

hFRET manual

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- sample_data_1
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- analyze_traces.fig
- analyze_traces.m
- coordinateprompt.fig
- coordinateprompt.m
- evidenceprompt.fig
- evidenceprompt.m
- hfret_gui_main.fig
- hfret_gui_main.m
- hfret manual.pdf
- hmmparametersprompt.fig
- hmmparametersprompt.m
- hist2Dprompt.fig
- hist2Dprompt.m
- port.fig
- port.m
- treeprompt.fig
- treeprompt.m
- vbscope_analyze_traces.fig
- vbscope_analyze_traces.m

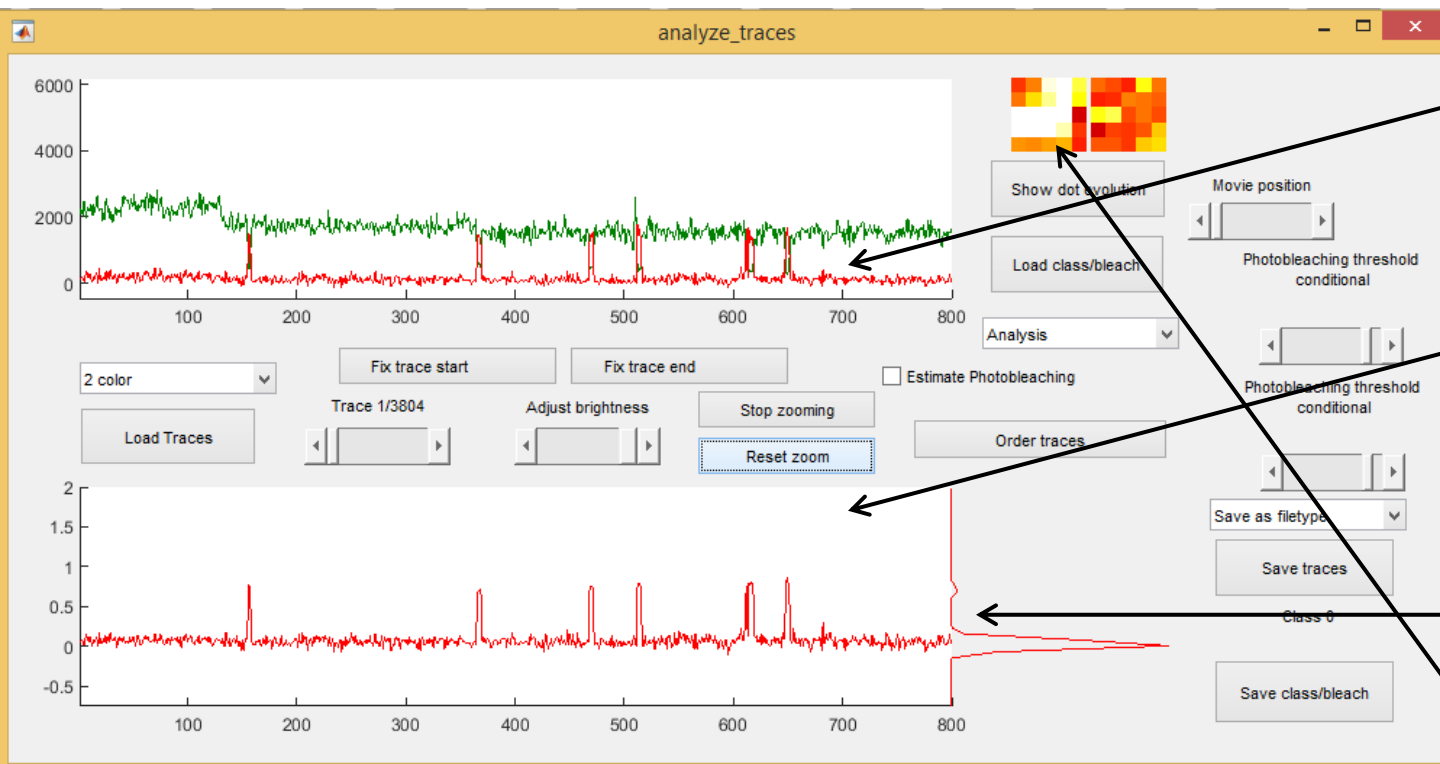
Details

Command Window

New to MATLAB? See resources for [Getting Started.](#)

```
>> analyze_traces  
fx >>
```

Open the trace viewer gui by typing as shown and pressing <Enter>

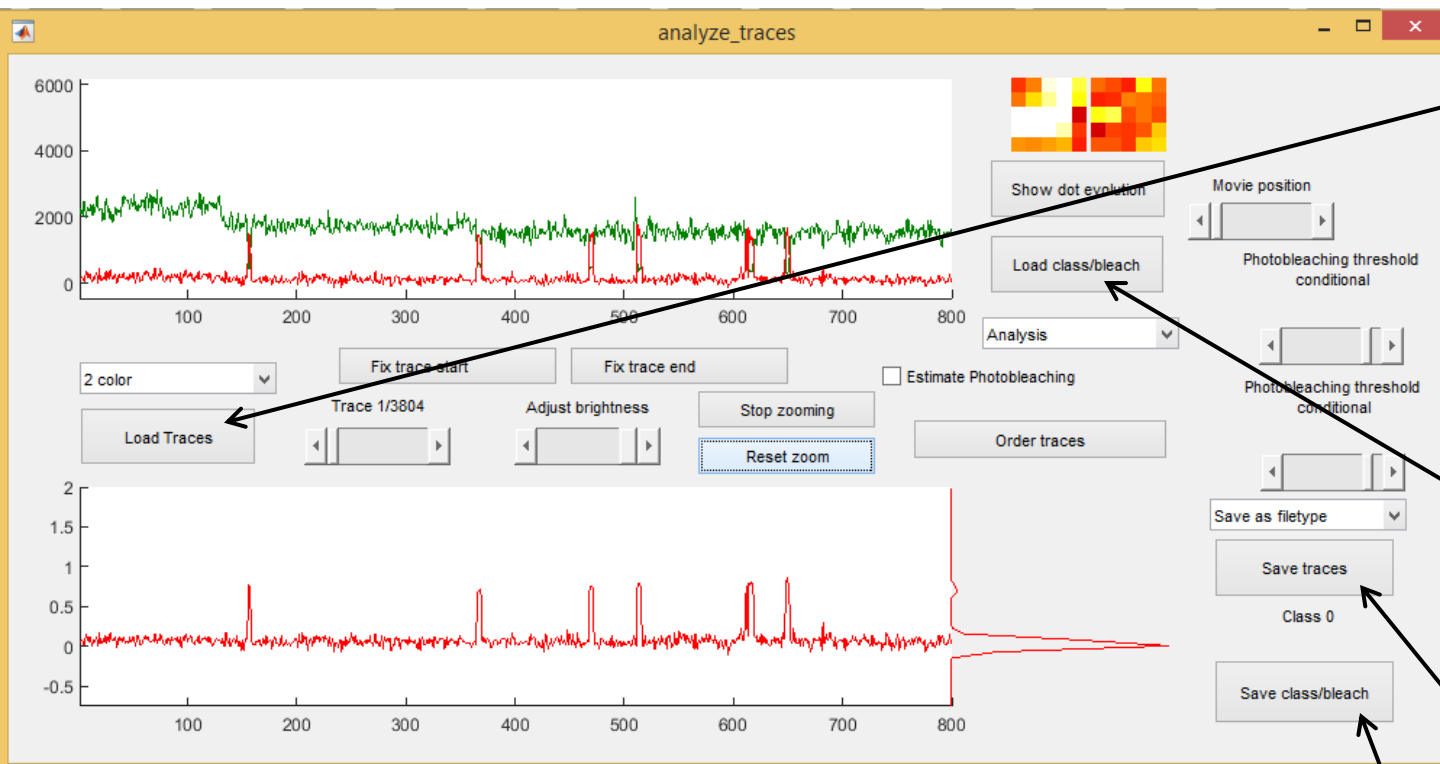


Intensities of
each color

Fractional
Intensities (for
two colors,
potentially
EFRET)

Histogram

Chromophore
context

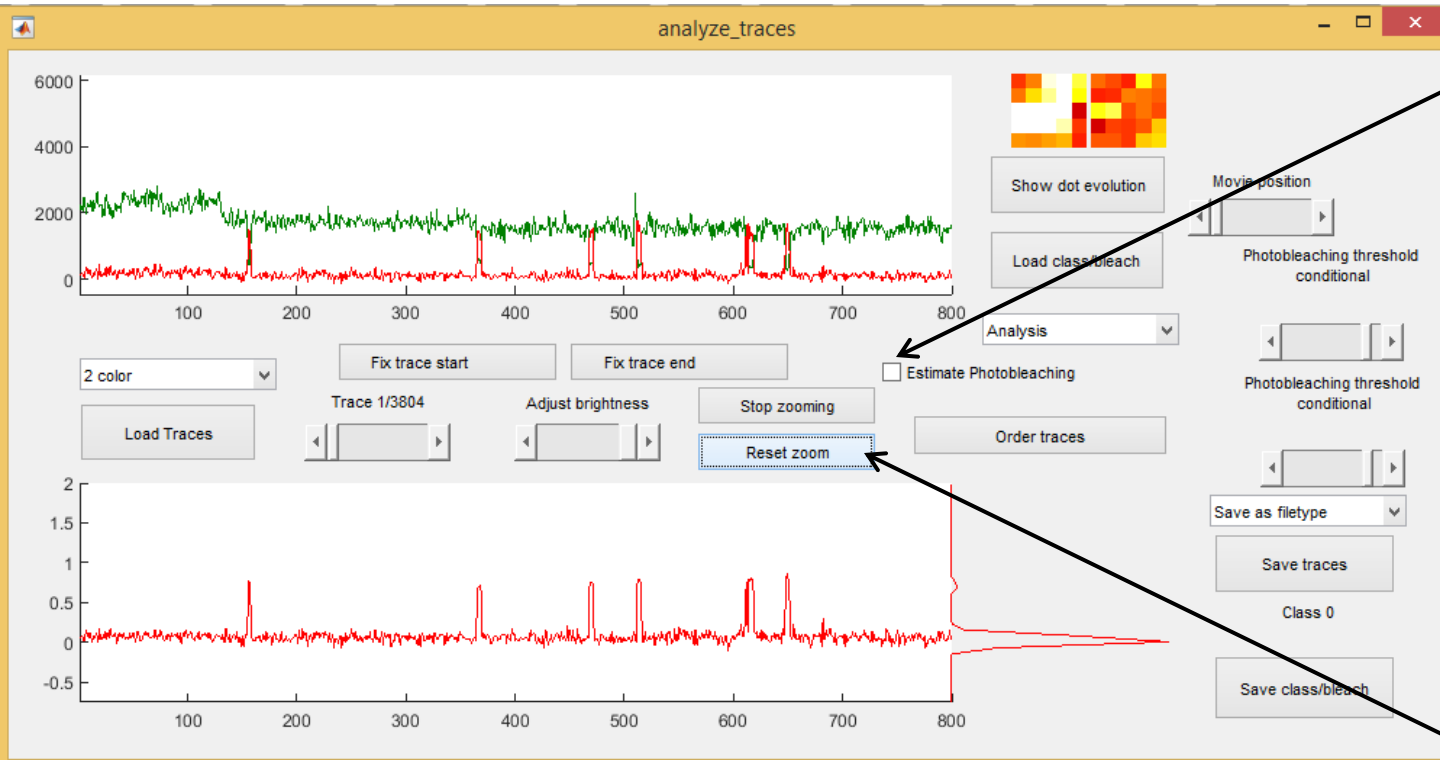


Load in data
(can take
multiple files;
number of colors
must be
specified
abovefirst)

