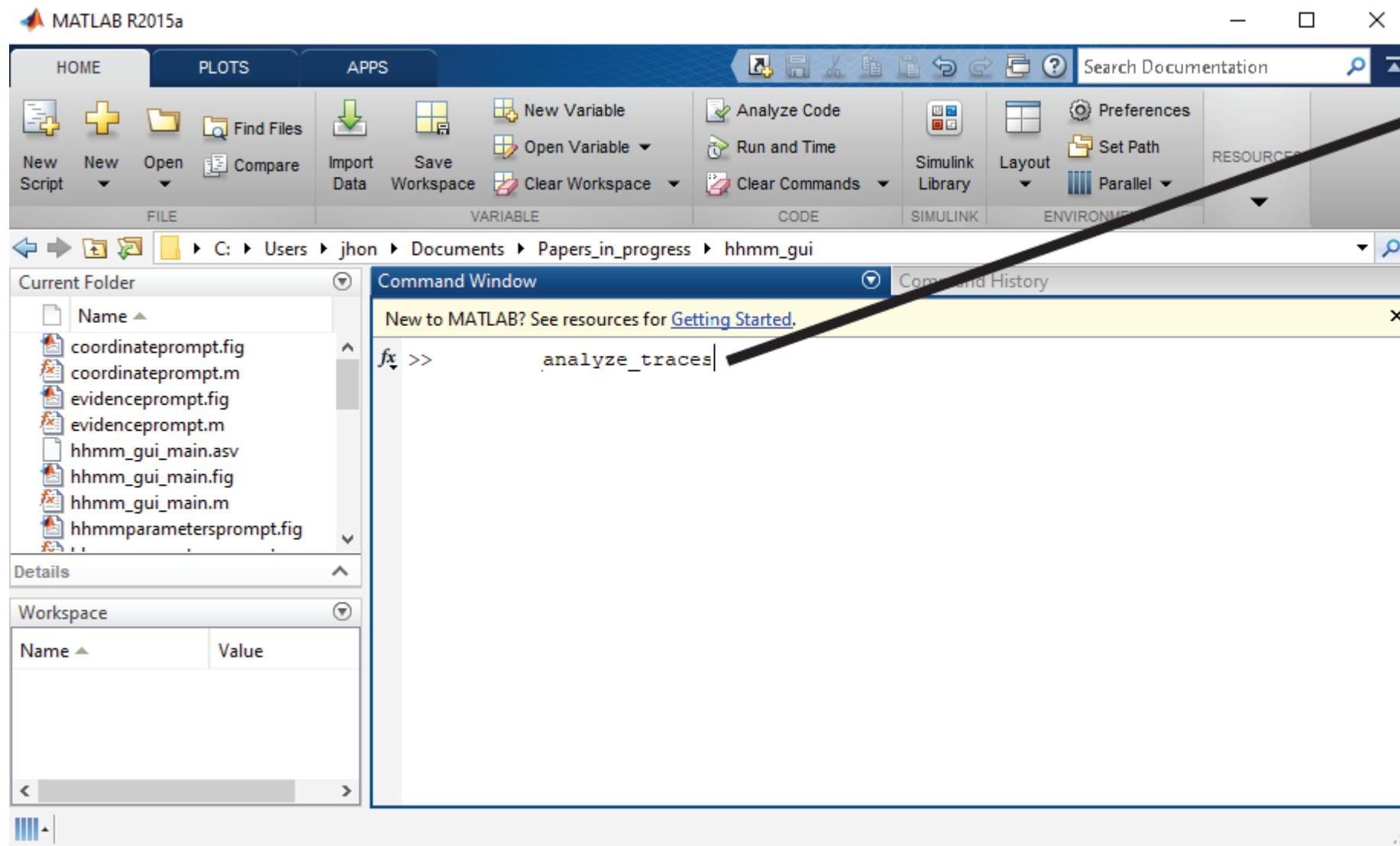
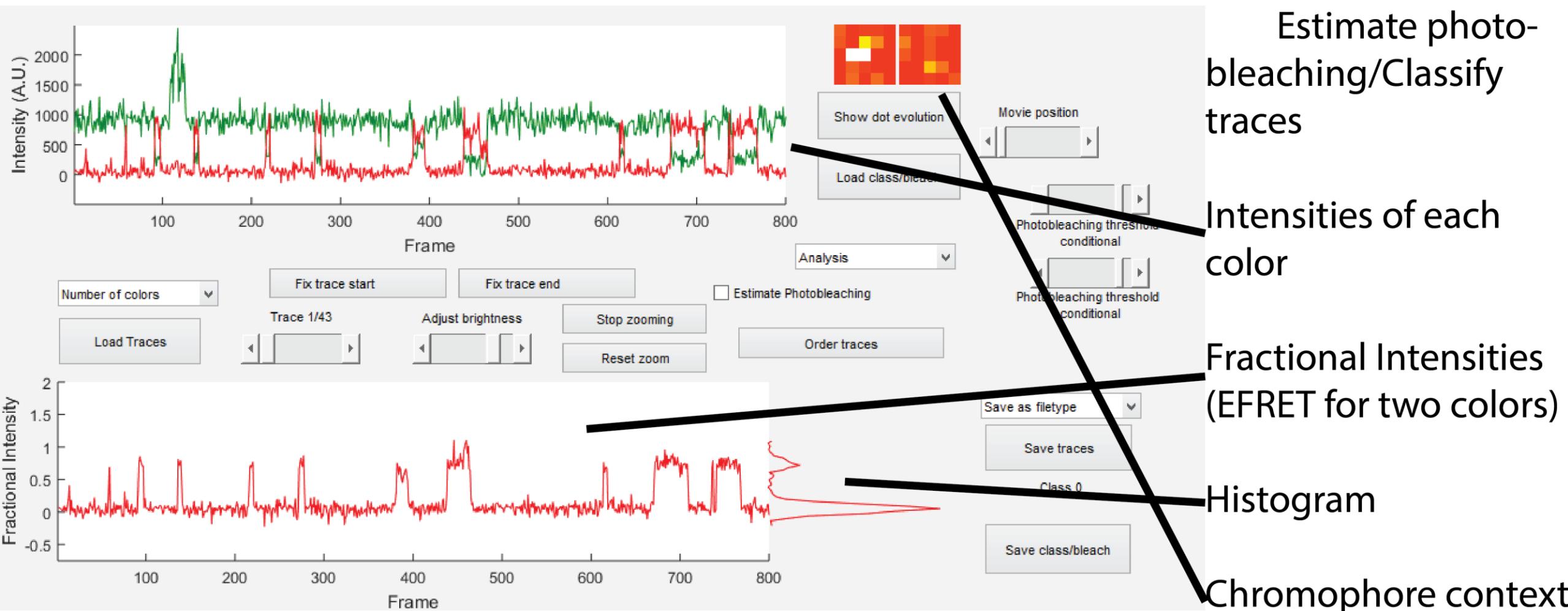
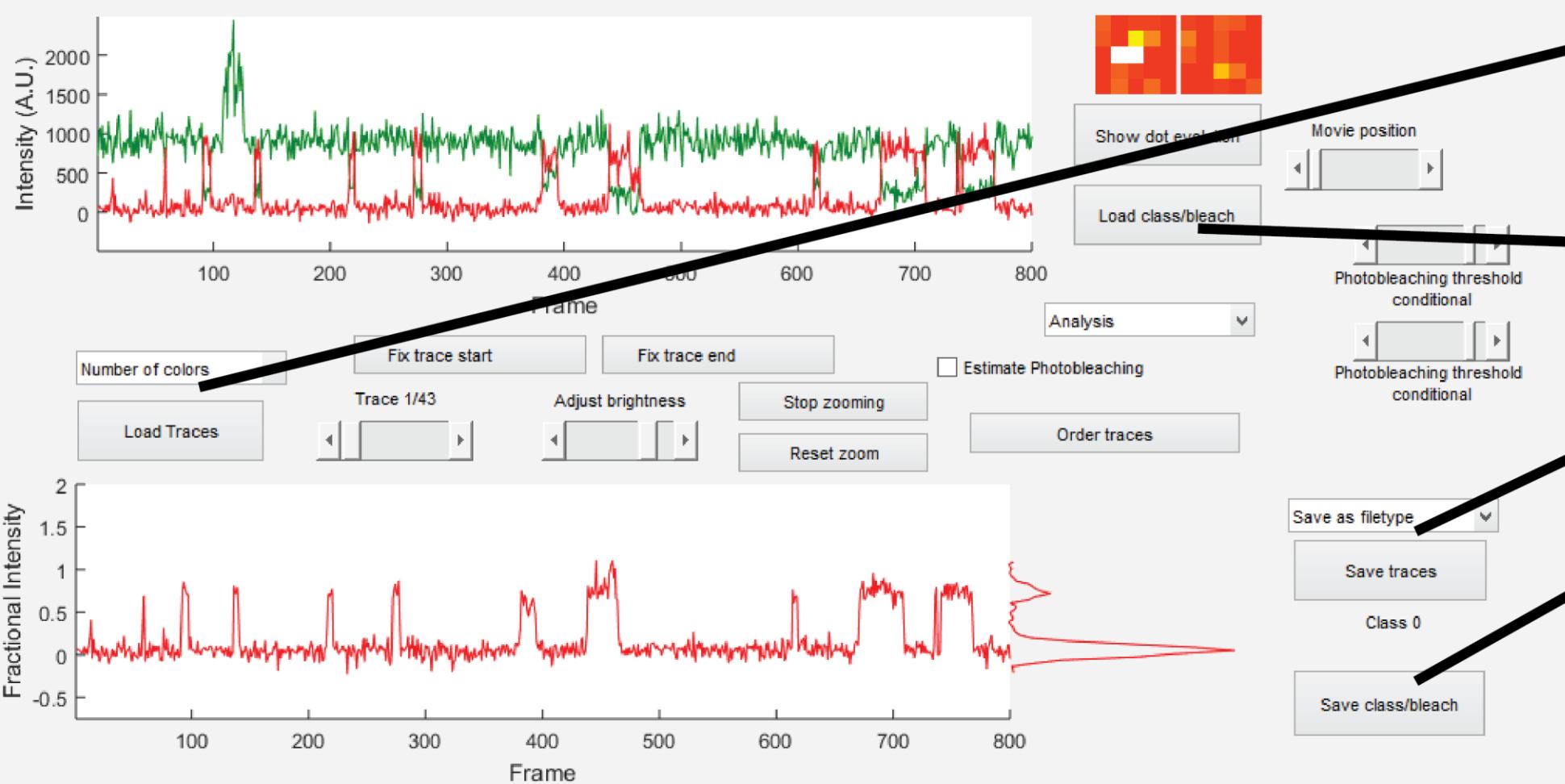


hFRET manual



Open the trace viewer gui by typing as shown and pressing "enter."





Load in data (can take multiple files)

Load in classifications (can take multiple files)

Save trajectories (.dat, just traces; vbscope - everything.)

