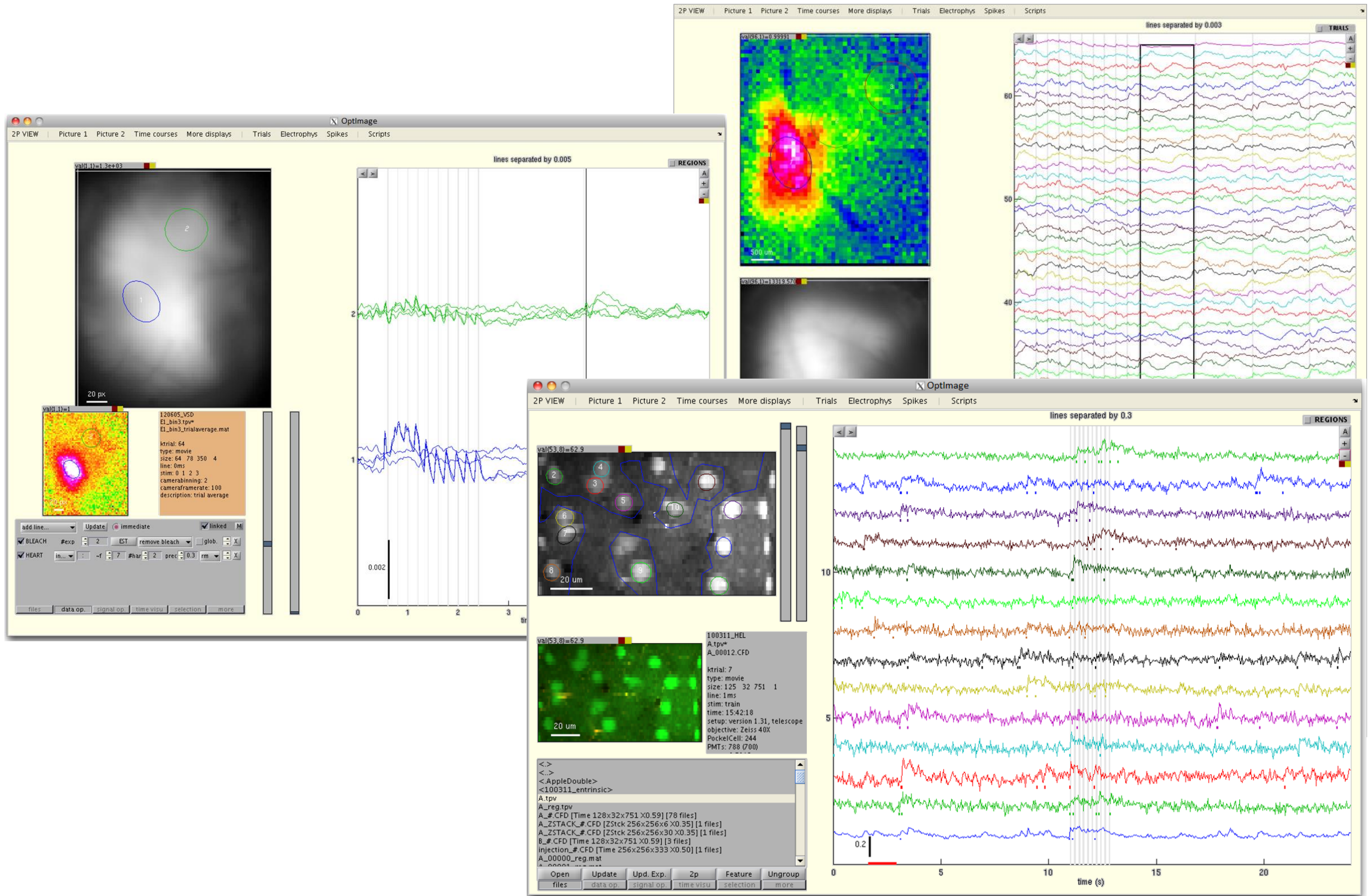


OptImage



Requirements

- Matlab 7.14 (R2012a) or later with
 - Image Toolbox
 - Optimization toolbox (necessary only for specific functionalities such as the correction for bleaching and for heart artifact)
- 8GB RAM or more is recommended for analyzing large data

Installation

- Unzip the program to a target location
- Run the function 'optimage.m' in Matlab
- Press the button 'request a license number' to get an identifier unique to your machine and send it to your provider
- Once your provider returned a license number to you, start again the program, press button 'activate your license' and copy the number there

I. Quick Tour

- 1) Processing the data
- 2) Visualizing the data
- 3) Other useful tools

1) Processing the data

a. Open the data

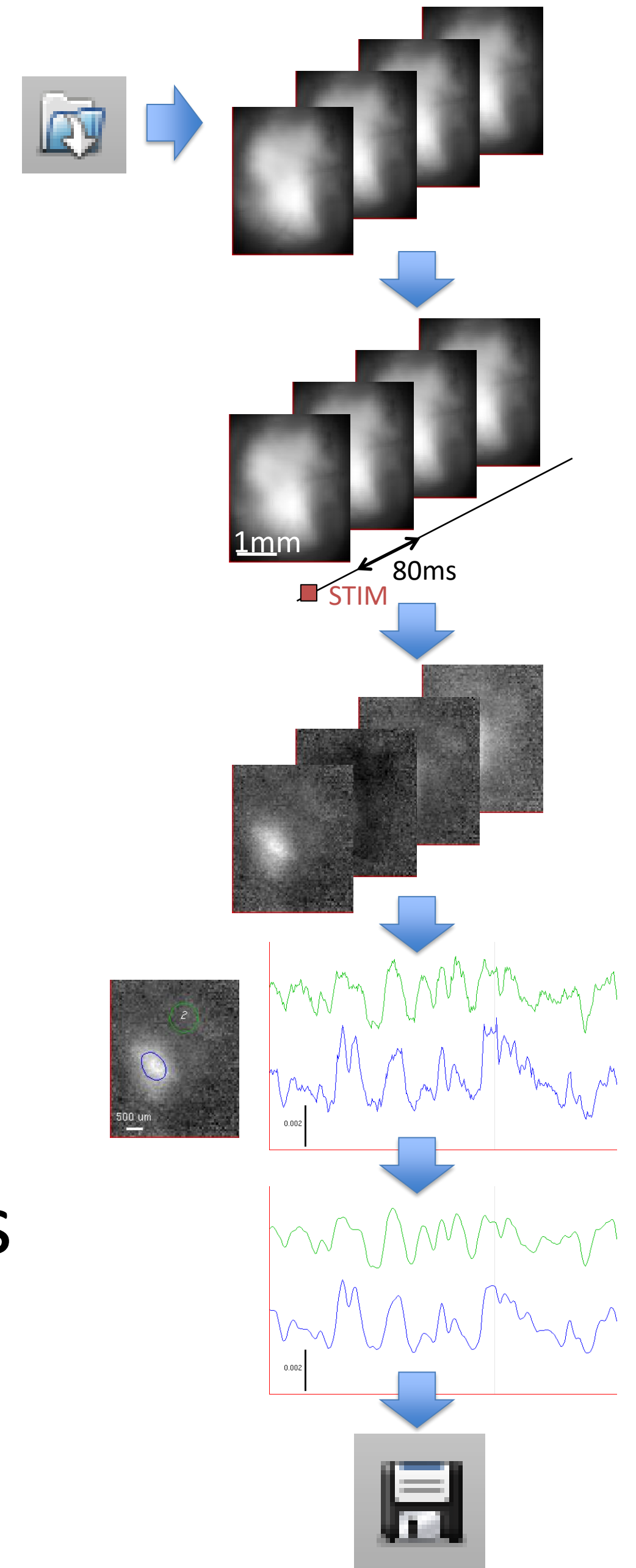
b. Header information

c. Operations on movie data

d. Extraction of time courses

e. Operations on time courses

f. Save



1)a. Open the data

The screenshot displays the 2P VIEW software interface. The top menu bar includes '2P VIEW', 'Picture 1', 'Picture 2', 'Time courses', 'More displays', 'Trials', 'Electrophys', 'Spikes', and 'Scripts'. The '2P VIEW' menu is open, showing options like 'Resize frames', 'Preset positions', 'Edit code', 'Reinit menus', 'Object in base workspace', 'Save PNG', 'Copy sub-part...', 'More', 'Preferences...', 'New window', 'Open...', 'Bin and open...', 'Save', 'Save as...', 'Comments', 'Auto-repair (light)', 'Auto-repair (heavy)', 'More repairs...', 'Edit code', 'access tpview object', and 'Trial-specific selection'. The 'Open...' option is highlighted with a red box and a callout bubble that says 'Open from the menu'. Below the menu, there is a small thumbnail image of a brain slice with a scale bar of 500 um. To the right of the thumbnail, a text box contains the following information: '120605_VSD', 'E1_bin3.tpv*', 'E1_bin3_trialaverage.mat', 'ktrial: 64', 'type: movie', 'size: 64 78 350 4', 'line: 0ms', 'stim: 0 1 2 3', 'camerabinning: 2', 'cameraframerate: 100', and 'description: trial average'. At the bottom left, a file list is shown with a red box around it and a callout bubble that says 'or use the « files panel »'. The file list includes: '<correlations>', '<data>', '<forpa>', '<vdaq>', 'E0(barrel).tpv', 'E1_bin3.tpv', 'E1_bin3_corrected.tpv', 'E1_bin4.tpv', 'E1_bin4_corrected.tpv', and '.DS_Store'. Below the file list are buttons for 'Open', 'Update', 'Upd. Exp.', '2P', 'VSD', 'Unaroup', 'files', 'data op.', 'signal op.', 'time visu', 'selection', and 'more'. The main window displays two time-series plots. The top plot shows a green line representing a signal over time, with a scale bar of 0.0075. The bottom plot shows a blue line representing a signal over time, with a scale bar of 0.002. The x-axis for both plots is labeled 'time (s)' and ranges from 0 to 6.

2P VIEW: E1_bin3

lines separated by 0.0075

REGIONS

Open from the menu

or use the « files panel »

120605_VSD
E1_bin3.tpv*
E1_bin3_trialaverage.mat

ktrial: 64
type: movie
size: 64 78 350 4
line: 0ms
stim: 0 1 2 3
camerabinning: 2
cameraframerate: 100
description: trial average

500 um

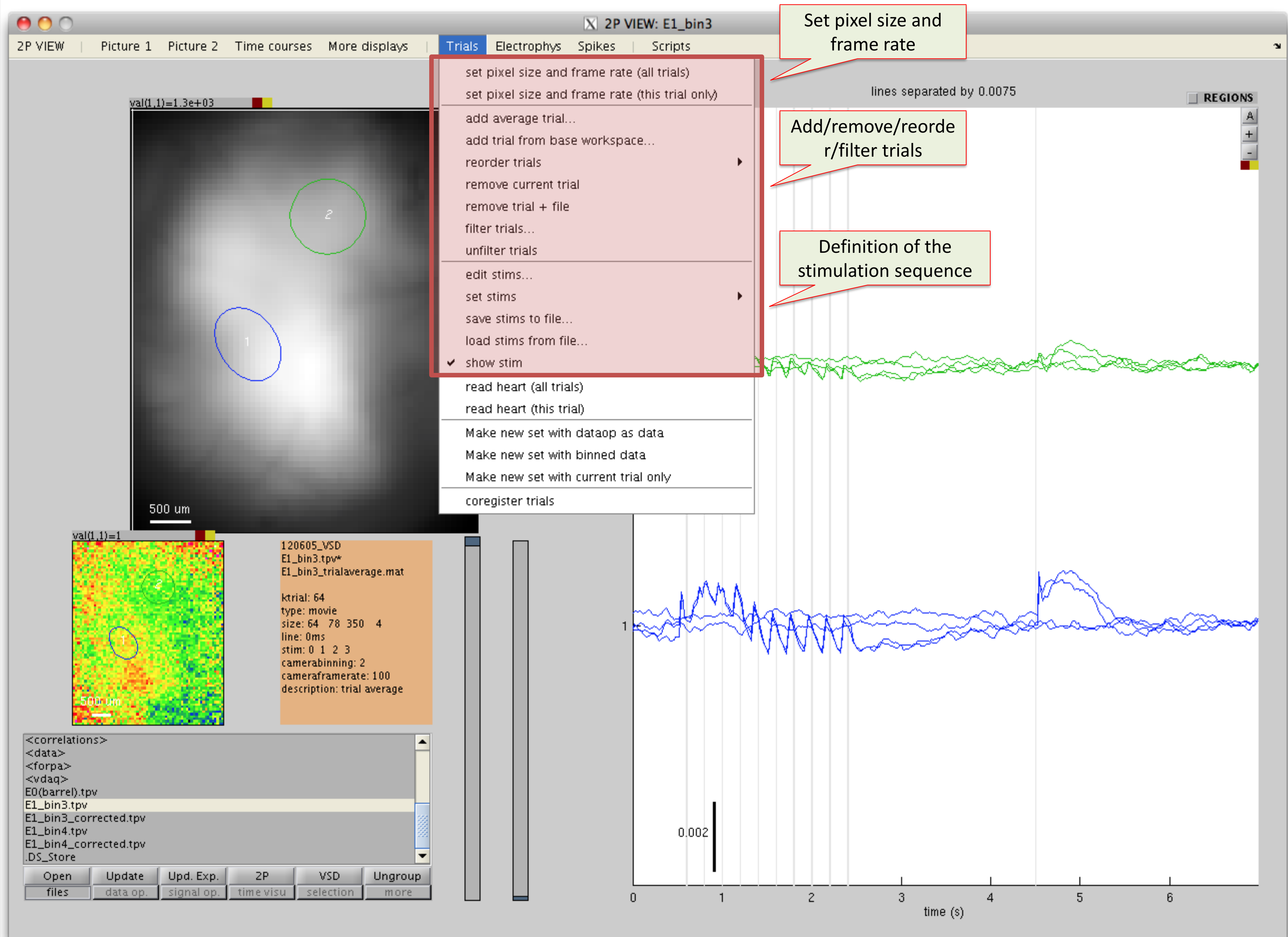
<correlations>
<data>
<forpa>
<vdaq>
E0(barrel).tpv
E1_bin3.tpv
E1_bin3_corrected.tpv
E1_bin4.tpv
E1_bin4_corrected.tpv
.DS_Store

Open Update Upd. Exp. 2P VSD Unaroup
files data op. signal op. time visu selection more