Load in
classifications
(can take
multiple files)

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

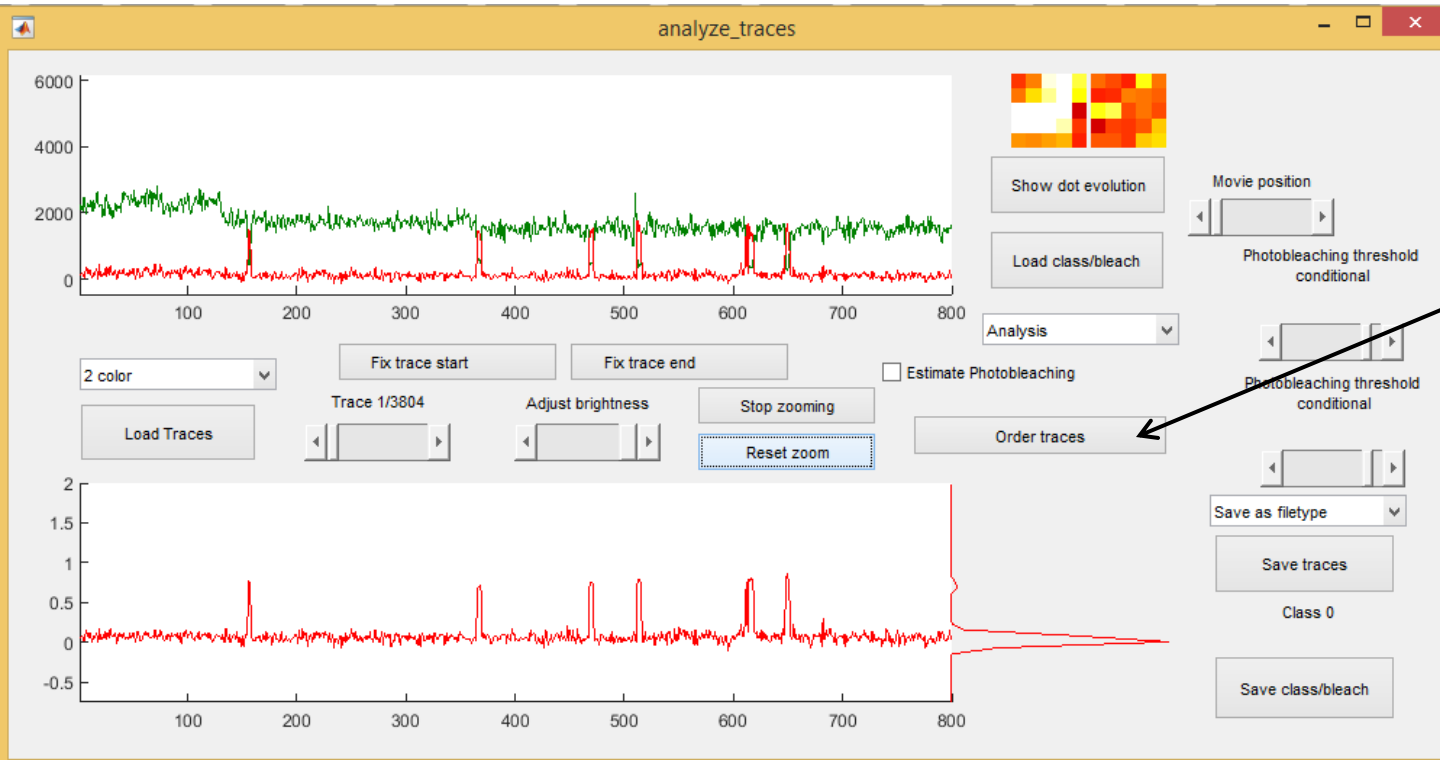
Save
classifications



Enable photobleach detection/correction

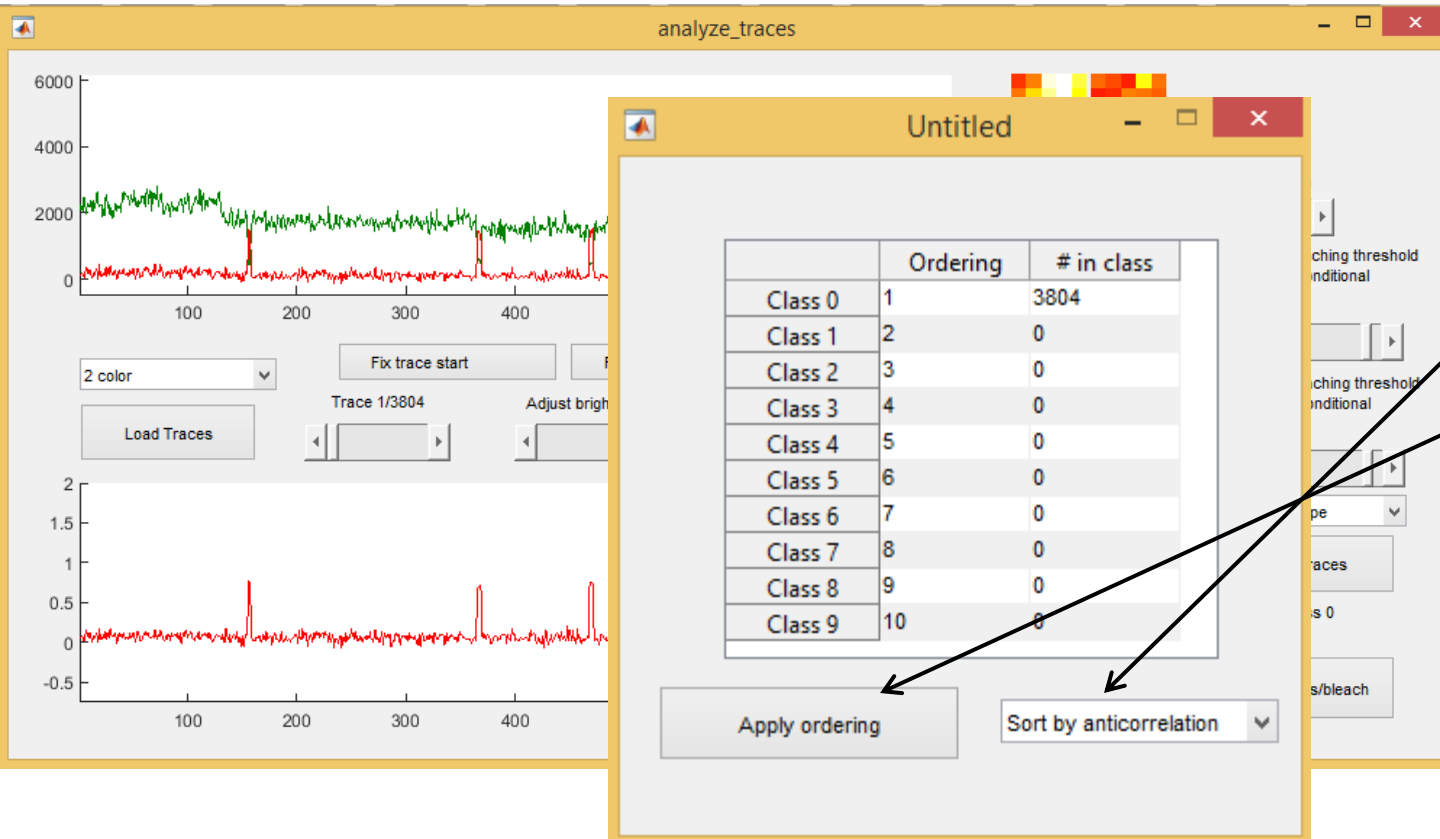
Keyboard shortcuts:
s: fix start (then shift-click each color)

f: fix finish
n: next trace
b: back one trace
z: zoom in. When done must hit “stop zooming”, here.