Save classifications



Enable photobleach detection/correction

Keyboard shortcuts:

s: fix start (then shift-click each color)

f: fix finish

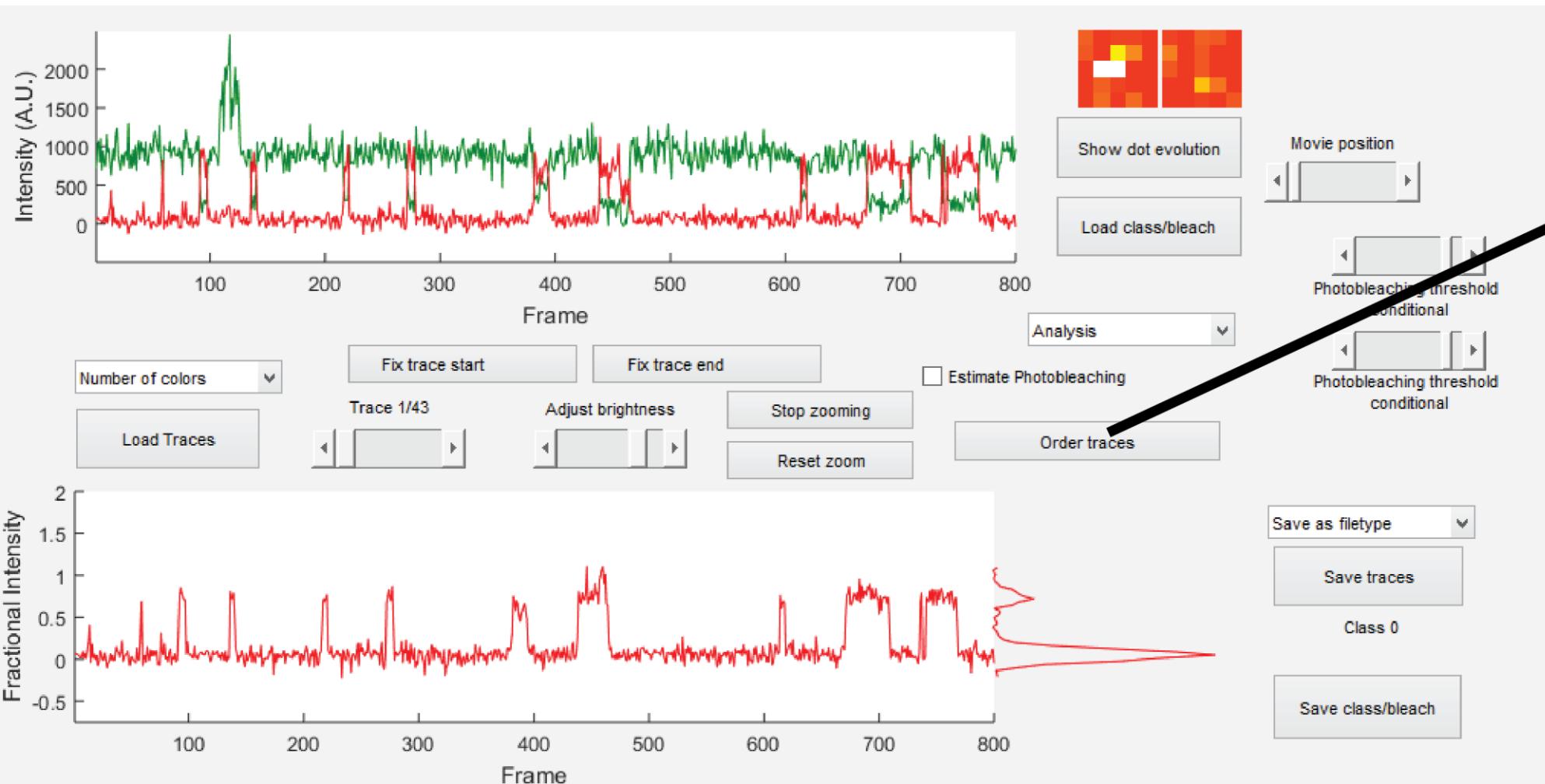
n: next trace

b: back one trace

z: zoom in. When done you must hit "stop zooming" here

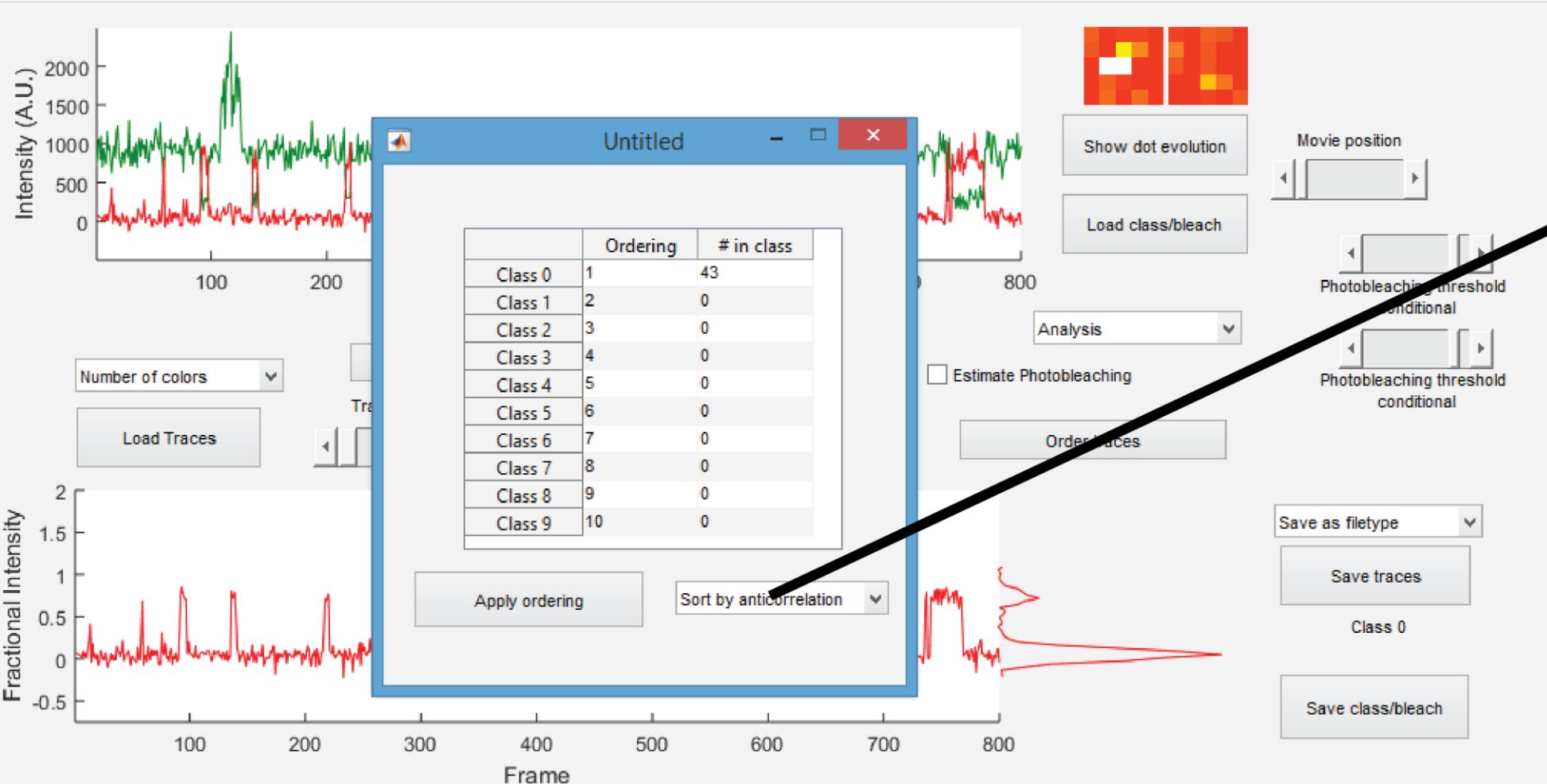
Sorting through the
traces

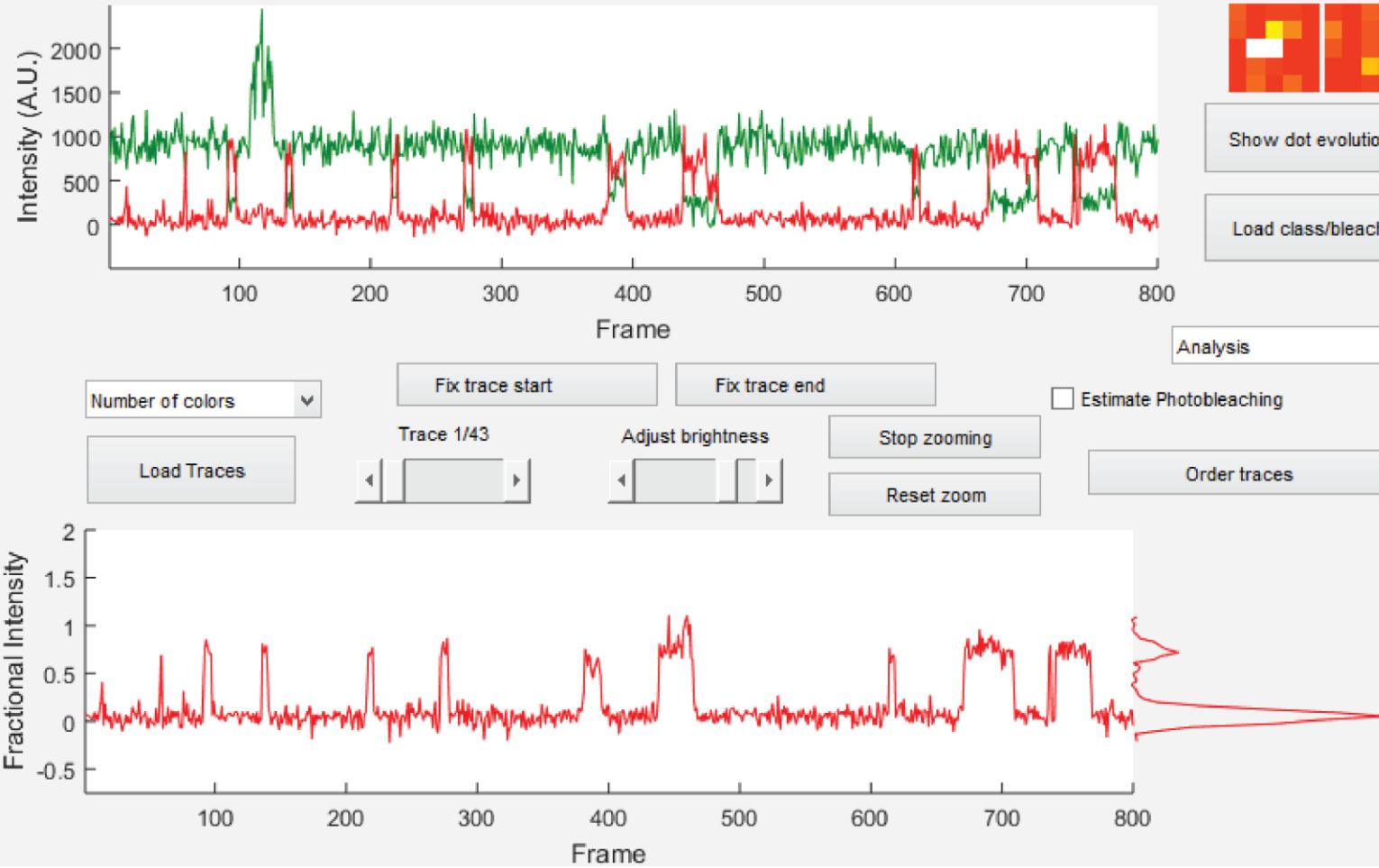
Automatic sorting



Sorting through the traces

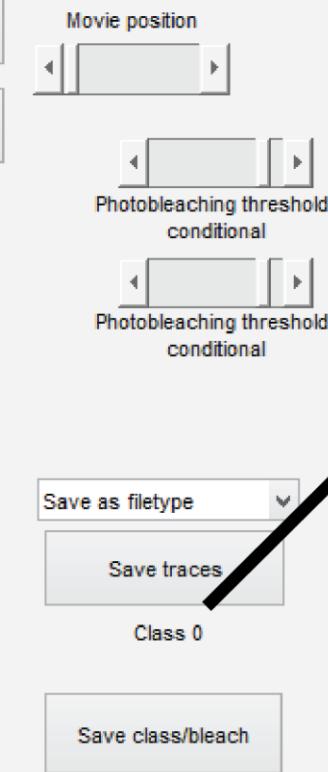
Calculates anticorrelation. Clicking “Apply ordering” places the traces in order from most to least anticorrelated.



