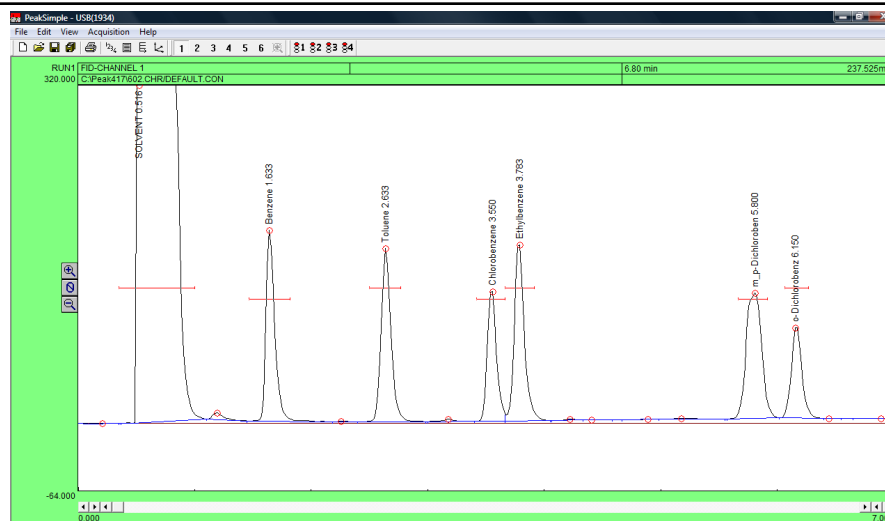


PeakSimple Basic Tutorial

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Installing PeakSimple from the CD or USB thumb drive:

- Start the Windows operating system in use on your computer. (Windows XP, Vista, or 7)
- Insert the CD or USB thumb drive into the computer.
- Open **My Computer** and open either the CD or thumb drive.
- Double-click on the **Setup.exe** file. Make sure to select the right version of PeakSimple to install (32- or 64-bit). Windows XP and some Vista computers need to install the 32-bit version, other Vista computers and Windows 7 need to install the 64-bit version. If you are unsure, right-click on **My Computer** then select **Properties** in order to determine what bit operating system you are using.
- To complete installation follow the onscreen instructions provided by the installation wizard.
- For instructions on loading the driver, please refer to the Quick Start Documents located in the PeakSimple folder or on the www.srigc.com website.

Installing PeakSimple from software download:

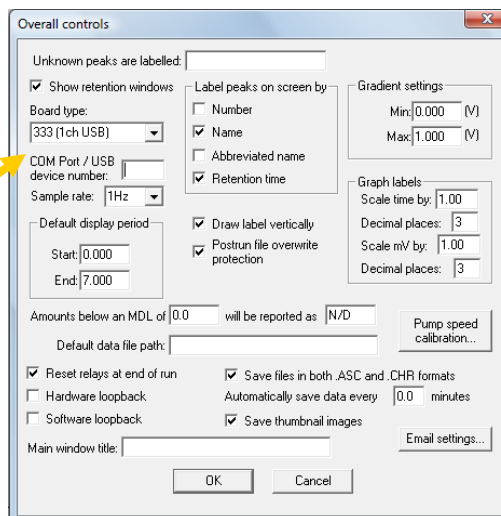
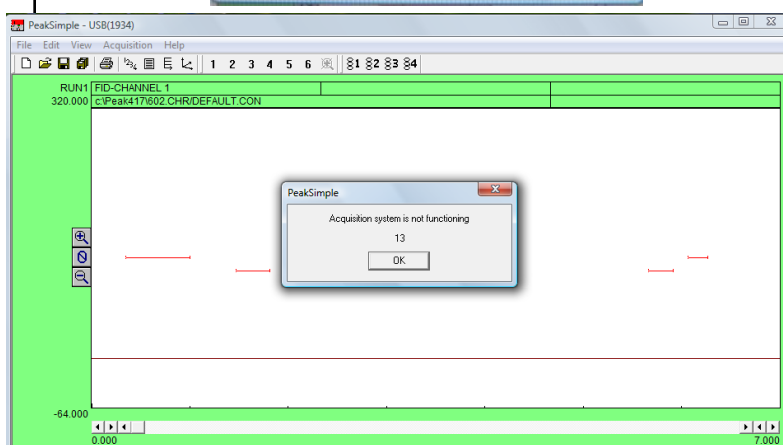
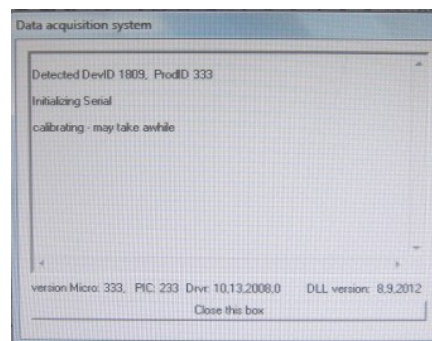
- Start the Windows operating system and use an online browser to access www.srigc.com.
- From the menu on the left hand side of the screen select **Download PeakSimple** and then download the latest version. Windows XP and some Vista computers need to download the 32-bit version, other Vista computers and Windows 7 need to download the 64-bit version. If you are unsure, right-click on **My Computer** then select **Properties** in order to determine what bit operating system you are using.
- Save the file to a temporary folder and double-click on the setup file when it is finished downloading, or, just click **Run** to install PeakSimple without saving the setup file.
- Follow the onscreen instructions provided by the installation wizard.
- For instructions on loading the driver, please refer to the Quick Start Document located in the PeakSimple folder or on the www.srigc.com website.

