OVERVIEW OF PEAK-ABC SYSTEM

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1. Acquiring Channel / Model

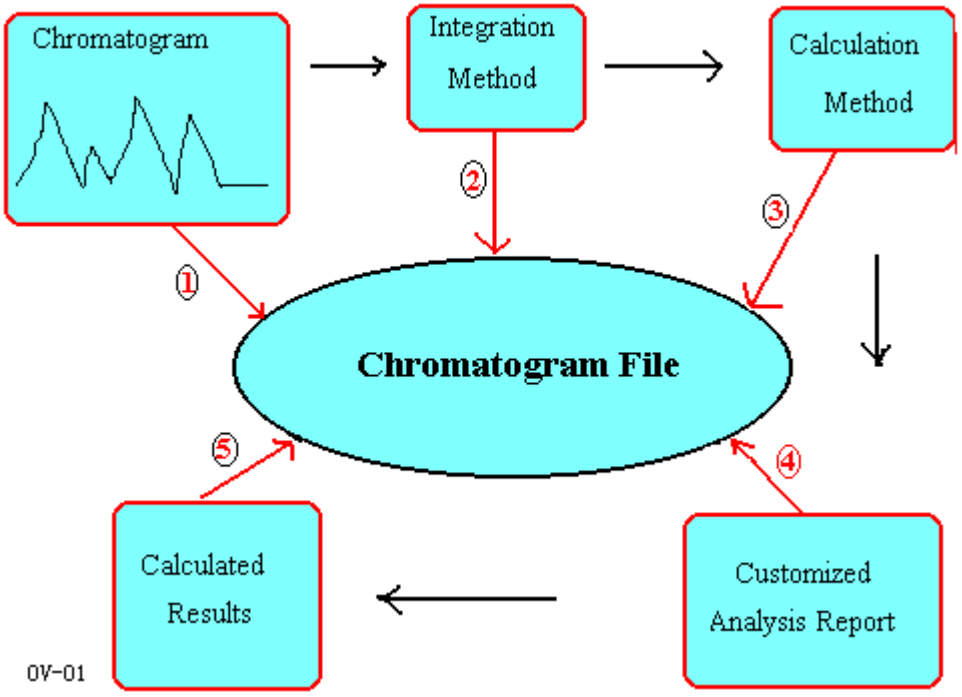
- This software system is compatible with any model of chromatographic instrument. Our state-of-the-art hardware comes in two different models, namely Single-channel Model and Dual-channel Model. The hardware for Single-channel Model is to be installed inside the computer.

- The hardware for Dual-channel Model is externally connected to the computer through a digital cable. While you can connect the two channels to the dual detectors of the same instrument for simultaneous data acquisition, you can also connect the two channels to two different instruments for independent signal acquisition.

- User has the option to define three different level of authority to access PEAK-ABC.

2. Data Storage

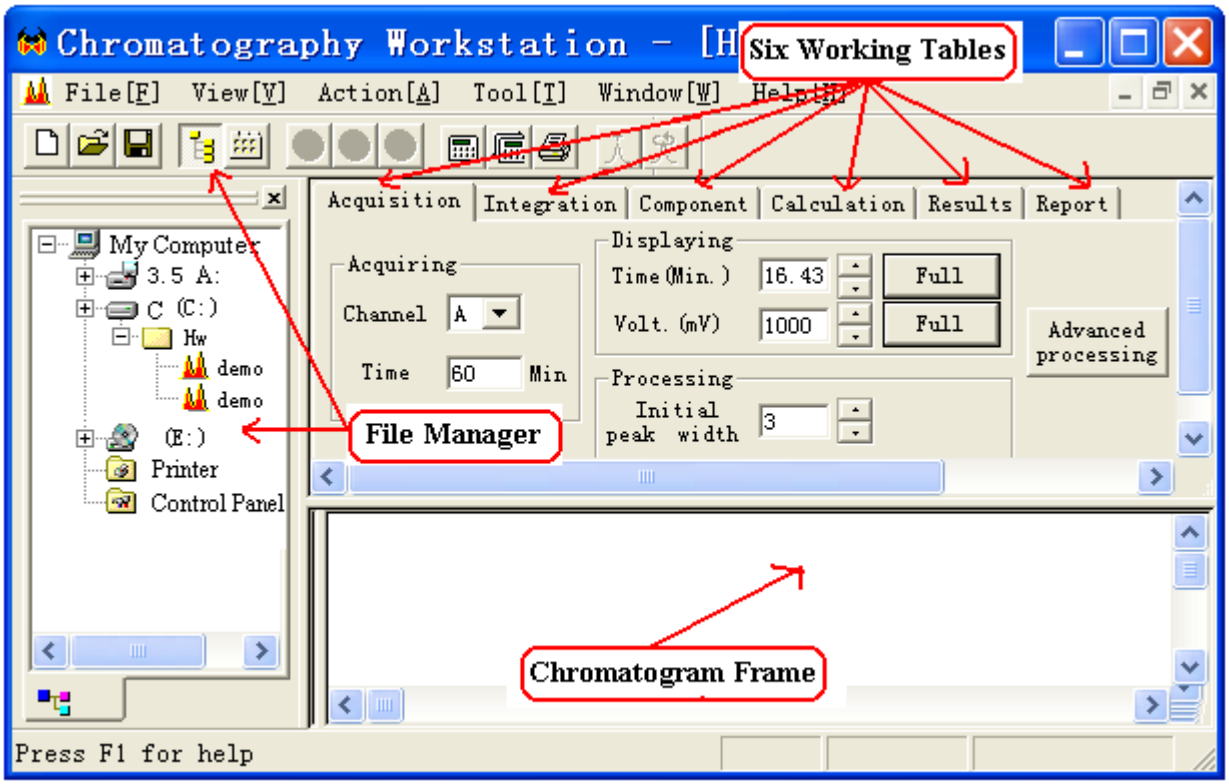
- This software system is structured in such a way that all the sequences of the data handling are neatly stored in one source document, entitled **"Chromatogram file"**. Should you need to recall the results of a particular analysis, you only need to locate one document file. Apart from being in compliance with GLP standards, this one-document structure saves you an enormous amount of time compared to other analytical software on the market today.



- Saving command could be automated at various stages of data handling to prevent loss of data.

3. Document Window Technique / Split Window Technique

- By applying **Document Window Technique** and **Split Window Technique,** a one-page Document window is designed to display all the working elements of a Chromatogram file in one screen for quick access and manipulation. Every time you start the software system, a new **Document Window** would be created ready for data acquisition. Each Document window consists of **Six Working Tables** and a **Chromatogram Frame**. After successfully installed the software, the following page would be displayed.

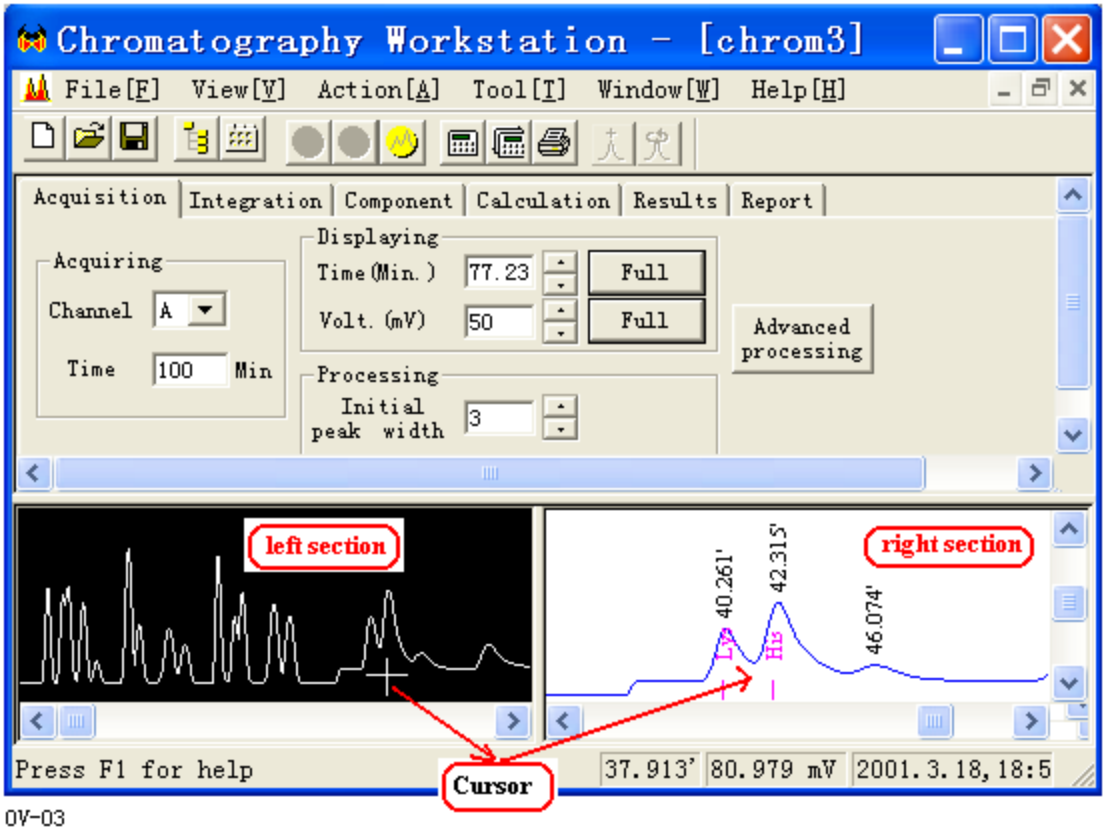


OV-02

- The **File Manager** displays the File folder contents of your computer system including the Chromatogram file folders. By clicking on the icon, you can hide the **File Manager** to create more space for the **Document Window**. You can make use of the **File Manger** to conveniently apply the various commands such as Cut, Copy, Paste and Rename to manage your files by right clicking on the mouse. Most importantly, by double clicking on the filename, you can quickly retrieve a Chromatogram file.

