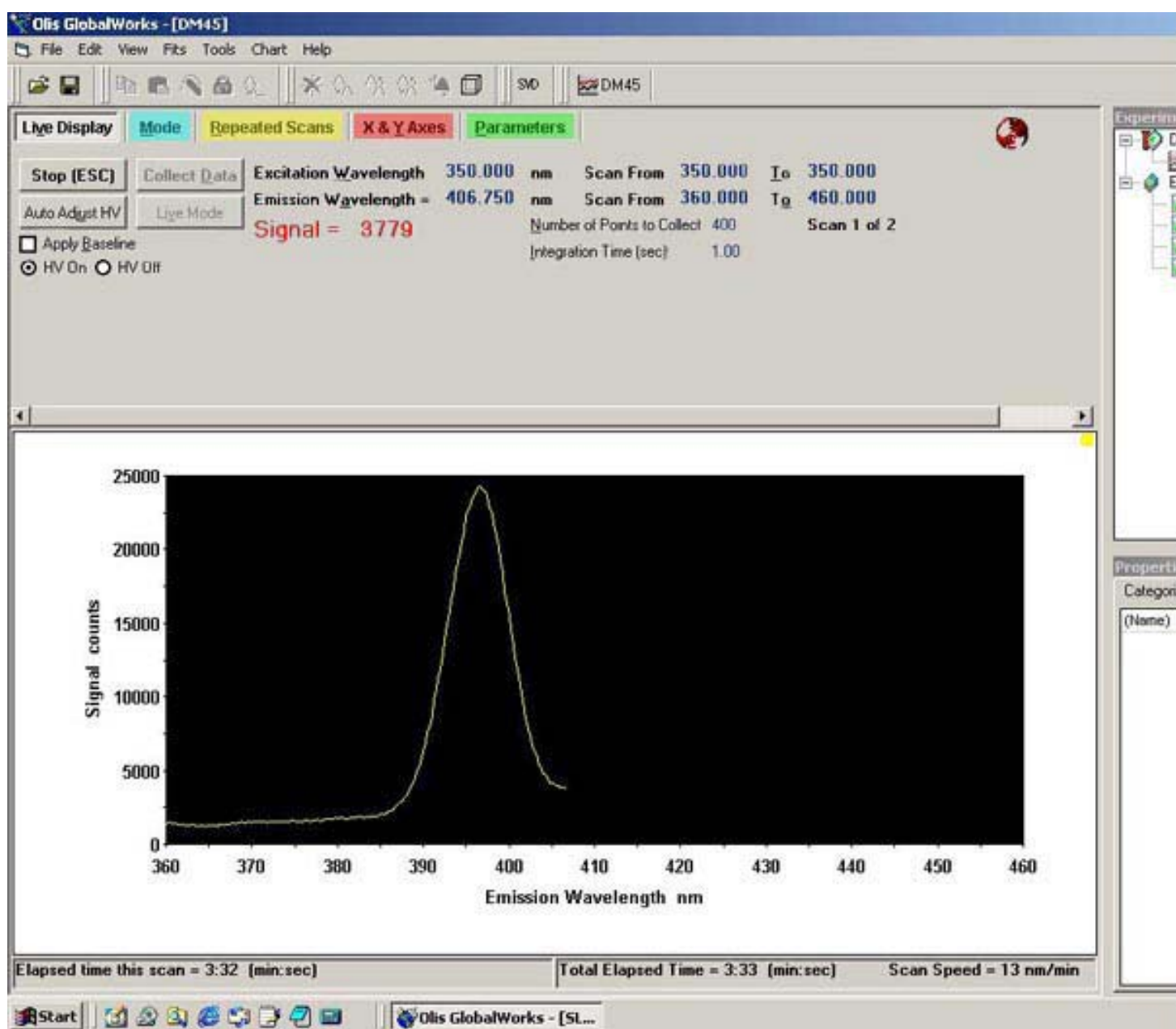
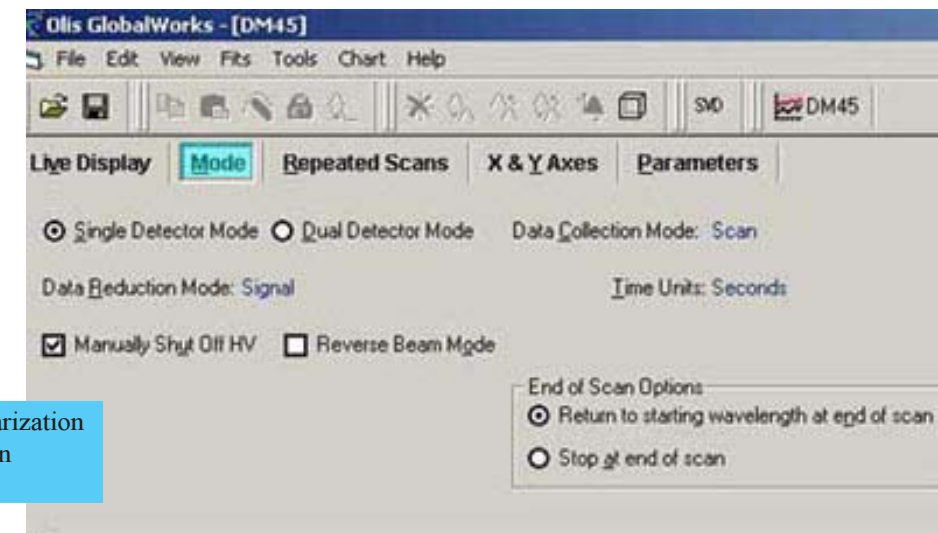