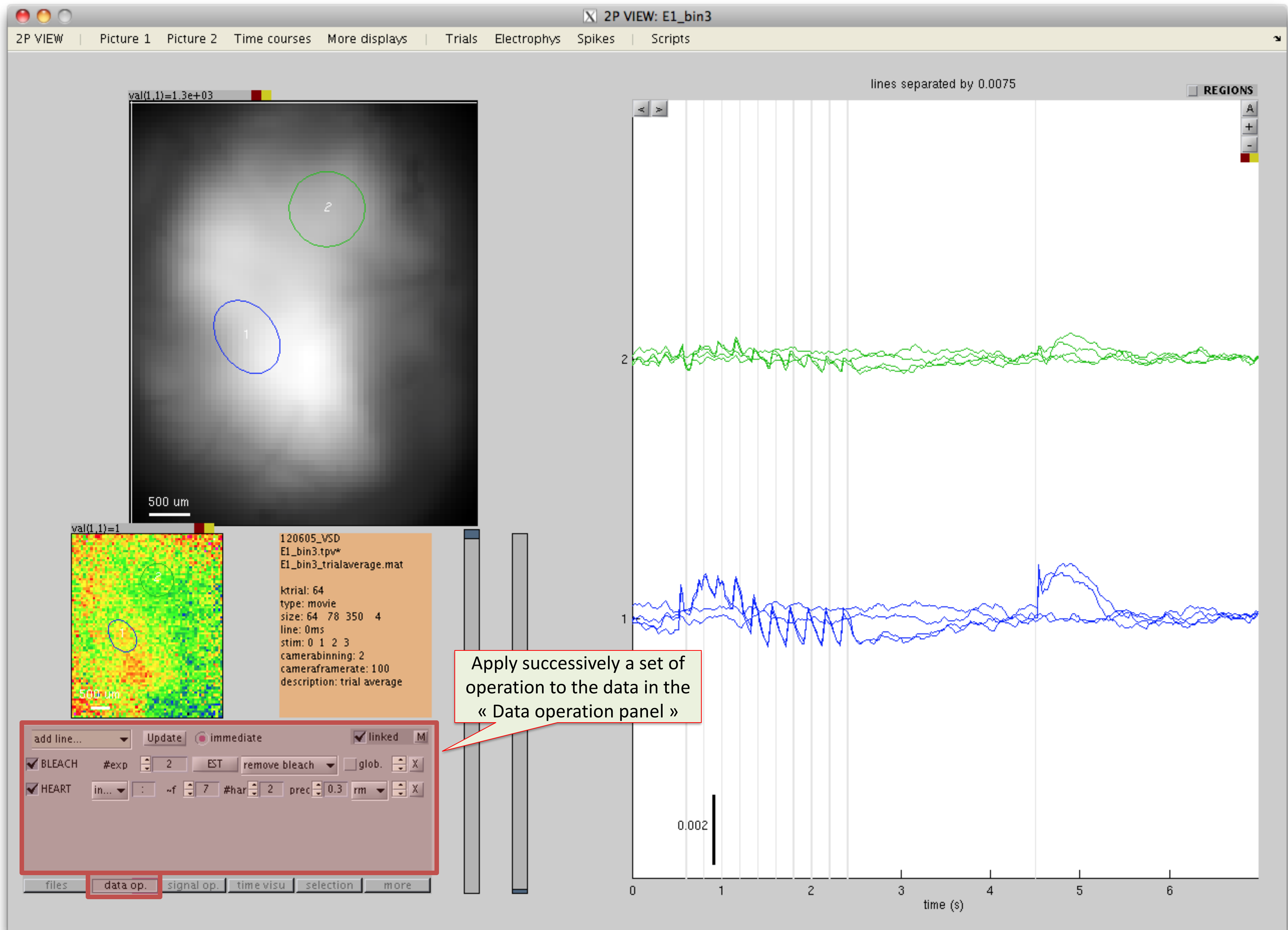
0.002

time (s)

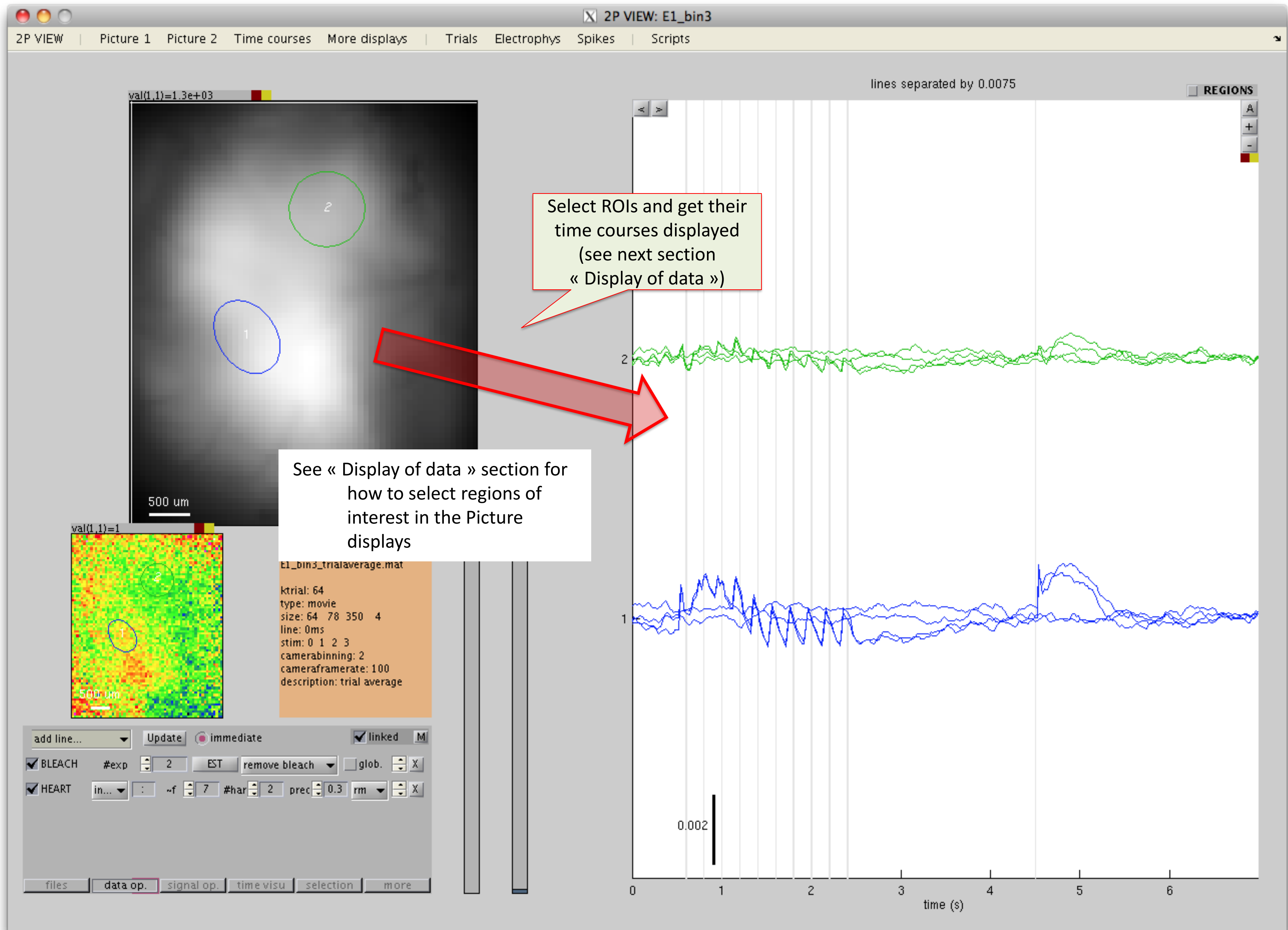
1)b. Header information



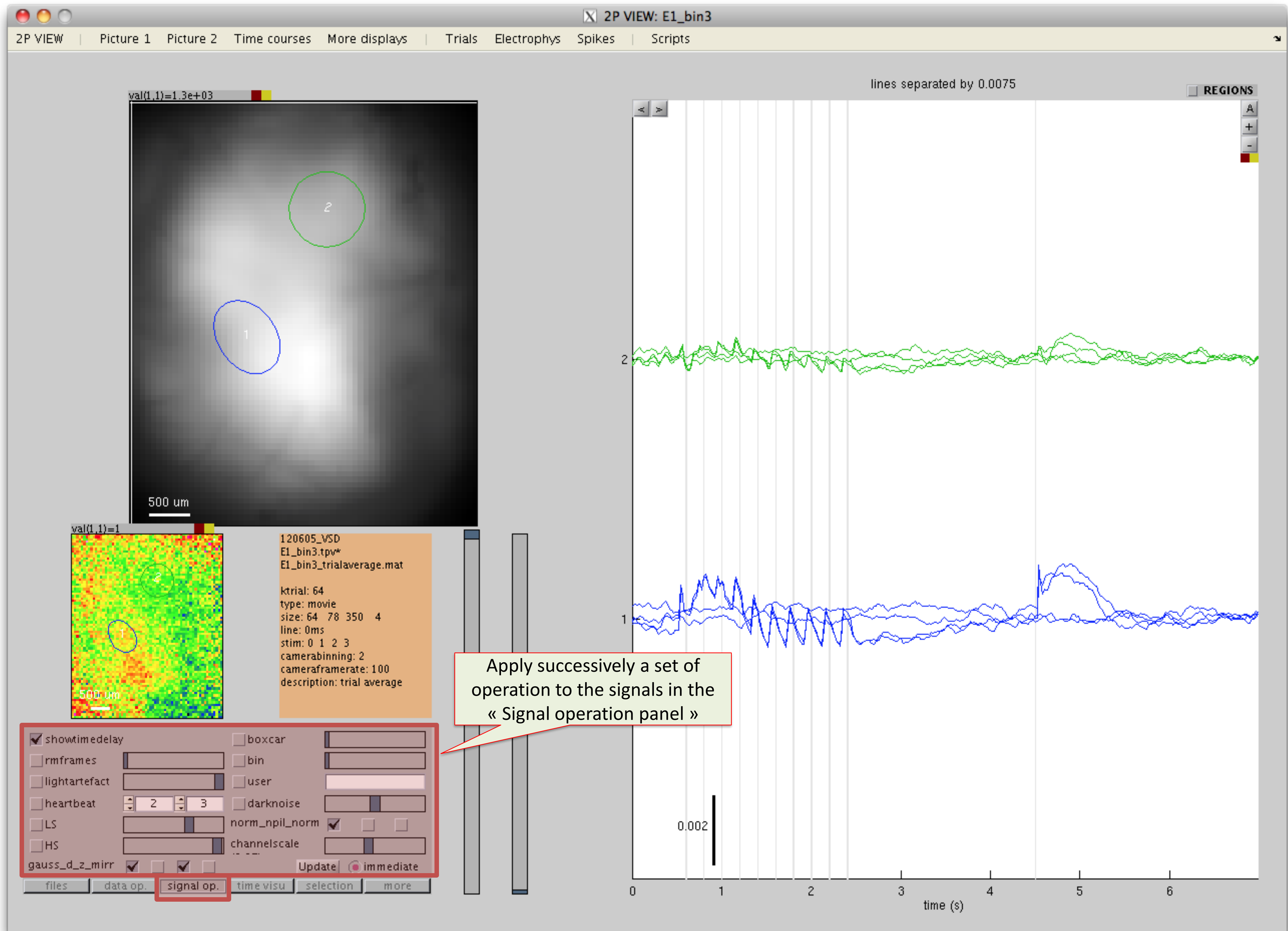
1)c. Operations on movie data



1)d. Extraction of time courses



1)e. Operations on time courses



1)f. Save

The screenshot displays the 2P VIEW software interface with the 'Trials' menu open. The menu options are as follows:

- Resize frames
- Preset positions
- Edit code
- Reinit menus
- Object in base workspace
- Save PNG (Ctrl+P)
- Copy sub-part...
- More
- Preferences...
- New window (Ctrl+N)
- Open... (Ctrl+O)
- Bin and open...
- Save (Ctrl+S)**
- Save as...
- Comments
- Auto-repair (light)
- Auto-repair (heavy)
- More repairs...
- Edit code
- access tpview object
- ✓ Trial-specific selection
 - load data at opening
 - avoid loading data
 - read data

Below the menu, a small heatmap shows a 500 µm scale bar. To its right, a text box contains the following information:

120605_VSD
E1_bin3.tpv*
E1_bin3_trialaverage.mat

ktrial: 64
type: movie
size: 64 78 350 4
line: 0ms
stim: 0 1 2 3
camerabinning: 2
cameraframerate: 100
description: trial average

The bottom of the interface features a control panel with various checkboxes and sliders, including 'showtimedelay', 'rmframes', 'lightartefact', 'heartbeat', 'LS', 'HS', 'gauss_d_z_mirr', 'boxcar', 'bin', 'user', 'darknoise', 'norm_npil_norm', and 'channelscale'. There are also 'Update' and 'immediate' buttons.

On the right side, two plots are visible. The top plot shows 'lines separated by 0.0075' with a 'REGIONS' button. The bottom plot shows 'time (s)' on the x-axis (0 to 6) and a y-axis with a '0.002' scale bar. A green line plot is overlaid on the top plot, and a blue line plot is overlaid on the bottom plot.

Two callout boxes highlight specific features:

- A red box around the 'Save' menu item with the text: "Save / export / write in a comments file".
- A red box around the 'Make new set with dataop as data', 'Make new set with binned data', and 'Make new set with current trial only' options with the text: "Save a modified version of the data".

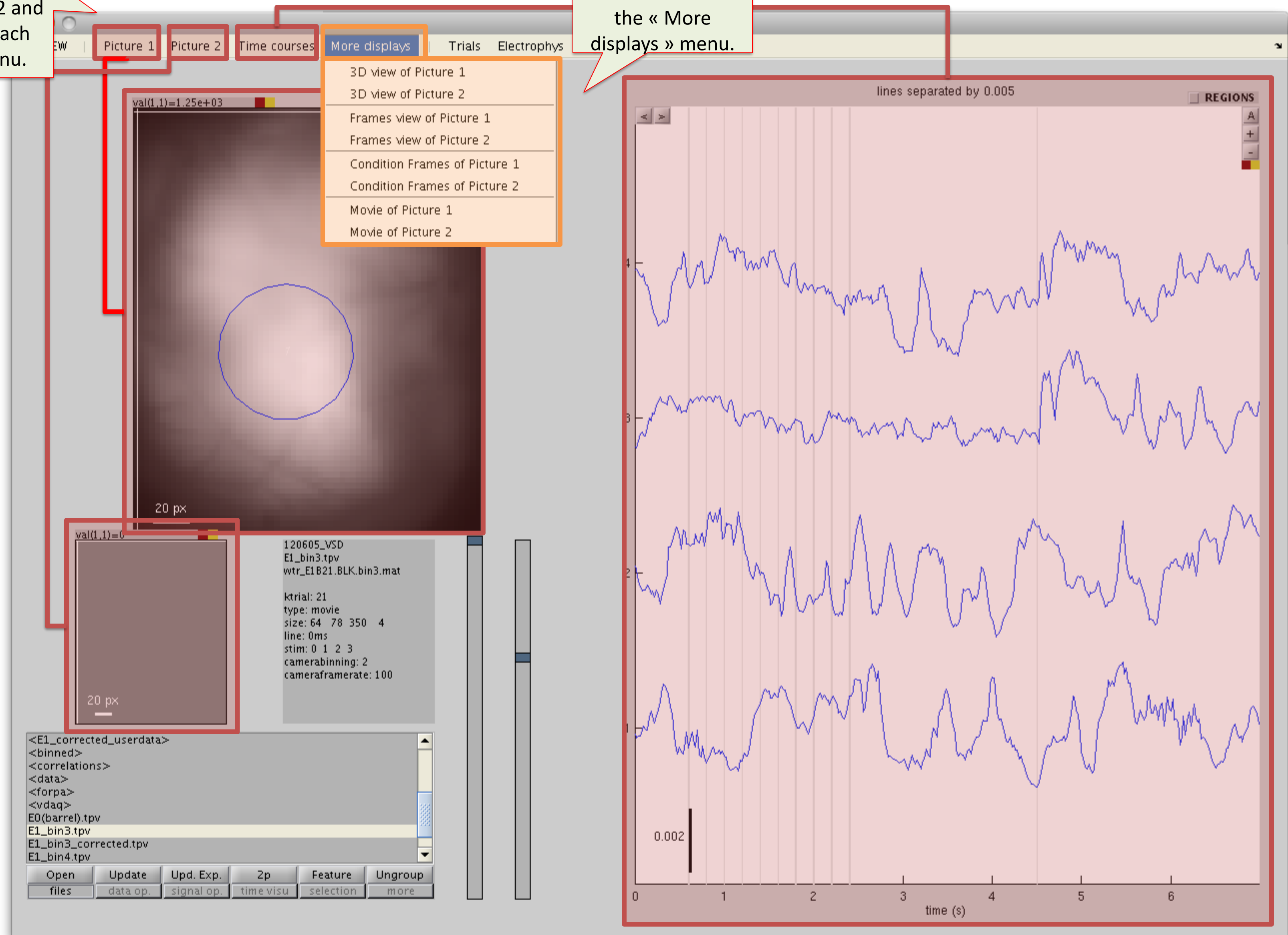
2) Visualizing the data

- a. Which displays are available?
- b. What to show in each display?
 - Picture1 and Picture2
 - Time Courses
- c. Display options
 - Picture1 and Picture2
 - Time Courses
- d. Mouse actions
 - Principles of region selection
 - Table of mouse actions