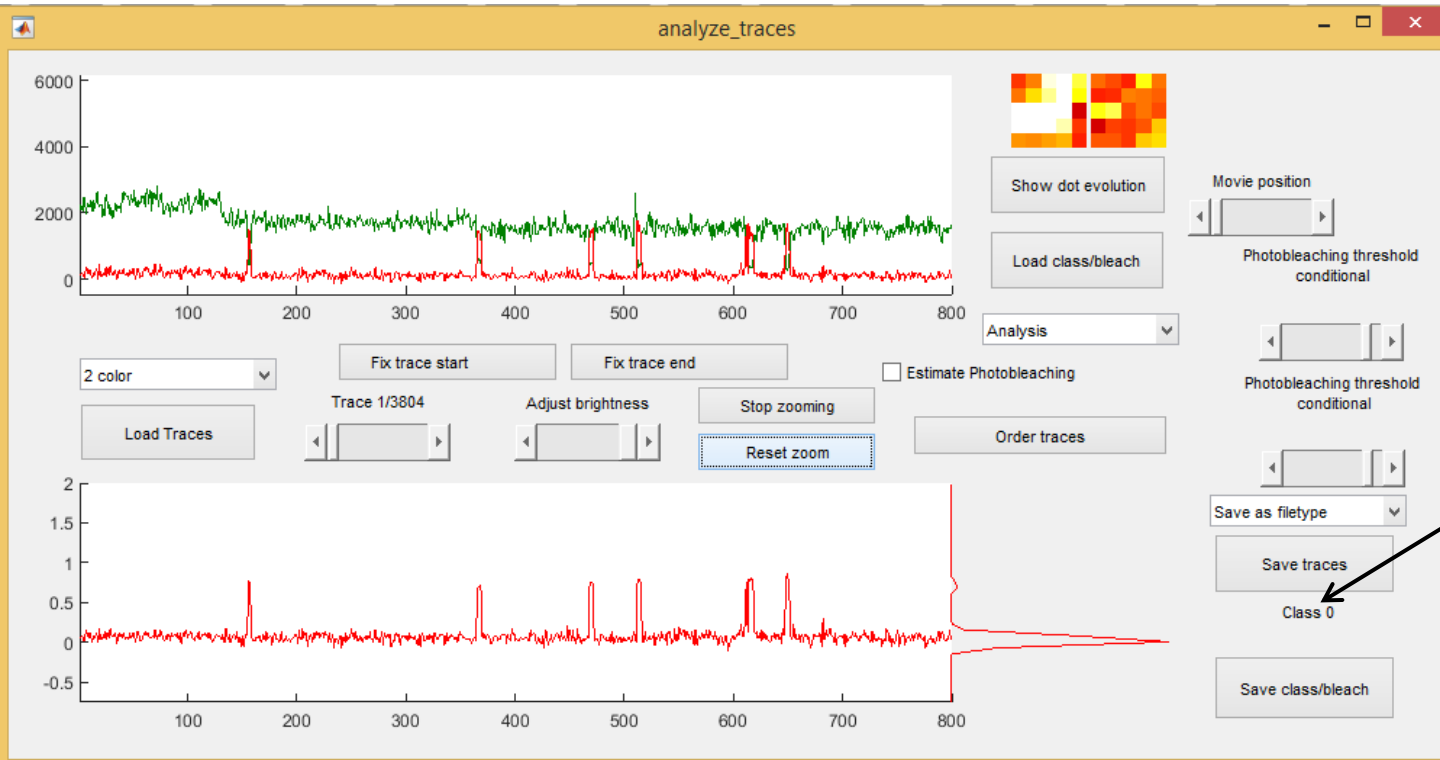
Sorting through
the traces

Automatic
sorting



Sorting through the traces

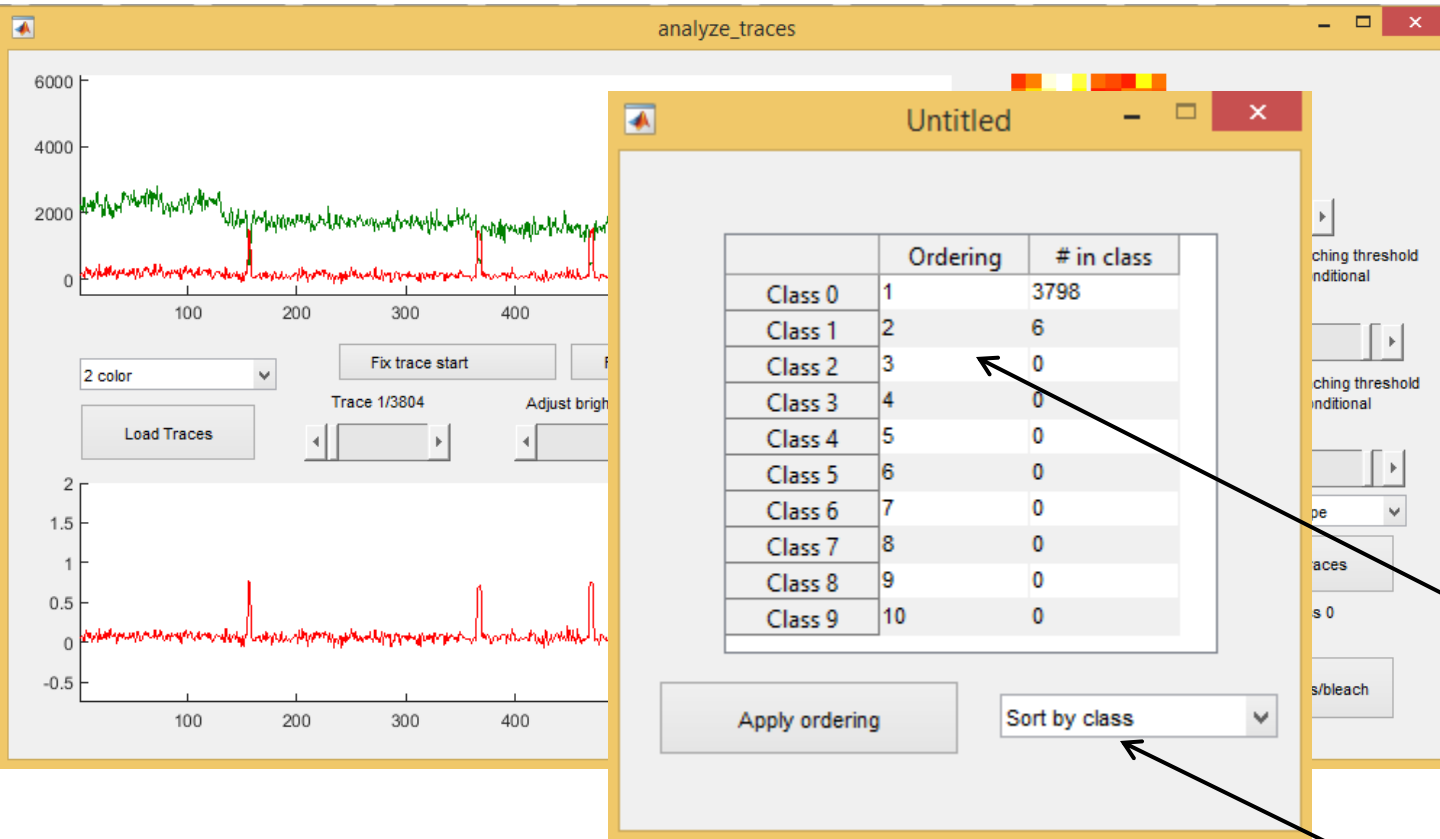
Calculates anticorrelation. Clicking “Apply ordering” places the traces in order from the most to the least anticorrelated.



Sorting through
the traces

Manual sorting

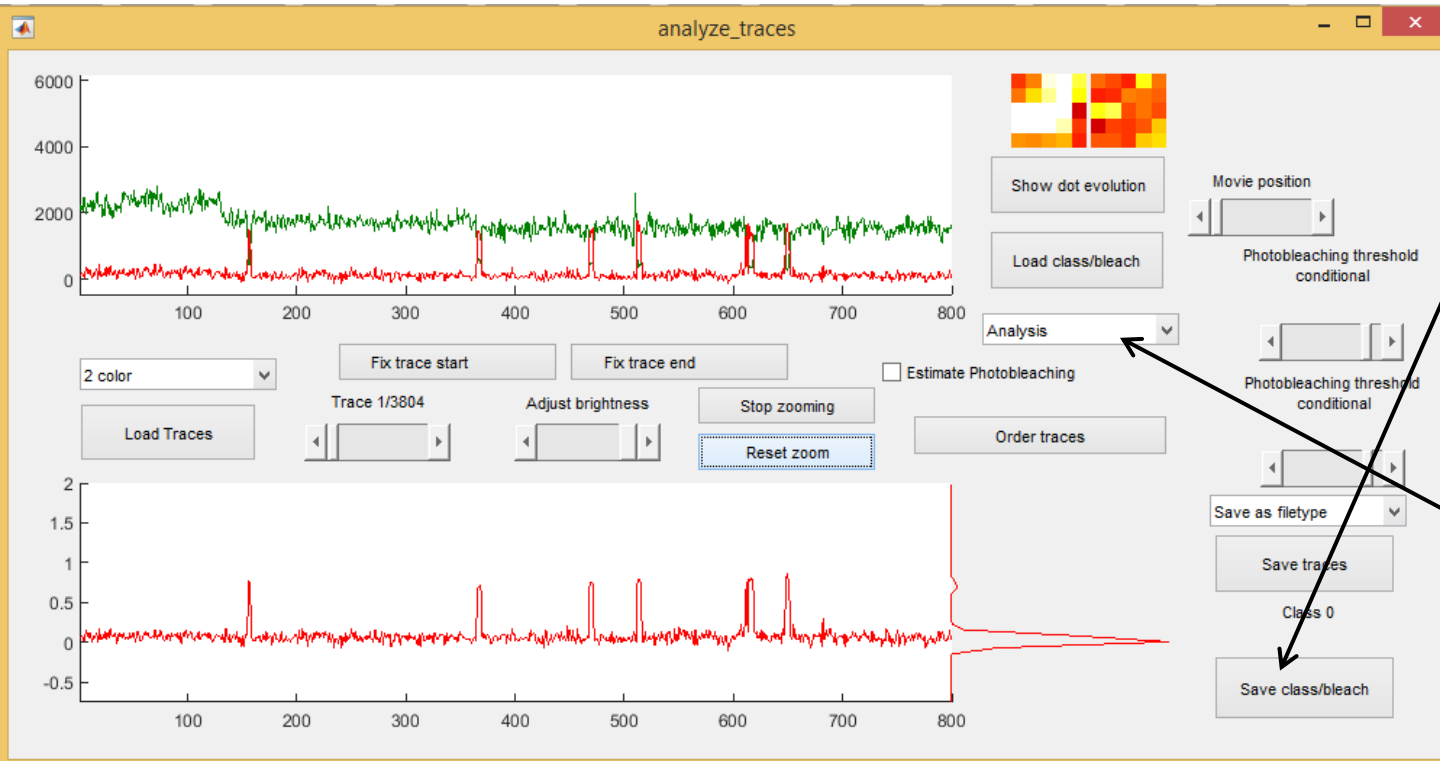
Click a number
between 0-9
after clicking a
graph. The
trace is now in
that class.
Readout is
here.



Sorting through
the traces

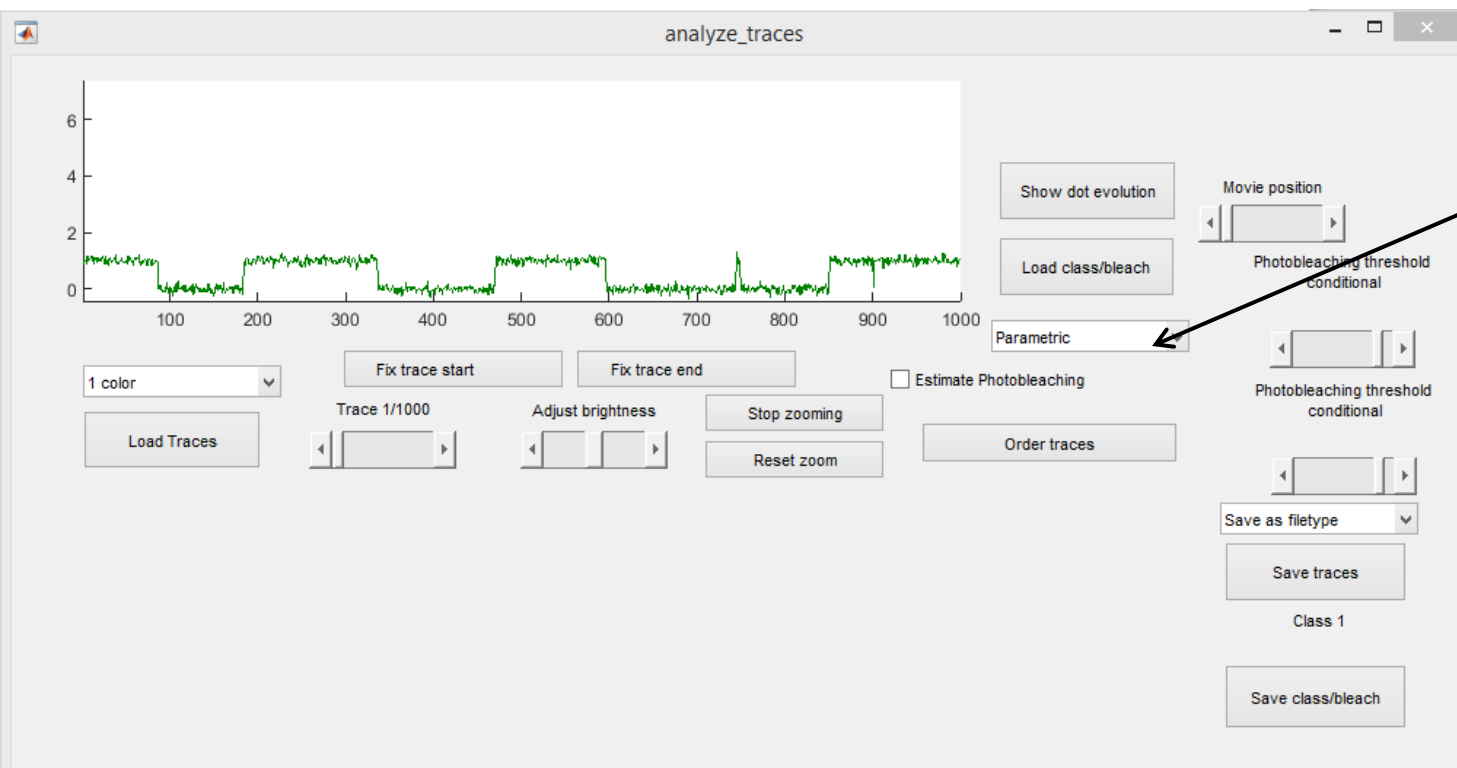
Manual sorting

Clicking
“Ordering traces”
again, this table
appears. The
“Ordering”
column is
editable and
allows the
classes to be put
in order from 0-9
(1-10), if “Sort by
class” is selected
when ordering is
applied.

