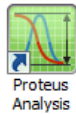


Basic Data Processing Tutorial 07/03/14

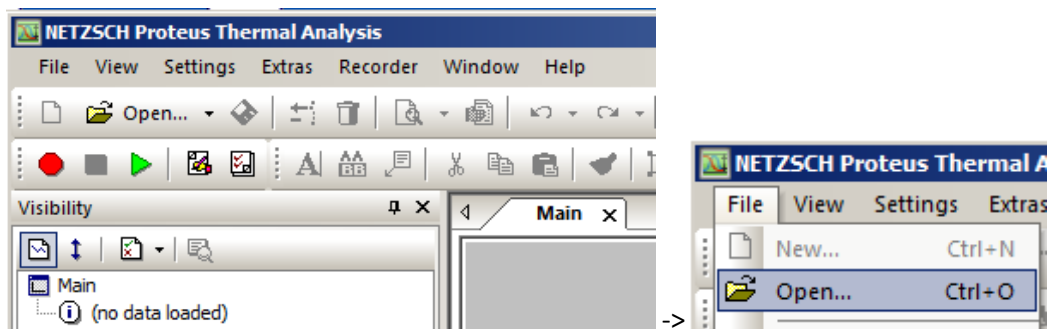
The data files you have acquired using the Autosampler program will be one of the following file types:

- *.ngb-bs1 -baseline correction file (empty sample crucible vs. reference crucible)
- *.ngb-ss1 -uncorrected sample file
- *.ngb-ds1 -automatically baseline corrected sample file (requires *.ngb-bs1 file first)

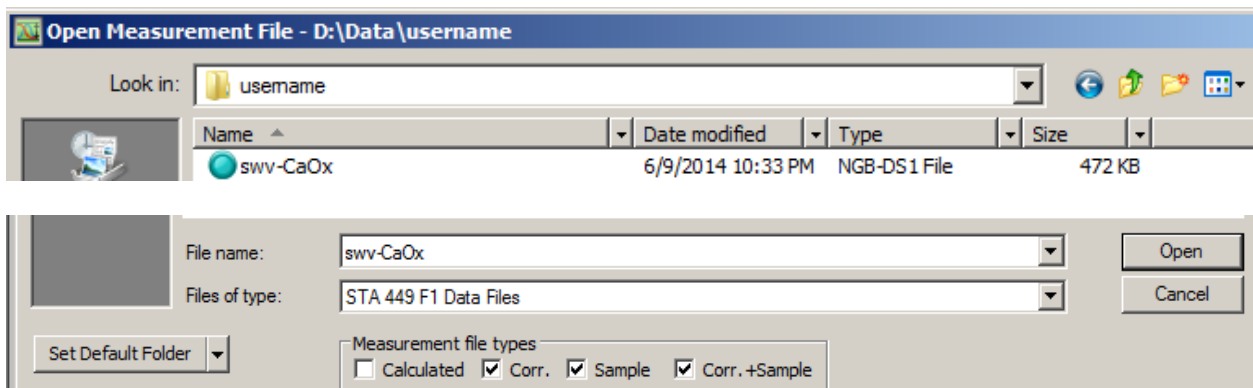
This tutorial only deals with processing TGA/DSC data, but if FTIR or MS has been enabled in the measurement, you will also have OPUS or Aeolos files that can be imported into the view. In this example we will use a data file that already includes a corrected baseline. Copies of this file have been put in each of your data directories.