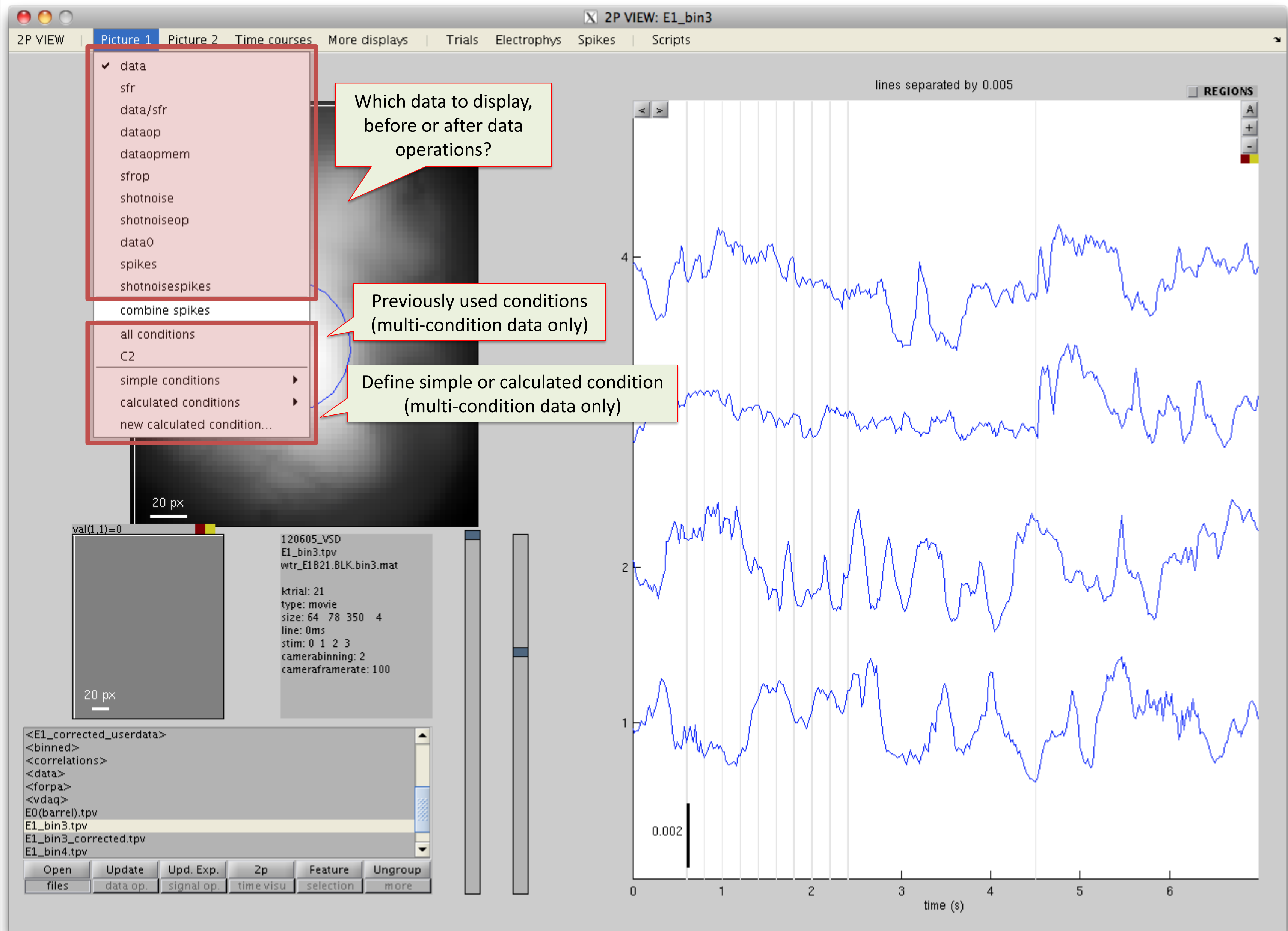
2)a. Which displays are available?

Three default displays:
Picture1, Picture2 and
Time courses. Each
has its own menu.

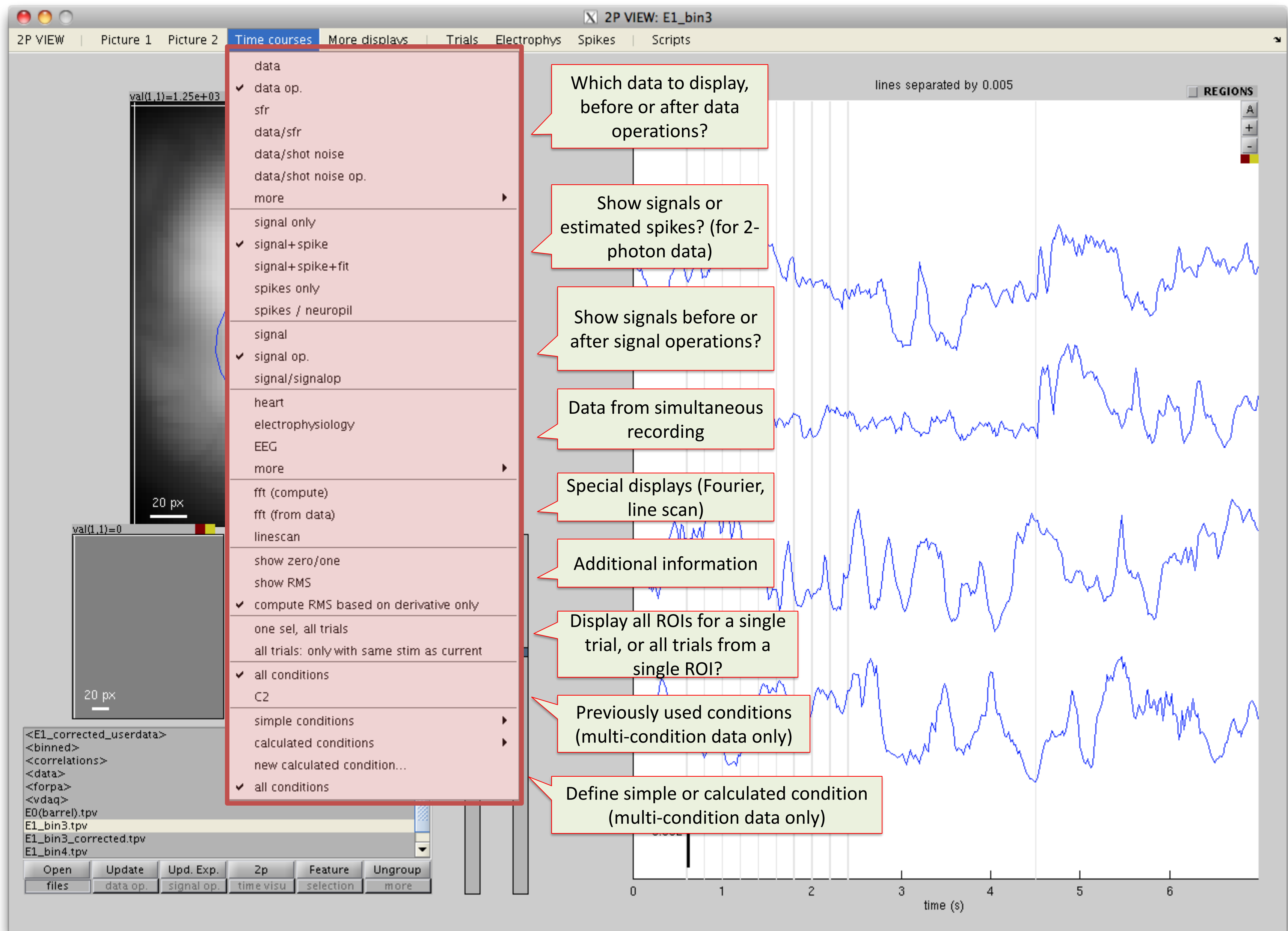
Additional displays
are available from
the « More
displays » menu.



2)b. What to display in Picture1 or Picture2



2)b. What to display in Time Courses?



2)c. Display options (Picture1 and Picture2)

Left-click on the red button to adjust the clipping

Right-click on the red button to make a menu of display options appear

- shape select poly
- shape select free
- shape select rectangle
- ✓ shape select ellipse
- shape select ring

- advanced selection
- ✓ display selection marks
- color selection marks
- reset selection display
- reset selection

- navigation
- scrollwheel zooming

- features
- color map
- clipping mode
- autoclip mode
- user clip
- binning

- distance tool
- show color bar

- duplicate in new figure
- duplicate in ...
- display in base workspace
- save picture
- repair communications

cameraframerate: 100

Shape of the ROI selection tool

Selection and display of ROIs

Rules for mouse control of zoom and pan

Display options: scale bar, color map, rules for changing the clipping, binning...

Additional tools: distance tool; show the color bar

<E1_corrected_userdata>
<binned>
<correlations>
<data>
<forpa>
<vdaq>
E0(barrel).tpv
E1_bin3.tpv
E1_bin3_corrected.tpv
E1_bin4.tpv

Open Update Upd. Exp. 2p Feature Ungroup
files data op. signal op. time visu selection more

2P VIEW: E1_bin3
Electrophys Spikes Scripts

lines separated by 0.005

REGIONS

A
+
-
■

20 px

20 px

0.002

time (s)

2)c. Display options (Time Courses)

Click on 'A' to switch between 3 automatic display modes:

- exact display
- dispatch regions
- dispatch conditions

Click on '+' or '-' to adjust the size.

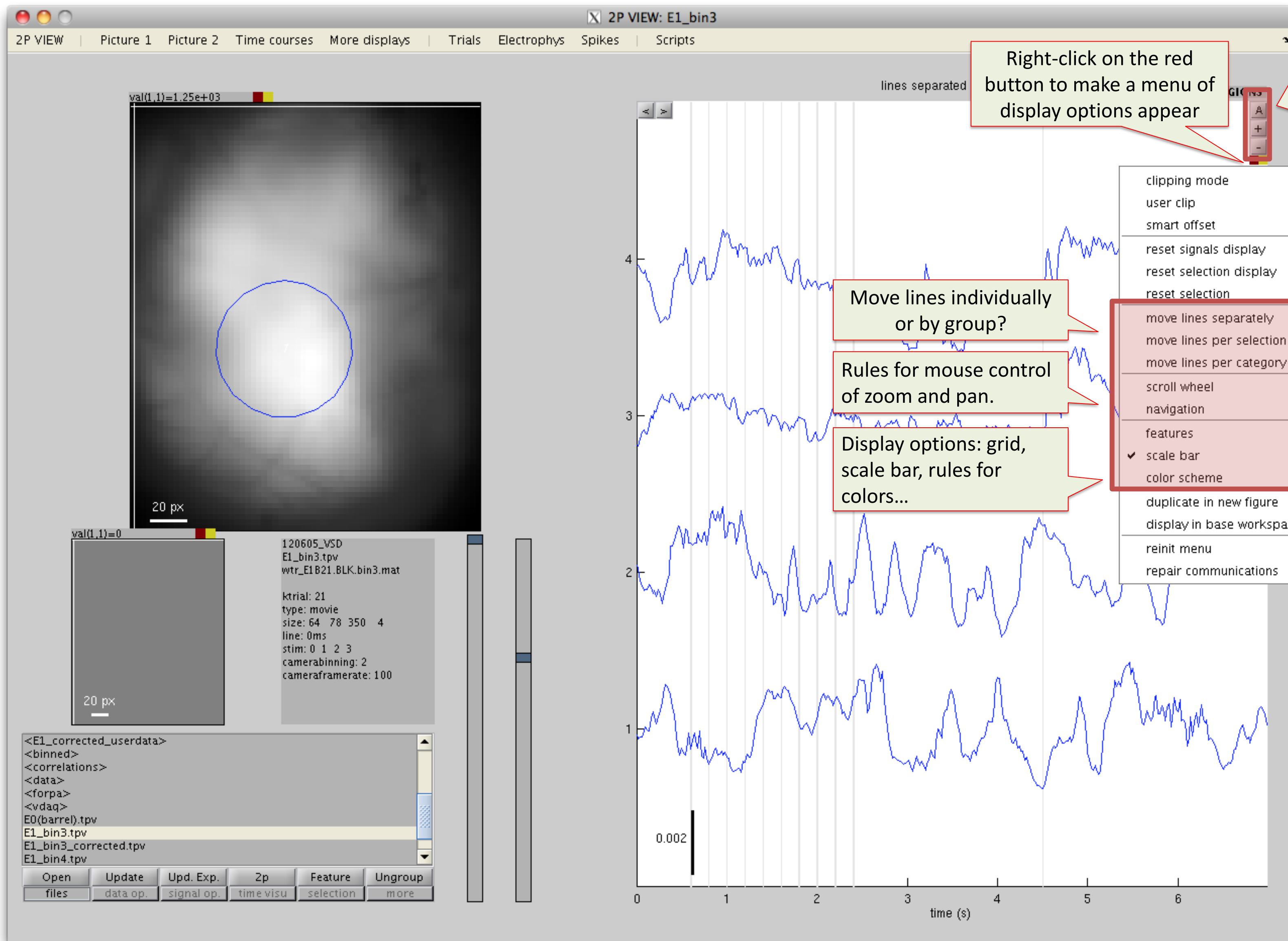
Right-click on the red button to make a menu of display options appear

Move lines individually or by group?

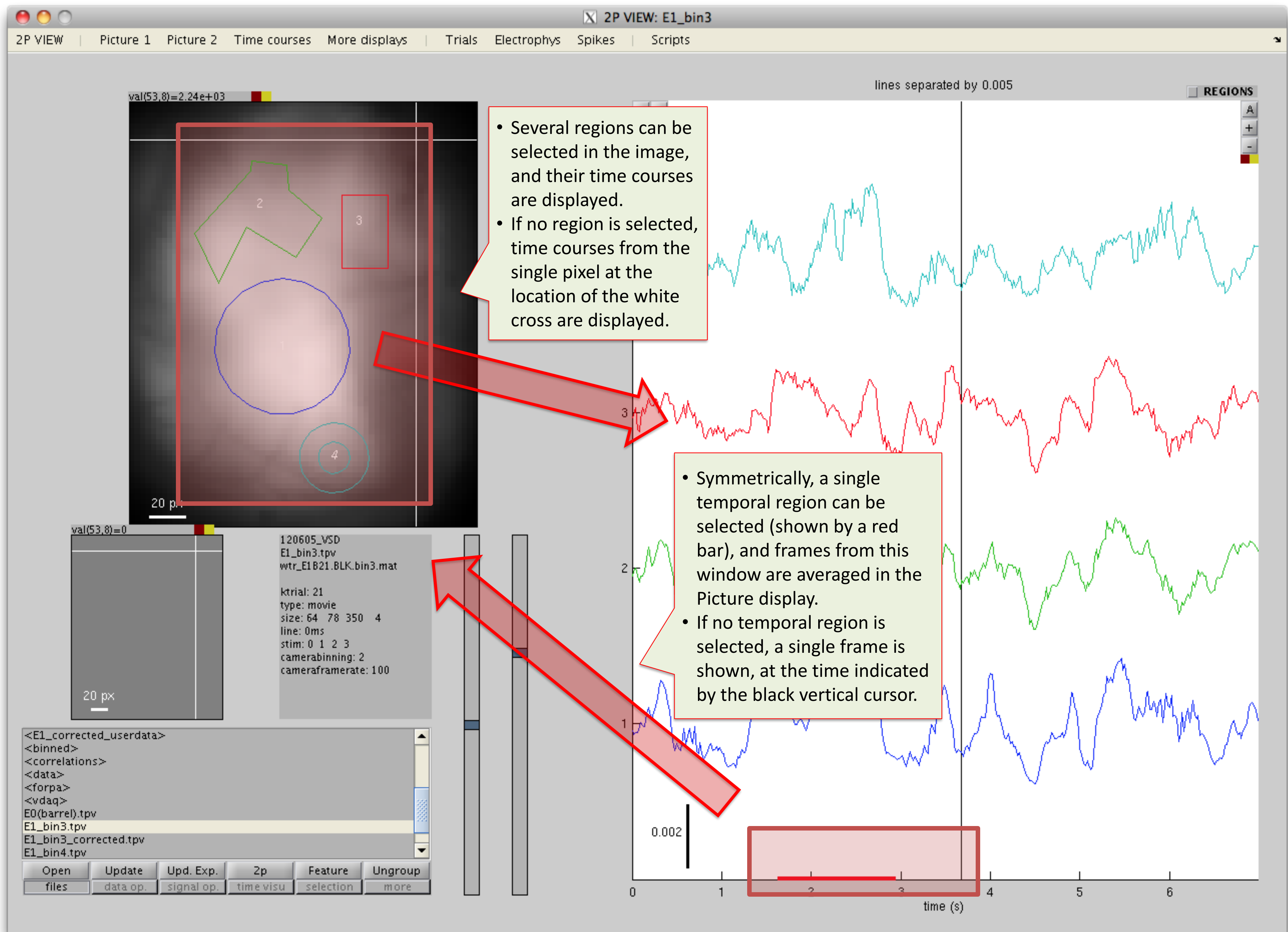
Rules for mouse control of zoom and pan.