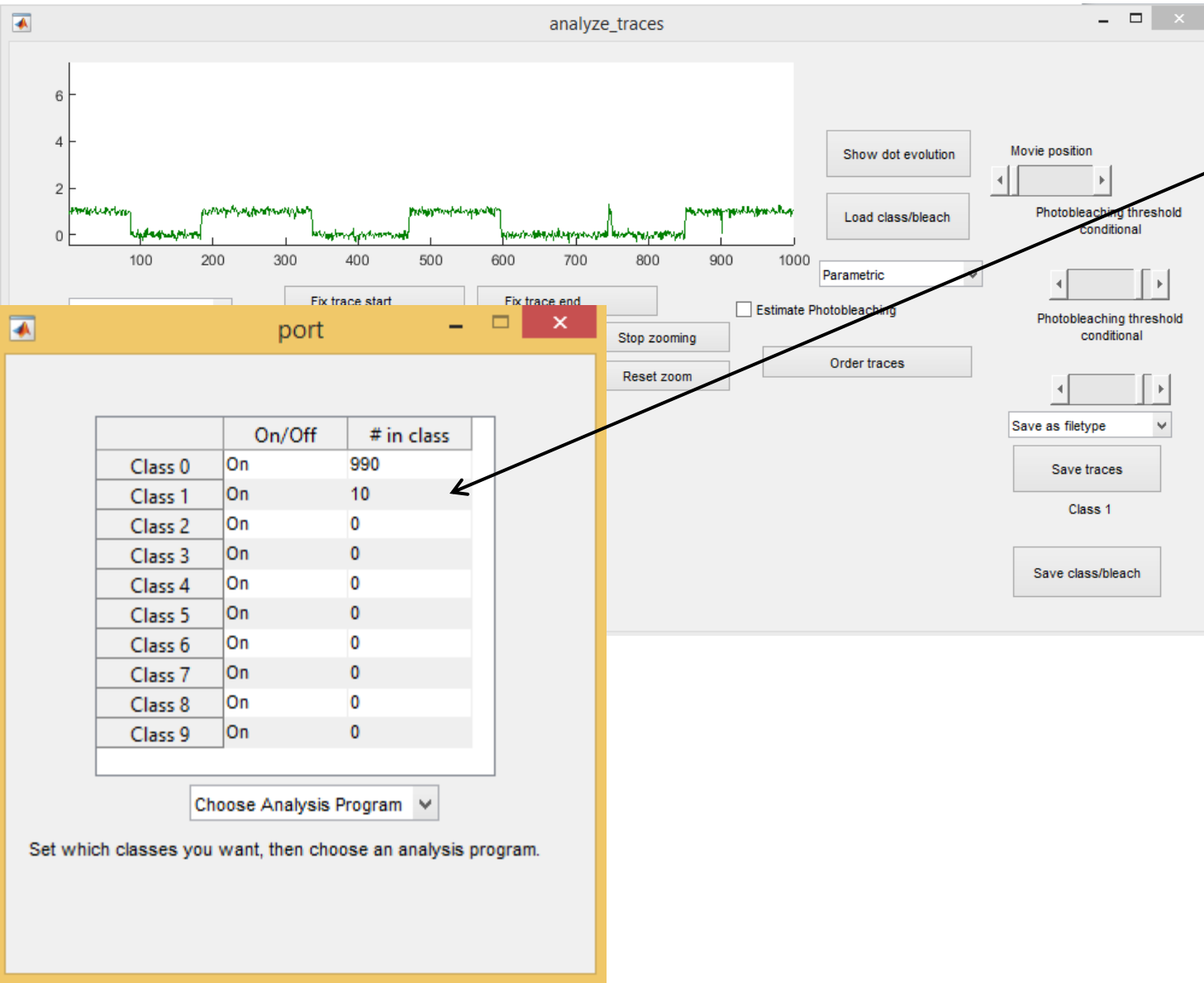


Once sorting/start/stop correction is complete, save class/bleach

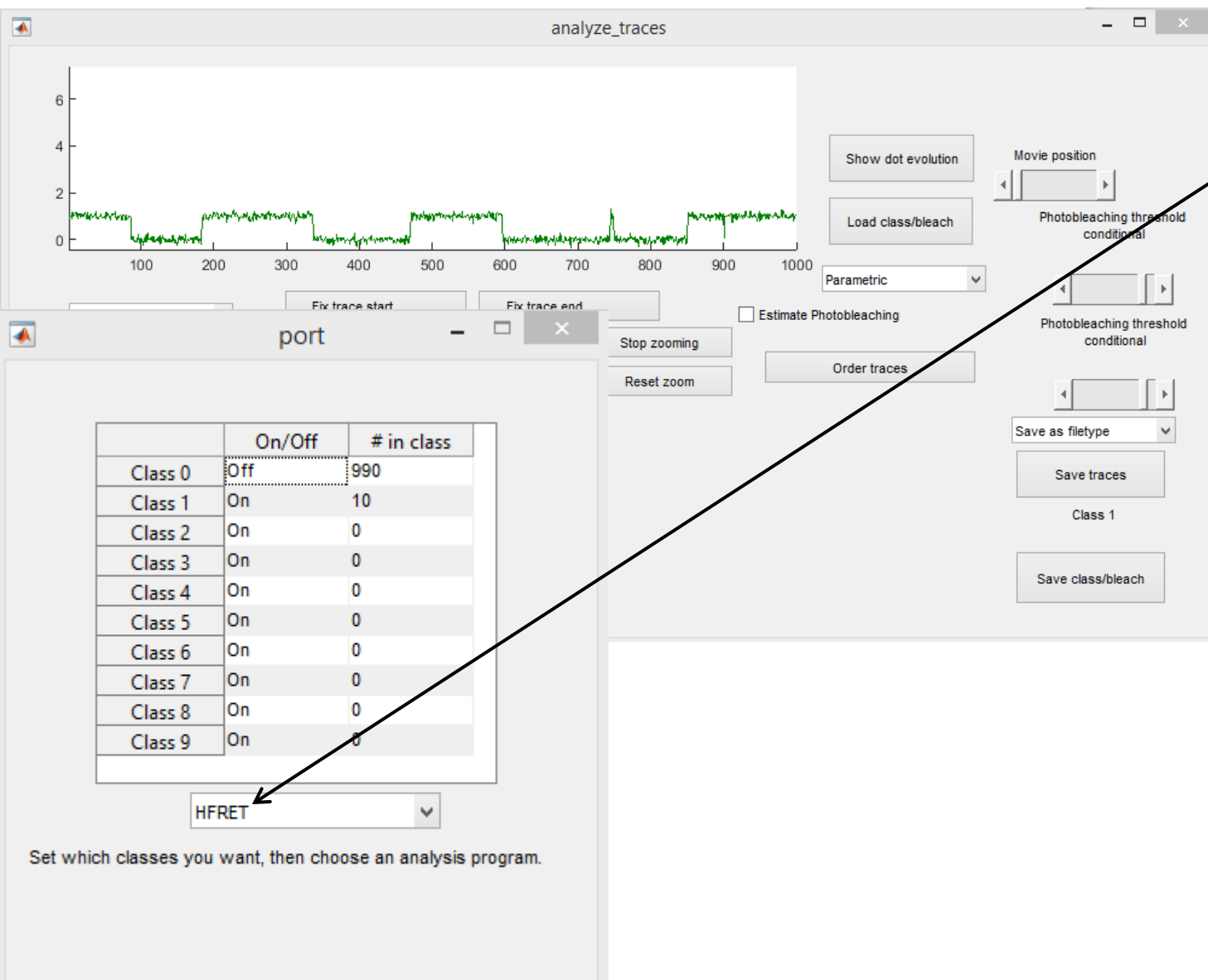
Next open a parametric or a nonparametric analysis type



Change from
“Analysis” to
“Parametric”



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



For hFRET,
choose
"HFRET"

