NIST EI Mass Spec Search Class
Part III: AMDIS (NIST) for Processing EI Mass Spectral Data Files

11/30/2024

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- *Retired* Research Fellow, Eastman Chem. Co.*
- *42 years experience unknown identification*
- *Now Consultant, MS Interpretation Services*
- *Specialties[1] EI GC-MS, LC-MS/MS, Chemical Ionization,[7] Accurate Mass, Derivatization,[8,9] MS library management, SciFinder,[10] Chemspider,[10] Surfactant ID,[11] NMR, GC-IR, organic synthesis, matrix ionization effects,[21] etc.*

Eastman Chemical Company, Main Site, Kingsport, TN
50 Manufacturing Sites Worldwide, ~14,500 Employees

>50 Mass Specs Networked
Worldwide

* https://en.wikipedia.org/wiki/Eastman_Chemical_Company

NIST EI Mass Spec Search Class

Part 0: Changes in EI NIST23 Program (V3.0)
Part I: Spectral Searches with NIST MS Search
Part II: Structure Searches with NIST Search and MS Interpreter
Part III: AMDIS (NIST) for Processing EI Mass Spectral Data Files
Part IV: Advanced NIST Hybrid Search of EI Spectra
Part V: Creating and Sharing User EI and MS/MS Libraries
Part VI: Creating and Using Retention Indices in NIST Software
Part VII: Tracking Complex Coelution with AMDIS and NIST Search

Link to Full Course

Table of Contents: *Basic* AMDIS Features Discussed in Handout

Very Diverse Program, *Many* More Features Discussed in Manual[3]

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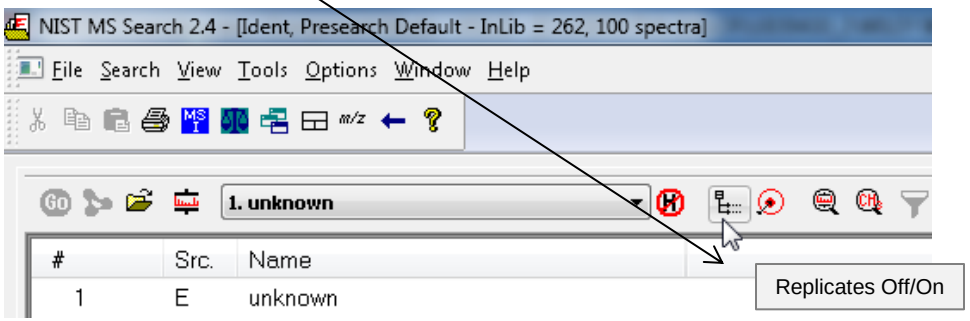
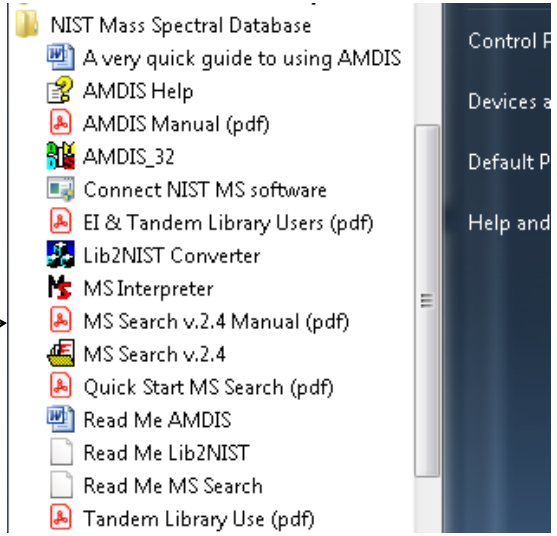
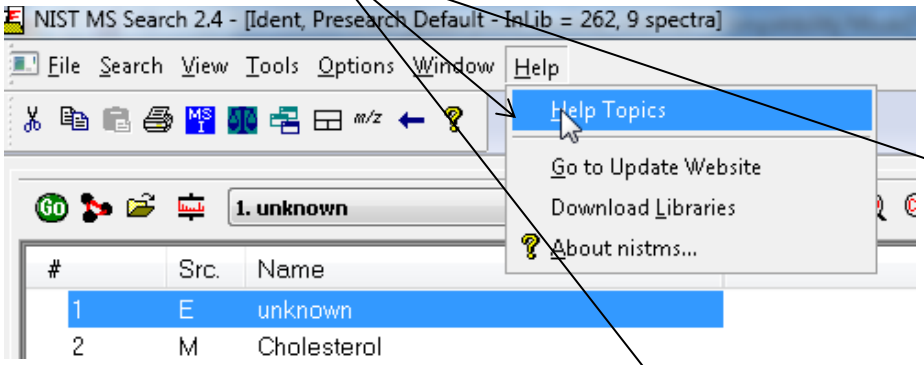
Help Files for NIST Search

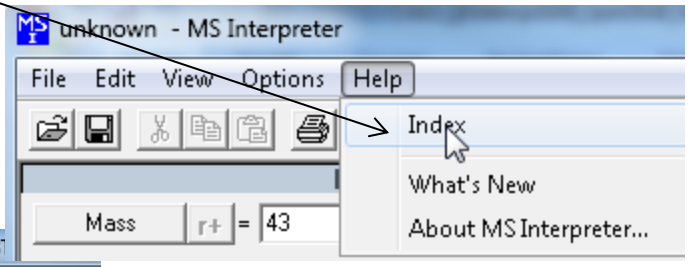
-"Hover" over Program Icon with mouse and function description displayed

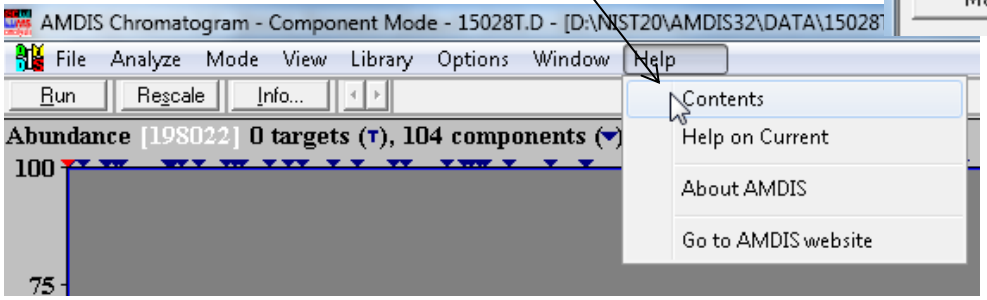


-Detailed documentation for NIST Search[2] and AMDIS[3,4,12]
-MS Interpreter included in NIST manual[2] and in posters[13-15]
-Windows Program Group
-"In program" assistance for all three programs









NIST Software in General is "Windows Compliant"

-***left click (LMB)*** to select an item, ***double LMB*** on that item to perform operation
-***right click (RMB)*** in area or item to see operations that can be performed or to change properties of window
-***LMB*** on first item and last item to select group ***while*** holding ***shift key***
-***LMB*** to select/deselect individual items ***while*** holding ***Ctrl button***
-use up and down arrows ***on keyboard*** to step between entries
-some NIST windows such as librarian have no delete button to delete ions, ***must*** use delete key on keyboard!
-***control a*** (select all), ***control x*** (delete selected), ***control c*** (copy); ***control v*** (paste)
-***control k*** copies entries into windows in tab-separated text format, e.g., ***paste*** into Excel
-F1 MS Search help
-F9 send spectrum to MS Interpreter
-***LMB*** and ***zoom*** mass spectral windows, ***RMB*** then ***LMB*** to ***zoom out***

Tip 3: ***LMB*** and **drag** to rearrange order of column headers

#	Lib.	Name	Match	Prob. (%)	RI	R.Match	Syn	DBs
1	R	Undecane	955	44.8	1100	955	4	8
2	M	Undecane	945	44.8	1100	945	4	8
3	R	Undecane	944	44.8	1100	958	4	8
4	w1	Undecane	937	44.8	-	955	11	0
5	w1	Undecane	933	44.8	-	950	11	0
6	w1	Undecane	932	44.8	-	939	11	0

-***LMB*** on column of interest
-Can sort in lower value first or higher
-Will show use in mixtures in example later in presentation

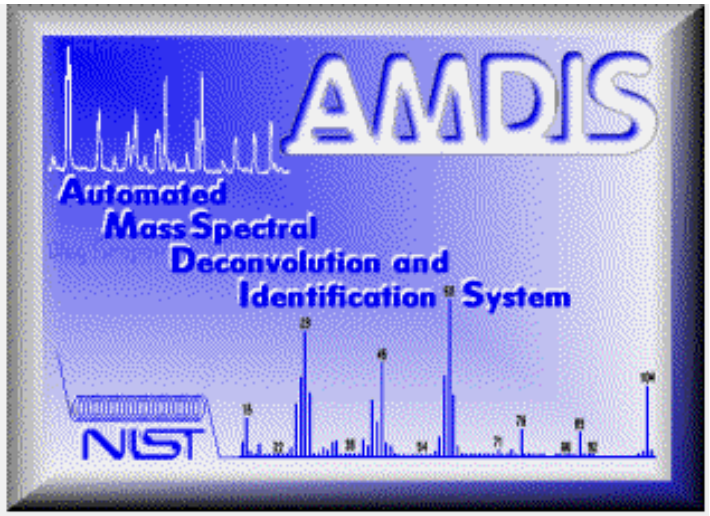
Tip 1: When reviewing search results, use up and down arrows on keyboard to quickly step through results!

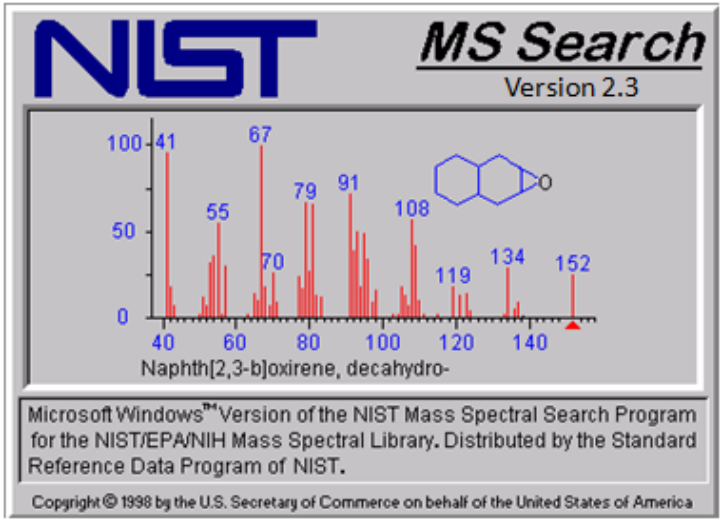
Tip 2: When viewing structures in MS Interpreter, use left and right arrows on keyboard to quickly review results!

*Modified** Basic Instructions for Using AMDIS with MS Search

By James L. Little, O. David Sparkman
Input from Gary Mallard
*9/6/2020 (Many additional slides on many topics added by JL)

See AMDIS Manual for Detailed Instructions





What is AMDIS?

Automated **M**ass spectral **D**econvolution and **I**dentification **S**ystem

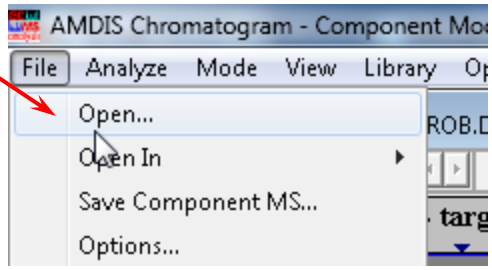
Developed to automatically detect chemicals in violation of Chemical Weapons Convention

- Software to ***automatically*** separate (deconvolute) chemical background in GC/MS data from signal for sample components
- Deconvoluted spectra can be ***sent*** to the NIST Mass Spectral Search Program for identification
- Spectra can also be searched automatically ***within*** AMDIS to give results yielding names, but not structures
- Software can be used to automatically ***find targeted species*** in complex mixtures
- If necessary, manual background subtraction performed
- Software can be used to compare “Good” and “Bad” samples analyzed by EI GC/MS and differences categorized
- Create Retention Indices using a calibration mixture for comparison to NIST values and adding to user libraries

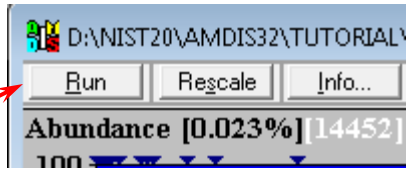
AMDIS Essentials

- ***Must always*** open a data file and run deconvolution ***before*** sending a spectrum to ***external*** NIST 2.4 Search Program
- ***Three ways*** to ***obtain a spectrum*** for searching: automatically, manually by ***LMB*** on spectrum, or manually with background subtraction
- AMDIS extracts the mass spectra of individual **Components** from chromatograms, these are symbolize with a ▼ on top of the chromatogram at the point of elution
- When AMDIS extracts the spectrum, that spectrum can ***also*** be automatically searched internally against an internal AMDIS **Target Compound Library** (MSL file) ***or*** a commercial database.
- If a component is identified in these ***internal*** searches, a **T** is place above the ▼

