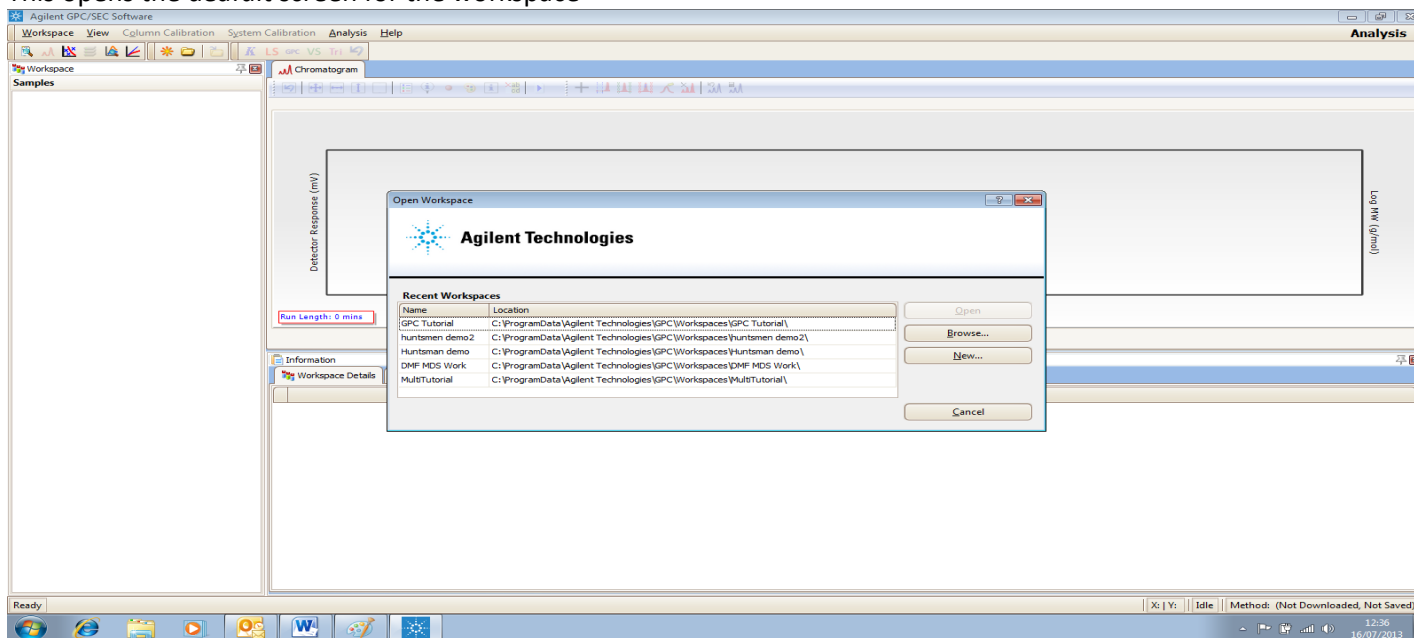


# GPC SOP

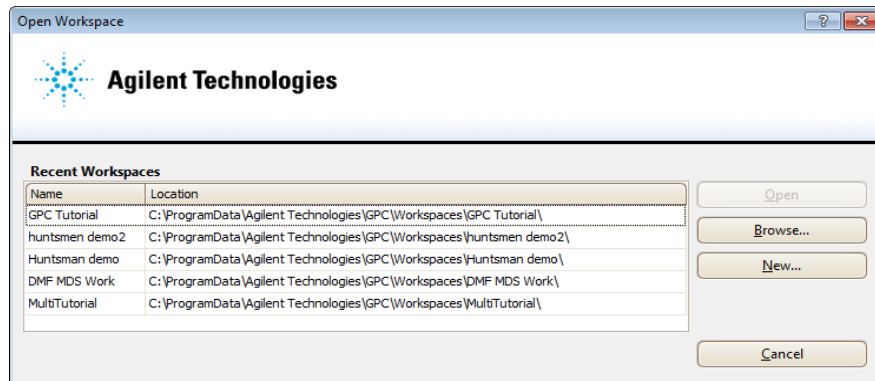
- 1) open the Agilent GPC by going to start all programs, then to the Agilent technologies , Agilent GPC and select



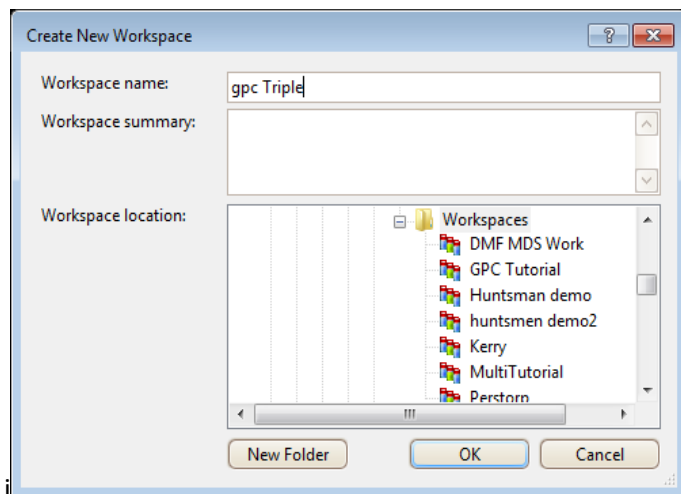
This opens the default screen for the workspace



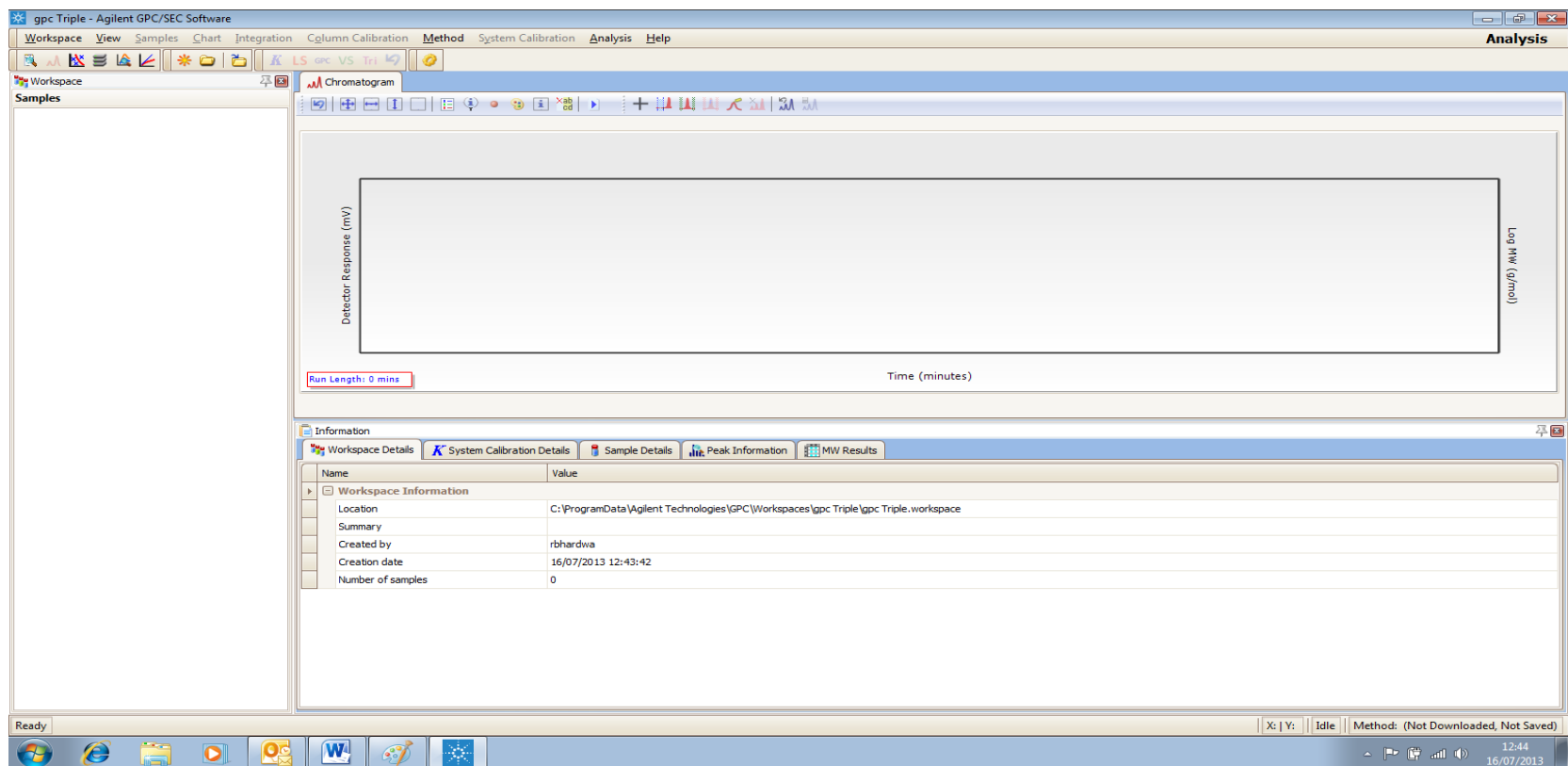
To create a new workspace for your analysis, click the tab New



You will now be prompted with the window below and you can give a name to your workspace e.g. gpc Triple.



Click OK



# Instrument Control

The *Instrument Control View* is accessed from the *View* menu, Figure 3.

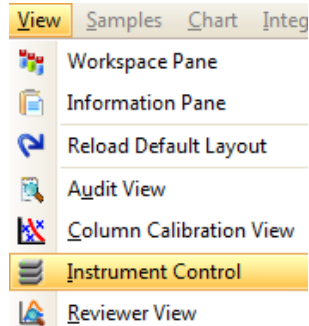


Figure 3 Accessing the Instrument Control view from the menu

Alternatively,



Now Click on the Icon and this opens the above window. Now select your instrument by high lighting the Icon gpc Triple & OK This will take a few moments to populate with the instrument control window as seen below (Figure 4).



Select the Instrument to connect to and click ok, upon connection the software will automatically synchronize with the current system parameters.

## 2.1 Overview of Instrument Control View

The Instrument Control View has two main sections, the **Instrument Dashboard** and the **Injection Sequence**.

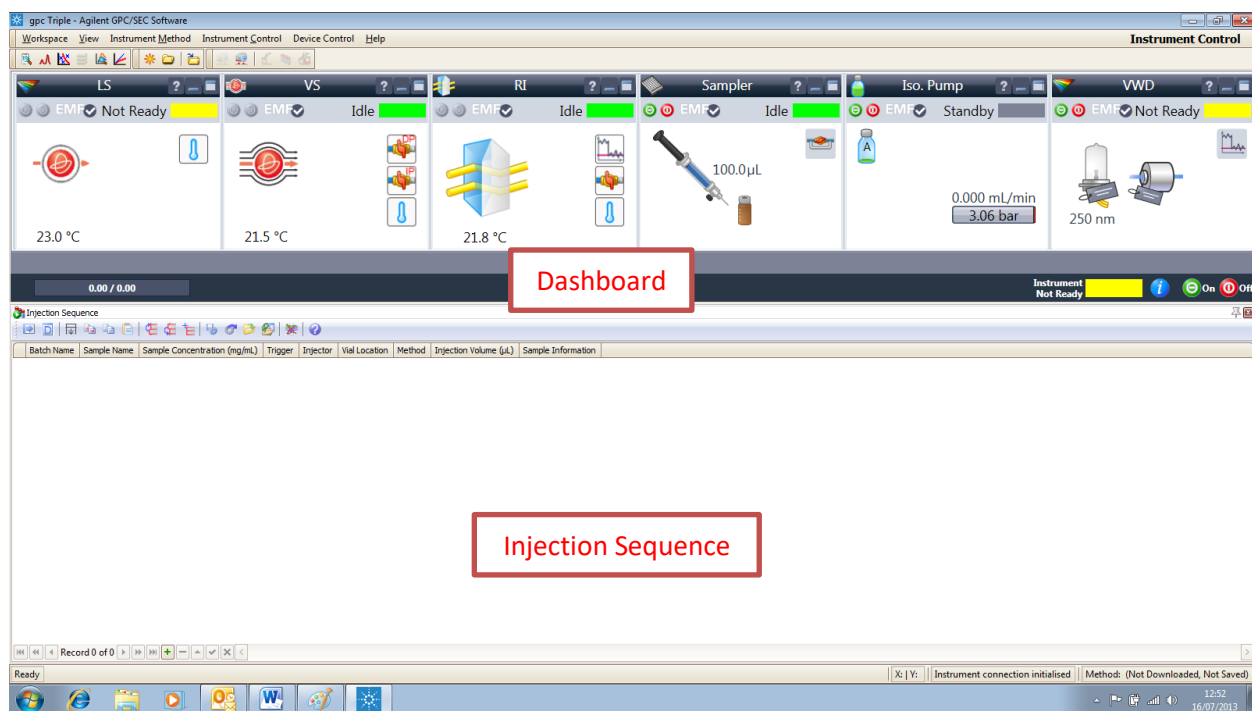
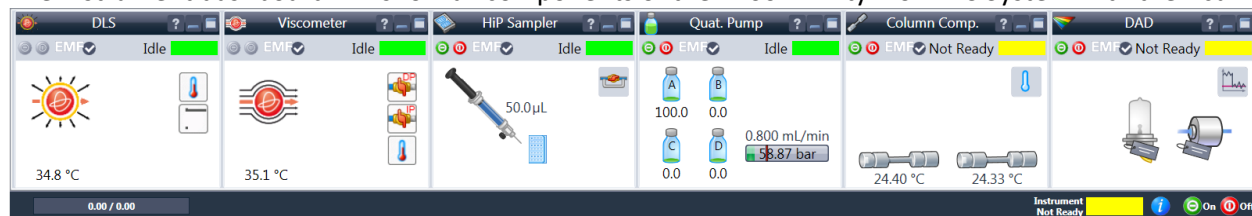


Figure 4

### Instrument Dashboard

The Instrument dashboard will show all components of the 1260 Infinity Bio-MDS System with their current status.



The dashboard will highlight the component status with a colored status bar. When in a **Ready** state a green bar will appear, a **Not Ready** state is yellow; if there is an **Error** they will appear red. The global status is shown on the bottom right.

Placing the mouse cursor over the yellow bar will provide information on why the system is **Not Ready**, i.e. if the column oven is heating.

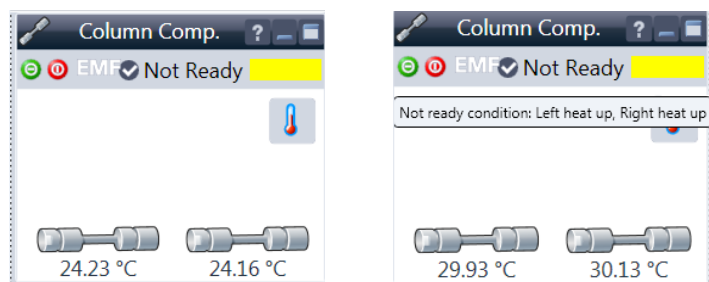
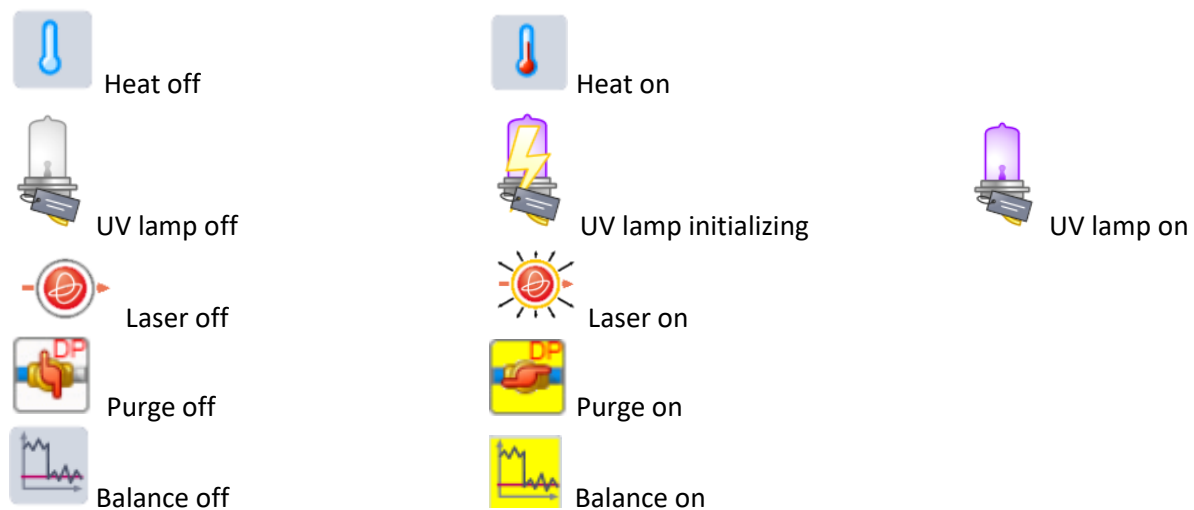


Figure 1 Dashboard tiles in *Not Ready* state

Icons show what action(s) the detector is currently performing:



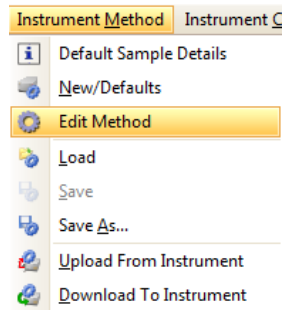
More detailed information can be seen by maximizing the dashboard tiles

## Purge the pump line to remove old solvent. (Necessary when changing the solvent/ Bubble in line)

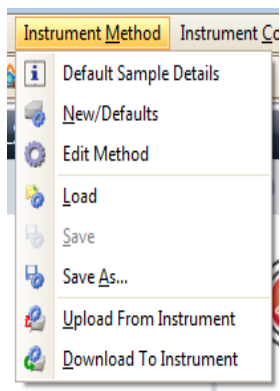
- 1) Open the pump purge valve anticlockwise.( Only loosen it, don't open it complete.
- 2) Right click on the Quat pump and give flow of 5 ml, select all 4 ports and increase the flow gradient to 100 from advance menu → Click OK.
- 3) While purging the pressure of the pump should be near to Zero, if pressure of the pump is high during the purge, frit needs replacement.
- 4) Select port one by one and purge at least for 2 minutes each port.
- 5) Once purging is done reduce the flow to 0.1 ml then reduce the flow gradient to 0.1

## Creating instrument methods/ Loading any existing method.

Upon connection the software will automatically synchronize with the current system parameters. Edit the method from the *Instrument Method – Edit Method*



Or in this case Select New Method; you'll now be prompted with a new window as seen below:



A screenshot of the 'Instrument Method' dialog box, specifically for the 'RI (G7801A)' module. The dialog has a tabbed interface with 'RI' selected. The settings are organized into several sections:

- Temperature:** Radio buttons for 'Not controlled' (selected) and '30 ± 0.1 °C'.
- Sampling Rate:** A dropdown menu set to '1 Hz'.
- Purge Time:** A numeric input field set to '60' s.
- Stop time:** Radio buttons for 'As pump/injector' (selected) and '10.00 ± 0.01 min'.
- Post time:** Radio buttons for 'Off' (selected) and '0.00 ± 0.01 min'.
- Advanced:**
  - Signal Polarity:** Radio buttons for 'Positive (+)' (selected) and 'Negative (-)'.
  - Autoczero:** A checkbox for 'Prerun'.
- Enable Analysis:** Radio buttons for 'With any temperature' and 'When temperature is within' (selected), with a temperature range input set to '± 1.0 °C'.
- Automatic Purge:** A checkbox for 'Automatic purge' and input fields for 'Purge time' (60 s) and 'Wait time' (0.00 min).
- Advanced Parameters:** Input fields for 'Zero offset (mV)' (0), 'LED power (% of Full Scale)' (100), 'Signal gain' (1.00), and 'Signal time constant' (1.0 s).

At the bottom of the dialog are buttons for 'Help', 'OK and Download', 'OK', and 'Cancel'.

Now populate each instrument module starting from the RI detector.



## Refractive Index Detector (RI)

The screenshot shows the 'Instrument Method' dialog for the 'RI (G7801A)' detector. The dialog is divided into several sections:

- Temperature:** Includes a radio button for 'Not controlled' (selected) and a temperature input field set to 30 °C.
- Sampling Rate:** A dropdown menu set to 1 Hz.
- Purge Time:** An input field set to 60 s.
- Stop time:** Includes a radio button for 'As pump/injector' (selected) and a time input field set to 10.00 min.
- Post time:** Includes a radio button for 'Off' (selected) and a time input field set to 0.00 min.
- Advanced:**
  - Signal Polarity:** Radio buttons for 'Positive (+)' (selected) and 'Negative (-)'.
  - Autozero:** A checkbox for 'Prerun'.
  - Enable Analysis:** Radio buttons for 'With any temperature' and 'When temperature is within' (selected). The latter has a temperature range input field set to ± 1.0 °C.
  - Automatic Purge:** A checkbox for 'Automatic purge'.
  - Purge time:** An input field set to 60 s.
  - Wait time:** An input field set to 0.00 min.
  - Advanced Parameters:**
    - Zero offset (mV):** An input field set to 0 mV.
    - LED power (% of Full Scale):** An input field set to 100.
    - Signal gain:** An input field set to 1.00.
    - Signal time constant:** An input field set to 1.0 s.

At the bottom of the dialog are buttons for 'Help', 'OK and Download', 'OK', and 'Cancel'.

### Important parameters

Setting	Comments
Temperature	<i>Not controlled</i> will turn the heaters off. Setting a temperature will turn the heaters on and the RI will start to heat to that temperature, 30 – 60 °C
Stoptime	Set <i>As Pump/Injector</i> to ensure collection time synchronization
Enable Analysis	If set to <i>When temperature is within</i> then the run will not start until the RI detector temperature is within those limits

## Viscometer (VS)

The screenshot shows the 'Instrument Method' dialog box for the 'VS (G7802A)' method. The 'VS' tab is selected. The settings are as follows:

- Temperature:** ☒ Not controlled, ☐ 30 °C
- Sampling Rate:** 1 Hz
- Purge Time:** 60 s
- Stop time:** ☒ As pump/injector, ☐ 10.00 min
- Post time:** ☒ Off, ☐ 0.00 min
- Advanced:**
  - DP Autozero:** ☐ Prerun, ☐ Postrun
  - Enable Analysis:** ☐ With any temperature, ☒ When temperature is within ± 1.0 °C
  - Automatic Purge:** ☐ DP Automatic purge, ☐ IP Automatic purge
  - Purge time (secs):** 60 s
  - Wait time:** 0.00 min

Buttons at the bottom: Help, OK and Download, OK, Cancel.

### Important parameters

Setting	Comments
Temperature	<i>Not controlled</i> will turn the heaters off. Setting a temperature will turn the heaters on and the Viscometer will start to heat to that temperature, 30 – 60 °C
Purge Time	A Viscometer has larger internal volumes than standard detectors, will require longer purges
Stoptime	Set <i>As Pump/Injector</i> to ensure collection time synchronization
Enable Analysis	If set to <i>When temperature is within</i> then the run will not start until the Viscometer detector temperature is within those limits

## Light Scattering Detector (LS)

The screenshot shows the 'Instrument Method' dialog box for the 'LS (G7803A)' detector. The 'LS' tab is selected. The settings are as follows:

- Temperature:** ☒ Not controlled, ☐ 30 °C
- Sampling Rate:** 1 Hz
- Stop time:** ☒ As pump/injector, ☐ 10.00 min
- Post time:** ☒ Off, ☐ 0.00 min
- Advanced Laser:** ☒ Laser on required for acquisition, Laser power (%) 100 %
- Enable Analysis:** ☐ With any temperature, ☒ When temperature is within ± 1.0 °C

Buttons at the bottom: Help, OK and Download, OK, Cancel.