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Launching PeakSimple

1. Double-click on the Desktop PeakSimple icon to launch PeakSimple.
2. The data acquisition system will attempt to initiate communications between the computer and the data system.
3. If PeakSimple comes up with an error message stating "Acquisition system is not functioning" with a countdown timer, it is indicating that there is a communication problem between the computer and the data system or that the data system and the hardware is not connected. Click OK to continue working with PeakSimple.
4. The first time PeakSimple connects to a GC or data system open the **Edit** menu and select **Overall** to get to the **Overall Controls** Screen.
5. Enter the proper **Board type** (202, 203, 302, or 333) and **COM Port/USB device number** (Found on data system or GC). Select OK and PeakSimple will establish communications with the data system.
6. Most of the commands and options in PeakSimple are equipped with tool tips that will automatically pop up to display useful information when the mouse cursor is held over a command. To turn off the tool tips deselect the tool tips option in the Help menu.



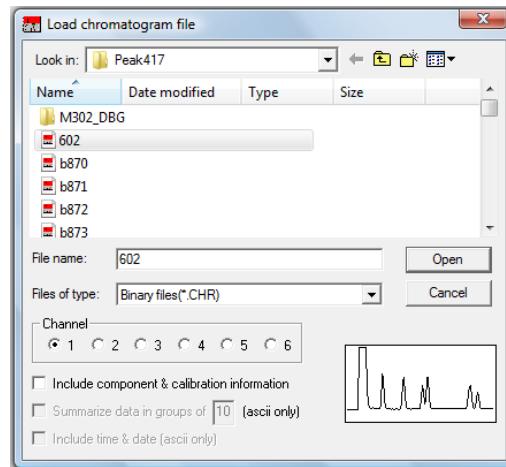
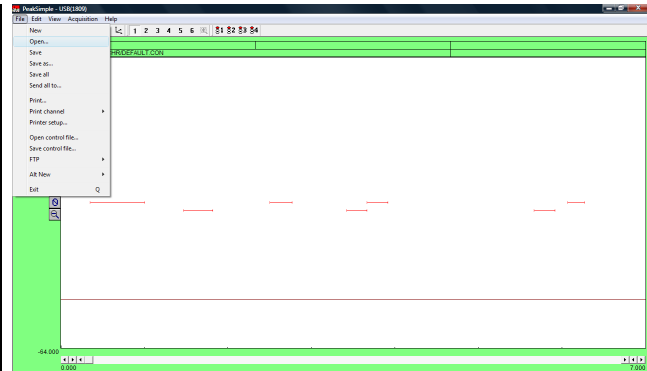
Enter the A/D board type. Your choices are Model 203 single channel serial connection, Model 202 4 channel serial connection, Model 333 single channel USB and Model 302 6 channel USB.

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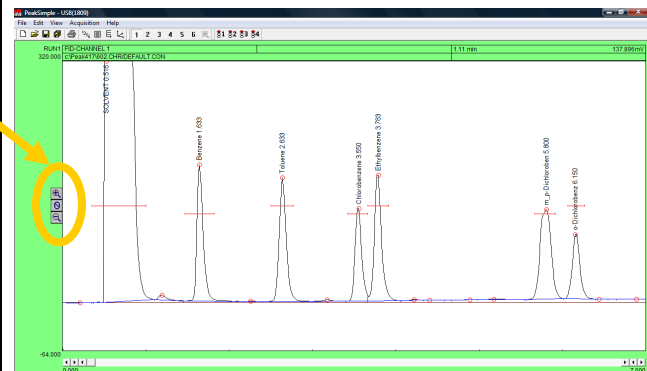
Opening a PeakSimple Data File

1. To open a PeakSimple data file or chromatogram, begin by selecting **File** in the PeakSimple menu bar and then choose **Open...** from the set of options.
2. The Load Chromatogram File window is now open. The PeakSimple software includes a number of sample chromatogram data files that can be opened, displayed, and manipulated. One file, 602.CHR, will be used throughout the rest of the tutorial. Select file **602.CHR** from the PeakSimple directory, choose **Channel 1** as a destination channel, and then select **Open** to load the file.