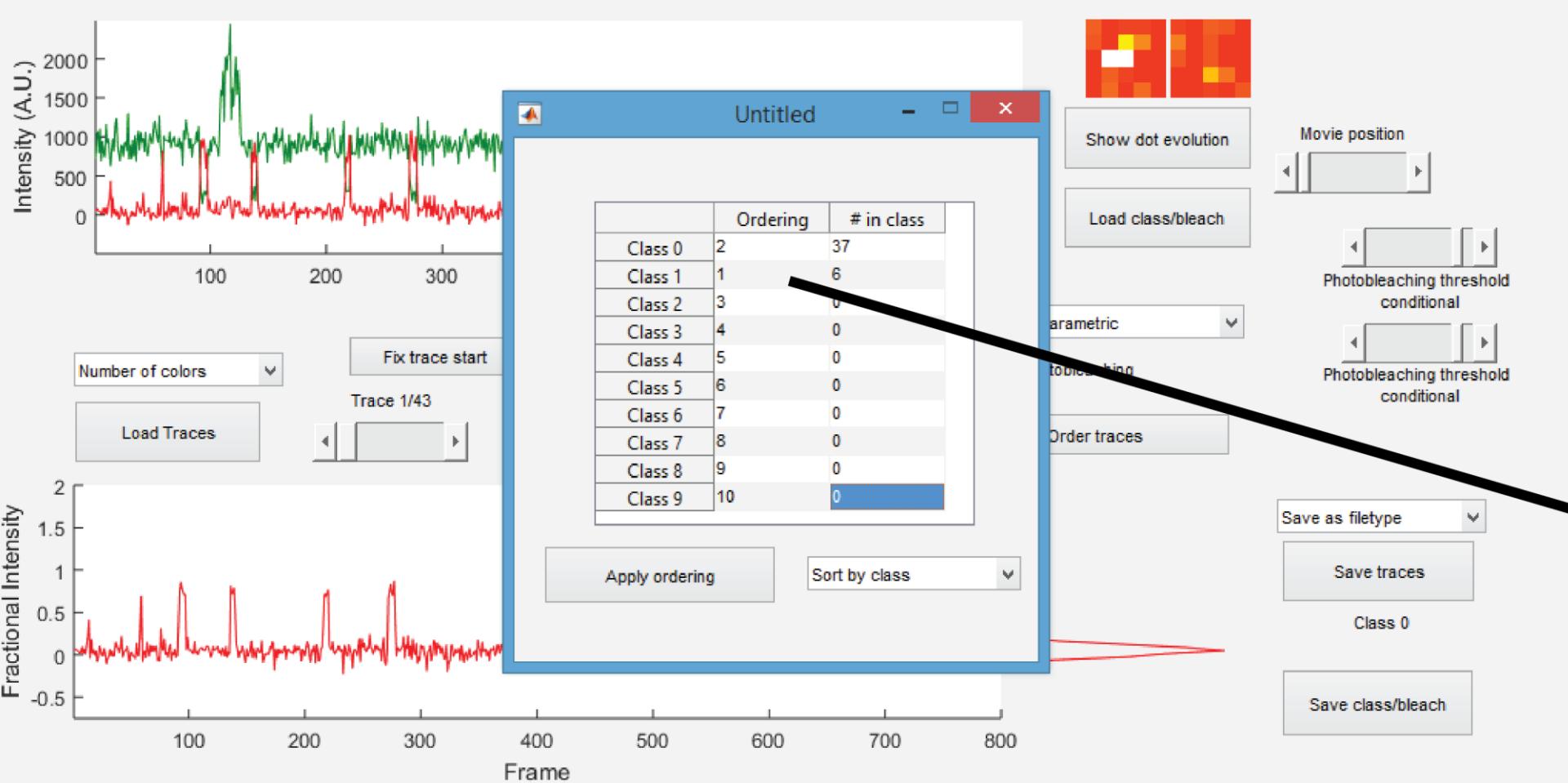


Sorting through the traces

Manual sorting



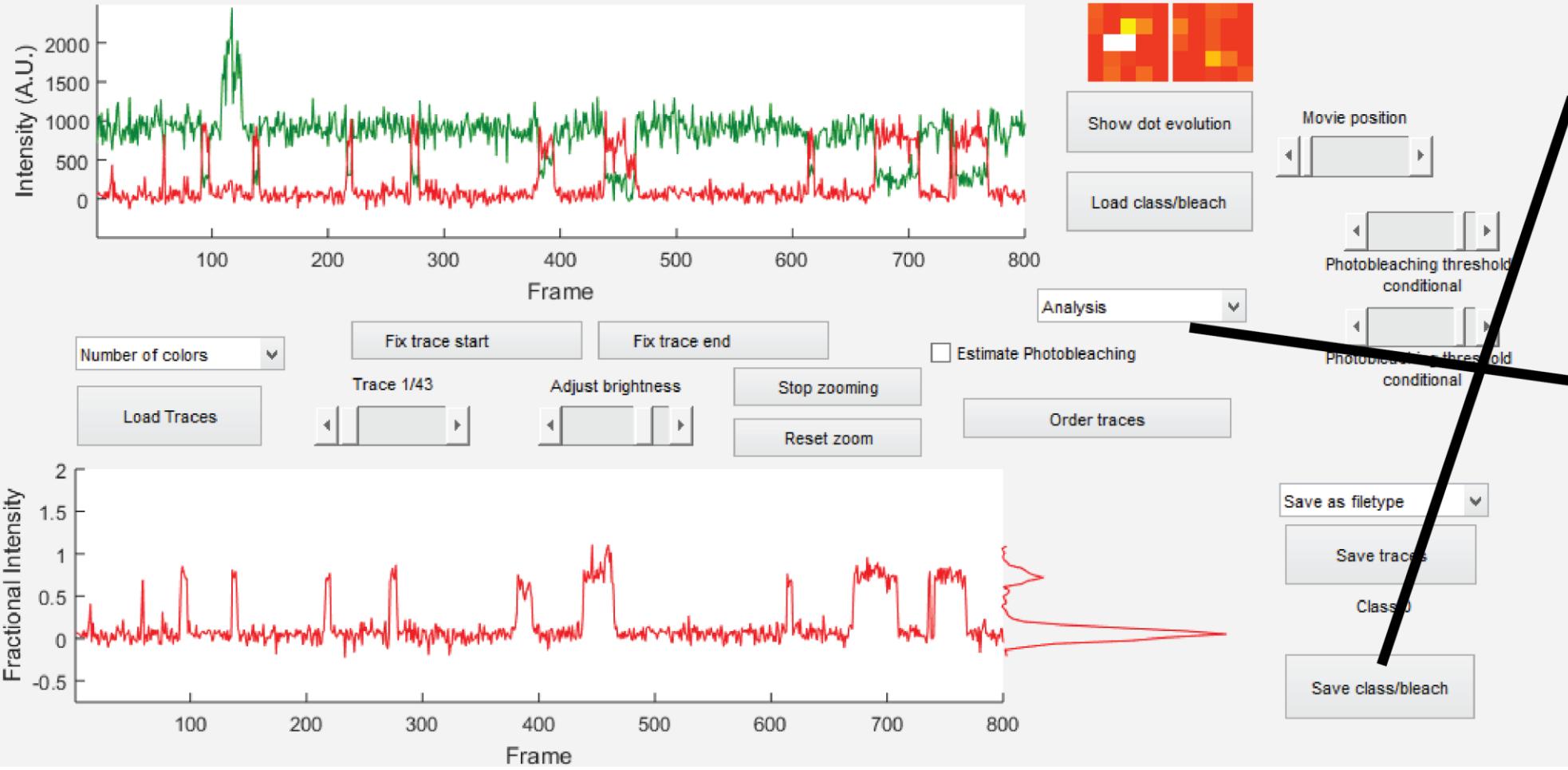
Click a number between 0-9 after clicking a graph. The trace is now in that class. Readout is here.



Sorting through the traces

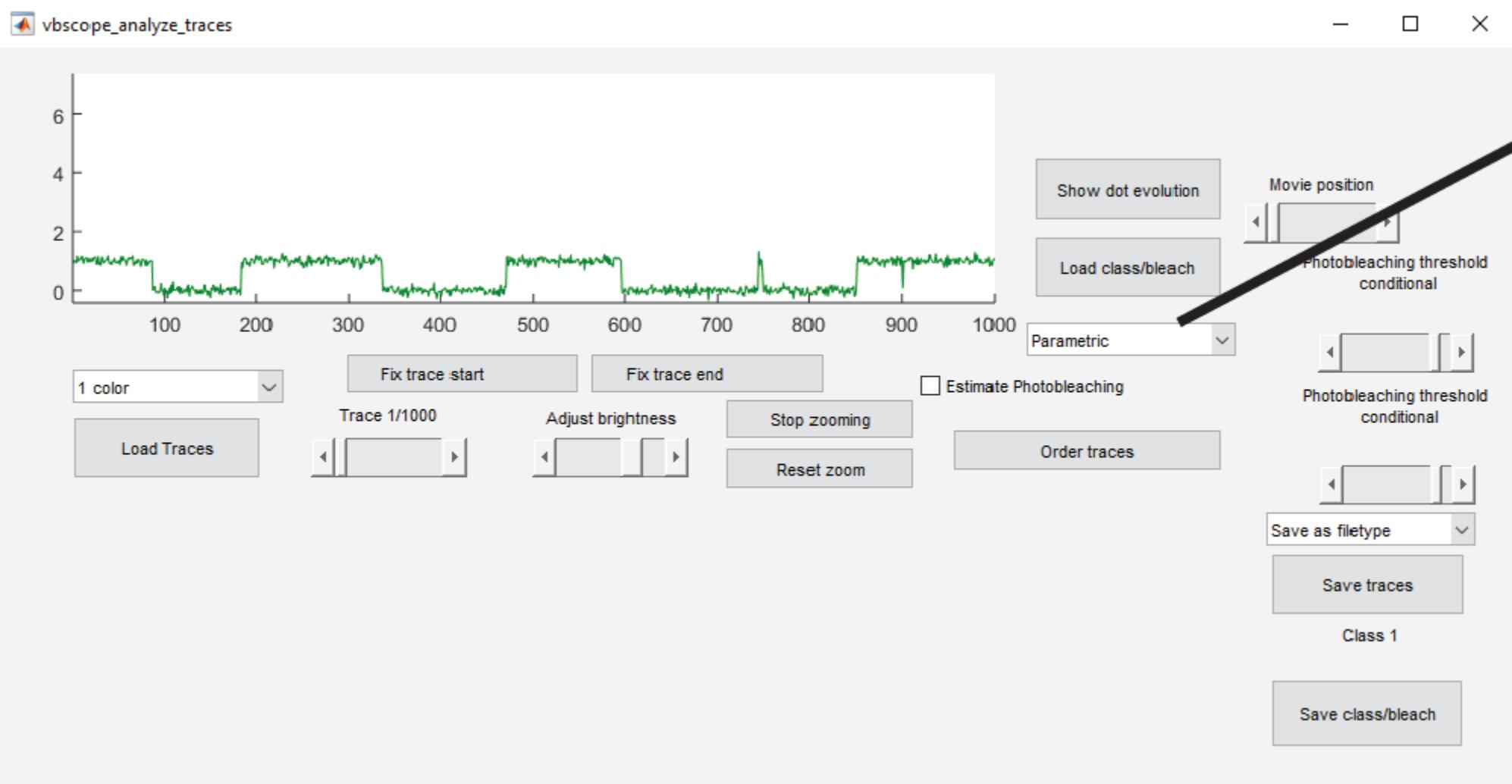
Manual sorting

Clicking “Ordering traces” again, this table appears. The “Ordering” column is editable, and allows the classes to be put in order from 1-10.



