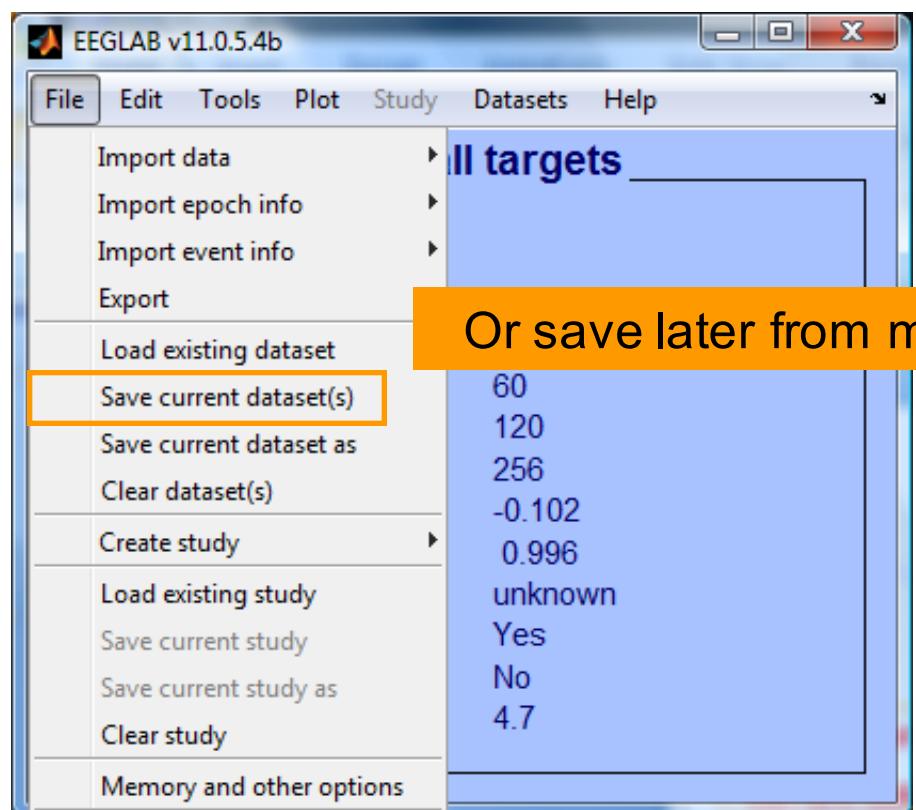
Help Cancel Ok



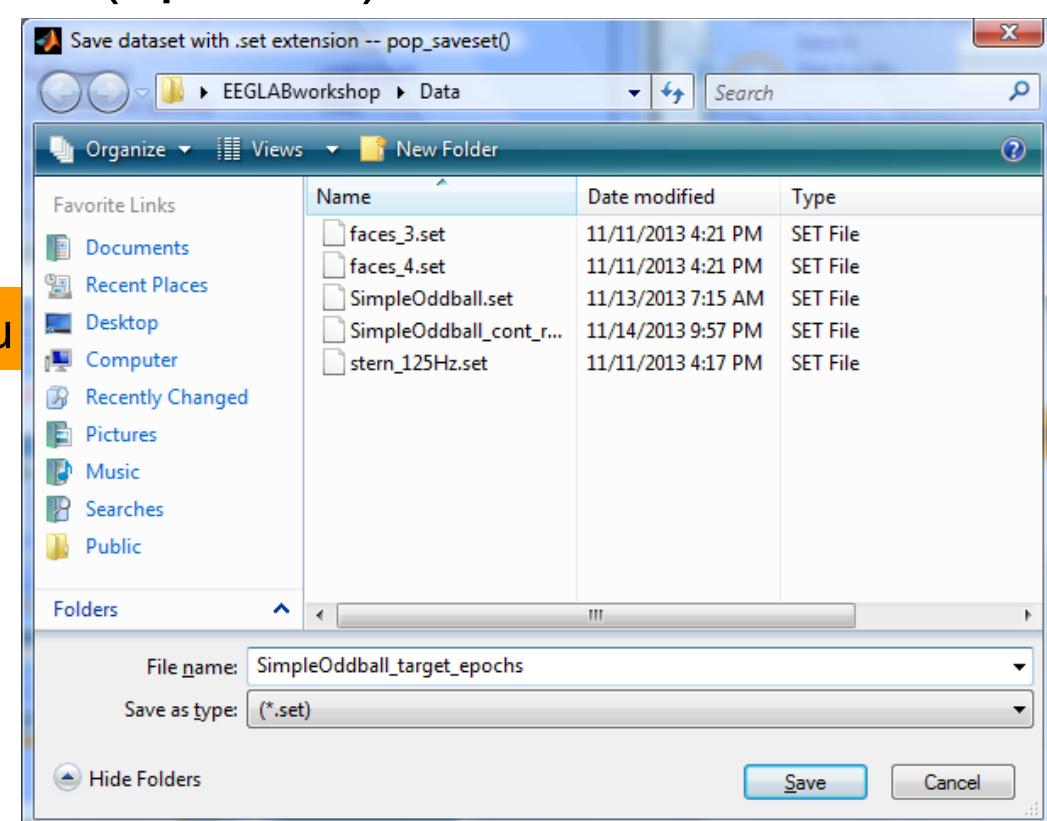
'Do not overwrite
current dataset'



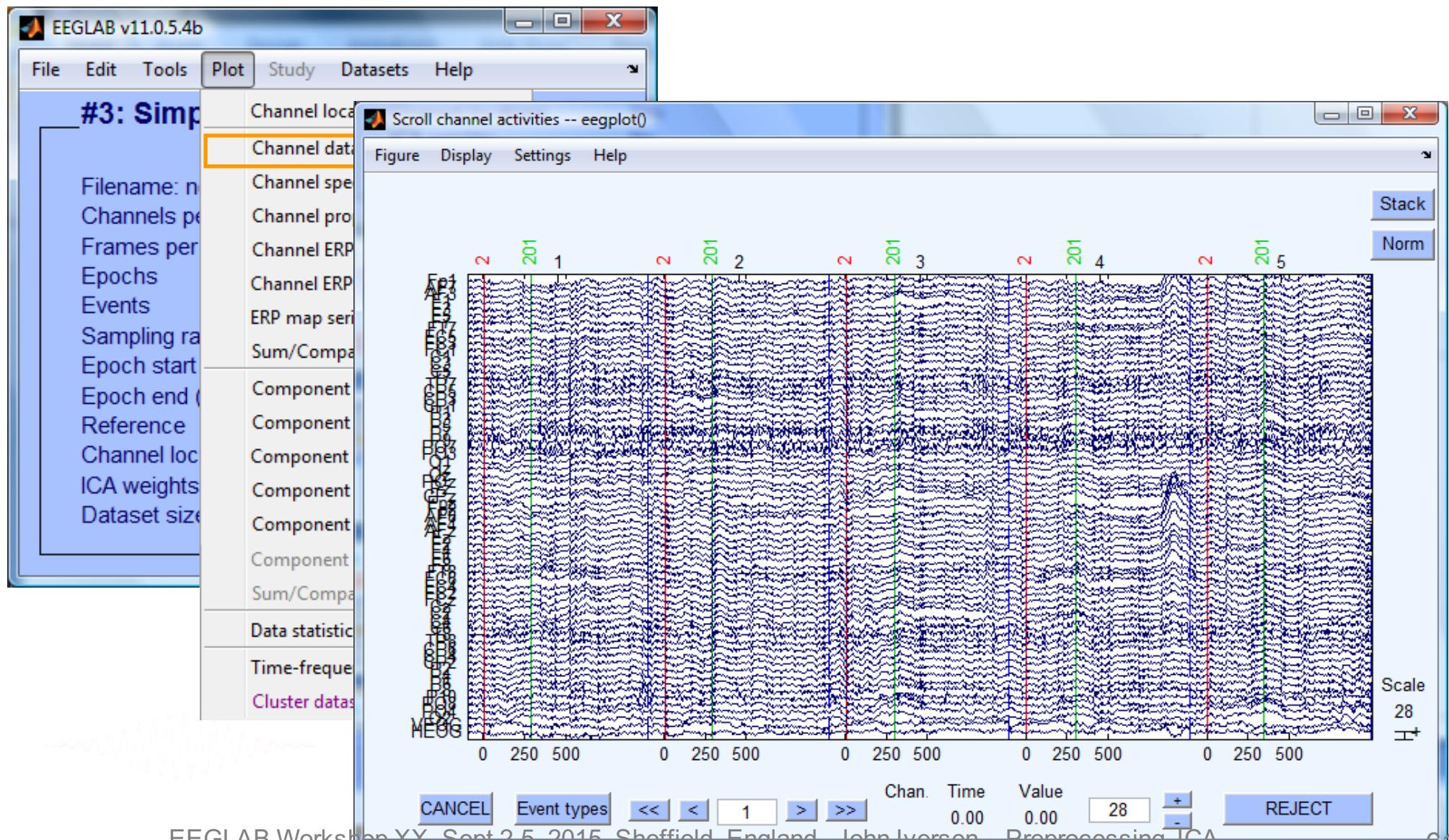
Save dataset (optional)