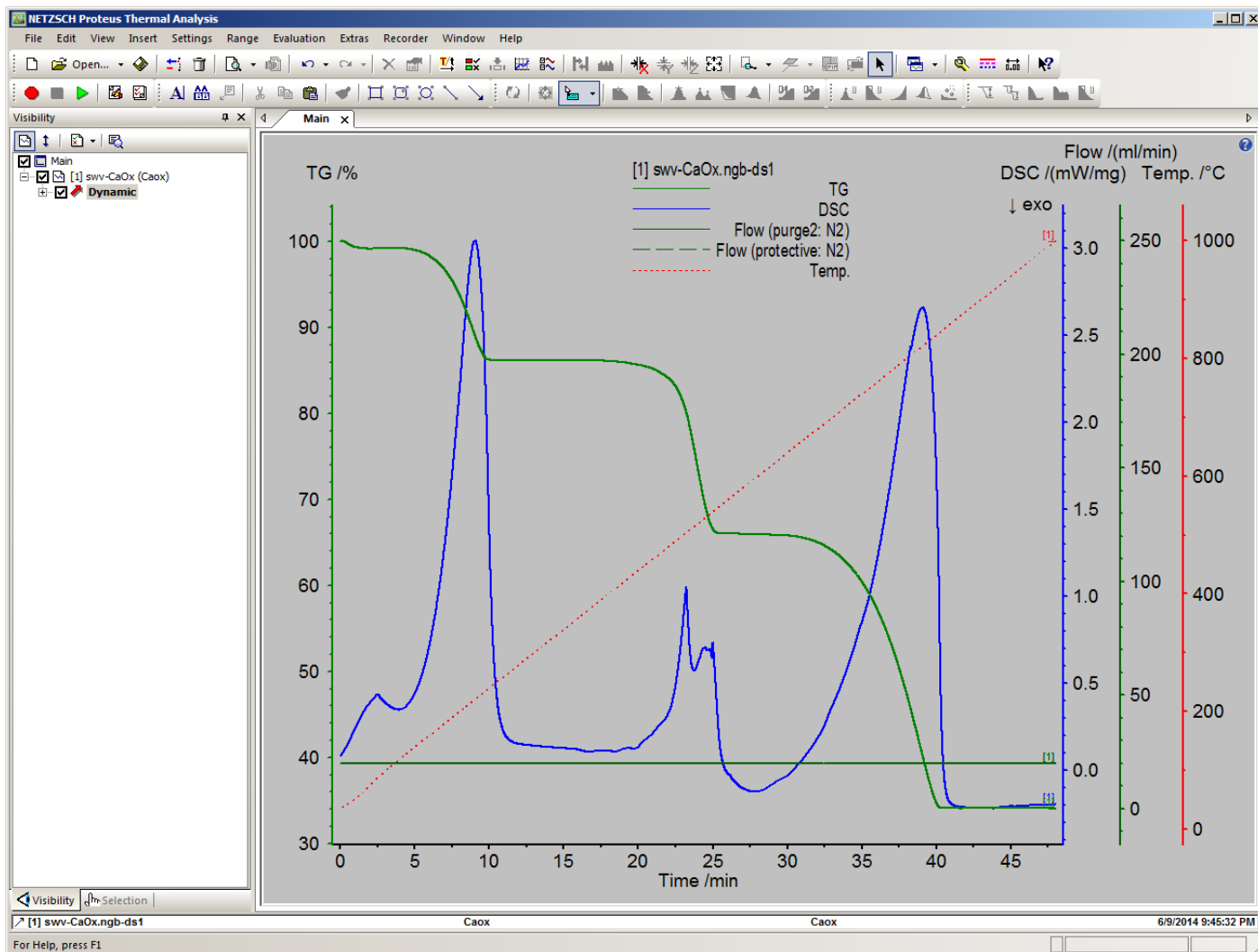
Start the Proteus Analysis program and choose File -> Open.



Select the file swv-CaOx, and choose OPEN. Note that all data files should start with the assigned three-letter code of the person who acquired the data. This is usually your initials.

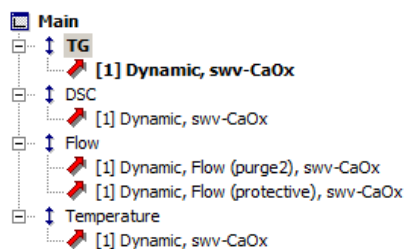


Exactly how the program looks when you open it will depend upon the program default settings or choices you have made in the layout configuration. As with most Windows-based software, the View and Settings drop-down menus are used to customize the program appearance.

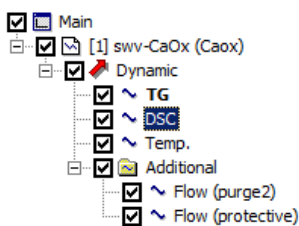


Take some time to explore each of the drop-down menus. Also, mouse over each of the icons in the ribbon bars to see their functionality.

Also note that the browser pane has two tabs at the bottom, corresponding to Visibility and Selection views. Clicking on the various rows in the browser pane will select or deselect the file and/or curve. Selection is normally indicated by the curve (and associated axis) changing from the default color to white, and by the text in the browser changing from normal to **bold** font.

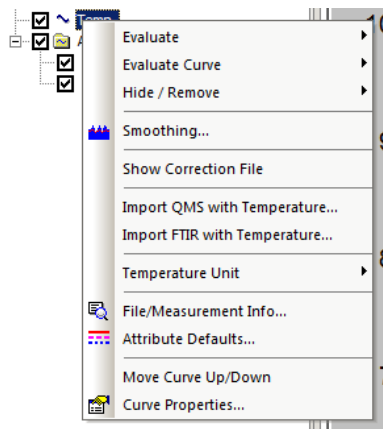


Selection view



Visibility view

Right-clicking on most of the items in the browser pane (Selection or Visibility view) will bring up a menu of additional choices or information pertaining to the item. Spend some time exploring the various actions and choices available in the two browser pane views. Many of these features are replicated in the ribbon bars and/or the drop-down menus.

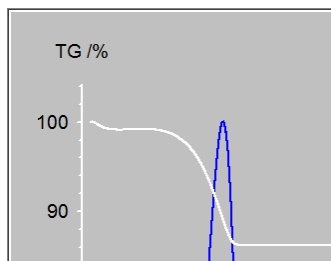


Converting the X-axis from Time <-> Temperature.

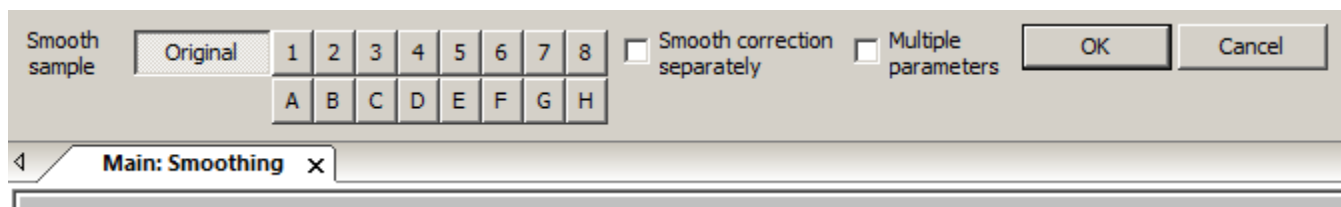
Using the ribbon bar icon , or the [Settings -> X-time -> X-temp] toggle, display temperature on the x-axis.