Must always first

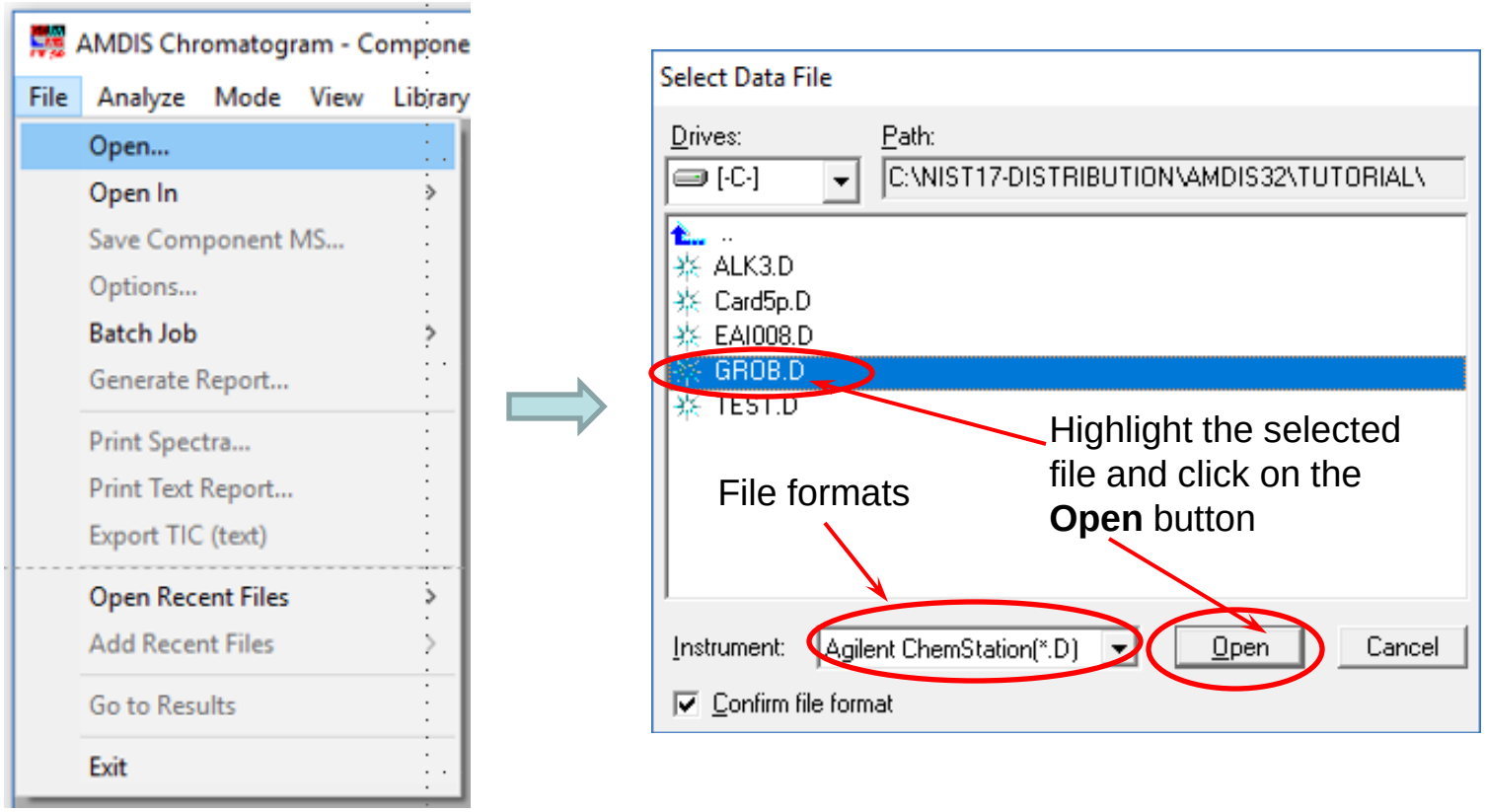


then



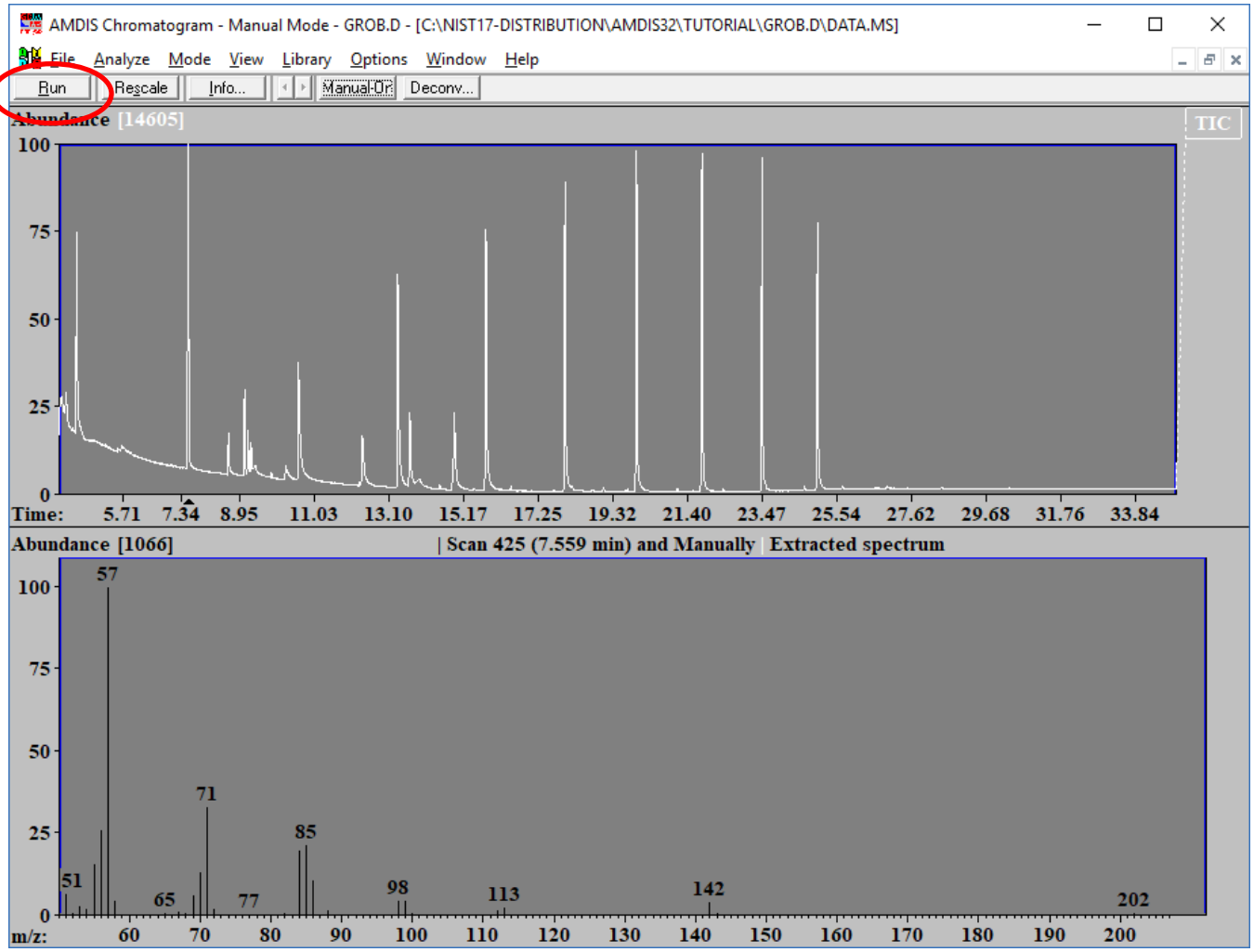
Opening File with AMDIS

- Can process many different file types with AMDIS including Agilent, netCDF, etc.
- Many manufacturers supply utility programs for conversion of files in their native format to the “standard” netCDF format
- File formats accessed by “pull down” menu
- ***Before*** sending components to library search, ***must*** open and run the file to get background corrected spectra



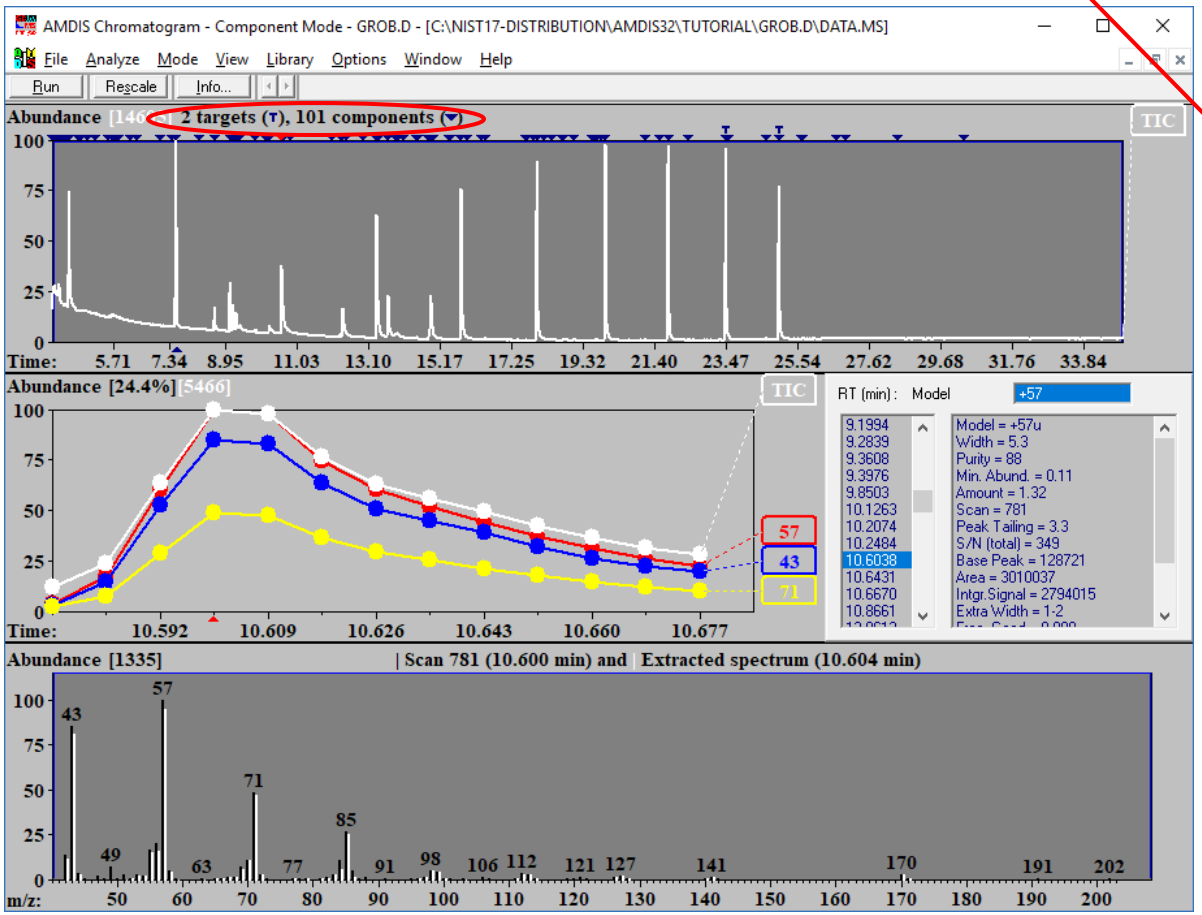
Deconvoluting Spectra

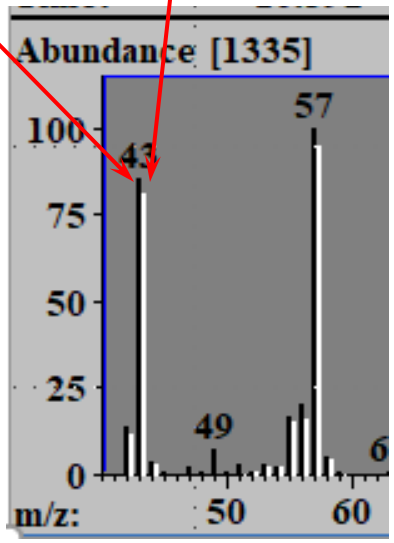
- First click the **LMB** with the **Pointer** on the **Run** button to deconvolute the file and search each spectrum against the selected **Target Compounds Library** (**Analyze\Settings\Lib**)
- The computer plots a chromatogram from every *m/z* value in the data file
- Then “looks” at the stacked plots to determine which ions “belong” with each other and subtracts out ions from air, column bleed, other nearby components, etc.



Evaluating Deconvoluted Results

1. Note the number of **Components** found (101)
2. Note the little blue upside-down triangles (▼), left click on any one to see deconvoluted spectrum
3. After selecting one blue triangle, can step through by using up or down arrows ***on your keyboard***
4. The left middle window shows what ions were “modeled” to define your spectrum
5. The right middle window show you the associated parameters for each peak
6. The bottom window shows the unsubtracted spectrum in black and the deconvoluted in white



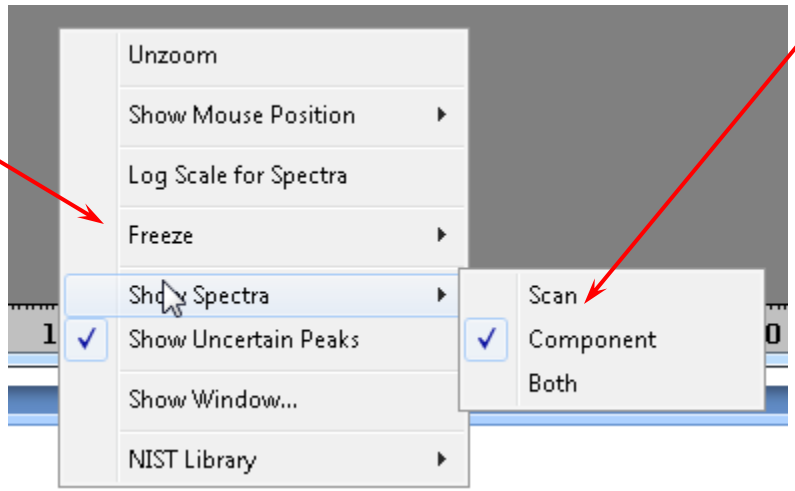


Evaluating Deconvoluted Results (continued)

- Can just show the **Component** (white peaks), the Scan (black peaks), or Both, but best to get accustomed to looking at both
- When the black matches the white, you probably have a good spectrum of a major **Component**
- For minor **Components**, possibly coeluting with a major **Component**, the white will be different than black and in many cases smaller
- With default “deconvolution parameters”, AMDIS will sometimes ID too many components
- The “deconvolution parameters” need to be adjusted to minimize this
- Very dependent on having a good stable signal from the instrument, but in my experience, just tends to do that without using the appropriate filters for processing (*more on that later*).

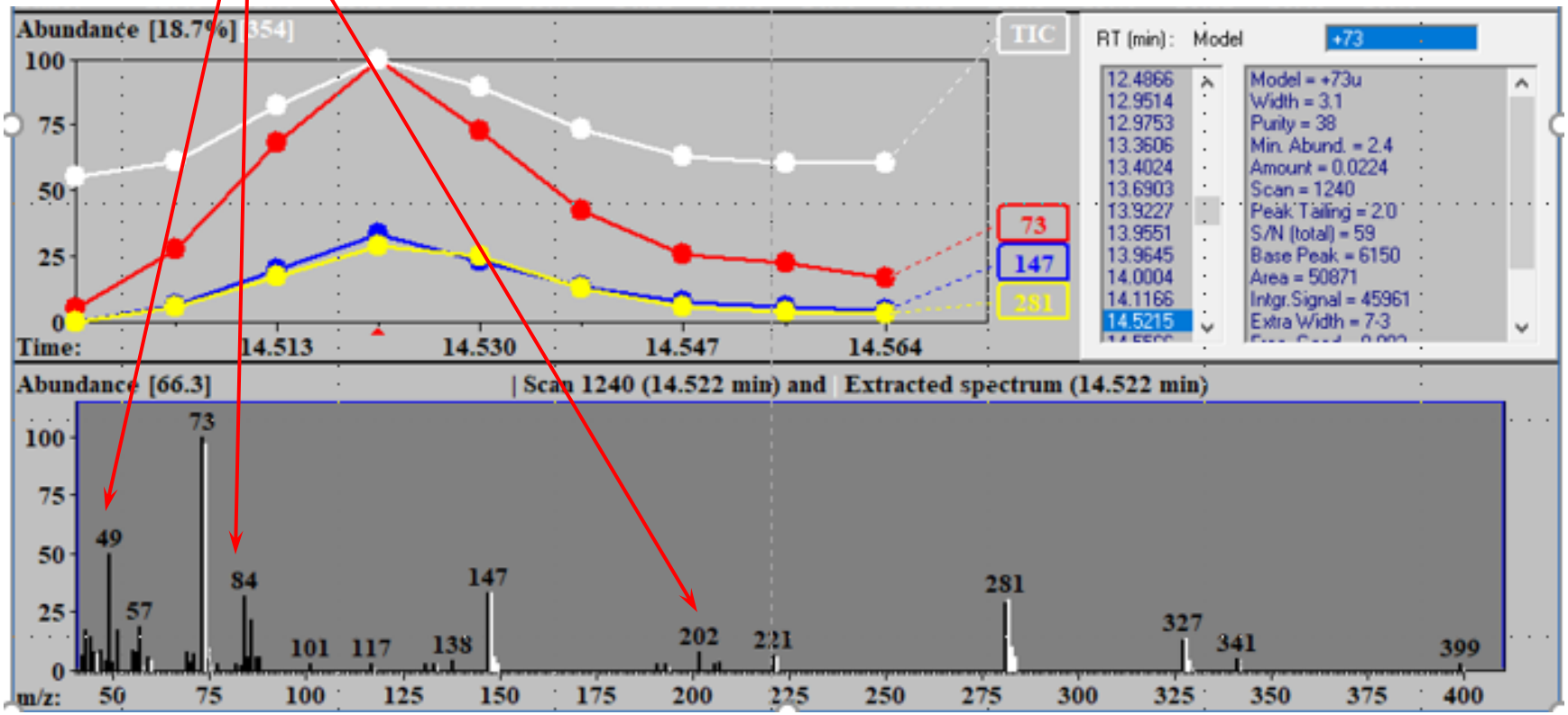
RMB Menu displayed by placing the **Pointer** on the Spectrum window and clicking the **RMB**

Which peaks will be displayed in the Spectrum window.