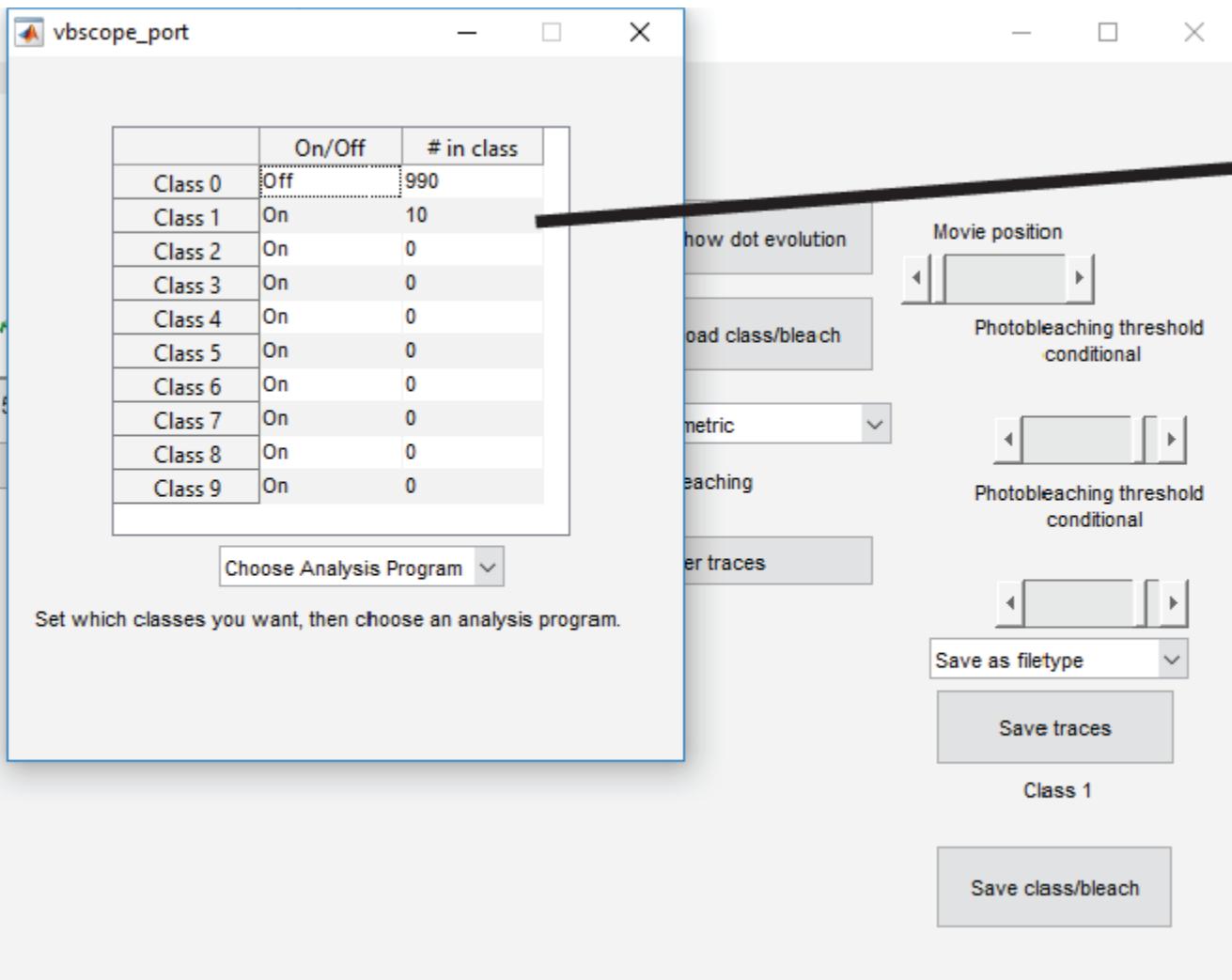
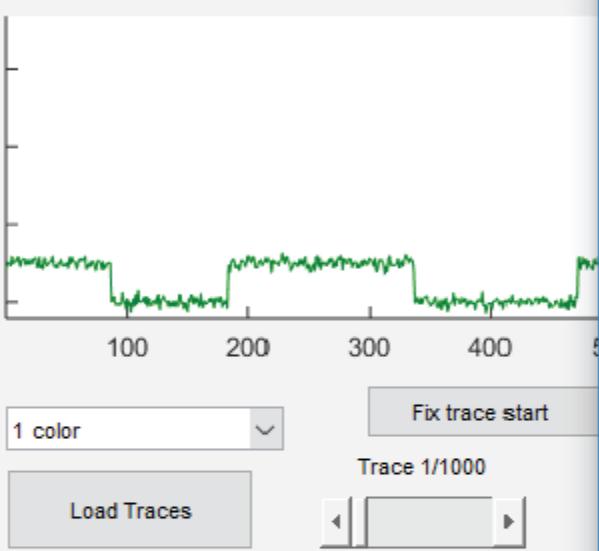
Once sorting/start/stop correction is complete, save class/bleach

Then open up a parametric or a nonparametric analysis type



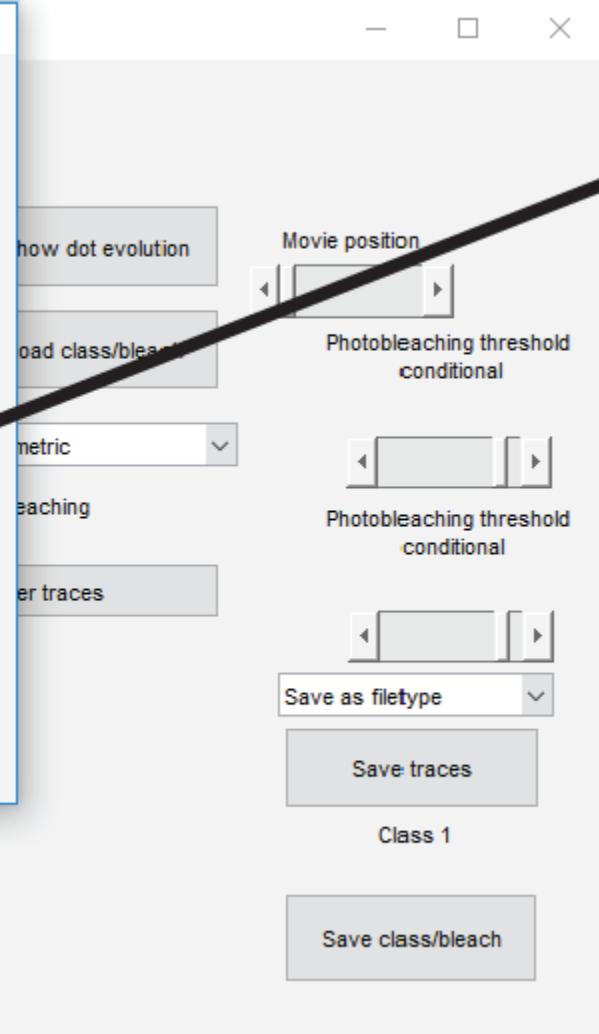
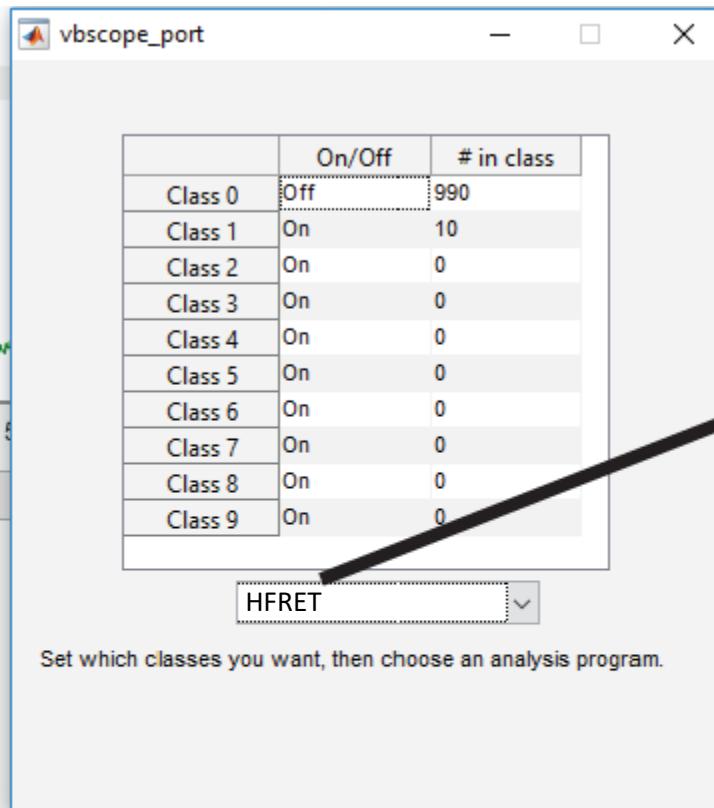
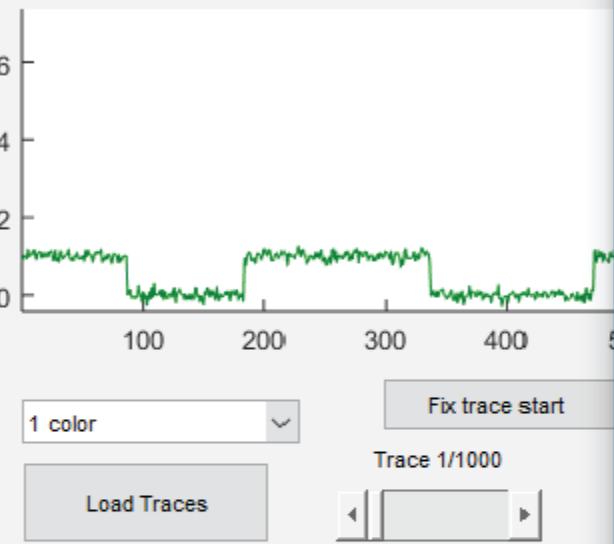
Change from
"Analysis" to
"Parametric"

vbscope_analyze_traces

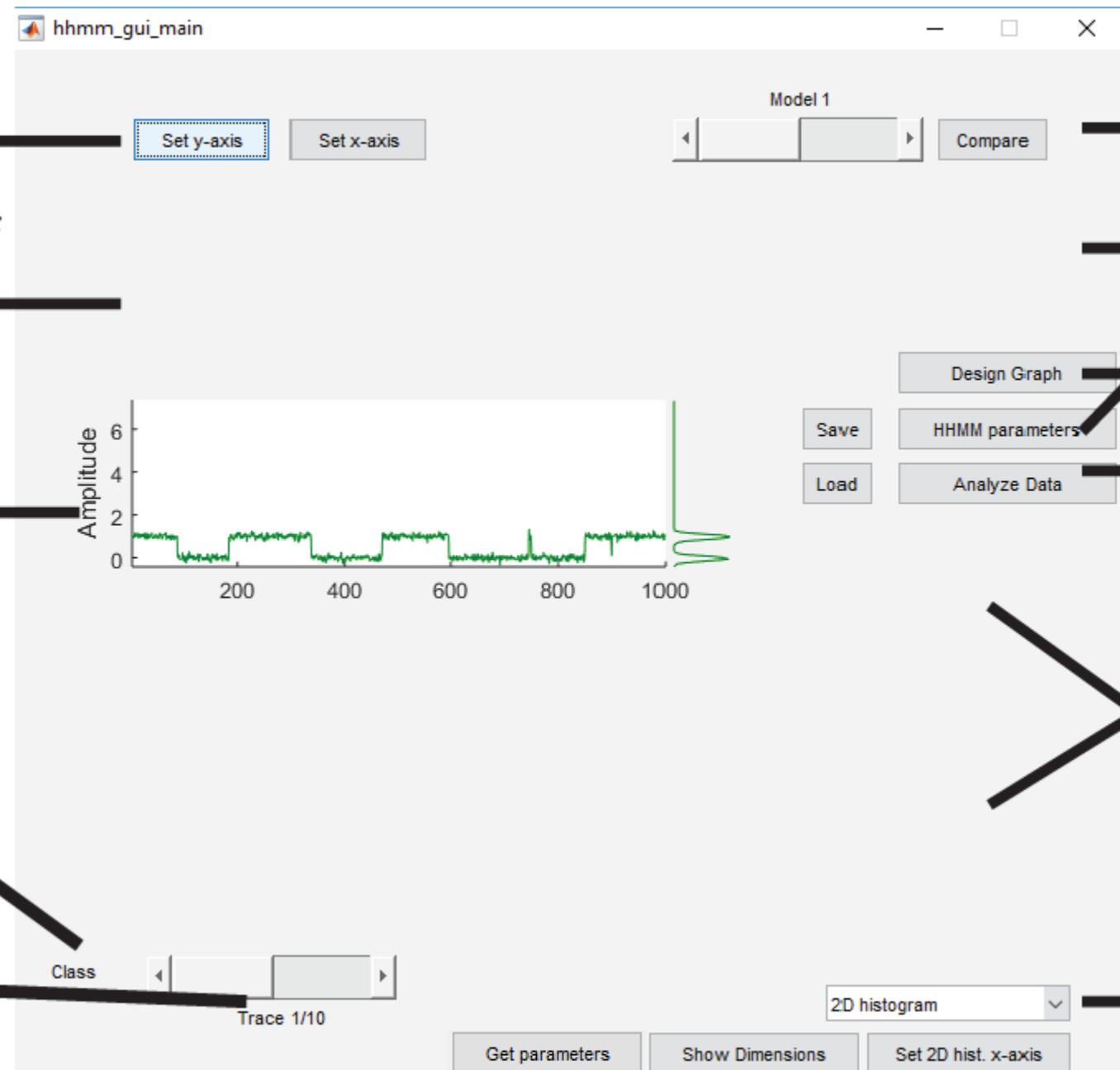


Choose which classes to port over by clicking on the table and toggling a class "on" or "off" by hitting the appropriate number on the keyboard

vbscope_analyze_traces



Choose "HFRET"



- Current Model
- Model Topology
- Model parameters
- Begin analysis
- Population plots
- Population plot parameters