Display options: grid, scale bar, rules for colors...

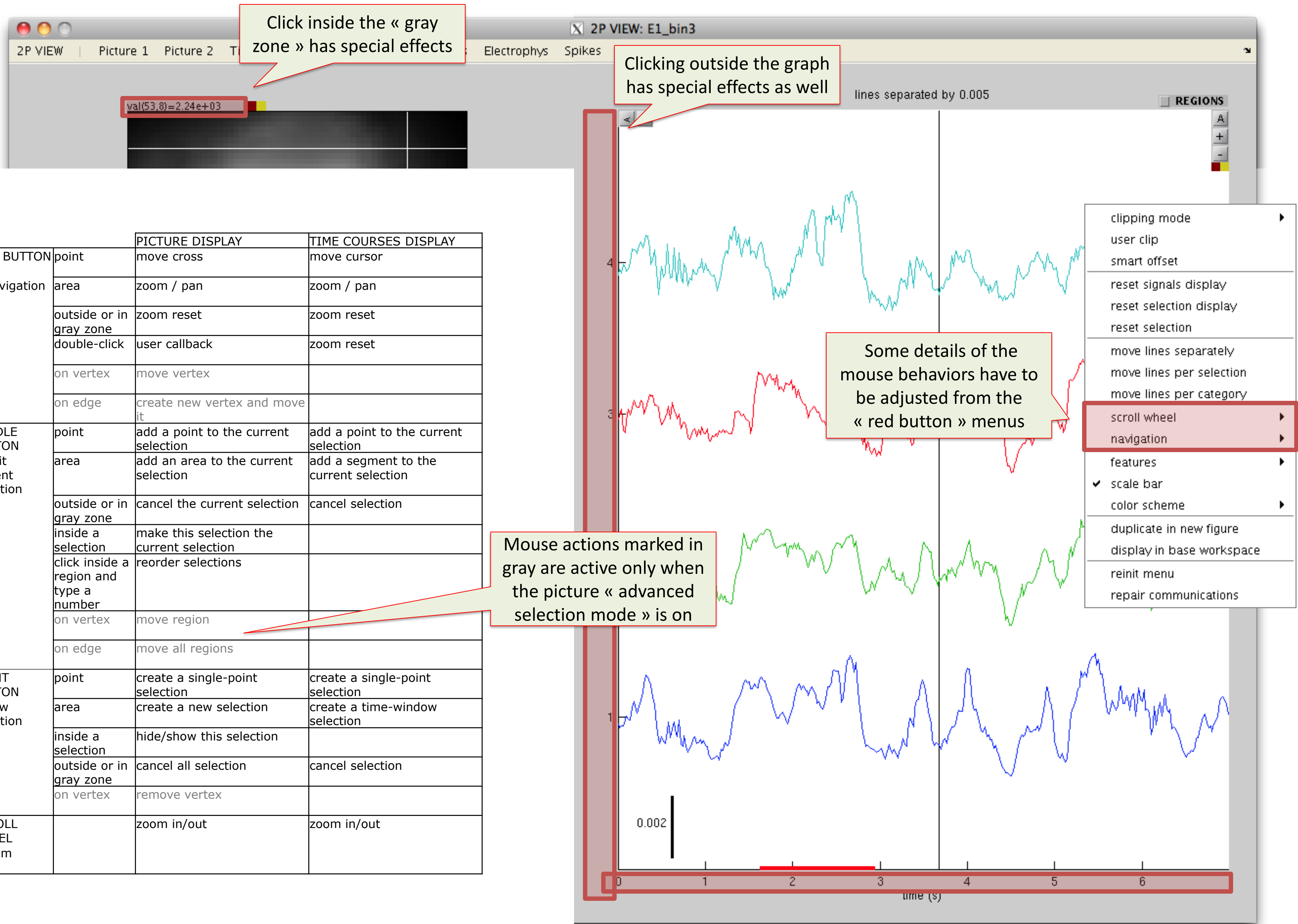
- clipping mode
 - user clip
 - smart offset
- reset signals display
- reset selection display
- reset selection
- move lines separately
- move lines per selection
- move lines per category
- scroll wheel
- navigation
- features
 - ☒ scale bar
 - color scheme
- duplicate in new figure
- display in base workspace
- reinit menu
- repair communications



2)d. Principles of region selection



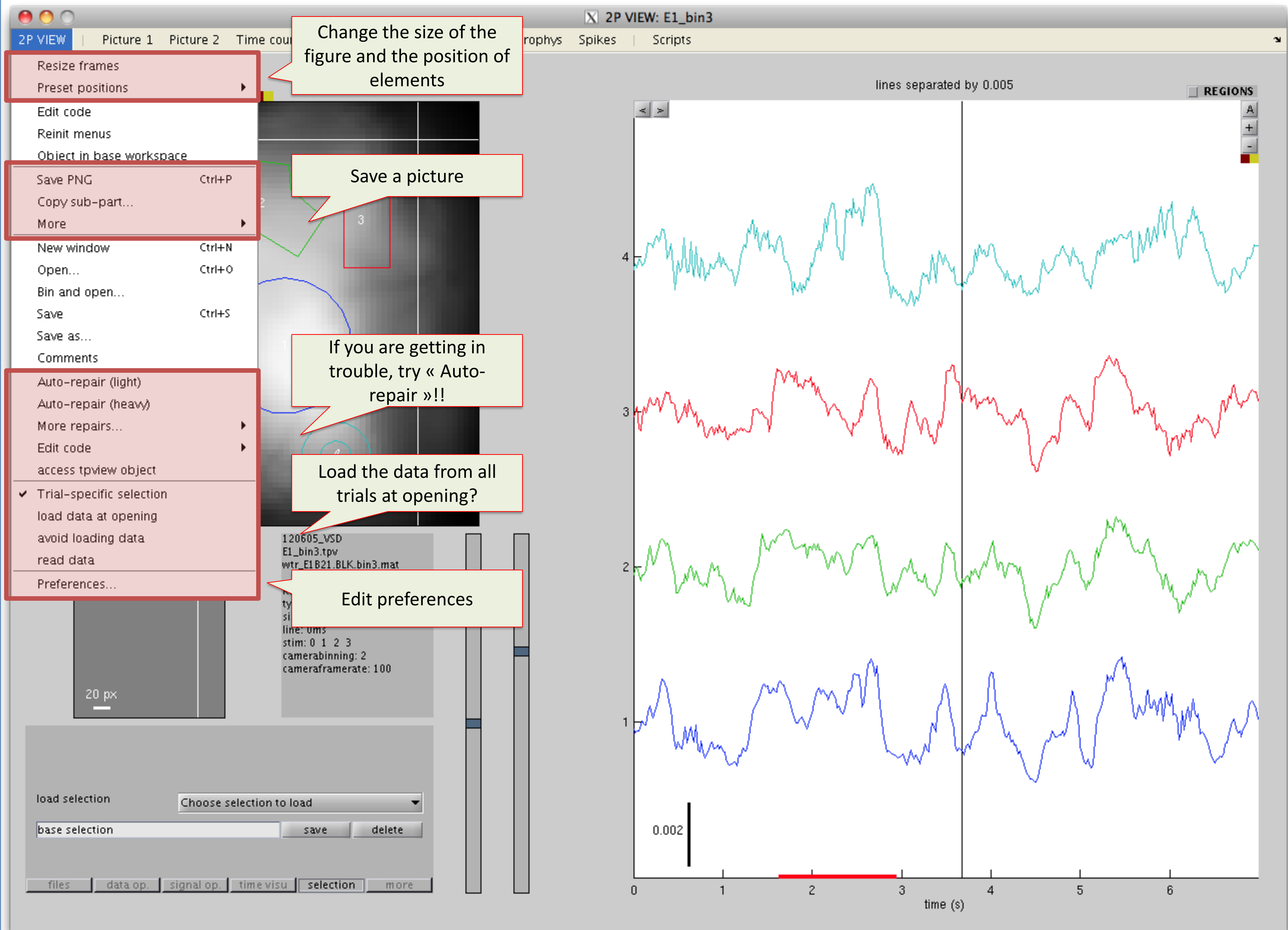
2)d. Mouse actions



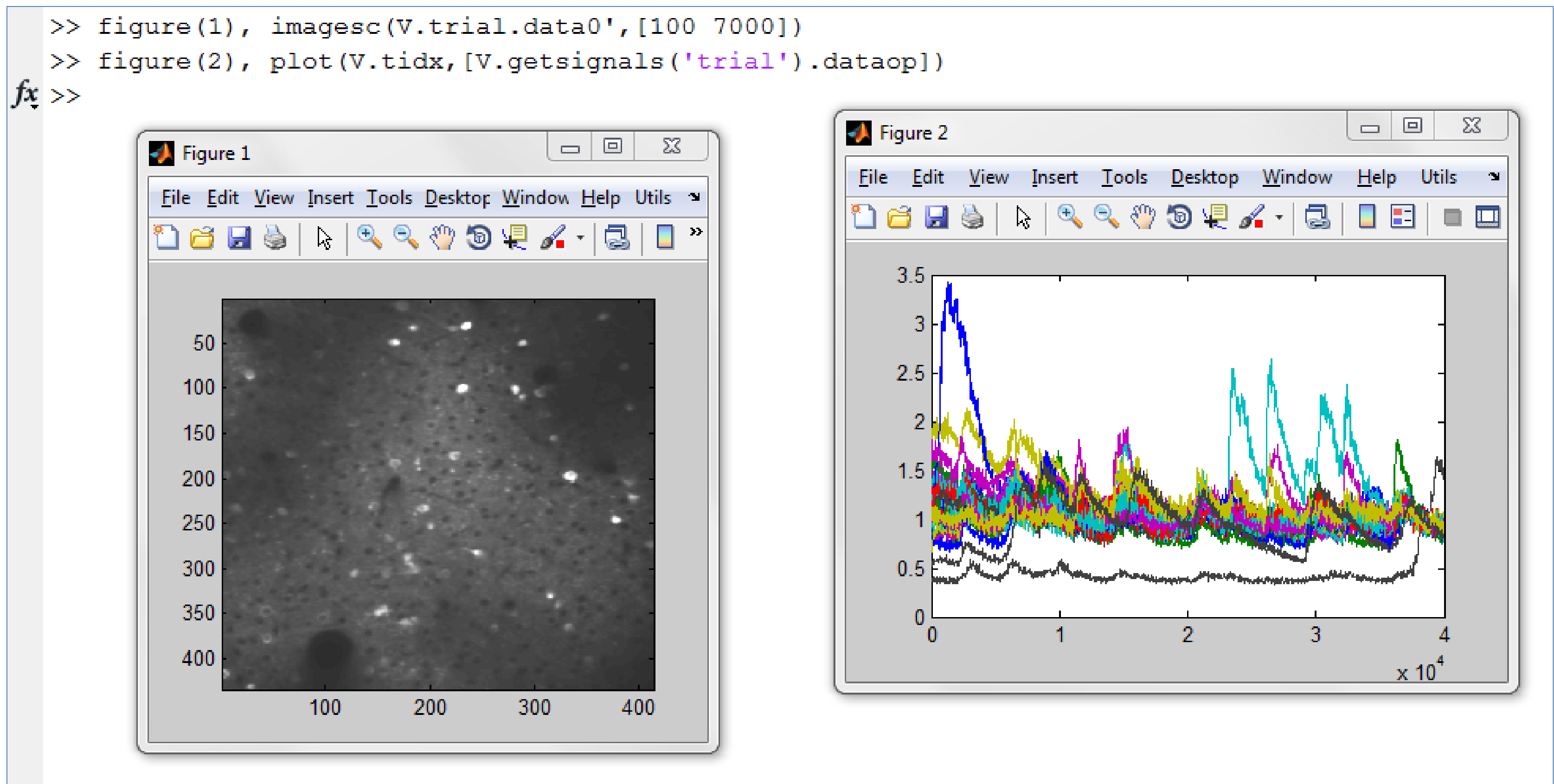
3) Other useful tools

- a. The 2Pview menu
- b. Access to the data from the command line

3)a. The « 2Pview » menu



3)b. Access from command line



Main variables of interest:

V.content all the data

V.content.trials all the trials

V.content.signals all the time courses

V. getsignals('current|sel|trial|all')

V.trial current trial

V.data current trial raw data

V.dataop current trial processed data

get specific time courses

II. More details

- 1) Processing the data
- 2) Visualizing the data
- 3) Other useful tools

1) Processing the data

a. Open the data

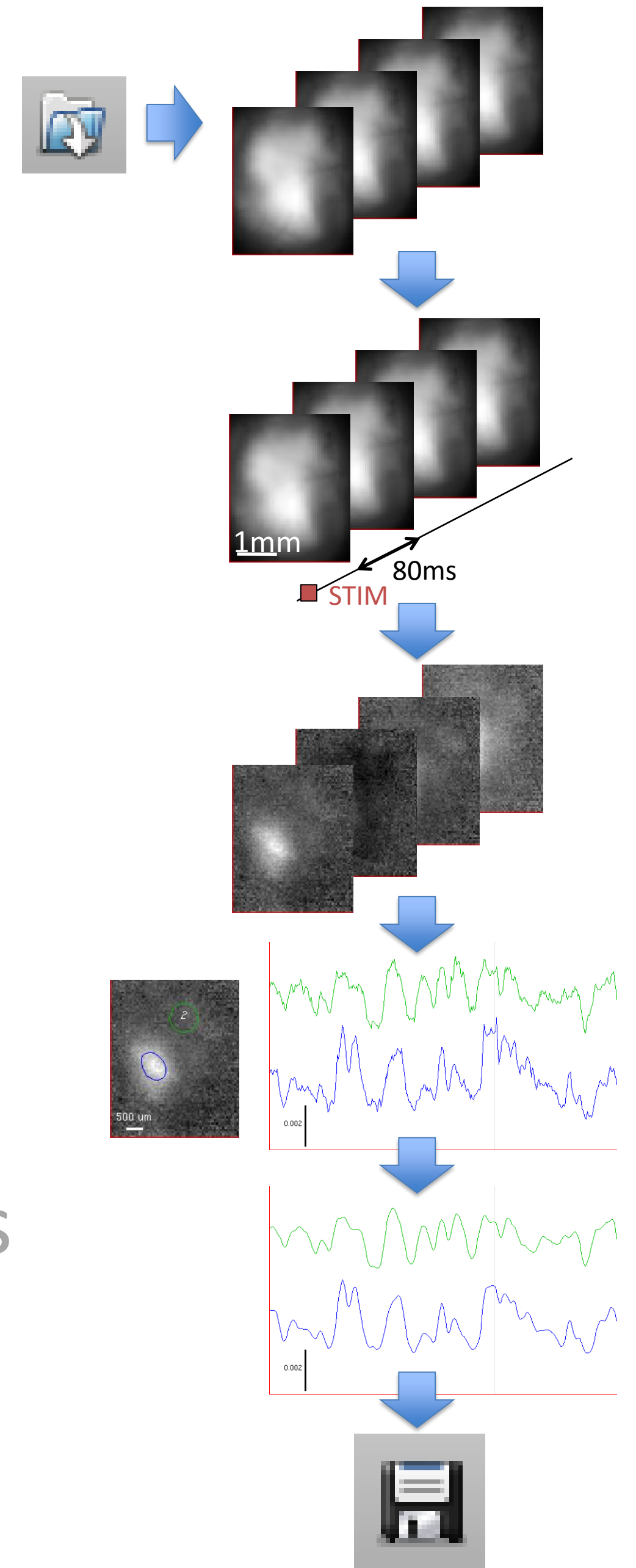
b. Header information

c. Operations on movie data

d. Extraction of time courses

e. Operations on time courses

f. Save



1)a. Open the data

The « file panel »



These two buttons provide the ability to create shortcuts to your two preferred data folders. Right-click on any of them to define these folders.