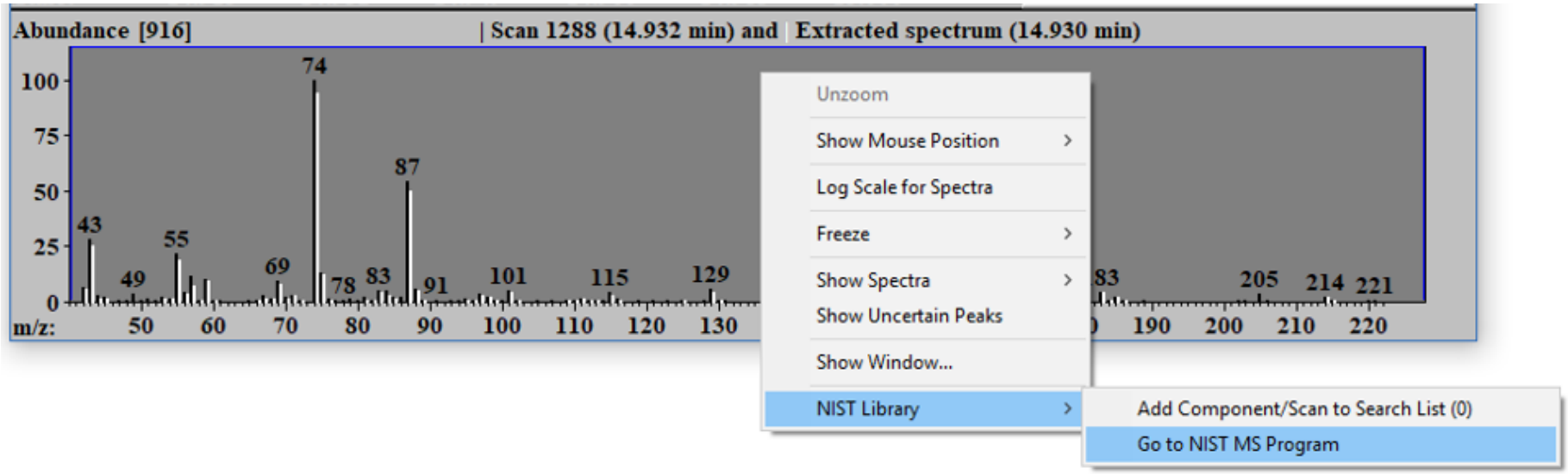
Evaluating Deconvoluted Results (continued)

- Note black (uncorrected peak with background)
- White is spectrum corrected for back ground and all non tracking ions removed



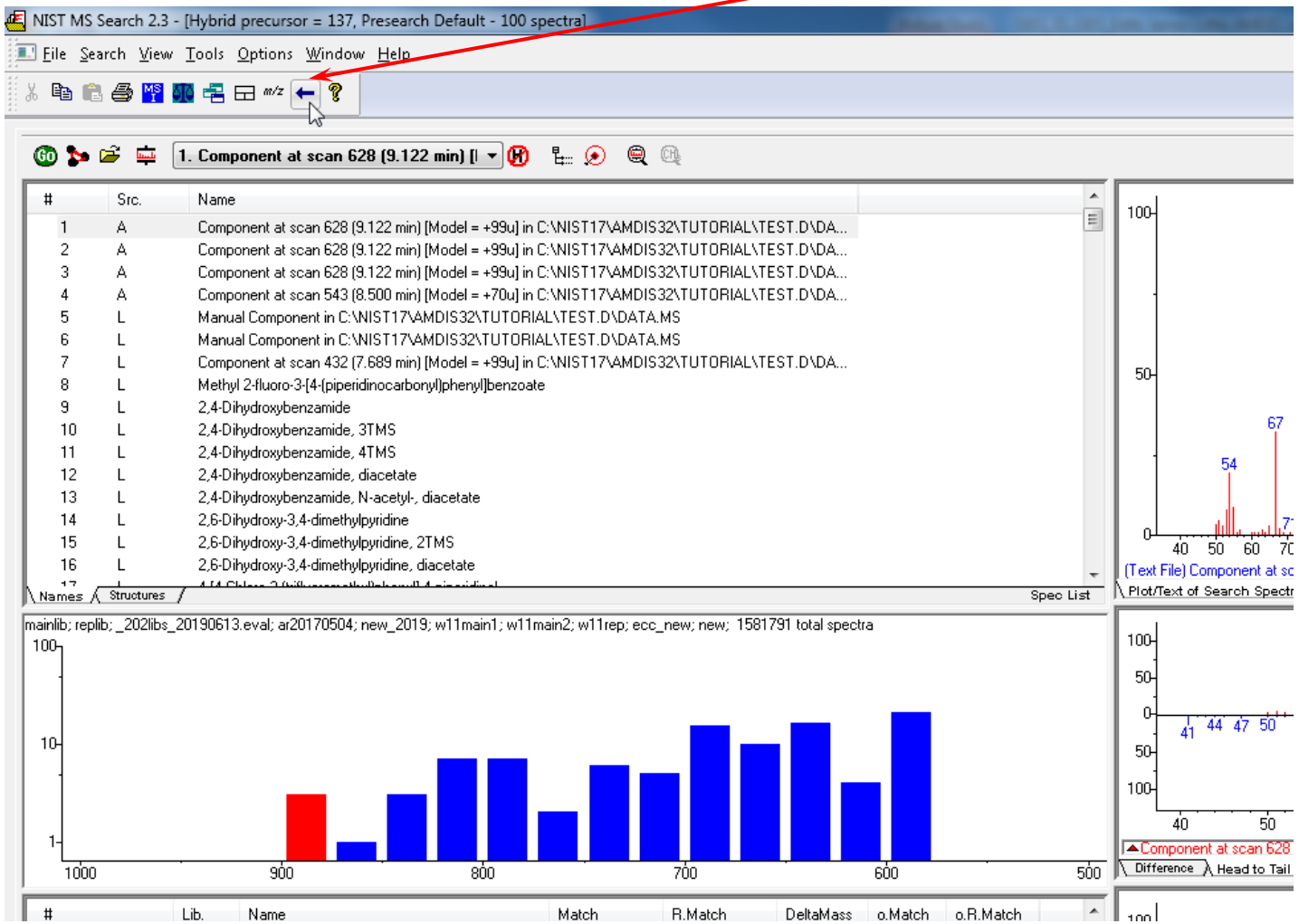
Sending Deconvoluted Spectra to NIST Search Program

- To send an individual mass spectrum to the NIST MS Search Program, click the **RMB** with the **Pointer** on the spectrum to display the **RMB** menu
- Select **Go to NIST MS Program**
- The spectrum will be sent to the NIST MS Search Program, if the Program is active; and, if not active, it will be started and the spectrum then sent
- If **Automation** is checked in the **Library Search Option's Search** tab, the search will occur automatically and the results will be displayed in the MS Search Program
- ***Tip:*** Can just LMB on chromatogram and obtain ***manual spectrum*** (*no background correction*) and send to MS Program for searching



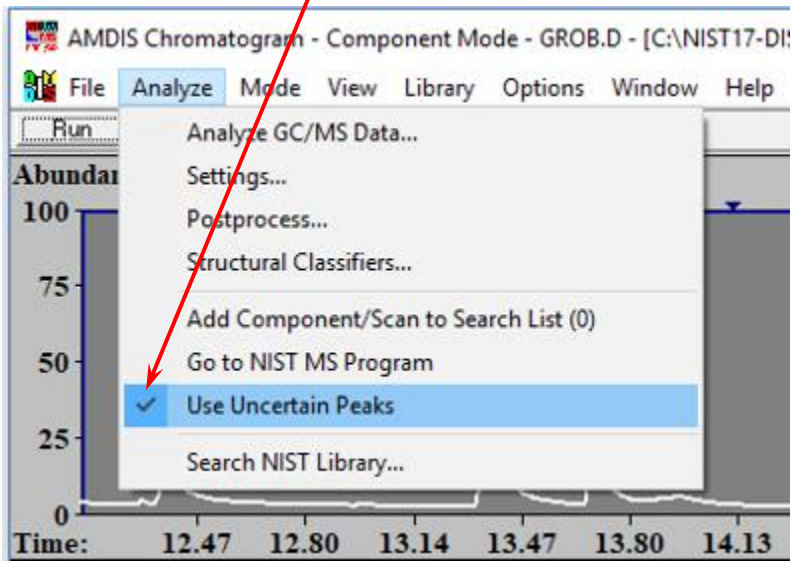
Returning to AMDIS Window after NIST Search

- After NIST search, return to AMDIS window by putting the **Pointer** on “Switch to Caller” button and click the **LMB.**

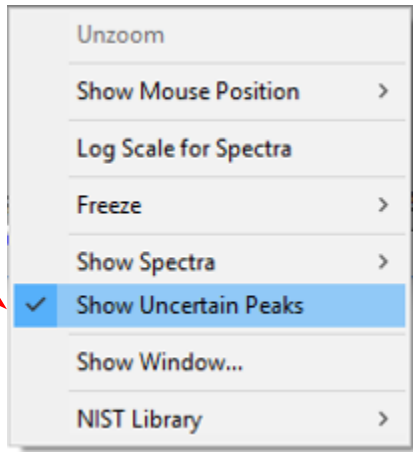


Uncertain Peaks, Dashed Lines, in Deconvoluted Spectrum

- Sometimes the AMDIS “decides” that some peaks “***might***” be associated with the deconvoluted spectrum, but it is not sure; you will need to change the basic settings if you want to use them
- These “***uncertain peaks***” are shown as dashed white lines in the spectrum
- To use them and send them for library searching, the Analyze settings have to be changed
- First, click the **RMB** with the **Pointer** on the spectrum to cause the display of the **RMB** menu and select **Show Uncertain Peaks**. Once selected, this will remain until changed.
- Then go to top of the **Analyze** menu, displayed from the Main Menu, and select **Use Uncertain Peaks**



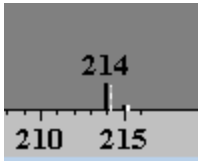
Analyze Menu

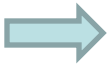


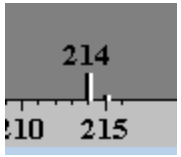
Right Mouse-button Menu with Pointer on Spectrum

Avoiding Uncertain Peaks in a Spectrum

- Often uncertain peaks ***can be avoided*** by changing the default settings for Resolution and/or Shape Requirements in the ***Analysis Settings*** menu
- ***Alert!*** Internal library searches ***do not use uncertain peaks***, so best results obtained by avoiding their formation!
- Of course, uncertain peaks ***not*** a concern with spectra obtained manually

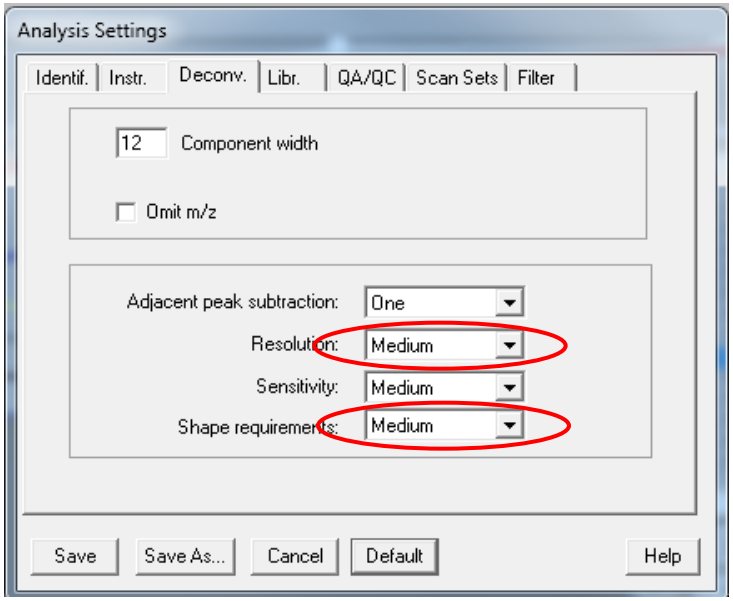


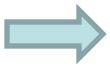


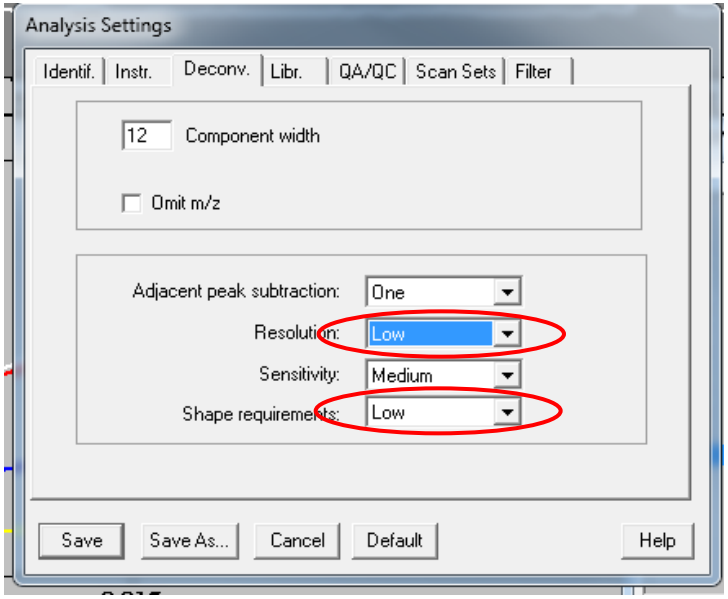


Default Settings

Modified Settings

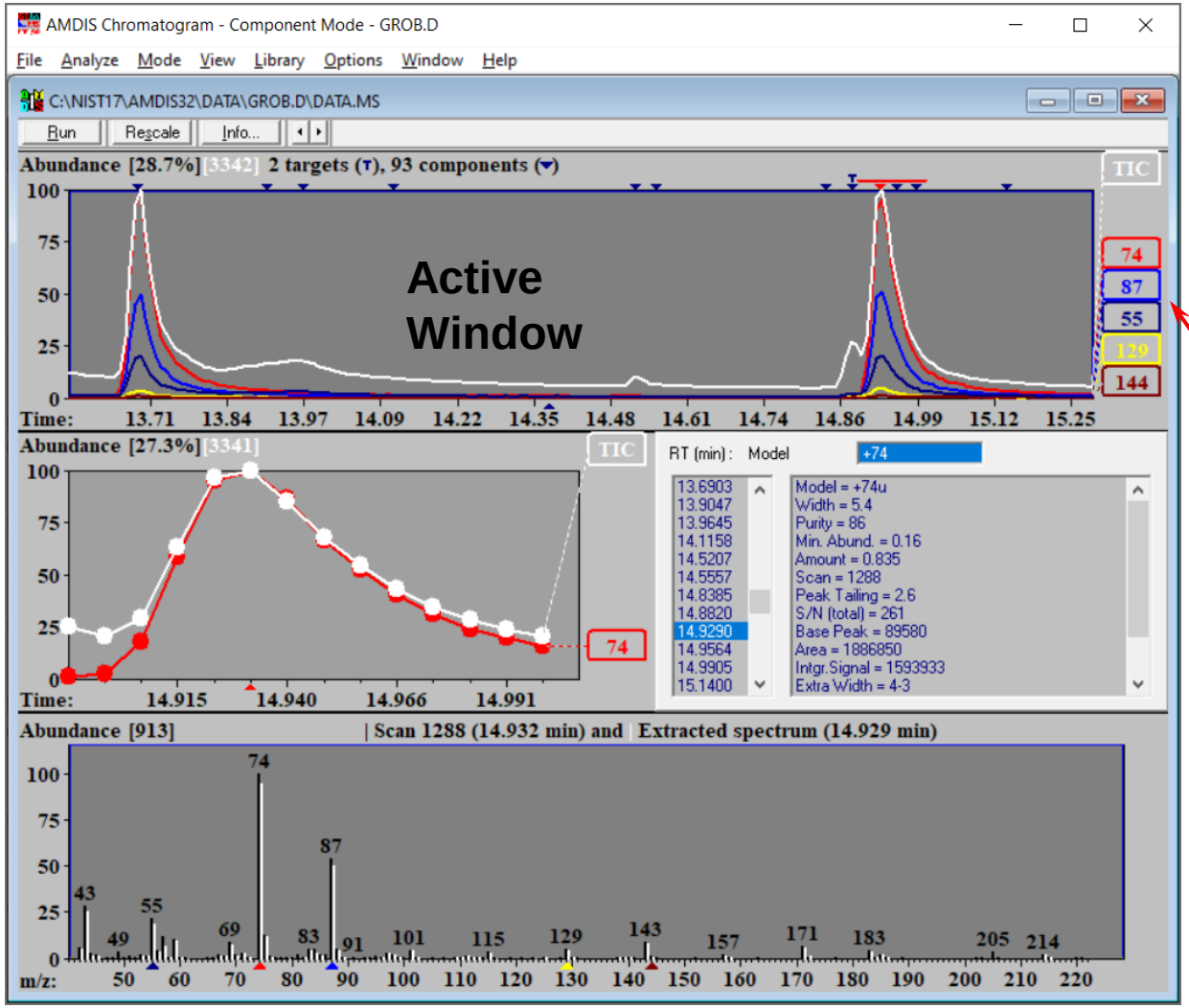






Plotting Single (or Extracted) Ion or (Mass) Chromatograms

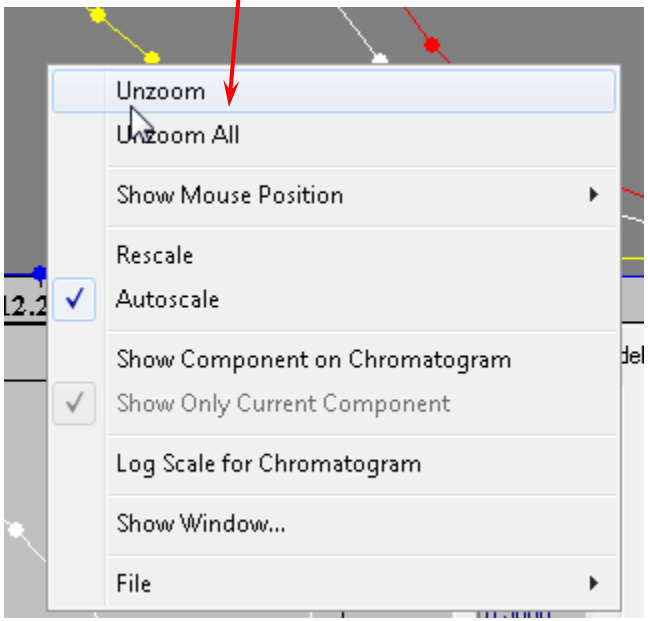
- To plot ion current *vs.* time (i.e., a mass chromatogram), just click the **LMB** with the **Pointer** on the peak representing the ion in the spectrum window, and the mass chromatogram will ***immediately*** be displayed in a different color in the active window. The intensity of the peak produced by the 1st selected ion is set to be 100%. If a subsequent ion is more abundant than that 1st selected ion, its plot will be off scale

