EcoSEC® GPC Workstation Software Multiprocessing Feature Auxiliary Instructions

Introduction

Common practice in the analysis of polymers via size exclusion chromatography is to perform multiple injections of several different sample dispersions to ensure repeatability and reproducibility in the molar mass averages obtained. It is widely accepted among those who regularly analyze size exclusion chromatography results that the reproducibility for the same sample, injected on the same instrument, with the same experimental conditions, e.g. concentration, injection volume, flow rate, etc., depends on the consistency of the signal from the detector, the long term accuracy of the pumping system, and data processing parameters.[1-3]

The hardware of the EcoSEC GPC System is designed to ensure detector signal consistency through the use of the dual flow refractive index detector and long term pumping accuracy through the use of a temperature controlled pump oven. In order to ensure reproducibility from data processing, the EcoSEC GPC System Workstation Software offers a multiprocessing feature.

As shown in Tosoh Application Note AN36, the standard deviation in the molar mass averages can be significantly decreased by implementing the use of the multiprocessing feature. The decrease in the standard deviations of the molar mass averages determined using the multiprocessing feature vs. the individual processing method is a direct result of the decrease in variation in baseline and integration limit settings. Step by step instructions on the use of the multiprocessing feature follow.

Using the Multiprocessing Feature

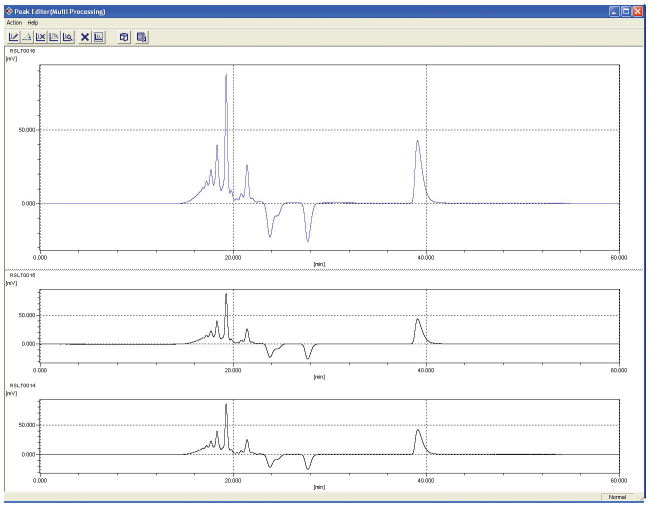
Step 1: Load the sample set of interest into the Analysis portion of the EcoSEC GPC Workstation software. From the chromatogram data list, highlight the replicate chromatograms to be analyzed by holding down the SHIFT key while clicking on the Data Name of each chromatogram. Samples to be included in the analysis will now be highlighted in blue.

Data Name	Sample Nam
RSLT0022	THF
RSLT0021	THF
RSLT0020	THF
RSLT0019	Polymer A (2)
RSLT0018	Polymer A (2)
RSLT0017	Polymer A (2)
RSLT0016	Polymer A
RSLT0015	Polymer A
RSLT0014	Polymer A
RSLT0013	DMSO
RSLT0012	DMSO

Step 2: Left click on the down arrow to the right of the Multiprocessing tool on the tool bar and select Peak Editor.

Step 3: Select either the RI or UV data channel for processing. Click OK. Once editing has been started, the detector cannot be changed.

Step 4: A new screen will open labeled “Peak Editor (Multiprocessing)”. The tool bar on this screen will look the same as that used for editing a single sample. All of the samples highlighted in blue in Step 1 will be displayed on this screen. The top chromatogram will appear in blue, while all other chromatograms will appear in black. All peaking editing will be performed on the top “blue” chromatogram and immediately applied to all of the other “black” chromatograms. The Peak Editor (Multiprocessing) window displays chromatogram data selected on the chromatogram data list in order from the top.



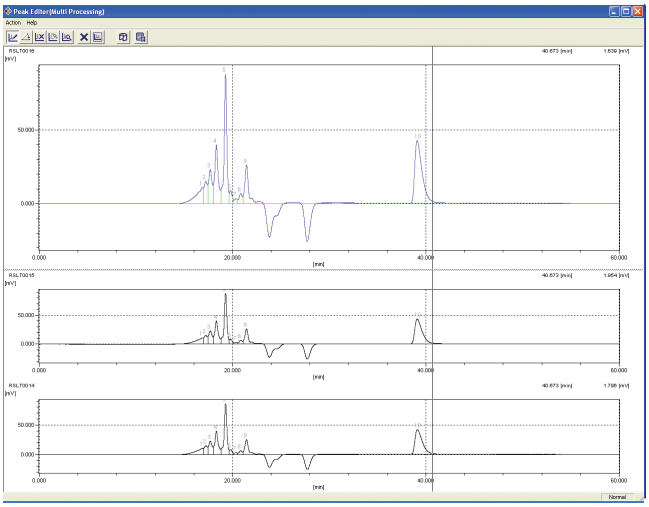
Step 5: The baseline and peak integration limits will be set for the top chromatogram and automatically applied to sequential chromatograms. If the top chromatogram is not the chromatogram to be used as the model chromatogram, continue to Step 6. If the top chromatogram is the chromatogram to be used as the model chromatogram, skip to Step 8.

Step 6: To change the top chromatogram data, click on the Model Chromatogram button or click the Data Select button to display the Data Select dialog box.

Step 7: Click on the data name of the chromatogram to be moved to the top position, then click Model Chromatogram and close. The selected chromatogram will then be displayed at the top of the Peak Editor (Multiprocessing) window.

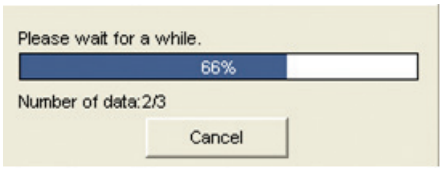
Step 8: Draw the baseline using the draw tool  on the top chromatogram. The baseline will appear in green on the top chromatogram and in black on all sequential chromatograms.

Step 9: Continue using the draw tool to assign the integration limits of each peak on the top chromatogram. All peaks will be labeled numerically on all chromatograms selected for multiprocessing.



Step 10: If needed, use the hide peak tool to hide any unneeded portions of the baseline or peaks previously assigned.

Step 11: Click on the calculator tool  to perform calculations. Each chromatogram selected for multiprocessing will be processed. Once processing is complete the "Peak Editor (Multiprocessing)" screen will disappear and the results screen for the first chromatogram processed will appear.



Step 12: The results for each chromatogram selected for multiprocessing can be obtained by toggling between the sample names on the left hand side of the results screen. The results being displayed correspond to the sample highlighted in blue.

Step 13: Repeat this procedure for each set of replicate measurements.

References

[1]Ritter, A.; Schmid, M.; Affolter, S. Polym. Test., 2010, 29, 945.
[2]Goetz, H.; Schulenberg-Schell,H. Int. J. Polym. Anal. Charact., 2001, 6, 565.
[3]Mori, S.; Kato, H.; Nishimura, Y. J. Liq. Chrom. & Rel. Technol., 1996, 19, 2077.

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