- The **Six Working Tables** are arranged in tag form for your easy access. Moving from one table to another is as simple as a click of the mouse on the respective tag. Each of them serves a specific function during the entire analysis process starting from acquisition of chromatogram, through to identifying and calculating of components quantities to preparing of analysis report. We shall explain more about the **Six Working Tables** in the later part of this overview.

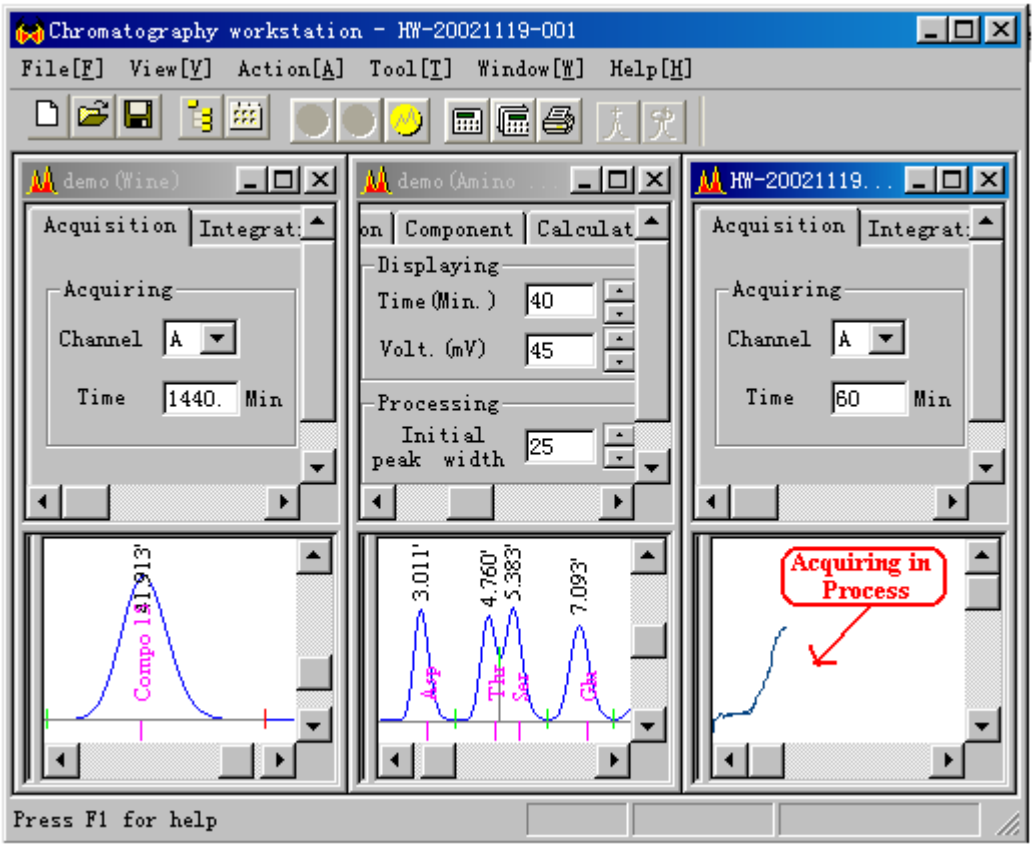
- The **Chromatogram Frame** displays the chromatogram on a real time basis as and when a chromatogram is being acquired. You can freely expand and shrink the **Chromatogram Frame** and also partition it into two sections. The **left section** displays the entire chromatogram while the **right section** displays the enlarged segment of the chromatogram following the movement of the cursor.



OV-03

4. Multi-Document Window Technique / Multi-thread Technique

- To improve the speed of operating this software, we apply **Multi-Document Window Technique** so that you can work with more than one Chromatogram files at one time. When you are working with more than one chromatogram files, there would be more than one corresponding **Document Windows** being displayed. This technique allows you to acquire a chromatogram in one **Document Window**, while re-processing an acquired chromatogram in another **Document Window**. When working with more than one **Document Window**, you are able to stack them together or display them side-by-side, for easy comparison.

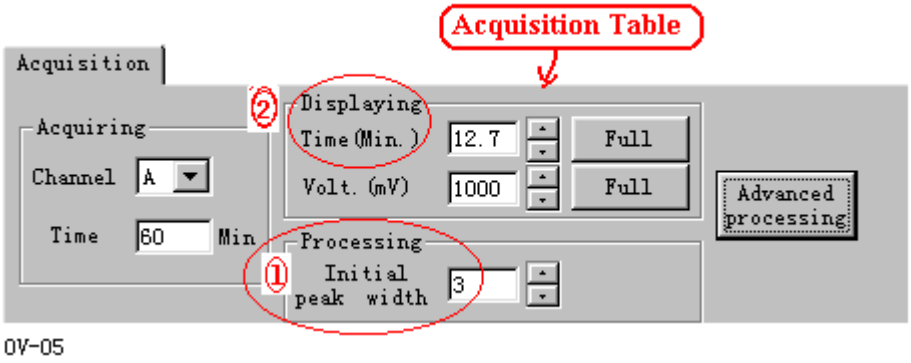


OV-04

- This software is based on the **Multi-thread Technique** so that you can perform other functions within a Document window when acquisition of signal is in process. For example, you are able to adjust the **Displaying** parameters as and when chromatogram is being acquired. You can also input the **Component Table** or **Report Table** while acquisition is in process.

5. Patented Noise Filtering Method / Acquisition Table / Display

- **Acquisition Table** is for you to input the acquiring parameters to be applied during chromatogram acquisition. When data signal is being acquired, we apply our patented **Noise Filtering Method** to eliminate noise so that we can detect even the weakest level of noise close to Baseline noise.

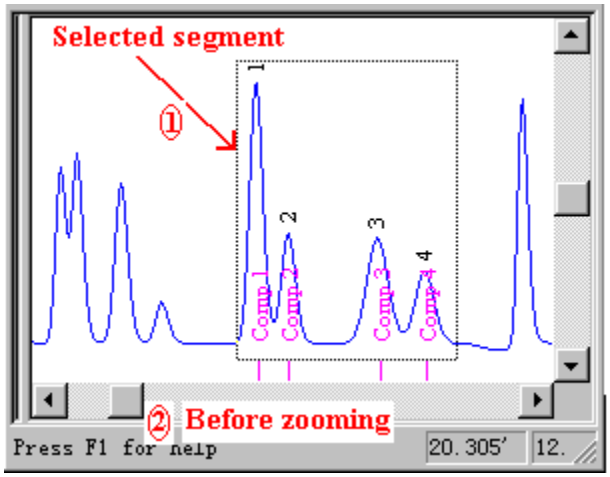


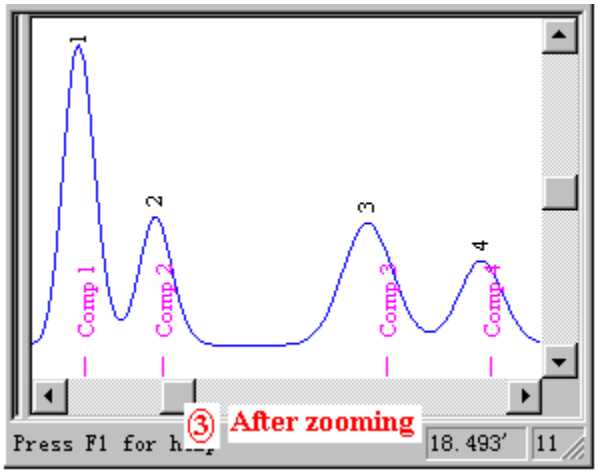
- Instead of having to adjust numerous parameters as is typical in other software, you only need to adjust one single parameter to process complicated chromatogram. This one and only one processing parameter is called **Initial Peak Width**.