1)c. Operations on movie data

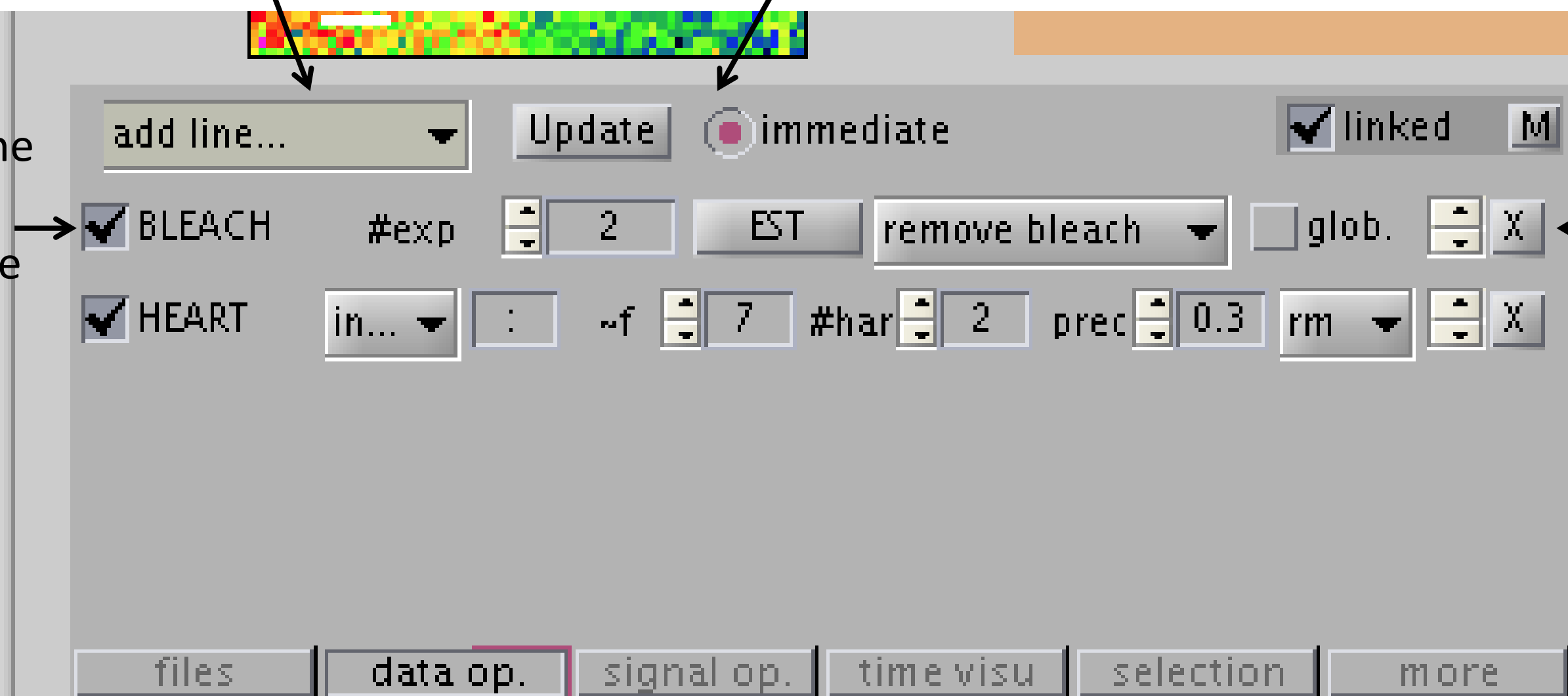
Apply successively a set of operations to the data in the « Data operation panel ». The processed data is called “dataop”. To see the result of the operations, the displays should show the variable “dataop” rather than “data”.

Start by pressing “add line...” to select an operation (all different operations are presented in the next slides).

If “immediate” is checked, the data is re-processed and re-displayed immediately after every change in the operation definitions.

To save computation time, uncheck “immediate” and press “Update” only after all operations have been properly defined.

Check/uncheck the box on the left to activate/inactivate each operation.



Press the cross to remove an operation. Use the arrows to change the order in which the operations are performed.

1)c “SPACE” operation : frame normalization

An average frame is calculated from the movie. There are 3 ways to specify which frames to average together:

- Define a frame range (e.g. 1:10) , or use “:” to use all frames
- Define a time range in seconds (e.g. 0-2)
- Use the current temporal selection in the Time Courses display (see section 2d).

frames	:
frames	1:10
time (s)	0-2
current selection	:

☐ SPACE

divide by	frames	:	
divide by	frames		
subtract	time (s)		
subtract without mean	current selection		

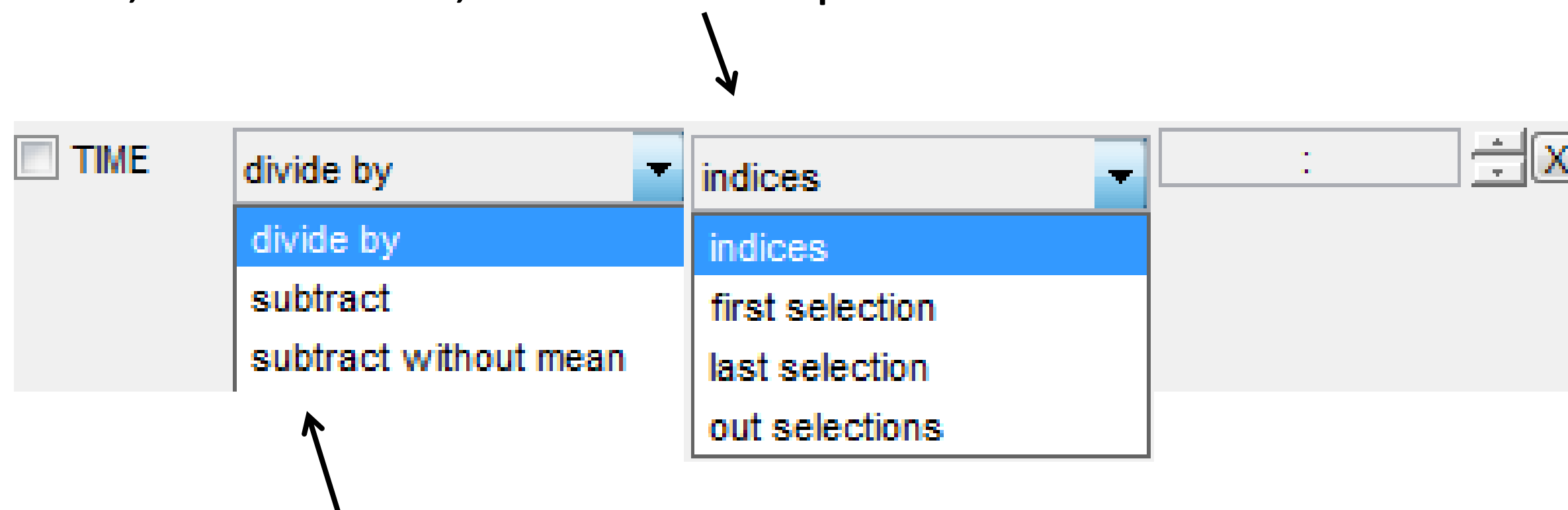
This average frame is then used to correct the movie in one of the 3 following ways:

- Each frame is divided by the average frame
- The average frame is subtracted from each frame
- The spatial pattern present in the average frame is subtracted from each frame, but not its mean value (this prevents the processed data to have all frames with their mean over all pixels equal to zero, i.e. the time courses of the data averaged over all pixels is preserved rather than being flattened to zero).

1)c “TIME” operation: time courses normalization

Symmetrically to the “SPACE” operation, an average time courses is first calculated. There are 2 ways to define which pixels to use:

- Define a set of pixel indices (e.g. 1:10, indexed as in Matlab) , or use “:” to use all pixels
- Use the manually defined ROIs (see section 2d)): use either the first ROI, the last ROI, or the set of pixels that are in none of the ROIs.



This average time courses is used to correct the movie in one of the following ways:

- The time courses of each pixel is divided by the average time courses
- The average time courses is subtracted to each pixel time courses
- The average time courses is subtracted but the mean pixel value over time is preserved (this results in the average movie frame to remain the same rather than being flattened to zero).

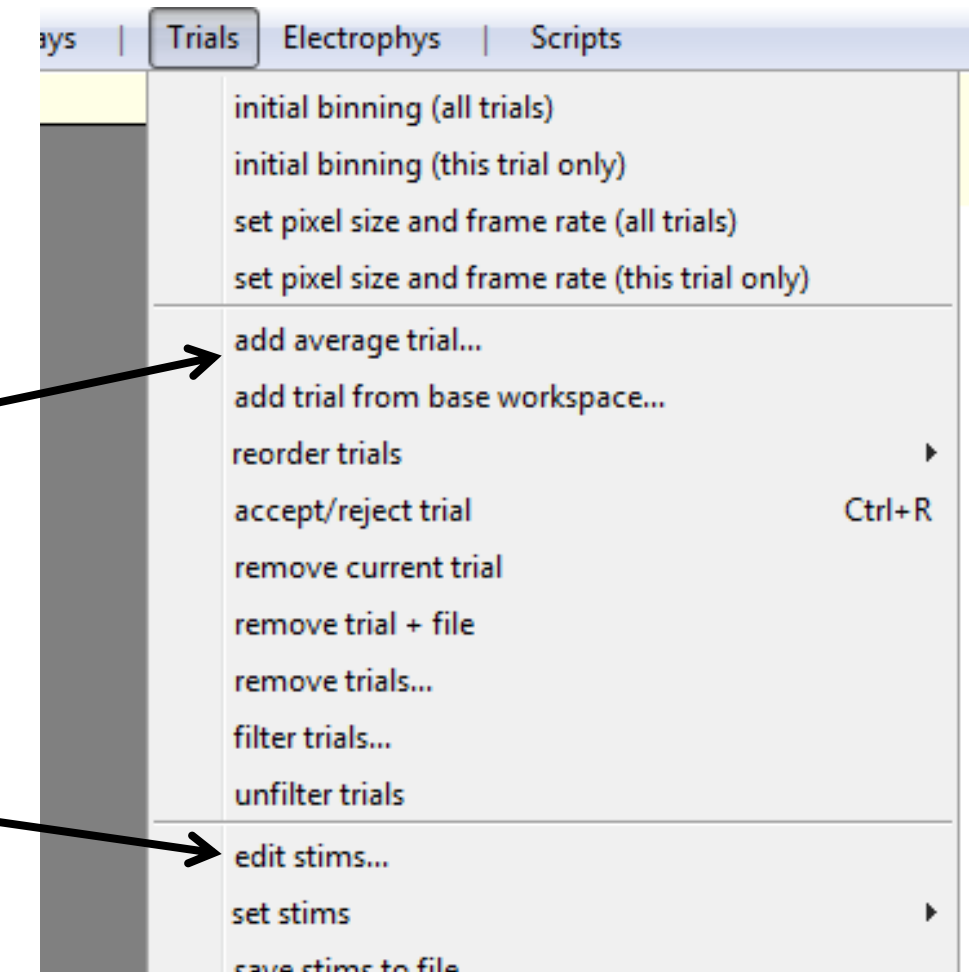
1)c Bleaching correction

Bleaching is modelled as a set of decaying exponentials. The time constants of these exponentials should be estimated once for all at the beginning ('EST' button).

Please follow the procedure below.

1) Time constants should be estimated on the average trial. First compute it in 'Trials > add average trial...'

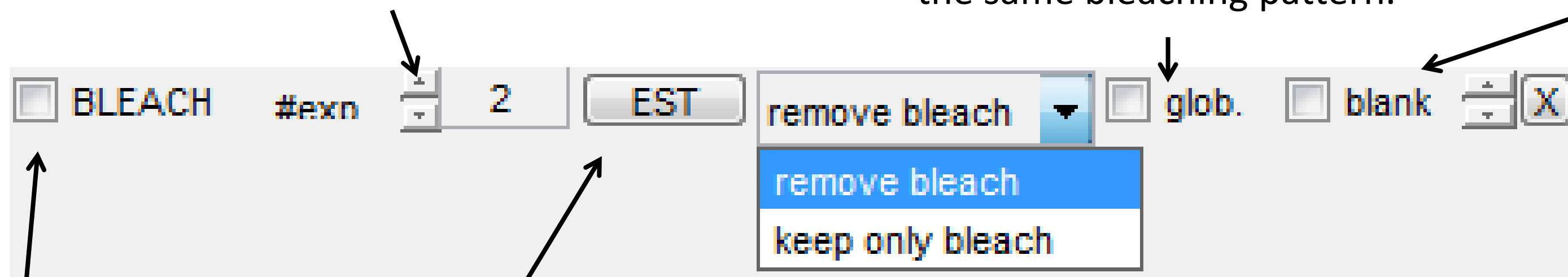
2) The algorithm needs to know which conditions are without stimulation: first do 'Trials > edit stims...' to set the 'type' of the appropriate conditions to 'blank'.



3) Set the desired number of exponentials to use (typically 2 or 3).

4) Optional: check 'glob' if all trials are assumed to share exactly the same bleaching pattern.

Alternatively, check 'blank' to make estimations only from the blank trials to avoid the specific patterns of the responses to be fitted by the bleaching exponentials.



5) Make sure that the current trial showing is the average trial and press 'EST' to estimate the global parameters of the bleaching.

6) Now only activate the correction.