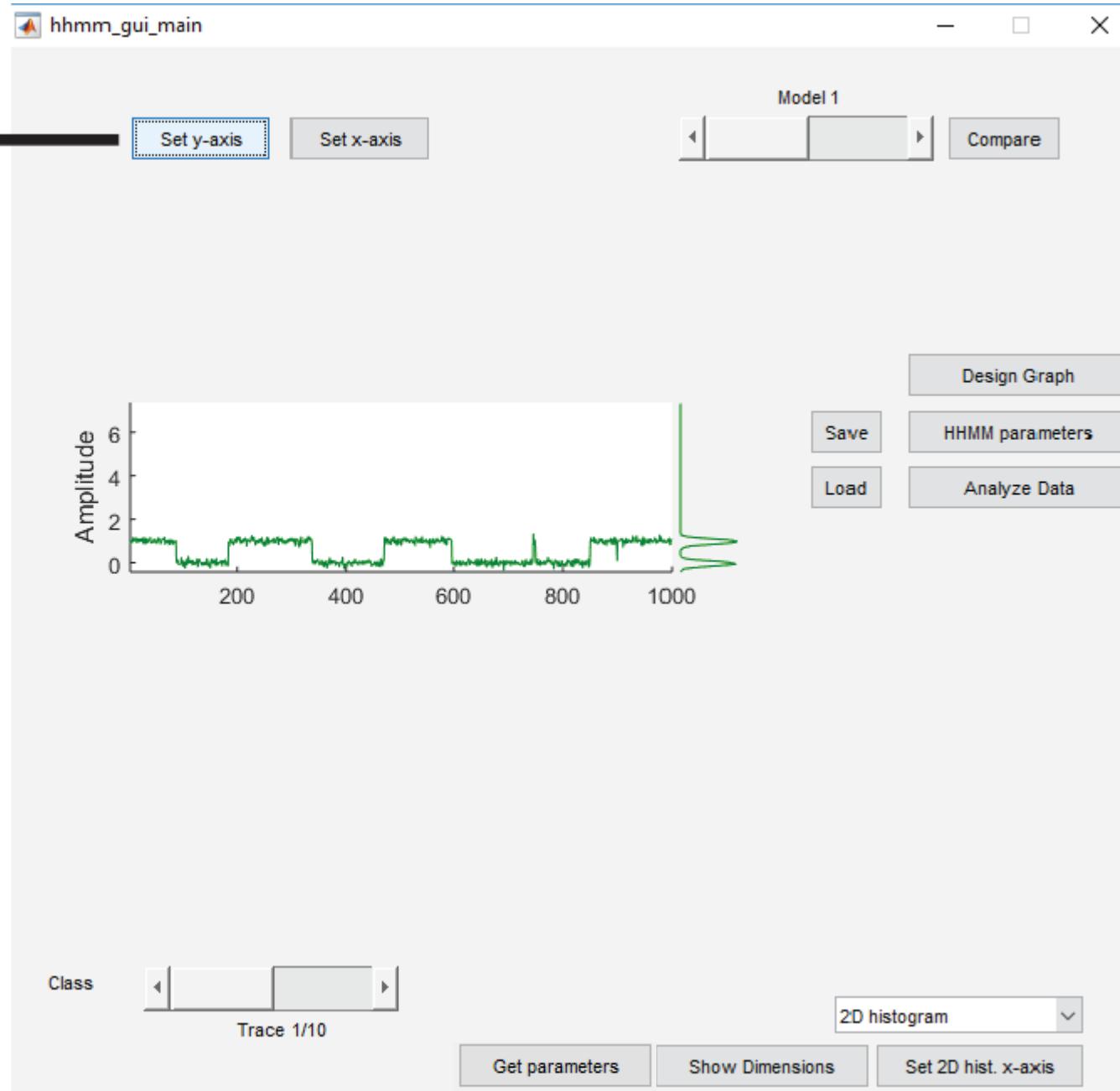
y axis adjustments

yaxisprompt

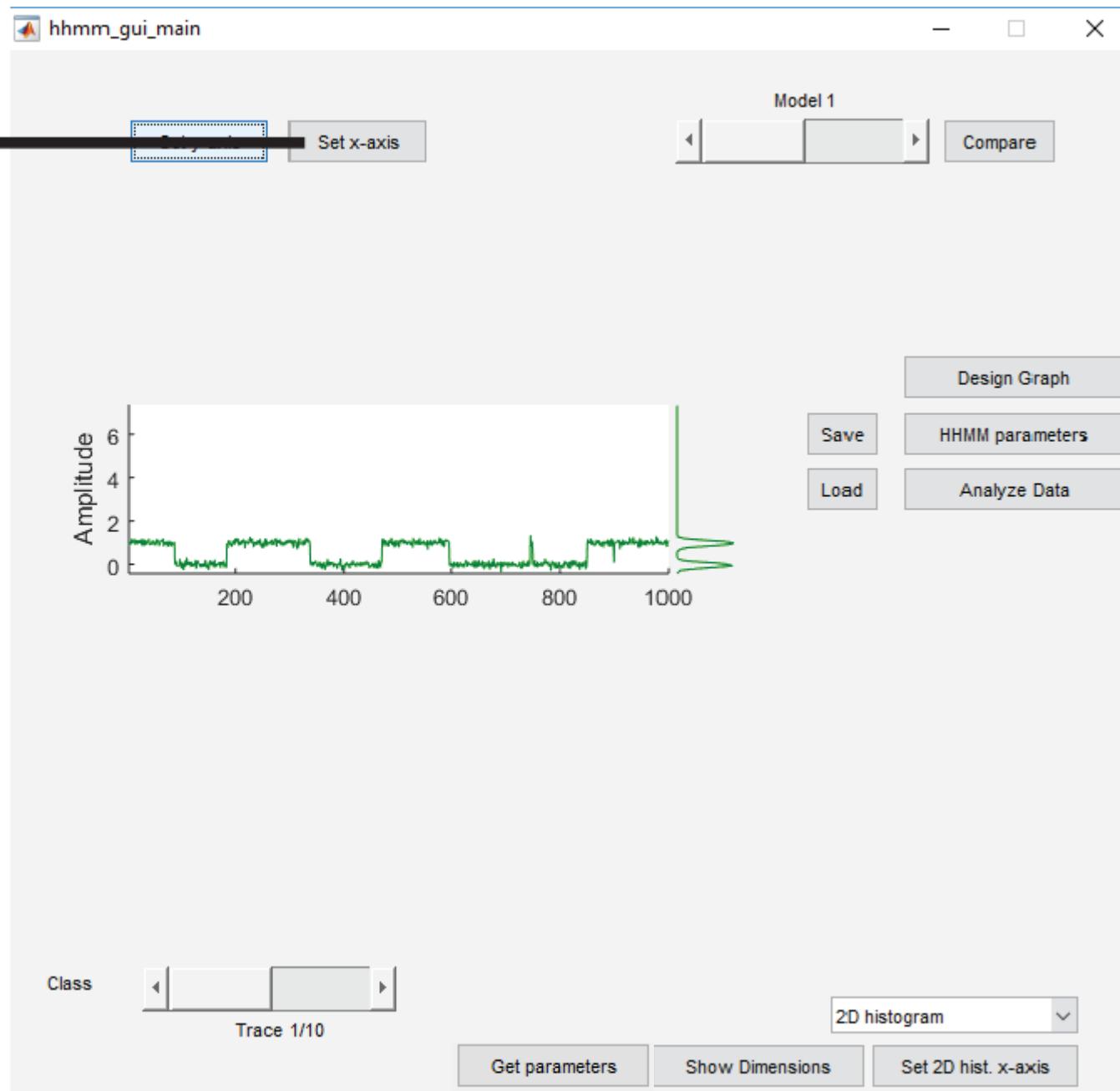
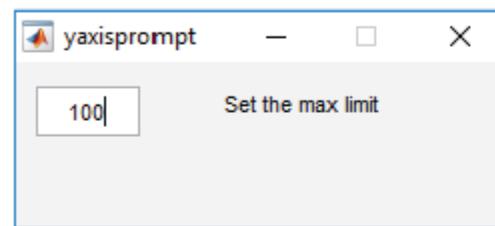
Set min limit

For all prompts like this, just type in the number and hit <Enter>. If more than one number is required, type the two numbers like so

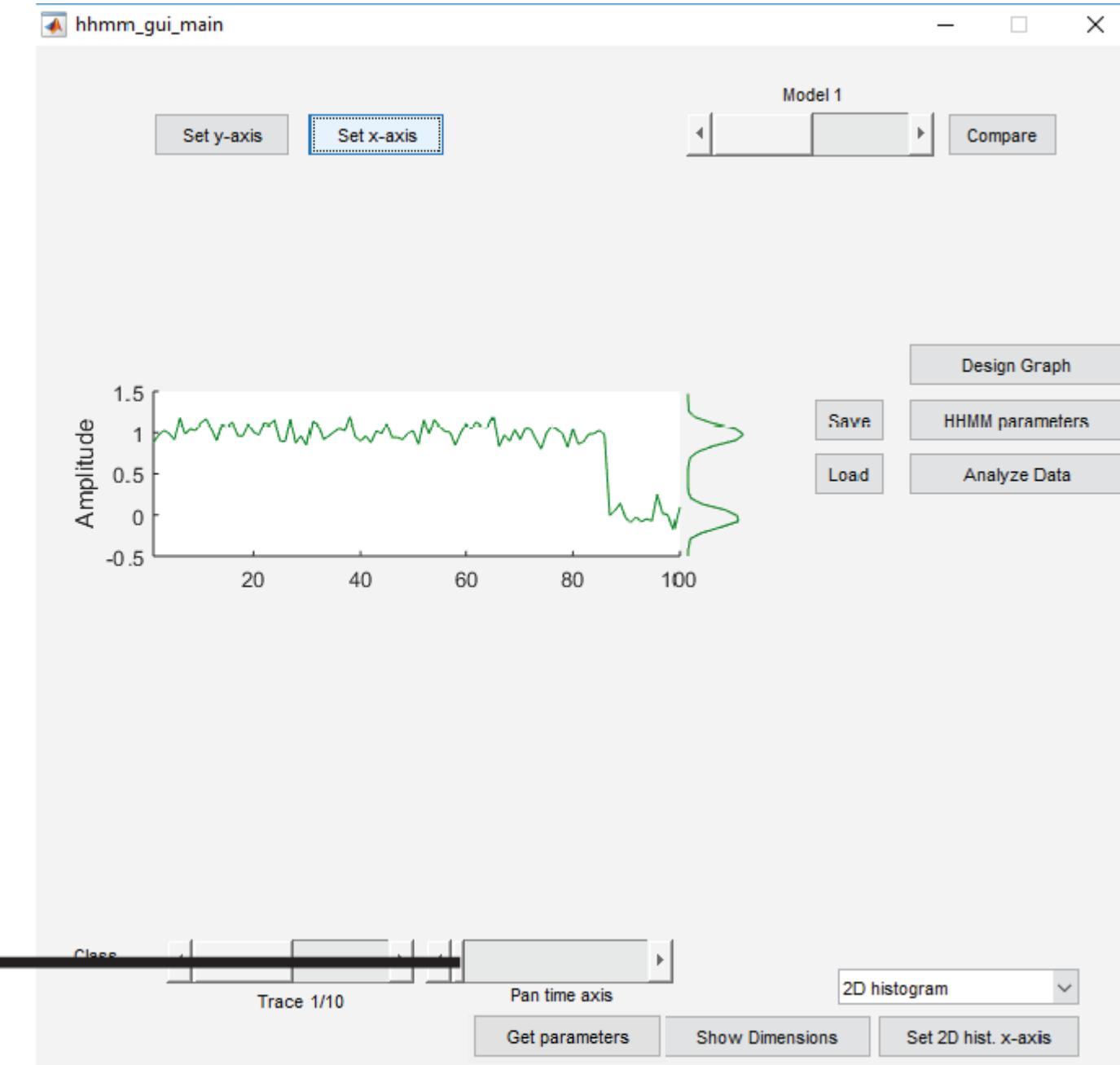
[1 2 ... etc]