- By applying **Multi-thread Technique**, user is able to make real time adjustment to the scale of the chromatogram horizontally and/or vertically as and when data signal is being acquired.

- User has the option to change the labeling of peaks and also the description and scales of the horizontal and vertical axes.

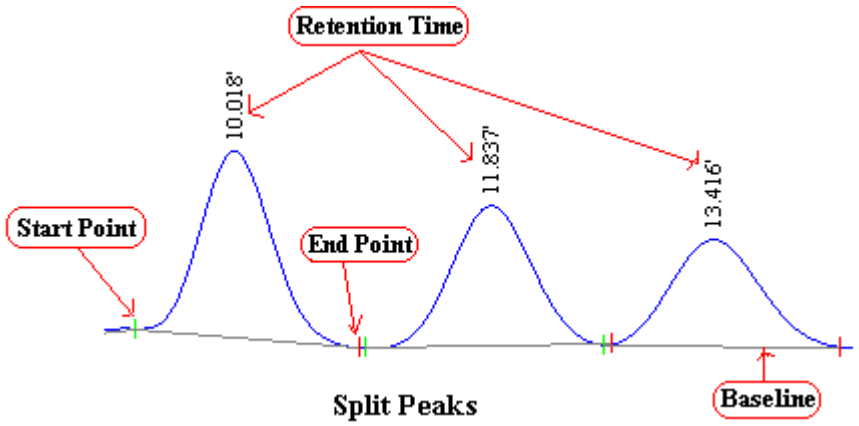
    - User can drag on the mouse to zoom in on a selected segment of the chromatogram for close examination of small peaks, Baseline noise and precision of manual integration method. Simply double click on the mouse if you wish to un-zoom.





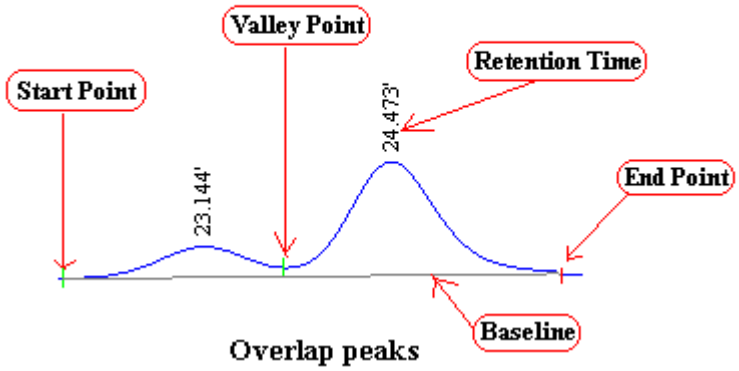
6. Marking of Detected Peak

- When an independent peak is detected, a short green line would be marked to indicate the **Start Point** and a short red line would be marked to indicate the **End Point** of the peak together with its **Retention time**. If a few connecting peaks are treated as split, (refer to the diagram below) each of the peak would have its own **Start Point** and **End Point** as shown below. Should the **End Point** of one peak coincides with the **Start Point** of the next peak, a short green line would be displayed instead. The **Baseline** that we use to integrate the area of each peak is the line that connects the **Start Point** of a peak to its respective **End Point**.



Split Peaks

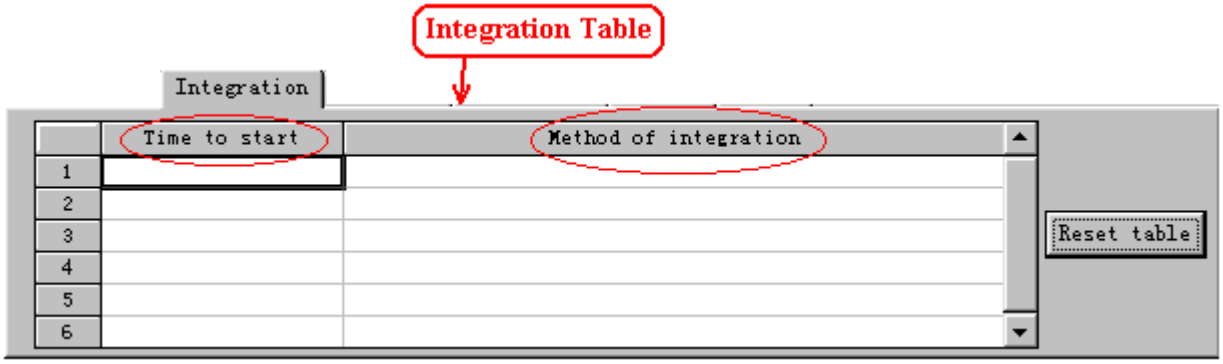
- If two connecting peaks are treated as overlap, (refer to the diagram below), a short green line would be marked to indicate the **Start Point** of the group of peaks, another short green line would be marked to indicate the **Valley Point**. A short red line would be marked to indicate the **End Point** of the group of peaks. When integrating the area of each peak, a vertical line is dropped from the **Valley Point** to the **Baseline,** which is the line that connects the **Start point** of the group of connecting peaks to the **End Point** of the group of connecting peaks.



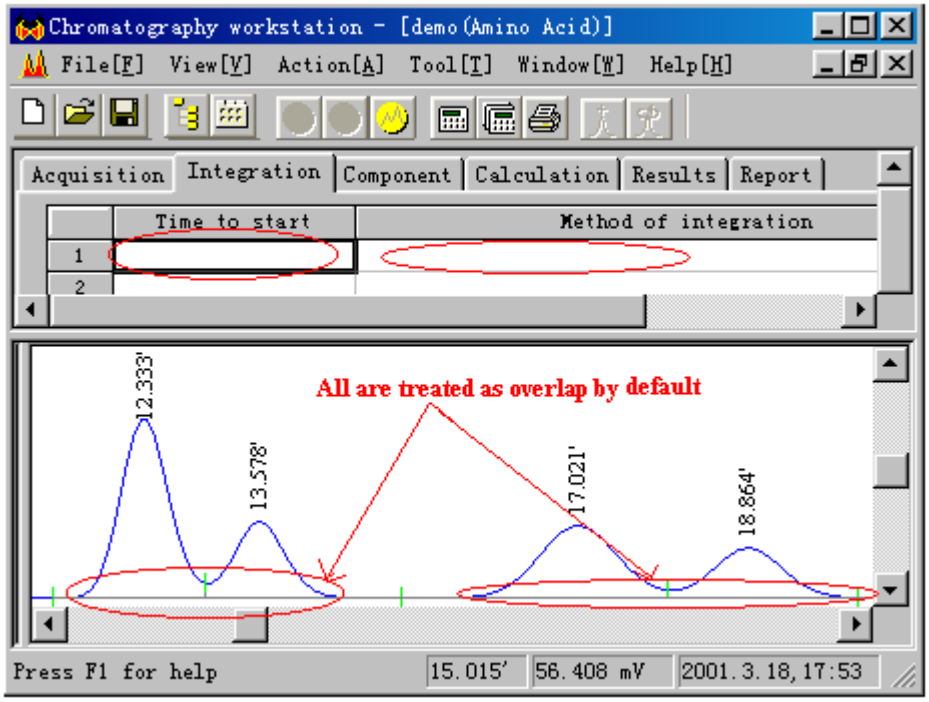
Overlap peaks

7. Fine-tuning the chromatogram / Integration Table

- If you need to apply Manual integration to certain segment of the chromatogram, we make it really easy for you to select the integration method and to specify the segment to apply the integration method by providing you with the **Integration Table**. Pre-acquisition input made in **Integration Table** would be applied as and when data signal (i.e chromatogram) is being acquired. Post-acquisition input made in the **Integration Table** would be applied immediately upon specification.



- For example, all the peaks in the following chromatogram are being treated as overlap by default as is indicative by the blank **Integration Table**.