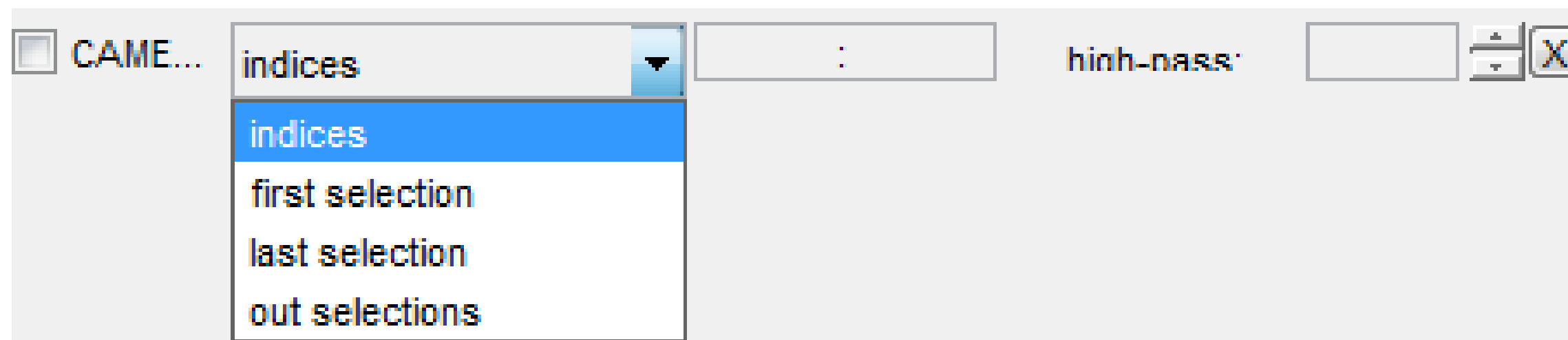
7) It can be useful to press 'keep only bleach' to show the estimated bleach pattern and check that it was properly estimated.

1)c Camera Noise removal

This operation can remove a specific camera noise which is common to all pixels.

Select a region which is rather dark in the image (in such a region the ratio between camera noise and physiological signals is higher) and press 'last selection': time courses from this region will be subtracted everywhere to correct the noise.

If the camera noise is known to be high-frequency, set a value for high-passing the time courses, and that way avoid to subtract lower-frequency physiologically meaningful signals.

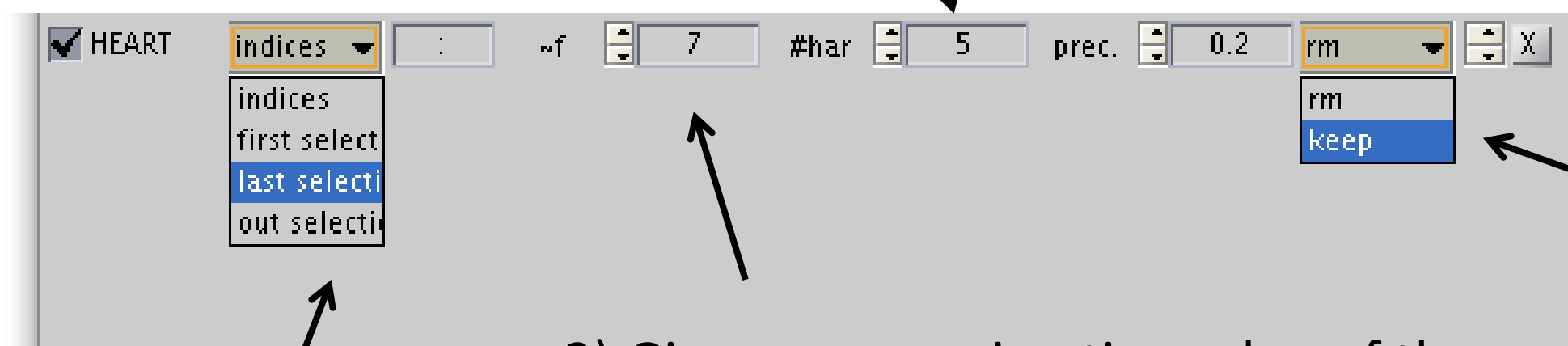


1)c. Heart correction

Removal of heart beat artefact: the underlying method first estimates the phase of the heart pulsation, based on a selected sub-region that is strongly contaminated; then a general linear model estimates the specific shape of heart signals in every pixel.

3) number of harmonics to use (1 would result in a sine wave estimation, more harmonics capture more high frequencies).

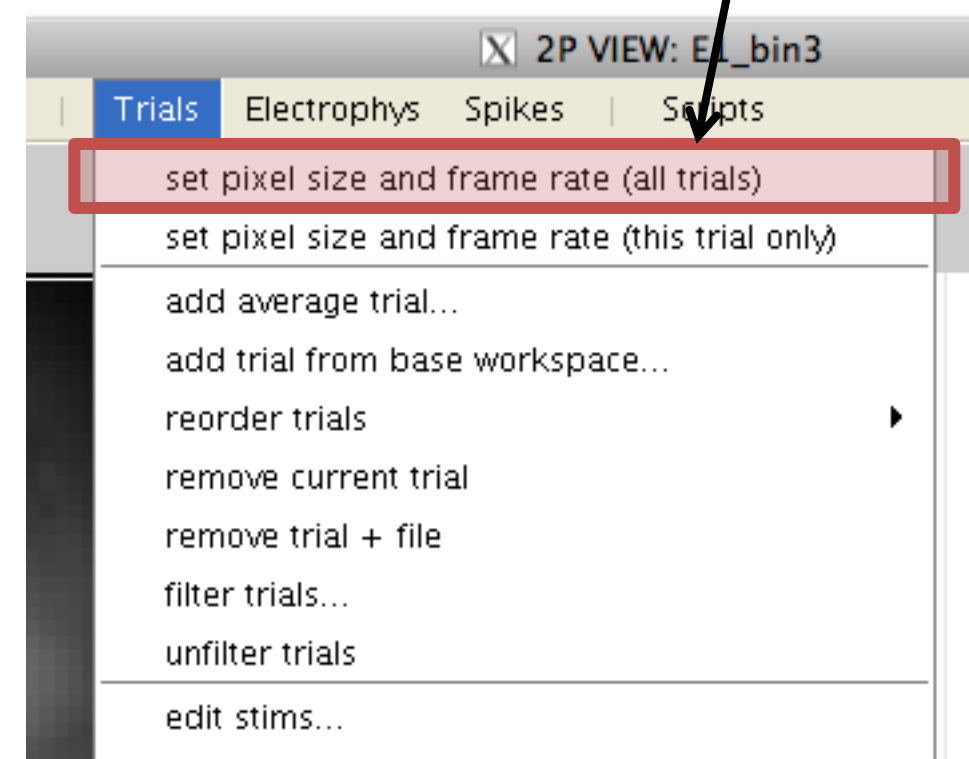
4) 'precision' parameter: the higher this parameter, the more fluctuations in the frequency are allowed.



2) Give an approximative value of the heart frequency. Note that it is necessary that the frame duration has been defined accurately before (here).

5) 'keep' keeps only the estimated heart artefact: use this option to double-check that the estimation was accurate. Then select 'rm' to remove this artefact from the data.

1) Draw a region of interest on a blood vessel or any place in the image that has a lot of heart contamination. Then choose option 'last selection' to use this region for estimating the phase of the heart pulsation.



1)c Motion correction

This coregisters and resamples the frames in a movie to correct for motion artefacts.

This computation can take time.

It is often preferable to create a whole new data set with all trials coregistered together from the 'Trial > coregister trials' menu rather than using this option.

The motion can be estimated from a sub-part of the image only. This can increase computation speed, or avoid misestimation due to high noises or high physiological signals in some parts of the image.

Limit to the amplitude of the motion, expressed as a fraction of the frame size



How many frames to take (counted from the first frame) to compute a reference image to which all frames will be aligned.

1)c Masking

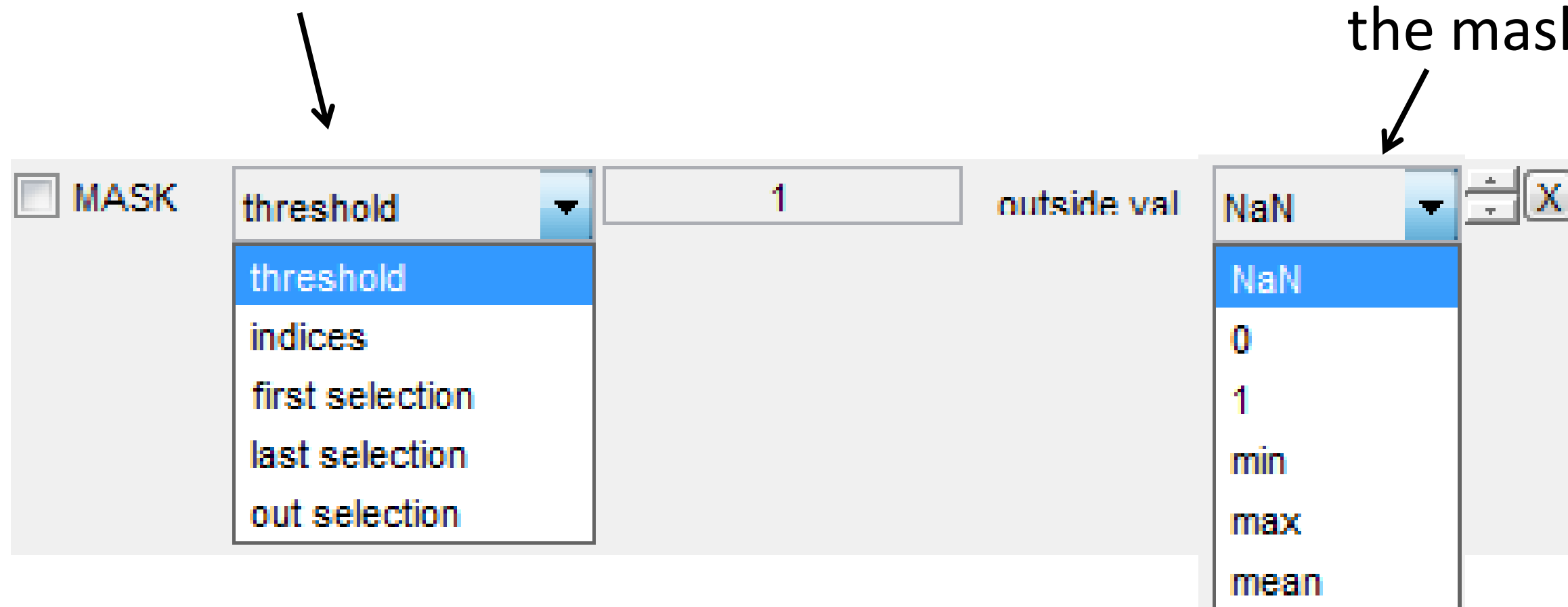
Keep only a part of the image.

Choose how to select the mask:

- All pixels whose average value is above a fixed threshold
- Manual selection of pixel indices
- Manual selection of a ROI

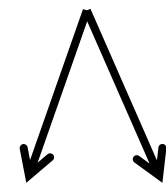
What value to use outside of the mask:

- A fixed value (NaN, 0 or 1)
- The minimum, maximum or average value inside the mask.

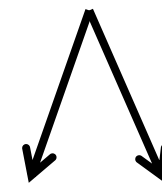


1)c Spatial and temporal filtering

Spatial low-pass and high-pass
cutoff distances expressed in pixels



Temporal low-pass and high-pass
cutoff periods expressed in seconds



Options:

- d: Use a detrend to minimize edge effects of the temporal filter
- z: If a high-pass is applied, keep the mean rather than make the mean zero
- ph: (special) get the phase of the signal after temporal filter has been applied
- s: 'sharp cut-off' - the transfer function of the filter has a sharper cut-off frequency, but this can cause enhanced oscillations near this frequency

1)c Temporal Detrending

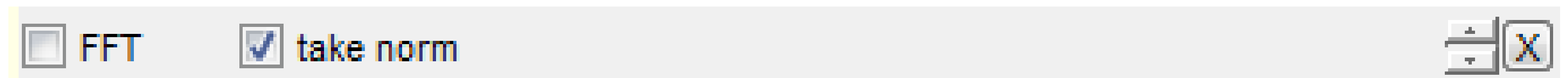
Remove a linear trend in the time courses. It is possible to specify specific frames from which this linear trend is estimated.



1)c Spatial and Temporal binning

☐ BIN space: time:

1)c Fourier Transform



Check 'take norm' to get the norm of the Fourier transform, otherwise the values remain complex (complex values can be visualized in the Image displays but not in the Time Courses displays)

1)c User-defined operation

Users can apply their own functions.

Define a function right inside the control using variable name “x” (1st example below), or write the name of the function to be applied (2nd example).

<input type="checkbox"/> USER	<input type="text" value="x./(1+x)"/>	<input type="button" value="edit"/>	<input type="button" value="recompute"/>	<input type="button" value="÷"/>	<input type="button" value="X"/>
<input type="checkbox"/> USER	<input type="text" value="my_custom_operation"/>	<input type="button" value="edit"/>	<input type="button" value="recompute"/>	<input type="button" value="÷"/>	<input type="button" value="X"/>

Press ‘edit’ to edit (or even create) the m-file.

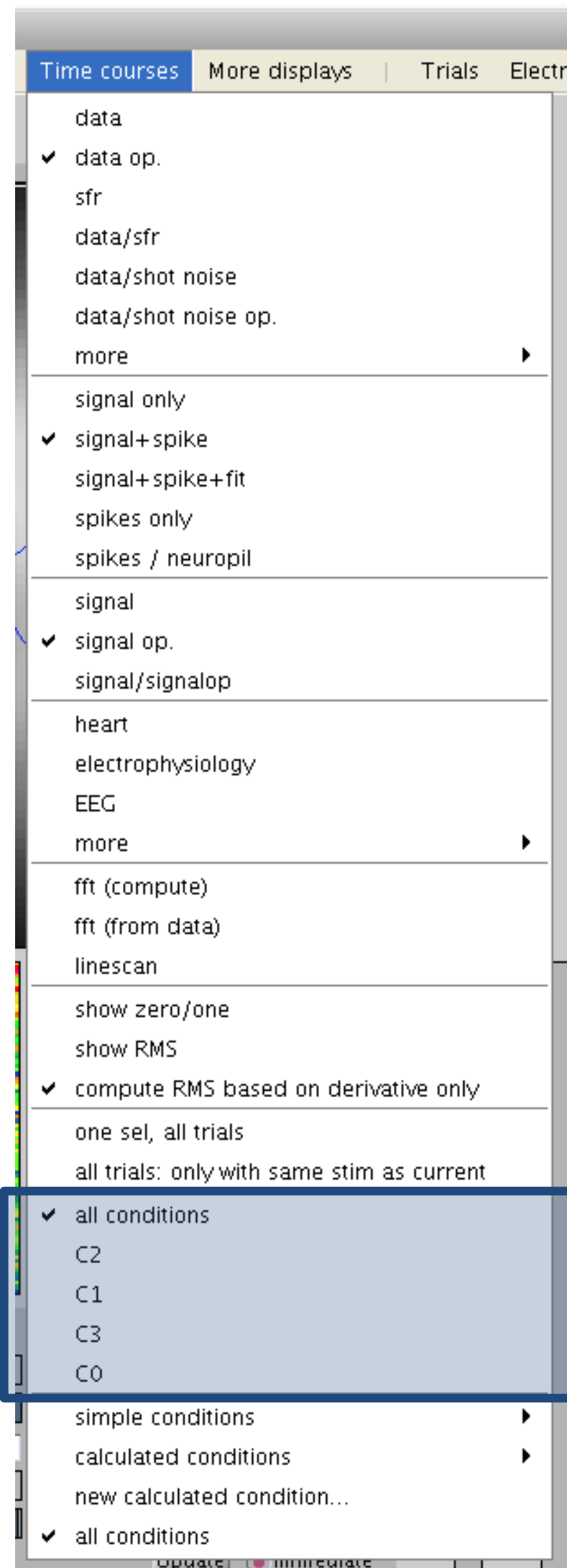
OptImage might not well detect that the m-file content has changed. Press ‘recompute’ to force a function call.