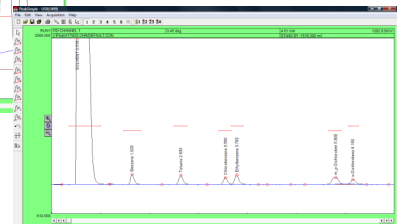
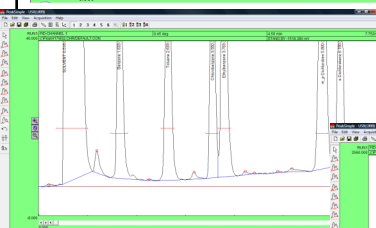


Adjusting Display Limits

1. To adjust the display limits of a chromatogram click on either the **+** magnifying glass icon or the **-** magnifying glass icon to the left of the chromatogram. This will increase or decrease the limits by a factor of two each time you click on the icons.



2. After opening chromatogram 602.CHR, practice making the display limits smaller but the peaks larger by clicking the **+** magnifying glass icon.
3. Practice making the display limits larger but the peaks smaller by clicking on the **-** magnifying glass icon.

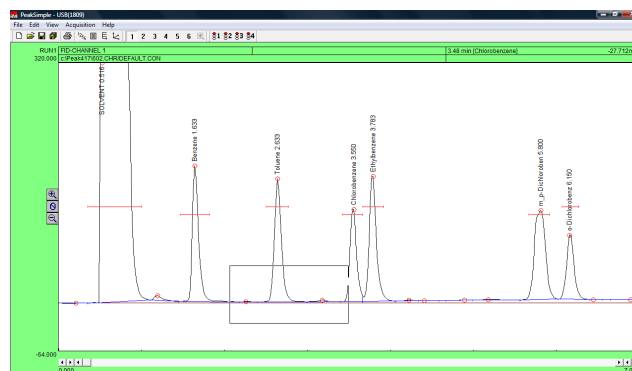


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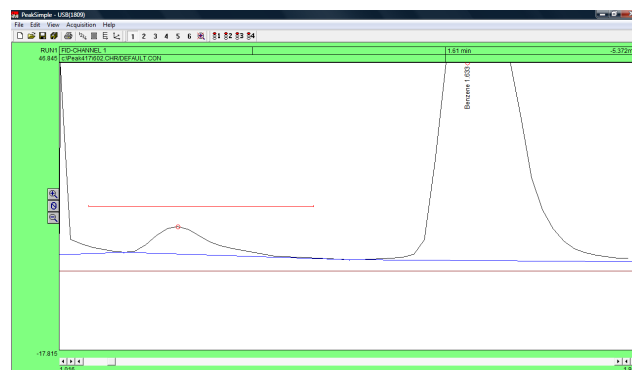
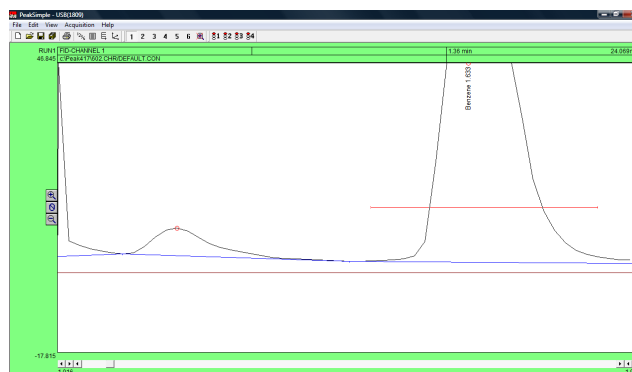
Zooming

1. To zoom in on a specific part of a PeakSimple chromatogram, click and hold the left mouse button and drag it over the desired area.
2. After opening chromatogram 602.CHR hold the left mouse button and drag it over the base of the toluene peak. Let go of the mouse button and there will be a larger view of the area that was selected.
3. To return to the original display limits of the chromatogram and unzoom the area selected press **F6** or select the unzoom icon located in the PeakSimple toolbar at the top of the screen or right-click and select **Unzoom**.



Dragging Retention Windows

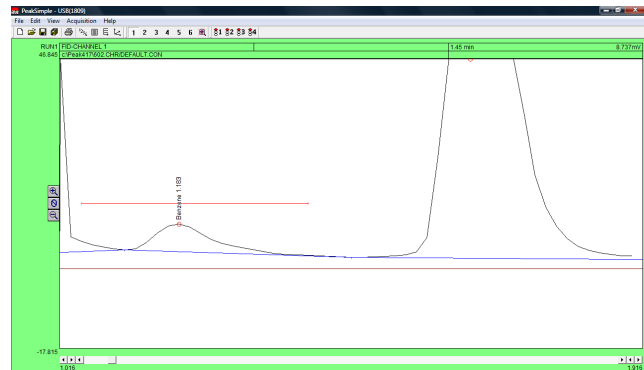
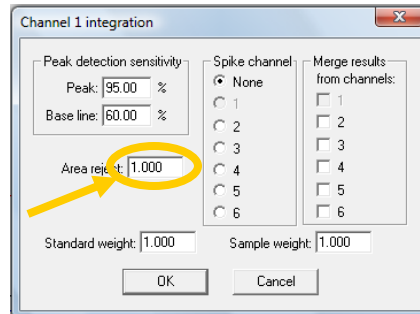
1. To drag a retention window bar place the mouse cursor on the bar until a double sided arrow pops up. Click on the left mouse button and hold and then drag the retention window bar to its desired place.
2. After opening the chromatogram 602.CHR zoom in on the benzene peak and the smaller peak to its left. Locate the benzene retention window bar and drag it over to the smaller unnamed peak to the left of the benzene. Because this is a small peak it is not immediately recognized.



