

Open the data

2P VIEW | Picture 1 | Picture 2 | Time courses | More displays | Trials | Electrophys | Spikes | Scripts

val(1,1)=0

0.2 um

val(1,1)=0

0.2 um

TC10190413140542_E008054.BLK
TC10190413142218_E008118.BLK
TC10190413142737_E008139.BLK
TC10190413144531_E018023.BLK
TC10190413145411_E018055.BLK
TC10190413151019_E018117.BLK
TC10190413151551_E018138.BLK
TC10190413153553_E018213.BLK
TC10190413154100_E018233.BLK
TC10190413155408_E018280.BLK
colorluminance1_6sRES.prm
colorluminance1_6sRES_lowC.prm
green0.RMD

open average
open concatenate
open add
bin and open
PMT test
rename file(s)

bin and open
bin and average
bin and concatenate

0.1

0.4 0.6 0.8 1 1.2 1.4 1.6 1.8 2

Select folder where to save binned data

Look In: 130419_billy

130419_billy_bin3

File Name: UX/Projects/1109_Feature/save/130419_billy/130419_billy_bin3

Files of Type: All Files

OK Cancel

Edit parameters

spatial binning 3
temporal binning 1

OK

Define pixel size and frame duration

The screenshot displays the 2P VIEW software interface. The main window is divided into several panels. On the left, there is a 'Picture 1' panel showing a grayscale image of a brain slice with a blue rectangular region of interest (ROI) labeled '1'. Below this, a 'Picture 2' panel shows a similar image with a scale bar labeled '50 px'. To the right of the 'Picture 1' panel, a text box displays the following information:

```
130419_billy_bin3
TC00190413135352_E008009.8
LK_bin3.mat*

ktrial: 1
type: movie
size: 128 168 143 1
frametime: 10ms
stim: 0
```

At the bottom left, a list of trial files is shown, including TC09190413140813_E008064.BLK, TC09190413142319_E008122.BLK, and others. The bottom of the interface features a series of buttons: 'Open', 'Update', 'Upd. Exp.', 'Projects', '2p', 'Ungroup', 'files', 'data op.', 'signal op.', 'time visu', 'selection', and 'more'.

The central 'Trials' panel contains a menu with the following options:

- set pixel size and frame rate (all trials)
- set pixel size and frame rate (this trial only)
- add average trial...
- add trial from base workspace...
- reorder trials
- accept/reject trial
- remove current trial
- remove trial + file
- remove trials...
- filter trials...
- unfilter trials
- edit stims...
- set stims
- save stims to file...
- load stims from file...
- show stim
- display events
- edit events
- read heart (all trials)
- read heart (this trial)
- Make new set with dataop as data
- Make new set with binned data
- Make new set with current trial only
- coregister trials

The 'Edit para...' dialog box is open, showing the following parameters:

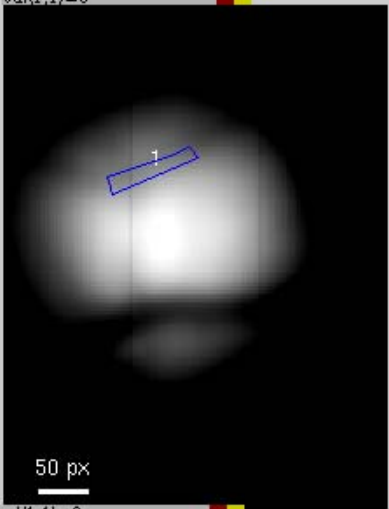
- dx: 3
- dy: 3
- dz: 0
- xyzunit: px
- dt: 1/110
- tunit: s

The 'OK' button is visible at the bottom of the dialog box. The background of the software shows a time course plot with a blue line representing the signal over time (0 to 1.4 seconds).