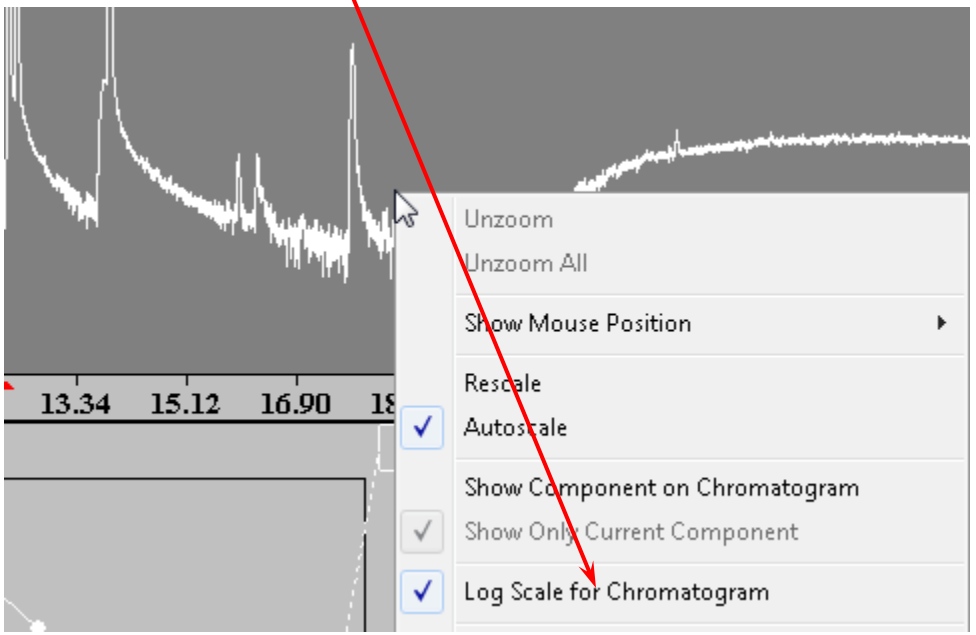


- Either the chromatogram (top) window of the model (middle left) window can be the active window
- To select the active window, put the **Pointer** on the bar above the window and click the **LMB**.
- The active window is dark gray
- To delete that mass chromatogram, just click the **LMB** with the **Pointer** on its box to the right of the top chromatogram
- ***Tip:*** the TIC (total ion chromatogram) box can be toggled off for easier viewing of low intensity mass chromatograms ***or*** use log scale as describe on next slide

Expanding Chromatograms or Plotting in Log Scale to See Small Peaks

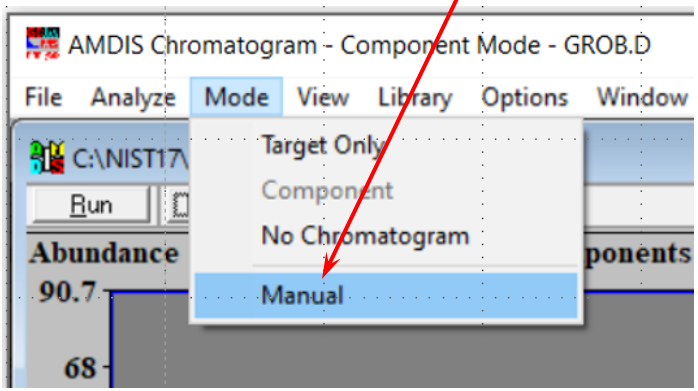
- To expand the chromatogram or spectrum, just hold down the **LMB** and drag (Drag-n-Drop)
- To unzoom, right click in the window and select **Unzoom** or **Unzoom All** from **RMB** menu
- Another way to see small peaks is to put Mouse-pointer on the chromatogram (or spectrum) window, click the **RMB**, and select **Log Scale for Chromatogram** or **Log Scale for Spectra** from the **RMB** menu

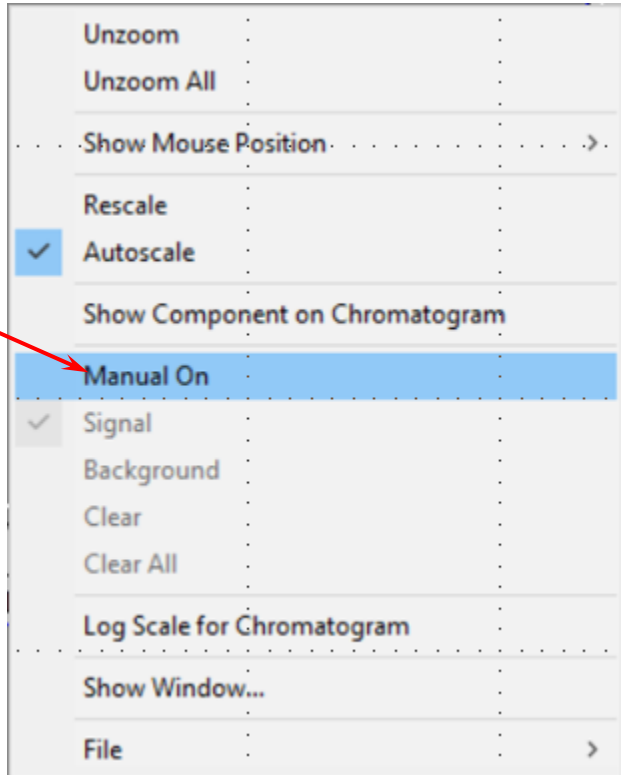




Manually Processing File in AMDIS

- If you just want an non-deconvoluted (uncorrected) spectrum of the background, click the **LMB** with the **Pointer** on the scan of interest, it can then be sent to the MS Search Program and searched against the NIST and/or other libraries
- AMDIS can produce a manual background-subtracted spectrum, typical of other MS software
- Often helpful for broad or peaks with excessive tailing
- First, go to top bar and select **Manual** from the **Mode** menu on the Main Menu bar
- Second, display the **RMB** menu and select **Manual On**

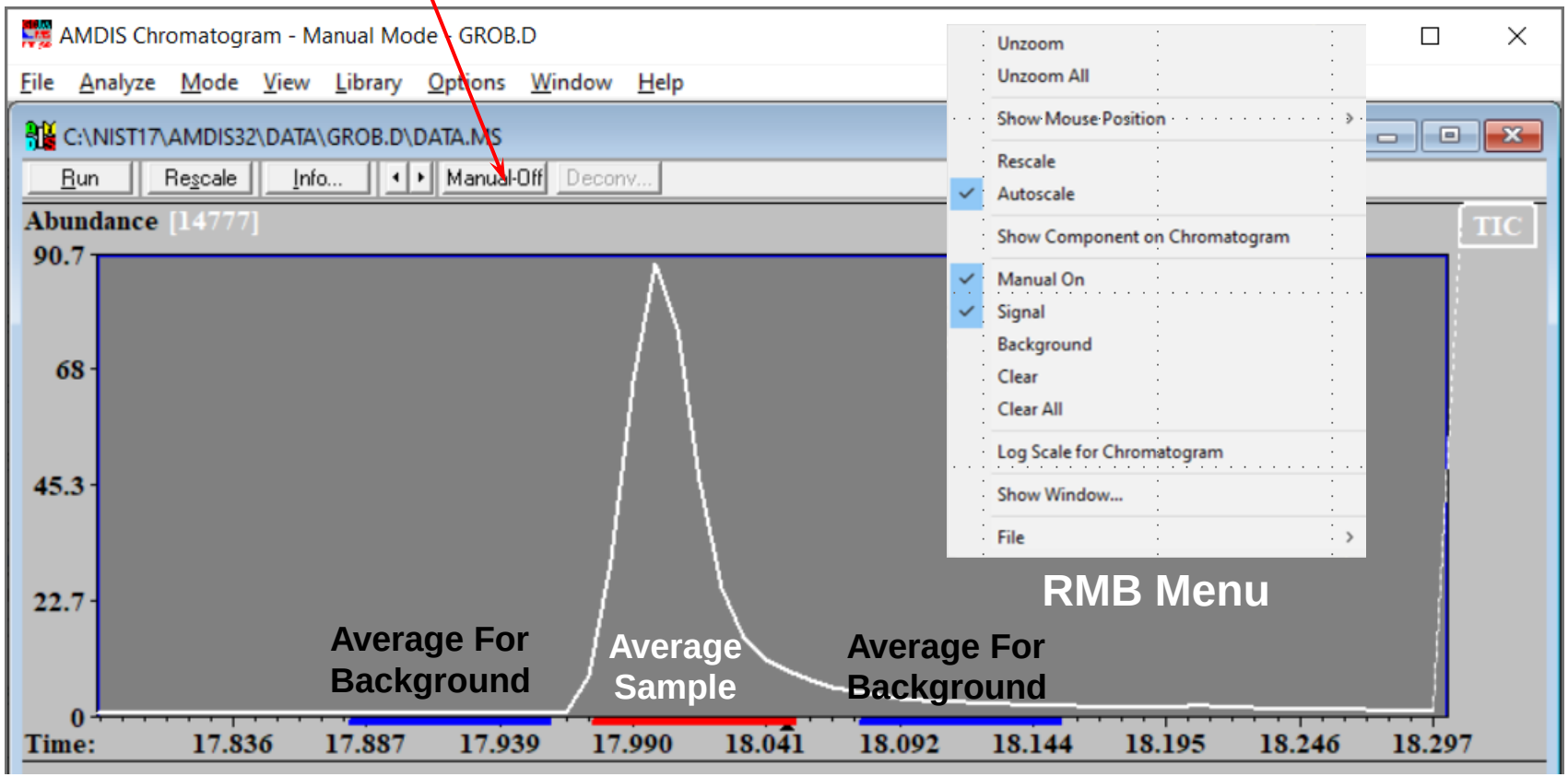




RMB Menu displayed by putting **Pointer** on Chromatogram window and clicking the **RMB**

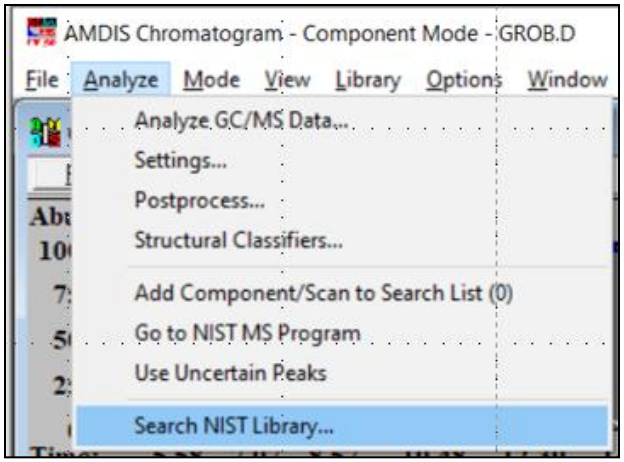
Manually Processing File in AMDIS (continued)

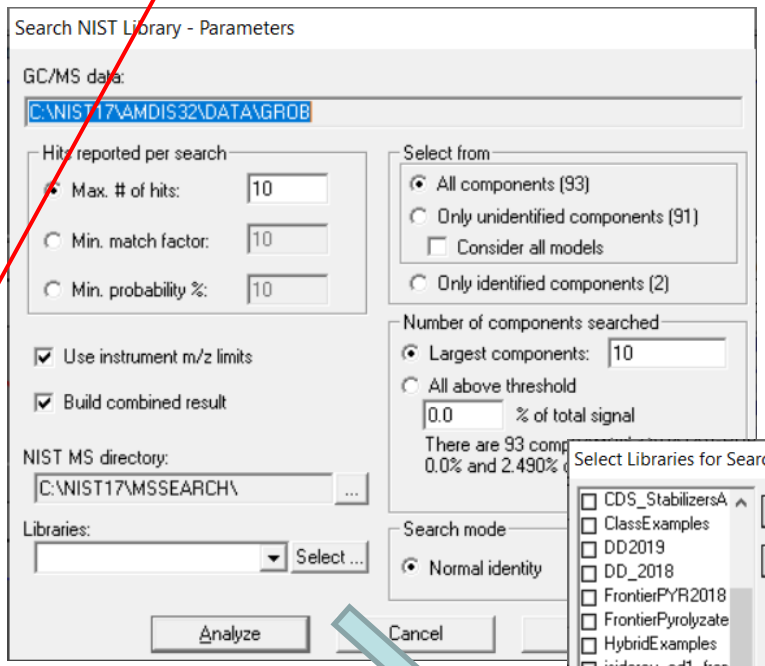
- From **RMB** menu displayed with **Pointe**r on the chromatogram window select (***one at a time***) in a sequence, **Signal** (one or more ranges to average) and **background** (one or more ranges)
- The manually background spectrum is shown in the spectrum window, (bottom of the two displayed windows; the model window (middle), used in deconvolution, is no longer present
- The chromatogram window can be unzoomed using the **RMB** menu; but, to zoom requires **LMB** clicking on the **Manual Off** button above the chromatogram turning it to **Manual On**
- The spectrum obtained can be sent to MS Search using the **RMB** menu

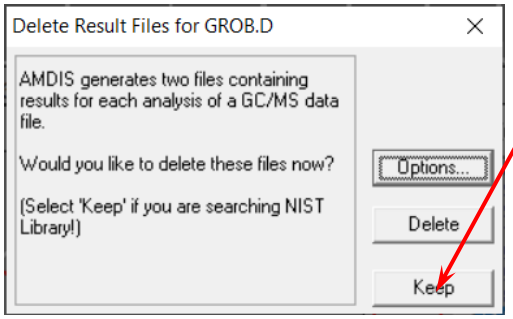


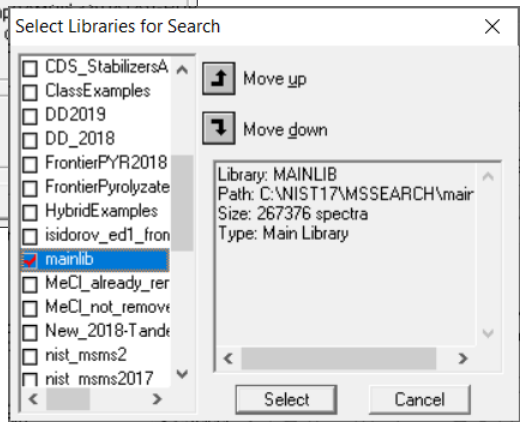
Automated Searching of Deconvoluted Spectra within AMDIS

- Searching Mass Spec Libraries with Results shown in AMDIS (names only, ***no*** structures!)
- Select **Search NIST Library…** from the **Analyze** menu on the Main Menu bar to send spectra to MS Search automatically
- Can select more than one library by clicking with the Left Mouse-button on the **Select** button in the **Search NIST Library – Parameters** dialog box (**Select Libraries for Search** dialog box)
- Set parameters to limit the search (use **Help** button if necessary)
- Left click on **Analyze** button and be sure to select ***Keep*** in **Delete Results File** dialog box