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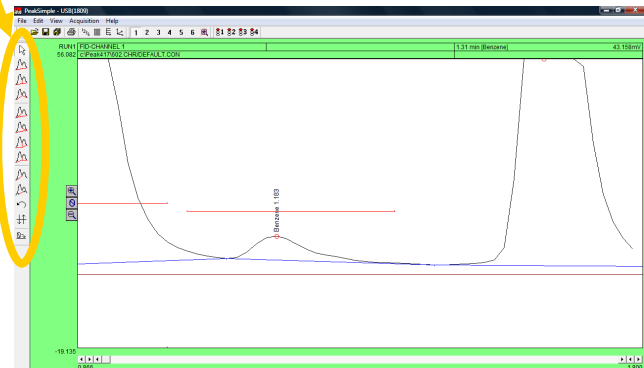
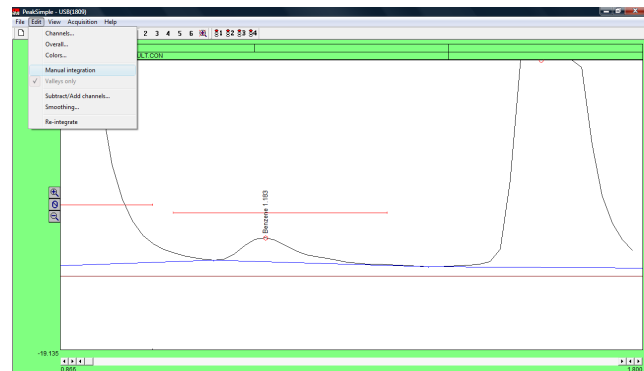
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- Right click on the chromatogram over the unnamed peak and select **Integration** from the resulting menu.
- From the integration window locate the **Area Reject** dialogue box, erase the 100.0 in the box, and add the number **1.0** to the dialogue box. Click **OK** and the integration window will exit.
- Press the **Enter** or **Return** key on your keyboard and the smaller peak will now be recognized as Benzene.



Manual Integration

- To manually adjust the integration baseline and peak separation in a chromatogram use the manual integration toolbar provided by PeakSimple. To open up the manual integration toolbar select **Edit** in the PeakSimple menu bar and then click on the **Manual Integration** option. The manual integration toolbar will now appear to the left of the chromatograph.
- The manual integration toolbar contains nine types of manual integration options. Four of the most commonly used options are **None** integration, **Drop** integration, **Based** integration, and **Rubber Band** integration.



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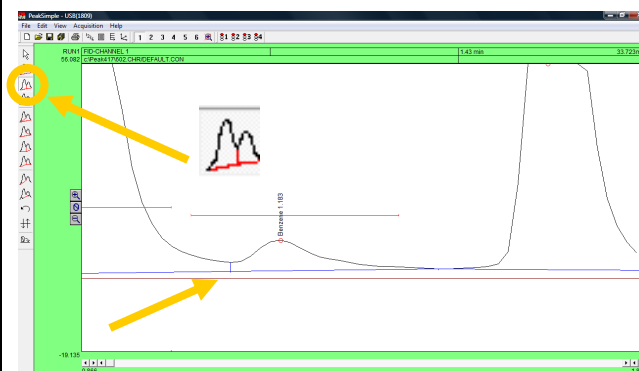
3. To make a baseline “ignore” a peak use the None integration tool. After opening chromatogram 602.CHR and the manual integration toolbar, zoom in on the baseline of the solvent peak and the smaller unrecognized peak immediately to its right. Click on the **None** integration tool in the manual integration toolbar with the mouse cursor and then click on the valley between the two peaks where they meet the baseline. The area of the small peak is now added to the solvent peak.



4. To undo the changes made to a chromatogram at any time simply click on the **Undo** integration tool in the manual integration toolbar. After selecting this tool all integration changes made to the chromatogram will be undone.



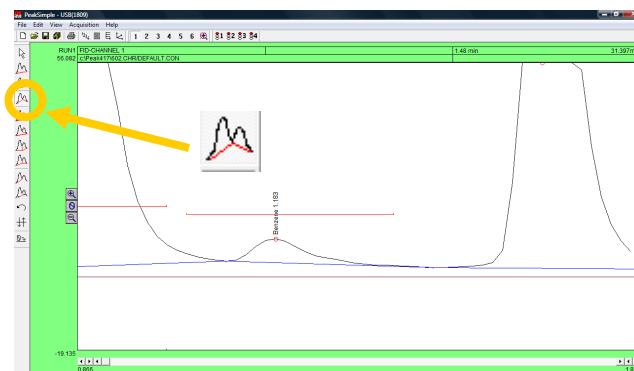
5. Click on the **Undo** tool with your mouse cursor and select the **Drop** integration tool to enable the dropping of the baseline below the two peaks. After selecting the Drop tool click where the valley of the peaks meet the baseline with the cursor. The baseline should now be dropped below the base of the peaks and a line should extend from it to the baseline.



