Short primer of RoiGui_005

0) Load plane (Fsig_<AnimalID>_<Date>_plane#_ch#_MinClust#.mat)

1) Left click to select an ROI, inspect its fluorescent trace.
2) Find Cellbody with good F-trace. Ctrl-Left to select multiple of them.
2.1) Register as Cellbody by clicking [CellBody] button in SVM panel.
2.2) Find noise as well and register as noise by clicking [noise].
3) [Update] to reflect changes.
Repeat 2-3 until all selected ROIs have good F-trace.

4) Right click to force flip the selection, if the fluorescence pattern does not look correct/incorrect.
This Right-clicked ROIs are labeled as "manually selected", and it overwrites the filtering conditions.
5) If there is any suspicious ROI, load movie and check the F-trace. Press [m] to load movie.
6) If there is an ROI that needs to be split, click [split-ROI] button.
click once to select a potential one ROI. Cross + cursor appears, then click the other potential ROI to split an ROI.
7) Save processed data [Save proc]. Fsig_<AnimalID>_<Date>_plane#_ch#_MinClust#_proc.mat is generated.
8) Back to HDBCellSCAN_Master and finalize signal.

Note: Skewness of F-trace is one of the features used to classify ROIs into soma, dendrite, noise.
Splitted ROI does not have this value. So, they have skewness=1 by default.

==== Keyboard and mouse click, short cut keys ====
Left click: select this ROI and show F(t).
Right click: flip selection (selected <-> non-selected ROI)

<Keyboard short cuts>
s   flip selected view/ unselected view
q   ROI view
w   mean (p=0) or normalized (p=1) image view.
p   flip mean <-> normalized mode.
m   load movie
<   role back movie
>   role forward movie
?   acceralate movie frame rate.
→   move one frame forward
←   move one frame backward
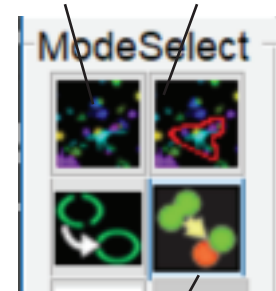c   show correlated cluster.
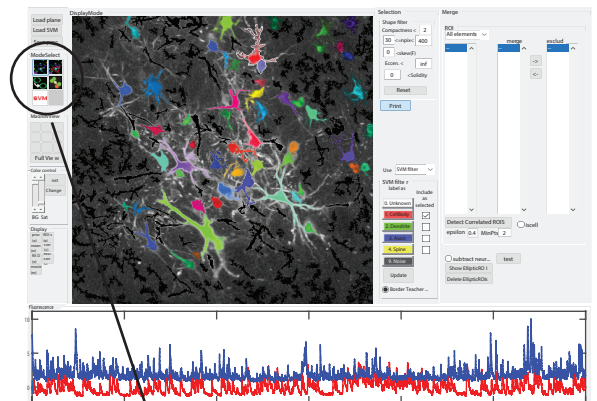
Correlaed cluster view [c]
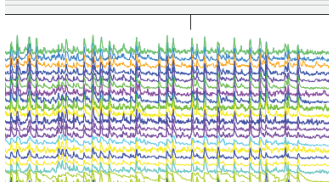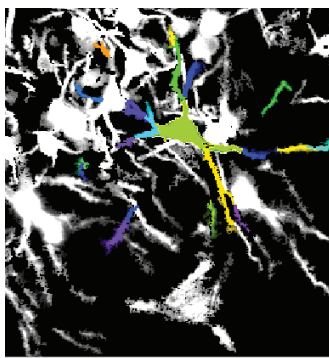
elliptic ROI mode:

It allows user to inspect potential
ROI area. It requires movies to load.
Press [m] to load movie before hand.

Display   elliptic ROI

split ROI