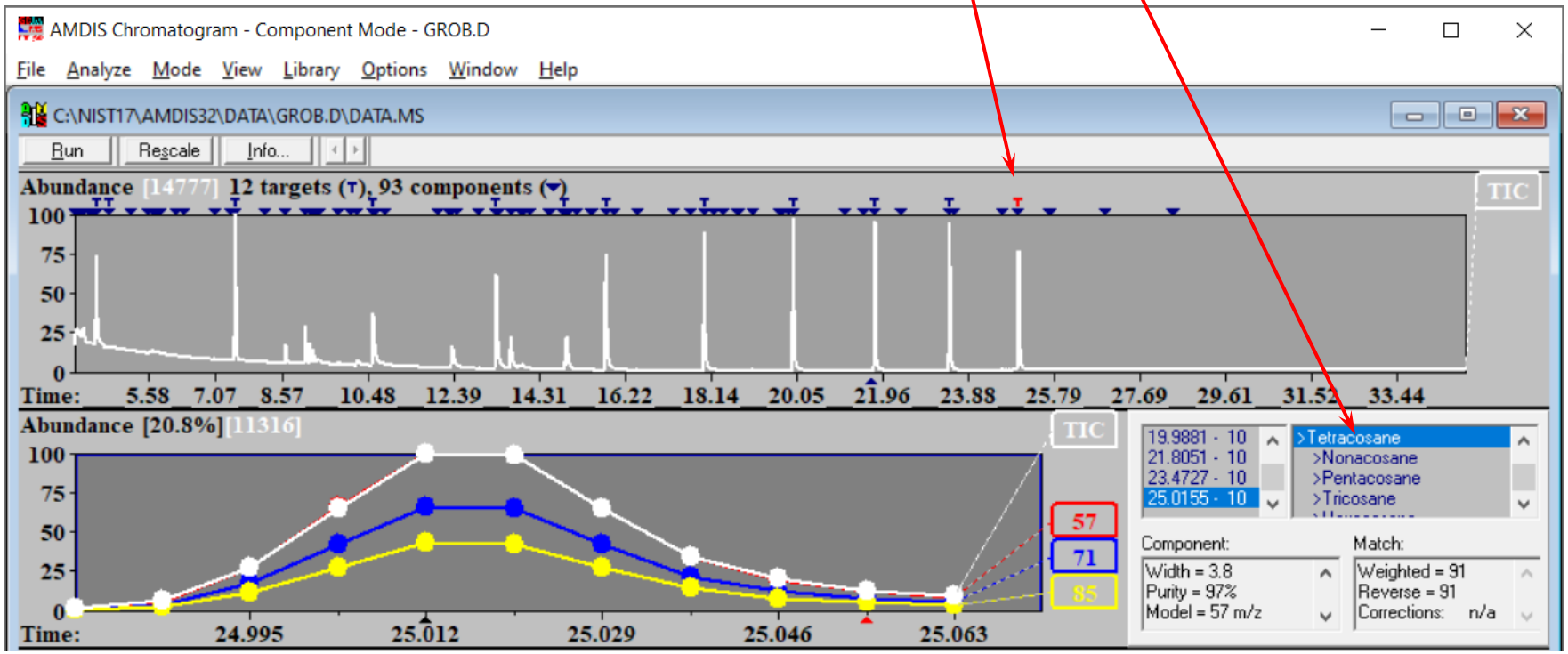


Be sure there is a check in the box next to the selected library

Examining Results of EI Mass Spectral Search with AMDIS

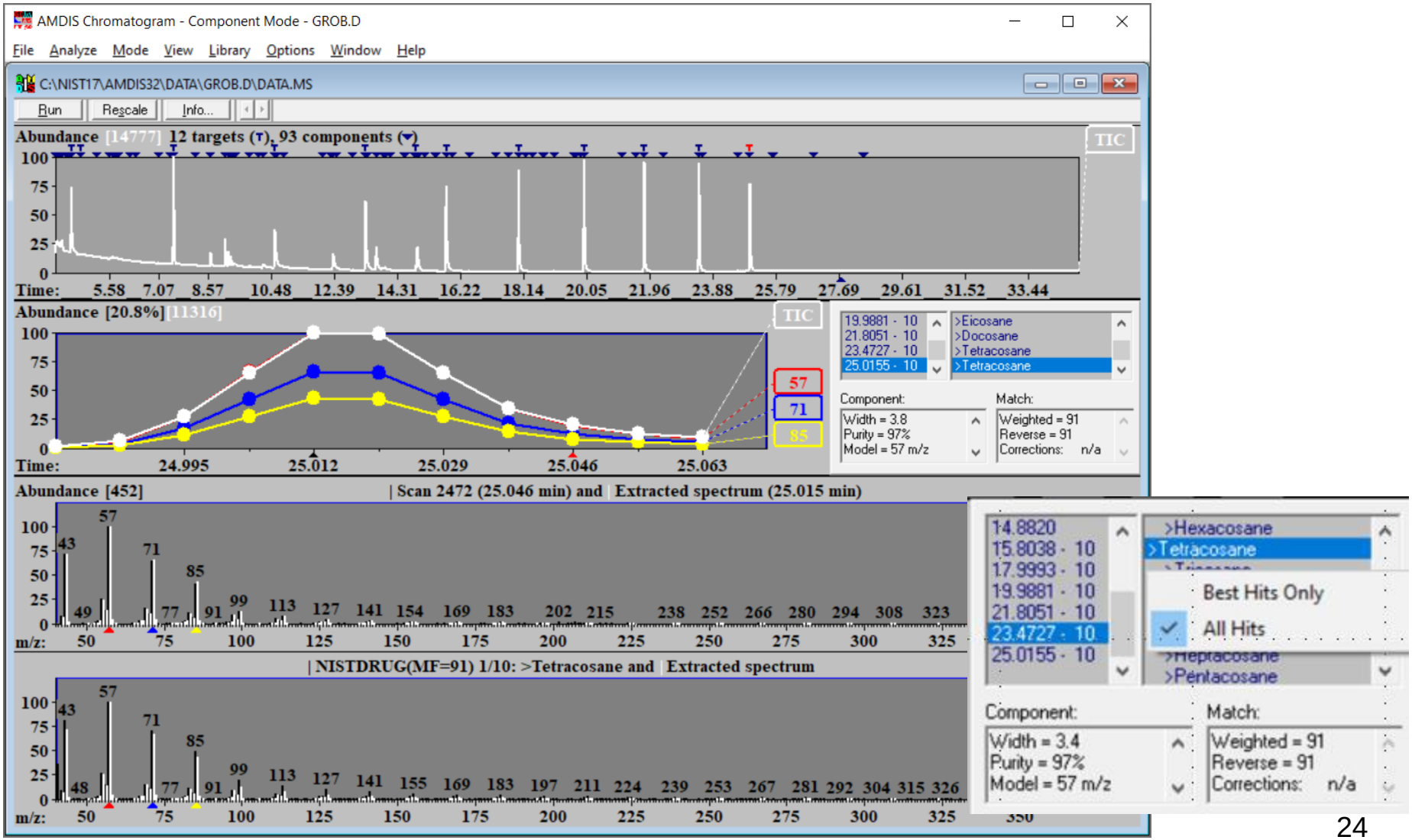
- Click **LMB** with the **Pointer** on any one blue **T** (turns **Red**) above chromatogram window
- **T** stands for target and that will be the library search results
- If the **T** furthest to the left, click on ***down arrow*** on keyboard to step through the results (L to R)
- The ***up arrow*** keys results in jumping from **T** to **T** from right to left*
- The list in the Results window is from using the NIST MS Search Program and ***not*** the search of the Target Compounds Library ***unless*** is checked (☑ Build combined result) in the NIST Search Library-Parameter menu

Bug Alert: Cannot ***currently*** step through from right to left in ***some*** instances



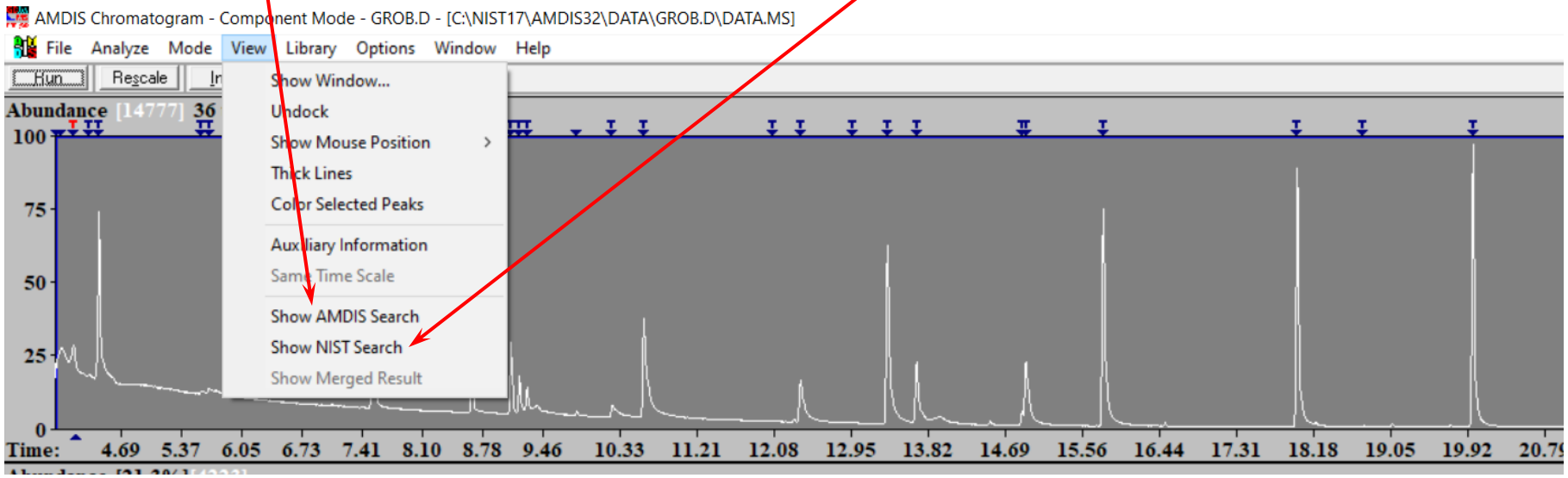
Examining Results of EI Search Results with AMDIS (cont'd)

- The unknown spectrum *vs.* spectrum library hit will be displayed in the lower window as you step through the results using the **up** and **down arrow** keys (**Note *Bug Alert*** previous slide)
- Can also click the **RMB** with the **Pointer** on the **Results** window to see all hits for a **Component**



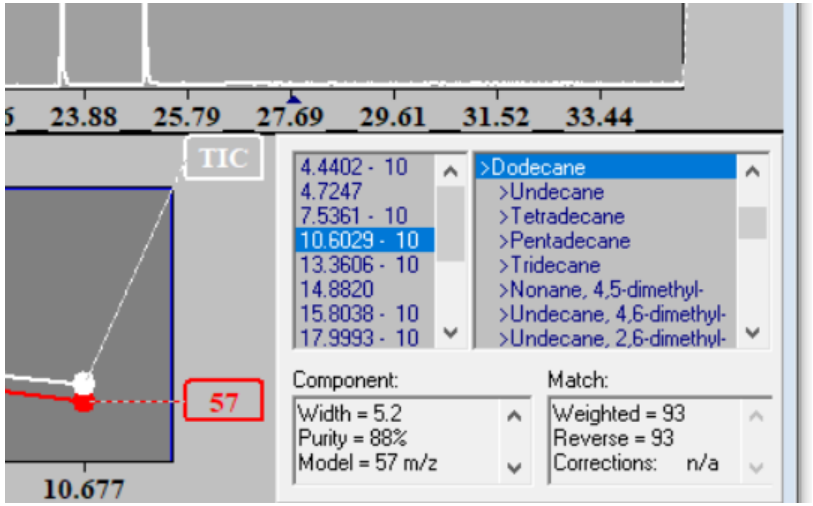
Examining Results of EI Search Results with AMDIS (cont'd)

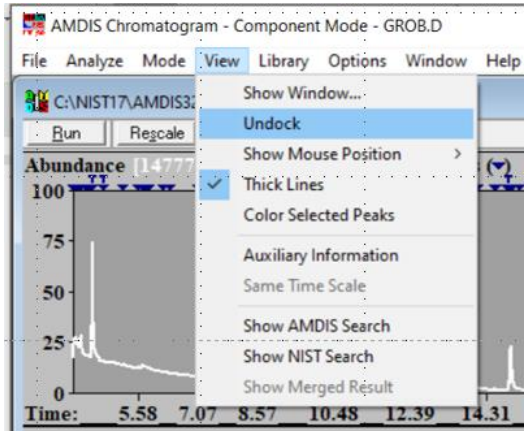
- Deconvoluted spectra can be searched using the AMDIS internal **Target Compounds Library** or libraries in the NIST MS Search Program using MS Search
- The library search results of either search can be displayed by selected **Show NIST Search** or **Show AMDIS Search from the View** menu right after the search using the NIST MS Program has been performed
- After one is selected, it will be grayed and the **Show Merged Result** selection will no longer be grayed. Once **Show Merged Result** is selected, it will be grayed and the other two will no longer be grayed
- More information can be found on these options on pg 62 of AMDIS manual (Section 3.1.4.8)

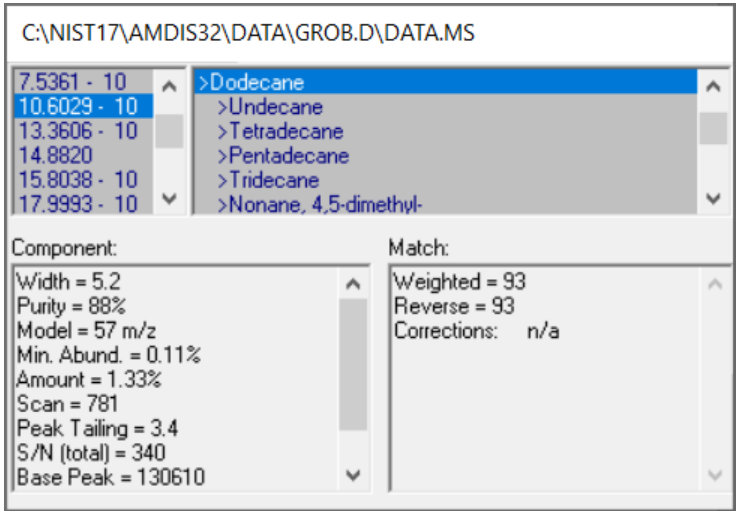


Undocking Library Results Windows for Viewing

- Viewing library search results is better done by undocking the Results window
- Undocking is accomplished by clicking the **RMB** with the **Pointer** on the frame of the window or from the **View** menu
- After **Undocking**, the window can be moved and resized as desired

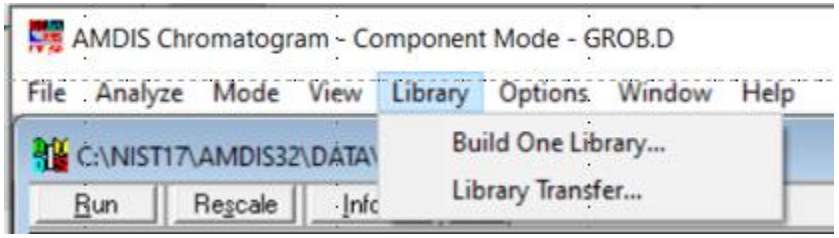




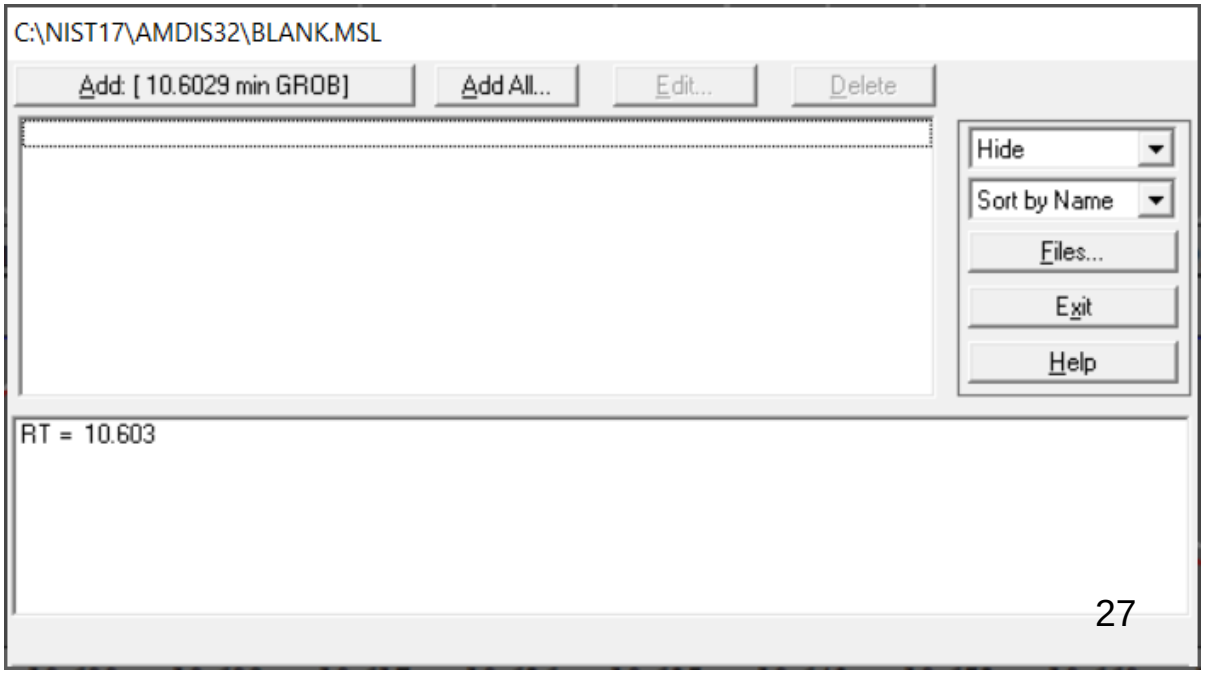


Creating Small Custom Libraries of Targeted Species within AMDIS

- Small custom libraries can be created in AMDIS and then searched like the NIST mainlib would be searched against a file to give targeted species; **T**, at top of the chromatogram
- The library can just be any spectrum of interest, not necessarily a traditional library entry