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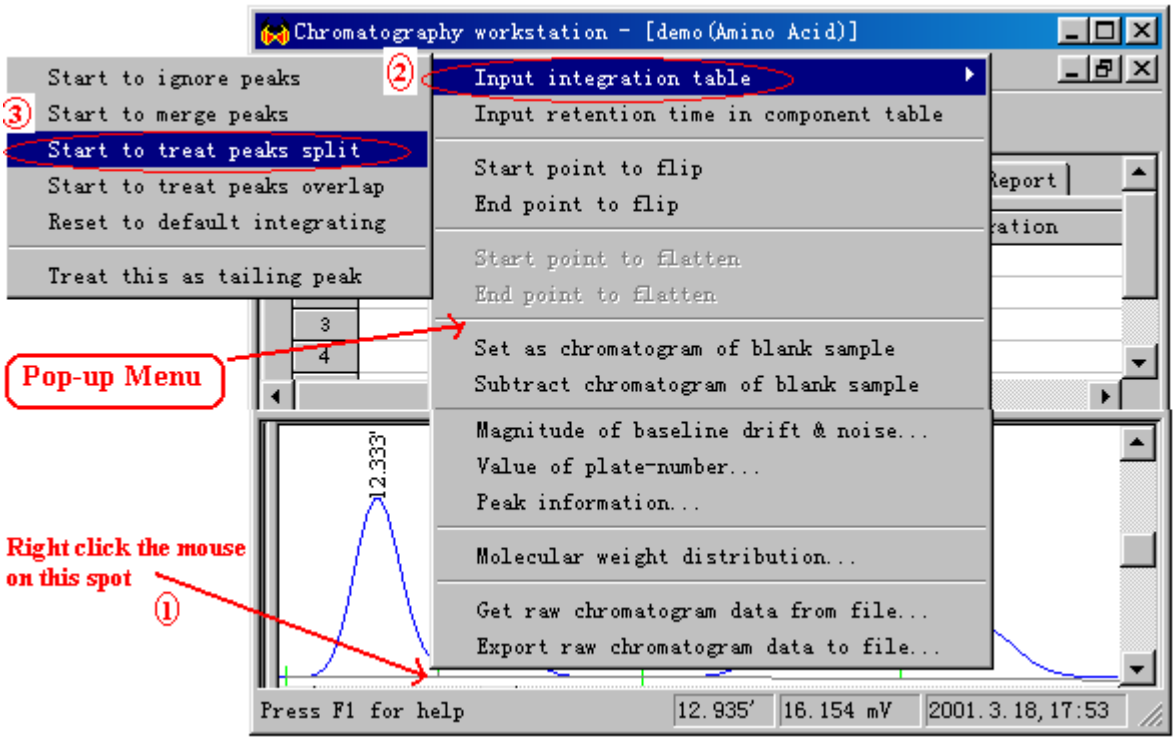
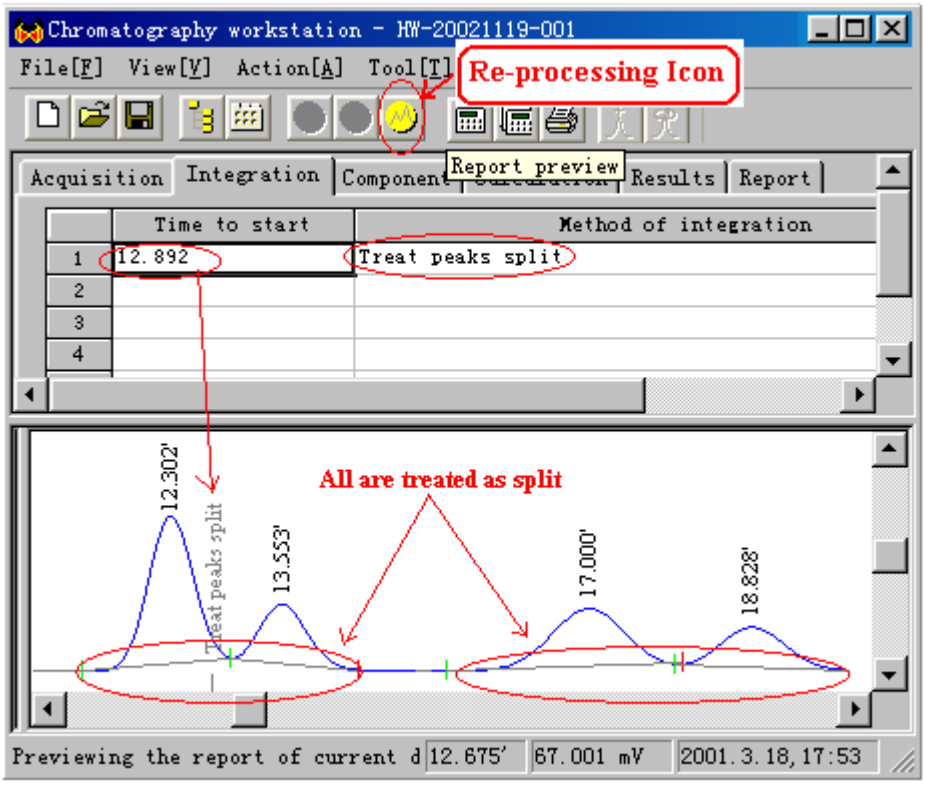
- If you think the first two peaks should be treated as split, position the cursor before the **Start point** of the second peak, right click on the mouse to access the **Pop-up menu**. Go to "**Input integration table**" to view the whole range of integration methods, click to select "**Start to treat peaks split**".



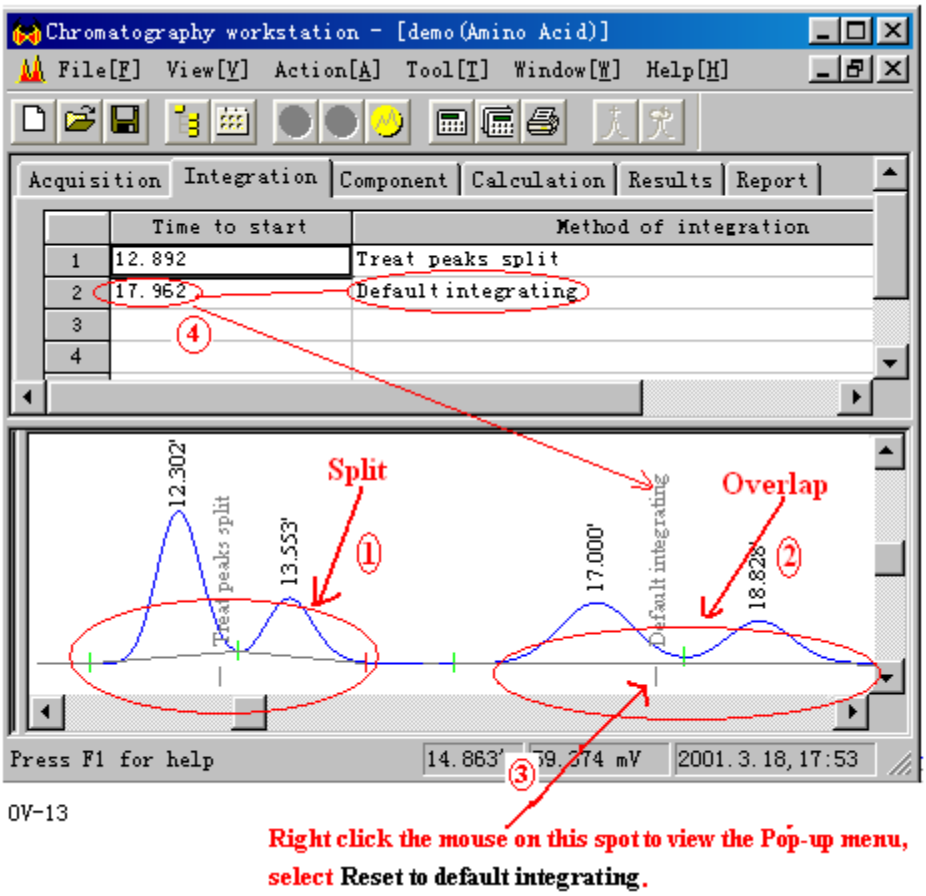
- The selected integration method and the time to start applying would automatically be captured in the **Integration Table**. Moreover a corresponding marking would be made on the x-axis to display the selected integration method, corresponding to the spot, where you right click on the mouse. You can adjust the time by simply repositioning the marking by dragging it using the mouse.



OV-12

- You will note that after applying this command, all the peaks towards the right of the marking are being treated as split. Since we only want to treat the first two peaks as split while leaving the rest unchanged, we need to input another integration method to end this command.

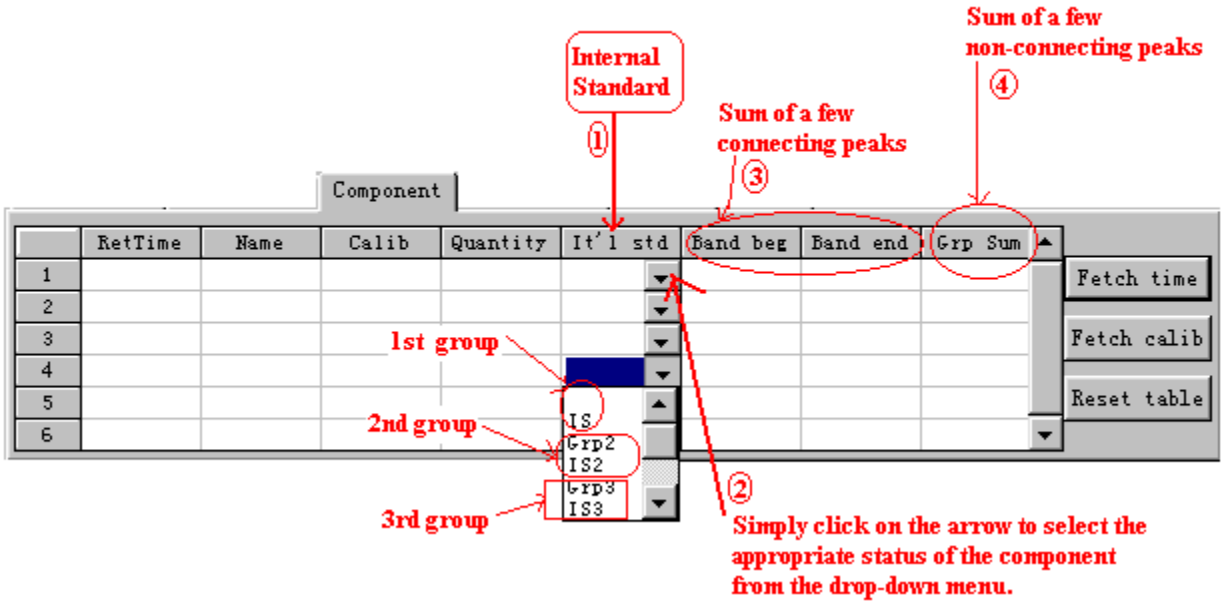
- Position the cursor before the **End Point** of the third peak, right click on the mouse to access the **Pop-up menu**. Go to **Input integration table**, select **Reset to default integration**. The selected integration method and the time to start applying would be captured in the **Integration Table**. A corresponding marking would be made on the spot where you right click on the mouse to display the selected integration method. You can adjust the time by simply repositioning the marking by dragging it using the mouse.