Reorder trials


2P VIEW | Picture 1 | Picture 2 | Time courses | More displays | **Trials** | Electrophys | Spikes | Scripts

val(1,1)=0



50 px

val(1,1)=0



50 px

130419_billy_bin3
TC00190413135352_E008009.8
LK_bin3.mat*

ktrial: 1
type: movie
size: 128 168 143 1
frametime: 9.0909ms
stim: 0

TC09190413140813_E008064.BLK
TC09190413142319_E008122.BLK
TC09190413143054_E008151.BLK
TC09190413144833_E018033.BLK
TC09190413145642_E018065.BLK
TC09190413151120_E018121.BLK
TC09190413151922_E018150.BLK
TC09190413153235_E018200.BLK
TC09190413153639_E018216.BLK
TC09190413155002_E018267.BLK
TC09190413160814_E018335.BLK
TC10190413135738_E008023.BLK

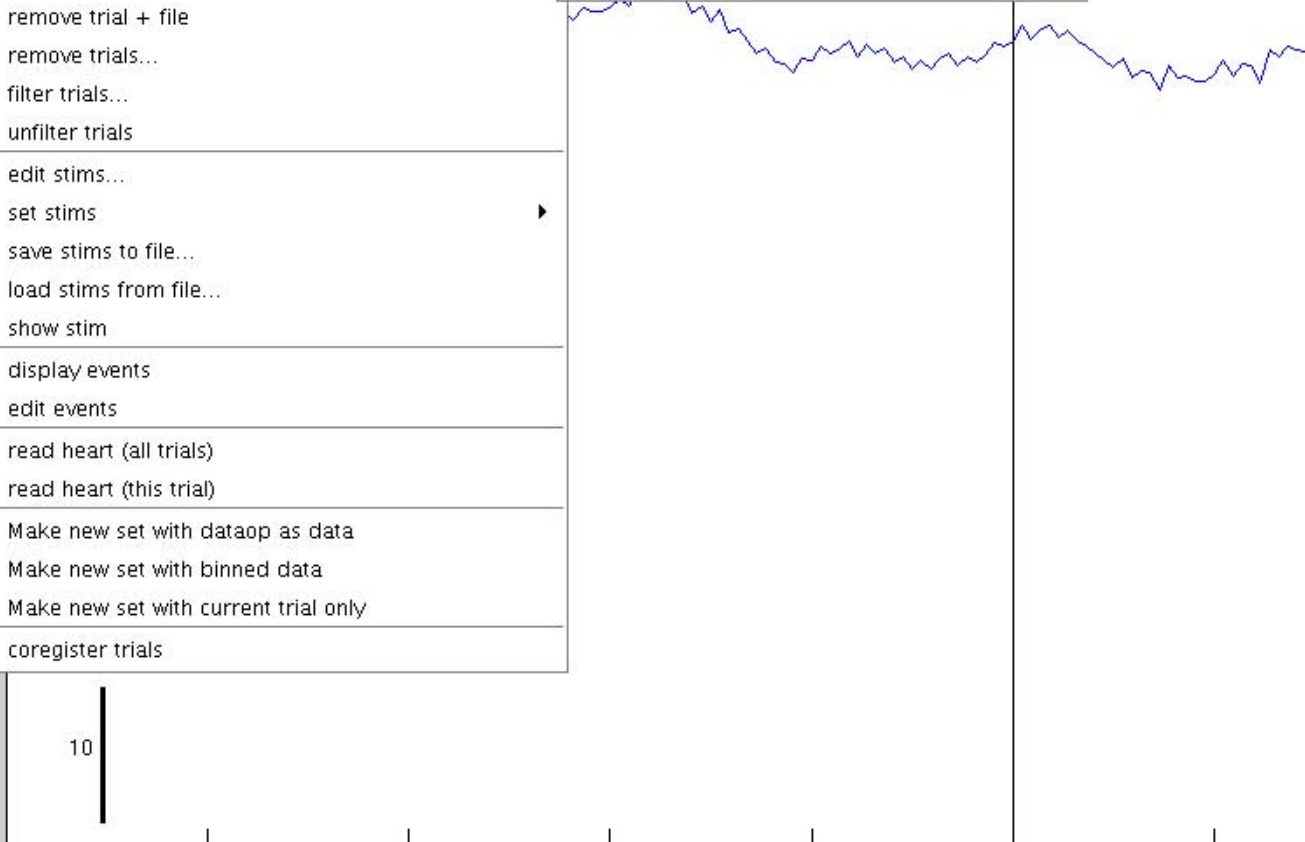
Open | Update | Upd. Exp. | Projects | 2p | Ungroup
files | data op. | signal op. | time visu | selection | more