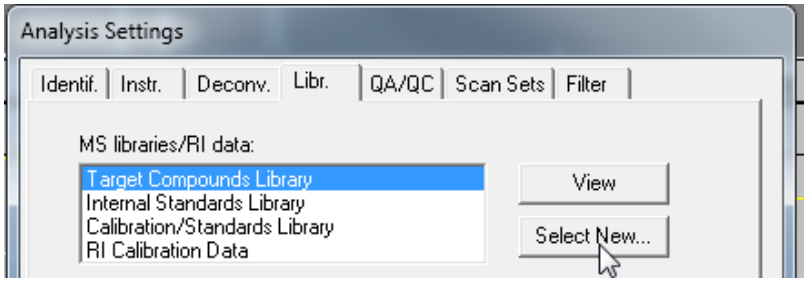


Information on Building AMDIS Custom Libraries Found in Help file or see AMDIS Manual pg 150 (Section 8.1.1)

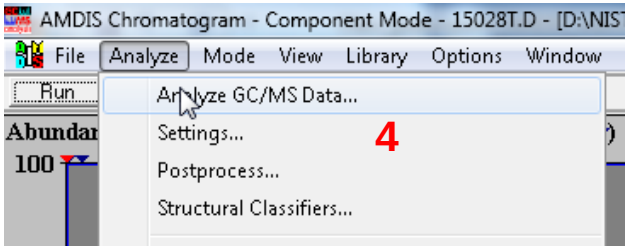


Tip: Quickly Search for Targeted Species within Data Files with Reference Spectra from NIST MS Search

1. Find reference ***spectrum*** or ***spectra*** of interest in NIST search program
2. Send to SpecList Window in MS Search (top left window)
3. ***RMB*** then ***LMB*** Export Selected (***can select more than one***)
4. Go to Analyze in AMDIS
5. ***LMB*** Target Library
6. ***LMB*** Select New..
7. ***LMB*** Simple MS Library (*.MSP)
8. ***LMB*** Save
9. ***Run*** [component(s) will be marked with “T” in chromatogram]

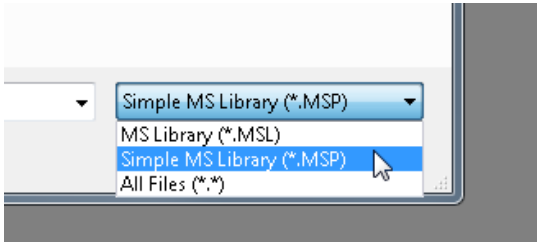


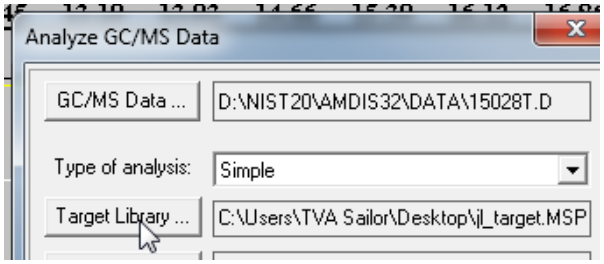
6



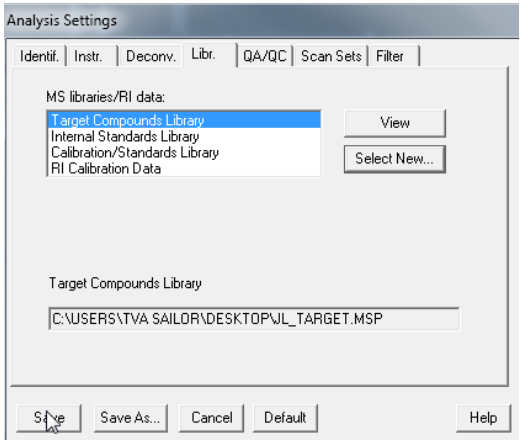
4

7

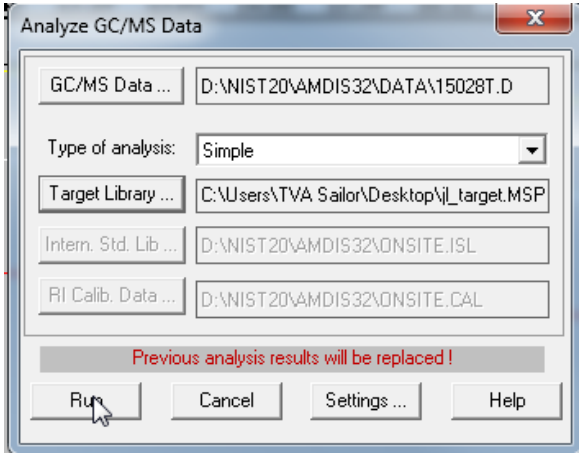




5



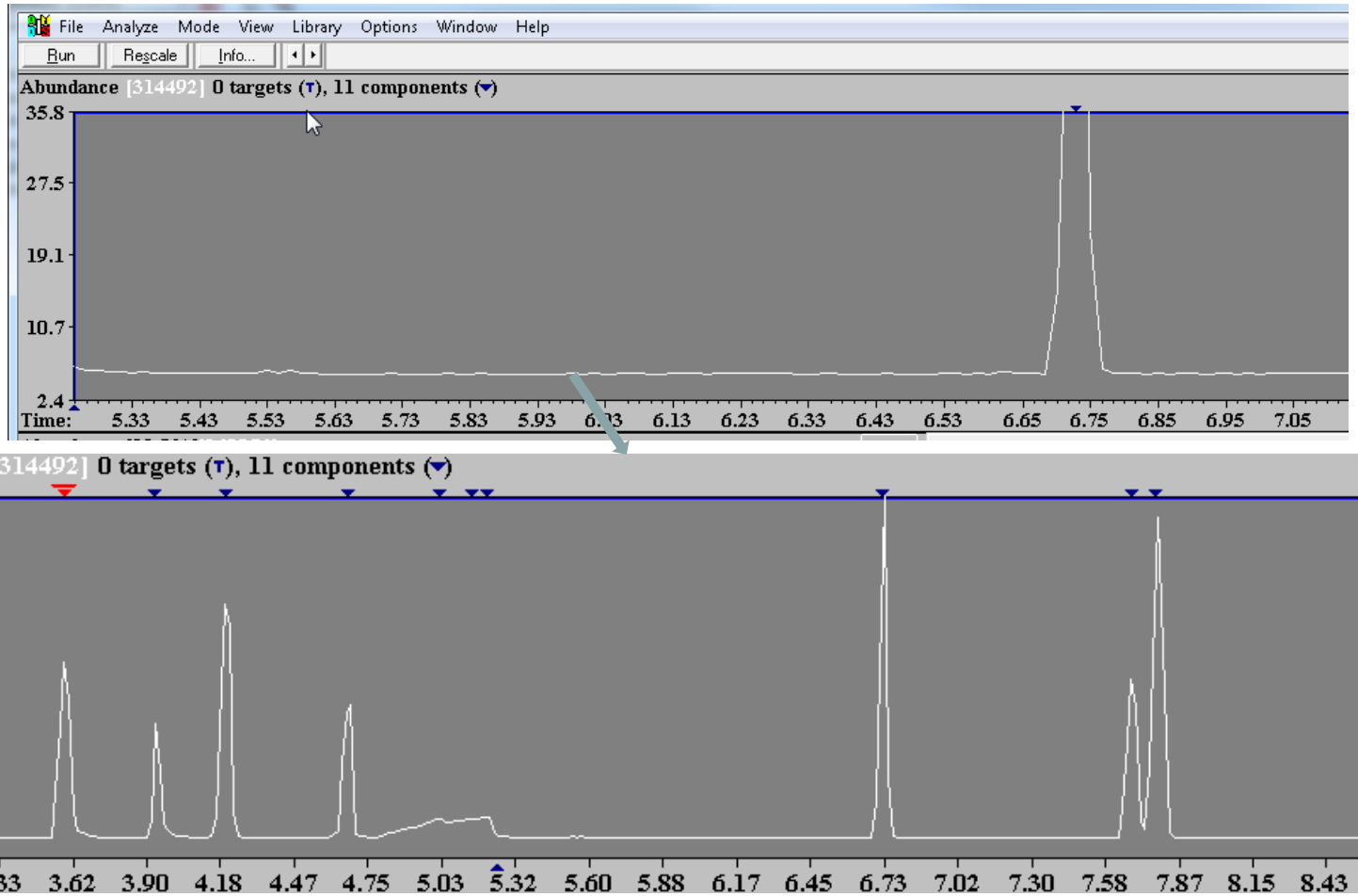
8



9

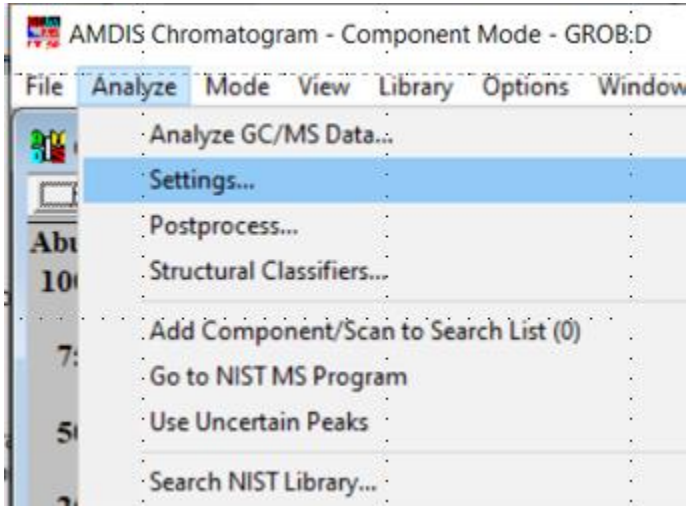
Adjusting Parameters for Optimized Peak Detection

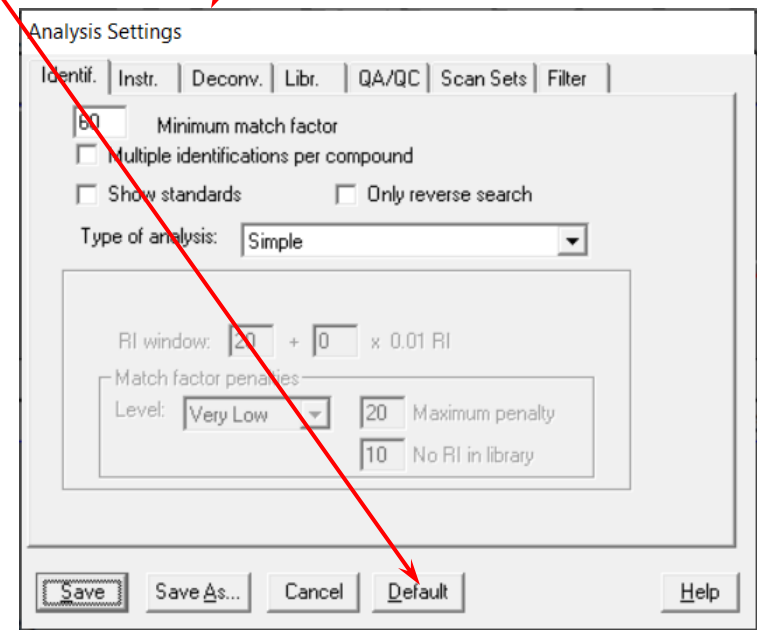
- When trying to determine proper parameters, expand the chromatogram to only show the most difficult areas
- Change to parameter and only the area shown will be reanalyzed
- After getting all the parameters as desired, then show the whole chromatogram and **Run** (Reanalyze) again
- This will greatly speed the process!
- ***Tip:*** NIST wrote 3 part series on suggested parameters for deconvolution[23]



Minimizing Marking Components in Chromatogram

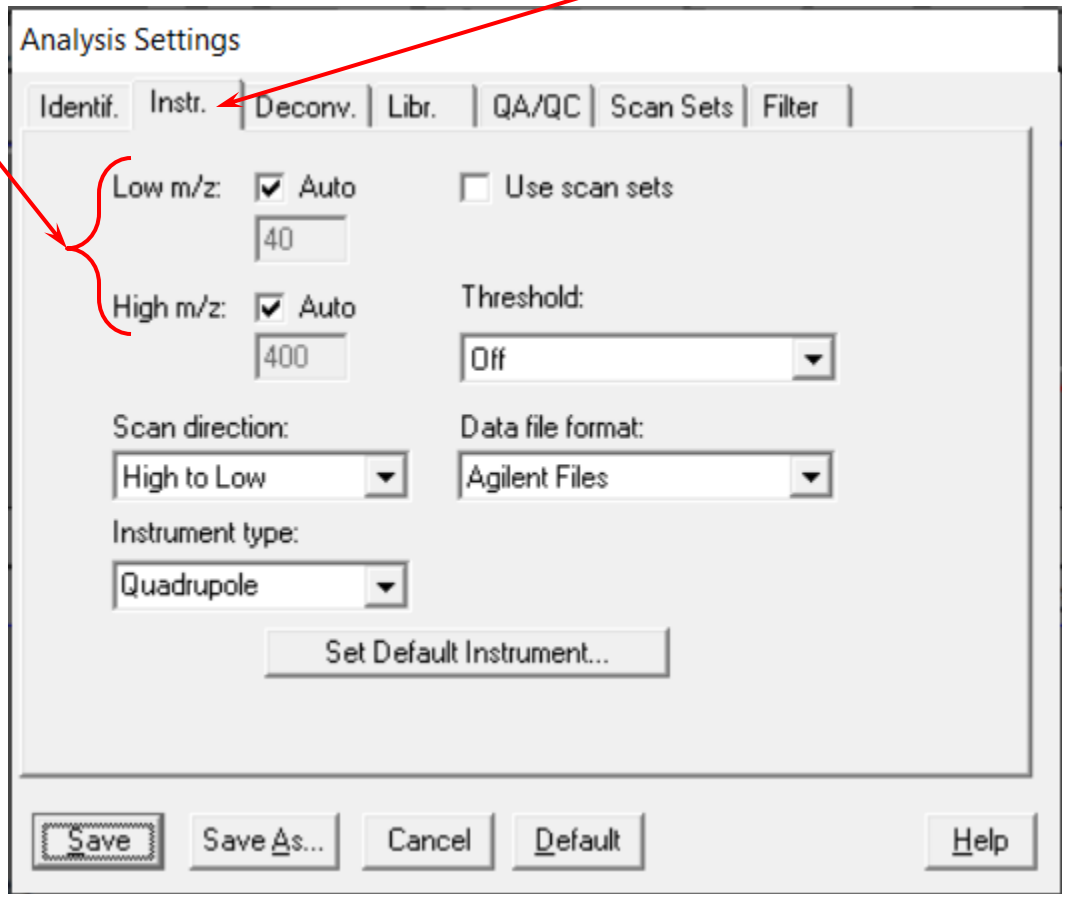
- The “multi-marking” of **Components** due to noise or instrument scanning irregularities can be annoying
- Almost all instruments under varying conditions tend to have this problem
- This can be minimized by adjusting some parameters In the **Analysis Settings** dialog box
- Note that there are multiple tabs with many parameters in this dialog box
- It is easy to restore the program’s **Default** settings