### Important parameters

Setting	Comments
Temperature	<i>Not controlled</i> will turn the heaters off. Setting a temperature will turn the heaters on and the LS will start to heat to that temperature, 30 – 60 °C
Stoptime	Set <i>As Pump/Injector</i> to ensure collection time synchronization
Laser	If selected the run will not commence until the laser is on and ready. The laser power can be adjusted to suit analysis. <b>Important</b> , the detector constants must be recalculated if the laser power is changed

## Enable Analysis

If set to *When temperature is within* then the run will not start until the LS detector temperature is within those limits

## Now the pump (Quat Pump)

Instrument Method

RI VS LS Iso. Pump Sampler VWD

Iso. Pump (G1310B)

Flow: 1.000 mL/min

Solvent A: THF

Pressure Limits: Min: 0.00 bar Max: 120.00 bar

Stoptime: ☒ As Injector/No Limit 1.00 min ☐ Off 1.00 min

Posttime: ☐ Off 1.00 min

Advanced

Timetable (empty)

☐ function centric view

Time [min]	A [%]	Flow [mL/min]	Max Pressure Limit [bar]
0.00	100.0	1.000	120.00

Add Remove Clear All Clear Empty Cut Copy Paste Shift Times min

Help OK and Download OK Cancel

## Setting

## Comments

### Flow

Set the flow rate (mL/min)

### Solvents

Set the solvent composition and what channels should be employed.

**Important**, SEC is always isocratic. Enter the buffer name and it will be stored with the sample.

### Pressure Limits

SEC columns typically have lower pressure limits than standard HPLC. Refer to the column guide.

### Stoptime

The length to collect data

### Posttime

The length after the data is collected before the next injection starts. This is useful when using a Viscometer to allow the delay peak through.

Compressibility	To ensure a smooth flow, enter the correct compressibility setting. For aqueous 46 is recommended.
Maximum Flow Gradient	Reduce this to 0.5 mL/min <sup>2</sup> to increase column lifetime and ensure detector stability.

## Now the Auto Sampler (Sampler)

The screenshot shows the 'Instrument Method' dialog box for the 'Sampler (G1329B)'. The 'Sampler' tab is selected. The 'Injection Mode' section has 'Injection volume' set to 100.00 µL, with 'Standard injection' selected. The 'Needle wash' section has 'Location' set to an empty field. The 'Stoptime' section has 'As Pump/No Limit' selected, and the 'Posttime' section has 'Off' selected. The 'Advanced' section has 'Auxiliary' settings: 'Draw speed' at 200 µL/min, 'Eject speed' at 200 µL/min, and 'Draw position' at 0.0 mm. The 'High throughput' section has 'Enable Optimization' checked, with 'Prefetch Vial' selected and 'Overlap Injection Cycle' set to 0.00 minutes after injection. The bottom of the dialog has buttons for 'Help', 'OK and Download', 'OK', and 'Cancel'.

Setting	Comments
Injection volume	Set the volume to be injection onto the column
Stoptime	Set <i>As Pump/Injector</i> to ensure collection time synchronization

## Column compartment (TCC)

Instrument Method

Viscometer | DLS | Quat. Pump | HiP Sampler | **Column Comp.** | DAD

**Column Comp. (G1316C)**

**Temperature**

Left:

☐ Not Controlled

☒ 30.0 °C

☐ As Detector Cell

Right:

☐ Not Controlled

☐ 20.0 °C

☐ As Detector Cell

☒ Combined

**Stoptime**

☒ As Pump/Injector

☐ 1.00 min

**Posttime**

☒ Off

☐ 1.00 min

**Advanced**

Enable Analysis

☐ when front door open

Left:

☐ With any temperature

☒ When temperature is within

± 0.8 °C

Right:

☐ With any temperature

☒ When temperature is within

± 0.8 °C

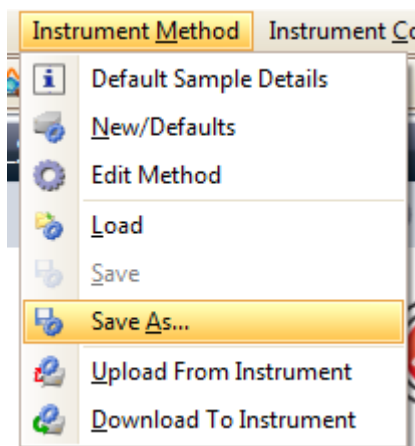
Timetable (empty)

Help OK and Download OK Cancel

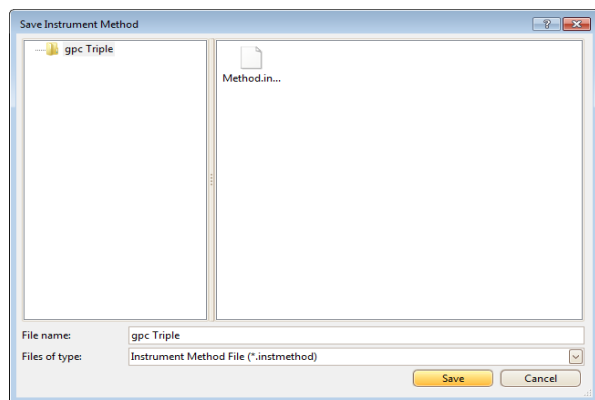
### Important parameters

Setting	Comments
Temperature	If a temperature is set, the oven still requires turning on. On the dashboard tile right-click and turn oven on. Select <i>Combined</i> to ensure column oven temperature consistent across oven
Stoptime	Set <i>As Pump/Injector</i> to ensure collection time synchronization
Enable Analysis	If set to <i>When temperature is within</i> then the run will not start until the column compartment temperature is within those limits

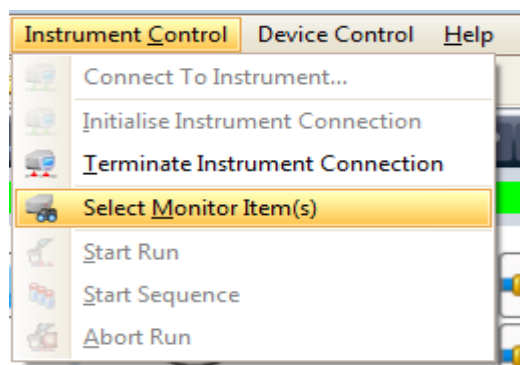
Once all parameters have been set the parameters can be sent to the instrument by selecting *OK and Download*. The method can then be saved *Instrument Method – Save As*. The method that is currently on the system is displayed on the lower right of the screen “see below”



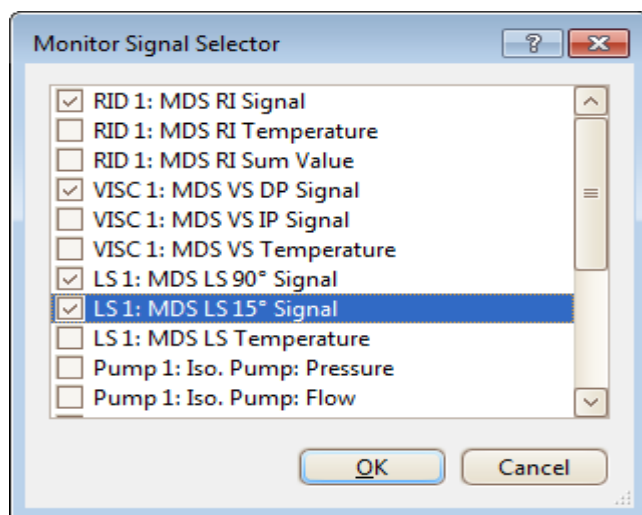
Now go to Instrument Method and click Save As..



High Light the gpc Triple Method and type in the file name and Save.



Now go to Instrument Control and select Monitor Items(s)

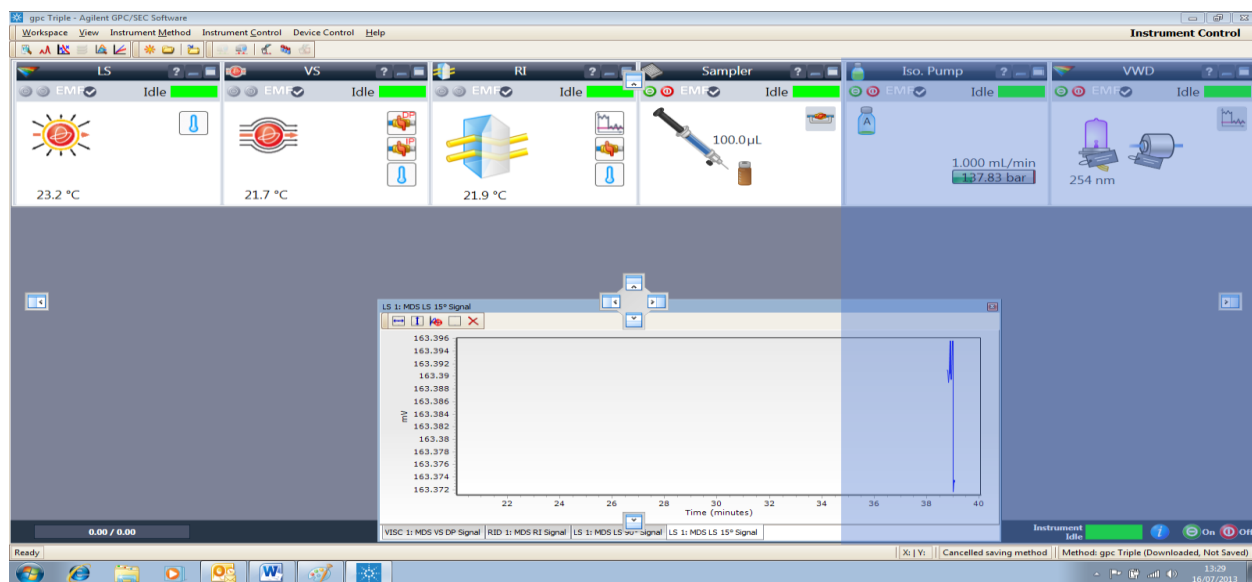


Place a tick in the appropriate box(s) to see the signals from these modules. Then drag the monitor signals screen to the bottom right hand corner by clicking on the left hand side of the mouse and fixing the screen to allocation tabs in the centre of the window below.

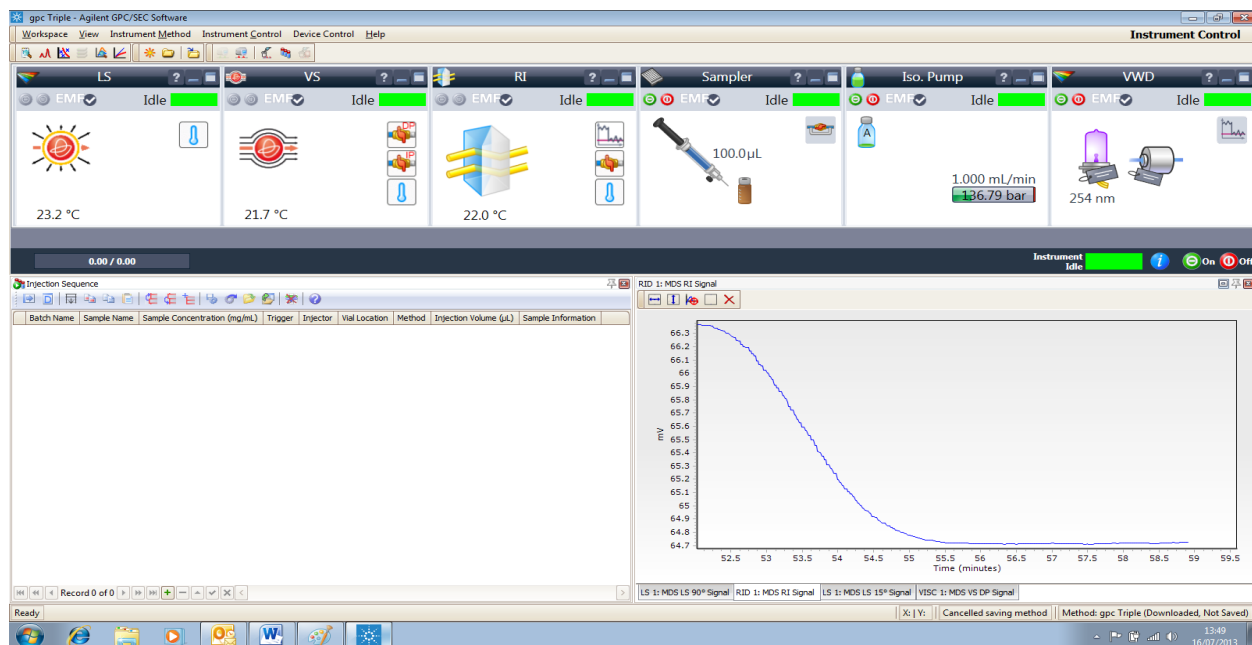


## Preparing the Detector

- Once the desired pump flow is reached and column is saturated, now RID and Visco Detector needs to be stabilised.
- Maximise the RID, LS and Visco Pane to see the detector values.
- Right click on the RI and purge the RI Detector reference cell for 10 minutes and repeat this step 3 times.
- Purge the Visco DP and Purge Visco IP 3 times to 10 minutes each.
- Autozero the RI and Visco both.
- Once the detectors and all the modules are ready and baseline is stabilised, system is ready for further use.
- If the system is completely stabilised and no run is in progress, Waste flow can be recycled if necessary.
- **Reminder: remove the waste tubing from the Solvent bottle before starting the sequence. (if Recycle is done)**



## Creating the Sequence.




Now we need to input the samples that are going to be collected. This is done in the Injection Sequence Screen.

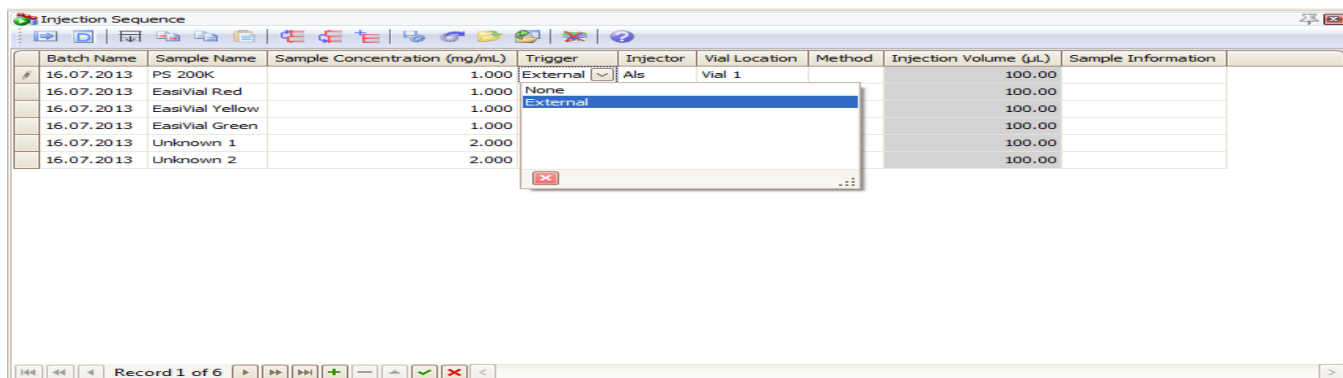
Click on the green button  at the bottom of the Injection Sequence screen and the following window pops up.

Injection Sequence

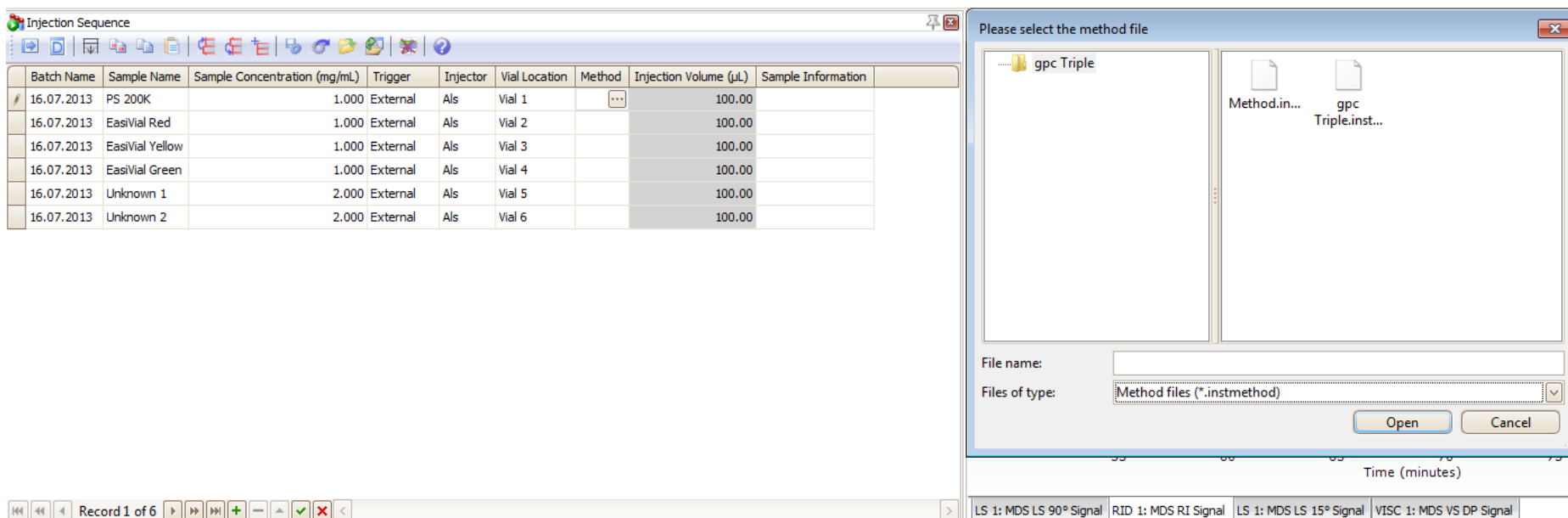
Batch Name	Sample Name	Sample Concentration (mg/mL)	Trigger	Injector	Vial Location	Method	Injection Volume (μL)	Sample Information
▶ 16.07.2013		1.000	External	Als	Vial 1		100.00	

Record 1 of 1

This can be populated by the number of samples that are going to be collected, in this case 6 samples by pressing the  button 6 times. Click under the Trigger tab and select External if autosampler is connected for each sample.



Then Click under the Method Tab next to the Vial location tab and the screen next to the injection sequence below will pop up.



High Light the gpc Triple Instrument Method and click Open to load the method.

Injection Sequence

Batch Name	Sample Name	Sample Concentration (mg/mL)	Trigger	Injector	Vial Location	Method	Injection Volume (μL)	Sample Information
16.07.2013	PS 200K	1.000	External	Als	Vial 1	...	100.00	
16.07.2013	EasiVial Red	1.000	External	Als	Vial 2		100.00	
16.07.2013	EasiVial Yellow	1.000	External	Als	Vial 3		100.00	
16.07.2013	EasiVial Green	1.000	External	Als	Vial 4		100.00	
16.07.2013	Unknown 1	2.000	External	Als	Vial 5		100.00	
16.07.2013	Unknown 2	2.000	External	Als	Vial 6		100.00	

Record 1 of 6

Please select the method file

gpc Triple

Method.in... gpc Triple.instmethod

File name: gpc Triple

Files of type: Method files (\*.instmethod)

Open Cancel

Time (minutes)

LS 1: MDS LS 90° Signal RID 1: MDS RI Signal LS 1: MDS LS 15° Signal VISC 1: MDS VS DP Signal

Injection Sequence

Batch Name	Sample Name	Sample Concentration (mg/mL)	Trigger	Injector	Vial Location	Method
16.07.2013	PS 200K	1.000	External	Als	Vial 1	C:\ProgramData\Agilent Technologies\GPC\Instruments\gpc Triple\gpc Trip
16.07.2013	EasiVial Red	1.000	External	Als	Vial 2	
16.07.2013	EasiVial Yellow	1.000	External	Als	Vial 3	
16.07.2013	EasiVial Green	1.000	External	Als	Vial 4	
16.07.2013	Unknown 1	2.000	External	Als	Vial 5	
16.07.2013	Unknown 2	2.000	External	Als	Vial 6	

Record 1 of 6

Copy down the method to each sample as shown below and select Icon




Injection Sequence

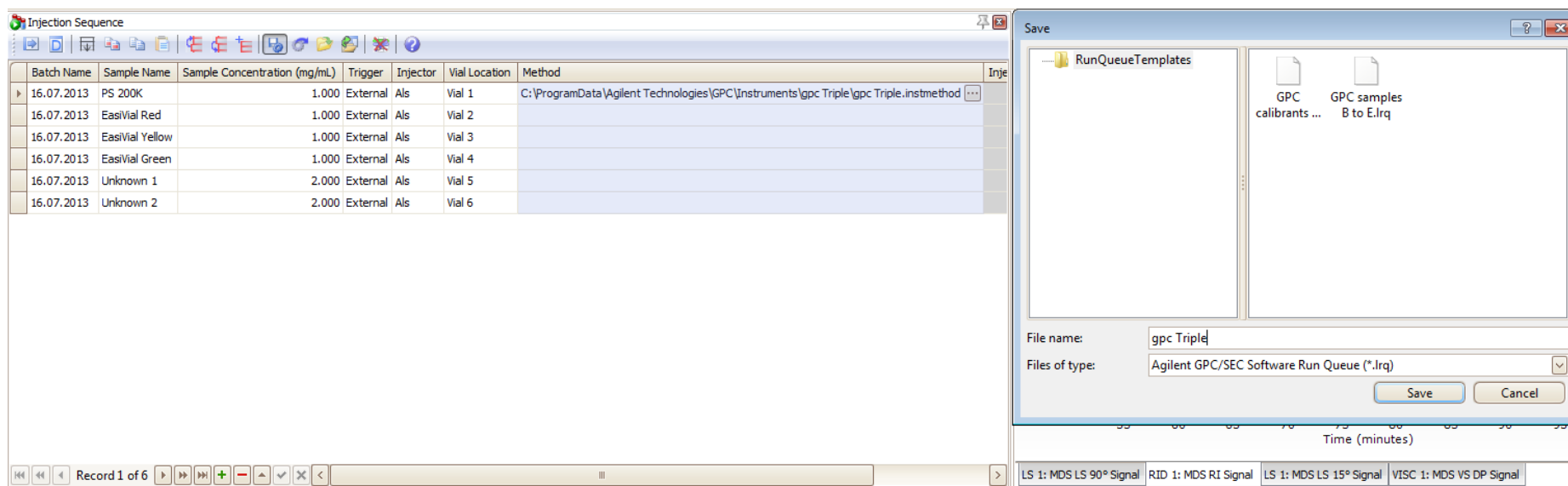
Batch Name	Sample Name	Sample Concentration (mg/mL)	Trigger	Injector	Vial Location	Method	Inje
16.07.2013	PS 200K	1.000	External	Als	Vial 1	C:\ProgramData\Agilent Technologies\GPC\Instruments\gpc Triple\gpc Triple.instmetho	
16.07.2013	EasiVial Red	1.000	External	Als	Vial 2	C:\ProgramData\Agilent Technologies\GPC\Instruments\gpc Triple\gpc Triple.instmetho	
16.07.2013	EasiVial Yellow	1.000	External	Als	Vial 3	C:\ProgramData\Agilent Technologies\GPC\Instruments\gpc Triple\gpc Triple.instmetho	
16.07.2013	EasiVial Green	1.000	External	Als	Vial 4	C:\ProgramData\Agilent Technologies\GPC\Instruments\gpc Triple\gpc Triple.instmetho	
16.07.2013	Unknown 1	2.000	External	Als	Vial 5	C:\ProgramData\Agilent Technologies\GPC\Instruments\gpc Triple\gpc Triple.instmetho	
16.07.2013	Unknown 2	2.000	External	Als	Vial 6	C:\ProgramData\Agilent Technologies\GPC\Instruments\gpc Triple\gpc Triple.instmetho	

Record 1 of 6

## Injection Sequence

This injection sequence can now be saved by clicking on Icon  and typing the file name gpc Triple as shown below  
Click Save

This section enables definition of all samples and/or calibrants to be injected into the system. It is good practice to include as much information as is known as this information is stored within the sample data file and can always be referred to at a later date



The screenshot shows the 'Injection Sequence' window with a table of injection data and a 'Save' dialog box open over it.








Batch Name	Sample Name	Sample Concentration (mg/mL)	Trigger	Injector	Vial Location	Method
16.07.2013	PS 200K	1.000	External	Als	Vial 1	C:\ProgramData\Agilent Technologies\GPC\Instruments\gpc Triple\gpc Triple.instrmethod
16.07.2013	EasiVial Red	1.000	External	Als	Vial 2	
16.07.2013	EasiVial Yellow	1.000	External	Als	Vial 3	
16.07.2013	EasiVial Green	1.000	External	Als	Vial 4	
16.07.2013	Unknown 1	2.000	External	Als	Vial 5	
16.07.2013	Unknown 2	2.000	External	Als	Vial 6	

The 'Save' dialog box is open, showing the file name 'gpc Triple' and the file type 'Agilent GPC/SEC Software Run Queue (\*.lrq)'. The 'Save' button is highlighted.