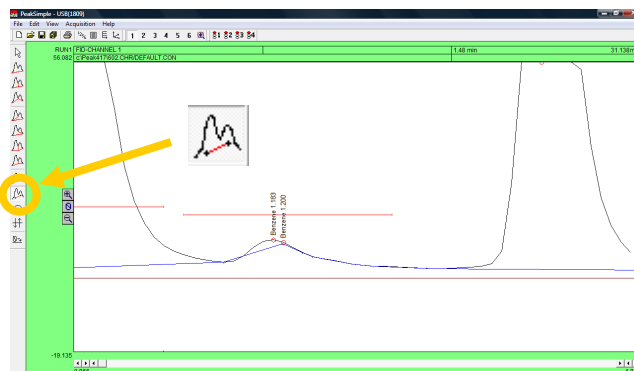
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6. After the manual integration between the two peaks is dropped use the **Based** integration tool to raise the baseline to the valley between the peaks. Once the Based integration tool is selected, click on the valley between the solvent peak and the smaller peak to its right with the mouse cursor. The baseline will now extend up to meet the valley of the two peaks.

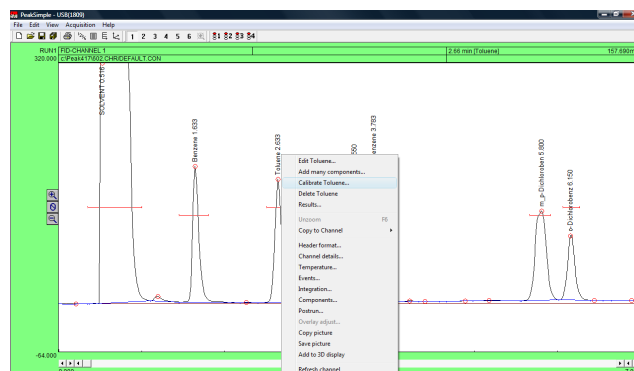


7. Once again click on the **Undo** tool in the manual integration toolbar to remove all changes done to the chromatogram. Select the **Rubber Band** integration tool to manually draw a baseline. Once the Rubber Band tool is selected take the mouse cursor and click on a part of the baseline. While holding down the left mouse button extend the line to another part of the baseline further to the right of the starting point and let go of the mouse button. The base line will now be drawn according to the line that was drawn using the Rubber Band integration tool.



Calibration

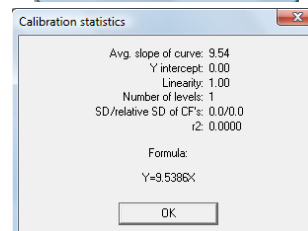
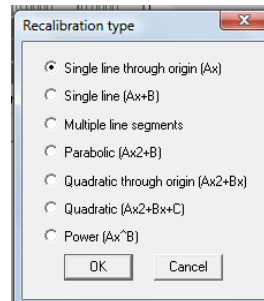
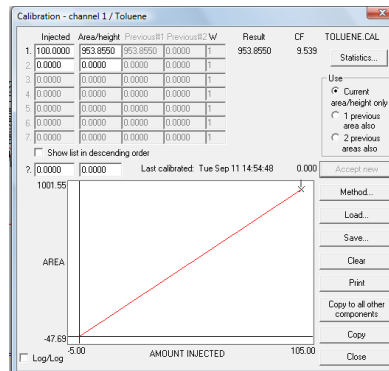
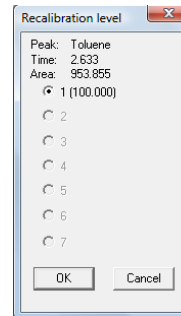
1. To turn the raw area of a peak into a real-world number the peak first needs to be calibrated. To calibrate the Toluene peak in chromatogram 602.CHR, open up the file and then right click using the mouse on the Toluene peak. After right clicking on Toluene select **Calibrate Toluene** from the resulting menu.



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- From the Recalibration level window click on the first level radio button **1 (100.000)** and then select **OK** with your mouse cursor.
- After selecting OK from the Recalibration level menu the Calibration menu for Toluene will pop up. Check to make sure the flashing asterisk on the calibration curve is on level 1 and then click on the **Accept New** button to the right of the window.
- Once the new data is accepted, click on the **Method** button immediately below the Accept New button. The Recalibration type window will now open allowing the user to select a method of calibration. By default the calibration type is set at Multiple Line Segments. Select the **Single line through origin (Ax)** radio button and then click on **OK** with the mouse cursor.
- After changing the method of calibration click on **Statistics** in the upper right hand corner of the Calibration level window. The Calibration statistics window will pop up revealing the statistics for the calibration of Toluene. Click **OK** with the mouse cursor to close the Calibration statistics window and then select **Close** from the Calibration window to finish calibrating Toluene.
- View the calibrated results in the Results screen by right-clicking on the chromatogram and selecting **Results**.