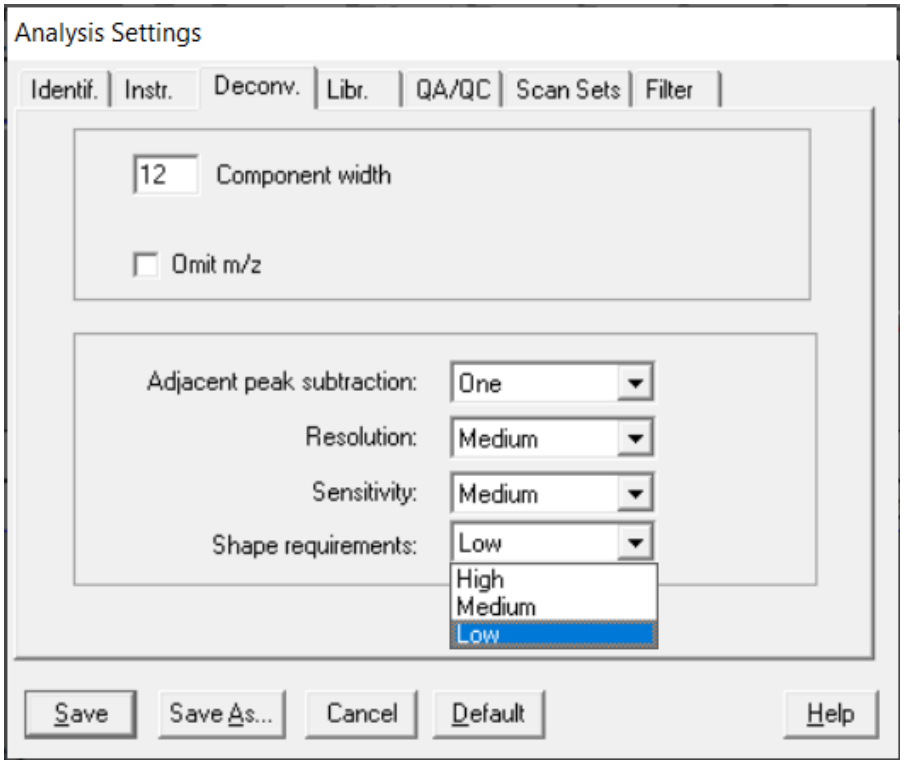
Minimizing Marking Components in Chromatogram (cont'd)

- Setup the processing parameters based on the instrument and its scan function (**Instr** tab)
- Can set the low and high m/z manually, or just automatically use those determined by AMDIS from the file



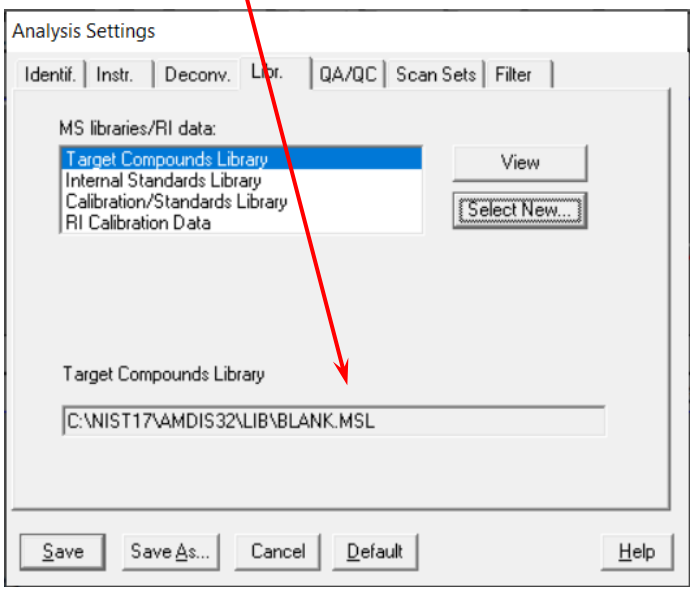
Minimizing Marking Components in Chromatogram (cont'd)

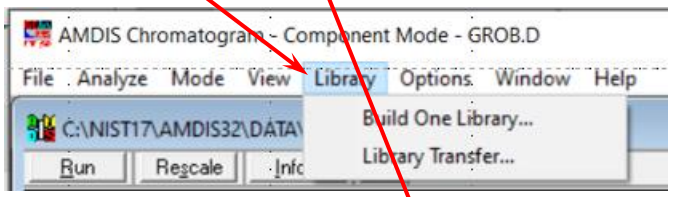
- The ***Deconvolution t***ab can be set to get rid of some peaks
- In particular, for tailing peaks, might want to set the **Shape** requirements to Low
- The default for **Shape** requirements is Medium
- The values show below are the **Defaults**
- In general, the **Filter** tab (*see slides 36-37 of this handout*) usually minimizes the multi-marking of **Components**

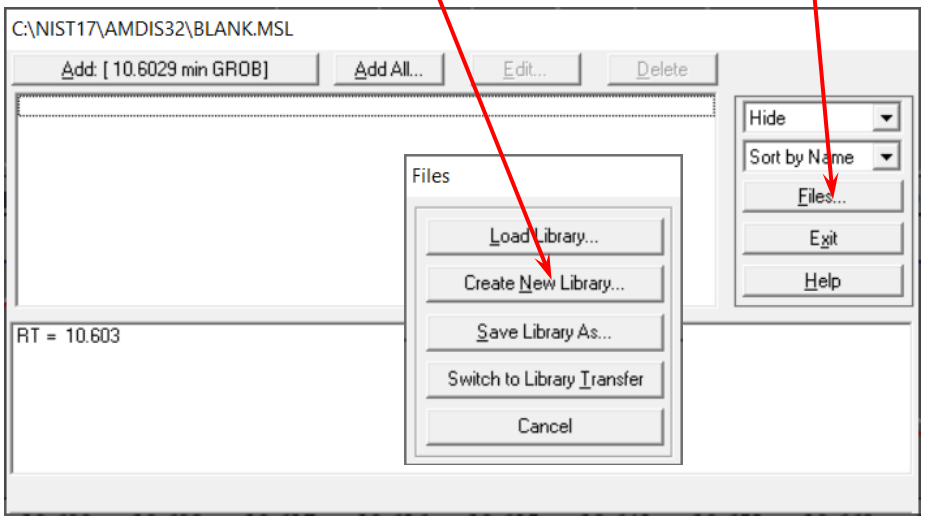


Minimizing Marking Components in Chromatogram (cont'd)

- Created a library named **Blank** so that when the file is deconvoluted, no **Components** are targeted with a **T**, they are marked with a ▼ to show that a **Component** was detected
- Created the library by first selecting **Library** from the Main Menu, then clicked on **File** button in the displayed dialog box, then click on the **Create New Library** in the **Files** dialog box

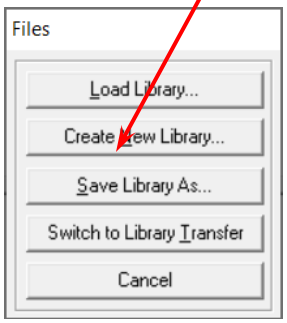


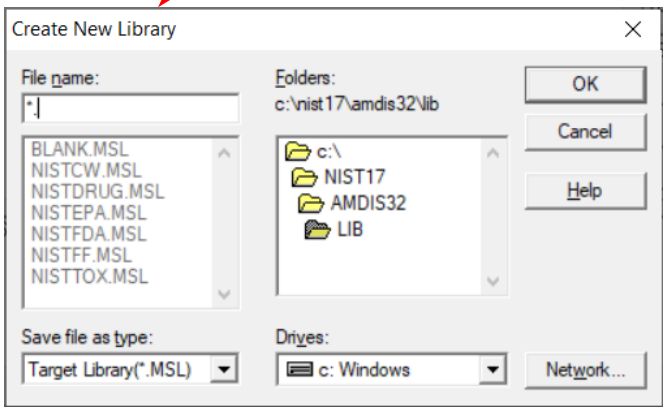




Minimizing Marking Components in Chromatogram (cont'd)

- After clicking on the **Create New Library** button in the **Files** dialog box the **Create New Library** file save dialog box will be displayed
- There is a known Bug in v.2.73 <build 149.31> (Apr 25, 2017) and earlier versions of AMDIS. In order for the file name entered in the **File name:** text entry box to have an extension, it has to be entered with the name. The dialog box has a section with the label **Save file as type:**. It shows the file should be saved as an ***.MSL** file; however, this does not work. Be sure to add the **MSL** extension to the file name or the file will be saved with no extension.

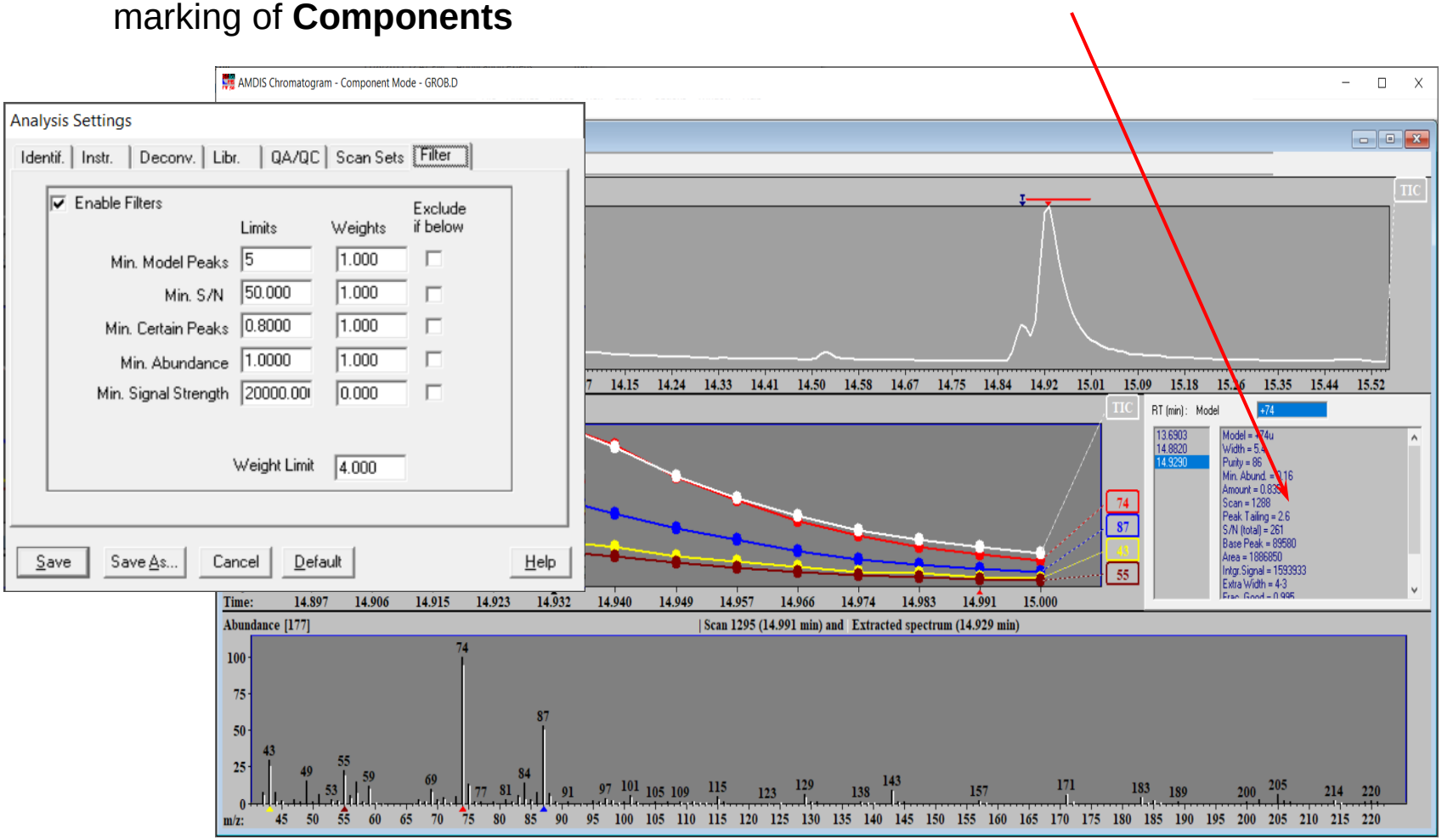




Bug Alert

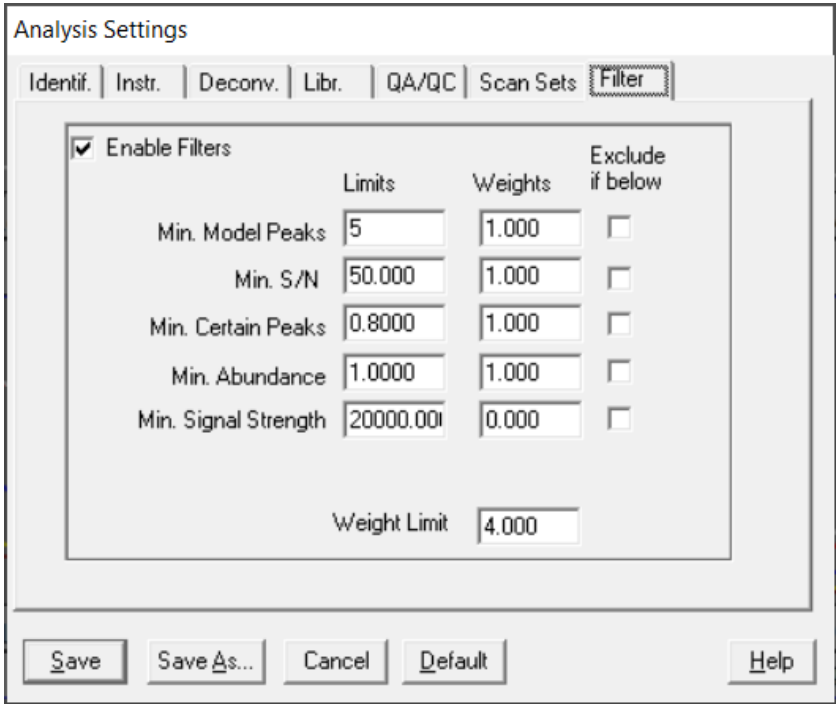
Minimizing Marking Components in Chromatogram (cont'd)

- The default filter settings are shown below; the default settings do NOT have the **Enable Filters** check box selected; unless checked, the fields are grayed
- The values associated with a particular **Component** can be viewed in the window next to the Model (middle-left) window
- Looking at these values gives an idea of how to limit parameters to minimize the marking of **Components**



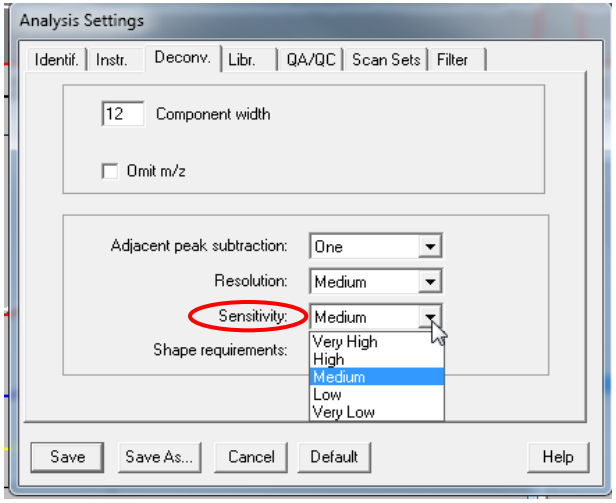
Minimizing Marking Components in Chromatogram (cont'd)

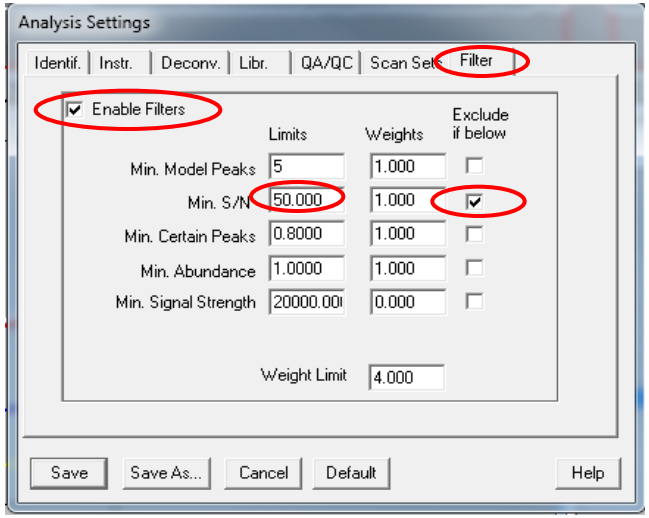
- ***Often*** just try LMB "Default" and "Run" file with "Enable Filters" checked, ***use my settings*** noted in window below if different from "Default" settings or try those suggested by NIST[23]; if these ***do not work***, try adjusting the weights and limits as described below manually[23]
- The limits are scaled, thus if "Min Model Peaks" below is set at 5 and there are less, the weight for this parameter is decreased below 1, if >5, the weight factor for this parameter is >1
- The scaling for these parameters are not linear and there is a maximum set for each
- If a **Component's** Σ of weights is >4, it is included as a deconvoluted peak, if not, it is excluded
- An absolute limit can also be set for any one of these parameters by checking **Exclude if below** and selecting a value
- Adjusting these parameters greatly determines the number of times a chromatographic peak will be marked and the total number of marked peaks (detected components)