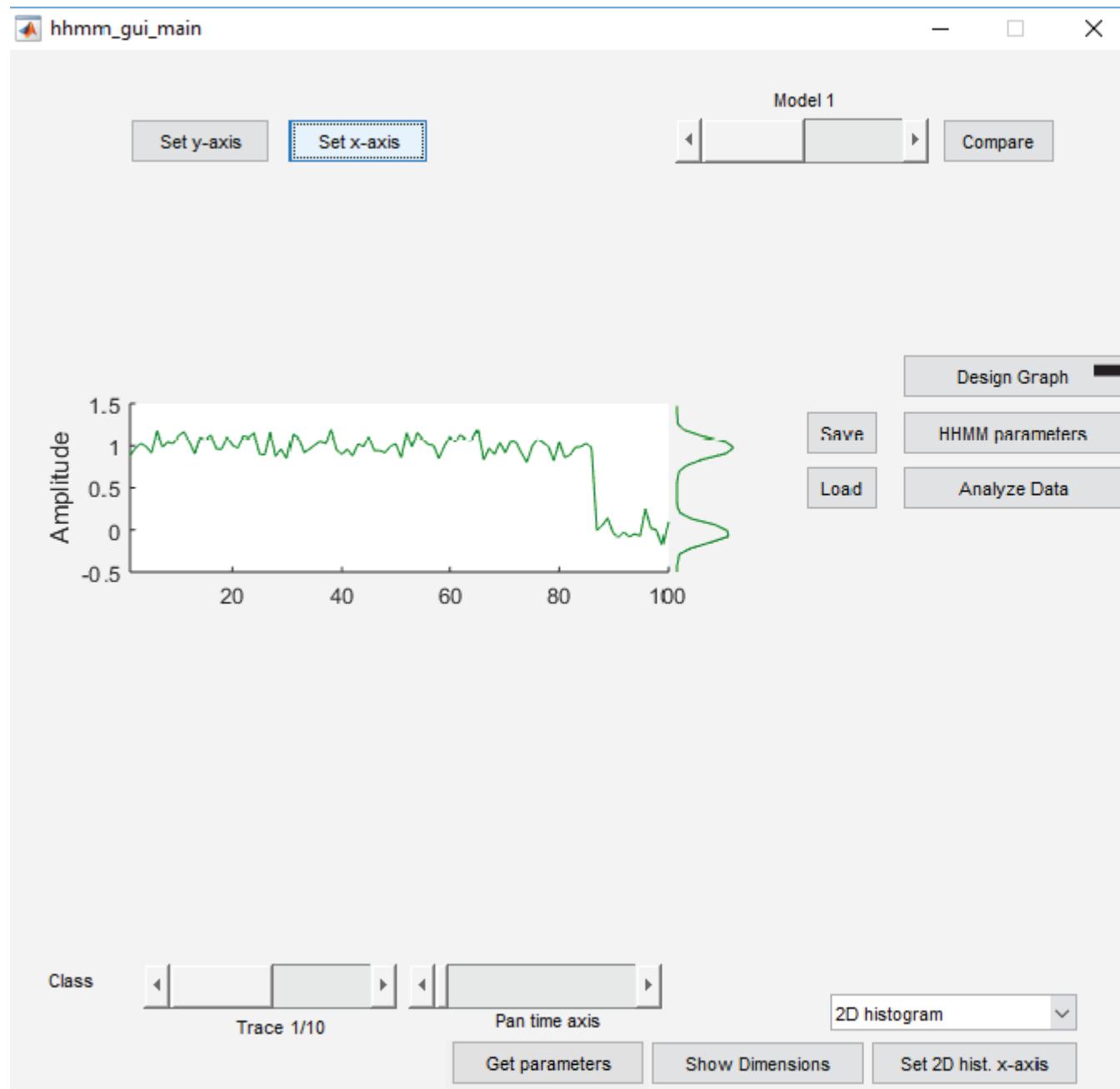


x axis adjustments

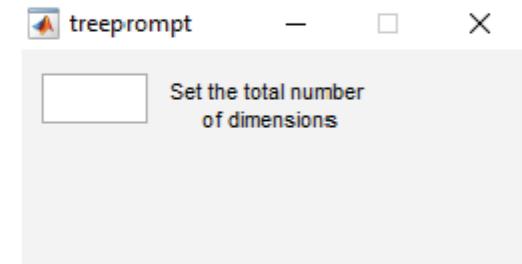


Time axis slider
will appear, allowing trajectory to
be panned



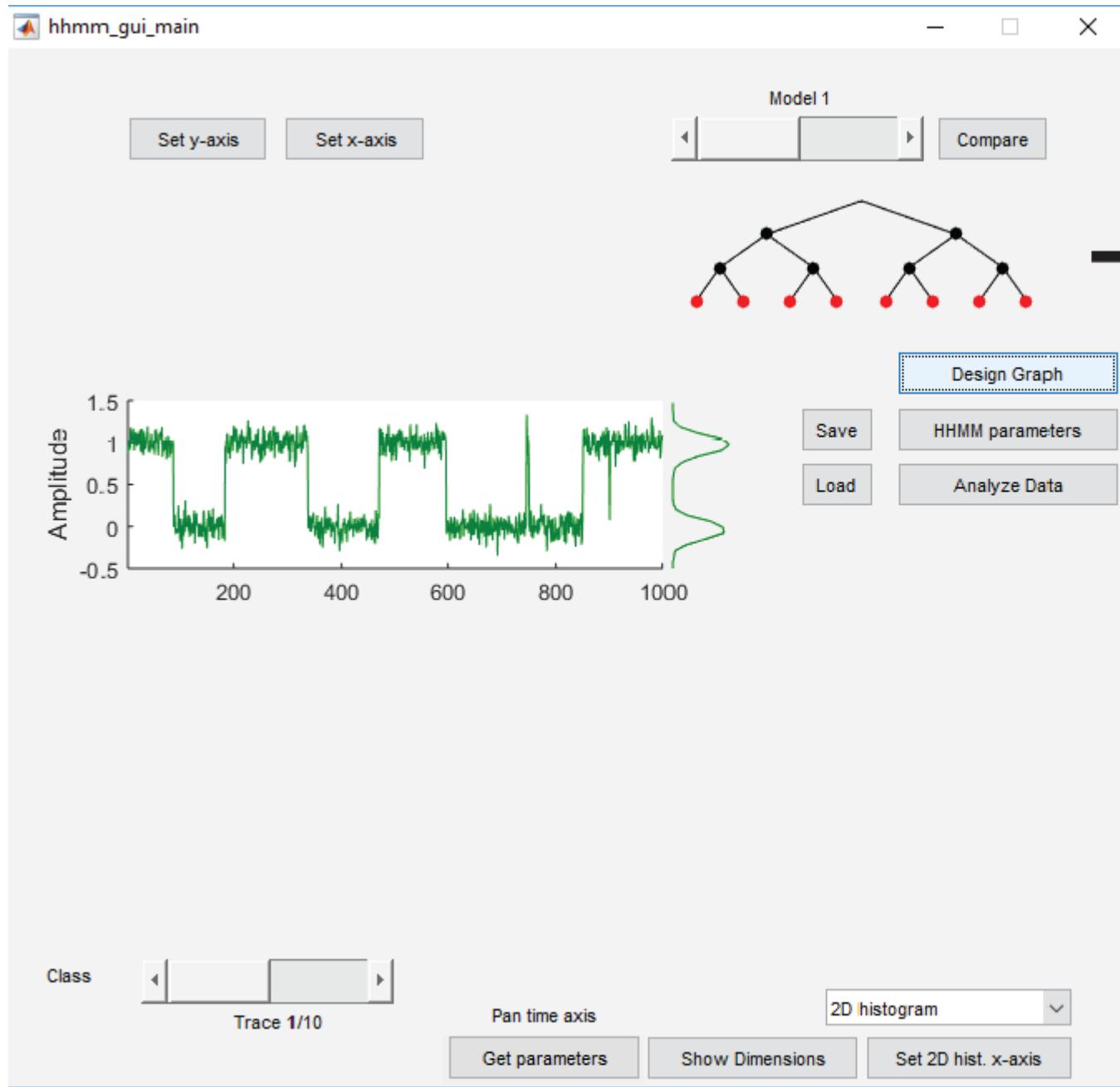


Design model topology

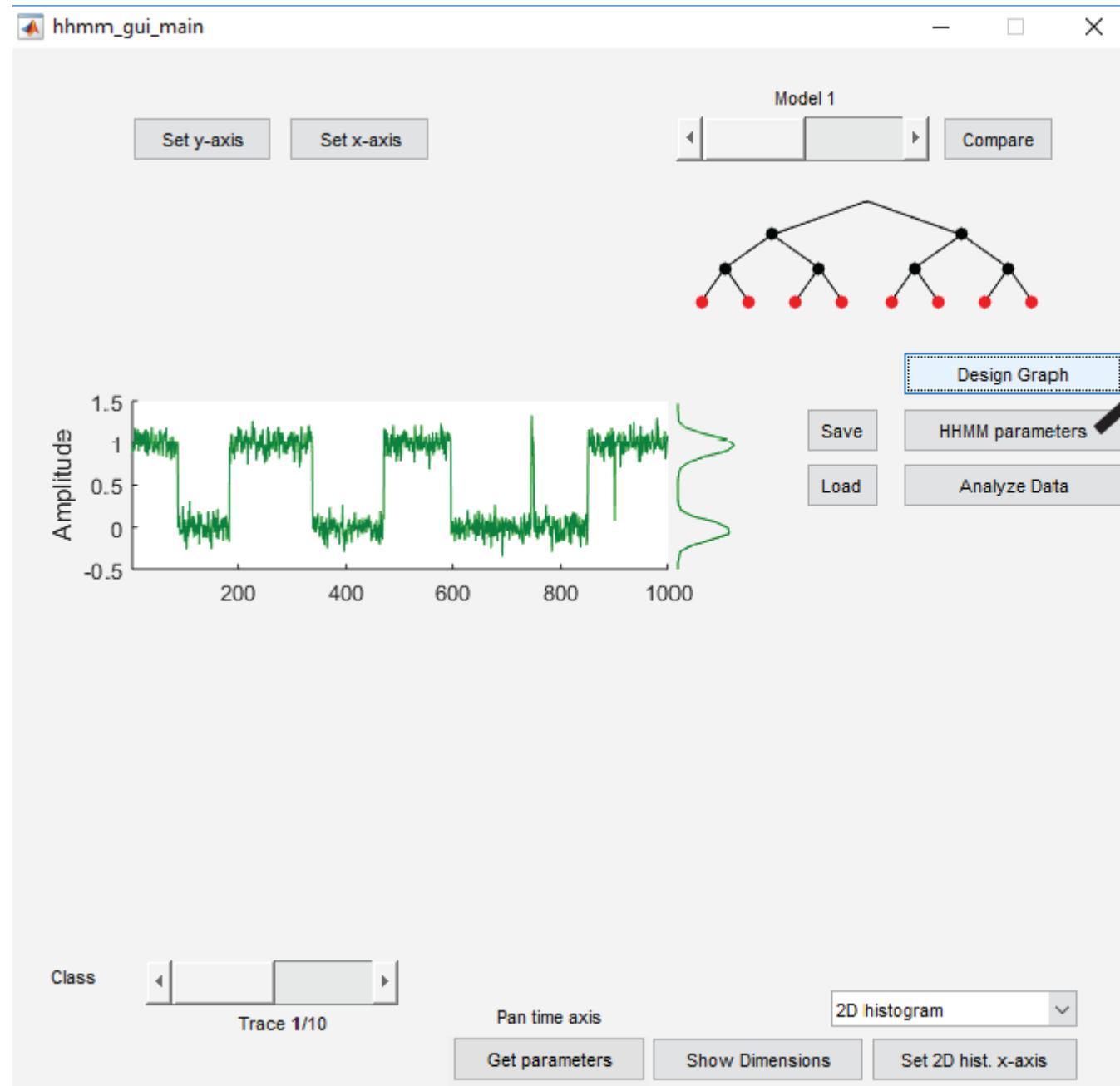


Prompts:

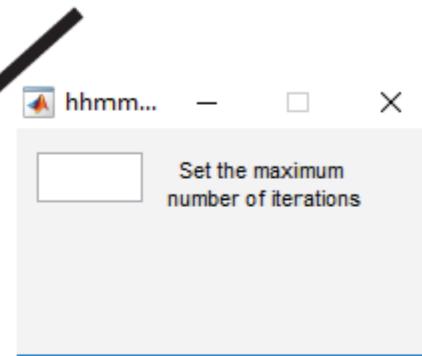
- (1) Total # of dimensions, D
- (2) # of distinct values at level $d > 1$
- (3) $d = 1$, # of distinct values of the direct dimension, $\tilde{\Omega}_1$