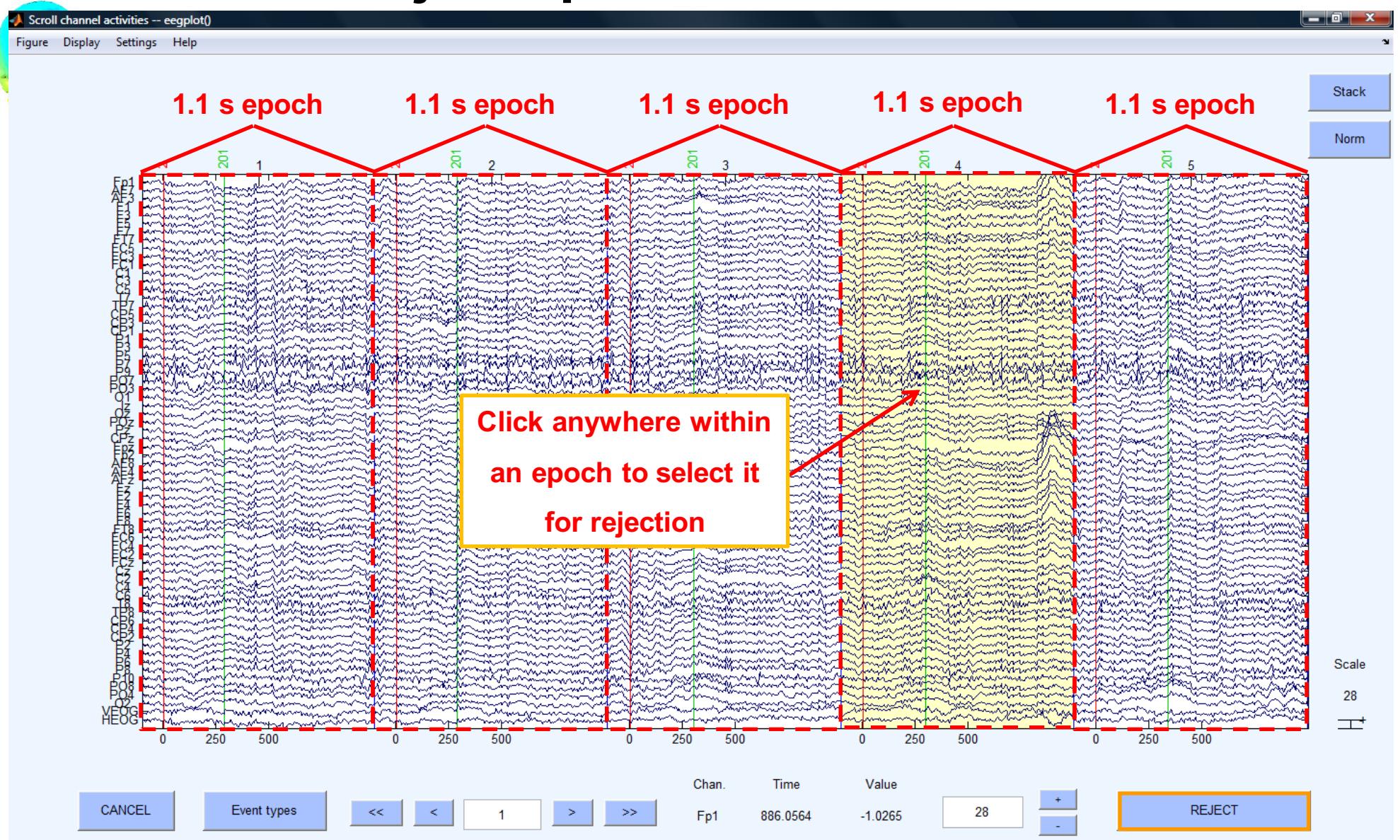
Or save later from menu



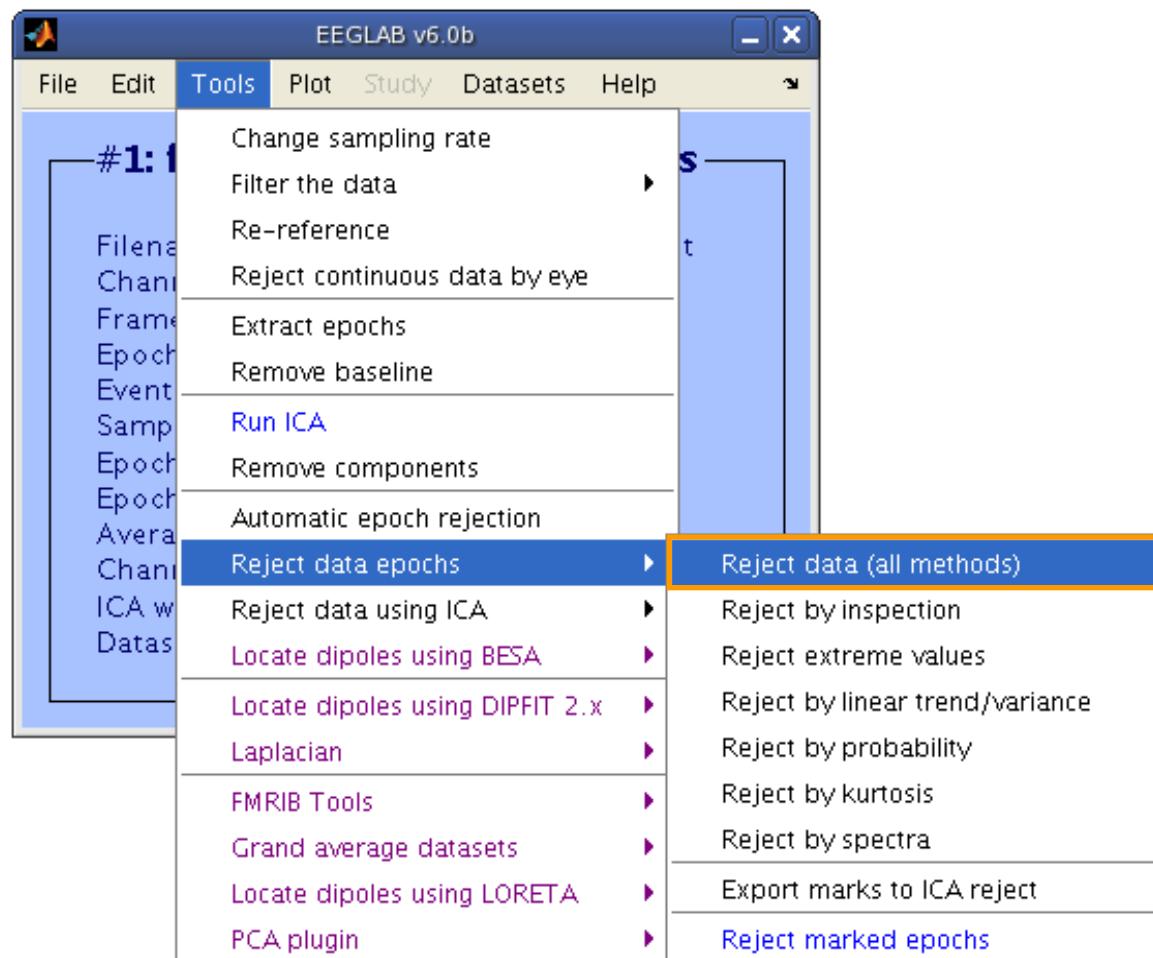
Scroll (epoched) channel data



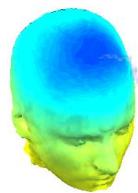
Reject epochs with artifact



Reject data epochs



Reject data epochs



visual
inspection

Reject trials using data statistics - pop_rejmenu()

Mark trials by appearance

Find abnormal values

Upper limit(s) (uV): 25
Start time(s) (ms): -1000
Electrode(s): 1:31

Find abnormal trends

Max slope (uV/epoch): 50
Electrode(s): 1:31

Find improbable data

Single-channel limit (std. dev.): 5
Electrode(s): 1:31

All channels limit (std. dev.): 5
Currently marked trials: 0

Find abnormal distributions

Single-channel limit (std. dev.): 5
Electrode(s): 1:31

All channels limit (std. dev.): 5
Currently marked trials: 0

Find abnormal spectra (slow)