set pixel size and frame rate (all trials)
set pixel size and frame rate (this trial only)
add average trial...
add trial from base workspace...
reorder trials ▶
accept/reject trial Ctrl+R
remove current trial
remove trial + file
remove trials...
filter trials...
unfilter trials
edit stims...
set stims ▶
save stims to file...
load stims from file...
✓ show stim
✓ display events
edit events
read heart (all trials)
read heart (this trial)
Make new set with dataop as data
Make new set with binned data
Make new set with current trial only
coregister trials

es separated by 20

REGIONS
A
+
-
[Color bar]

based on experiment and block numbers
based on file times
manual permutation



10

0 0.2 0.4 0.6 0.8 1 1.2
time (s)

Add average trial

The screenshot shows a software interface with a top menu bar (2P VIEW, Picture 1, Picture 2, Time courses, More displays, Trials, Electrophys, Spikes, Scripts) and a main workspace. The 'Trials' menu is open, displaying options such as 'set pixel size and frame rate (all trials)', 'add average trial...', 'add trial from base workspace...', 'reorder trials', 'accept/reject trial', 'remove current trial', 'remove trial + file', 'remove trials...', 'filter trials...', 'unfilter trials', 'edit stims...', 'set stims', 'save stims to file...', 'load stims from file...', 'show stim', 'display events', 'edit events', 'read heart (all trials)', 'read heart (this trial)', 'Make new set with dataop as data', 'Make new set with binned data', 'Make new set with current trial only', and 'coregister trials'. The 'add average trial...' option is highlighted, and an arrow points to the 'Edit parameters' dialog box. The dialog box has fields for 'Based on' (data), 'Filter indices' (1:38), 'Filter out indices', 'Stim id', 'Keep rejected trials' (unchecked), 'Average different conditions together' (unchecked), and 'Description of new trial' (trial average). The 'OK' button is at the bottom right of the dialog. The main workspace shows a 2D view of a brain slice with a blue rectangular region of interest (ROI) labeled '1'. Below the 2D view is a list of trial files, including 'TC09190413140813_E008064.BLK', 'TC09190413142319_E008122.BLK', 'TC09190413143054_E008151.BLK', 'TC09190413144833_E018033.BLK', 'TC09190413145642_E018065.BLK', 'TC09190413151120_E018121.BLK', 'TC09190413151922_E018150.BLK', 'TC09190413153235_E018200.BLK', 'TC09190413153639_E018216.BLK', 'TC09190413155002_E018267.BLK', 'TC09190413160814_E018335.BLK', and 'TC10190413135738_E008023.BLK'. At the bottom of the interface are buttons for 'Open', 'Update', 'Upd. Exp.', 'Projects', '2p', 'Ungroup', 'files', 'data op.', 'signal op.', 'time visu', 'selection', and 'more'.

2P VIEW | Picture 1 | Picture 2 | Time courses | More displays | **Trials** | Electrophys | Spikes | Scripts

set pixel size and frame rate (all trials)
set pixel size and frame rate (this trial only)
add average trial...
add trial from base workspace...
reorder trials
accept/reject trial
remove current trial
remove trial + file
remove trials...
filter trials...
unfilter trials
edit stims...
set stims
save stims to file...
load stims from file...
✓ show stim
✓ display events
edit events
read heart (all trials)
read heart (this trial)
Make new set with dataop as data
Make new set with binned data
Make new set with current trial only
coregister trials

es separated by 20

Edit parameters

Based on: data
Filter indices: 1:38
Filter out indices:
Stim id:
☐ Keep rejected trials
☐ Average different conditions together
Description of new trial: trial average
OK

val(1,1)=0
50 px
130419_billy_bin3
TC00190413135352_E008009.B
LK.bin3.mat*
ktrial: 1
type: movie
size: 128 168 143 1
frametime: 9.0909ms
stim: 0