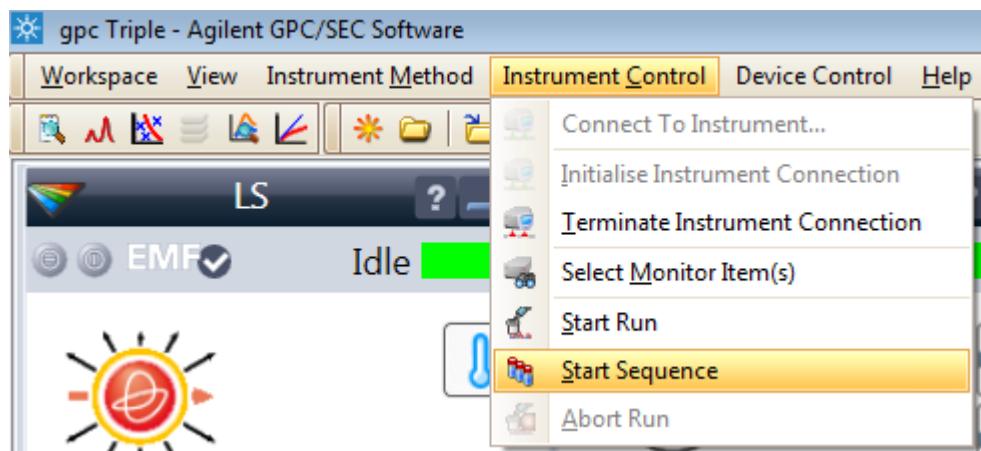
Below the table, there is a status bar showing 'Record 1 of 6' and a time axis labeled 'Time (minutes)' with a scale from 50 to 90. At the bottom, there are signal labels: 'LS 1: MDS LS 90° Signal', 'RID 1: MDS RI Signal', 'LS 1: MDS LS 15° Signal', and 'VISC 1: MDS VS DP Signal'.

## Example Injection Sequence

## Key icons

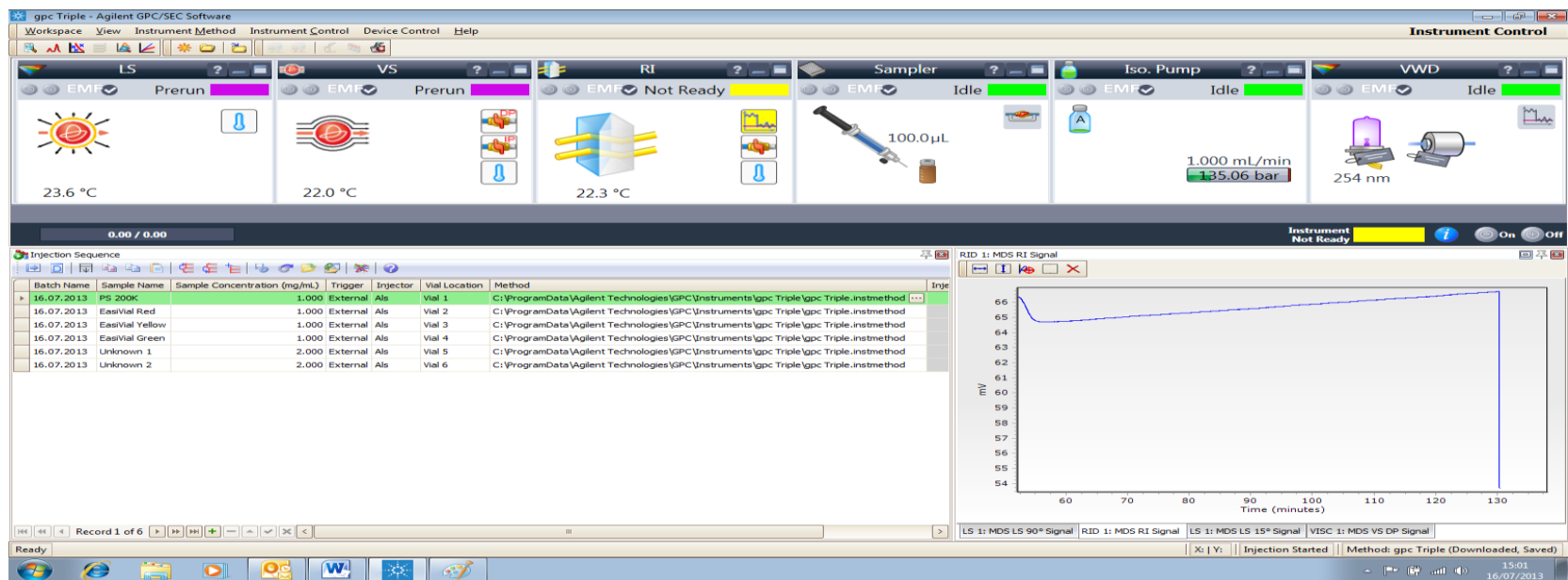
Icon	Command	Description
	Append	Add a single line to injection sequence
	Delete	Delete highlighted row from injection sequence
	Add Multiple Runs	Displays dialog to define number of samples to add to sequence
	Promote Run	Moves the selected run up one row in the sequence
	Demote Run	Moves the selected run down one row in the sequence
	Save Injection Sequence	Displays Dialog in which the sequence can be named and saved
	Open Injection Sequence	Load an existing injection sequence - <u>replacing</u> the current

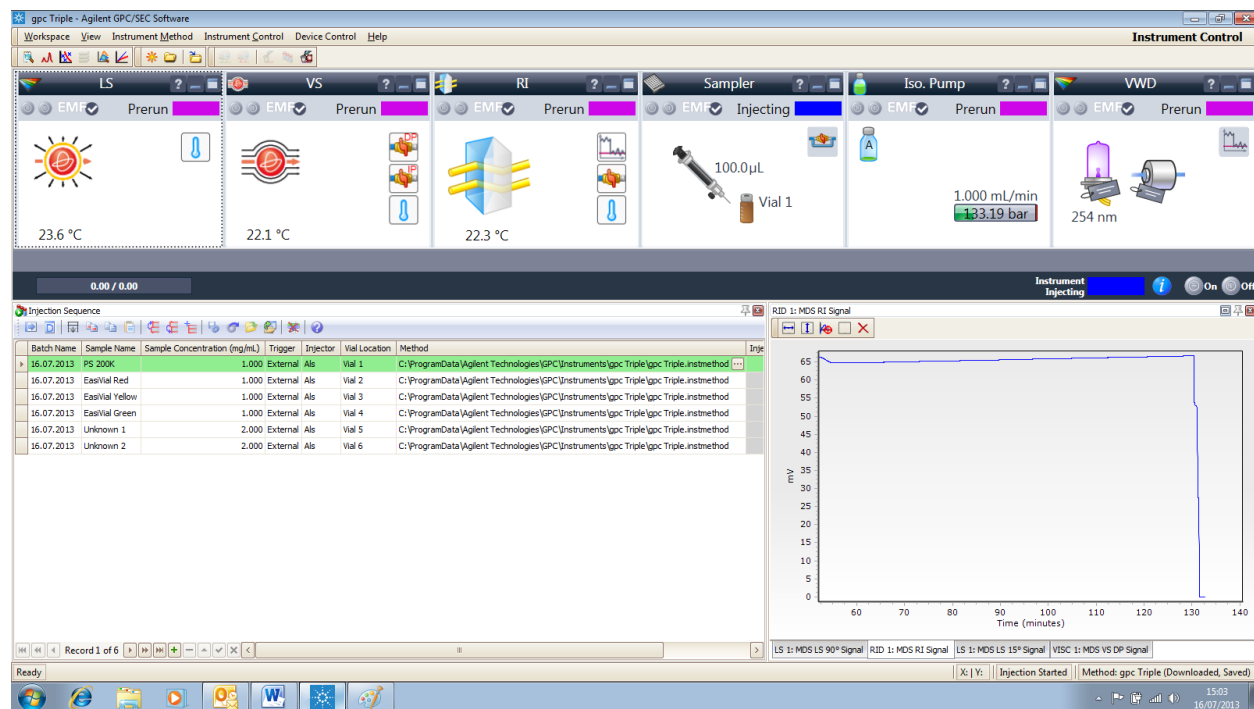
Now go to Instrument Control tab and click Start Sequence. This will start the data collection of the 6 samples.

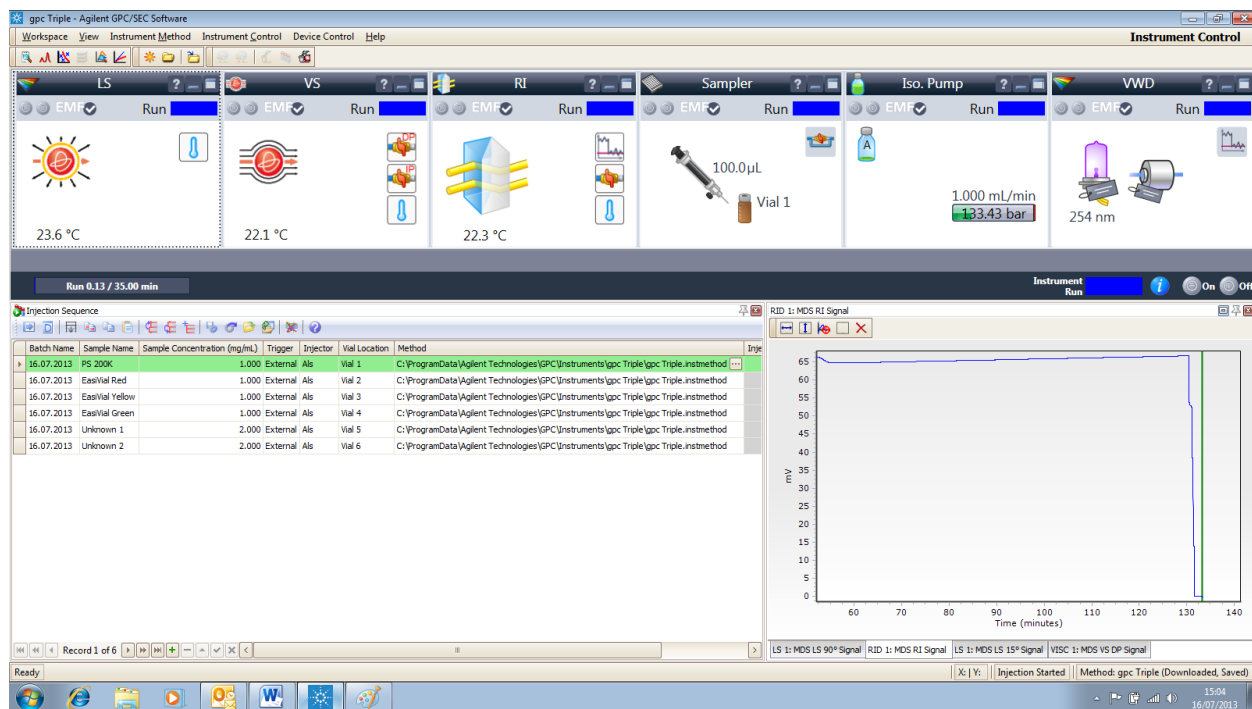


The following screen will be shown









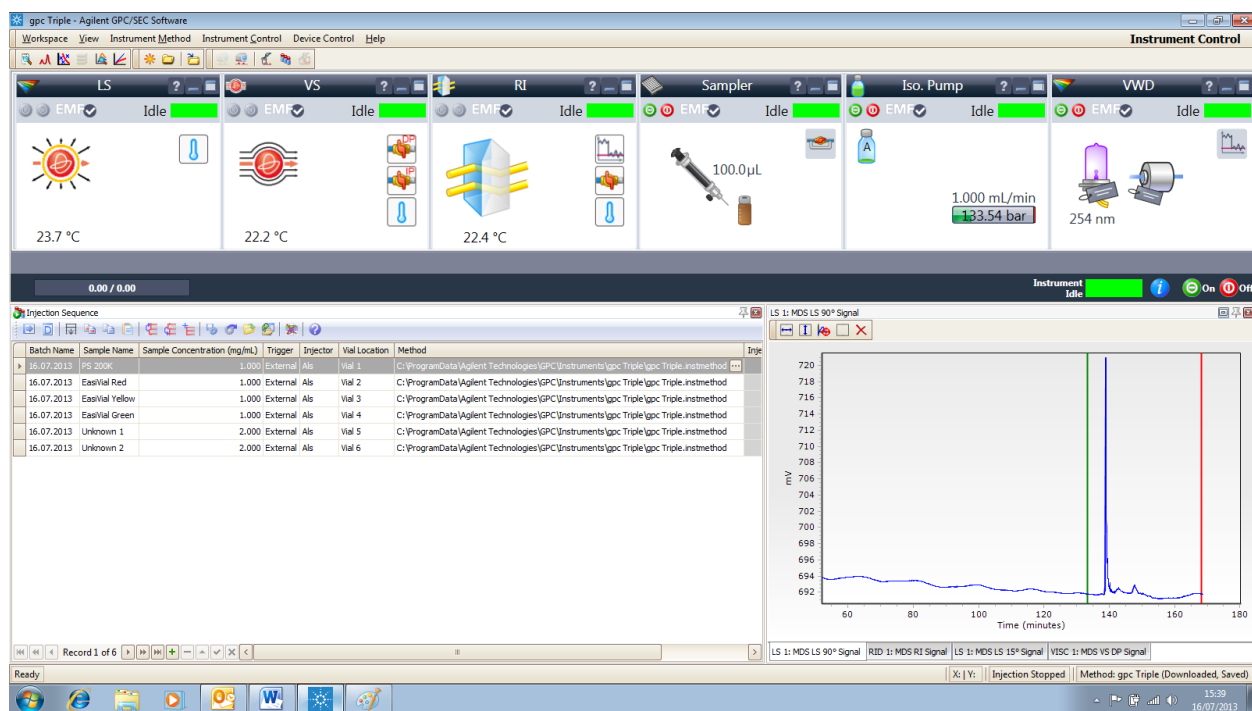


Figure2

The 1<sup>st</sup> sample has finished highlighted in grey. The system will continue until the last sample has been injected.


The *Injection Sequence* will always run in order, starting from the first non-completed run.

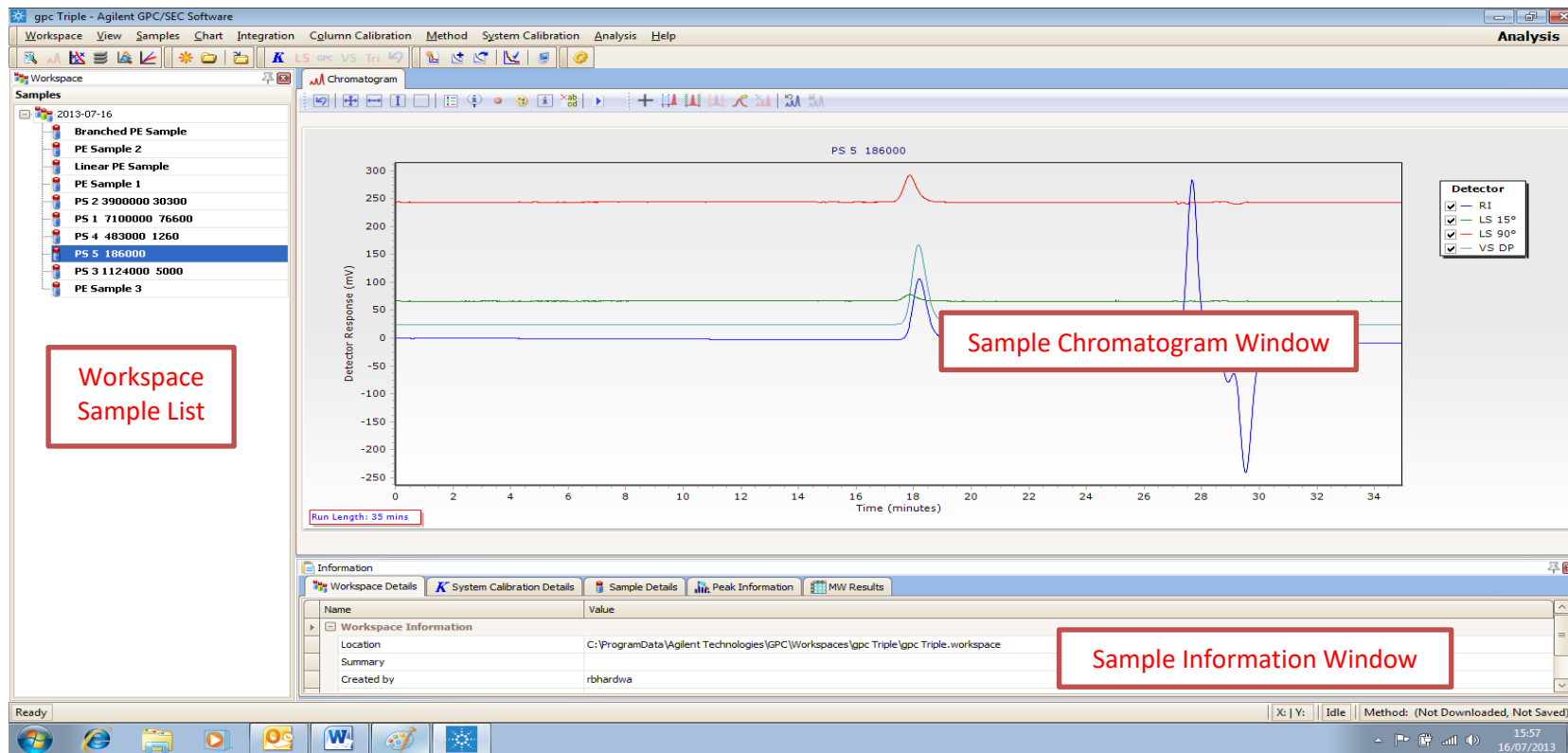
Figure 2 shows an example sequence, the initial run has been completed and are now grayed out, the data will be viewable in the **Analysis View**. These lines cannot be rerun, a new line will need to be added and the details can be copy and pasted if required. To remove these completed lines from the *Injection Sequence* highlight and *Delete*.

The next run will highlighted in green while running, the data for this is being collected and will be viewable only once the run has completed. No cells can be edited at this point.

The lines with a white background are the next to be injected, all entered information can still be edited. If a sample is added at the end of the sequence but is required to run sooner, *Promote run* to the top available slot.


# Processing of GPC Triple data

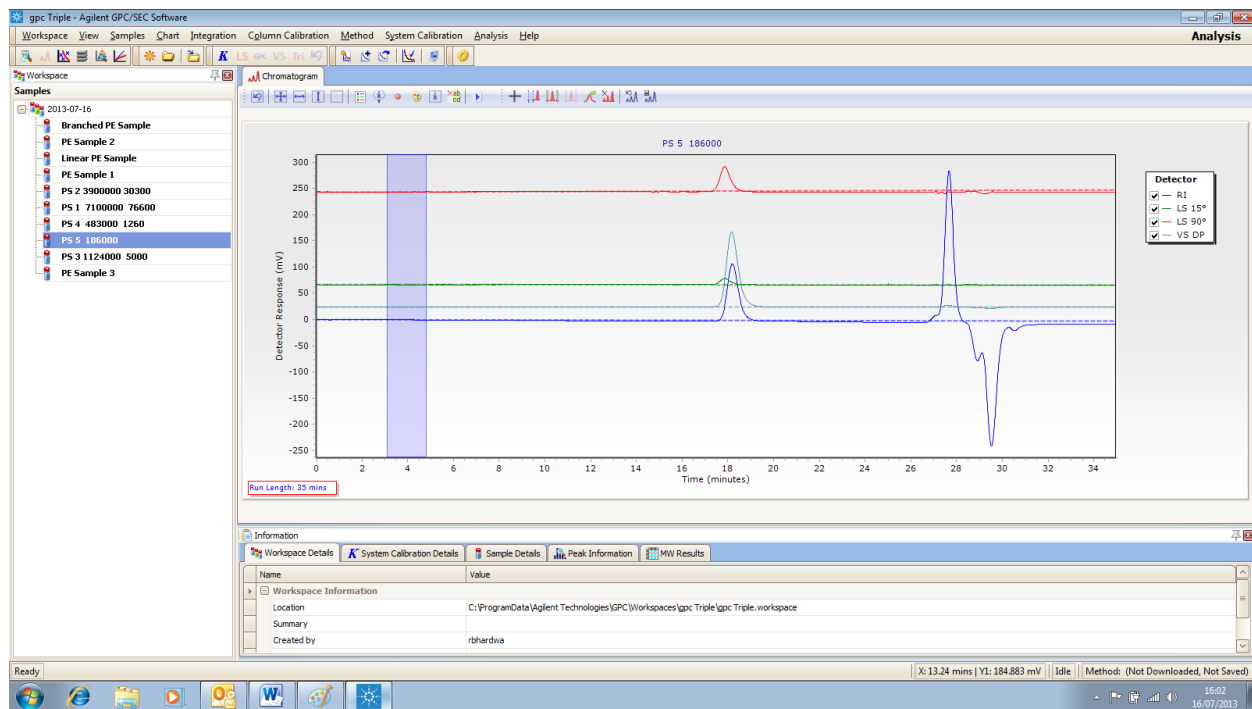
Click on the Icon  and your data for the 6 samples will be in the workspace under samples ready to be processed. Alternatively you can import samples collected previously or load other workspaces in this analysis View.



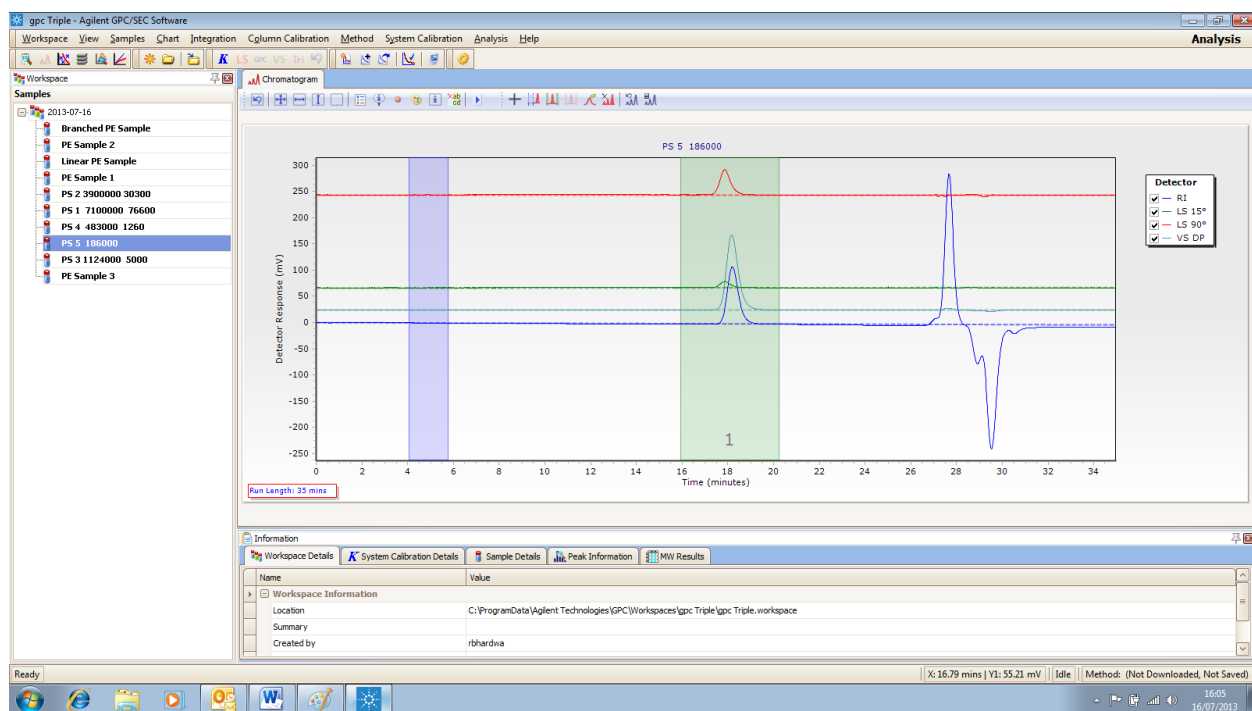
The *Analysis View* has three main sections, the **Workspace Sample List**, **Sample Chromatogram Window** and the **Sample Information Window**. Once a sample has been analyzed a fourth section will be added, the **Data Results Window**.