Results window showing a table of component data. Channel: 1. Buttons: Update, Save, Integration, Format, Close, Calibrate, Calibrate all, Copy, Copy results log, Clear results log, Show results log, Add to results log.

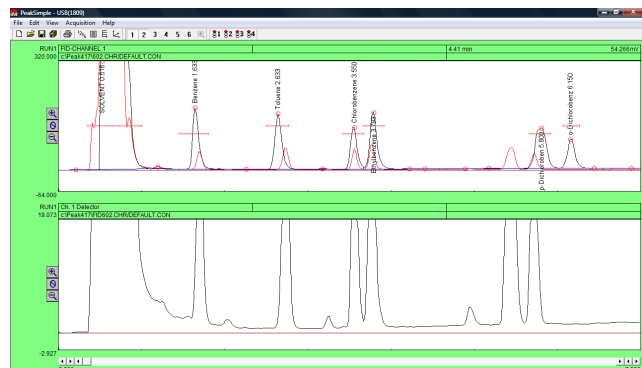
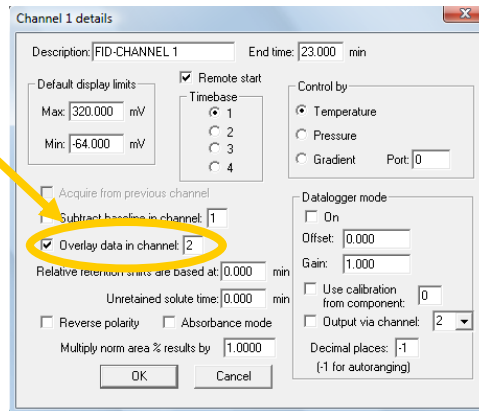
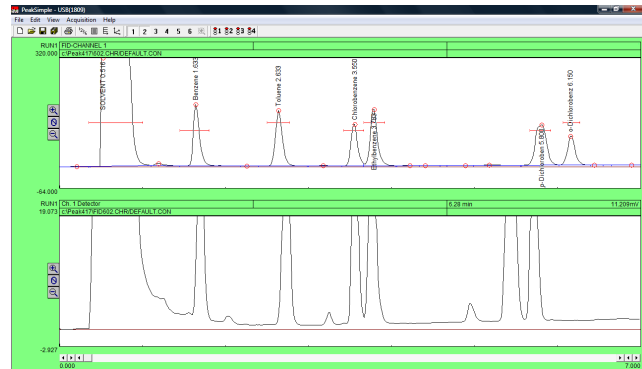
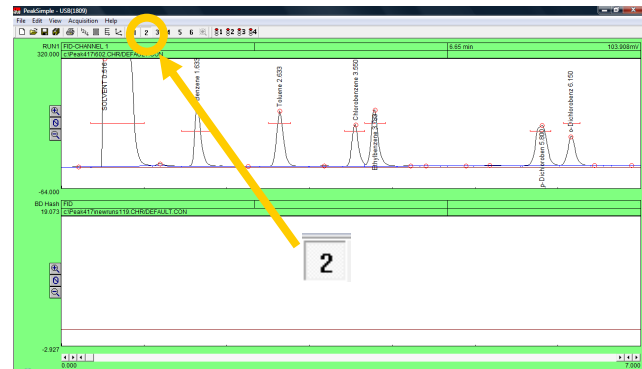
Component	Retention	Area	Height	External	Units
SOLVENT	0.016	71603.5420	8895.161	0.0000	%
Benzene	1.633	359.6270	180.764	100.0000	ppm
Toluene	2.633	953.8550	163.090	100.0000	ppm
Chlorobenzene	3.650	676.9720	122.832	72.1215	ppm
Dibromobenzene	3.763	998.4470	168.671	112.2659	ppm
m,p-Dichlorobenz	5.800	1093.8760	119.019	124.2345	ppm
o-Dichlorobenz	6.150	537.4520	95.187	54.6815	ppm
		76860.7715		963.3434	

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Overlay

1. To compare two or more chromatograms overlay them using PeakSimple. To overlay two chromatograms first open chromatogram 602.CHR and then click on the **2** button in the PeakSimple toolbar. A second chromatogram channel is now open in the PeakSimple window.
2. Once the second channel is open select **File** from the PeakSimple menu bar and then click on **Open**. The Load chromatogram file window will open up displaying a list of files to load. Select chromatogram **FID602.CHR** to load and then select the **2** channel radio button to load the chromatogram in the second channel.
3. Once FID602.CHR is open in the second channel right click using the mouse on the first channel and select **Channel Details** from the list of options.
4. After the Channel 1 details window appears on the screen locate the **Overlay data in channel** check box and select it. Look to the dialogue box to the right of the Overlay data in channel check box and insert the number **2** in place of the 1. Click on **OK** with the mouse cursor to exit the Channel 1 details window.
5. The chromatogram FID602.CHR is now in place overlaid on top of chromatogram 602.CHR in channel 1. Chromatogram 602.CHR is in black while FID602.CHR is in red.