TC09190413140813_E008064.BLK
TC09190413142319_E008122.BLK
TC09190413143054_E008151.BLK
TC09190413144833_E018033.BLK
TC09190413145642_E018065.BLK
TC09190413151120_E018121.BLK
TC09190413151922_E018150.BLK
TC09190413153235_E018200.BLK
TC09190413153639_E018216.BLK
TC09190413155002_E018267.BLK
TC09190413160814_E018335.BLK
TC10190413135738_E008023.BLK

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

10
0 0.2 0.4 0.6 0.8 1 1.2
time (s)

Define the conditions

The screenshot shows a MATLAB R2012a environment with several windows open:

- Trials Menu:** A list of actions for managing trials, including "edit stims...", "set stims", "save stims to file...", "load stims from file...", "show stim", "display events", "edit events", "read heart (all trials)", "read heart (this trial)", "Make new set with dataop as data", "Make new set with binned data", "Make new set with current trial on", and "coregister trials".
- Variable Editor - STIMTABLE:** A table with 7 columns (1-7) and 10 rows. The data is as follows:

	1	2	3	4	5	6	7
1	'id'	'name'	'stim'	'type'	'dir'	'freq'	'contrast'
2	0	'blank1'	[]	'blank'	[]	[]	[]
3	9	'blank2'	[]	'blank'	[]	[]	[]
4	10	'lum5'	[0.1000;1.2000]	'lum'	90	1	5
5							
6							
7							
8							
9							
10							
- Command Window:** Contains the following MATLAB commands:


```
>> STIMTABLE{4,3} = [.1; 1.2];
>> STIMTABLE{1,5} = 'dir';
>> STIMTABLE{4,5} = 90;
>> STIMTABLE{1,6} = 'freq';
>> STIMTABLE{4,6} = 1;
>> STIMTABLE{1,7} = 'contrast';
>> STIMTABLE{4,7} = 5;
```
- Dialog Box:** A message box at the bottom right says "Edit variable 'STIMTABLE', then press 'OK'. Close this figure to Cancel" with an "OK" button.

Save

The screenshot displays the 2P VIEW software interface. The left sidebar contains a menu with the following items: Resize frames, Preset positions, Edit code, Reinit menus, Object in base workspace, Save PNG (Ctrl+P), Copy sub-part..., More, 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, read data & compute dataop, and Preferences... The 'Save' menu item is highlighted, and an arrow points from it to the 'Save tpview data in' dialog box. The dialog box shows the 'Save In' folder as '130419_billy' and the file name as '130419_billy_bin3'. The 'Files of Type' is set to '*.tpv) 2P VIEW file format'. Below the dialog box, a 'confirmation needed' dialog box is open, asking 'Save or Remove temporary trials?'. An arrow points from the 'Save' button in the 'Save tpview data in' dialog box to the 'confirmation needed' dialog box. The 'confirmation needed' dialog box has three buttons: 'Save', 'Remove', and 'Cancel'. An arrow points from the 'Save' button in the 'confirmation needed' dialog box to the 'Enter file names' dialog box. The 'Enter file names' dialog box shows the file name '9_billy_bin3_trialaverage' and has 'OK' and 'Cancel' buttons. The main window shows a plot of 'lines separated by 20' with a time axis from 0 to 1.2 seconds. The plot shows three traces, with the top trace being a blue line. The bottom trace is a black line. The middle trace is a grey line. The plot is labeled 'trial 39' and 'type: movie'.

2P VIEW

Picture 1 Picture 2 Time courses More displays Trials Electrophys Spikes Scripts

lines separated by 20

REGIONS

Save tpview data in

Save In: 130419_billy

130419_billy_bin3

File Name: 130419_billy_bin3

Files of Type: (*.tpv) 2P VIEW file format

Save Cancel

confirmation needed

Save or Remove temporary trials?

Save Remove Cancel

Enter file names

trial 39

9_billy_bin3_trialaverage

OK Cancel

TC09190413151922_E018150.BLK
TC09190413153235_E018200.BLK
TC09190413153639_E018216.BLK
TC09190413155002_E018267.BLK
TC09190413160814_E018335.BLK
TC10190413135738_E008023.BLK

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

Reject the bad trials: Press 'r' to reject a trial. After having rejected all bad trials, repeat the procedure to compute the average trial.