2) Visualizing the data

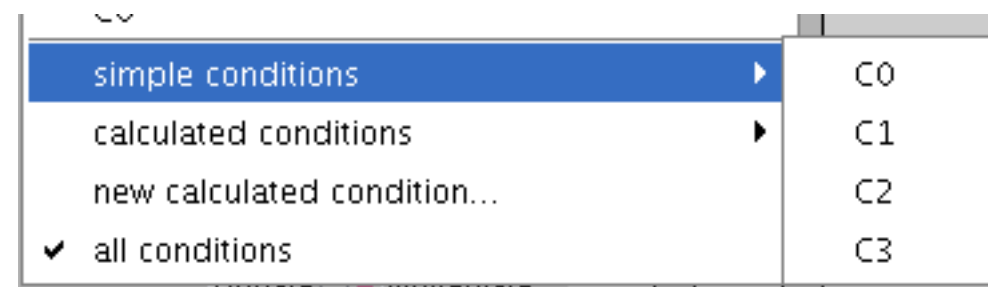
- a. Which displays are available?
- b. What to show in each display?
 - How to select conditions
- c. Display options
- d. Mouse actions

2)b. Select condition(s)

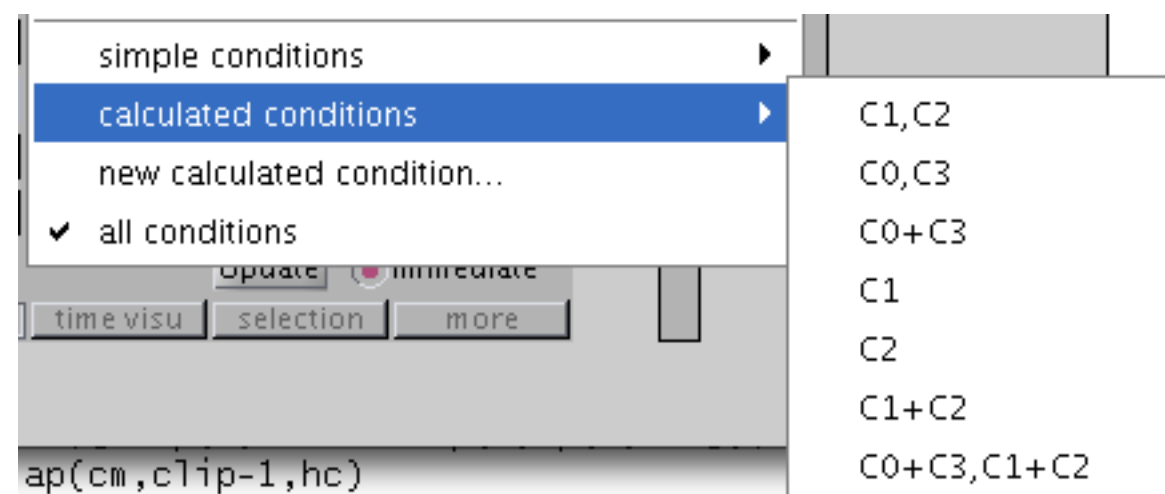
When data has multiple conditions, it is possible to choose which to display in Picture1, Picture2 or Time Courses. Several options exist:



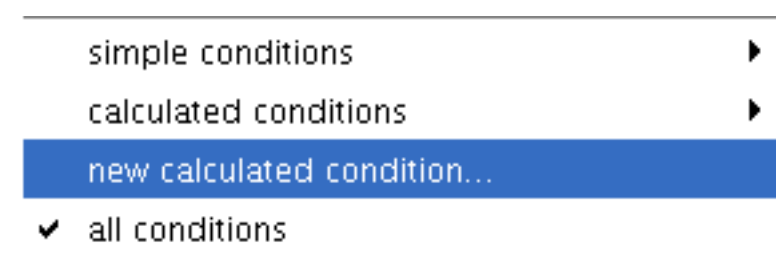
1) Choose one of the recently used conditions



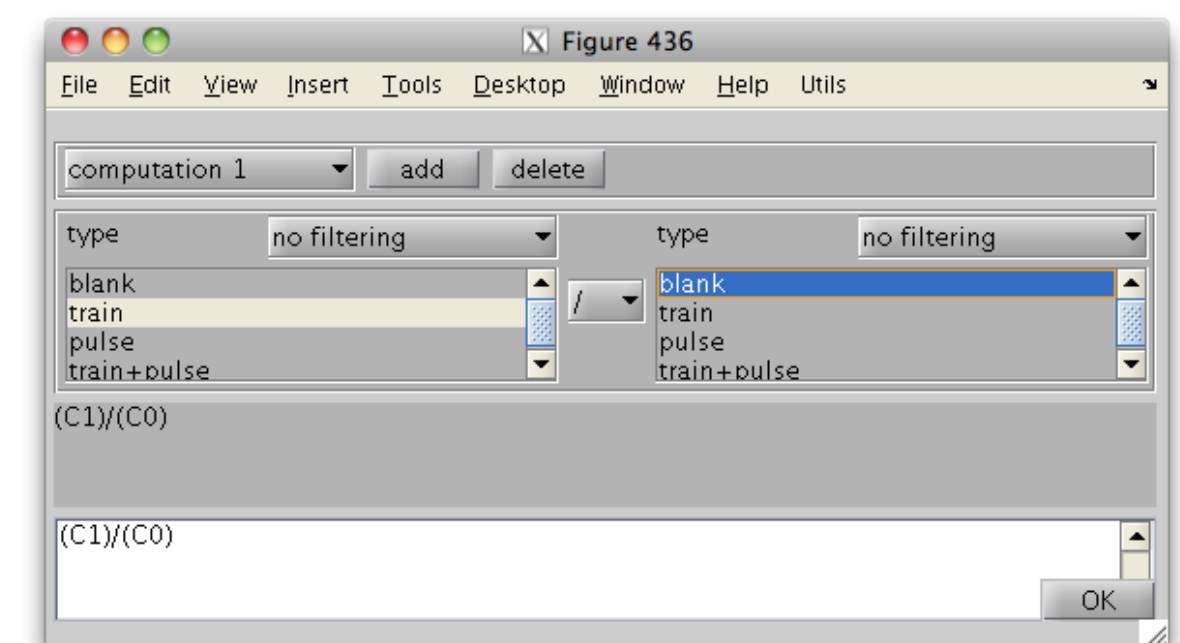
2) Choose a simple conditions



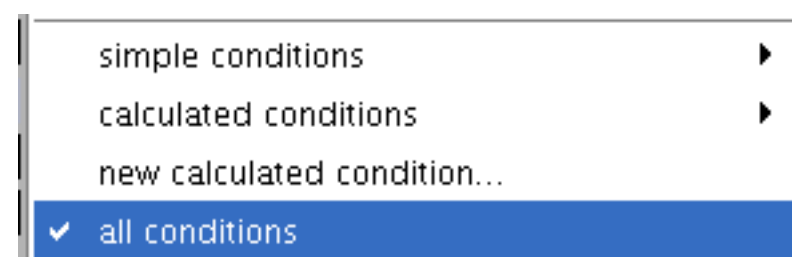
3) Choose a recent calculated condition



4) Create a new calculated condition: a new window opens that lets you define it



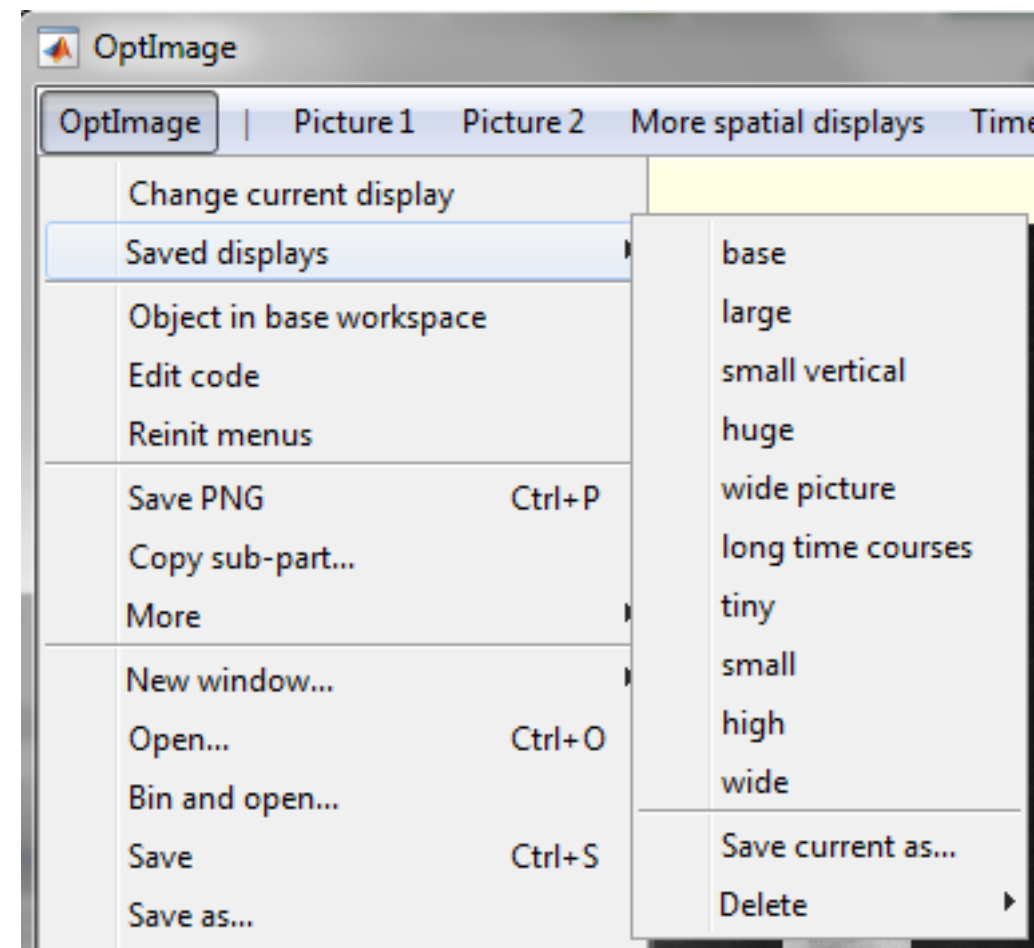
5) Display all simple conditions together



3) Other useful tools

- a. The 2Pview menu
 - Changing the program size and display
 - Preferences
- b. Access to the data from the command line

3)a. Changing the program size and display



A number of different **configurations** are pre-defined. Select one of them to change the program size and display.

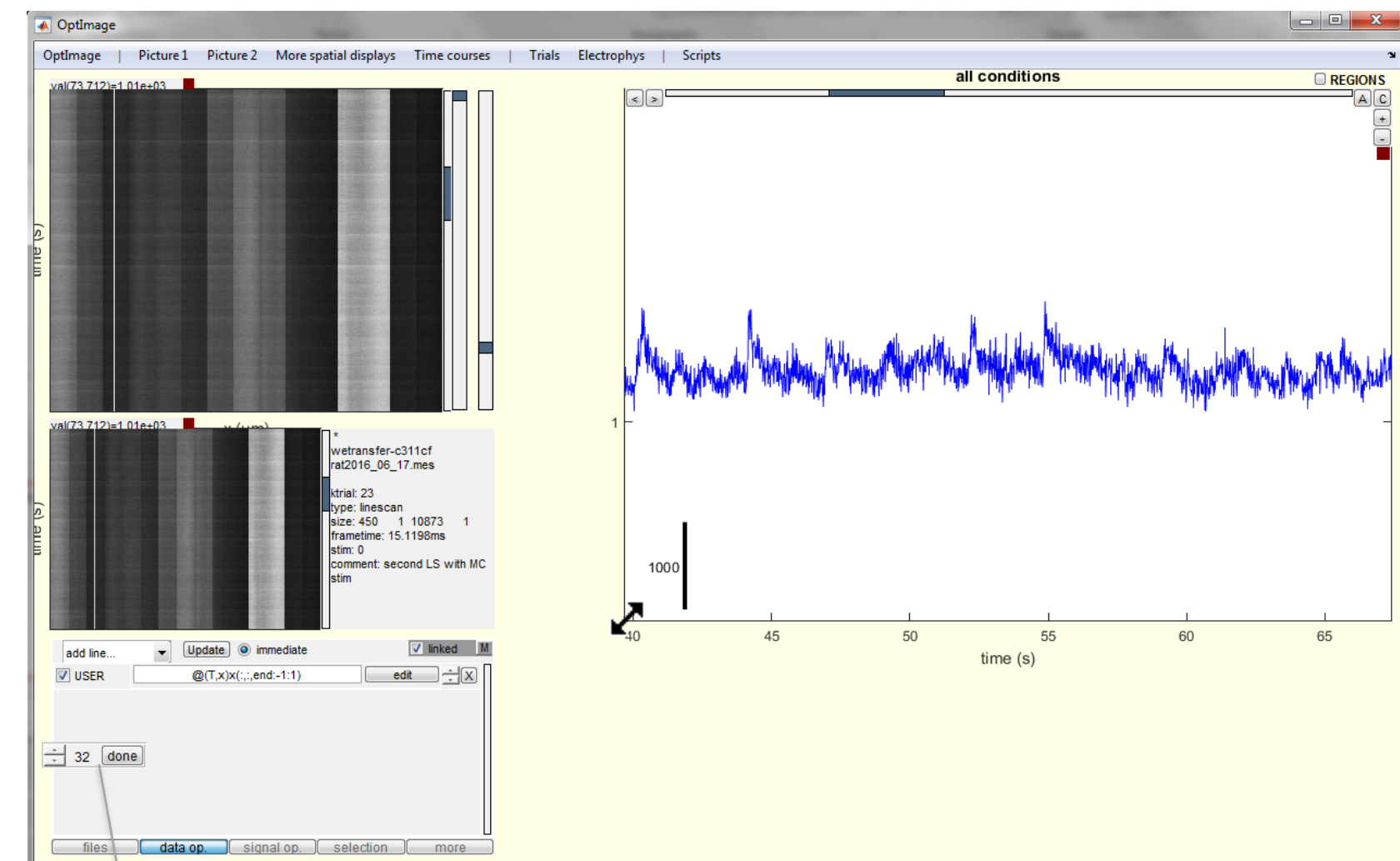
New configurations can be created with '*Change current display*' and then '*Save current as...*'.

When '*Change current display*' is pressed, the different elements of the program and the figure itself become **resizeable**.

For easy alignment of the elements, position coordinates will be automatically rounded to a given number that can be adjusted (here: 32).