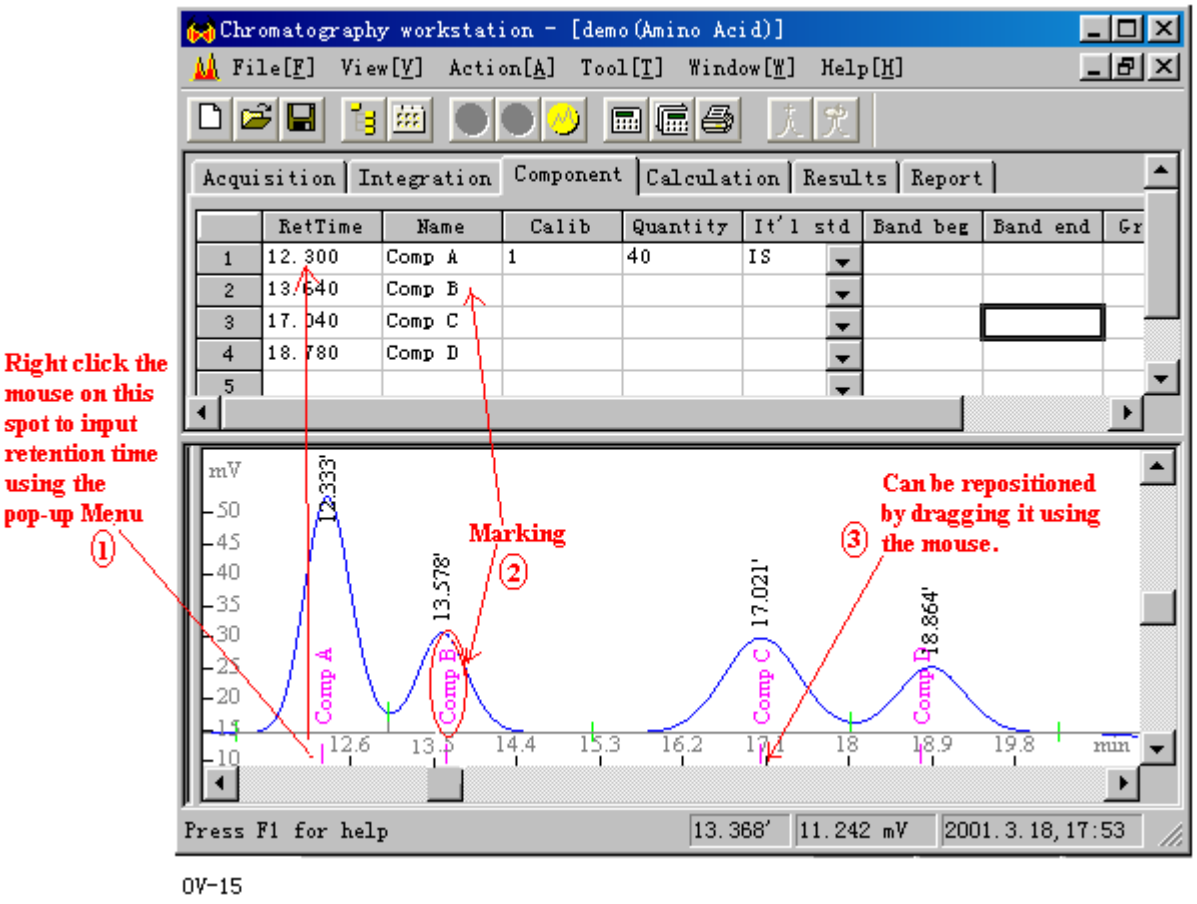
- The first two peaks are now treated as split while the last two peaks are being treated as overlap.

8. Identifying Components / Component Table

- The **Component Table** is for you to conveniently identify the components and Internal standard by their expected retention times, their name, their calibrators and their known quantities, if applicable. This software permits you to add more than one Internal standard to be applied to different groups of components. This way of identifying component and Internal standard is indeed very convenient. You can make use of the remaining three columns to calculate the aggregated quantity of a few components. For connected peaks, you can make use of the "**Band beg** (begin)", and "**Band end**". For non-connecting peaks, you can make use of the **Grp** (group) **sum** column to identify the peaks.



- For each component identified in this table, a marking would be made on the x-axis accompanied by its given name. When deciding whether a component is present or not, so long as the marking on the x-axis lies within the **Start Point** and **End Point** of a peak, the component corresponding to that peak is regarded as present. Input of retention time can be done by right clicking on the mouse to select the command from the **Pop-up menu**. The time corresponding to the position where you right click on the mouse would be captured in the **RetTime** (retention time) column. In the case of changes in retention time, you can conveniently reposition the marking by simply dragging it with the cursor. The time captured in the **RetTime** column will also be adjusted automatically.



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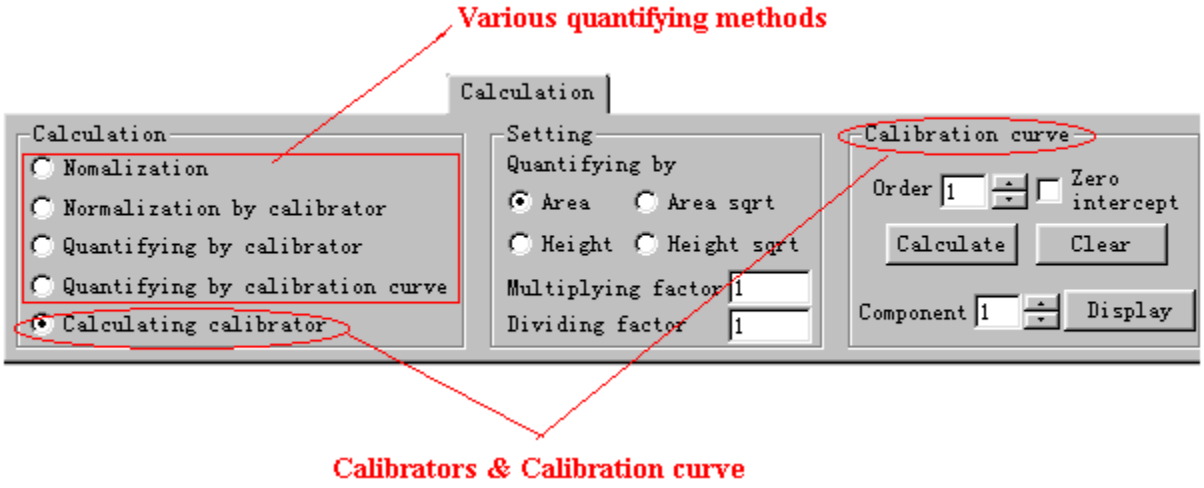
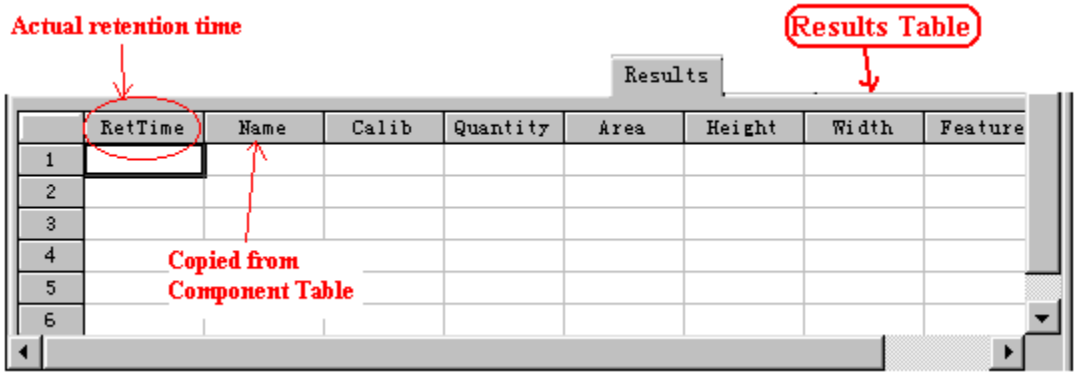
9. Quantifying Methods / Calculating Table

- The **Calculation Table** has two functions. The first function is for you to calculate the calibrator and to construct the calibration curve. The second function is for you to select the desired quantifying method, namely: Normalization, Normalization by calibrator, Quantifying by calibrator and Quantifying by Calibration curve.