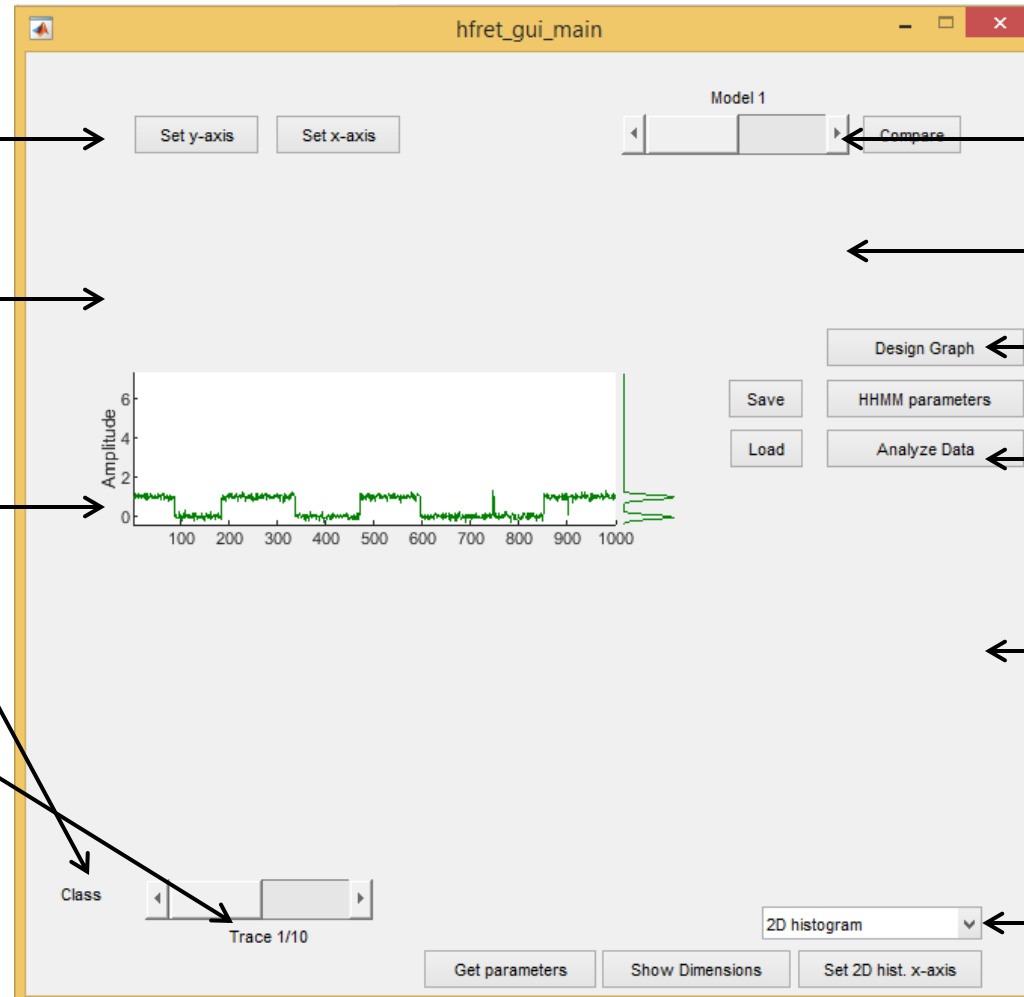
Axis adjustments

Trajectory (below,
if only one
dimensional

Trajectory
(fractional units)

Class

Plotted trajectory



Current model

Model topology

Model parameters

Begin analysis

Population plots

Population plot
parameters

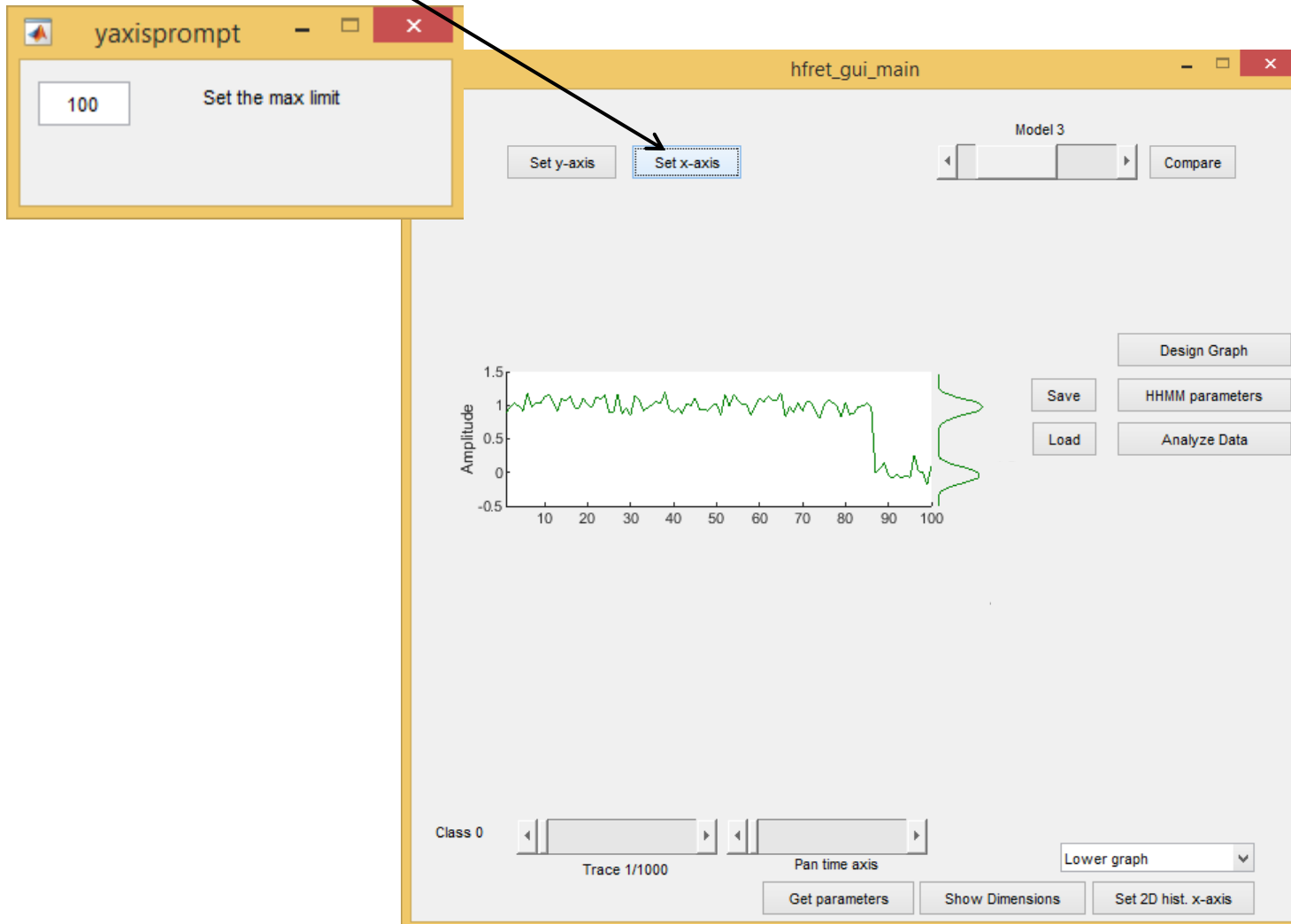
Y axis adjustments

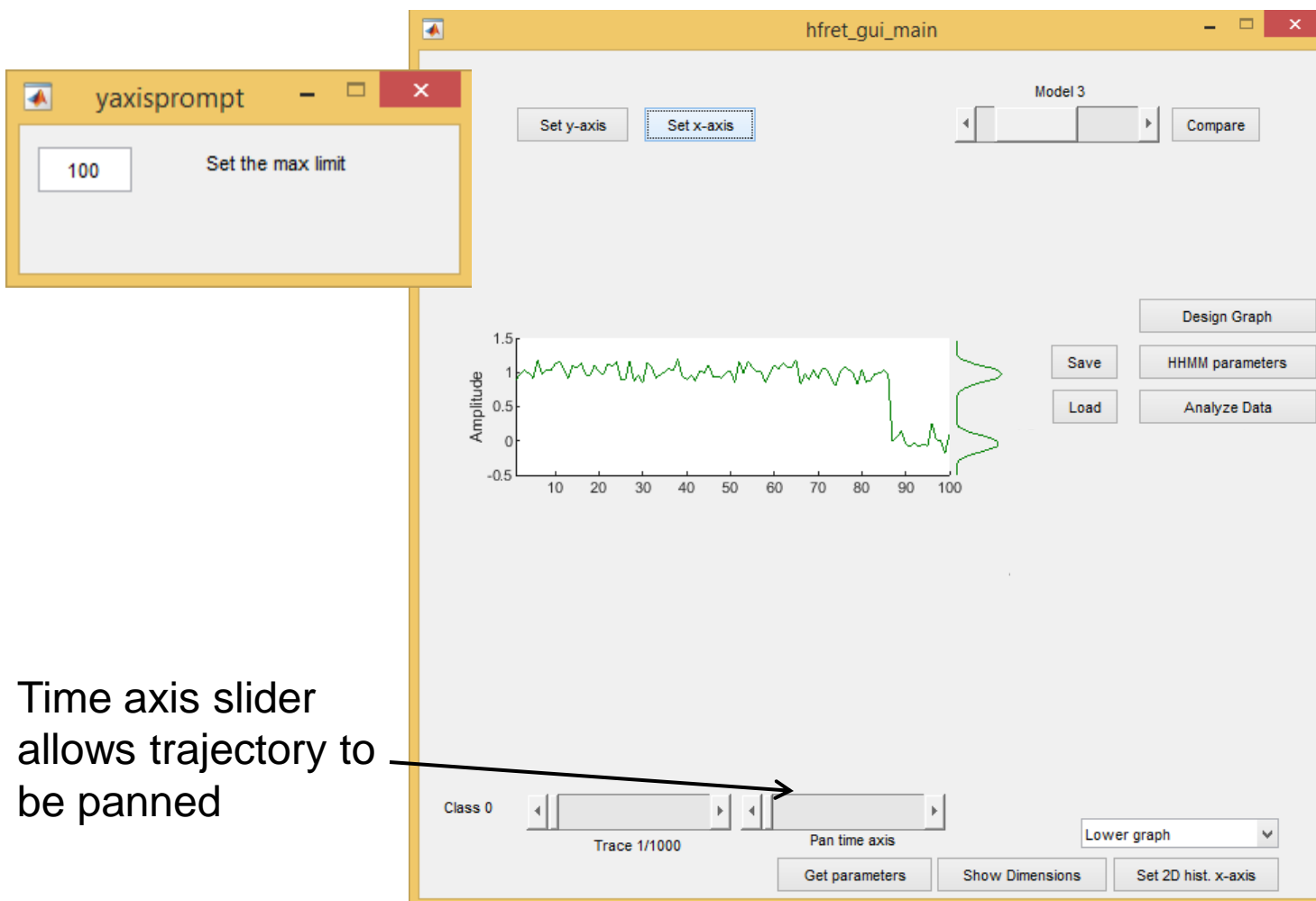
The screenshot displays the `hfred_gui_main` window. At the top, there's a title bar with standard window controls. Below it, a panel contains a 'Set min limit' input field and a 'Set y-axis' button. An arrow points from the 'Y axis adjustments' text to this button. The main area features a plot of 'Amplitude' (y-axis, -0.5 to 1.5) against time (x-axis, 0 to 1000). The plot shows a green signal with a step-like pattern. To the right of the plot are buttons for 'Design Graph', 'Save', 'Load', 'HHMM parameters', and 'Analyze Data'. At the bottom, there's a 'Class 0' label, a 'Trace 1/1000' label, a 'Pan time axis' label, and a 'Lower graph' dropdown menu. Below these are buttons for 'Get parameters', 'Show Dimensions', and 'Set 2D hist. x-axis'.