Highlight the sample PS 186,000, as shown above, and the right side of the screen will show the raw data. This sample will be used to measure the Detector Constants for the RI/LS & Viscometer and the Inter-detector Delay (IDD). In general this sample should be between Mp 60,000 to 200,00.

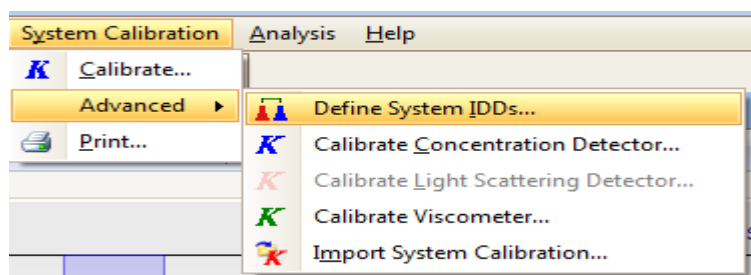
Now put in the base line by clicking on the Icon  and clicking on the raw data



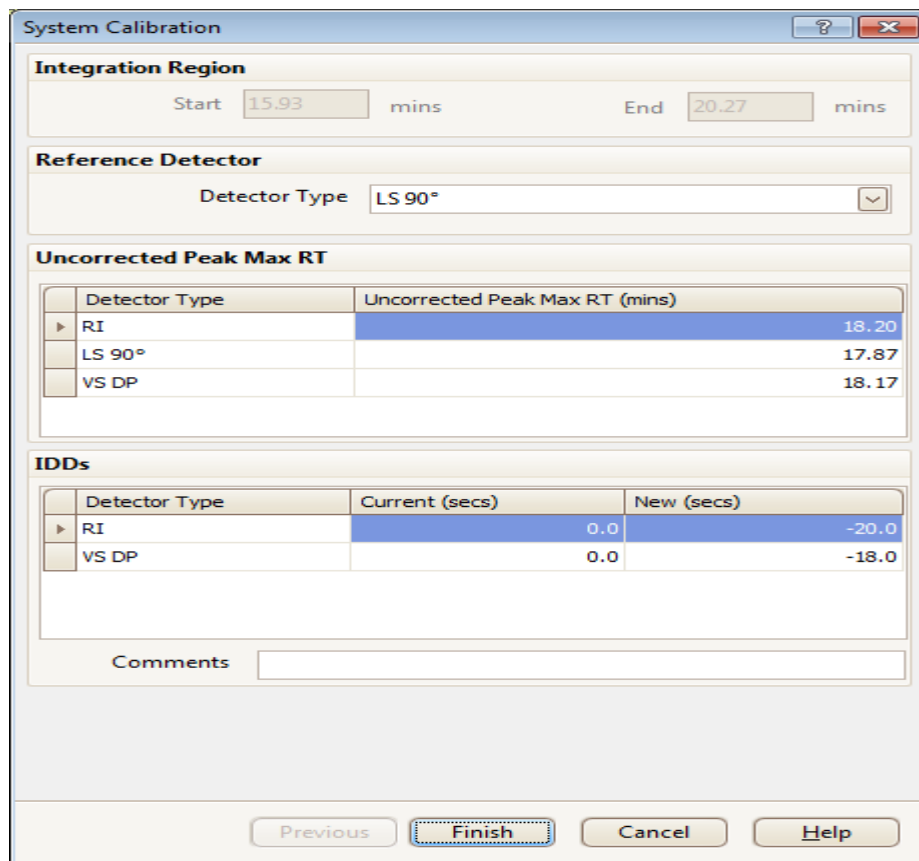
Then put the integration area by clicking on the Icon  and click and drag the area around the sample peak.



Now click on System Calibration, Advanced, Define System IDD's



And the following window comes up



The 'System Calibration' dialog box contains the following sections:

- Integration Region:** Start: 15.93 mins, End: 20.27 mins
- Reference Detector:** Detector Type: LS 90°
- Uncorrected Peak Max RT:**

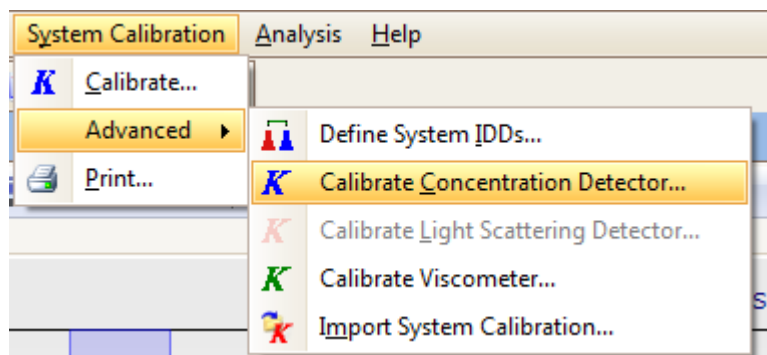
Detector Type	Uncorrected Peak Max RT (mins)
RI	18.20
LS 90°	17.87
VS DP	18.17
- IDDs:**

Detector Type	Current (secs)	New (secs)
RI	0.0	-20.0
VS DP	0.0	-18.0
- Comments:** [Empty text box]
- Buttons:** Previous, Finish (highlighted), Cancel, Help

Click the Finish tab



Now we need to generate from this sample the detector constants for each of the detectors  
Click System Calibration, advanced & Calibrate Concentration Detector as shown below

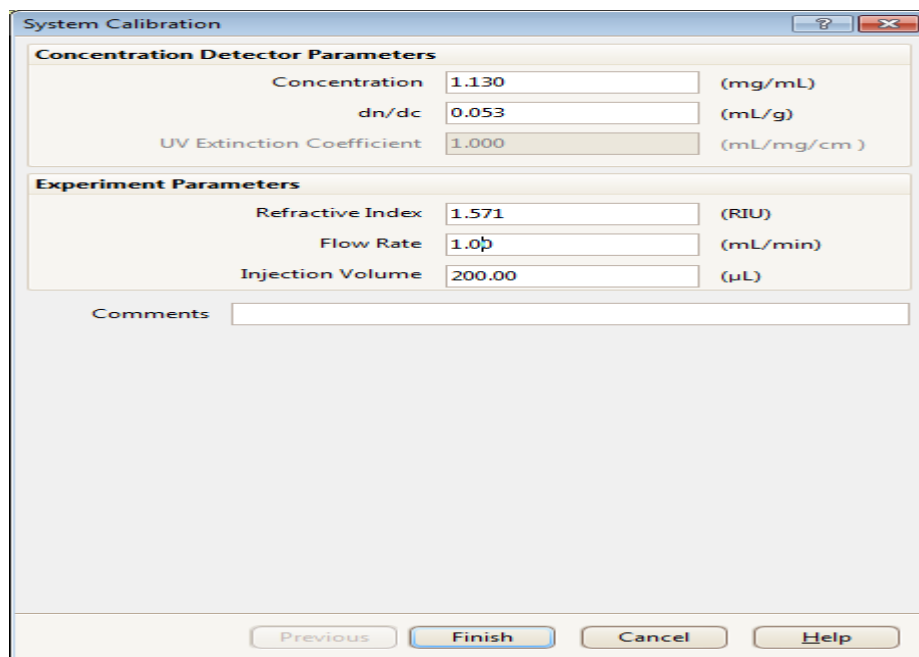


The following screen pops up

A screenshot of a dialog box titled 'System Calibration'. The dialog box is divided into two main sections: 'Concentration Detector Parameters' and 'Experiment Parameters'. The 'Concentration Detector Parameters' section contains three input fields: 'Concentration' (0.100 mg/mL), 'dn/dc' (1.000 mL/g), and 'UV Extinction Coefficient' (1.000 mL/mg/cm). The 'Experiment Parameters' section contains three input fields: 'Refractive Index' (1.000 RIU), 'Flow Rate' (0.00 mL/min), and 'Injection Volume' (200.00 µL). Below these sections is a 'Comments' text area. At the bottom of the dialog box are four buttons: 'Previous', 'Finish' (which is highlighted with a blue border), 'Cancel', and 'Help'.

This screen needs to be populated with the following information for this sample.

Conc of the sample,  $dn/dc$  of PS in TCB is 0.053, RI of TCB is 1.571, Flow rate of Pump and injection volume



The image shows a 'System Calibration' dialog box with two main sections: 'Concentration Detector Parameters' and 'Experiment Parameters'. The 'Concentration Detector Parameters' section contains three input fields: 'Concentration' (1.130 mg/mL), 'dn/dc' (0.053 mL/g), and 'UV Extinction Coefficient' (1.000 mL/mg/cm). The 'Experiment Parameters' section contains three input fields: 'Refractive Index' (1.571 RIU), 'Flow Rate' (1.00 mL/min), and 'Injection Volume' (200.00 µL). Below these sections is a 'Comments' text area. At the bottom of the dialog are four buttons: 'Previous', 'Finish' (highlighted with a blue border), 'Cancel', and 'Help'.

Concentration Detector Parameters		
Concentration	1.130	(mg/mL)
$dn/dc$	0.053	(mL/g)
UV Extinction Coefficient	1.000	(mL/mg/cm)

Experiment Parameters		
Refractive Index	1.571	(RIU)
Flow Rate	1.00	(mL/min)
Injection Volume	200.00	(µL)

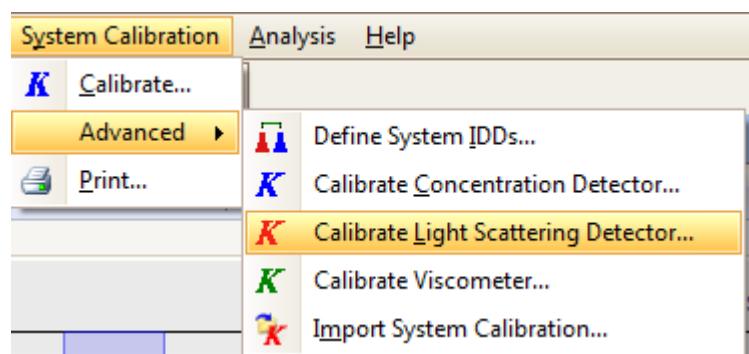
Comments

Previous Finish Cancel Help

Click Finish now

Now we need to calibrate the LS detector

Click System Calibration, Advanced & Calibrate Light Scattering Detector



Following screen comes up

The 'Light Scattering Detector Parameters' dialog box contains the following fields and controls:

- Calculated Concentration (mg/mL):** A text field with the value '1.130'.
- Detector type:** A dropdown menu showing 'RI'.
- Molar Mass:** A text field with the value '1' and a unit label '(g/mol)'.
- Laser Wavelength:** A text field with the value '650' and a unit label '(nm)'.
- Comments:** A large text area for additional notes.
- Buttons:** 'Previous', 'Finish' (highlighted), 'Cancel', and 'Help'.

This screen now needs to be populated with the Mp 186,000 as shown below

System Calibration

**Light Scattering Detector Parameters**

Calculated Concentration (mg/mL)	Detector type	Concentration
	RI	1.130

Molar Mass: 186000 (g/mol)

Laser Wavelength: 650 (nm)

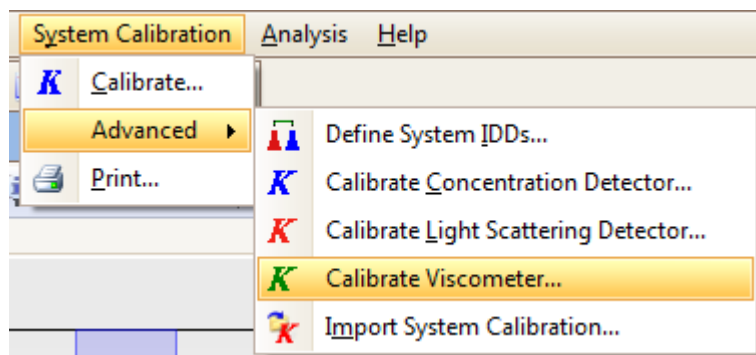
Comments

Previous Finish Cancel Help

Click Finish

Now we need to calibrate the Viscometer

Click System Calibration, Advanced & Calibrate Viscometer



The following window pops up

The 'System Calibration' dialog box displays the 'Viscosity Detector Parameters' section. It includes a table for detector data, a checkbox for 'Use Constant Inlet Pressure', and input fields for 'Inlet Pressure' and 'Known IV'. A 'Comments' text area and a row of action buttons ('Previous', 'Finish', 'Cancel', 'Help') are at the bottom.

Detector type	Concentration
RI	1.130

☐ Use Constant Inlet Pressure

Inlet Pressure:  (kPa)

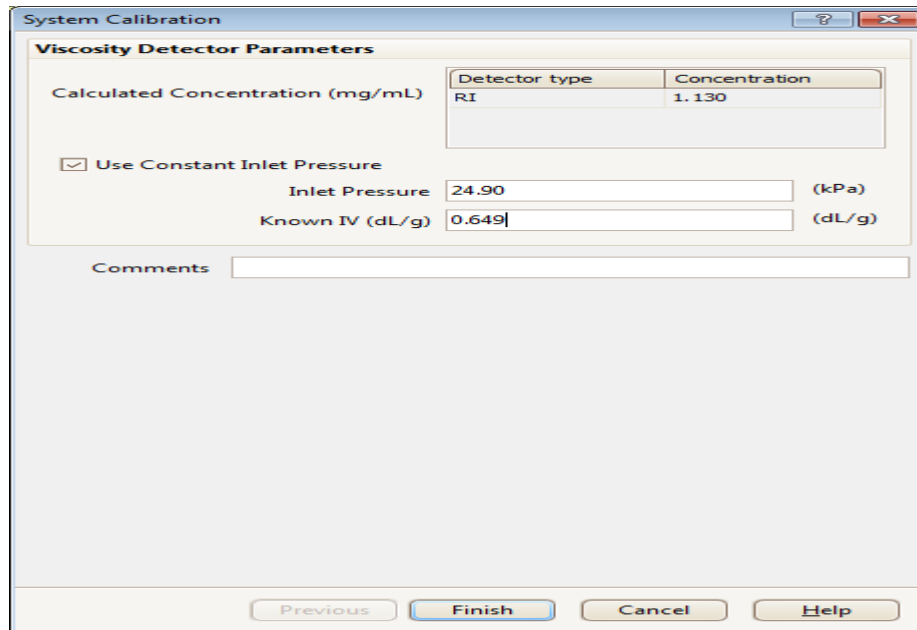
Known IV (dL/g):  (dL/g)

Comments:

Buttons: Previous, Finish, Cancel, Help

This screen needs to be populated as :

IV is provided for this sample as 0.649 and the Inlet Pressure reading is obtained from the instrument read out (24.9KPa).



The image shows a software window titled "System Calibration" with a sub-tab "Viscosity Detector Parameters". The window contains several input fields and a checkbox. A table at the top right lists "Detector type" as "RI" and "Concentration" as "1.130". Below this, the checkbox "Use Constant Inlet Pressure" is checked. The "Inlet Pressure" field is set to "24.90" with the unit "(kPa)". The "Known IV (dL/g)" field is set to "0.649" with the unit "(dL/g)". There is also a "Calculated Concentration (mg/mL)" label and a "Comments" text area. At the bottom, there are four buttons: "Previous", "Finish", "Cancel", and "Help".

Detector type	Concentration
RI	1.130

☒ Use Constant Inlet Pressure

Inlet Pressure:  (kPa)

Known IV (dL/g):  (dL/g)

Calculated Concentration (mg/mL):

Comments:

Buttons: Previous, Finish, Cancel, Help

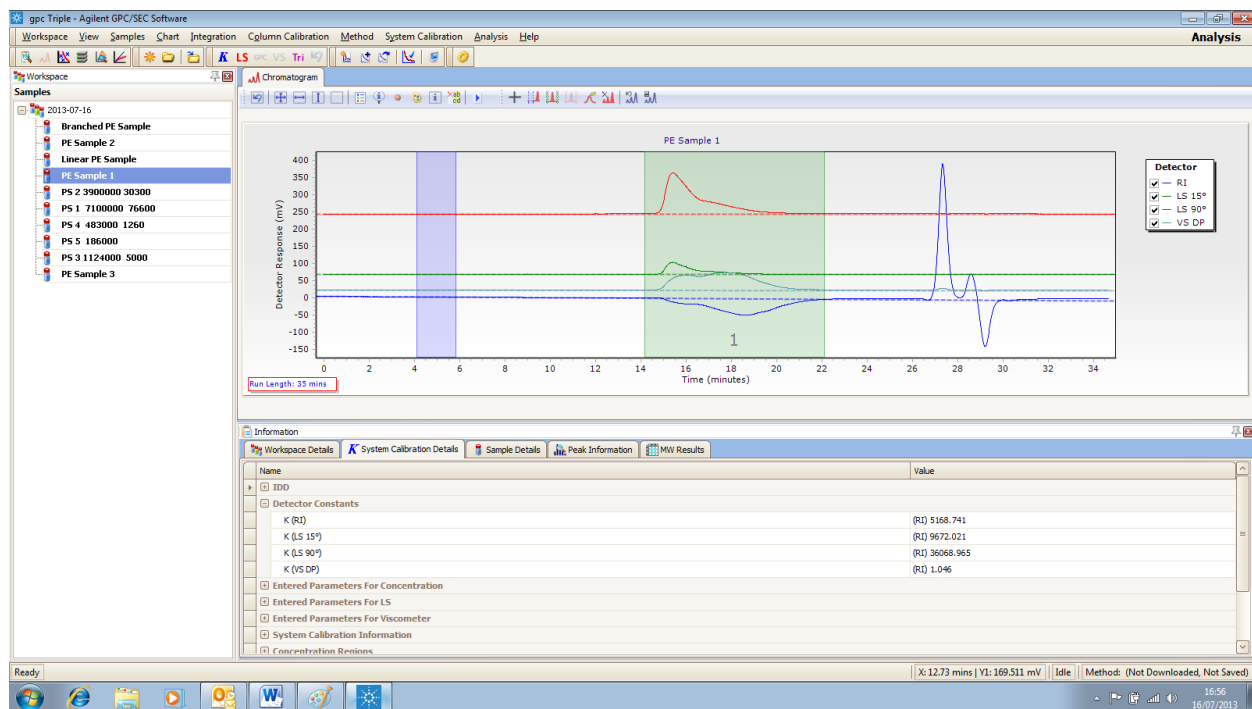
Click Finish

We can now look at the constants generated in the Information window below

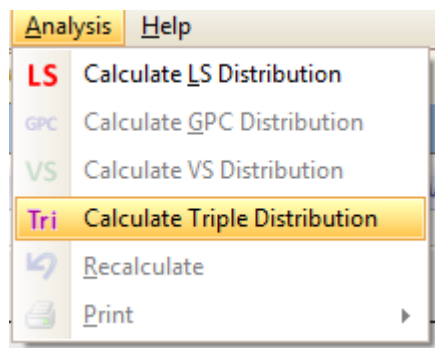
Information	
Workspace Details System Calibration Details Sample Details Peak Information MW Results	
Name	Value
+	IDD
-	Detector Constants
	K (RI) (RI) 5168.741
	K (LS 15°) (RI) 9672.021
	K (LS 90°) (RI) 36068.965
	K (VS DP) (RI) 1.046
+	Entered Parameters For Concentration
+	Entered Parameters For LS
+	Entered Parameters For Viscometer
+	System Calibration Information
+	Concentration Regions

X: | Y:
Idle
Method: (Not Downloaded, Not Saved)

Now let's process the unknown samples and start with PE Sample 1  
Highlight this sample and set base line and integration area as before:

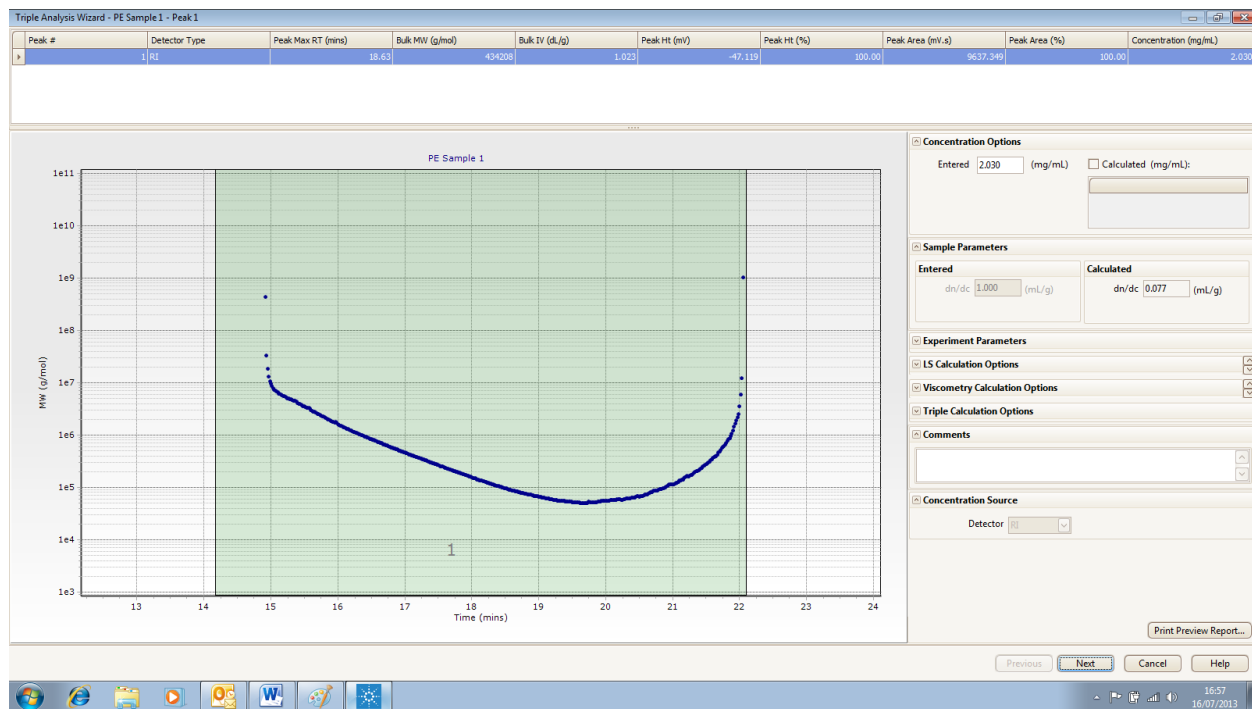


Now go to Analysis, Calculate Triple Distribution as shown below

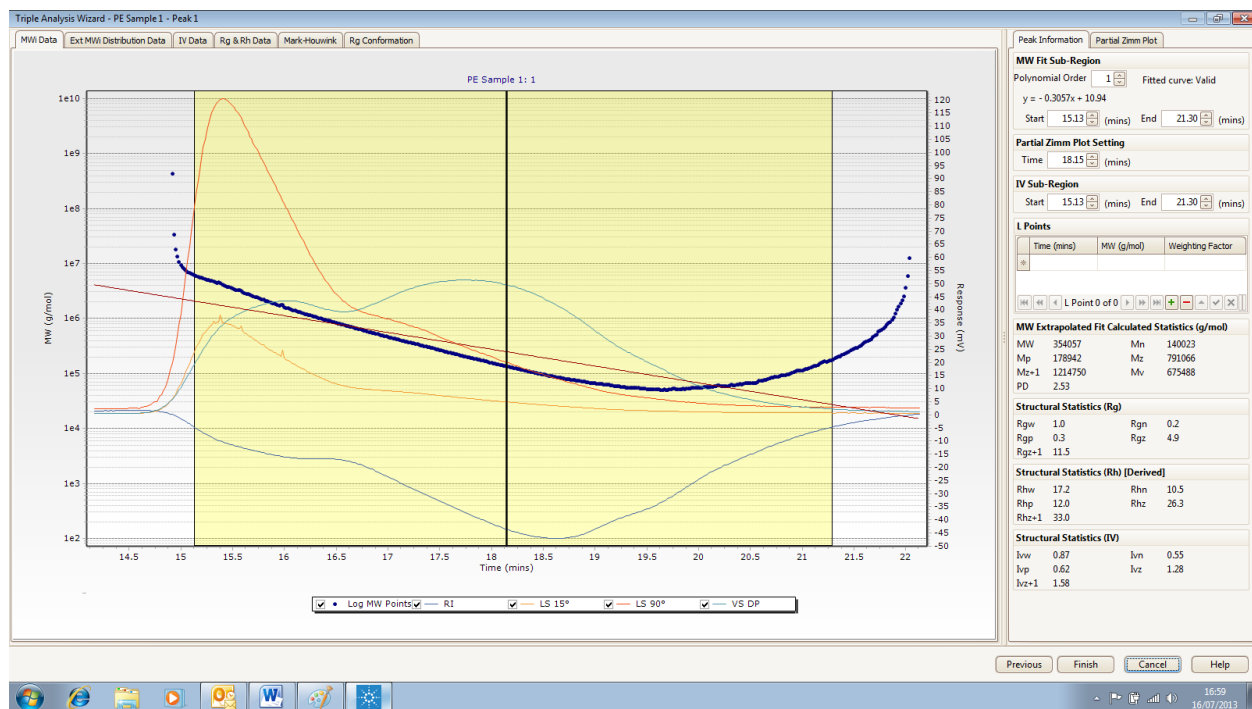




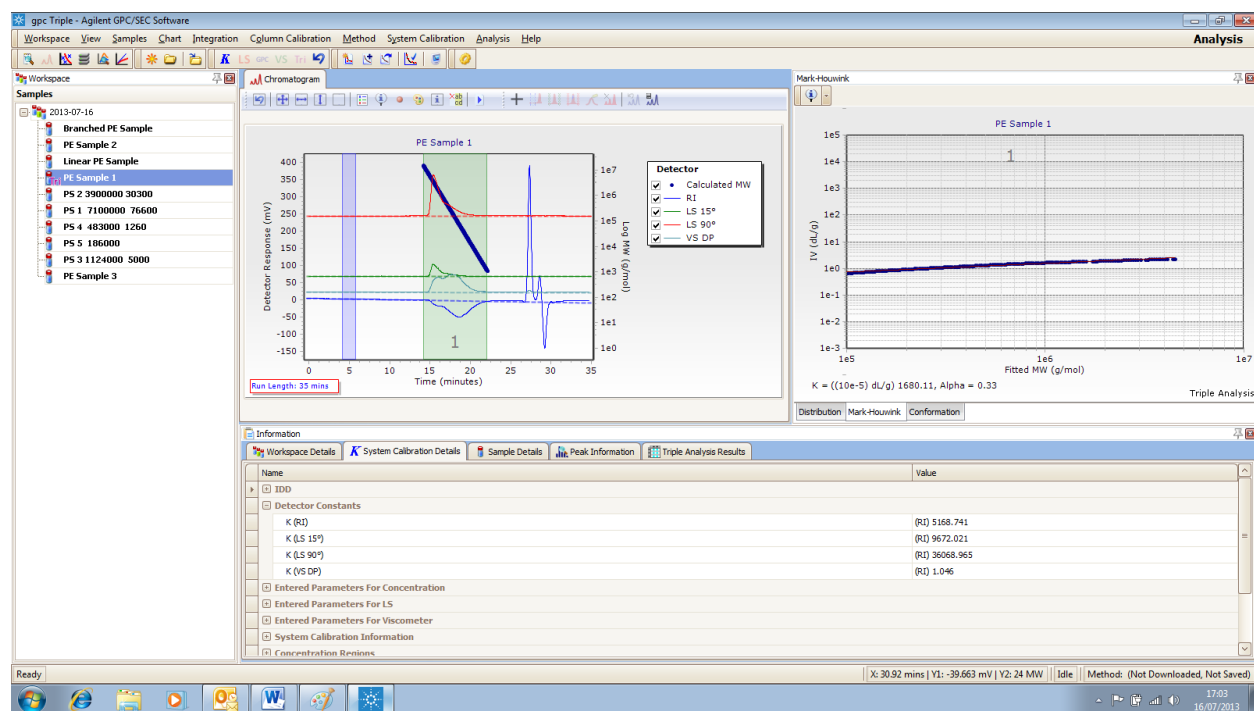
The following screen pops up



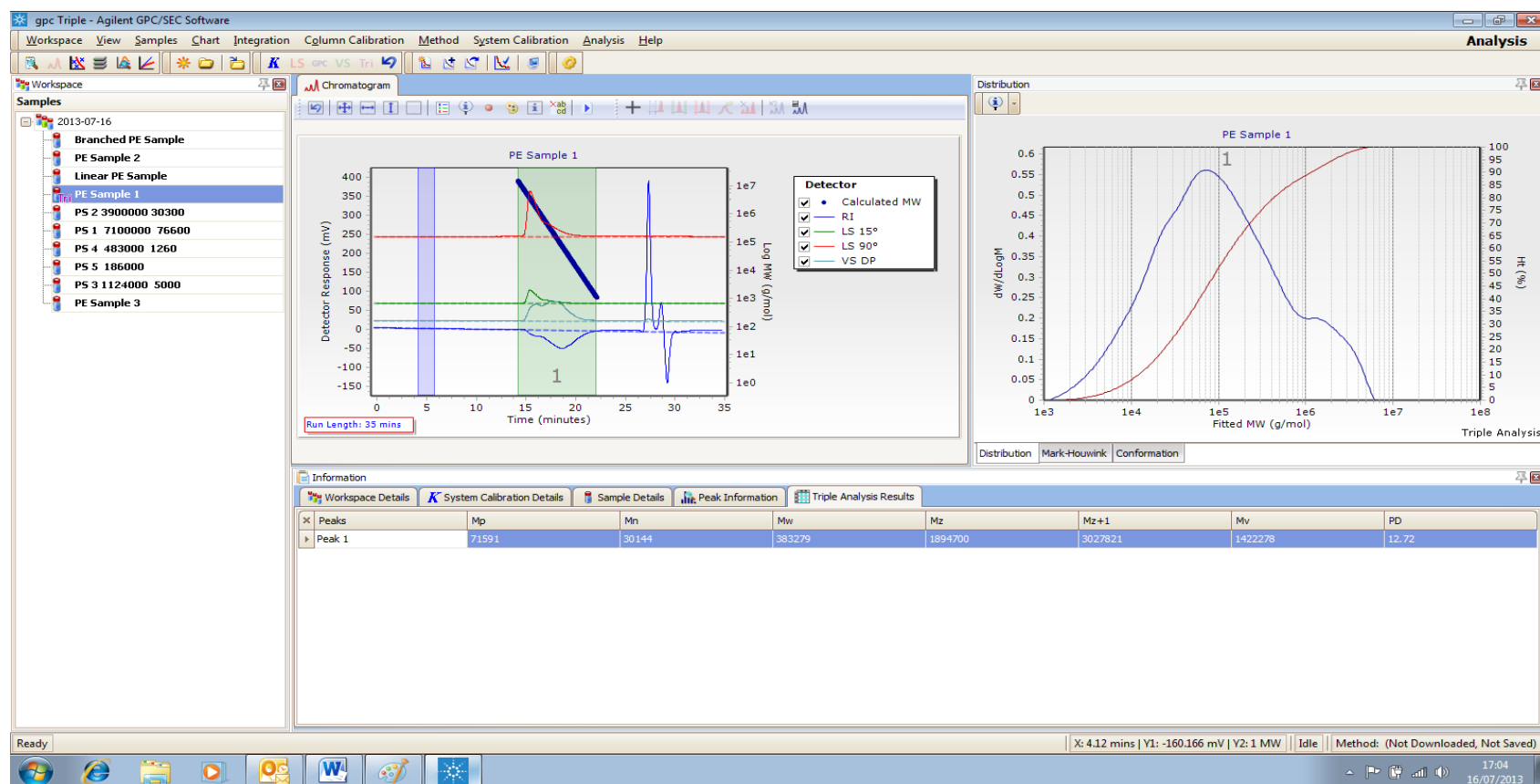
Click the Next button and the following screen pops up



Set the data fit limits – do not include the upturned part of the data which is created by weak signal from the LS detectors, Move the limits on the above screen so that the blue line is close to the linear red as above. Data is processed in the yellow area. Then click Finish button and the following screen will be shown.



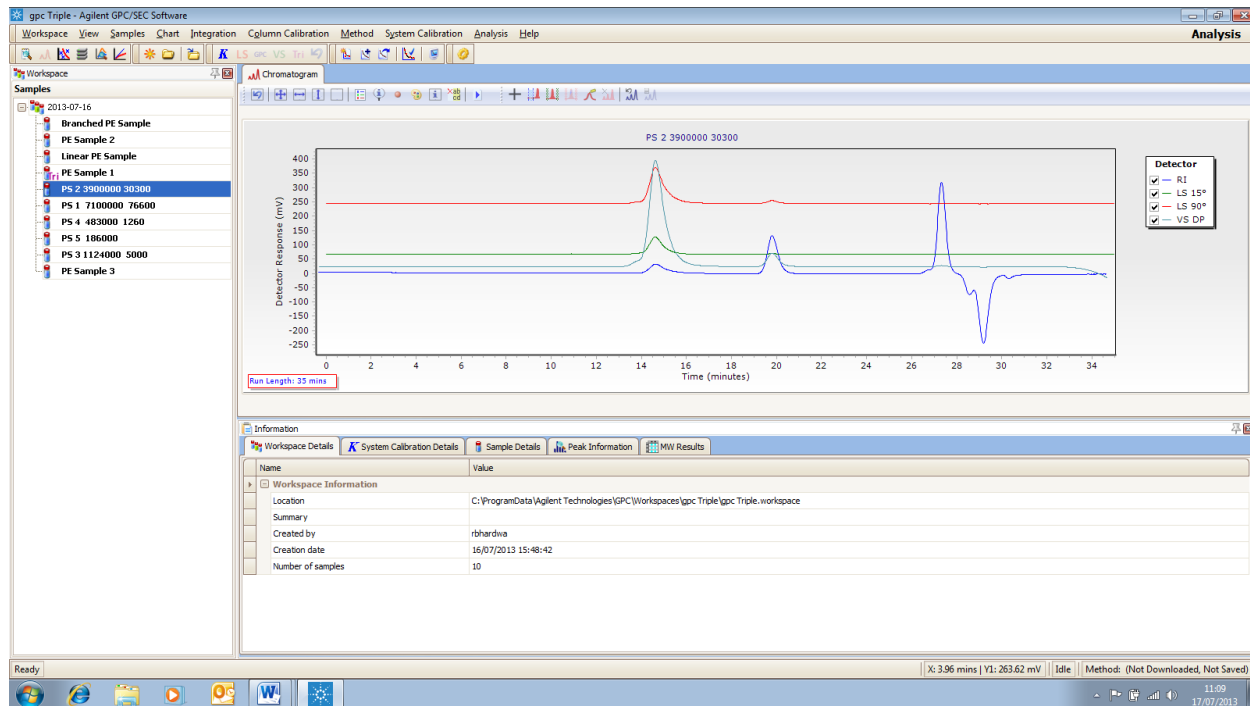
The Triple GPC analysis results are shown as below.



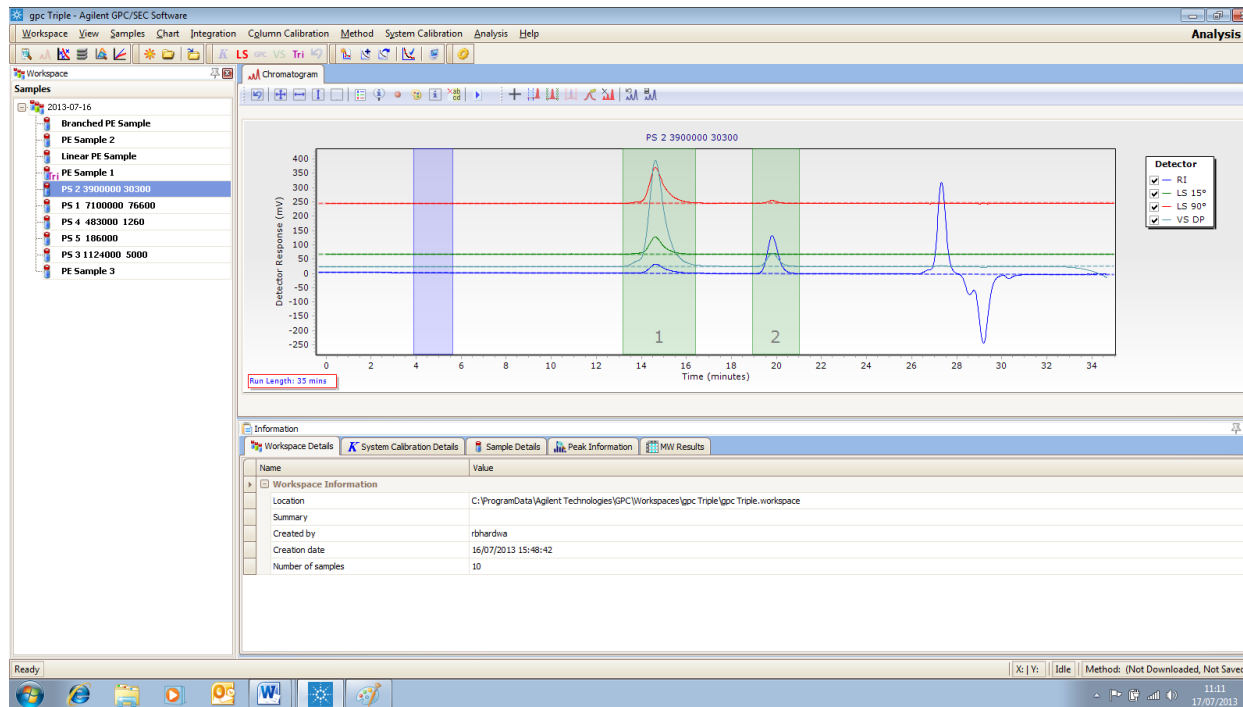
The above procedure is also applicable for RI/LS detector options also.

# Generating Universal Calibration

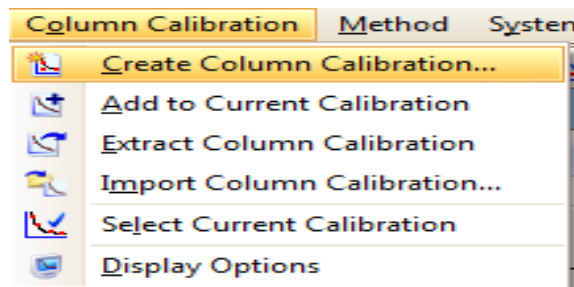
For generating a Universal Calibration we need to perform a column calibration using well characterised polymer standards. In this example we will use four PS EasiVial Mix standards. Highlight the first standard file to be processed, as shown below.



Now set the base line and the integration areas on the peaks as shown below



Then go to Column Calibration and Select Create Column Calibration



The window below will pop up

**Create Column Calibration**

**Calibration Type**  
☒ GPC Narrow Standard ☐ Universal

**Calibration Information**  
Concentration Detector: RI  
Sample Name: PS 2 3900000 30300  
Calibration Name: 2013-07-17-001  
Comments: GPC Column Calibration created 17 July 2013 by rbhardwa

**Mark-Houwink**  
K ((10e-5) dL/g): 14.100 Alpha: 0.700 FRM RT (mins): 0.00

**Assign Peak Molecular Weights**

Max. RT (mins)	Peak MW
14.63	3900000
19.80	30300

OK Cancel

Select Universal Calibration as shown below

**Calibration Type**  
☐ GPC Narrow Standard ☒ Universal

Then populate as below by inputting the Mw values for both peaks with their corresponding accurate Molecular weights. This will automatically generate the IV values for both peaks. At this stage you can type in a Calibration name for this calibration. In this example we have called it Universal.

Create Universal Calibration

**Calibration Type**

☐ GPC Narrow Standard ☒ Universal

**Calibration Information**

Concentration Detector: RI

Sample Name: PS 2 3900000 30300

Calibration Name: Universal

Comments: Universal Calibration created 17 July 2013 by rbhardwa

FRM RT (mins): 0.00

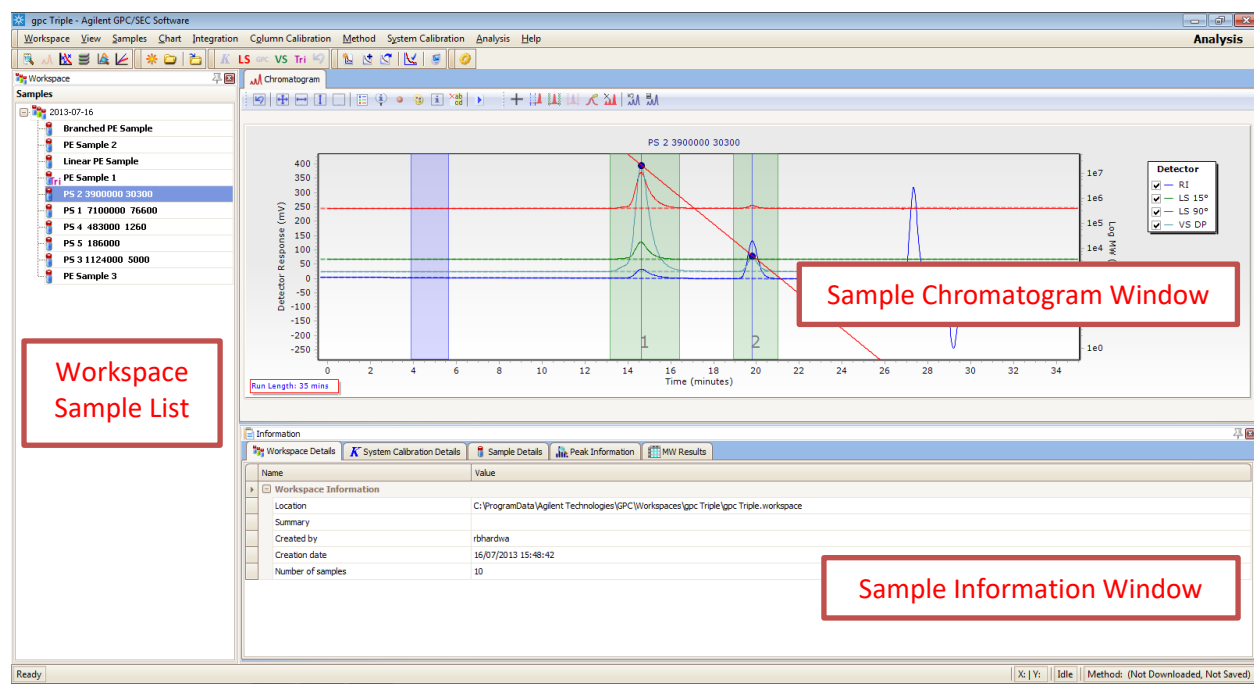
**Assign Peak Molecular Weights**

	Max. RT (mins)	Peak MW	Concentration (mg/mL)	IV (dL/g)
	14.63	3900000	0.500	5.240
	19.80	30300	1.340	0.1659

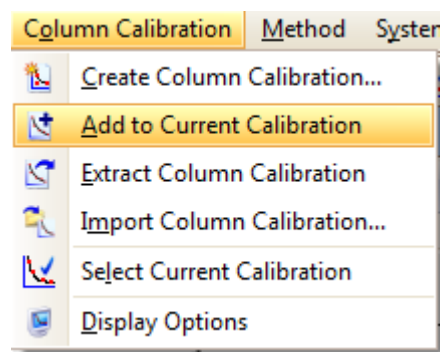
OK Cancel

Then Click OK tab to show the window below

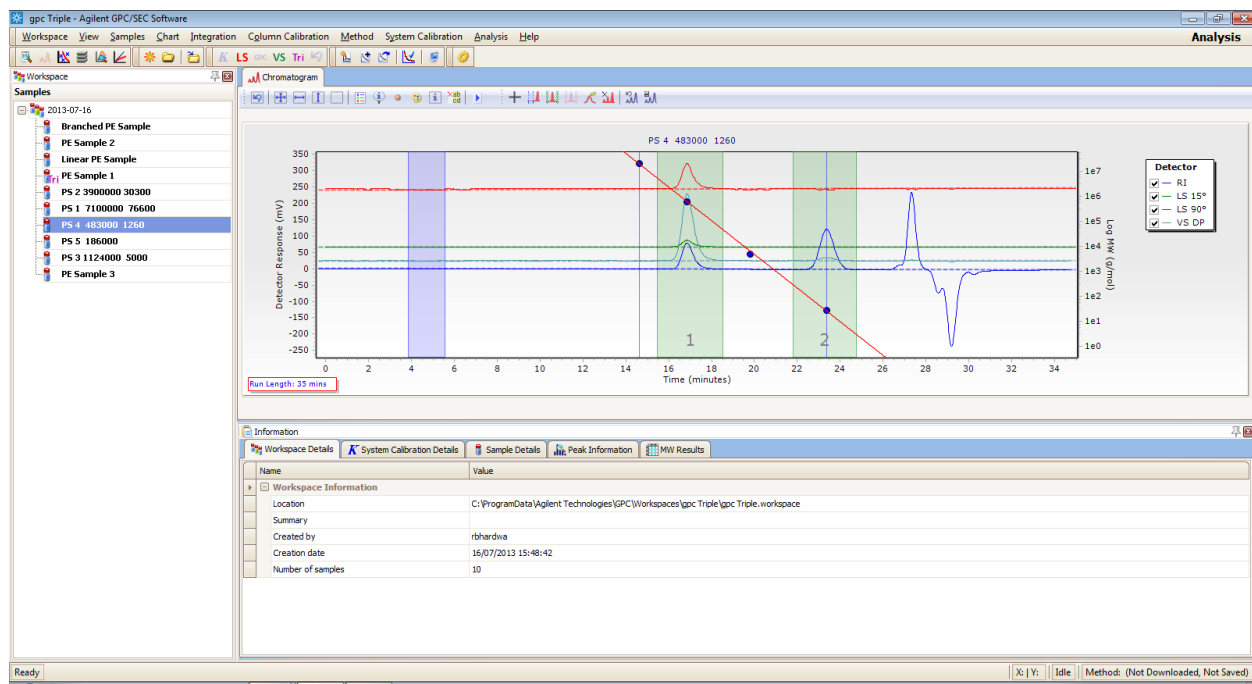




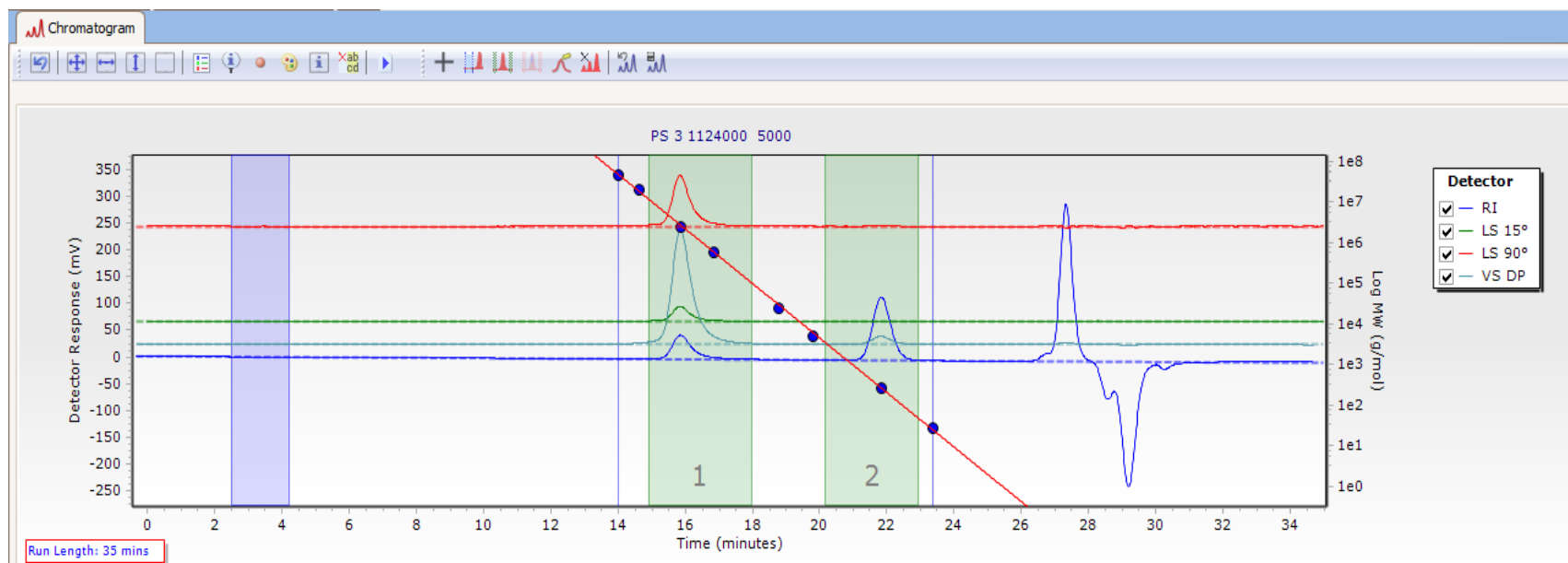
Now highlighting the 2<sup>nd</sup> sample and put base line and area integration for both peaks as with the 1<sup>st</sup> sample, and then go to Column Calibration tab and select Add to current Calibration