Data Collection Screen



Set collection parameters and watch incoming data on the primary SpectralWorks screen (this page) and from the secondary menus (facing page).

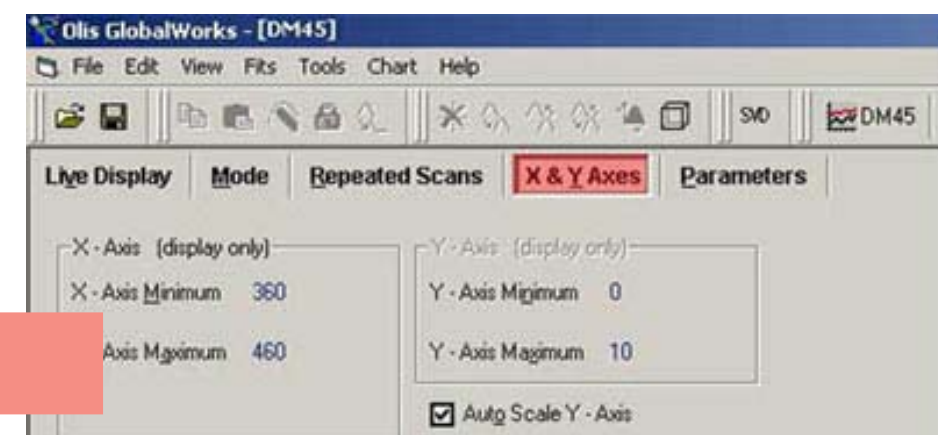
Choose mode of detection, which includes polarization and anisotropy; other collection modes based on accessories activated.



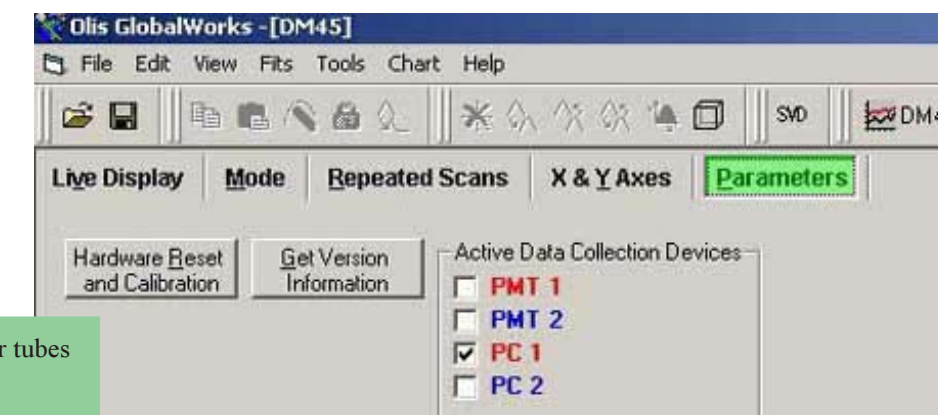
Repeated scans can be taken as a function of time, temperature, or concentration of reagents. Any number can be collected and retained or accumulated and averaged.