For all such prompts, if only one number, just type in the number and hit `<Enter>`. If more than one number is required, type the two numbers as:

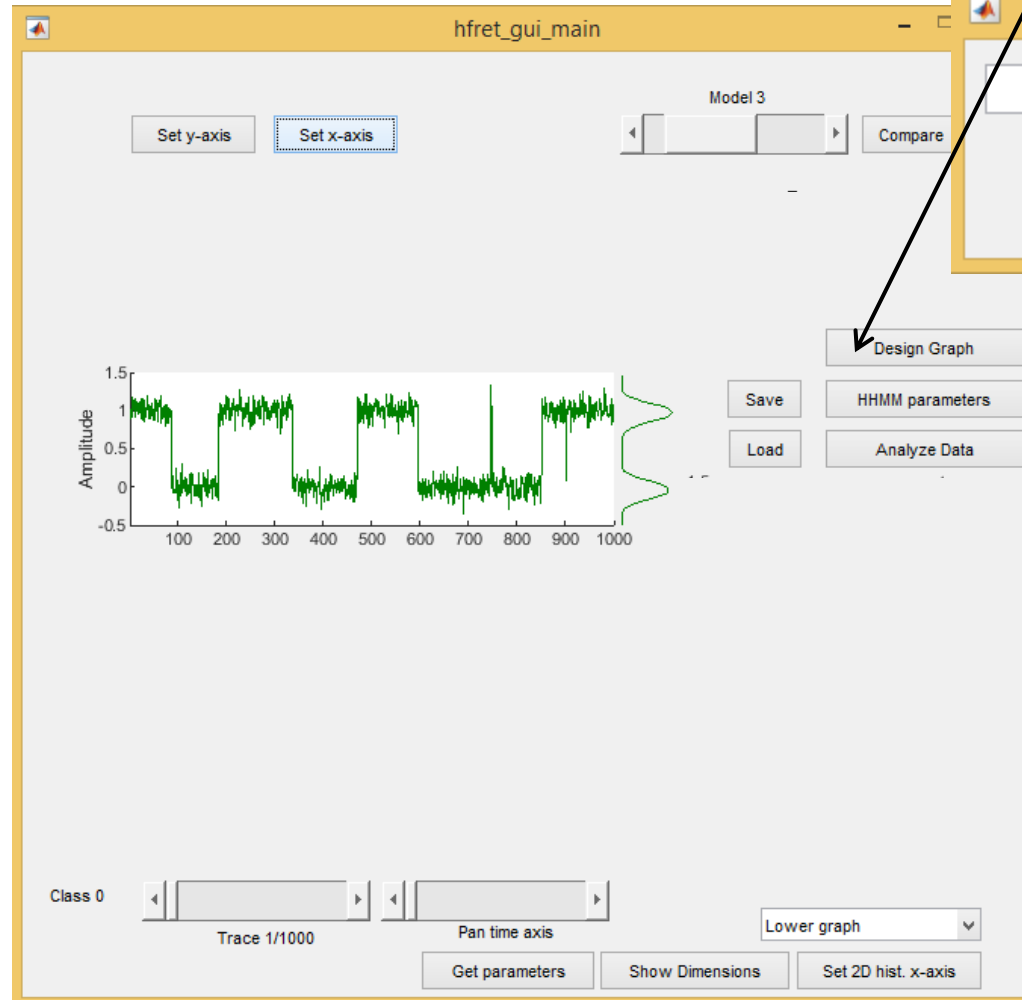
[1 2 ... etc]

X axis adjustments





Design Model Topology

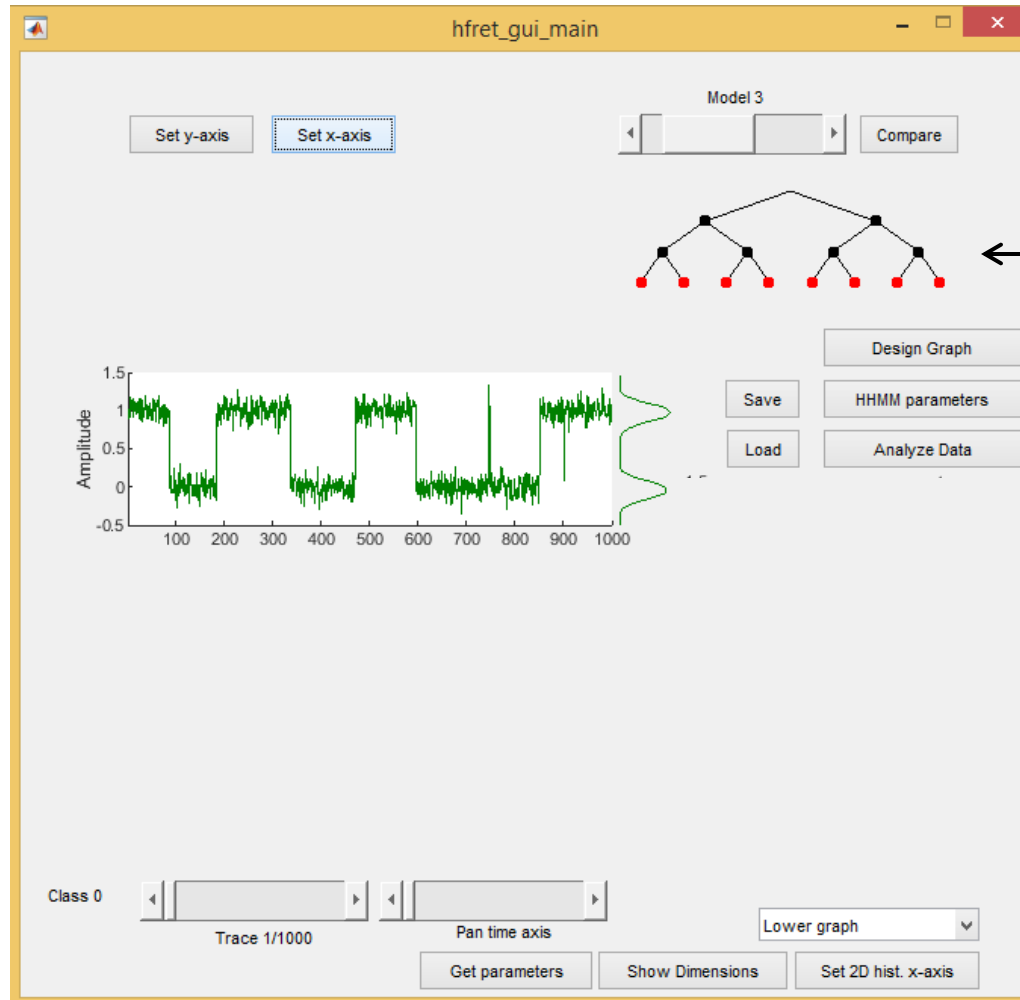


treeprompt

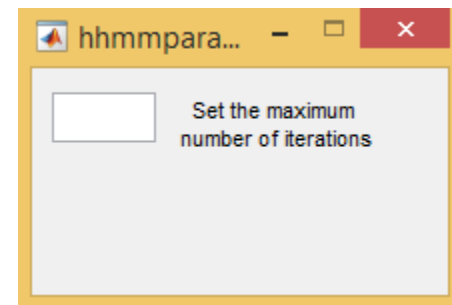
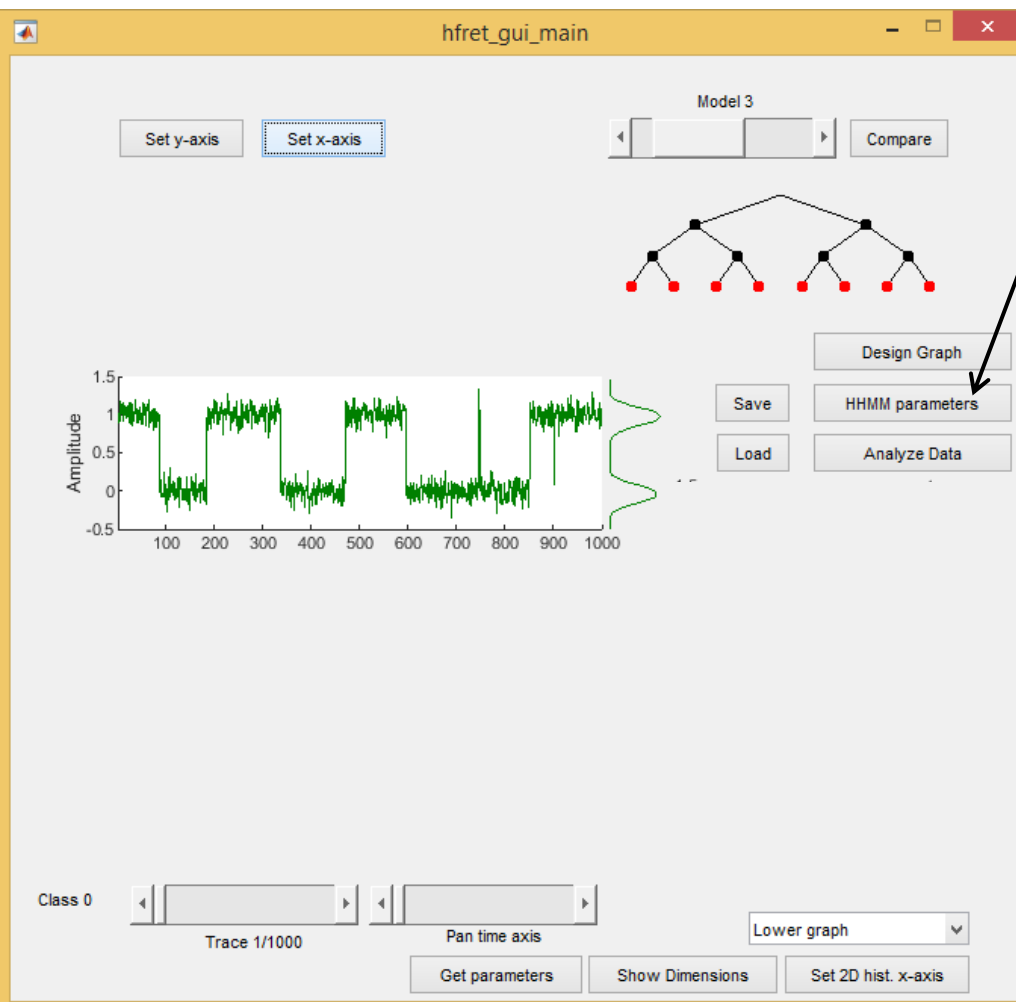
Set the total number of dimensions

Prompts:

- (1) Total # of dimensions, D
- (2) # of distinct values at level $d > 1$
- (3) $d=1$, # of distinct values of the direct dimension