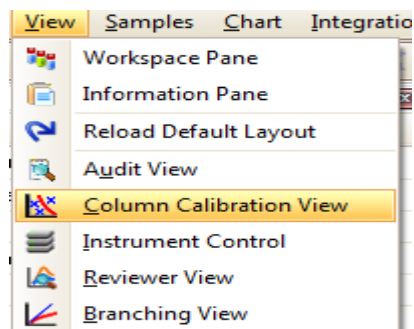
This will generate the following window

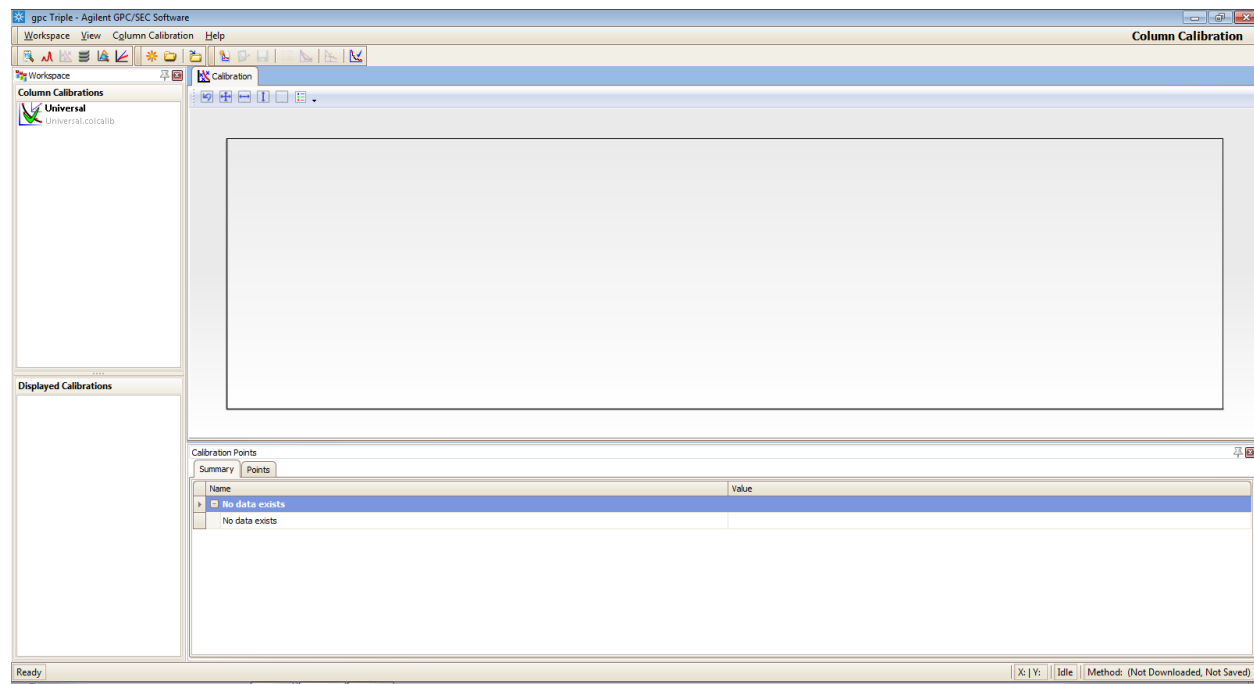



As seen above the 4 point calibration has been performed. Repeat for the next 2 standard runs to generate the following 8 point calibration

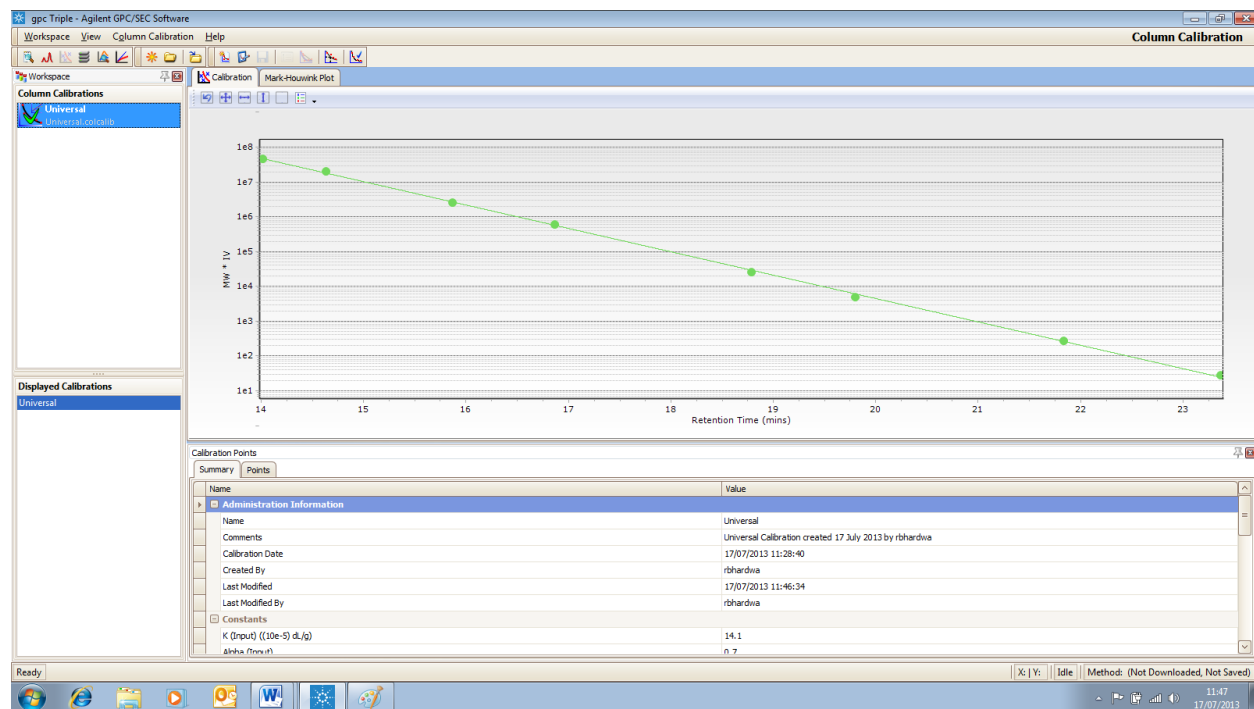


To view the created 8 point Universal Calibration go to View ,Select Column Calibration View

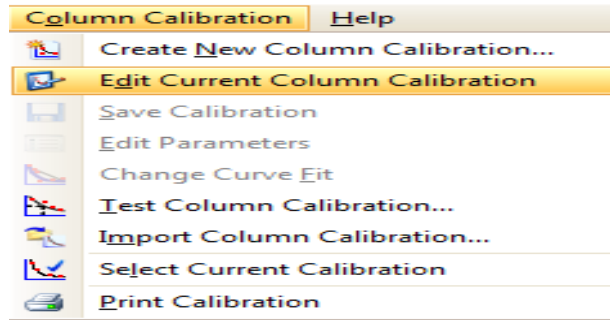




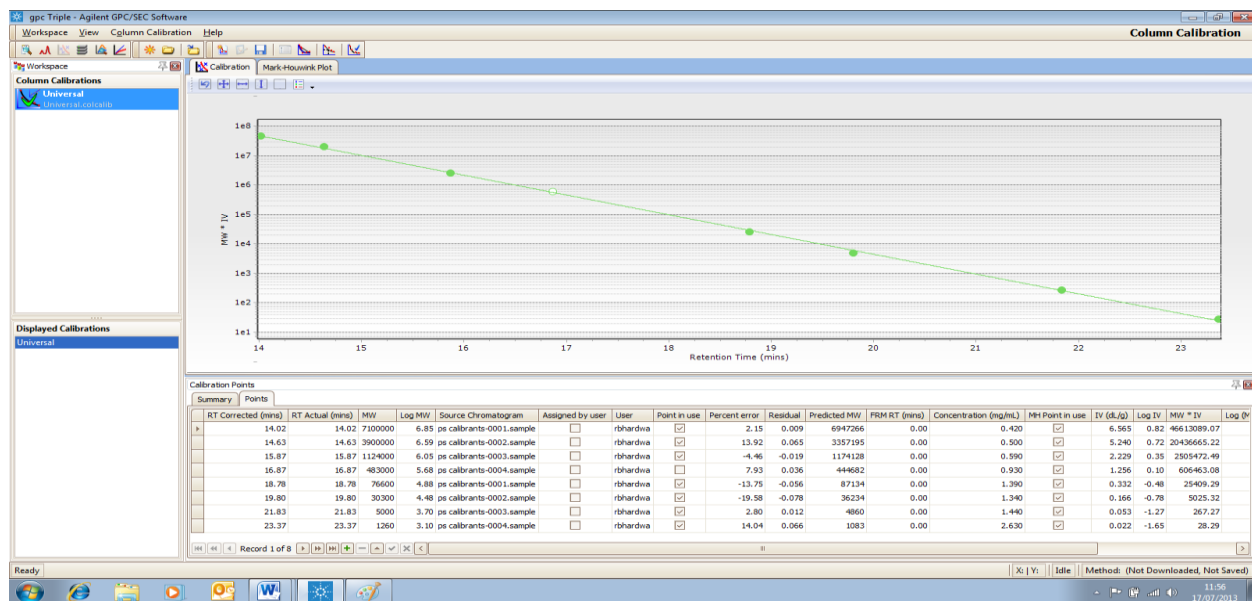
Click on the  **Universal** [Universal.colcalib](http://Universal.colcalib) and the following calibration window pops up



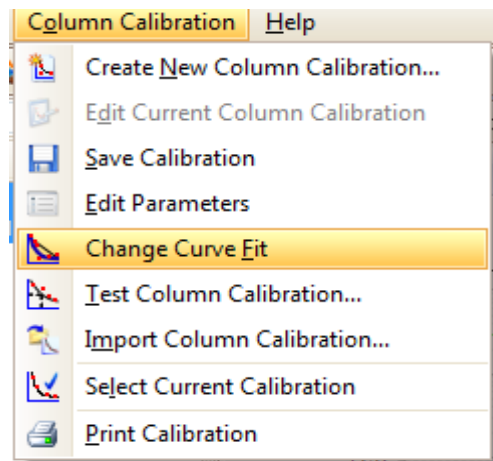
You can edit the generated calibration (add or remove points) go to Column Calibration tab and select Edit Current Column Calibration



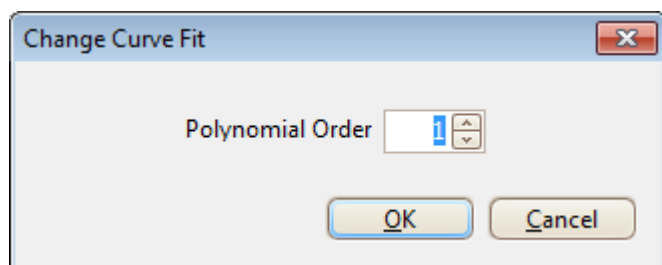
And click on any point to remove it from the calibration. In this example we have deselected the 4<sup>th</sup> point (Mp 48,3000) as shown below. This can be selected again by simply clicking onto the point to reactive it.



The curve fit can also be changed if required. Highlight Column Calibration tab and select Change Curve Fit



This will show the following window

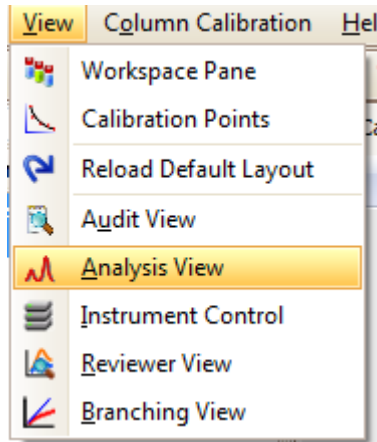


Change the order fit 1-5, but generally a good fit is 1-2. And select OK

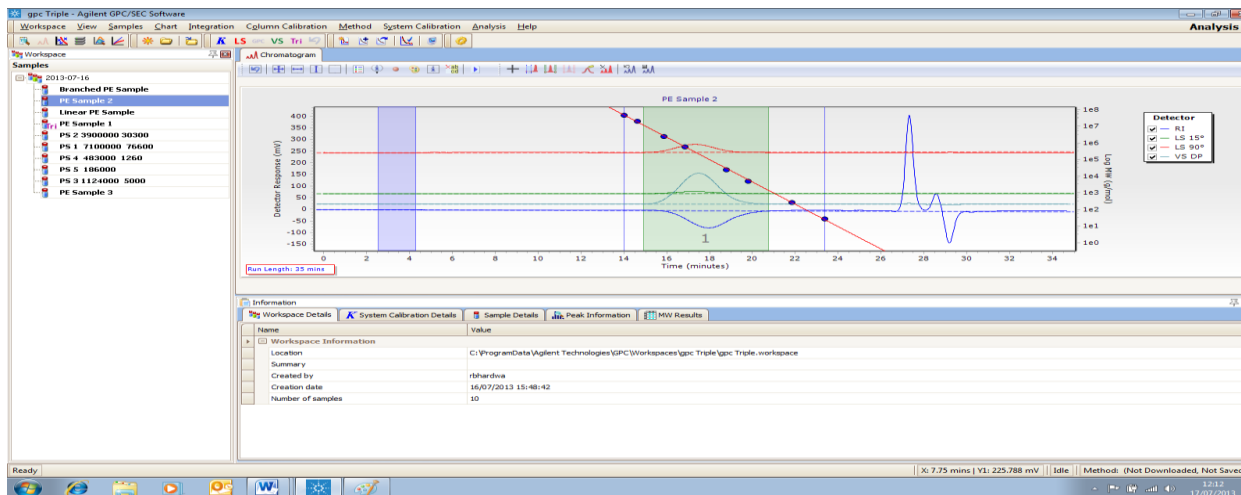
This will now save your calibration.



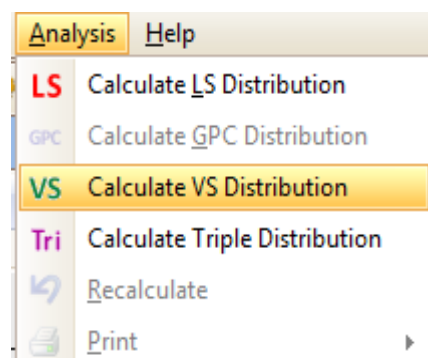
Now proceed to Analysis View as below to process the unknown samples



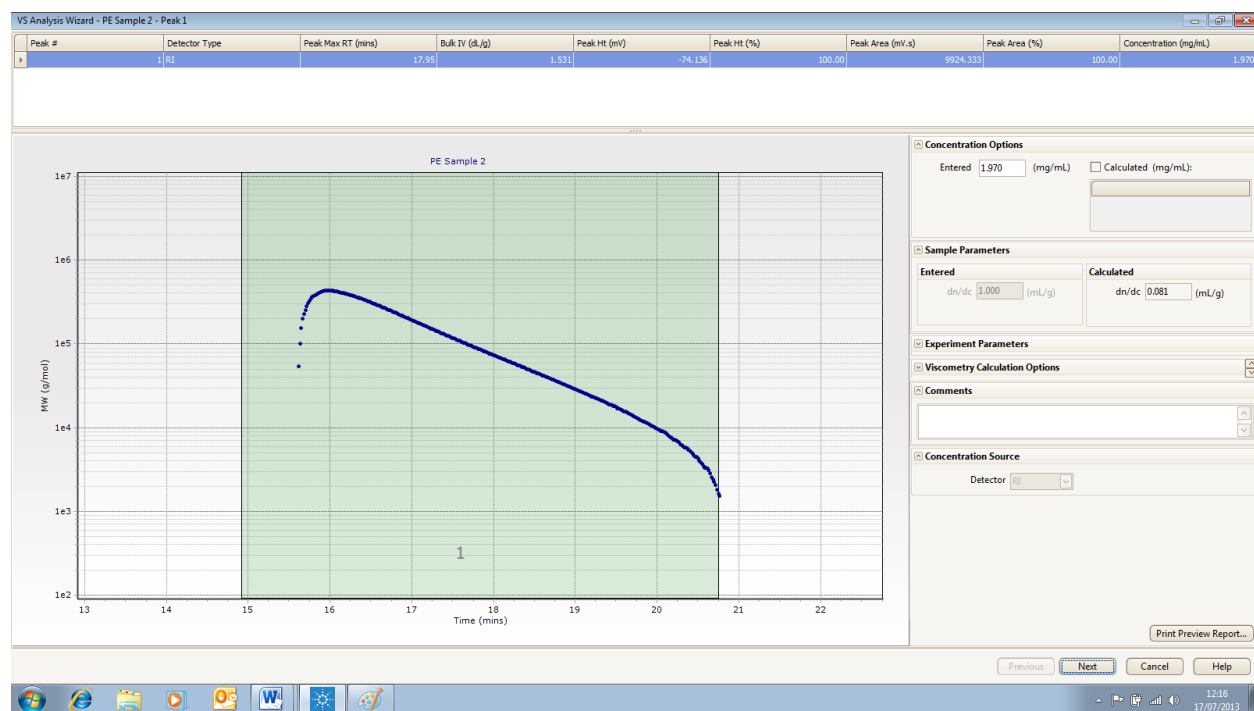
Highlight sample PE Sample 2 put in base line and area integration as before and the following window is seen



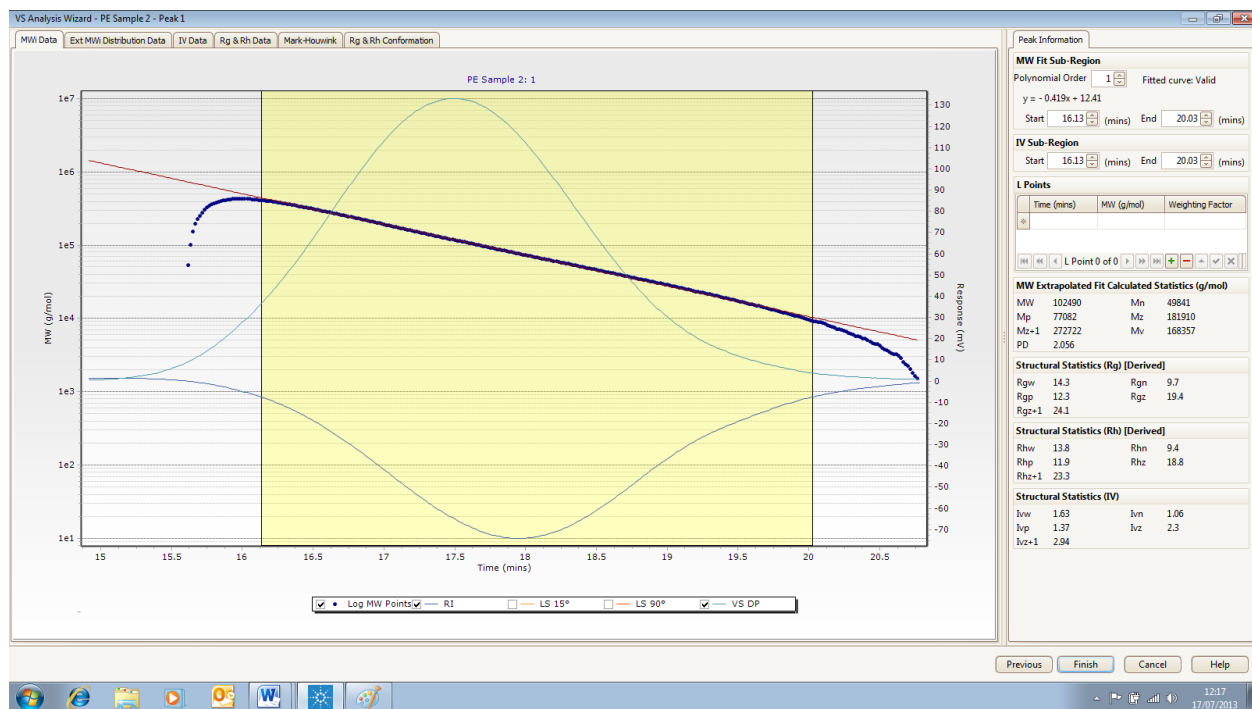
Now go to Analysis lab and select Calculate VS Distribution



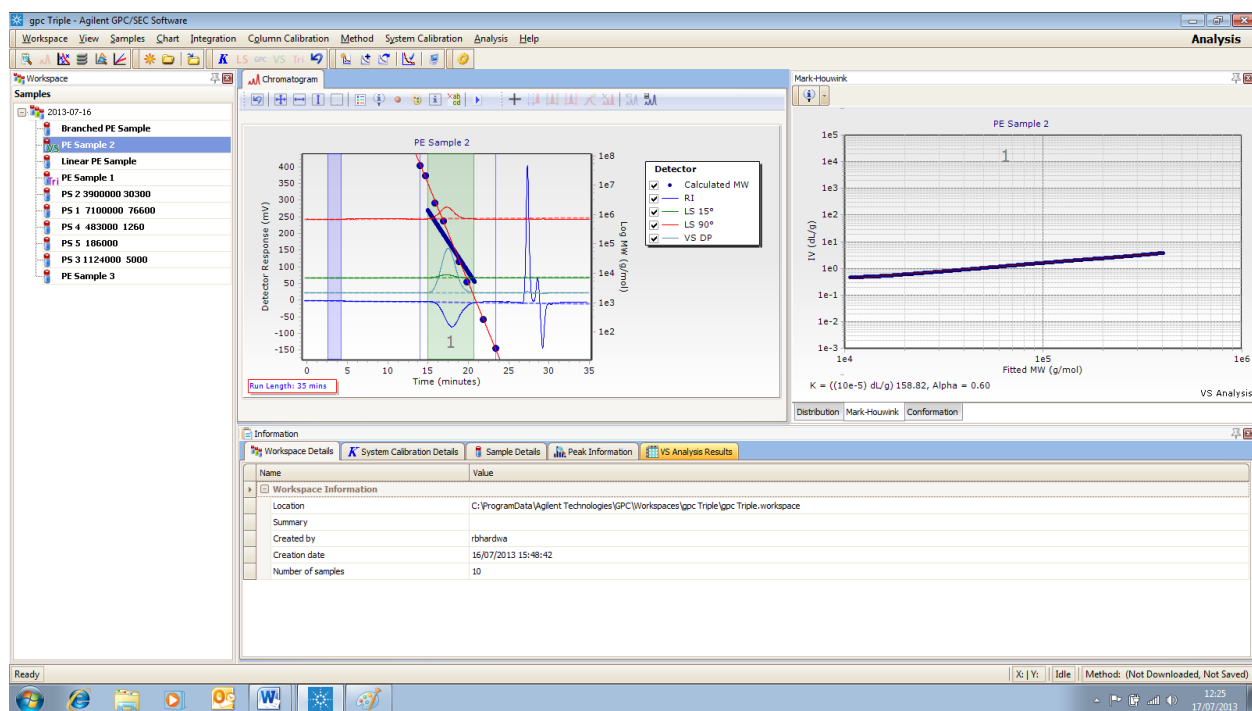
The following screen pops up



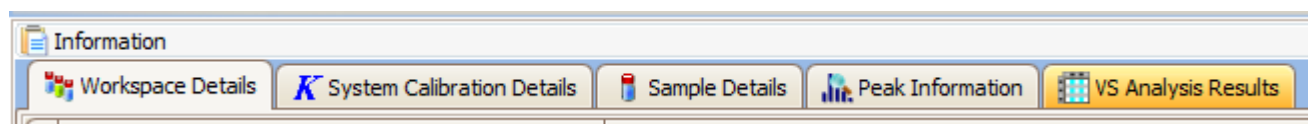
Click Next to go to the following screen



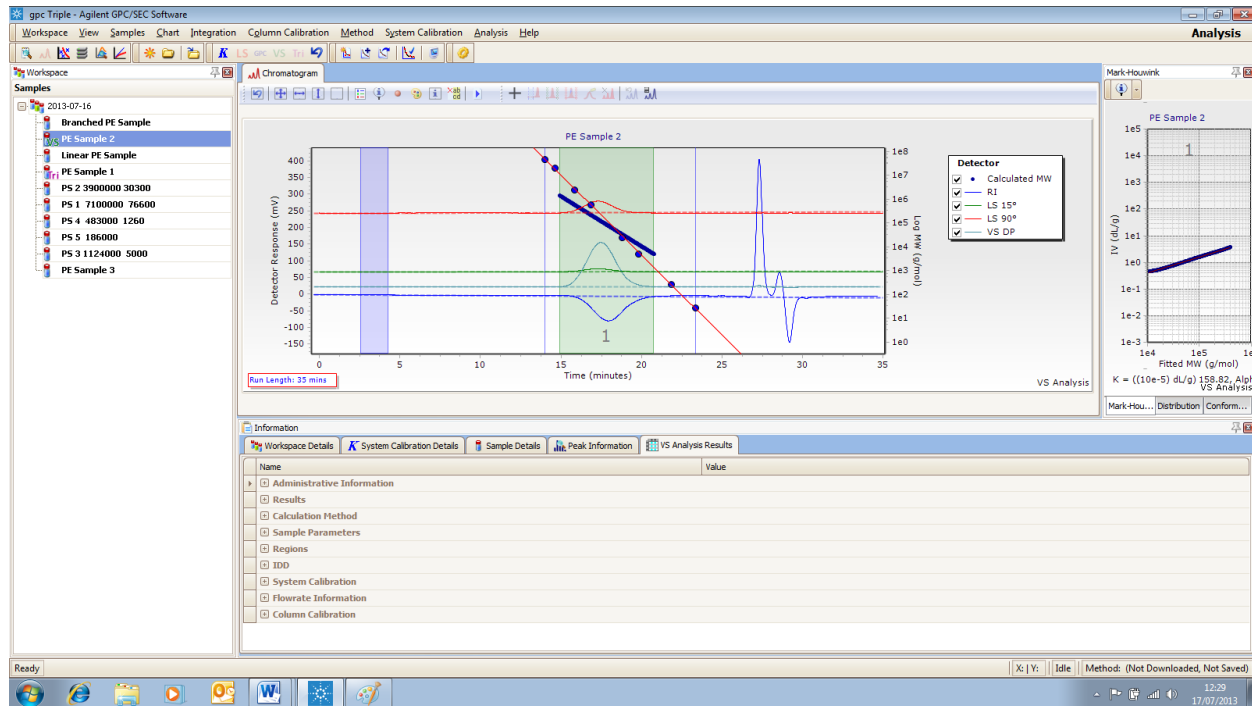
Set the data fit limits – do not include the upturned part of the data which is created by weak signal from the detectors, Move the Mw Fit start cursor and Mw Fit End Cursor to define the linear part of the curve fit.  
 Once you have done this Click Finish and the following screen is displayed



Now to see the data for this sample select VS Analysis Results tab



The following screen pops up



Now Click on the +Results tab, as highlighted below.