Upper limit(s) (dB): 25
Low frequency(s) (Hz): 0
Electrode(s): 1:31

Lower limit(s) (dB): -25
High frequency(s) (Hz): 50
Currently marked trials: 0

Plotting options

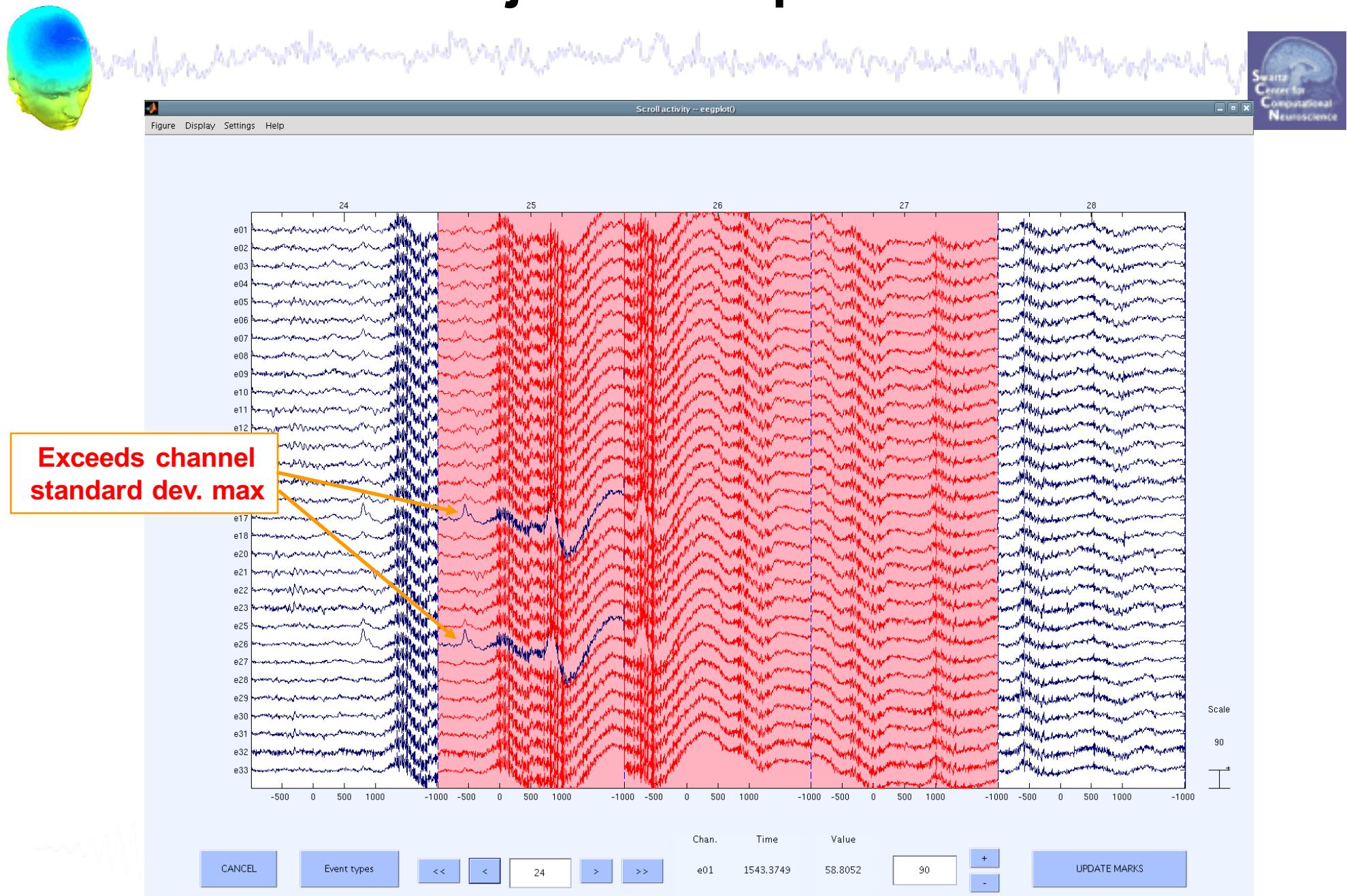
Show all trials marked for rejection by the measure selected above or checked below:

Abnormal appearance Abnormal values Abnormal trends
 Improbable epochs Abnormal distributions Abnormal spectra

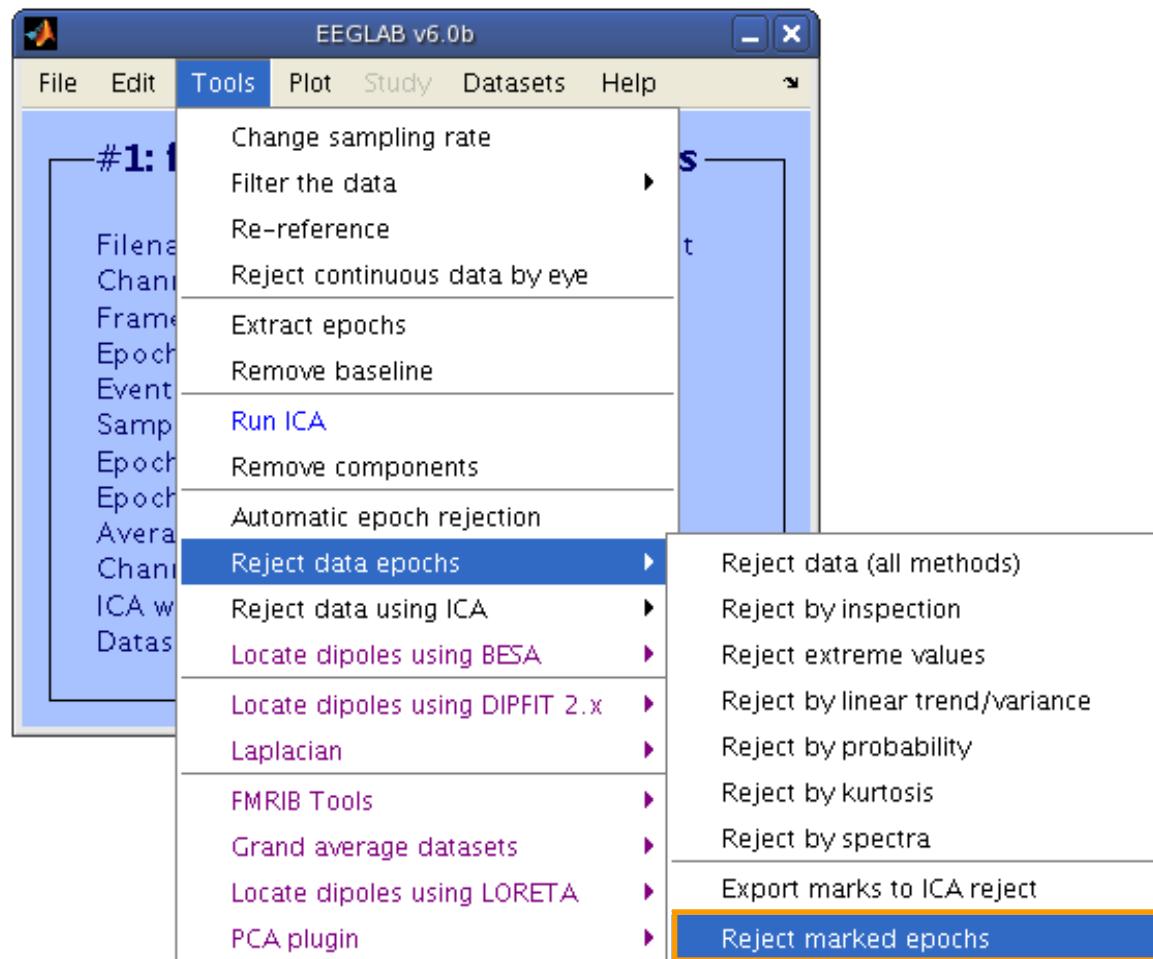
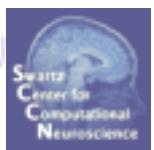
Buttons: Close (keep marks), Clear all marks, Reject marked trials