Smoothing Curves

Click on the TG curve (or the TG item in the browser pane) to select the curve. The curve and axis should turn white.



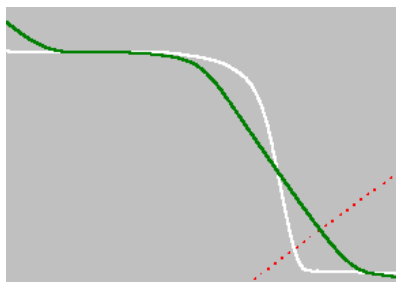
Enable the smoothing icon , or use [Settings -> Smoothing]. Smoothing choices will appear.



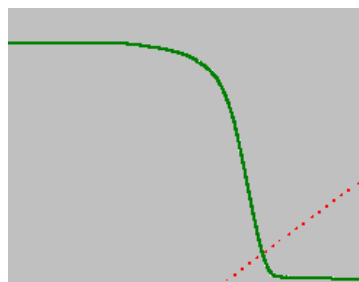
The strength of the smoothing increases from 1 -> 8 -> A-> H. Explore the various levels of smoothing. As long as you don't select OK, you will stay in the smoothing program. Click on the Zoom icon. It should change color to indicate that it is active.



The left-mouse button can now be used to drag a bounding box and zoom in. Select the highest level of smoothing (H) and compare the smoothed curve with the original. Finish by choosing level 5 smoothing, and pressing OK. When properly smoothed, there should be almost difference between the original (white) and smoothed (colored) curves.