Information

Workspace Details System Calibration Details Sample Details Peak Information VS Analysis Results

Name	Value
+ Administrative Information	
+ Results	
+ Calculation Method	
+ Sample Parameters	
+ Regions	
+ IDD	
+ System Calibration	
+ Flowrate Information	
+ Column Calibration	

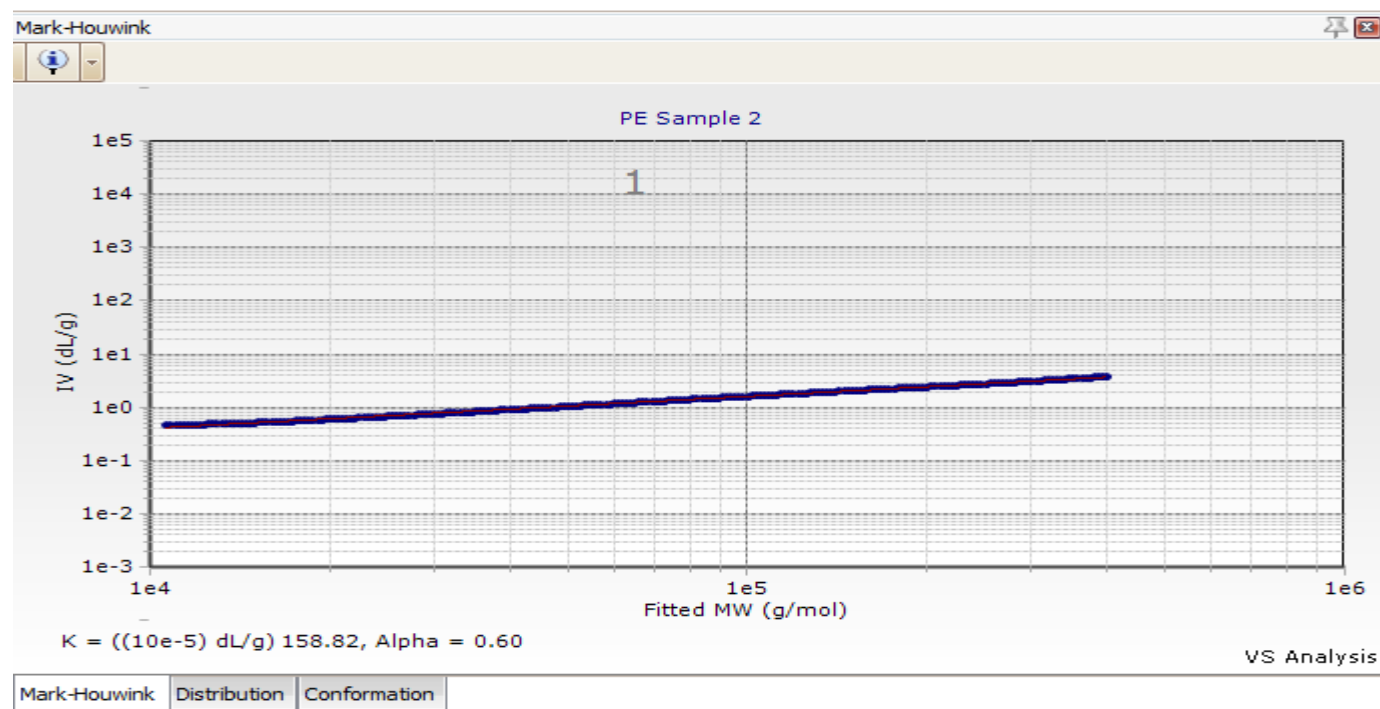
The results can be seen as below.

Information

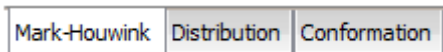
Workspace Details System Calibration Details Sample Details Peak Information VS Analysis Results

Name	Value
+ Administrative Information	
+ Results	
Recovery (%)	100.00
+ Peaks	
[-] Molecular Weight Averages	
Peaks	
Peak 1	77308 49932 102872 182825 274275 169179 2.06
+ Rg Averages	
+ Rh Averages	
+ IV Averages	

In addition to the molecular weight data, Mark-Houwink , Distribution and Conformation plots can also be displayed, as shown below.



Each plot can be displayed by selecting their individual tabs





# Branching In Polymer Analysis

## Introduction

Branching can be measured by LS/Vic by looking at changes in the molecular size (Rg) or Intrinsic Viscosity (IV) as a function of increasing Molecular Weight. Branched polymers always have lower Rg & IV values than linear analogs, this is due to presence of branched points. The calculations can be done by either IV (measured or calculated) or radius of gyration (Rg measured or calculated) data.

The quality of the results depends on the quality of the source data e.g Rg or IV.

Contraction factors are determined from Mark-Houwink (log IV Vs log Mw) or Conformation (log Rg Vs log Mw) plots using the relationship below:

$$g = (Rg_{\text{branched}} / Rg_{\text{linear}})_{Mw}$$

Where g is Radius of gyration contraction factor or branching Ratio

=====

For many polymers and applications this is as far as the branching analysis can be taken

This is especially true if the nature of the polymer is not known or if it is complex, or if the nature of the branches is not certain

At this point a qualitative indication of the level of branching is obtained

The analysis can only be advanced to give values if the exact repeat unit structure of the polymer is understood and the nature and rough distribution of the branching is known

Many of the methods that are used when measuring branching numbers only really apply to polyolefins

This is because polyolefins have a very simple structure and also because the presence of branching has proved of great commercial significance

The ratio of the intrinsic viscosity or radius of gyration of a branched polymer compared to a linear polymer of the same molecular weight is known as a contraction factor:

$$g = \frac{Rg \text{ (branched)}}{Rg \text{ (linear)}}$$

$$g' = \frac{IV \text{ (branched)}}{IV \text{ (linear)}}$$

At any given molecular weight:

- The Rg contraction factor measures a contraction in size
- The IV contraction factor measures an increase in molecular density

and they are not equivalent

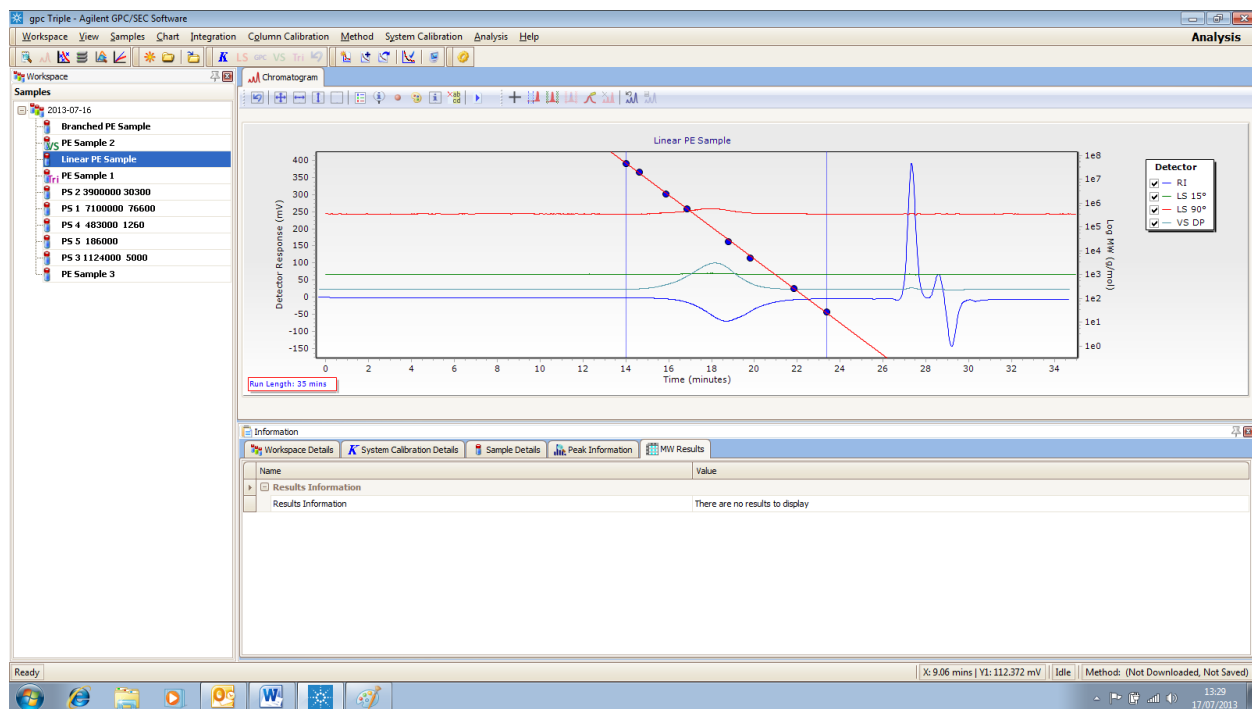
The value of g can be obtained from g' using the following relationship where  $\epsilon$  is the structure factor, a value between 0.5 and 1.5

$$g = g'^{(1/\epsilon)}$$

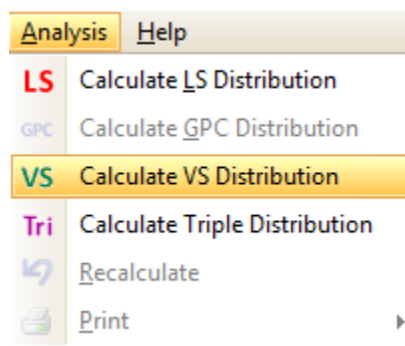
All branching models are based on g, therefore for accurate determination of Branching numbers and frequency using a Viscometer, a robust value of  $\epsilon$  is required.

### **Doing Branching Calculations on collected data**

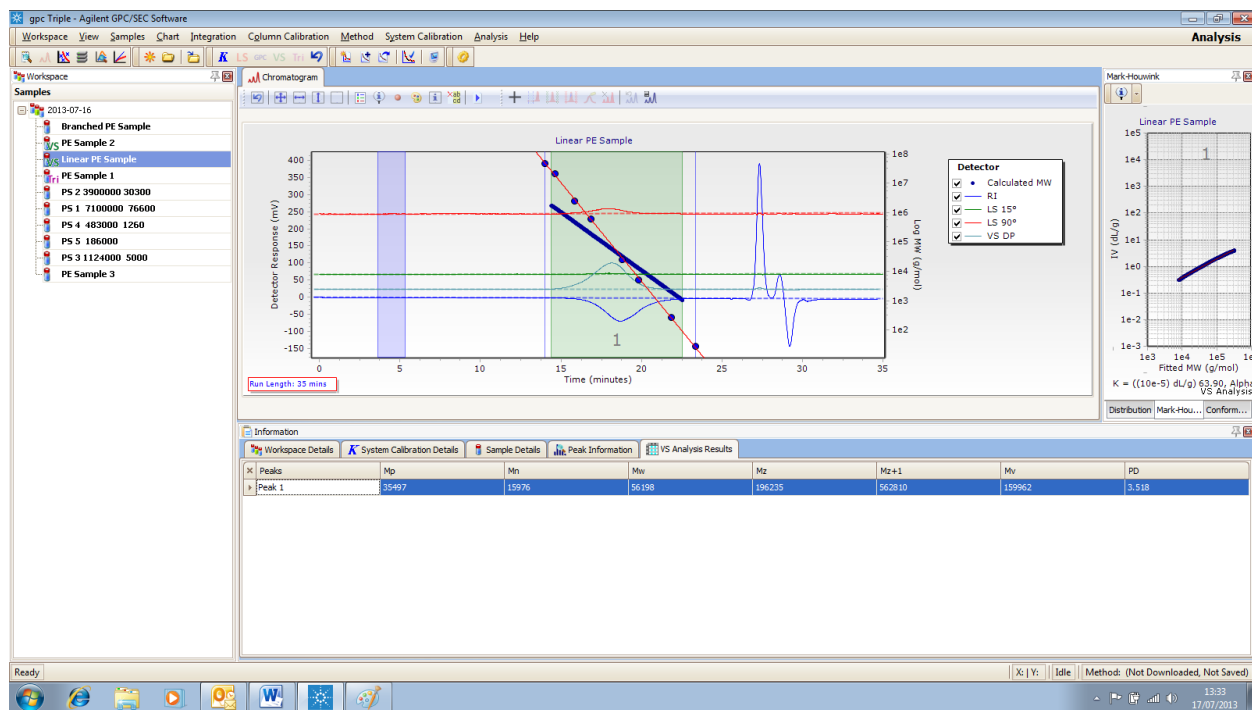
Highlight the Linear analogue (Linear PE Sample)



Draw the base line and area Integration and then calculate the results by selecting Calculate Vs Distribution

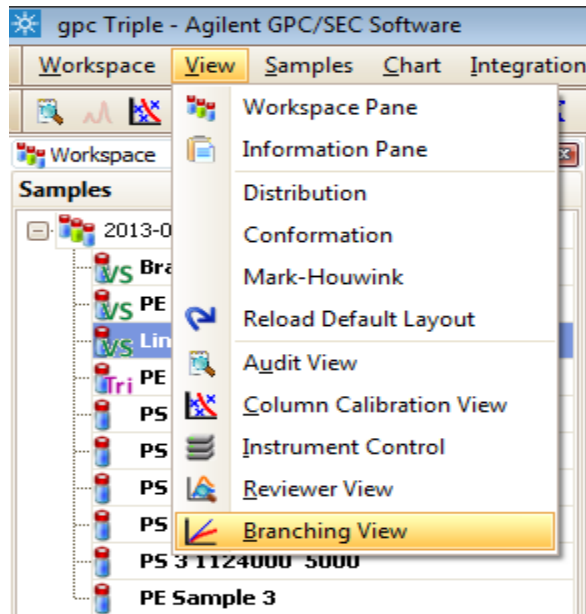


This will give the results molecular weight data for the linear sample, as seen below.

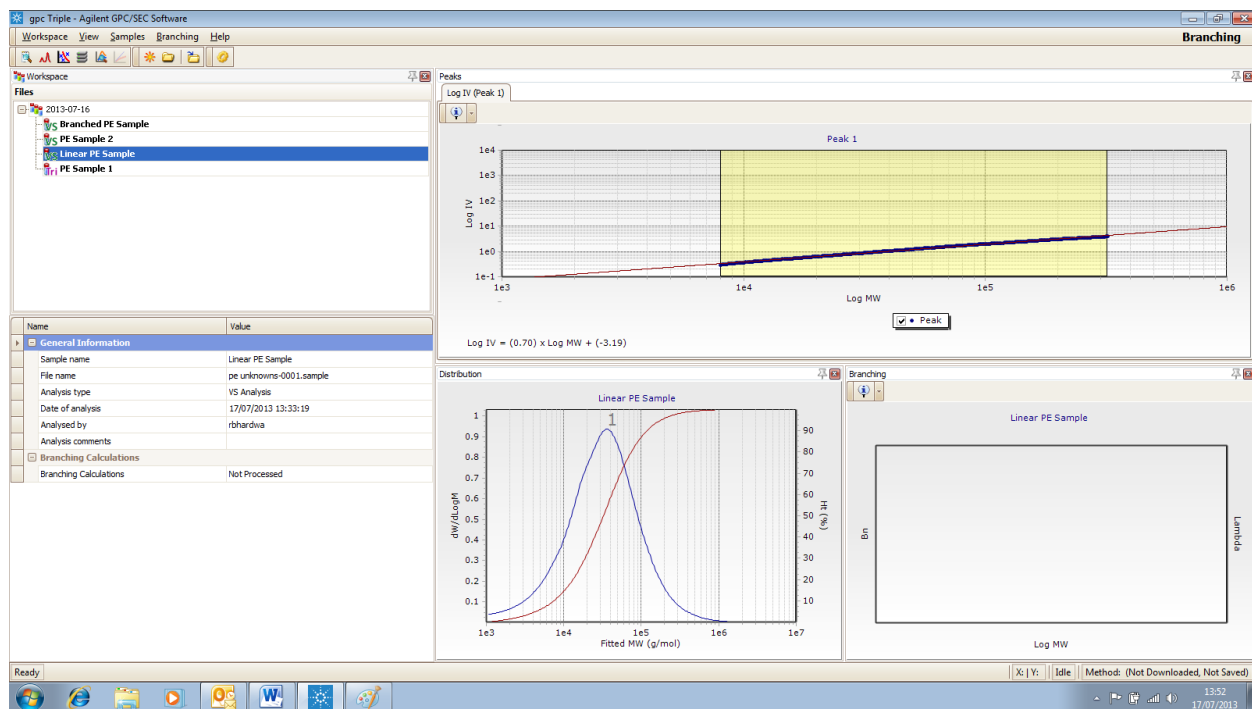


Now repeat the above steps for the branched PE Sample.

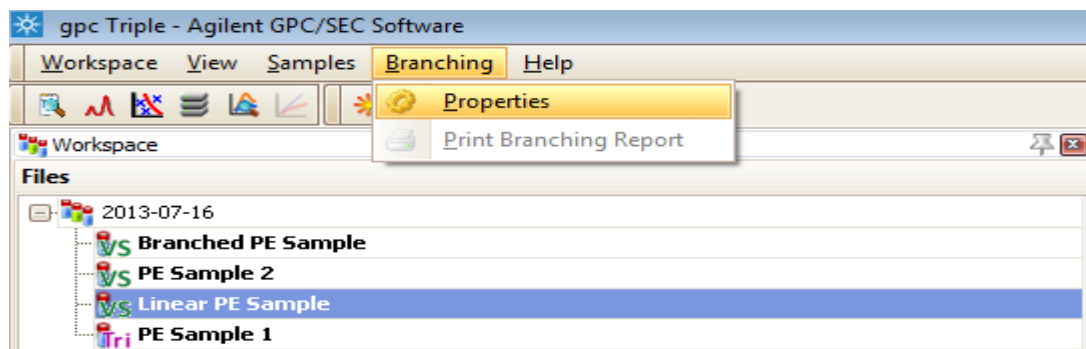
Once you have done this highlight the linear sample again and go to View & select the Branching View



The following screen pops up



Then go to Branching Tab and select Properties



The window below will pop up. Edit the window with the appropriate information as shown.

**Branching Parameters**

**Source of linear model**

☐ Use reference file      Source data: Use IV to calculate g

☒ Calculate from data fit

Fit start: 1.0 LogM      Fit end: 2.0 LogM

☐ Supply slope and intercept

Slope: 0.7      Intercept: 14.1

**Calculation parameters**

Structural model, E: 0.70 If E = 1 then calculating g'

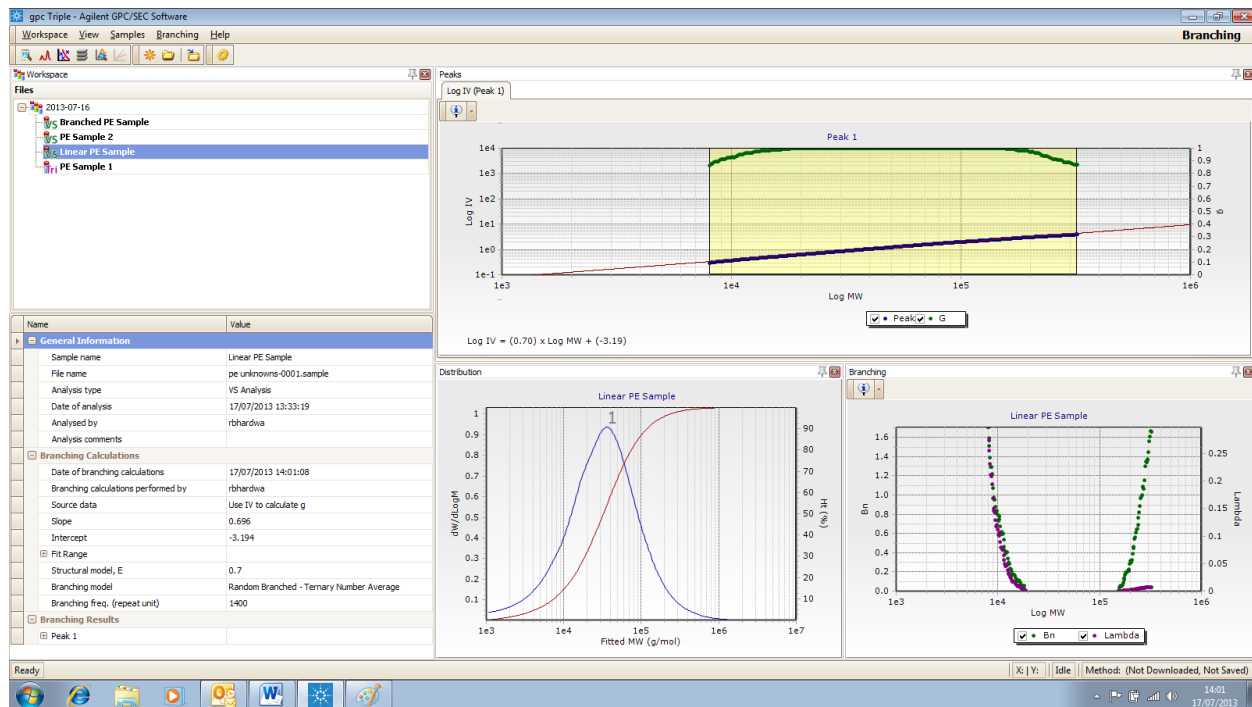
Branching model: Random Branched - Ternary Number Average

Branching freq. (repeat unit): 1400

Set as Defaults      OK      Cancel

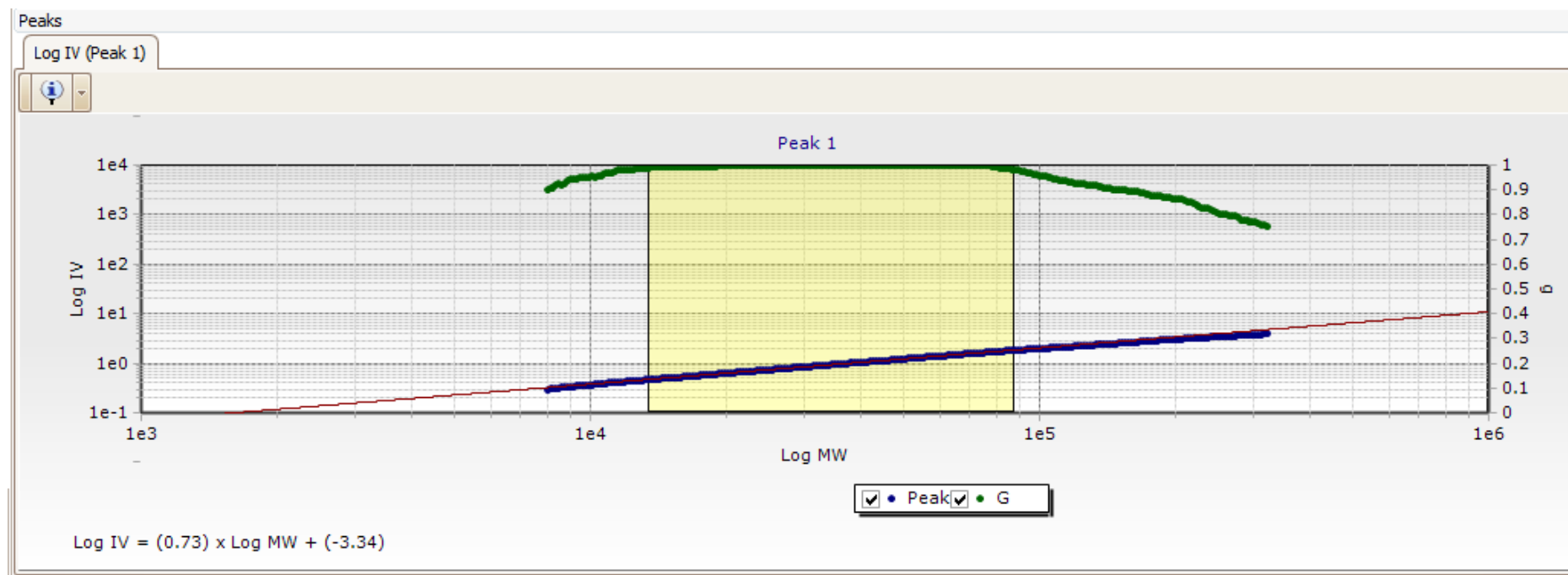
Click OK

And the following screen will pop up.