- **move** elements **sides and corners** with mouse left button
- **drag** elements with mouse middle button
- **round** an element coordinates to the set number with a right-button click

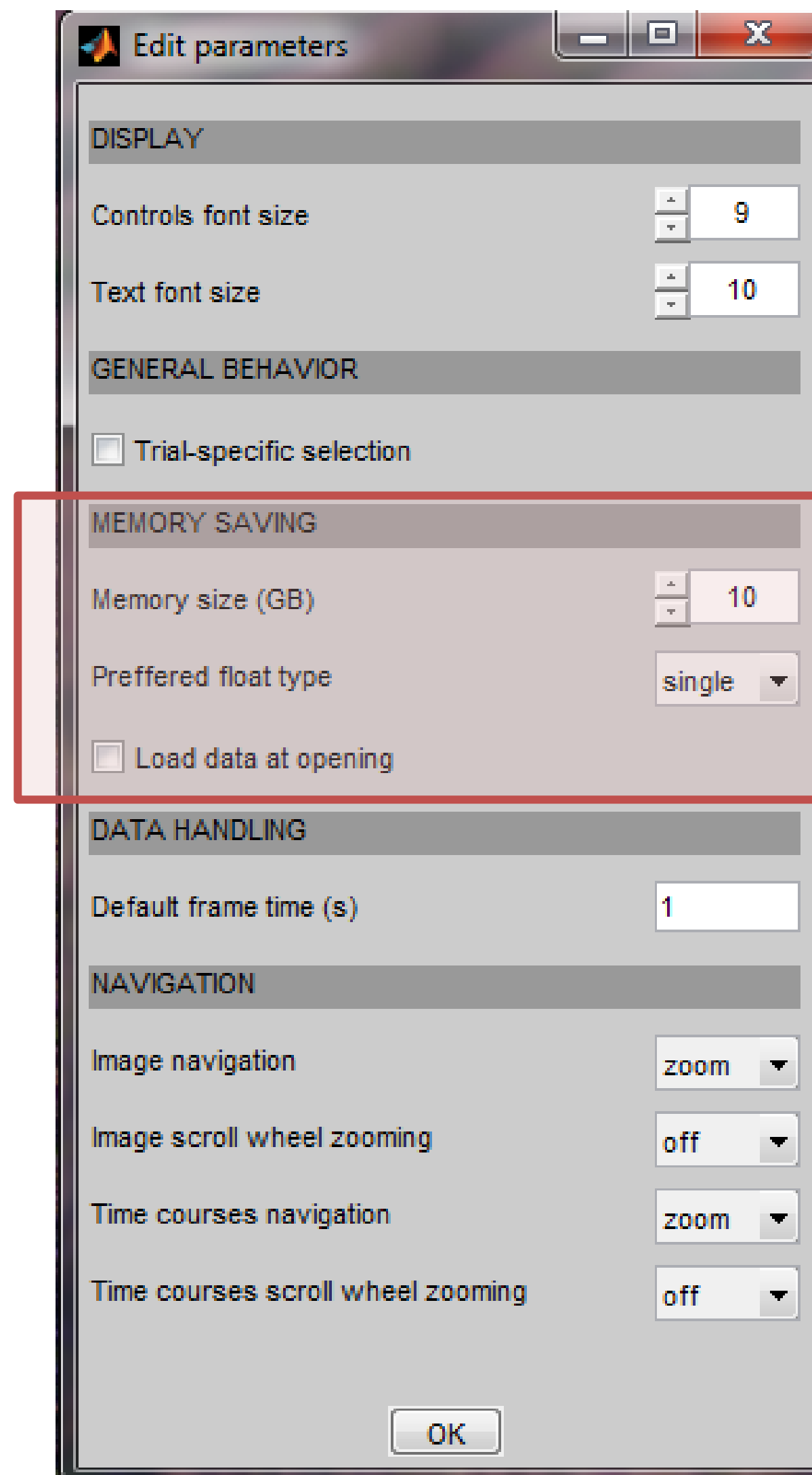
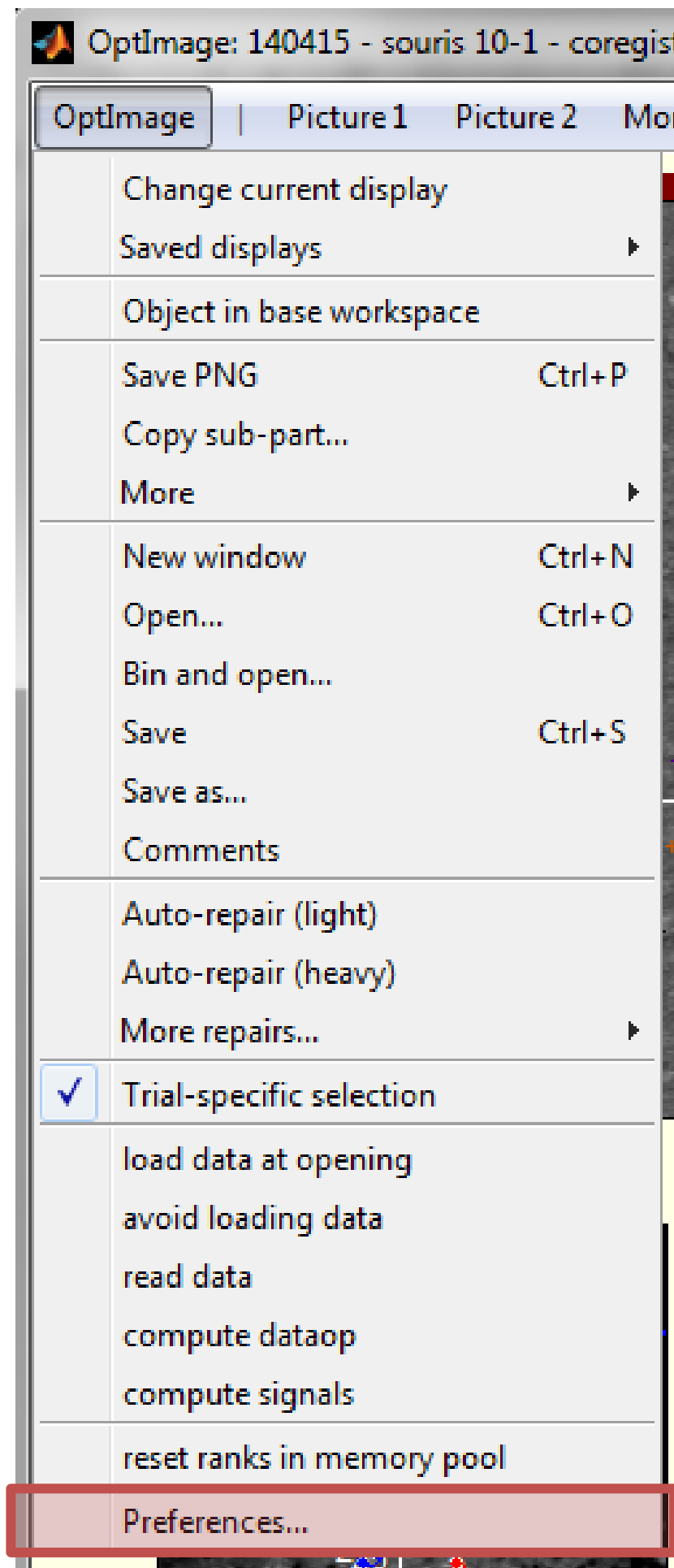
Press '*done*' once finished!



In the '*more*' panel, button '*toggle display*' allows to switch image and time courses display when one temporarily needs to see the images larger.

Finally, font sizes can be change in the '*Preferences*' (see next page).

3)a. Preferences



Change font sizes

If checked, the position of the ROIs can be different for different trials

Parameters to arbitrate between increasing speed and saving memory

If frame time is not set by user, some functions will assume this frame time

Choose between zoom and pan for image and time courses navigation. Decide whether it is possible to zoom in and out with the scroll wheel.

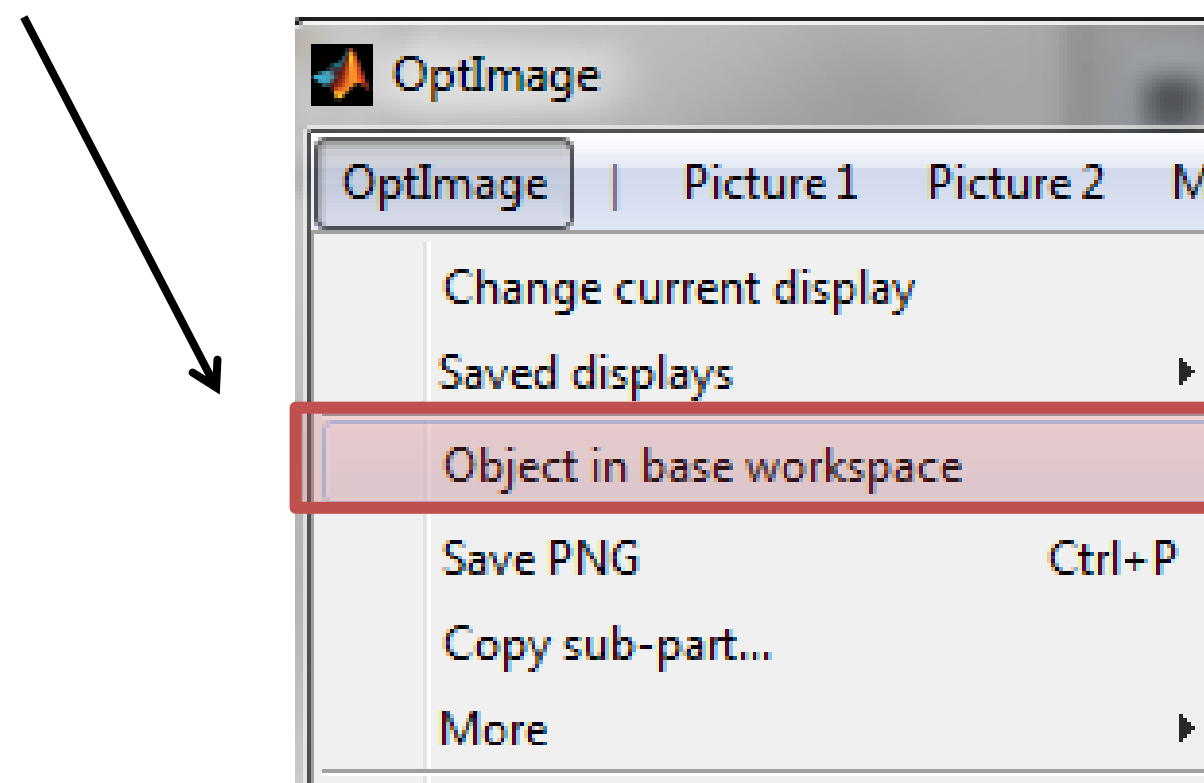
This section is very important. Raw data and processed data are stored inside a 'pool' whose size is limited. When the pool is filled some data is forgotten and will need to be loaded/computed again when accessed again. *If Matlab runs out of memory, decrease the pool size; if data is permanently forgotten and recomputed, try increasing it.*

Preferred float type should normally be set to 'double' to avoid numerical errors in computations. However in some circumstances, one can set it to 'single' to further save memory.

3)b. Access from command line

Variable 'V' contains all the information used by current OptImage window.

If 'V' has been cleared, or overwritten by another OptImage window, use this menu option to create it again.



```
>> V
V =
    tpview with properties:
        skin: 'OptImage'
        panels: [1x1 struct]
        a4d: [1x1 struct]
        timer: [1x1 timer]
        precomp: [1x1 struct]
        content: [1x1 tpv_content]
        internpar: [1x1 tpv_internpar]
        disppar: [1x1 struct]
        savingpar: [1x1 struct]
        ntrial: 64
        trial: [1x1 tps_trial]
        data: [414x434x1400 uint16]
        dataop: [414x434x1400 single]
        sfr: []
        file: [1x130 char]
        fullinfo: [1x1 struct]
        sizes: [414 434 1400 1]
            nx: 414
            ny: 434
            nfr: 1400
            nc: 1
        linedur: 0.0658
        tidx: [1x1400 double]
        nsel: 35
        signal: [1x1 tps_signal]
        ktrial: 2
        addinfo: [1x1 struct]
            type: 'movie'
        scanning: 1
            dx: 1.1921
            dy: 1.1921
            dz: 0
            dt: 28.5660
            t0: 0
        hf: 173.0052
        grob: [1x1 struct]
        options: [1x1 struct]
        menus: [1x1 struct]
        interfacepar: [1x1 struct]
```

The most important field is V.content

Number of trials
Current trial

Shortcuts to properties of the current trial

Number of ROIs
Shortcut to time courses
Index of current trial

Other fields are for internal use only

'V.content' contains all the data.

It is saved in a file with extension 'tpv'. Load 'tpv' files as follows:

load('mydata.tpv','-MAT')

```
>> V.content
```

```
ans =
```

```
    tpv_content with properties:
```

```
    version: 1.4100
```

```
    trials: [1x64 tps_trial]
```

```
    signals: [1x1 tps_signal]
```

```
    ktrial: 2
```

```
    electrophys: [1x64 tps_electrophys]
```

```
    nsel: 35
```

```
    ij: [2x1 double]
```

```
    seldotrial: 1
```

```
    timeline: 0
```

```
    ntrial: 64
```

```
    nfr: 1400
```

```
    nx: 35
```

```
    datamodes: {'data' ''}
```

```
    datacond: 'all conditions'
```

```
    trial: [1x1 tps_trial]
```

```
    signal: [1x1 tps_signal]
```

```
    channel: [1x1 tps_signalx]
```

```
    stimtable: [1x1 tps_stimtable]
```

```
    docfile: []
```

```
    user: [1x1 struct]
```

All the trials

All the time courses

User can store additional
information in this structure.

'V.content.trials(k)' contains the information relative to trial k.

```
>> V.content.trials(1)
```

```
ans =
```

```
tps_trial with properties:
```

```
version: 1.7000
```

```
file: [1x130 char]
```

```
fileflag: ''
```

```
analogfile: {[1x81 char] [1]}
```

```
origin: 'user [MESC header]'
```

```
sizes: [414 434 1400 1]
```

```
sizes0: [414 434 1400 1]
```

```
sfrchannel: 0
```

```
fullinfo: [1x1 struct]
```

```
addinfo: [1x1 struct]
```

```
status: 'n'
```

```
type: 'movie'
```

```
scanning: 1
```

```
xbin: 1
```

```
tbin: 1
```

```
dx: 1.1921
```

```
dy: 1.1921
```

```
dz: 0
```

```
dt: 28.5660
```

```
t0: 0
```

```
xunit: 'um'
```

```
tunit: 'ms'
```

```
user: [1x1 struct]
```

```
nx: 414
```

```
ny: 434
```

```
nfr: 1400
```

```
nc: 1
```

```
linedur: 0.0658
```

```
tidx: [1x1400 double]
```

```
dt_sec: 0.0286
```

```
usertransient: [1x1 struct]
```

```
stimtable: [1x1 tps_stimtable]
```

```
eventlist: [1x0 struct]
```

```
stimid: 63873
```

```
stim: [2x12 double]
```

```
stimdetails: [1x1 struct]
```

```
opdef: [1x1 tps_dataopdef]
```

```
opmem: [1x0 tps_dataopdef]
```

```
data0: [414x434 single]
```

```
data: [414x434x1400 uint16]
```

```
sfr: []
```

```
shotnoise: [414x434x1400 single]
```

```
dataop: [414x434x1400 single]
```

```
sfrop: []
```

```
shotnoiseop: [414x434x1400 single]
```

```
dataopmem: [414x434x1400 single]
```

```
recording: [1x1 struct]
```

```
heartcycle: []
```

File where data is saved: note that the data is not read until it is actually used.

Trial status: 'n'ormal, 'r'ejected or 's'pecial

Main header information

Header information related to stimulation

Processing applied to the data

Average frame of the raw data
Raw data

Processed data

'V.content.signal.x(k,i)' contains the information relative to time courses for trial k and region of interest i.

```
>> V.content.signal
```

```
ans =
```

```
tps_signal with properties:
```

```
    name: ''
  datamode: 'data'
 datacond: 'all conditions'
dataopdef: [1x64 struct]
  opdef: [1x1 struct]
seldotrial: 1
  timeline: 0
         x: [64x35 tps_signalx]
        shift: [64x2 double]
    spikepar: []
         nx: 35
        nfr: []
       nfrop: []
        nex: 64
         data: {64x35 cell}
        data2: {64x35 cell}
       dataop: {64x35 cell}
      data2op: {64x35 cell}
         sel: [64x35 selectionND]
        spikes: {64x35 cell}
```

Processing applied to the signals

```
>> V.content.signal.x(1,1)
```

```
ans =
```

```
tps_signalx with properties:
```

```
    tag: []
   active: 1
      sel: [1x1 selectionND]
    spikepar: []
        kcond: 1
        delay: 0.0141
delayshown: 0.0141
      tid: [1x1400 double]
      data: [1400x1 double]
     data2: []
    dataop: [1400x1 double]
    data2op: []
      spikes: []
    spikefit: []
 validspike: 0
      spikes2: []
    spikefit2: []
 validspike2: 0
```

Coordinates of the region of interest

Vector of time instants

Time courses before signal processing

Time courses of secondary data before signal processing

Time courses after signal processing

Time courses of secondary data after signal processing

Signals can be accessed also using the following method:

V.getsignals(ktrials,iregions), or V.getsignals('all'), V.getsignals('trial'), V.getsignals('sel'), V.getsignals('current')