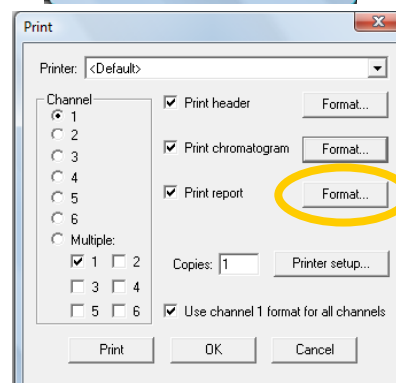
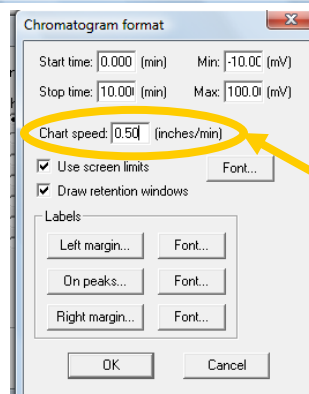
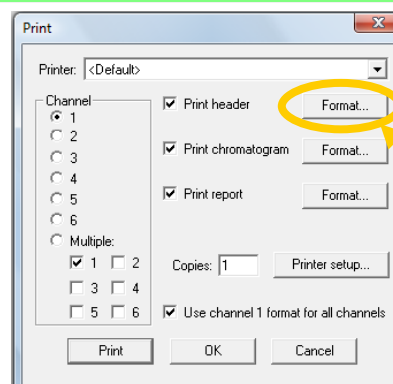
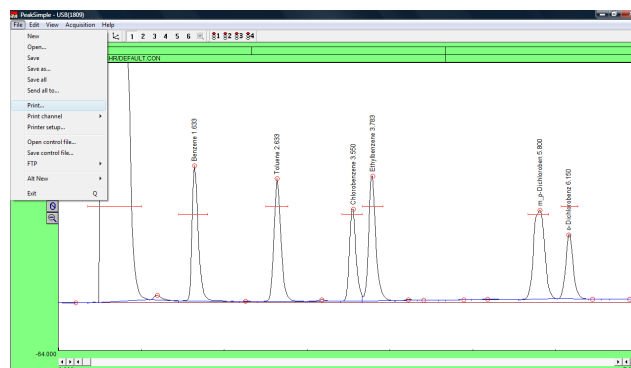


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Printing a Chromatogram

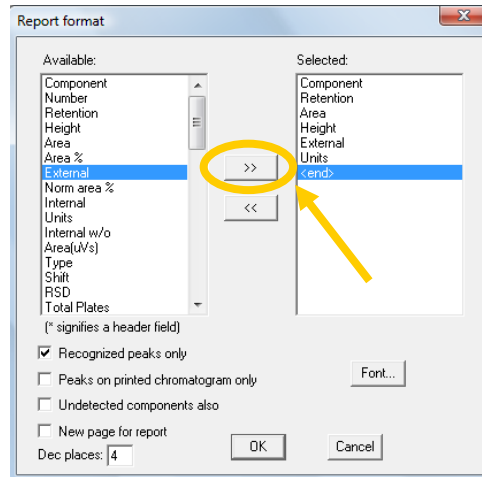
1. To print a chromatogram first open chromatogram 602.CHR. Once the chromatogram is open select **File** from the PeakSimple menu bar and then select **Print** from the drop-down menu.
2. The Print window will open and will allow the user to customize the printing of a chromatogram. Click on the **Format** button for the Print header to open up the Header format window. Add or delete any information in the window by clicking on the fields and inserting the desired information. Click on the **OK** button when all the desired information is inputted to close the window.
3. In the Print window click on the **Format** button for Print chromatogram to open up the Chromatogram format window. Locate the **Chart speed** dialogue box and insert the number of inches each minute on the chromatogram will take up when printed (for a nine minute run try **0.50** inches per minute). After the Chart speed is entered click on **OK** to exit the window.
4. In the Print window locate the Print report check box and click on the **Format** button to its right.



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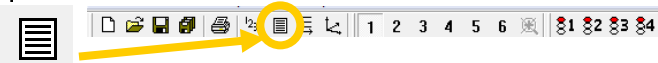
5. Once the Report format window is open click on **External** in the Available dialogue menu (on the left) and then click with the mouse cursor on the right facing arrow button to add External to the Selected dialogue box (on the right). After External is added to the Selected dialogue box click on **Units** with the mouse cursor and click on the right facing arrow button to add Units to the Selected dialogue box. Click on **OK** with the mouse cursor to exit out of the Report format window.