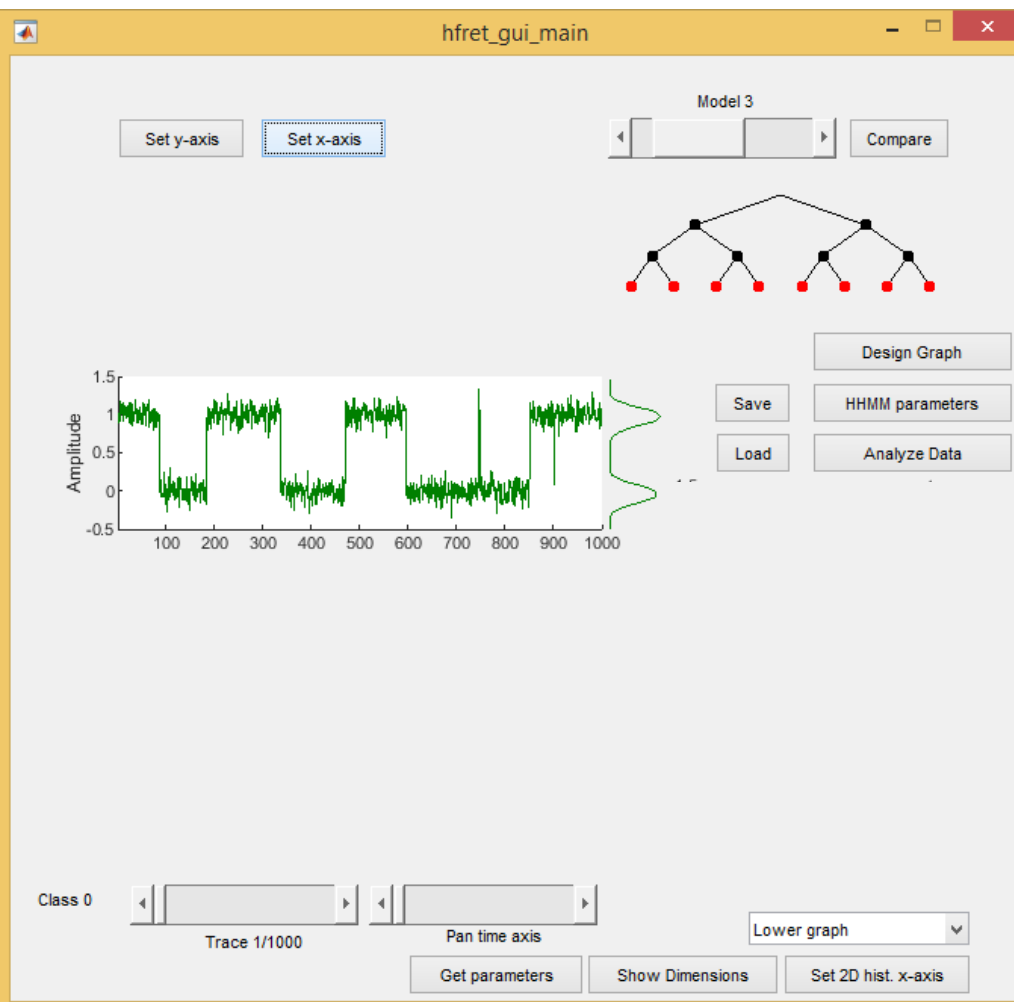
Model topology
appears here.
Shown: $D=3$, $\#=2$
for all values of d .



Set algorithm control parameters

Prompts:

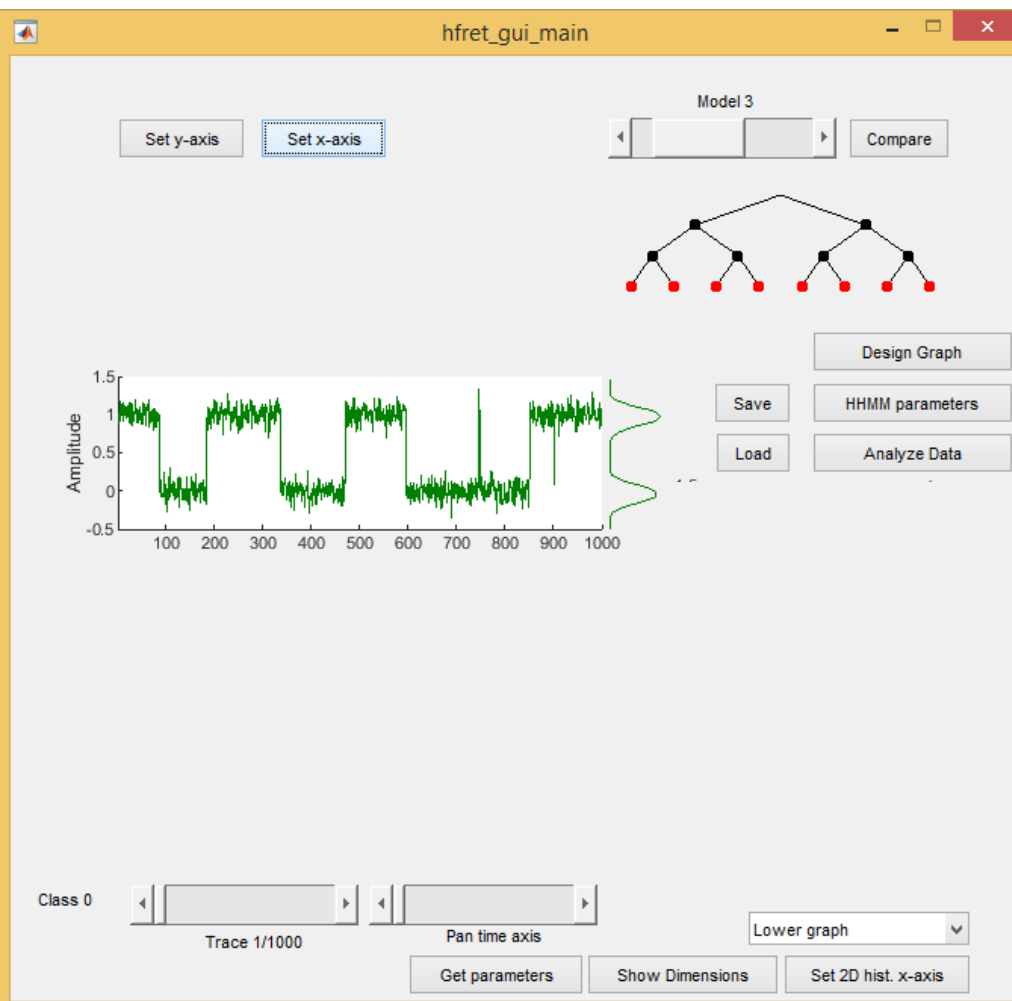
- (1) Maximum number of iterations
- (2) Number of restarts (kinetic parameters randomly drawn)
- (3) Whether each trajectory has the same emission distribution (type “y” or “n”)
- (4) Automatic or manual entry of normal distribution means(if “n,” the means are entered next; here, entering [0 1] would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



Analyze data

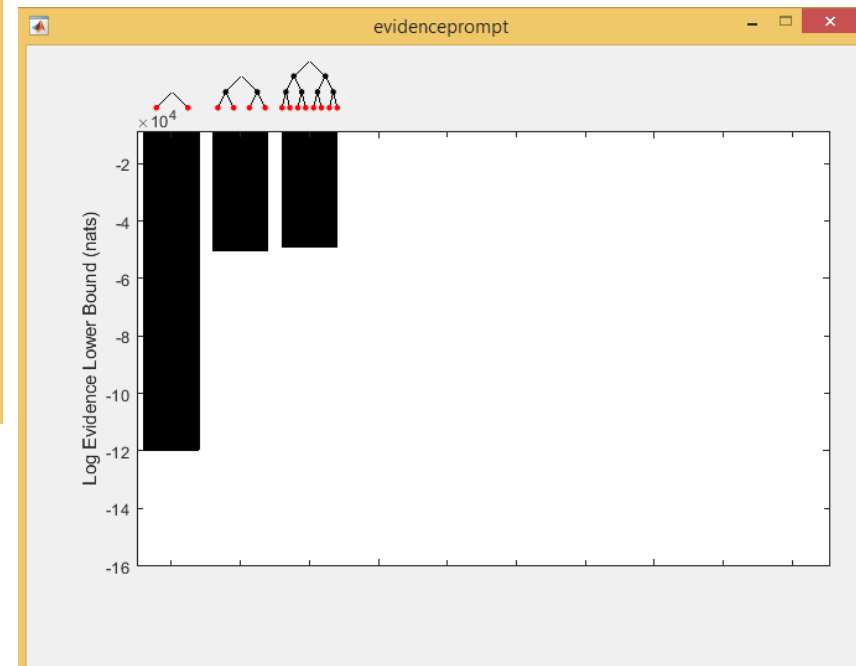
This can be a very time consuming step. Do not press other buttons while this occurs. A prompt in the command window will alert on completion.

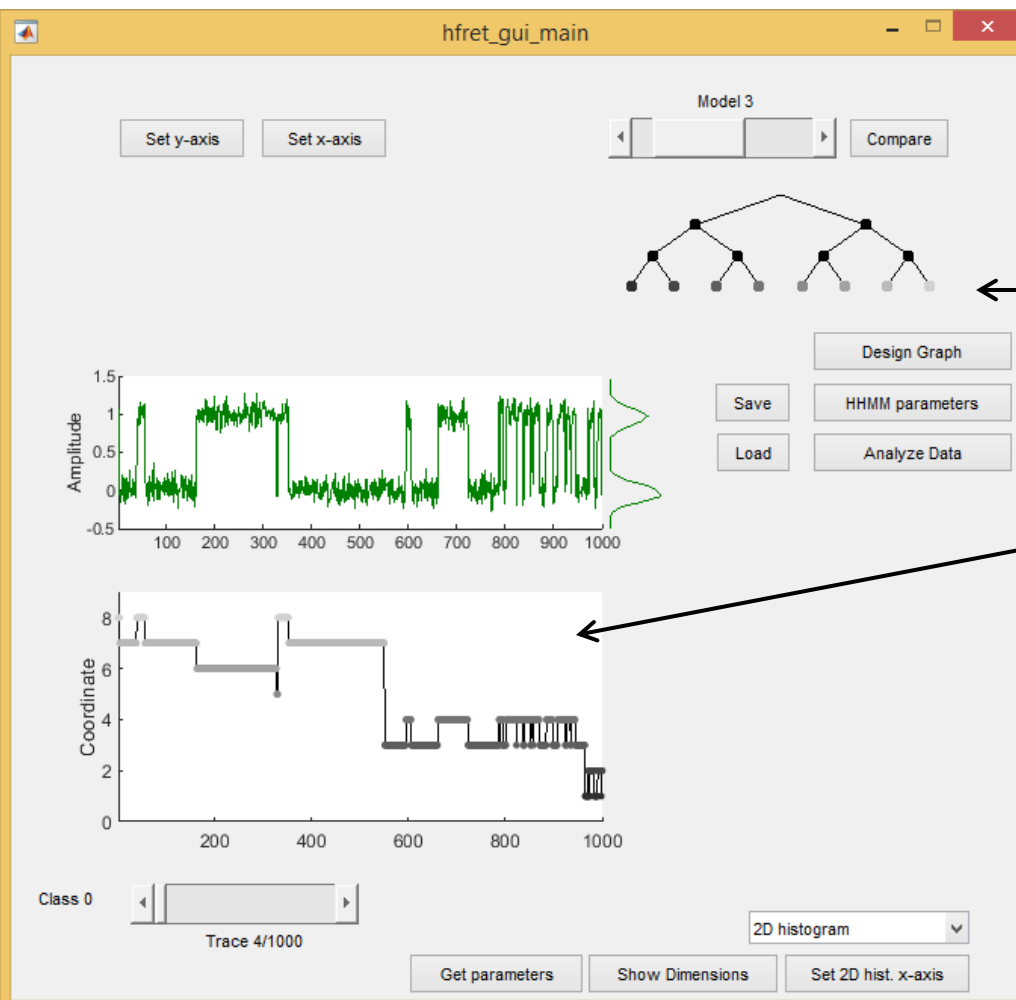
With two 3.6 GHz cores, shown model takes ~ 1 hr on 10^6 datapoints.