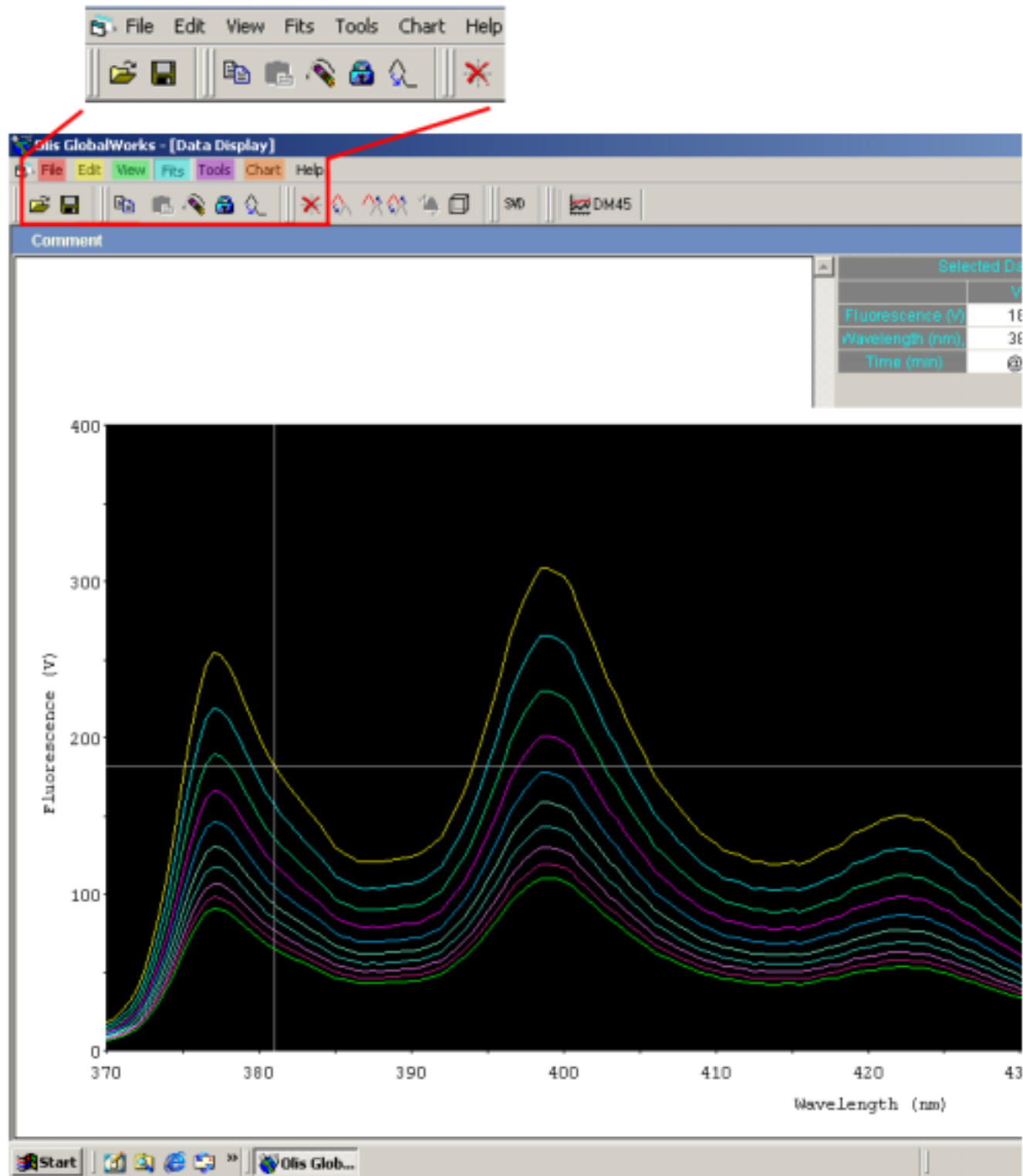
The X- and Y-axes can be changed during data collection with an option to override autoscale.