probability

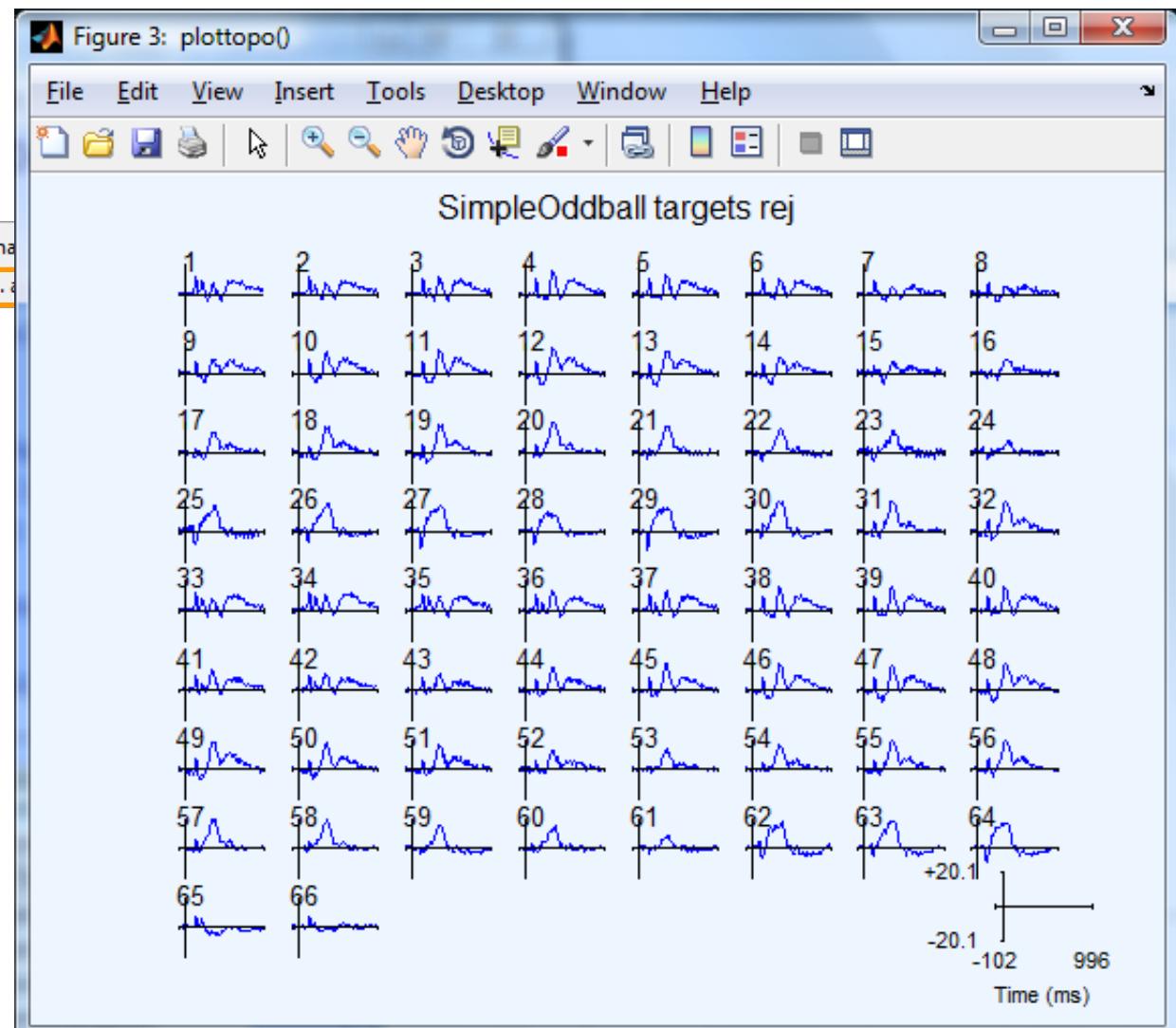
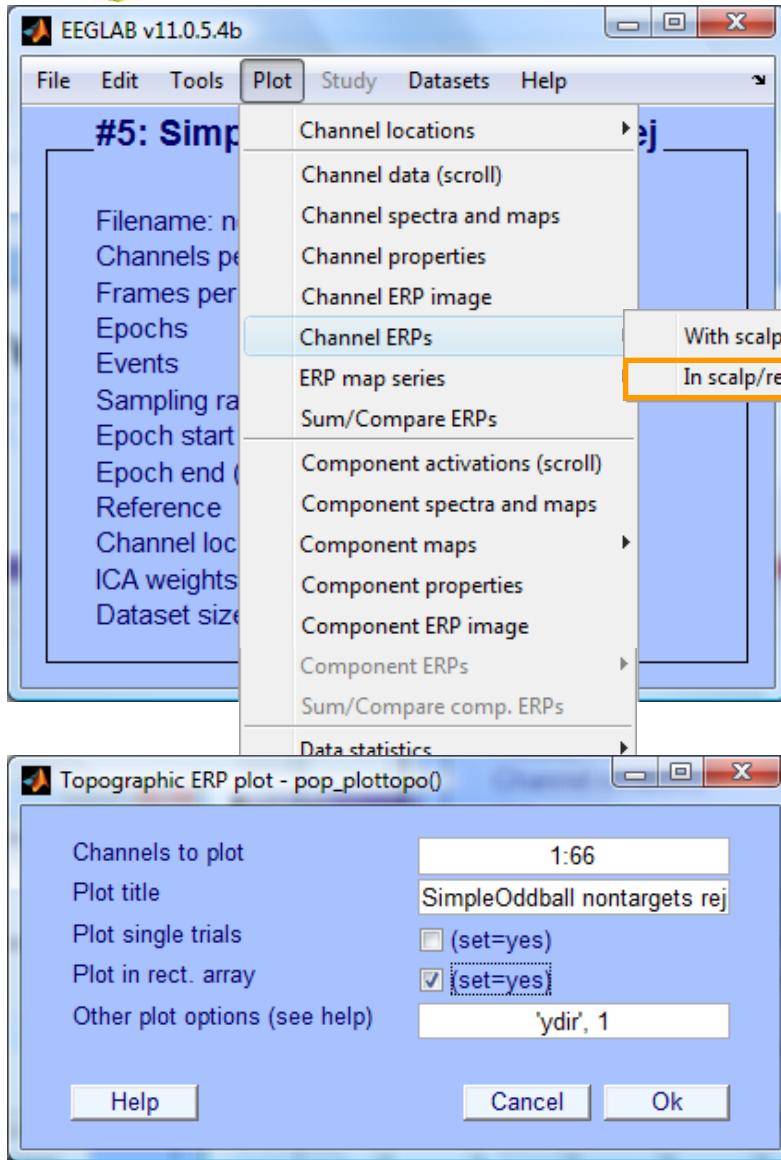
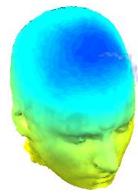
Reject data epochs