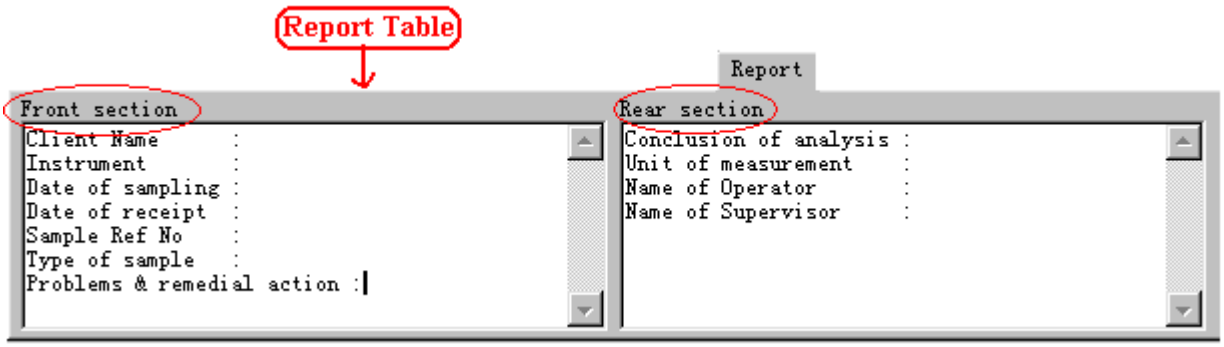
10. Results of Analysis / Results Table

- After activating the **Calculating** command, you can go to the **Results Table** to view the results of the calculation. When calculating the calibrators of a Standard sample, the calculated calibrators would be shown in the **Calib** (calibrator) column. When calculating components quantities of an unknown sample, the calculated quantities would be shown in the **Quantity** (quantity) column.



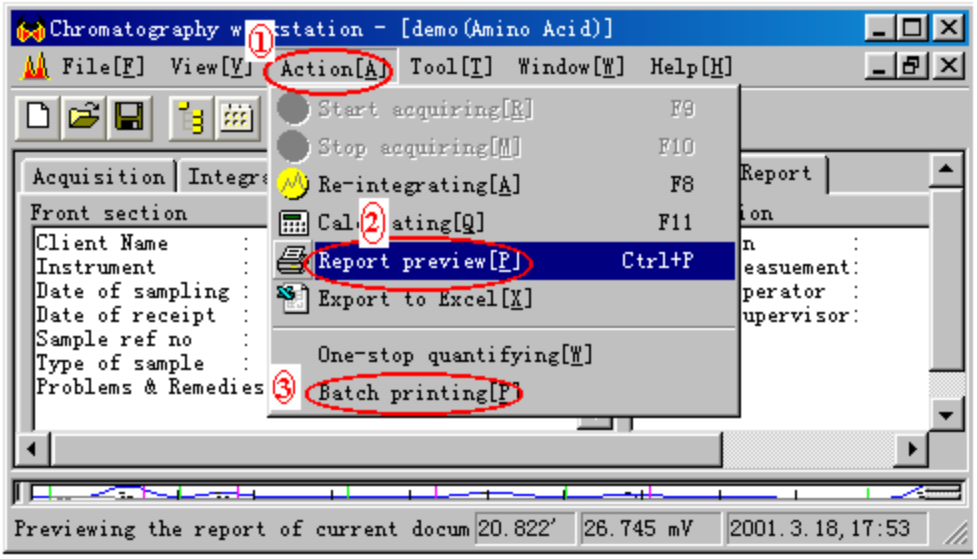
11. Customized Analysis Report / Report Table

- **Report Table** is for you to key in external reference information about the analysis to be included in the analysis report and also for future reference. The **Front section** and the **Rear section** of the **Report Table** are for you to key in additional reference information pertaining to the analysis for future reference. Examples of such reference information are Name of client, Date of sample, Name of operator, Method of sampling, Problems encountered and remedial actions taken and Conclusion etc. Such information would be permanently stored as part of the chromatogram file and is readily available for your viewing every time you revisit the file.



- You will recall, of course, that all the working elements of an analysis are permanently stored in one source document entitled "**Chromatogram File**". It is this structure that enables us to generate the analysis report to be inclusive of not only the chromatogram, but also the results of the calculations as well as the reference information which you had keyed in. This is in compliance with the standards of GLP (Good Laboratory Practice) requirements.

- The analysis report can be printed in Microsoft Words or WordPad. This Report preview function is for you to pre-view the report before printing. This batch printing command is for you to print a few analysis reports in one go.



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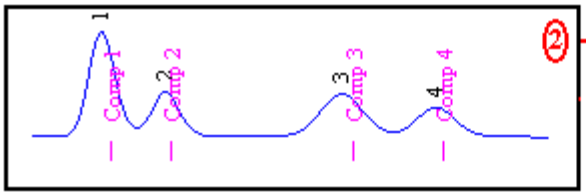
- Please refer to the following diagram for the format of a typical analysis report. Apart from the reference information that can be keyed in the **Front Section** and **Rear Section** of the **Report Table**, you are also given the option to include or exclude certain calculated results in the analysis report. Thus, you have the flexibility to customize a report format that best suit your need.

XXXX Report → Title

time: Wed Nov 27 17:31:51 2002
Injection time: Sun Mar 18 17:53:47 2001
Client Name :
Instrument :
Date of sampling :
Date of receipt :
Sample ref no :
Type of sample :
Problems & remedies :

① → Front Section of Report Table

File opened: C:\HW\Program\demo(Amino Acid)2.hw



② → Chromatogram

Selected Calculated results ③

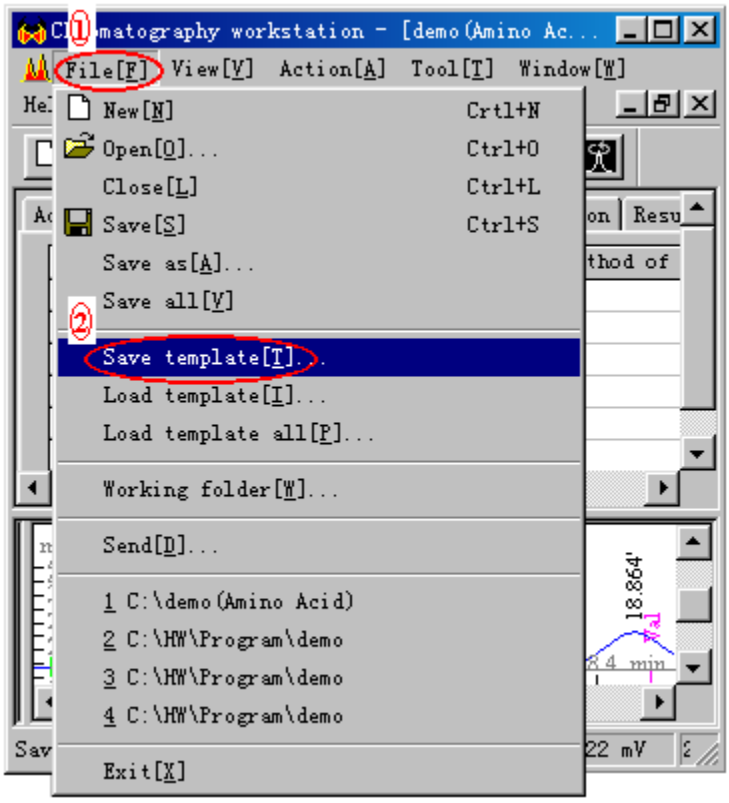
S/N	RetTime	Name	Qty	Calib	Area	Height	Width
1	12.333	Comp 1	0		1442623	38146	35.516
2	13.578	Comp 2	0		685290	16381	39.287
3	17.021	Comp 3	0		1022361	15789	60.809
4	18.864	Comp 4	0		708217	11220	59.278
Total			0		3858491	81536	

Conclusion :
Unit of measurement :
Name of operator :
Name of supervisor :