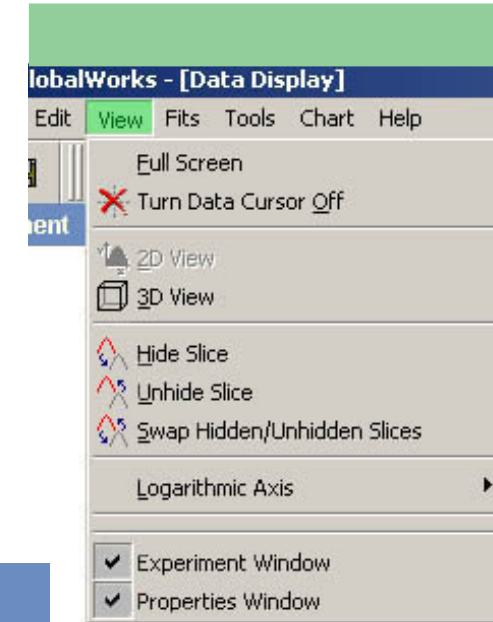
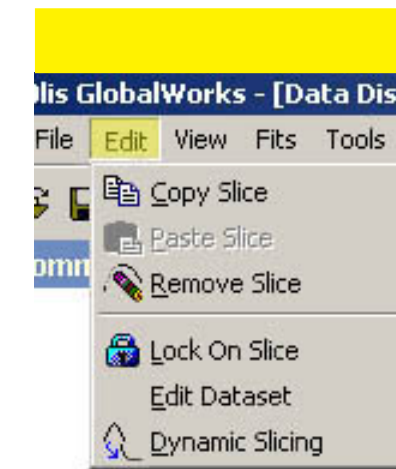
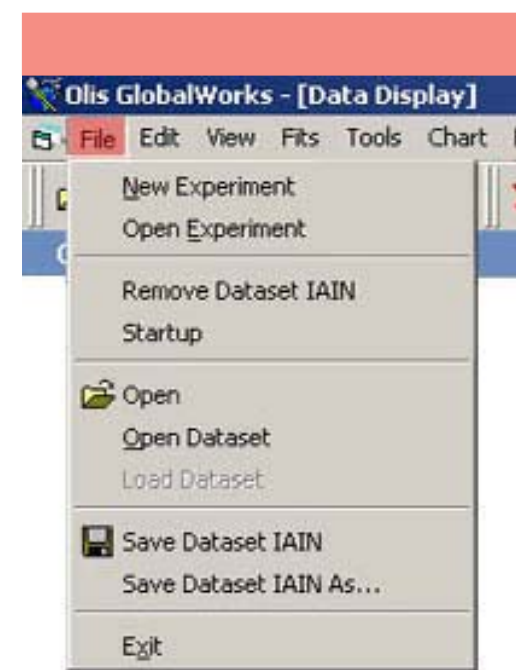
Photon counting (PC) or analog photomultiplier tubes (PMT) are selected for use.



Post Acquisition Options



Primary screen after data collection (this page) and secondary pulldowns (facing page).



The pull down menus from the post-collection screen of SpectralWorks are largely self-explanatory, save a few terms, defined here.

“Experiment” is a collection of “datasets.” A “dataset” can be a single scan or trace (2D) or a series of scans or traces (3D).

“Slice” is the scan or kinetic trace on which the cursor is resting. “Dynamic slicing” creates a 2D trace from a 3D data set based on the current cursor position on the X axis (e.g., wavelength) to create the Z axis plot (e.g., temperature).

“Logarithmic Axis” can be X or Y.

“SVD” is “singular value decomposition,” the first step in 3D fitting and the modern way to remove random noise from the data. “Compton fit” is an algorithm for determining the secondary structure of proteins acquired as CD scans.