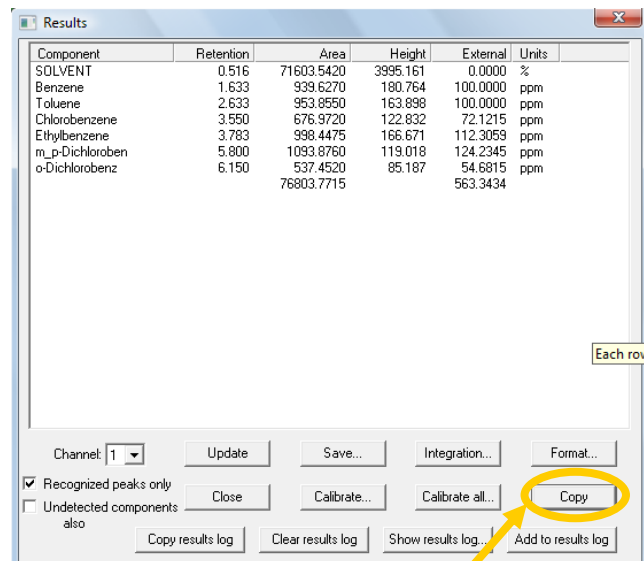
6. Select **Print** in the Print window to print the chromatogram or click on **OK** in the Print window to exit the window.

Exporting to Excel

1. In the PeakSimple toolbar click on the **Results** window button to open up the Results window. Once the Results window is open click on the **Copy** button to copy the results data to the Windows clipboard.



2. Make sure Microsoft Excel is loaded on the computer. If Excel is not loaded you can copy results data and chromatograms to Microsoft Word or PowerPoint. Open up Microsoft Excel by clicking with the mouse cursor on the **Start** button in the bottom left of the Windows screen and then **Programs** and then **Microsoft Excel** in the Windows Program menu.

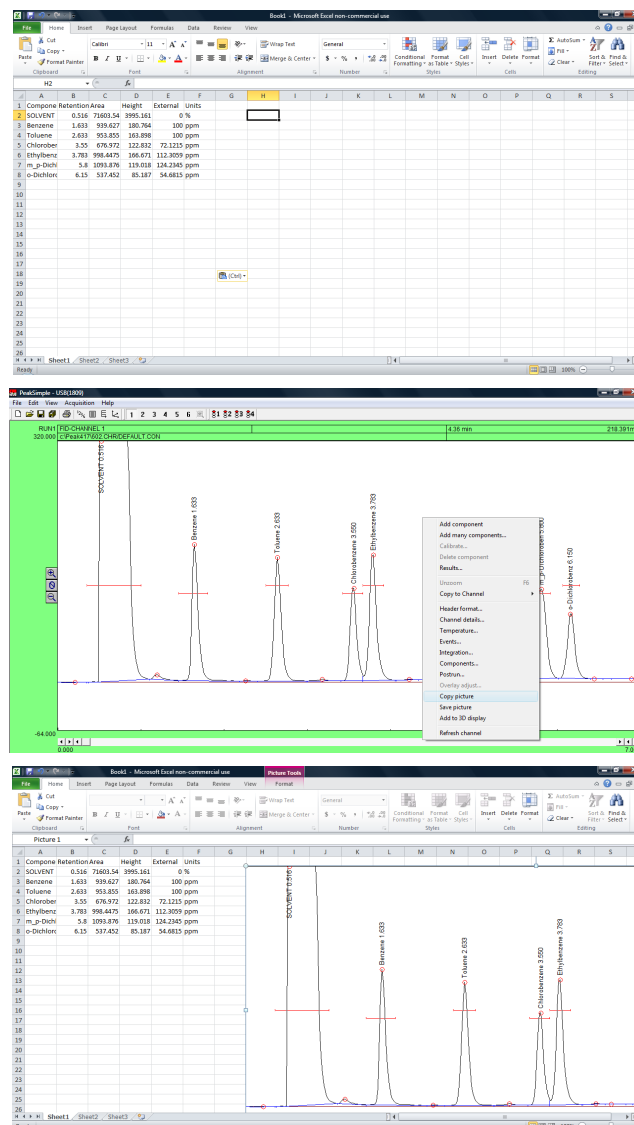


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3. Once Excel is opened select **Edit** from the Excel menu bar and then **Paste** from the drop down menu. The results data is now placed into the columns and rows of Excel. Using the mouse cursor, select a box to the right of the results data in the Excel spreadsheet. Go back into the PeakSimple program and hit **Close** to exit the Results window.

4. Right click with the mouse cursor anywhere on chromatogram 602.CHR and select **Copy picture** from the resulting menu. Go back into Excel and select **Edit** from the Excel menu bar and then **Paste** from the drop down menu. The PeakSimple chromatogram will now be displayed next to its results data in the rows and columns of Microsoft Excel.



This concludes the PeakSimple Basic Tutorial.

An Advanced Tutorial can be obtained by going to:
www.srigc.com

If you have questions or would like to place an order, call:
(310) 214-5092

SRI Tech Support 310-214-5092
www.srigc.com