Model topology appears here. Shown: D = 3, # = 2 for all values of d

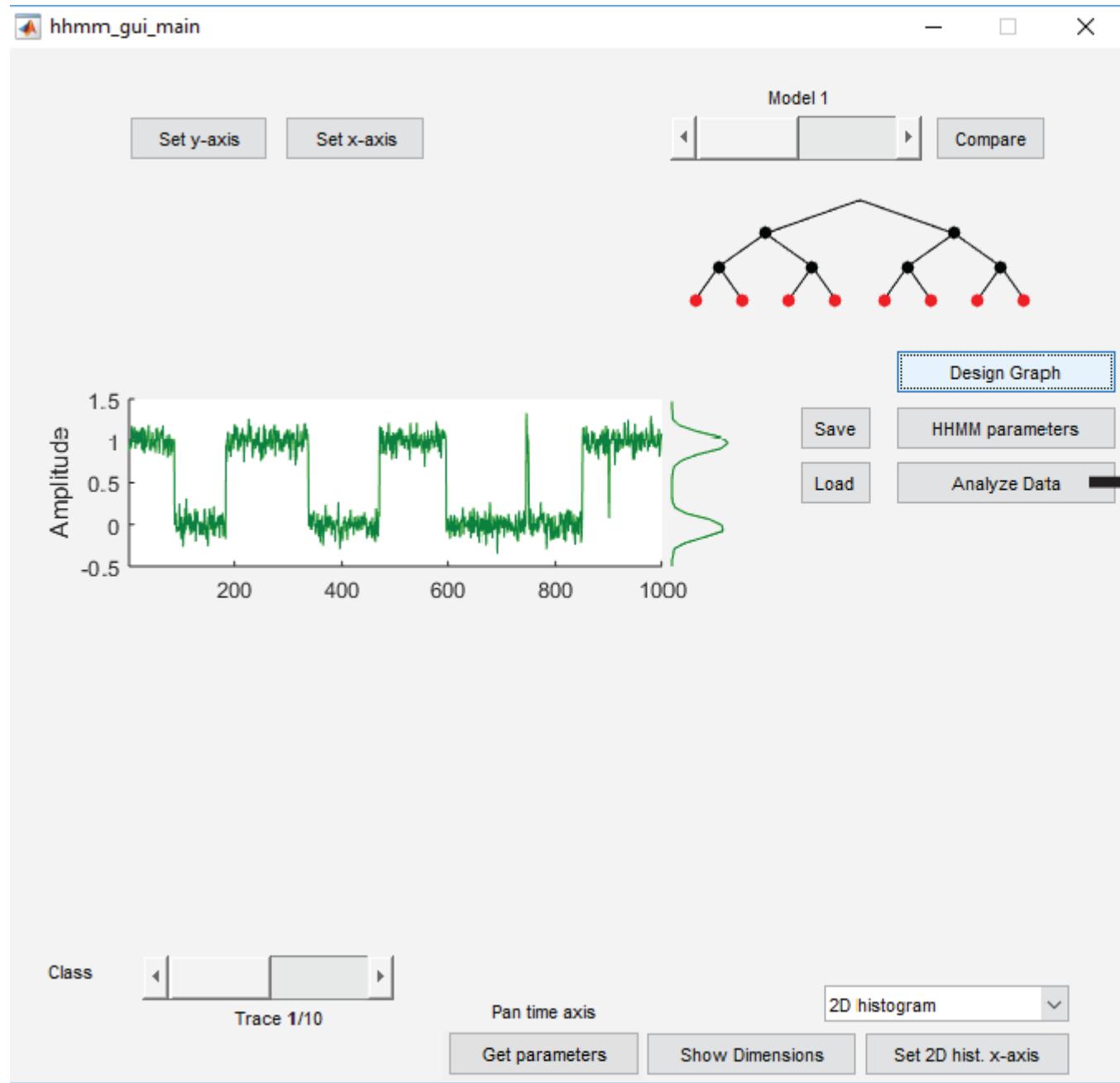


Set algorithm control parameters



Prompts:

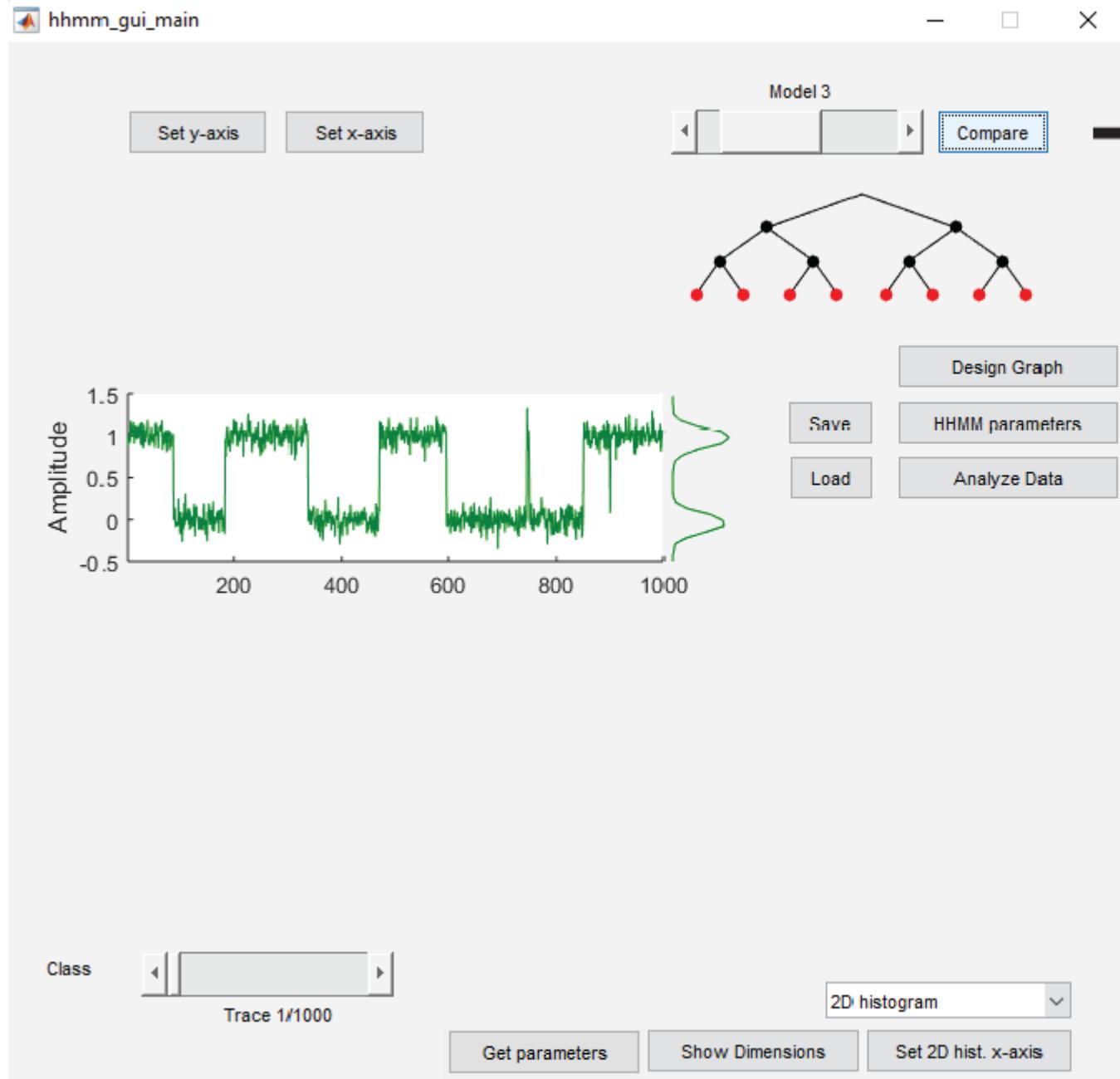
- (1) Maximum number of iterations
- (2) Number of restarts (kinetic parameters randomly drawn)
- (3) Whether each trajectory has the same emission distribution (type "y" or "n")
- (4) Automatic or manual entry of normal distribution means (if "n," entered next; here, [0 1] would do)
- (5) Analysis of amplitudes or fractional amplitudes (if "n," amplitude channel entered next; here, "1" would do)



Analyze data

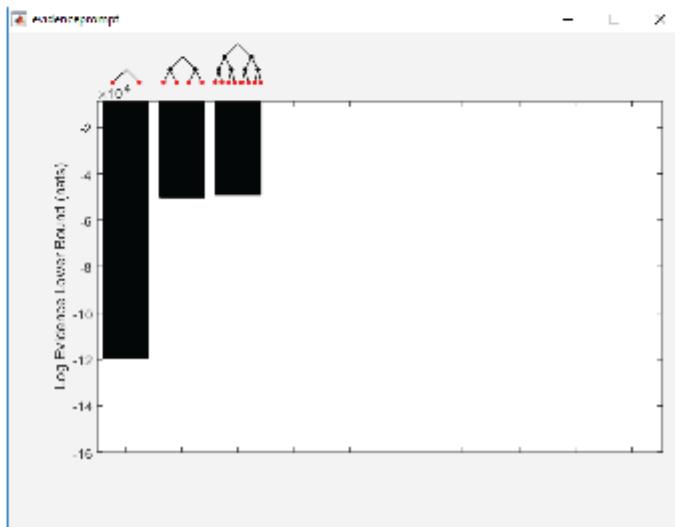
This can be very time consuming. Do not press other buttons while this occurs. A prompt in the command window will alert on completion.

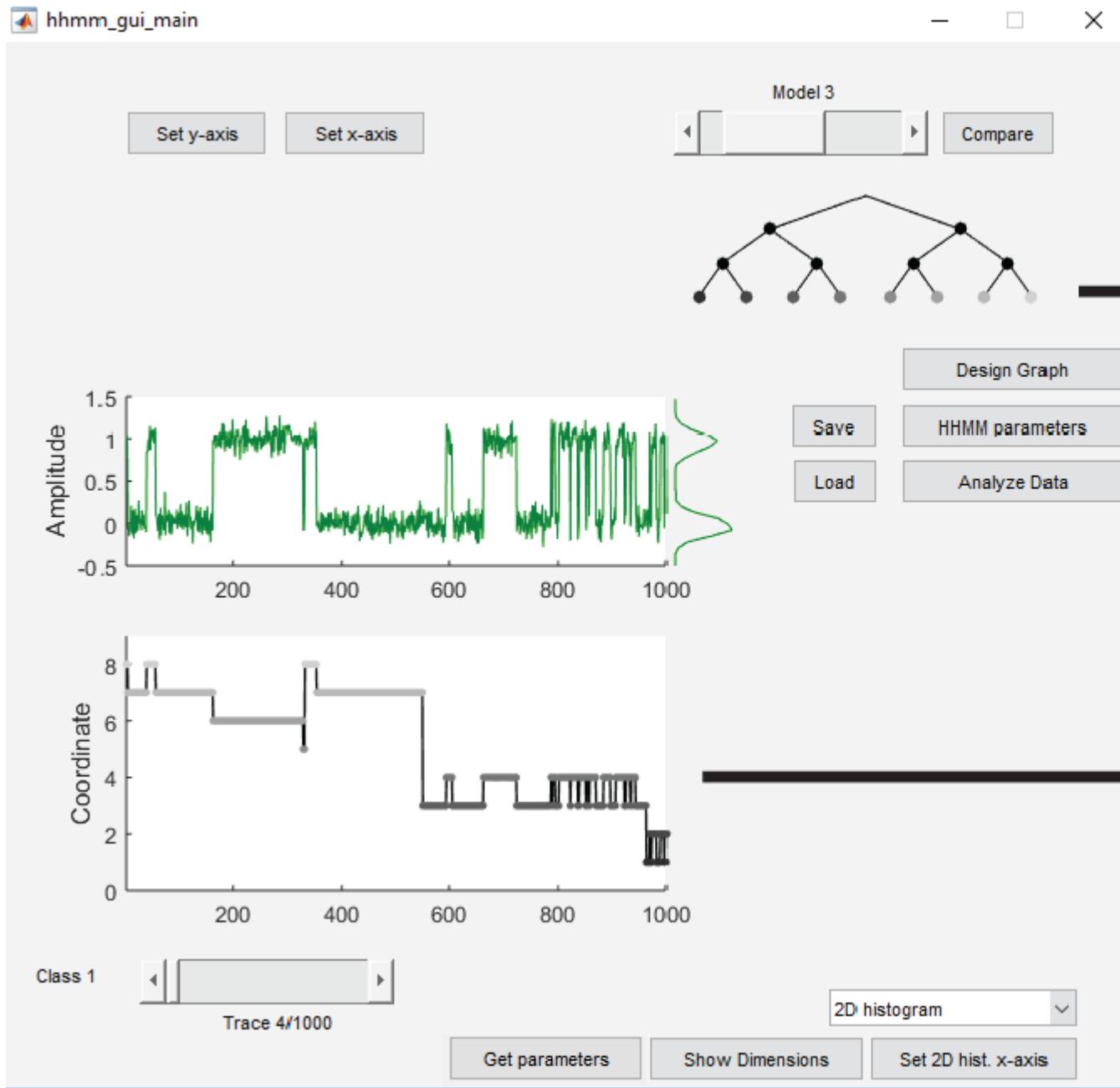
Shown model takes ~ 1 hr on 10^6 datapoints.