④ → Rear Section of Report Table

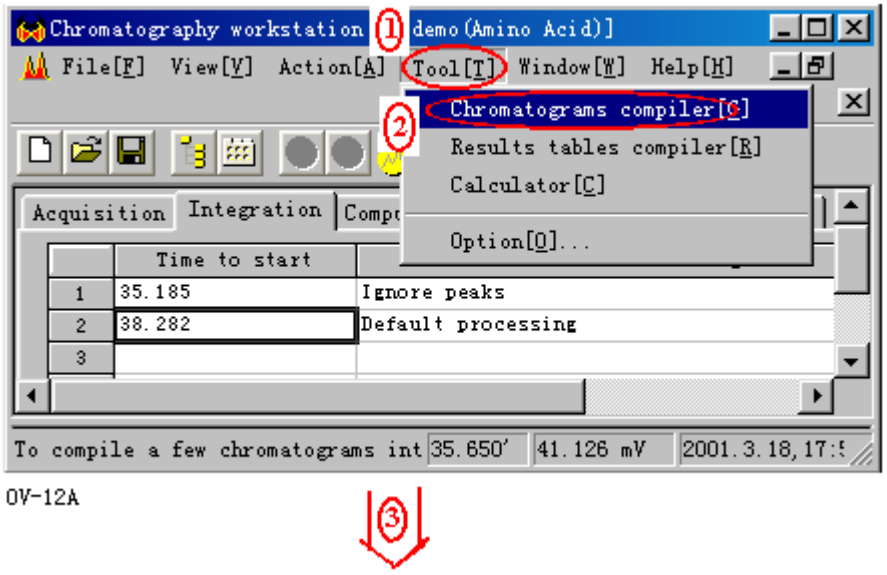
12. Save Template Command

- For repeated analysis of samples of a similar nature, some of the settings made in the working tables are applicable for subsequent analysis. We provide you with a **Save template** command to store these common settings for easy retrieval.

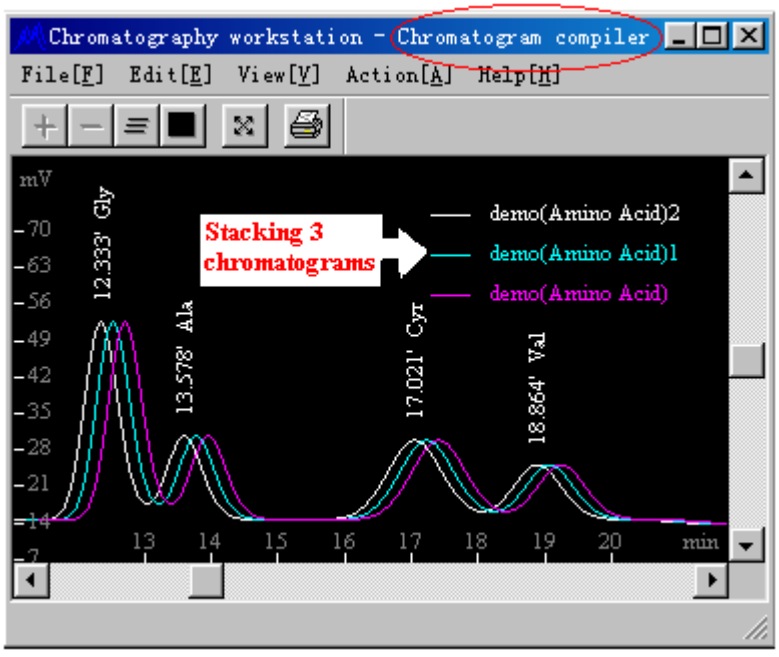


13. Chromatograms Compiler / Overlay Chromatograms

- Another distinct feature of this software is the **Chromatograms compiler**. You can conveniently overlay or stack a few chromatograms for comparison.



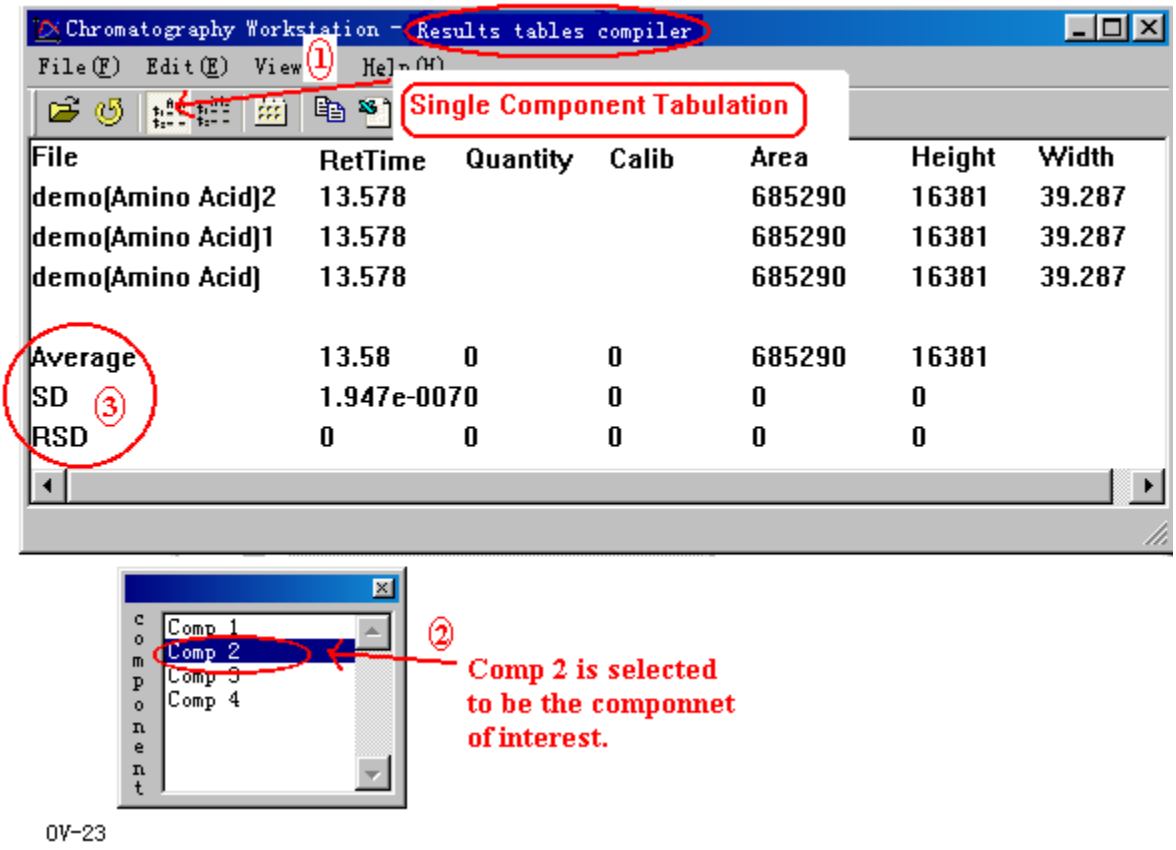
OV-12A



14. Results Tables Compiler

- Another distinct feature of this software is the **Results Tables compiler**. You can conveniently tabulate the results of past analysis in a **single-component tabulation** and **multiple-component tabulation** to calculate the average component quantity and relative standard deviations.

- Single-component tabulation



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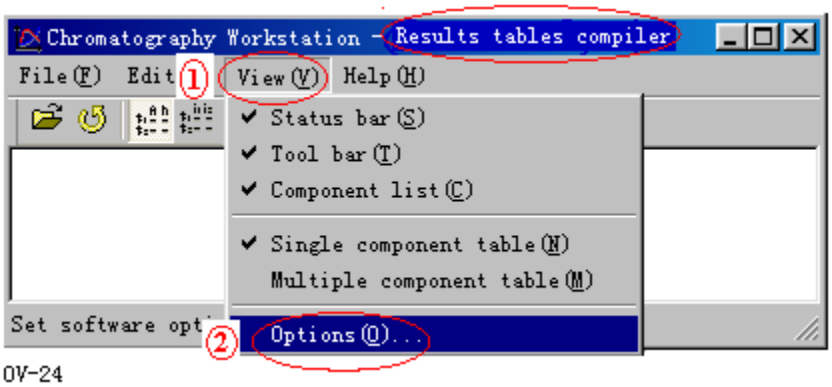
- Multi-component tabulation