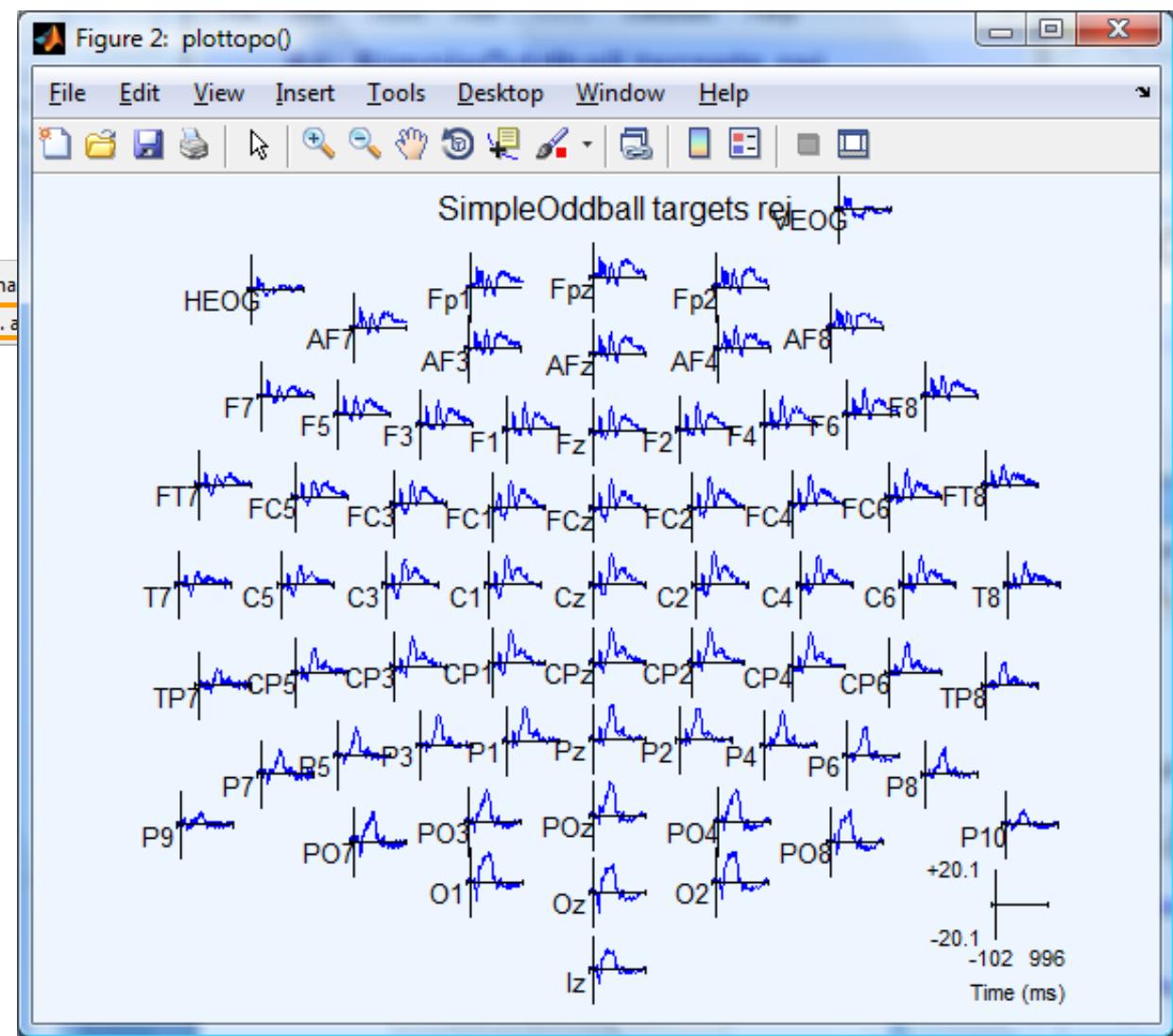
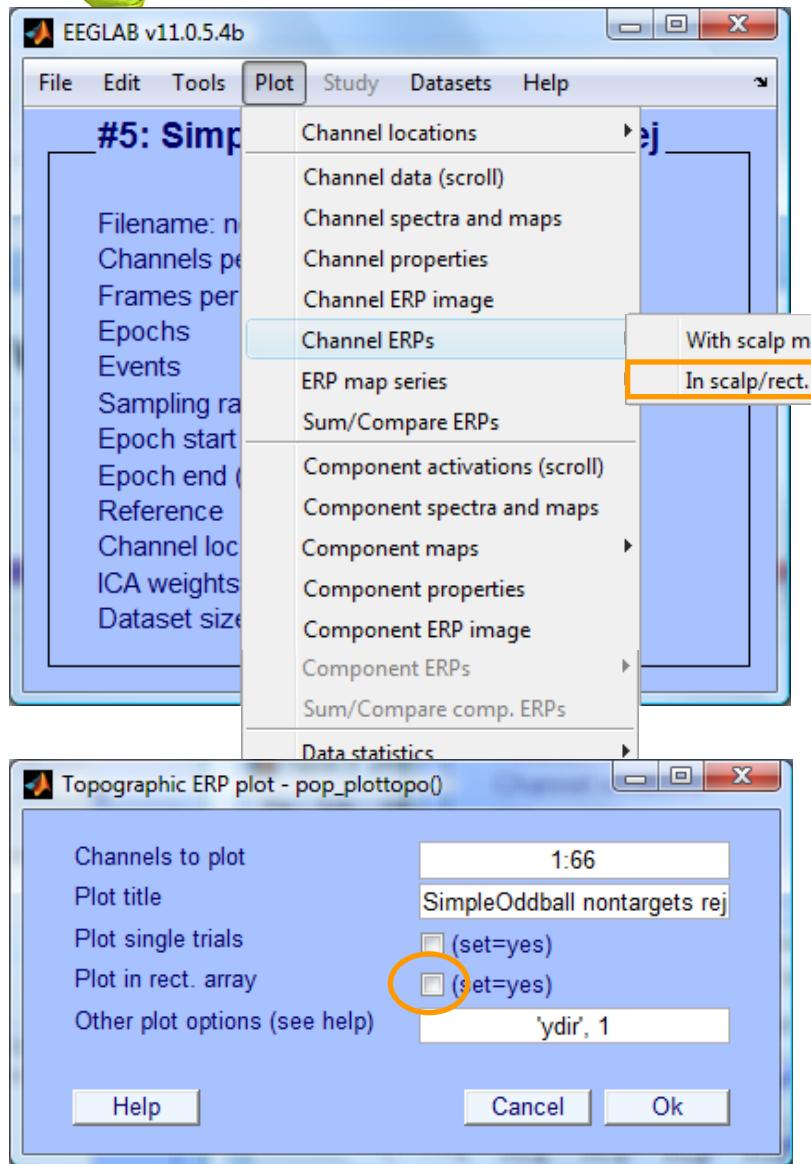
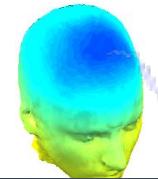
Reject data epochs



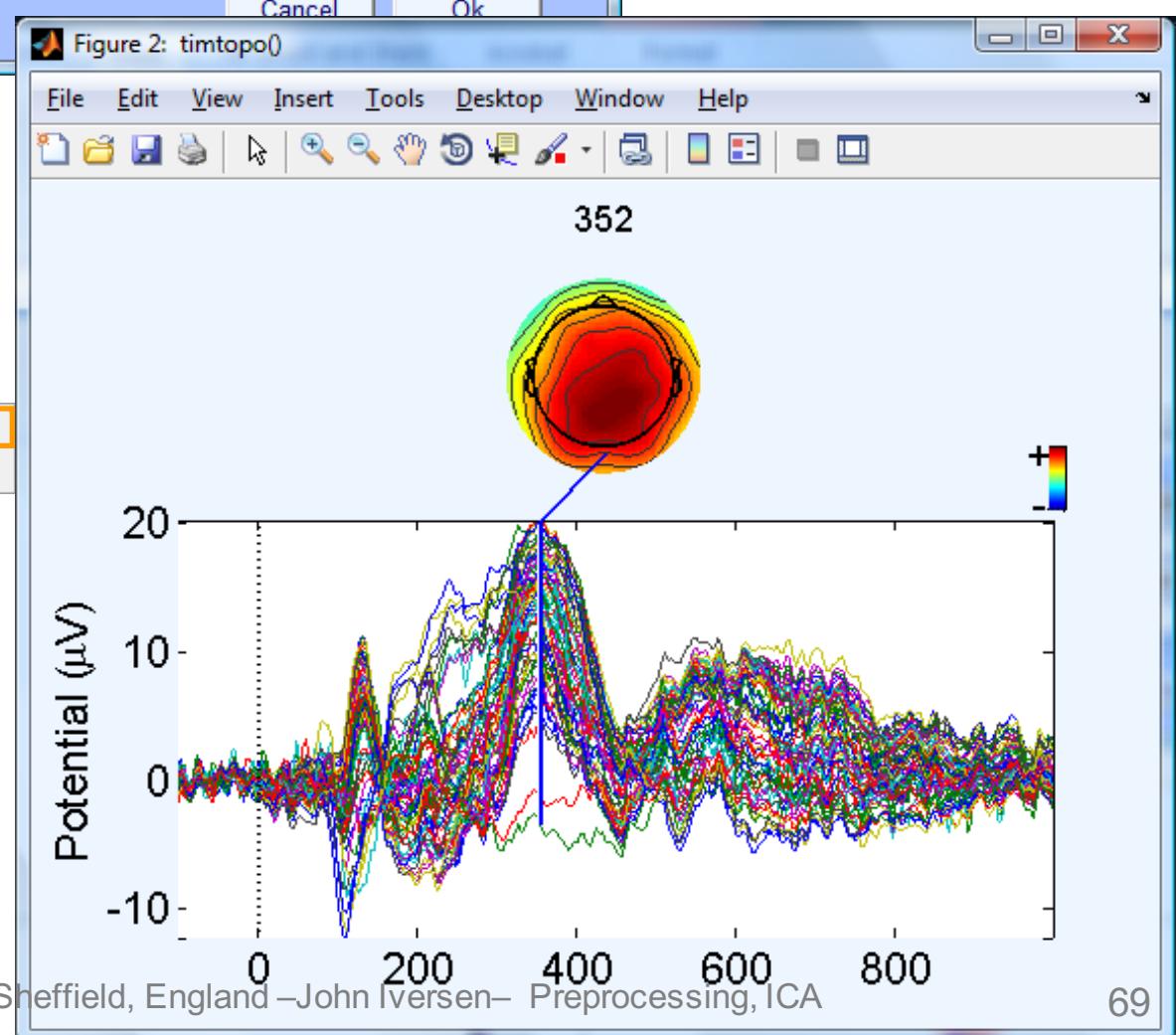
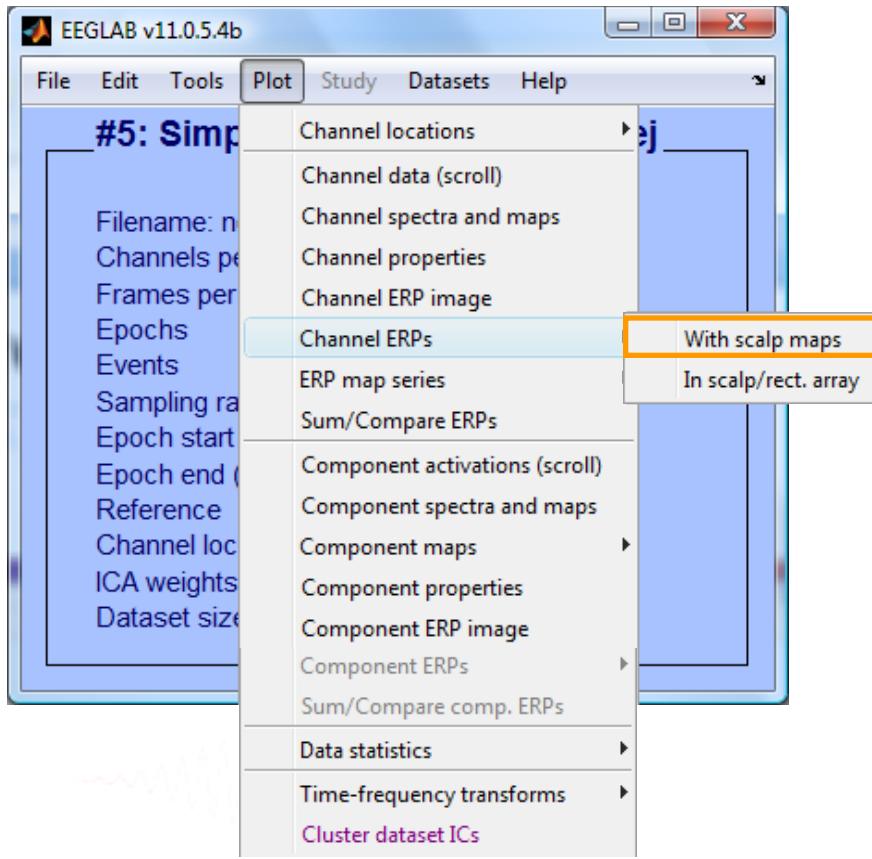
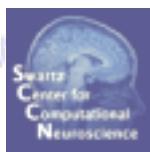
Visualize ERP in rectangular array