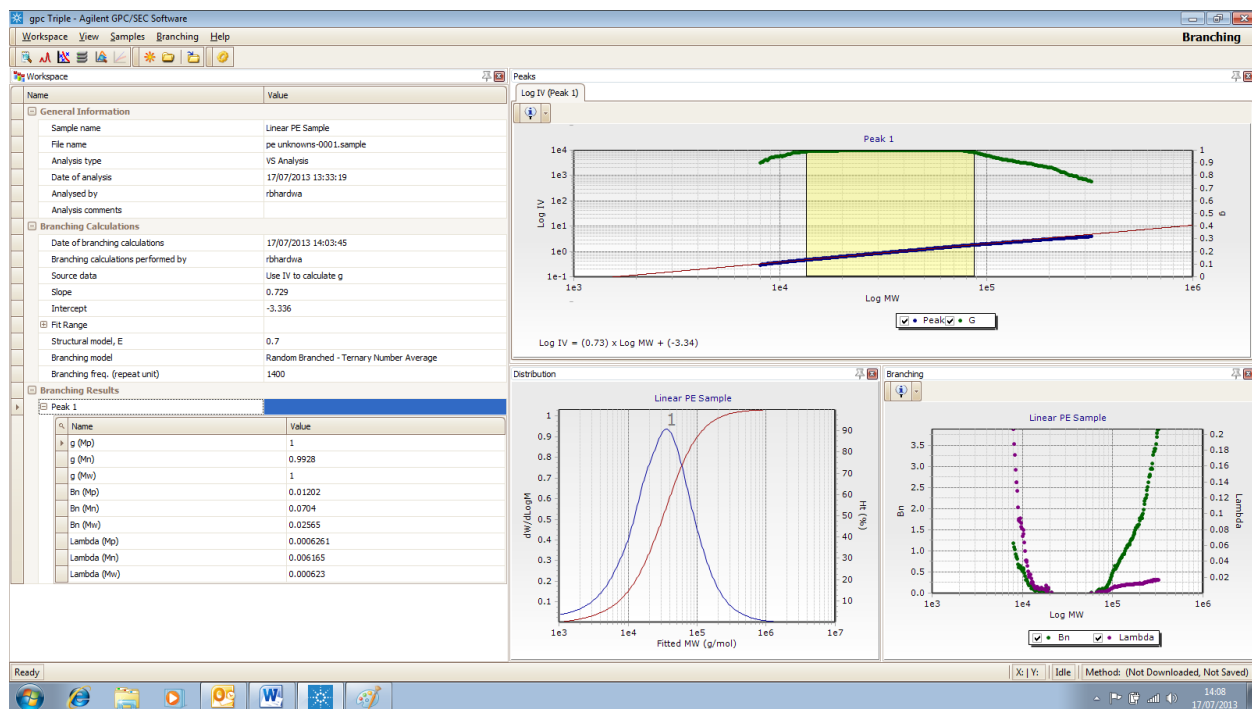


Move the highlighted region in yellow to get a good linear fit (as shown below)

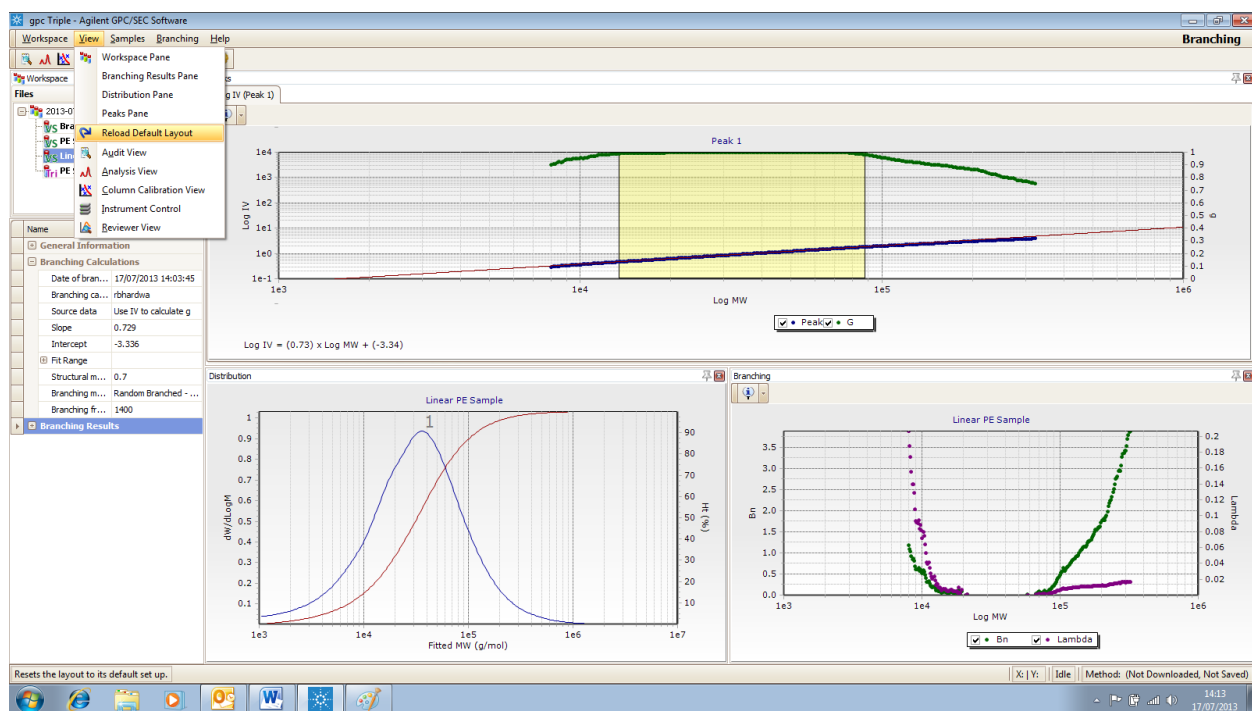




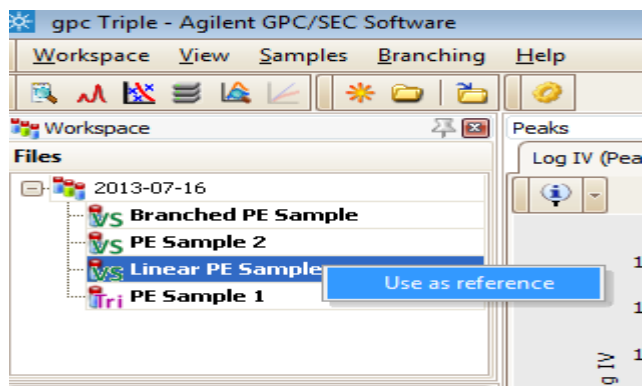
To see the results for the linear sample go to the branching Results window and click on + Peak 1, as shown below.



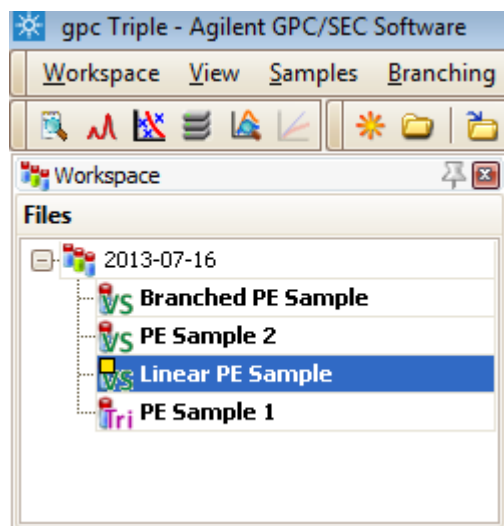
Now in order to view the linear highlighted sample go to View tab and select Reload Default layout. This will show the following window



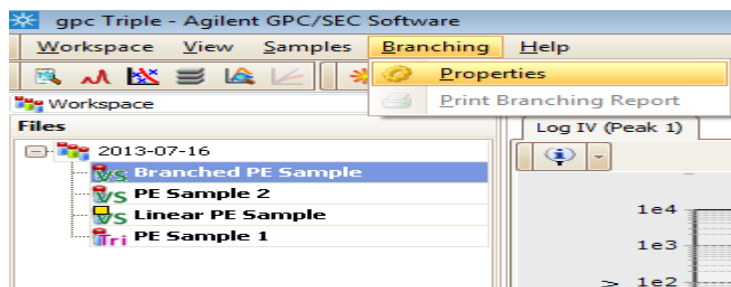
Then Right Click on the Linear PE Sample



Then left click on the Use as reference button to set this sample as the reference model that you will be using.



Now highlight the Branched sample and go to Branching tab and select Properties



Then the following window pops up

**Branching Parameters**

**Source of linear model**

☐ Use reference file      Source data: Use IV to calculate g

☒ Calculate from data fit

Fit start: 1.0 LogM      Fit end: 2.0 LogM

☐ Supply slope and intercept

Slope: 0.7      Intercept: 14.1

**Calculation parameters**

Structural model, E: 0.40 If E = 1 then calculating g'

Branching model: Random Branched - Ternary Number Average

Branching freq. (repeat unit): 1

Set as Defaults      OK      Cancel

Now we need to populate the above window as;

Branching Parameters

**Source of linear model**

☒ Use reference file      Source data Use IV to calculate g

☐ Calculate from data fit

Fit start 1.0 LogM      Fit end 2.0 LogM

☐ Supply slope and intercept

Slope 0.7      Intercept 14.1

**Calculation parameters**

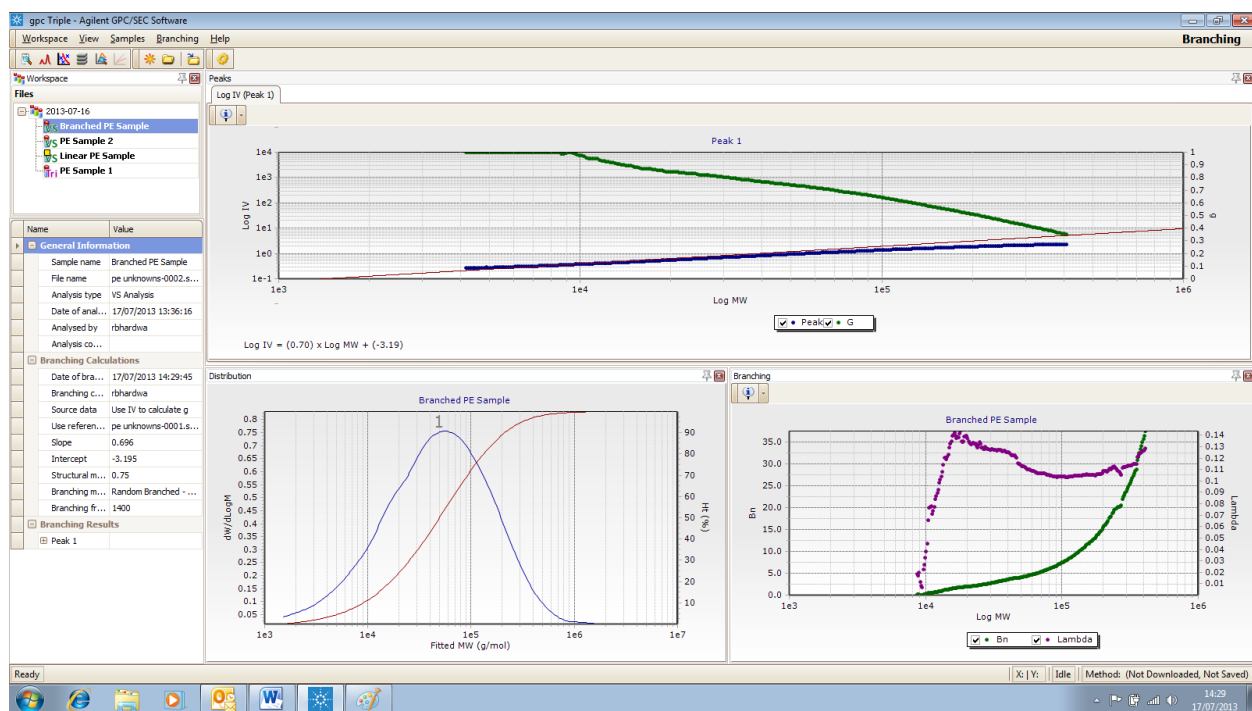
Structural model, E 0.75 If E = 1 then calculating g'

Branching model Random Branched - Ternary Number Average

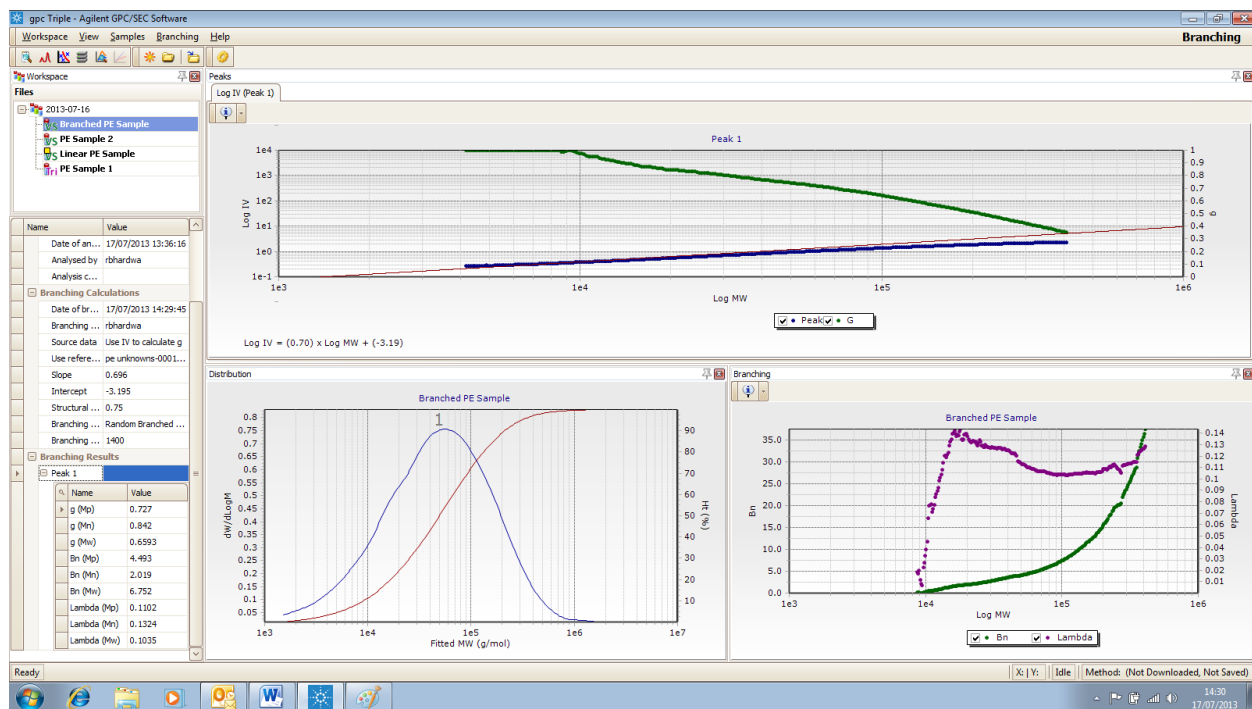
Branching freq. (repeat unit) 1400

Set as Defaults      OK      Cancel

Click OK and the screen below pops up



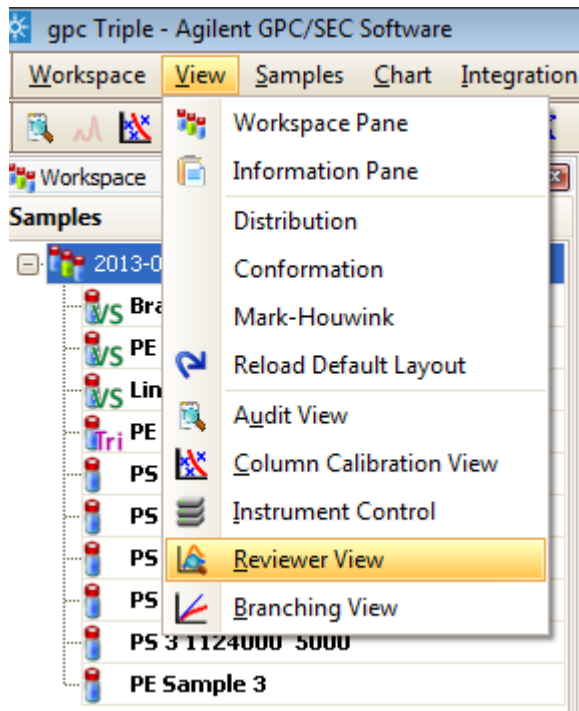
Click + Peak 1 tab to get branching data results;



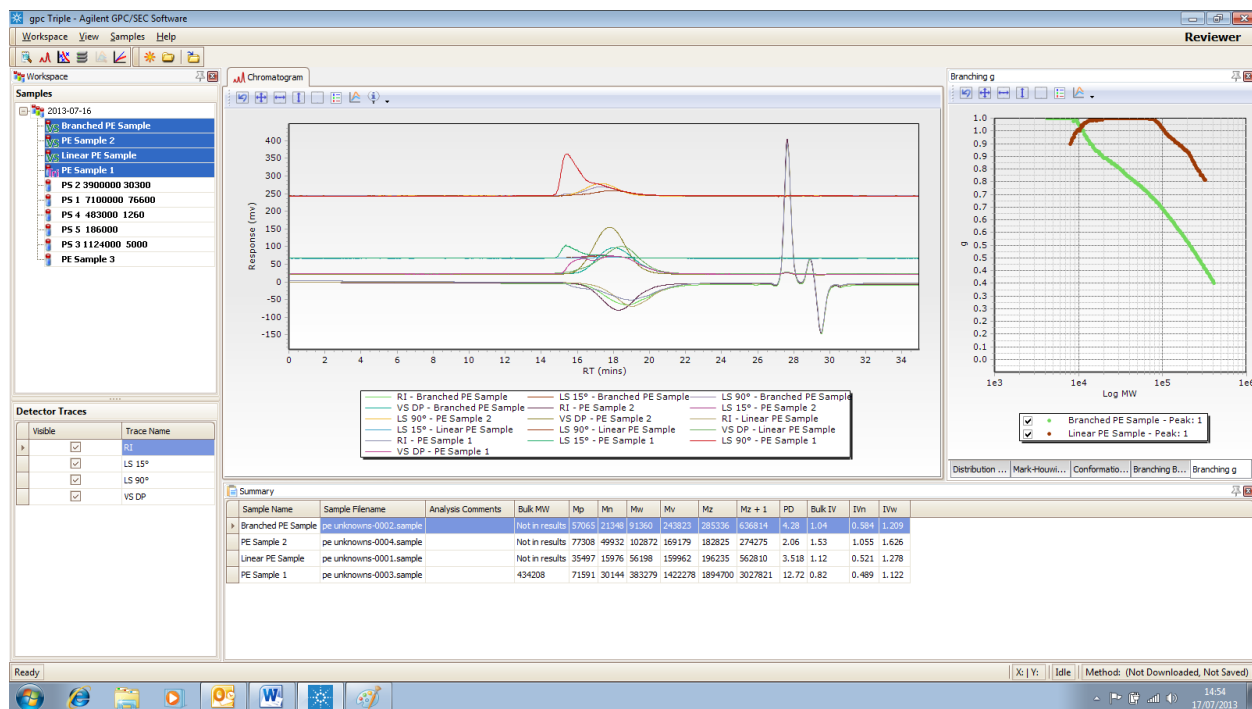


# Reviewer

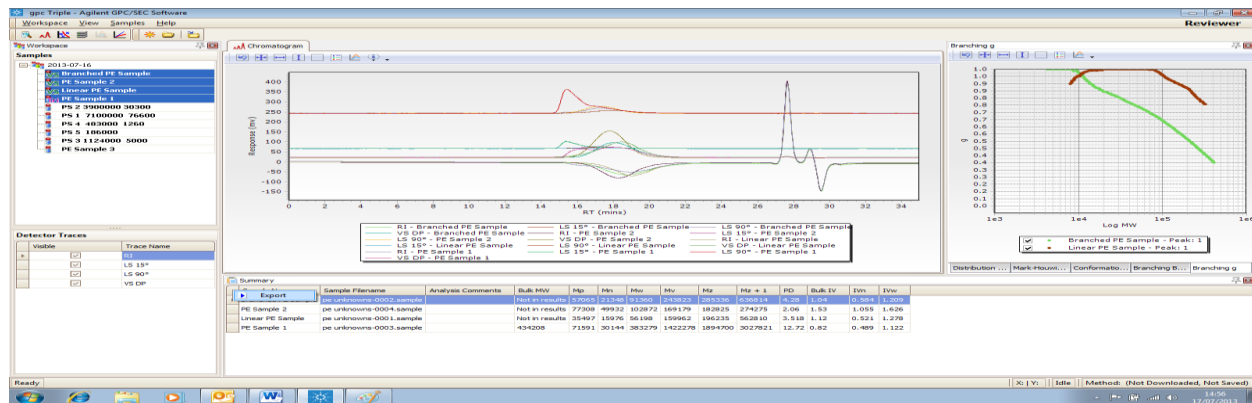
Once the samples have been collected they can all be viewed in the Reviewer window.  
Go to the View tab and select Reviewer.



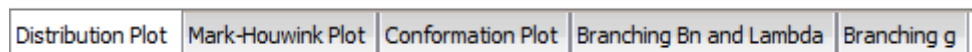
This will open the window below where you can select the files that you want to look at and the detector signals can also be selected by going to the detector traces.



The results can be exported into excel or word by right clicking the forward arrow in the summary tab.



Also by selecting the individual tabs samples can be displayed.



information generated for the