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 (as below.)

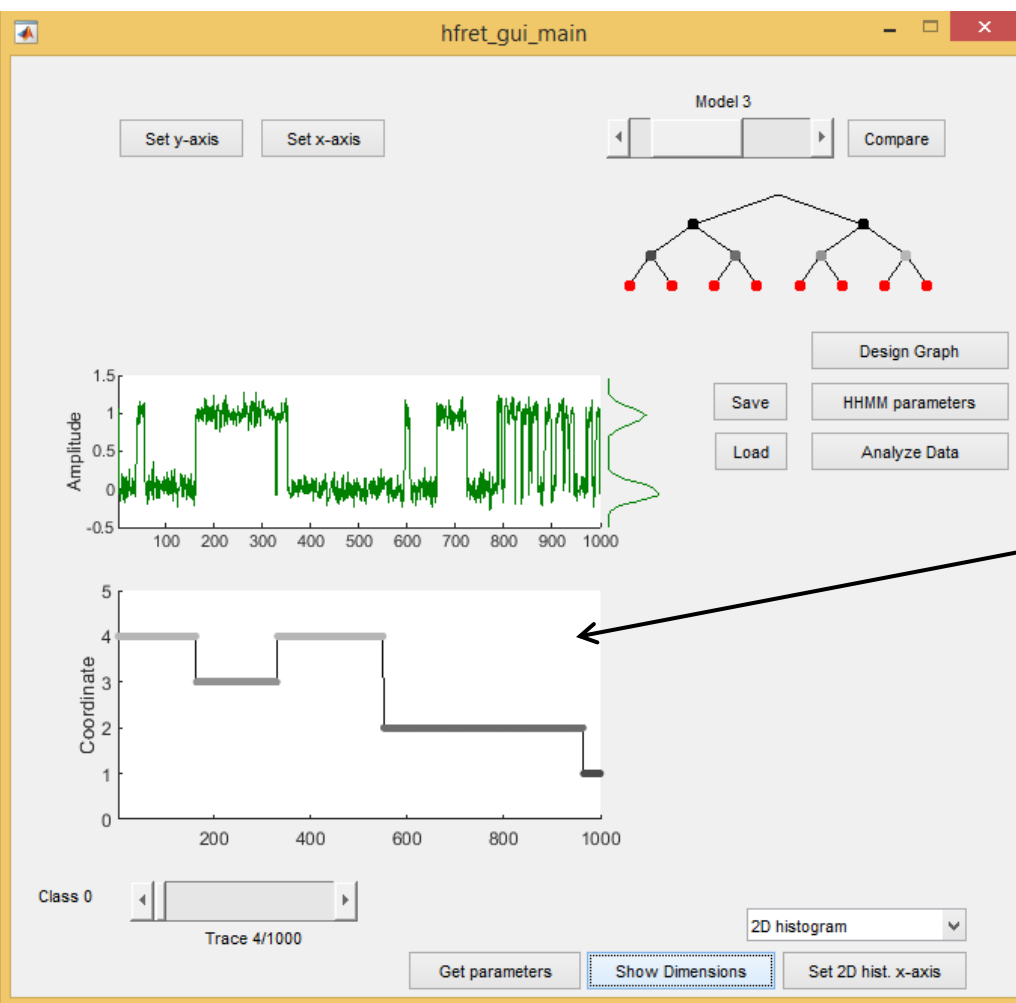




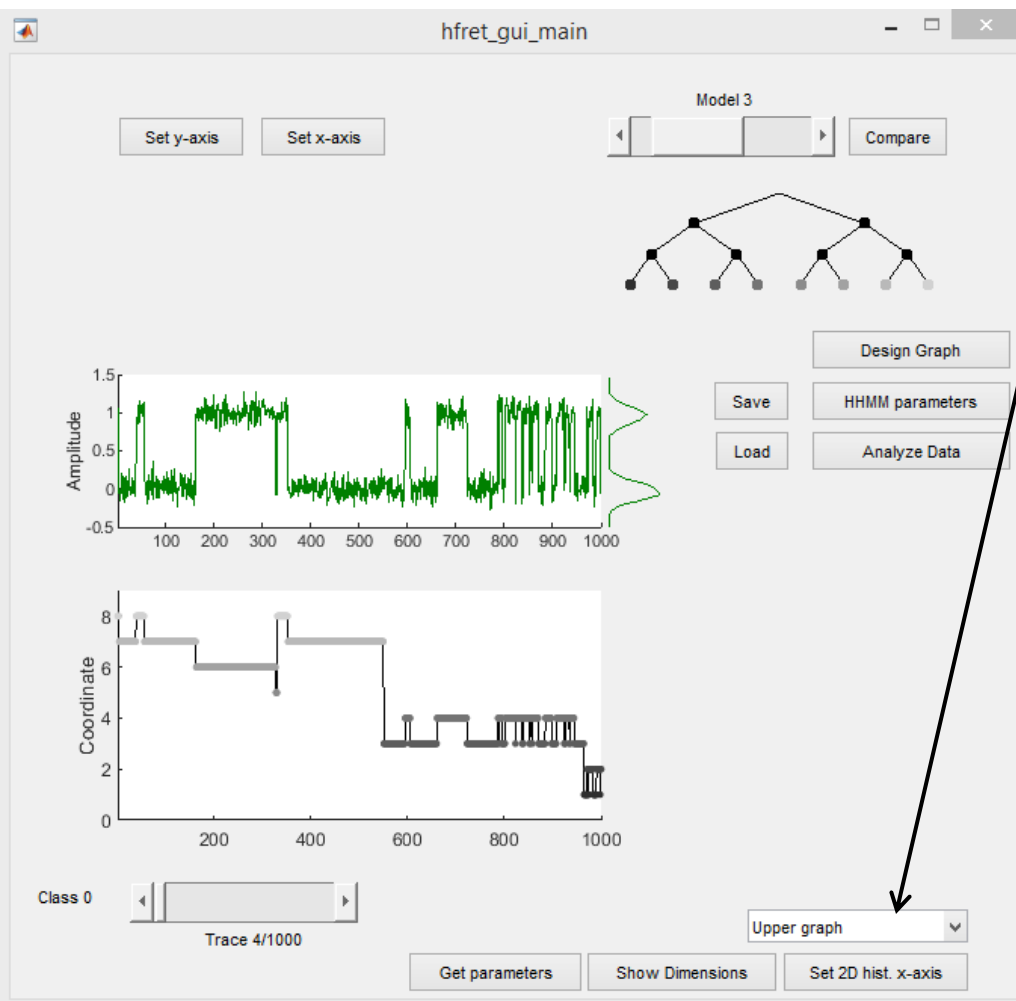
Click “Show dimensions.”

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

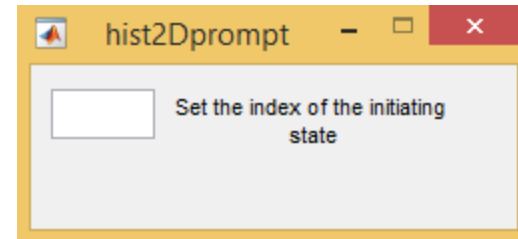
Values are both numbered (1-8) and color coded to correspond to the model topology diagram.



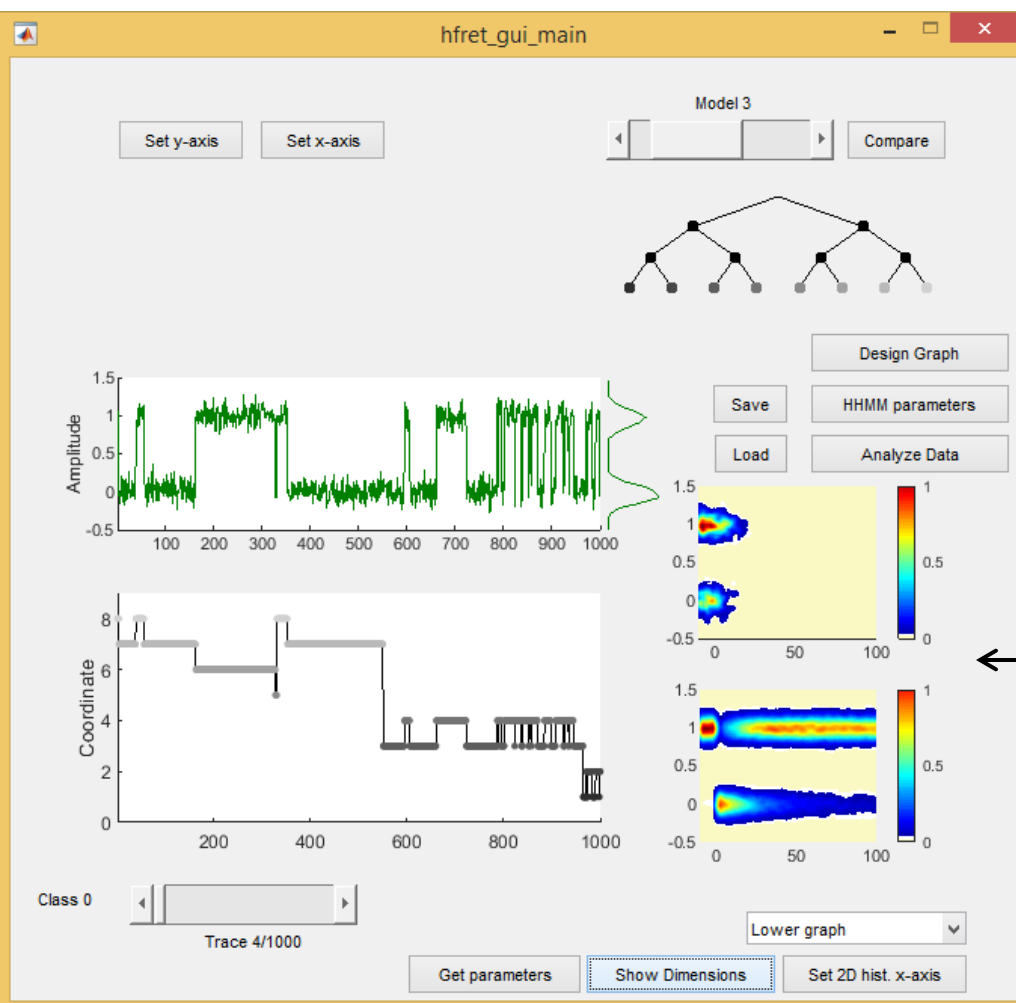
Intermediate level ($d = 2$) shown.
Values are both numbered (1-4) and
color coded to correspond to the
model topology diagram.



For population plots (or 2D histograms), change to “Upper graph” or to “Lower graph”



Enter the initiating and then the terminating state index, which correspond to the index shown in the coordinate plot. The index always refers to the index at the bottom level.



Two graphs can be shown. They need not be from the same model.