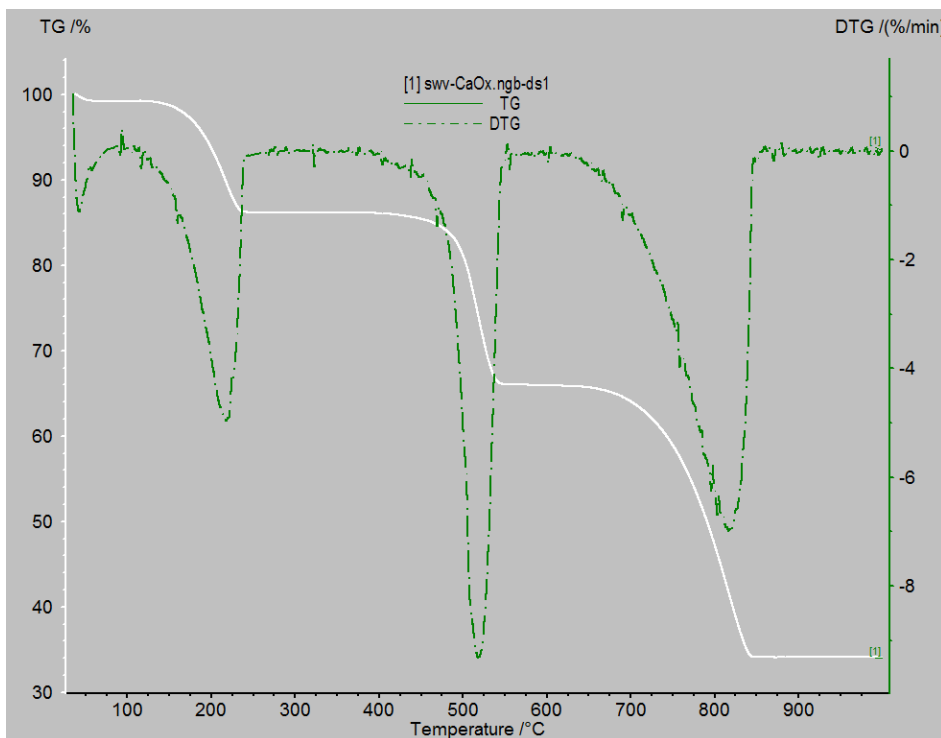
Level "H" smoothing




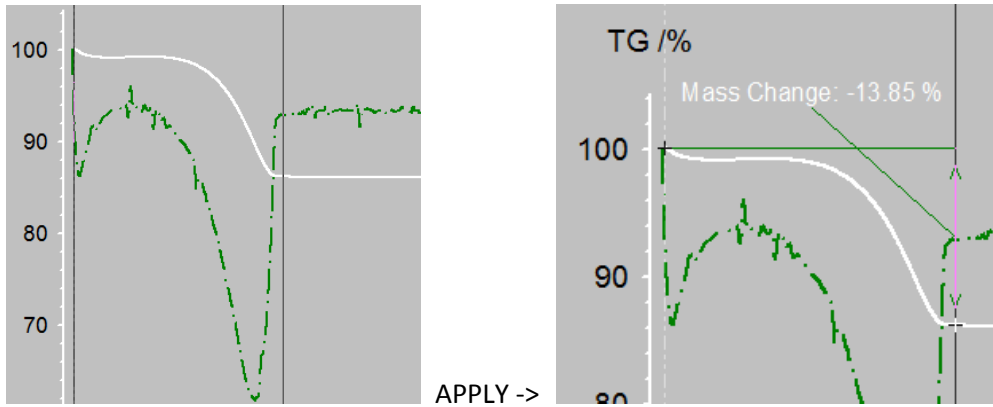
Level "5" smoothing

Determining Weight Losses

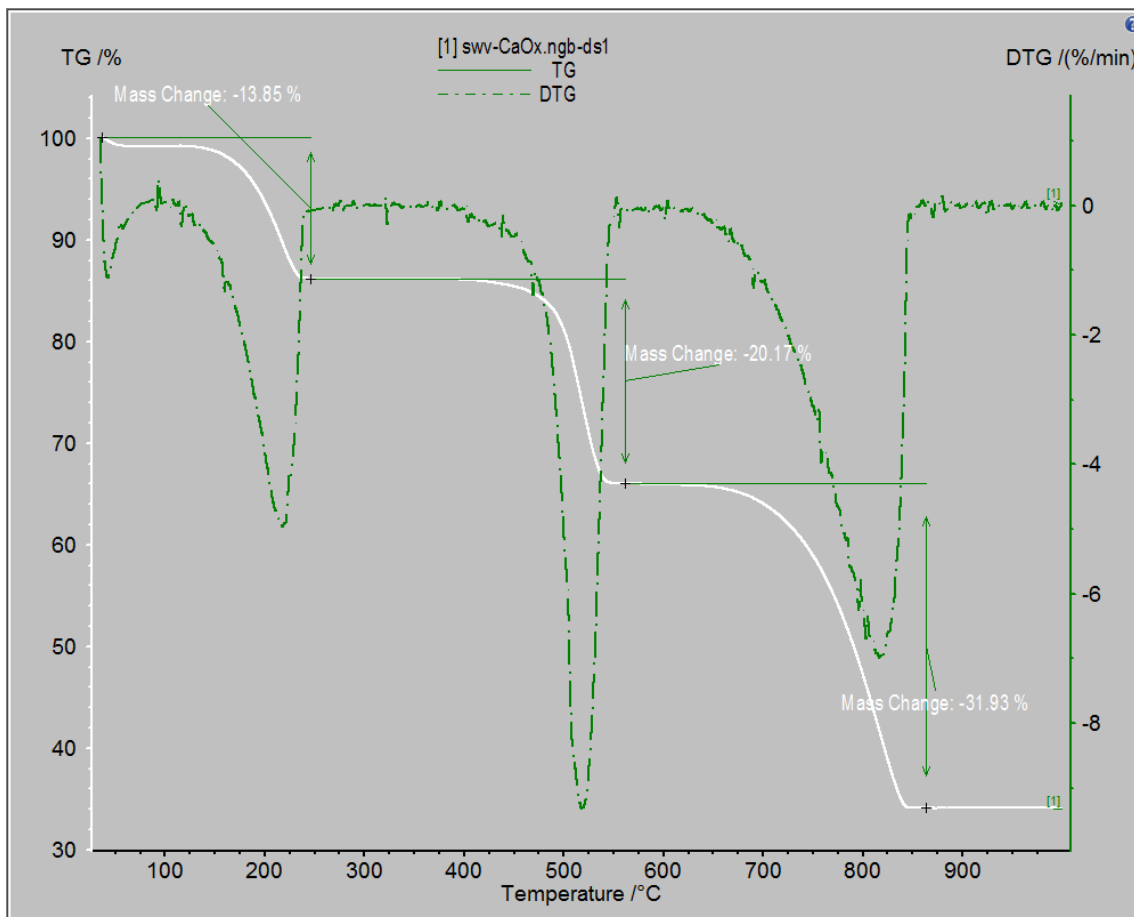
From the Evaluation menu select 1st Derivative. You may also use the ribbon bar icon . This is used to help calculate the mass changes reflected in the TG curve. Deselect (uncheck) all of the items in the browser pane except the TG and Temp curves so that the display is less crowded. Your display should look like this:



Select Mass Change  Mass Change... from the Evaluation menu or the ribbon bar. Move the left-cursor to the very beginning, and the right cursor to the sharp corner of the first derivative. Click APPLY.

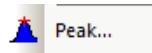


Move the cursors to define the second mass loss. Note that each measurement should start from where the previous one ended. There should be no gaps. Use APPLY to calculate the value and move to next area to be defined. When all of the weight losses have been defined, select OK. Your display should look like this:

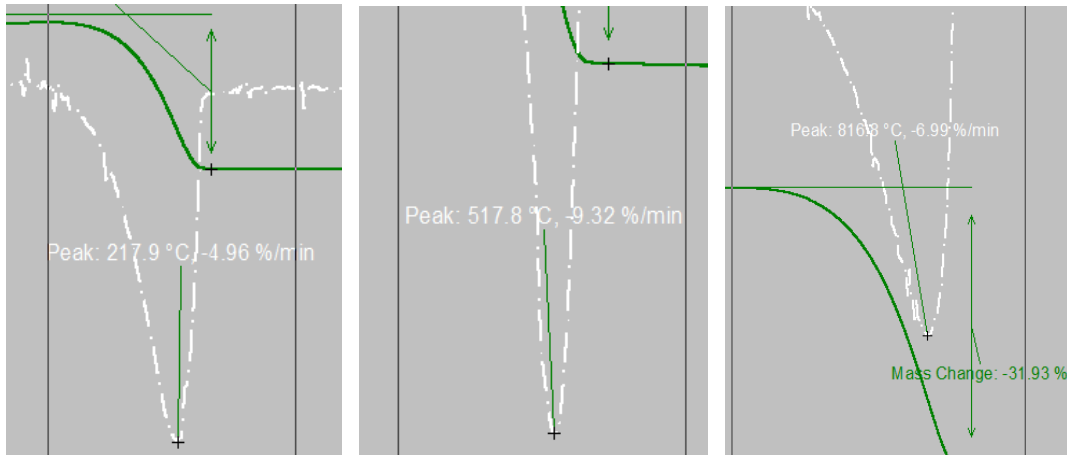


Evaluating Maximum Temperature and Rate of Mass Change

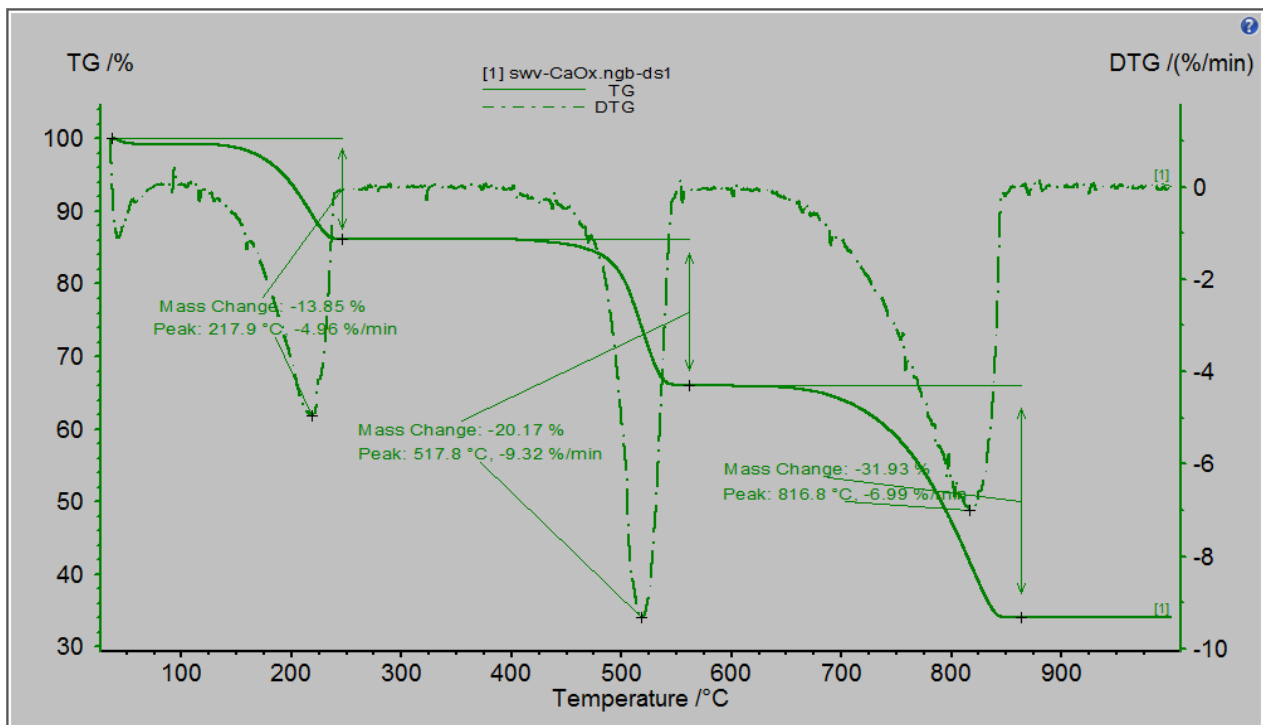
Select the 1st-derivative in the view. Select Peak in the Evaluation menu or ribbon bar.



Position the left and right cursors so that the first peak is approximately centered. Select APPLY. Move the cursors to bracket each additional peak, using APPLY each time.