Can store up to 10 models in the gui session for comparison. Models are not stored until after analysis completes.

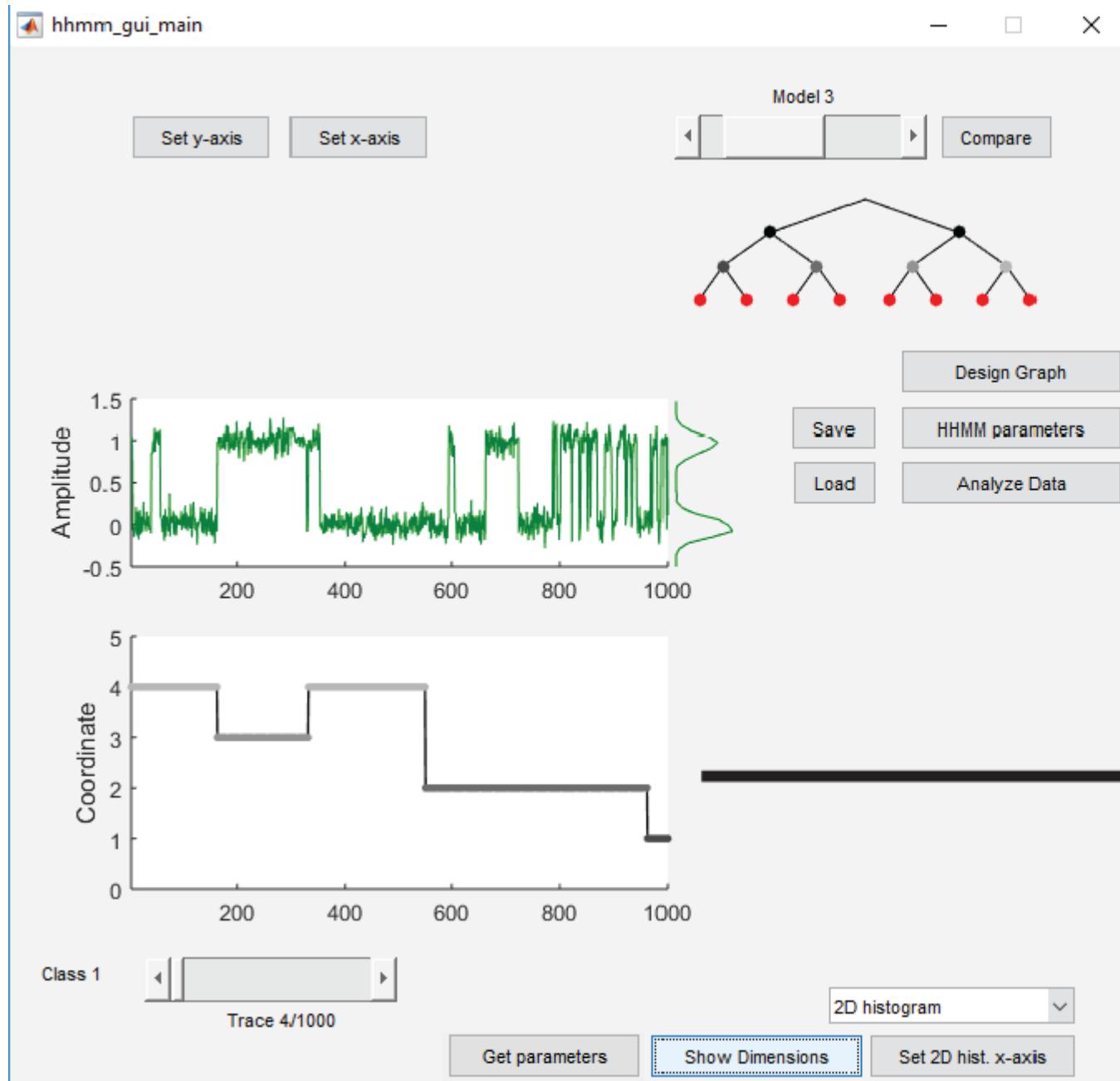
On pressing “Compare,” evidence lower bounds of the stored models are shown

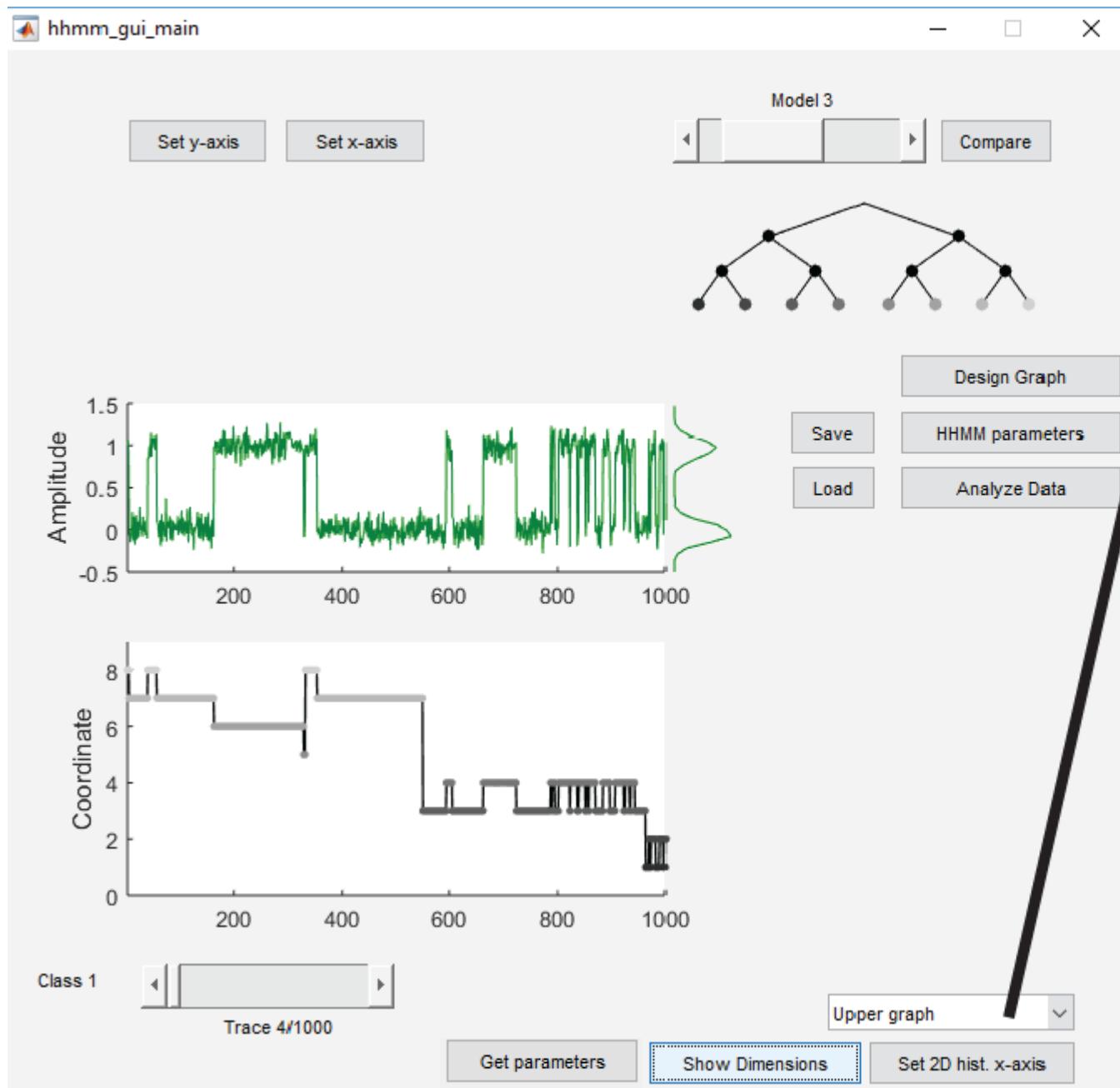


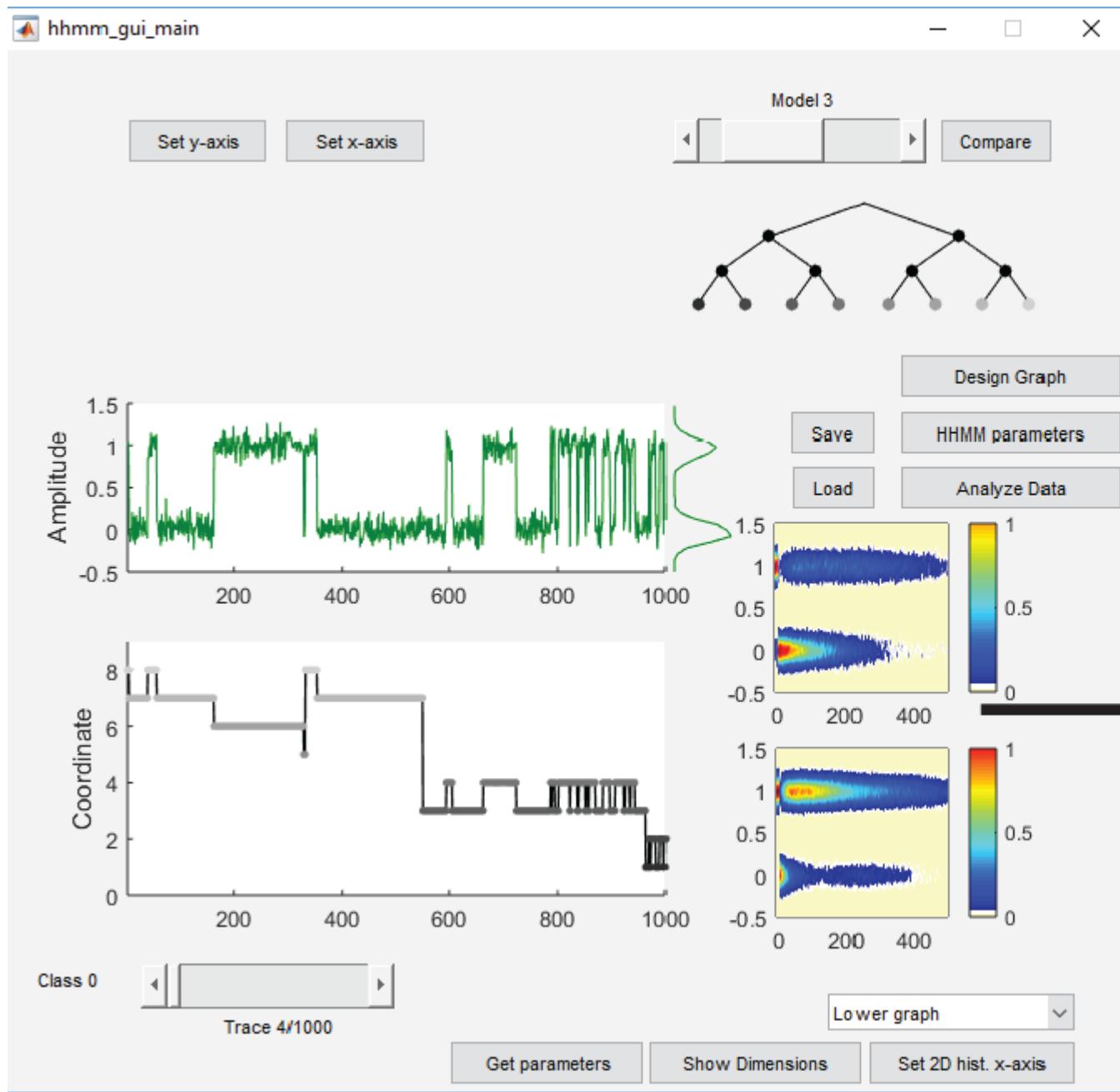


If a non-direct representation is chosen, the level is indicated here by a gradient of grayscale, here shown bottom level

Bottom level ($d=1$) shown. Values are both numbered (1-8) and color coded to correspond to the model topology diagram







2 graphs can be
shown, and need not
be from the same
model