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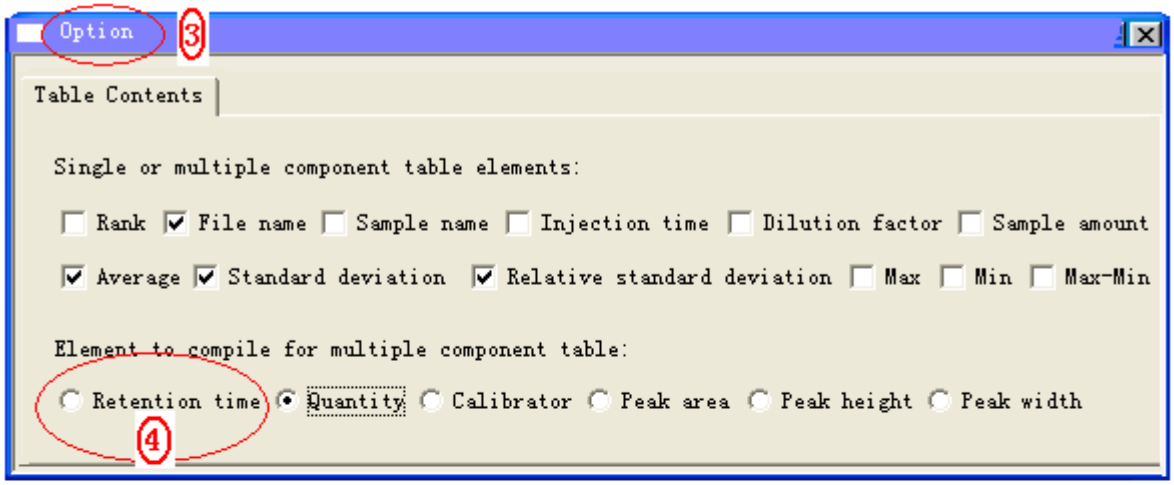

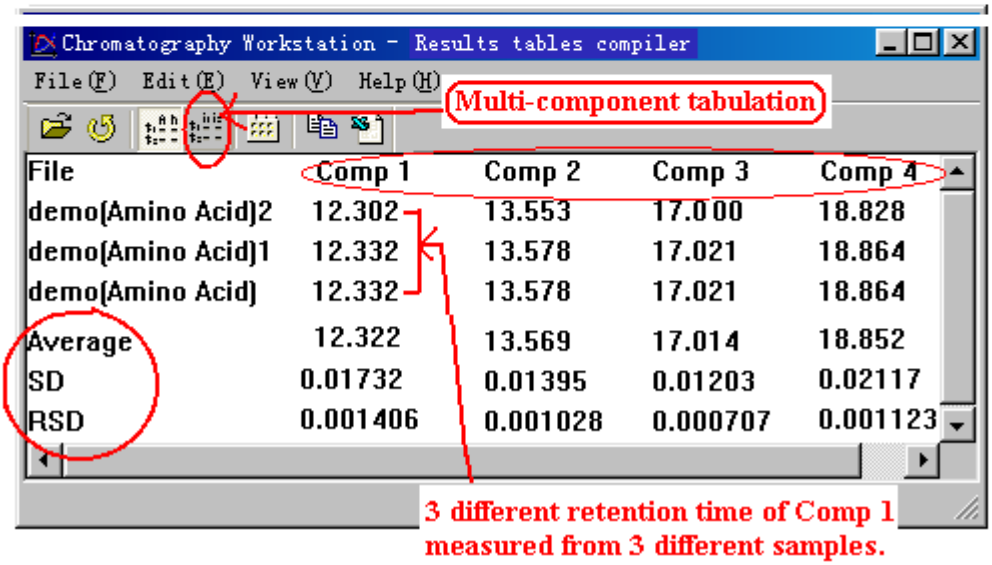

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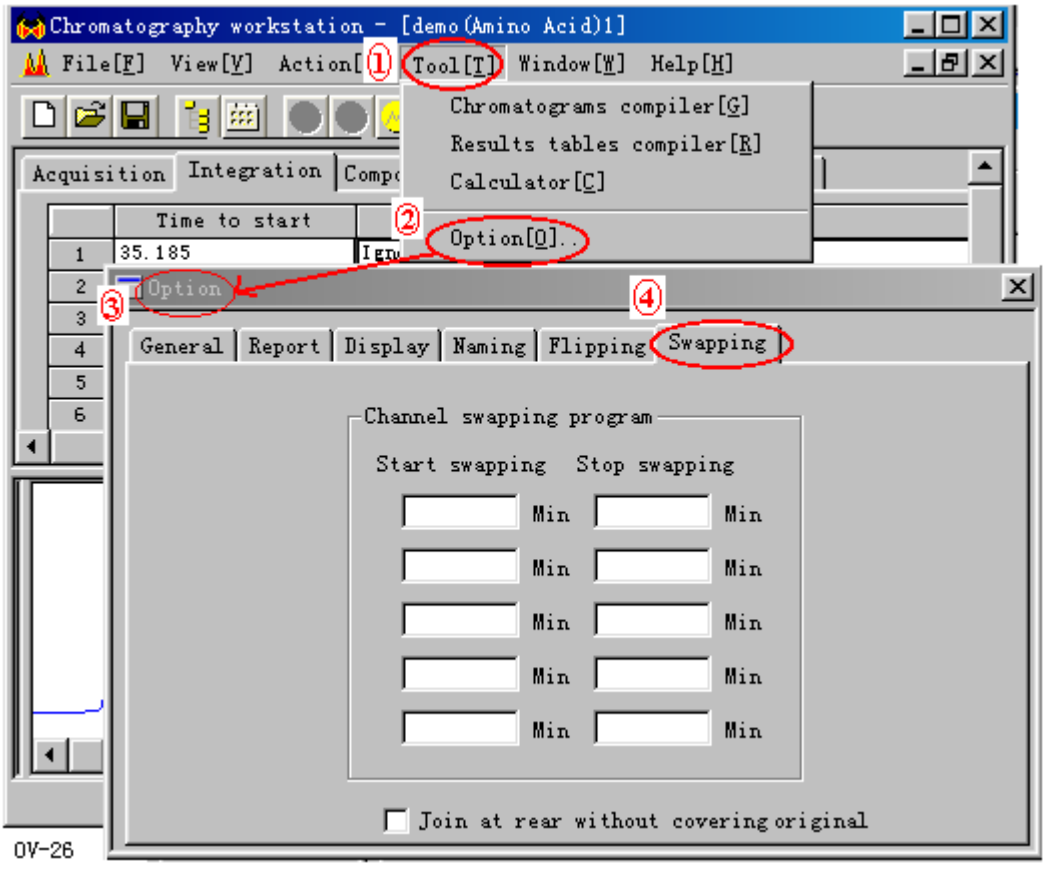
15. Swapping segment of chromatogram during simultaneous acquisition

- For the two chromatograms acquired from the two detectors of the same instrument, we provide you with real time **Swapping** command to merge the two chromatograms into one before you proceed to identify and quantify the components.

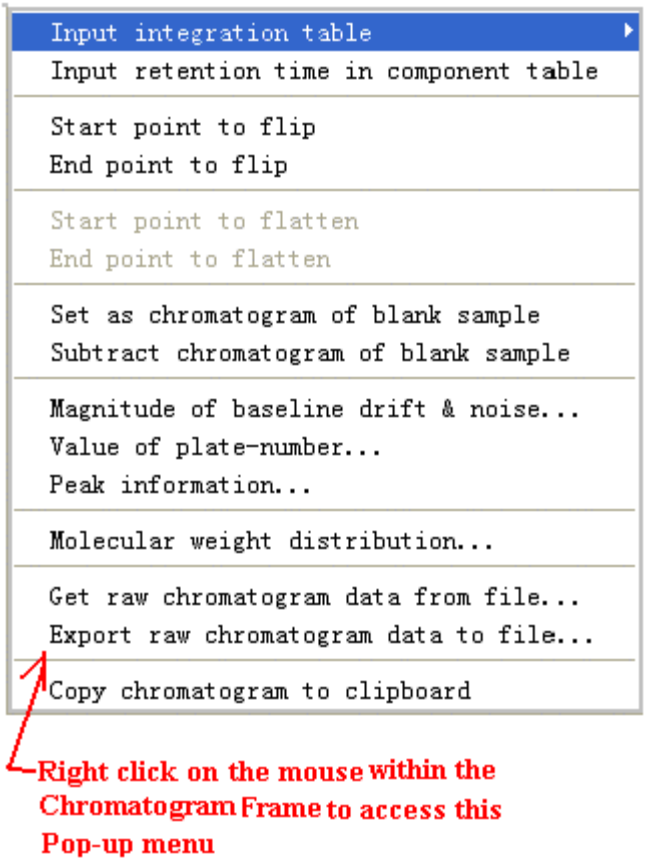


16. Other features available in this software

- Fully automate the entire data handling process starting from acquisition of data signal, through to integration of the chromatogram, to calculation of components quantities, to printing of the analysis report.

- Fully automated to work with Auto-sampler to analyze batch sample of same mixture and also batch sample of different mixtures. For batch sample of different mixtures, user can set different acquisition duration and different quantifying methods for each sample in the queue.

- Please refer to the following diagram for other commands contained in the **Pop-up menu.**



17. Special Versions for specific industries

- Before we end this overview, we would like to bring to your attention that different versions have been developed to cater for the need of different industries. Special versions are available for:
  - Amino acid analysis;
  - Natural gas analysis;
  - Liquid gas analysis;
  - GPC analysis;
  - Insulation oil analysis;

Thank you for your attention and time.