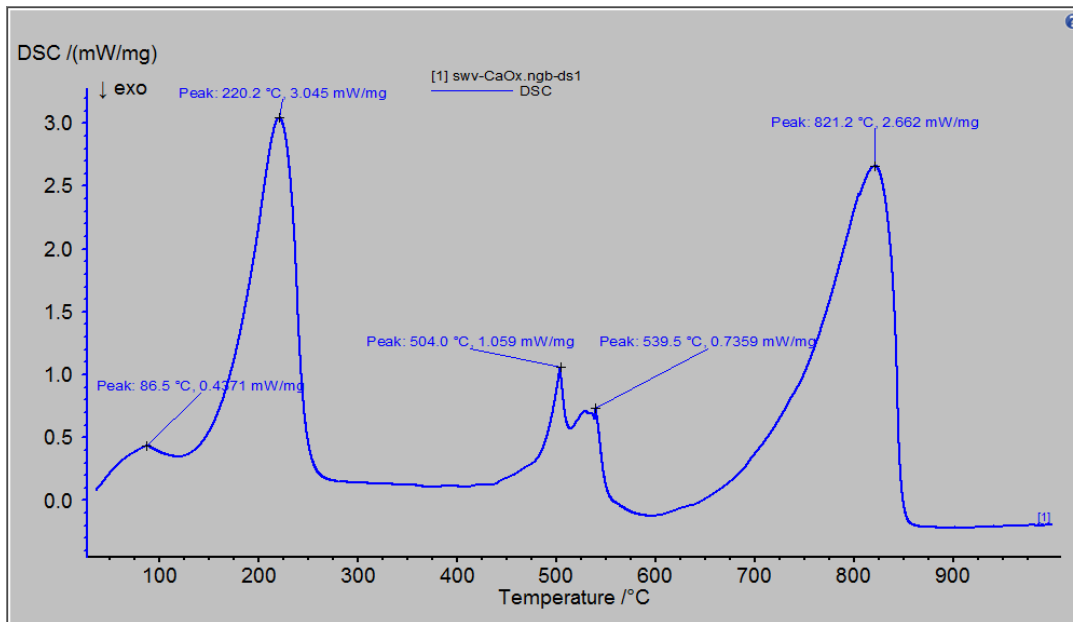


Click OK when finished. The view should look like this:



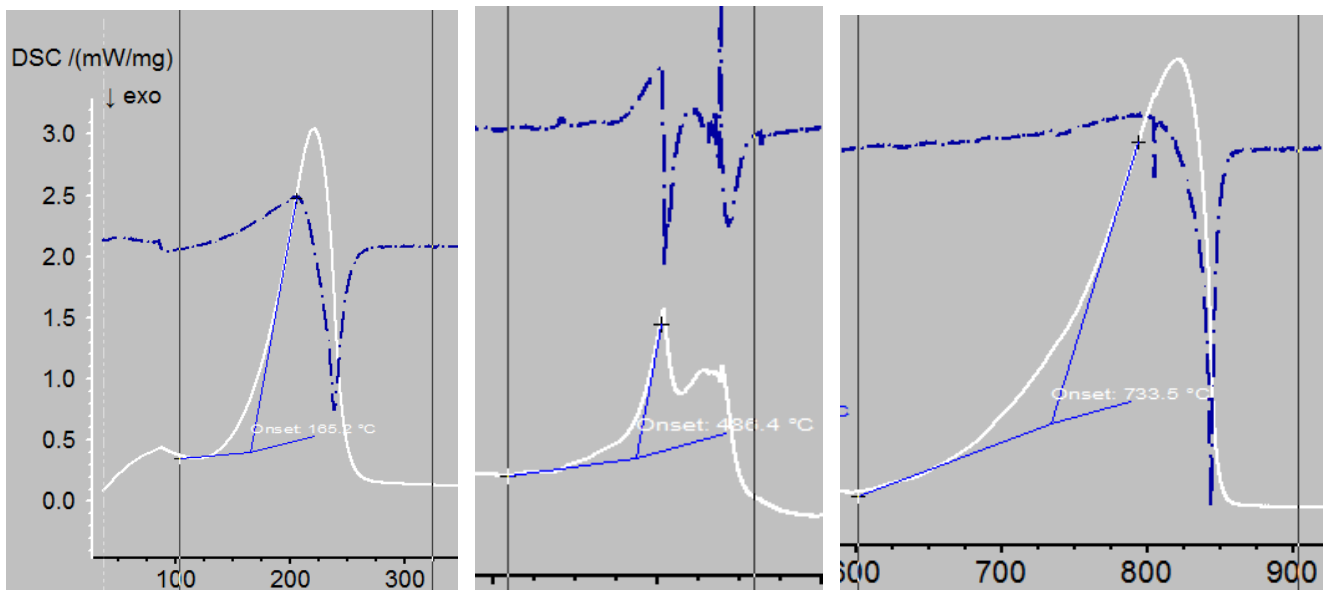
Evaluating DSC Peak Temperature

In the browser, uncheck the TG and DTG curves and check the DSC curve. Click on the curve to select it. When selected, the color of the trace will be white. Move the left and right cursors to bracket the peak. Select APPLY. Move the cursors to bracket each additional peak, selecting APPLY in each case. When finished, select OK. The view should look like this:

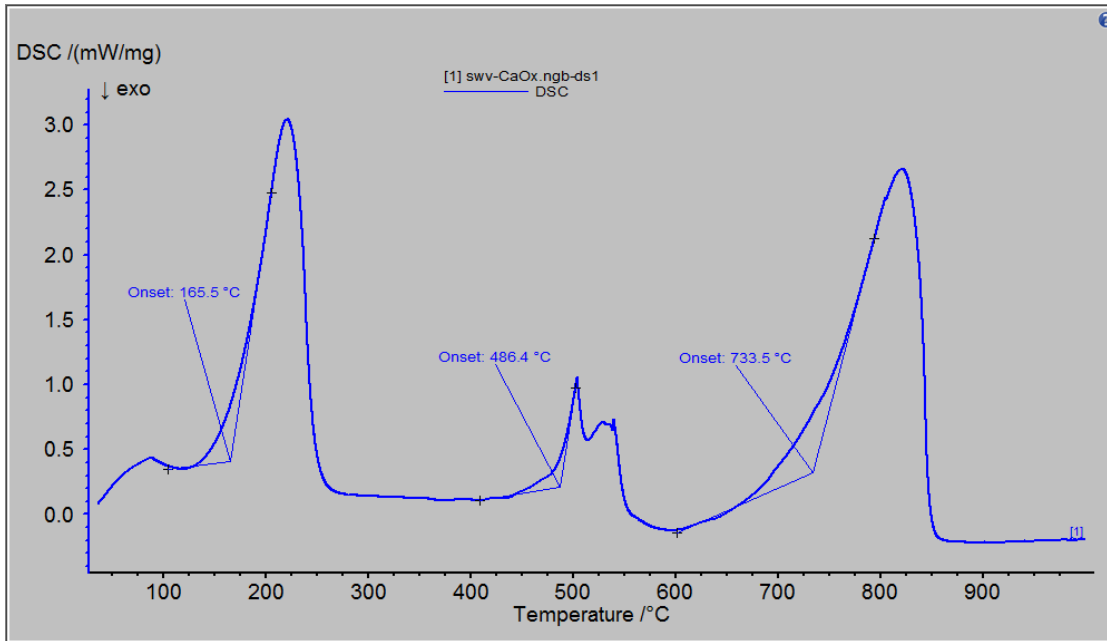


Evaluating DSC Onset Temperature

Verify that the DSC curve is selected in the view. If necessary, clean up the view by clicking on each of the text objects in the view and deleting them. Select Onset in the Evaluation menu. Onset...

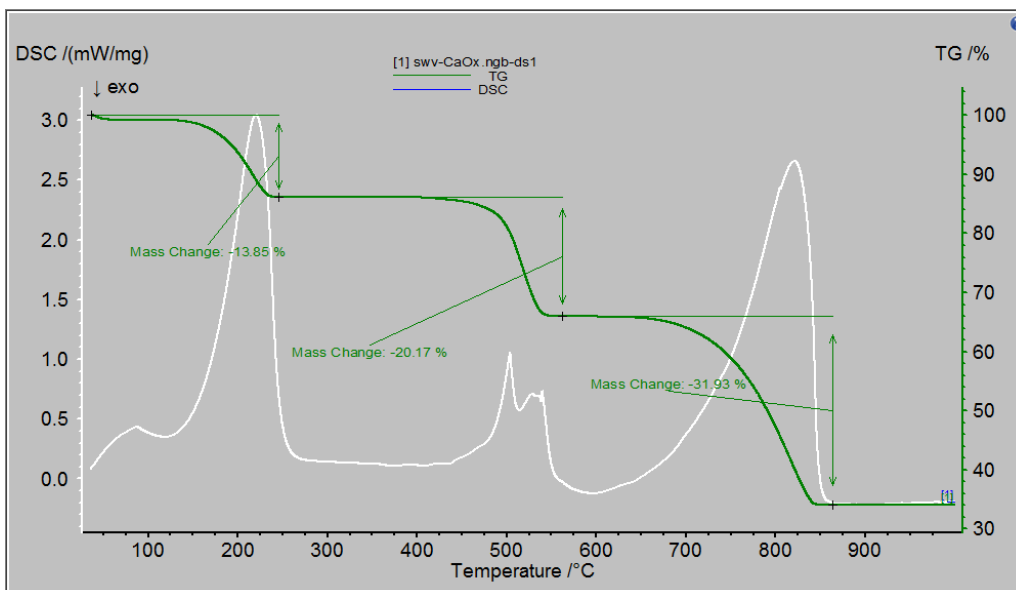
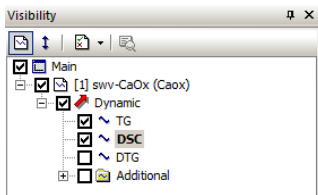


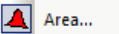
The left cursor should be positioned to include the most linear range of the baseline leading into the peak. The right cursor is positioned after the peak. Click APPLY. Move the cursors and determine onset positions for each additional peak. When finished, select OK. Your view should look like this:

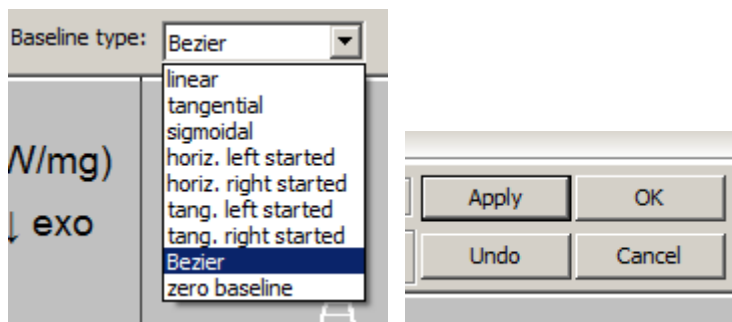


Evaluating DSC Peak Area (Enthalpy Change)