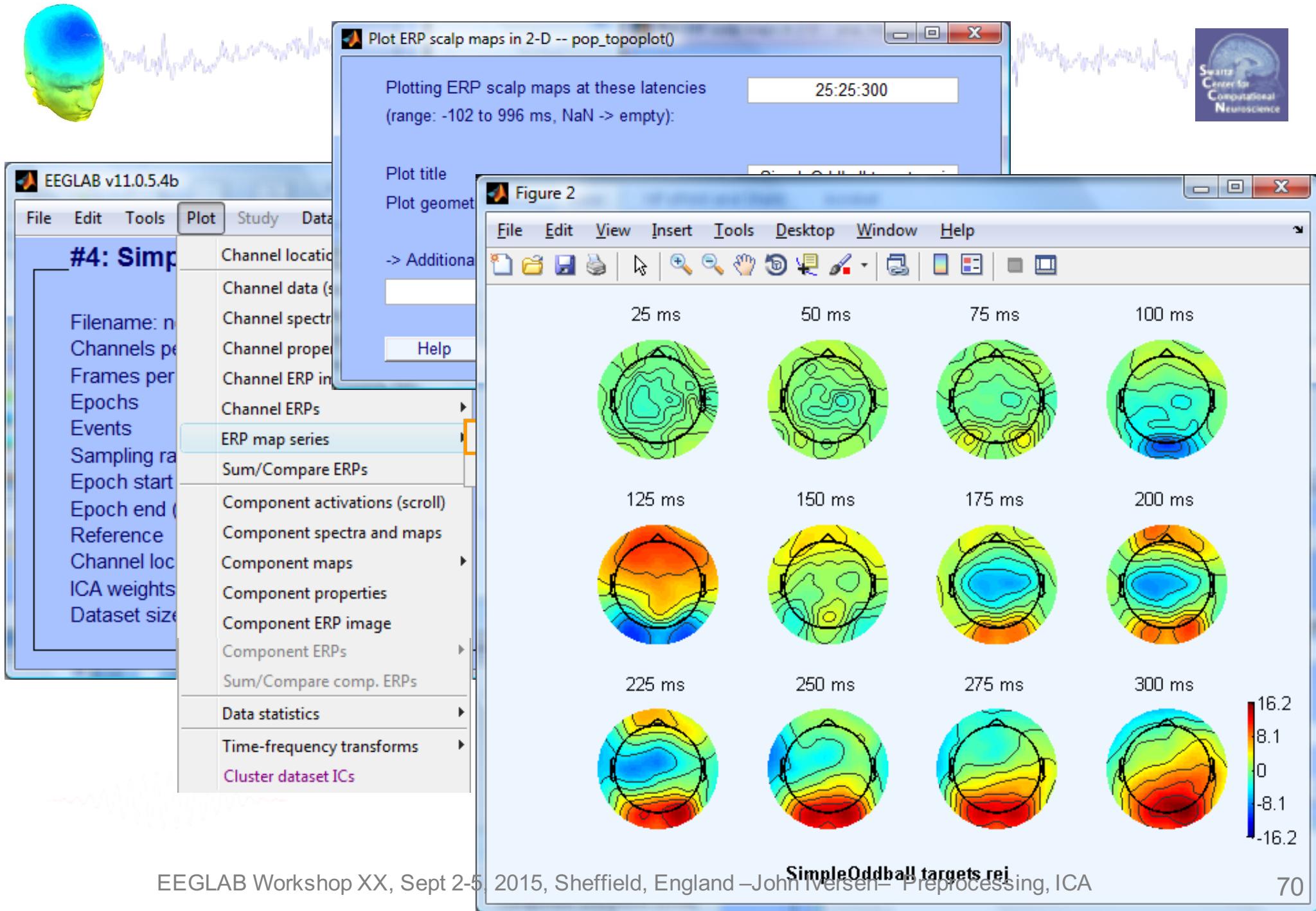
Visualize ERP in topographic array



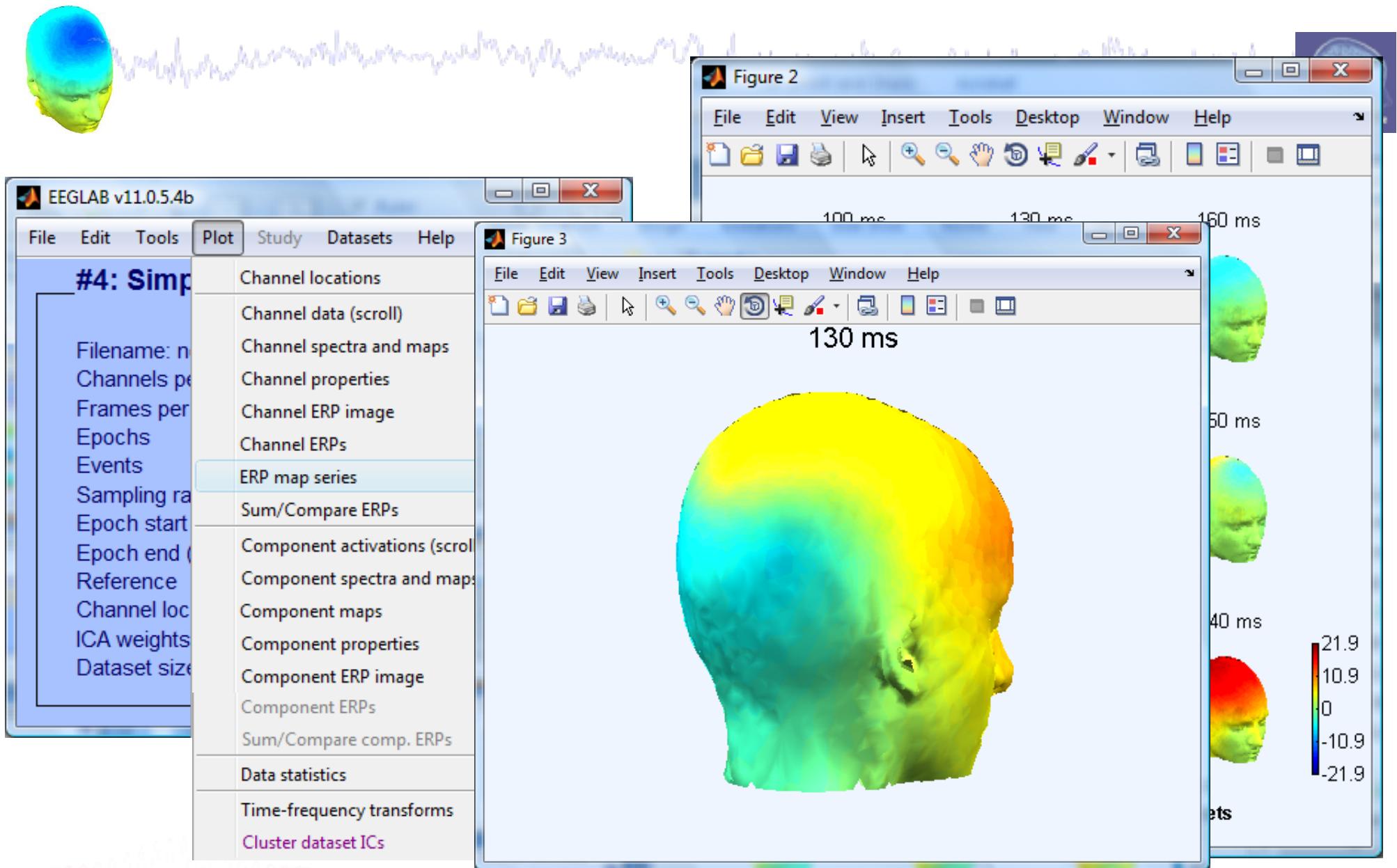
Visualize ERP scalp distribution



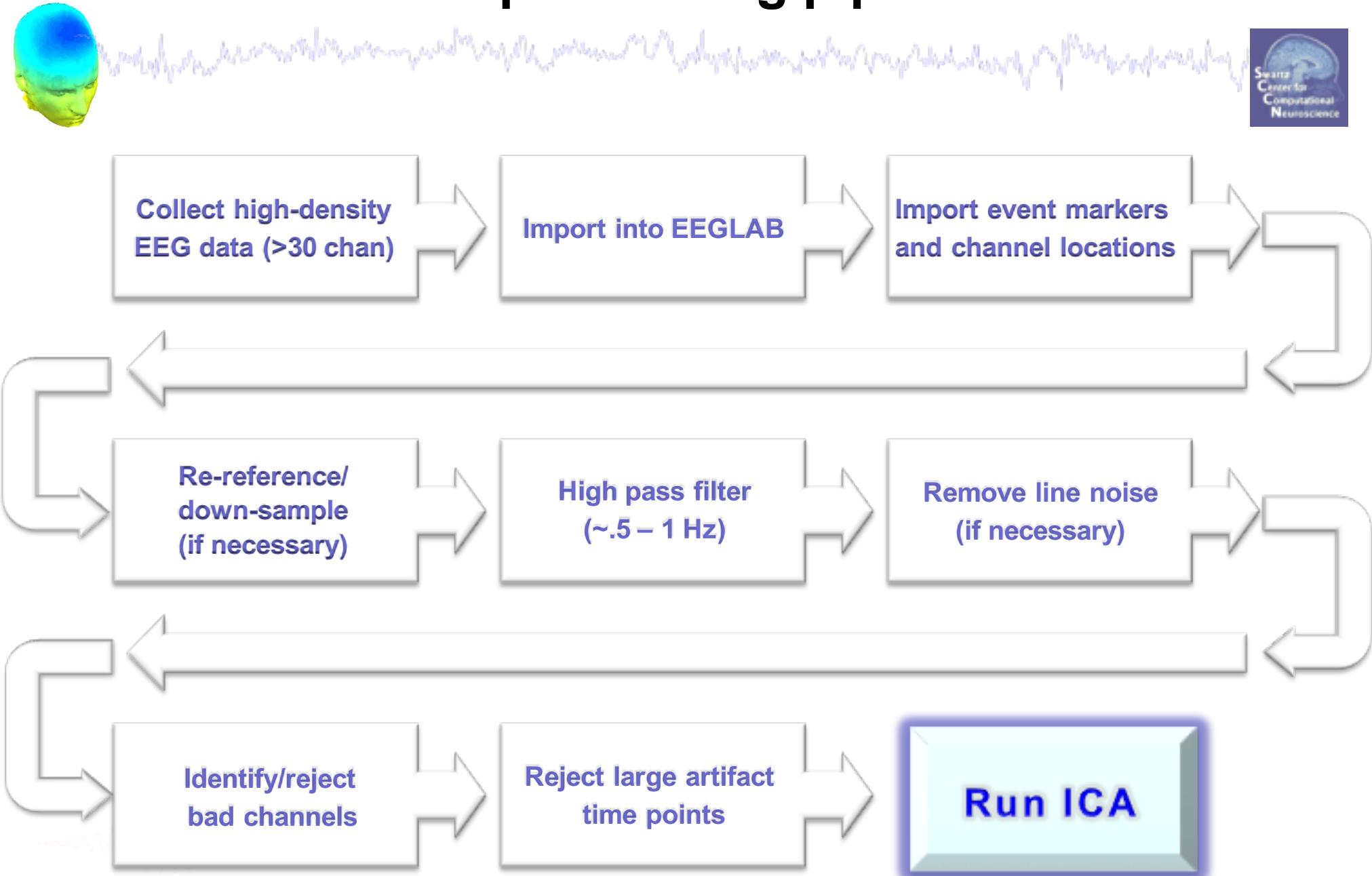
Visualize channel ERPs in 2D



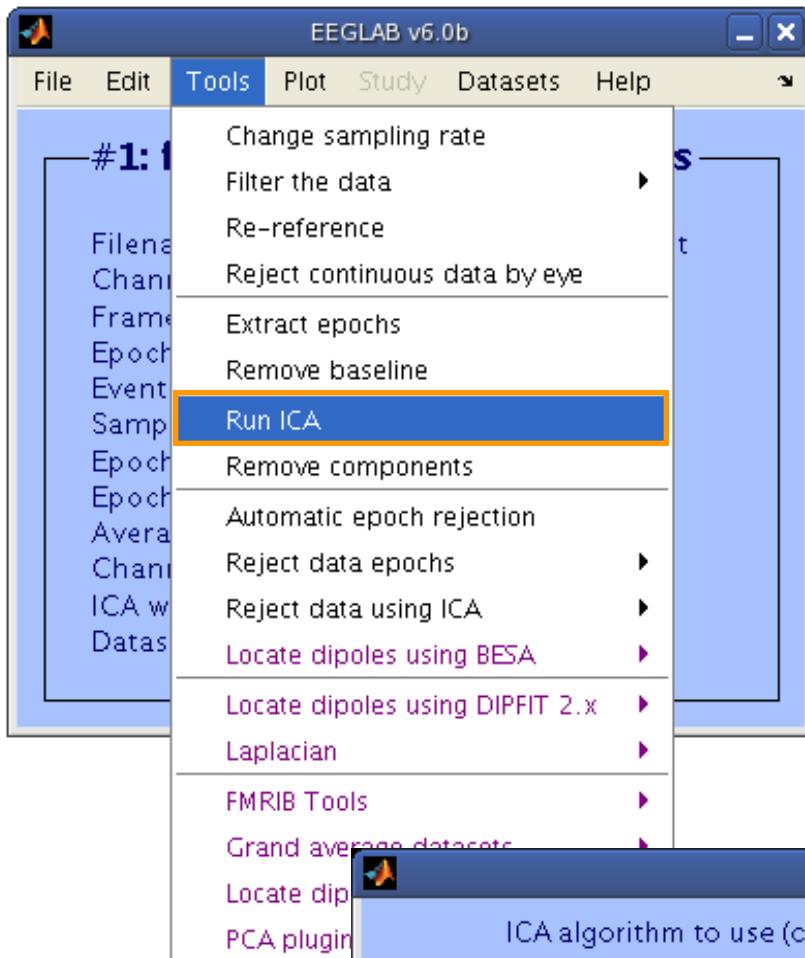
Visualize channel ERPs in 3D



Pre-processing pipeline



Finally: Runica options

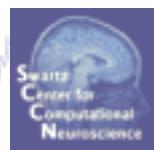
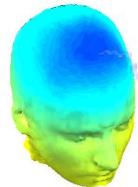


<u>Option</u>	<u>Default</u>	<u>Comments</u>
'extended'	0	1 is recommended to find sub-gaussians
'stop'	1e-7	final weight change → stop
'lrate'	determined from data	too small → too long... too large → wts blow up
'maxsteps'	512	more channels → more steps
'pca'	0 or EEG.nbchan	Decompose only a principal data subspace

Other algorithms:
binica,amica,sobi,acsobiro



Runica progress...