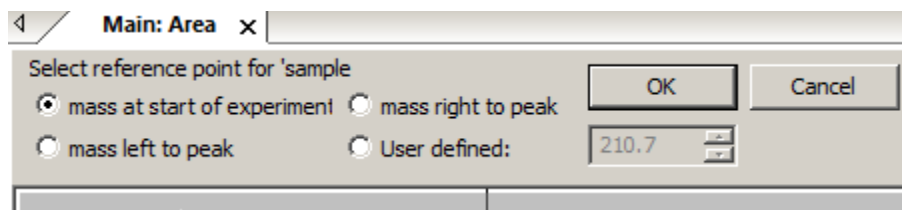
Check that the DSC curve is selected. Delete any text boxes in the view that are cluttering the display. For this exercise, you must also enable the TG curve by checking the box in the Visibility browser pane. The view should still show the mass change values.

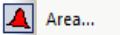


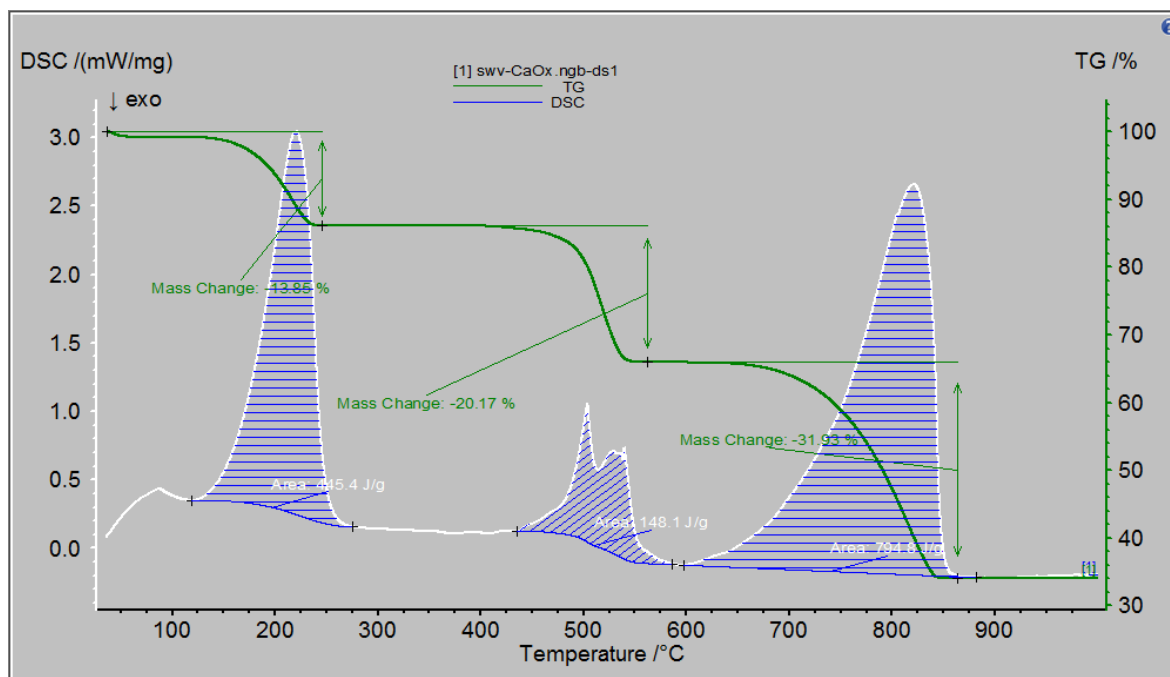
Select Area in the Evaluation menu.  Position the left and right cursors to include the entire peak. Note that a range of baseline types can be selected. Experiment with several choices of cursor positions and baseline types, by using the APPLY and the UNDO buttons.



Note that after selecting APPLY, the view header will change to show choices for the mass reference points for the peak you have just defined.

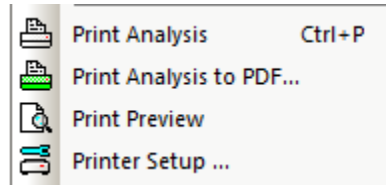


Set the checkmark for “*mass at start of experiment*”, then click OK. In order to evaluate the next peak, select Area again . Set the cursors and select APPLY. Ensure that “*mass at start of measurement*” is still checked, then click OK. Repeat the process again for the third peak. If you use Bezier for peak 1, Sigmoidal for peak 2, and linear for peak 3, your view should look like this:

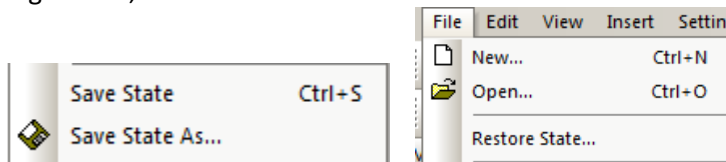


Printing and Saving Results

At any point you can use *File -> Print Preview* or *File -> Print* to print any of the views. Note that you can also print directly into a PDF file.



Often it is useful to save the results as a “*Saved State*”. This allows you to come back to a particular data file and reopen it at just the point in the processing where you left it. The file is saved in the same location as the original file, but with a different extension. *Saved States* can also be opened from the File drop-down menu.



END OF BASIC TUTORIAL