Press Button to interrupt runica
Interrupt

```
csh
Input data size [33,133175] = 33 channels, 133175 frames/nFinding 33 ICA components using extended ICA.
Kurtosis will be calculated initially every 1 blocks using 6000 data points.
Decomposing 122 frames per ICA weight ((1089)^2 = 133175 weights, Initial learning rate will be 0.001, block size
Learning rate will be multiplied by 0.98 whenever angledelta >= 60 deg.
More than 32 channels: default stopping weight change 1E-7
Training will end when wchange < 1e-07 or after 512 steps.
Online bias adjustment will be used.
Removing mean of each channel ...
Final training data range: -171.806 to 179.094
Computing the spherling matrix...
Starting weights are the identity matrix ...
Spherling the data ...
Beginning ICA training ... first training step may be slow ...
step 1 - lrate 0.001000, wchange 16.85061324, angledelta 0.0 deg
step 2 - lrate 0.001000, wchange 0.26760405, angledelta 0.0 deg
step 3 - lrate 0.001000, wchange 0.79058323, angledelta 104.0 deg
step 4 - lrate 0.000980, wchange 0.66700031, angledelta 147.2 deg
step 5 - lrate 0.000960, wchange 0.62849071, angledelta 146.5 deg
step 6 - lrate 0.000941, wchange 0.73967955, angledelta 150.7 deg
step 7 - lrate 0.000922, wchange 0.73727229, angledelta 151.6 deg
step 8 - lrate 0.000904, wchange 0.74051387, angledelta 137.9 deg
step 9 - lrate 0.000886, wchange 0.74536137, angledelta 156.0 deg
step 10 - lrate 0.000868, wchange 0.72101402, angledelta 143.7 deg
step 11 - lrate 0.000851, wchange 0.14690114, angledelta 102.5 deg
step 12 - lrate 0.000834, wchange 0.11822100, angledelta 114.3 deg
step 13 - lrate 0.000817, wchange 0.75552966, angledelta 100.6 deg
step 14 - lrate 0.000801, wchange 0.26739750, angledelta 109.1 deg
step 15 - lrate 0.000785, wchange 0.12123251, angledelta 94.2 deg
step 16 - lrate 0.000769, wchange 0.10285606, angledelta 110.7 deg
step 17 - lrate 0.000754, wchange 0.09770499, angledelta 118.6 deg
step 18 - lrate 0.000739, wchange 0.09544428, angledelta 117.1 deg
step 241 - lrate 0.000002, wchange 0.00000082, angledelta 101.5 deg
step 242 - lrate 0.000001, wchange 0.00000061, angledelta 96.1 deg
step 243 - lrate 0.000001, wchange 0.00000057, angledelta 97.5 deg
step 244 - lrate 0.000001, wchange 0.00000054, angledelta 93.7 deg
step 245 - lrate 0.000001, wchange 0.00000055, angledelta 100.3 deg
step 246 - lrate 0.000001, wchange 0.00000047, angledelta 96.9 deg
step 247 - lrate 0.000001, wchange 0.00000046, angledelta 91.3 deg
step 248 - lrate 0.000001, wchange 0.00000045, angledelta 101.5 deg
step 249 - lrate 0.000001, wchange 0.00000041, angledelta 103.1 deg
step 250 - lrate 0.000001, wchange 0.00000036, angledelta 95.5 deg
step 251 - lrate 0.000001, wchange 0.00000033, angledelta 92.1 deg
step 252 - lrate 0.000001, wchange 0.00000029, angledelta 97.4 deg
step 253 - lrate 0.000001, wchange 0.00000030, angledelta 95.8 deg
step 254 - lrate 0.000001, wchange 0.00000023, angledelta 94.2 deg
step 255 - lrate 0.000001, wchange 0.00000023, angledelta 97.6 deg
step 256 - lrate 0.000001, wchange 0.00000023, angledelta 97.1 deg
step 257 - lrate 0.000001, wchange 0.00000021, angledelta 92.0 deg
step 258 - lrate 0.000001, wchange 0.00000020, angledelta 99.1 deg
step 259 - lrate 0.000001, wchange 0.00000019, angledelta 95.0 deg
step 260 - lrate 0.000001, wchange 0.00000015, angledelta 98.3 deg
step 261 - lrate 0.000001, wchange 0.00000014, angledelta 99.0 deg
step 262 - lrate 0.000001, wchange 0.00000014, angledelta 94.3 deg
step 263 - lrate 0.000001, wchange 0.00000013, angledelta 95.4 deg
step 264 - lrate 0.000001, wchange 0.00000012, angledelta 94.1 deg
step 265 - lrate 0.000001, wchange 0.00000011, angledelta 96.1 deg
step 266 - lrate 0.000001, wchange 0.00000010, angledelta 94.8 deg
step 267 - lrate 0.000001, wchange 0.00000010, angledelta 94.5 deg
step 268 - lrate 0.000001, wchange 0.00000010, angledelta 97.7 deg
step 269 - lrate 0.000001, wchange 0.00000008, angledelta 95.1 deg
Sorting components in descending order of mean projected variance ...
Permuting the activation wave forms ...
>>
```

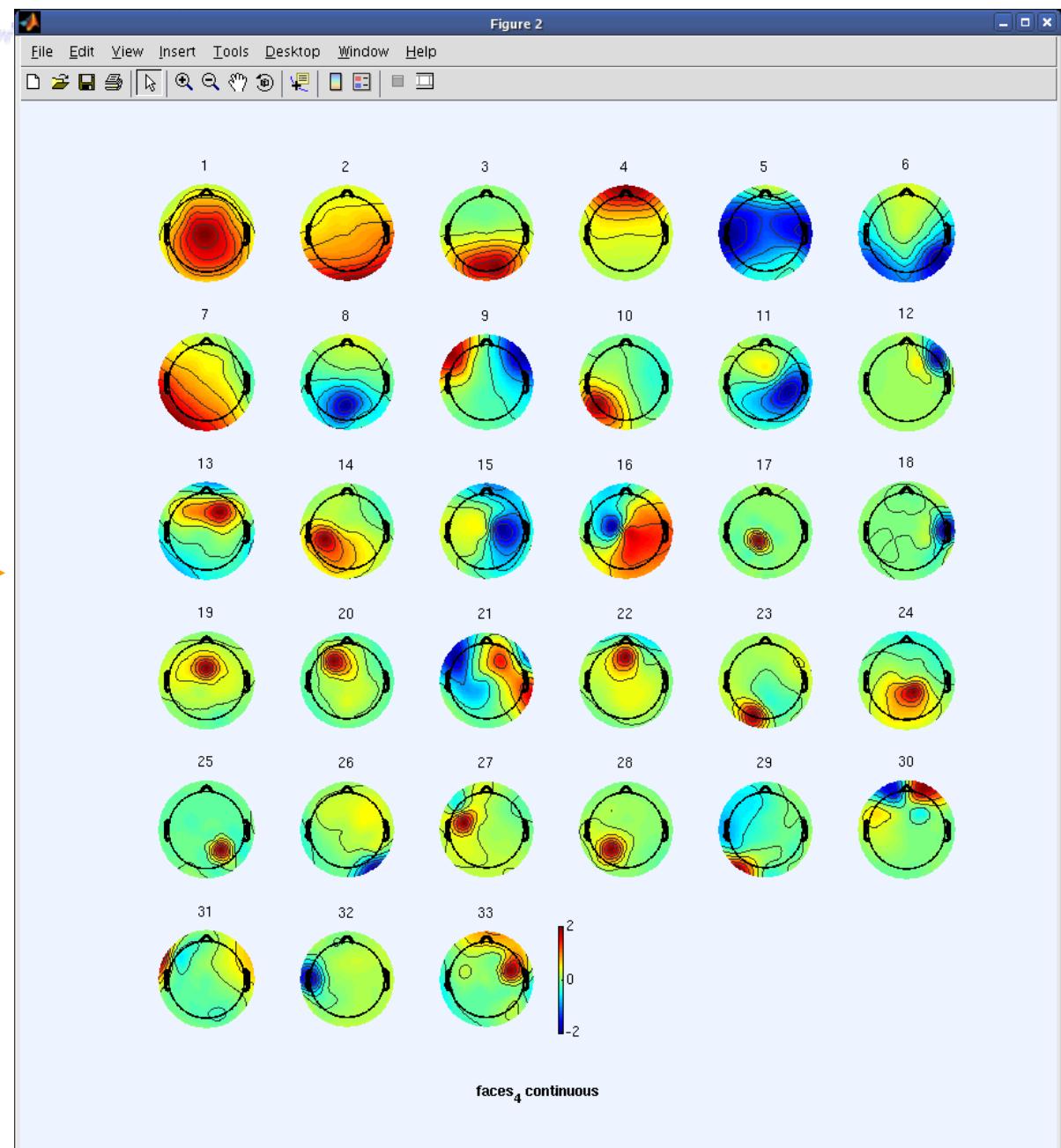
ICA weights in EEG structure

```
Terminal
File Edit View Terminal Tabs Help
>> EEG

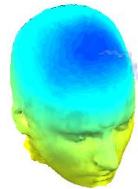
EEG = 

    setname: 'faces_4 continuous'
    filename: 'faces_4.set'
    filepath: '/home/julie/workshop06/'
    subject: ''
    group: ''
    condition: ''
    session: []
    comments: [15x48 char]
    nbchan: 33
    trials: 1
    pnts: 133175
    srate: 250
    xmin: 0
    xmax: 532.6960
    times: []
    data: [33x133175 single]
    icaact: [33x133175 single]
    icawinv: [33x33 double] —————>
    icasphere: [33x33 double]
    icaweights: [33x33 double]
    icachansind: [1x33 double]
    chanlocs: [1x33 struct]
    urchanlocs: []
    chaninfo: [1x1 struct]
    ref: 'common'
    event: [1x731 struct]
    urevent: [1x731 struct]
    eventdescription: {[[]]}
    epoch: []
    epochdescription: {}
    reject: [1x1 struct]
    stats: [1x1 struct]
    specdata: []
    specicaact: []
    splinefile: ''
    icasplinefile: ''
    dipfit: [1x1 struct]
    history: [1x1633 char]
    saved: 'no'
    etc: []

>>
```



Exercises (optional homework)



- Preprocess data of your choice or load a previously filtered dataset e.g. faces_4.set
- Identify bad channel(s) using auto-detection tool; plot channel properties of flagged channels
- Identify and remove non-task portions of continuous data; see if the previously flagged channels are still identified as bad
- Epoch on event of interest. Scroll the epoched data and perform visual rejection of epochs
- Explore the automated artifact rejection tools
- Run ICA