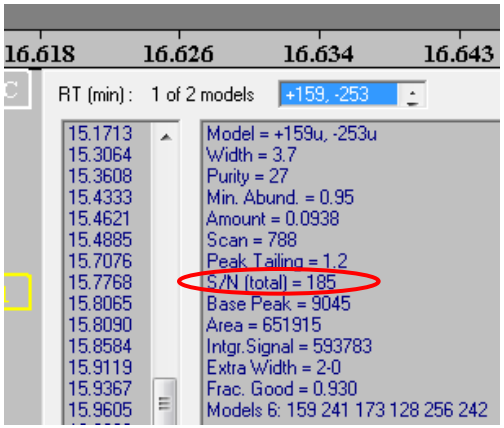


Minimizing Number of Components Detected

- The number of components detected can be minimized by many approaches
- One approach is to change the **Sensitivity** setting in the **Analysis Settings**
- Another approach is to use the filter settings and **Exclude if below** a specified **Min S/N**
- To optimized, expand the chromatogram and find a suitably sized “small” peak to find an appropriate S/N to mark the number of components detected

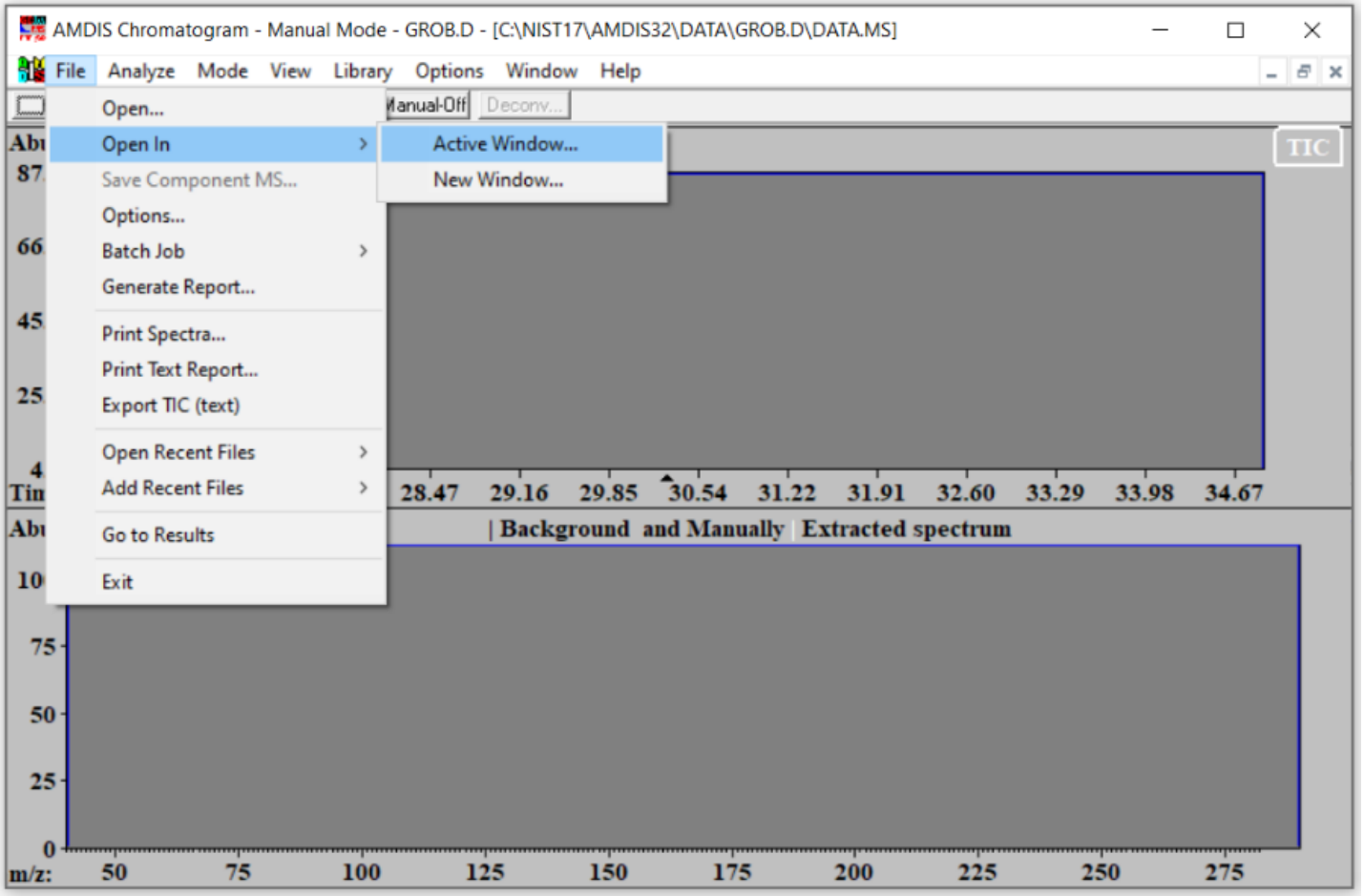






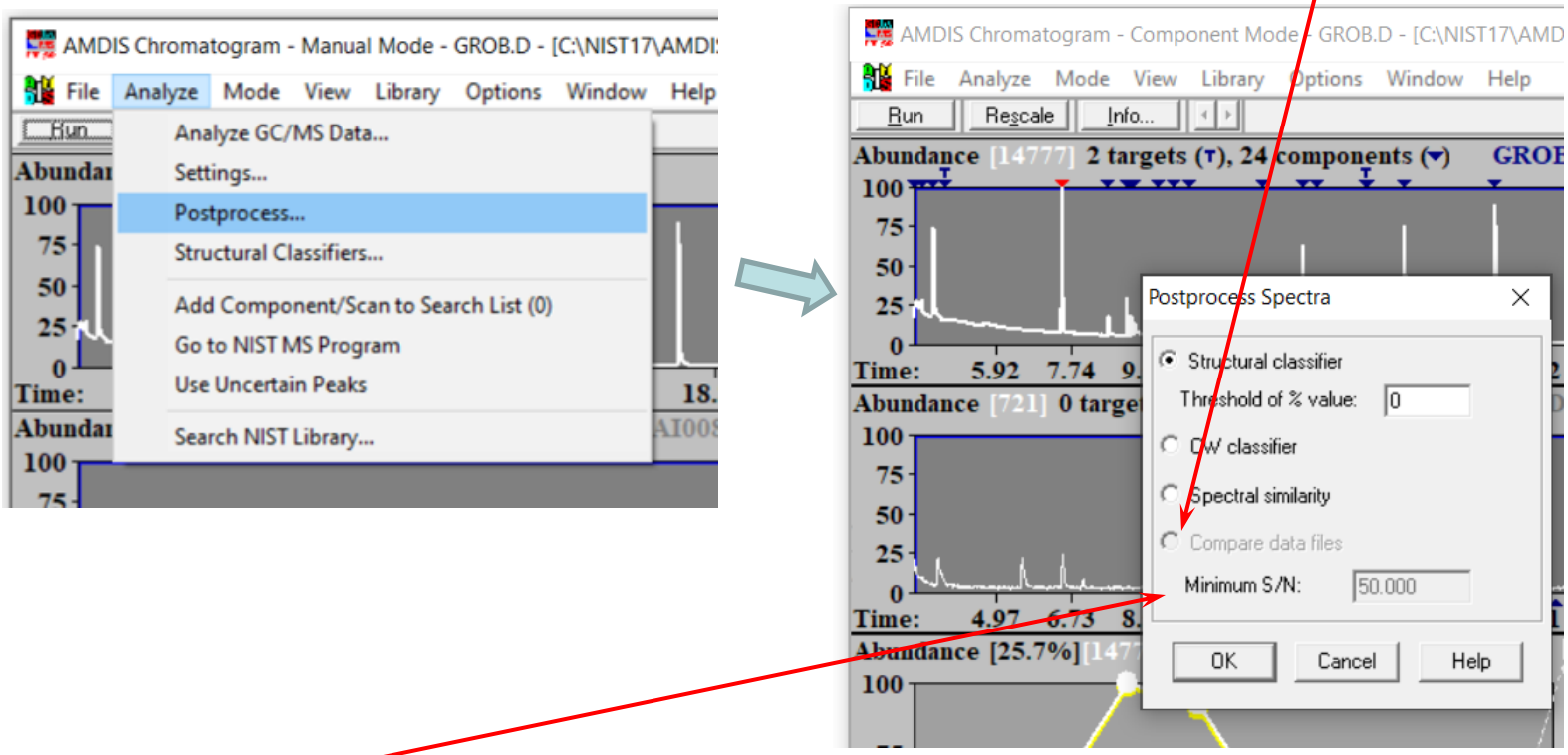
Comparing Two Chromatograms for Differences

- Two data files can be compared to determine differences, *i.e.*, "*Good*" and "*Bad*" samples
- Both ***must be loaded into the same window*** and both analyzed (run deconvolution)
- A good description of this process begins on pg 143 of the AMDIS Manual
- First, **Open** one file as normal
- Then open the file to be compared using **Open In/Active window…** as shown below



Comparing Two Chromatograms for Differences (cont'd)

- Put the **Pointer** on the top chromatogram and click the **LMB** followed by putting the **Pointer** on the **Run** button and clicking the **LMB** to deconvolute the file as normal using the appropriate settings. Repeated this process for the second chromatogram.
- Then, select **Postprocess** from the **Analyze** menu on the Main Menu and select "Compare data files"
- This process will compare both files to find differences
- Pick an appropriate S/N (bottom of pg 143 of manual)

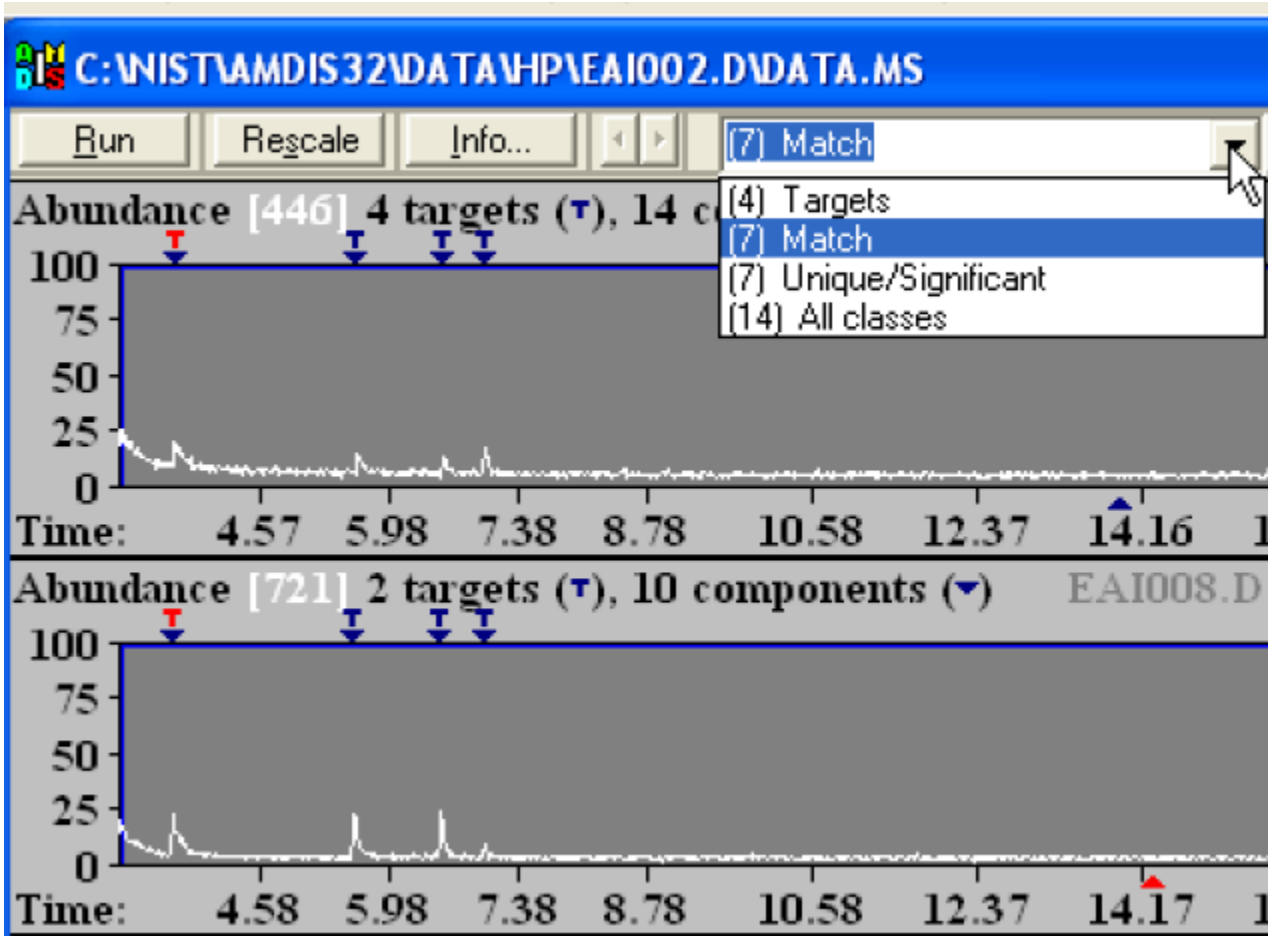


Specify a **Minimum S/N** to suit situation and then click the **OK** button

Note: The specified **Minimum S/N** should be adjusted to a level sufficiently high to prevent very low unique **Components** from appearing as **Unique/Significant**

Comparing Two Chromatograms for Differences (cont'd)

- The classes will be shown with a **T** when the menu is pulled down
- Can select either the top or bottom file, and the results are then with respect to the selected file (pg 144 of manual)



Classes of Comp'ds Compared in Post Process of Two Files

- The classes that are shown in the pull down menu for each file are shown below from pg 146 of the AMDIS User's manual

To compare results for both data files, it is necessary to make each active and perform the Compare Data Files analysis technique on each. Whenever the other file is made active by putting the **Pointer** on it and clicking the **LMB**, the drop-down list box changes to reflect that file's values

A **Component** will be assigned to one of the following groupings:

Match/Larger a pair of **Components** match, but one items is at least 3X larger than the other;

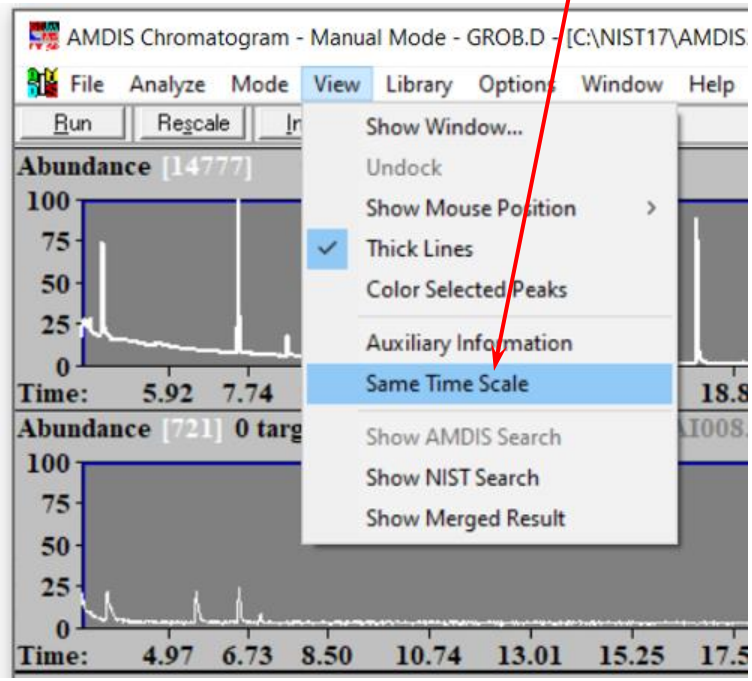
Match a pair of **Components** match and neither is 3X, or more larger than the other

Unique/Significant a **Component** that is only present in the active data file and whose signal is equal to or exceeds the signal-to-noise threshold describe above

Unique/Trace a **Component** that is only present in the active data file and whose signal is less than the signal-to-noise threshold described above

Displaying Chromatograms So That Time Scales Expand Together

- To get the files to expand together, select **Same Time Scale** from the **View** menu, as shown



Retention Indices (Kovat) Determined *by Users* in AMDIS

Name: Cholesterol
Formula: $C_{27}H_{46}O$
MW: 386 Exact Mass: 386.354866 CAS#: 57-88-5 NIST#: 332884 ID#: 7754 DB: mainlib
Other DBs: Fine, TSCA, RTECS, EPA, USP, HODOC, NIH, EINECS
Compound_ID: 0
Compound_Hash:
Contributor: NIST Mass Spectrometry Data Center
Related CAS#: 218965-24-3; 262418-13-3; 378185-03-6; 676322-57-9; 793670-51-6; 80356-14-5; 80356-33-8; 849593-11-9; 856708-55-9
InChIKey: HVYWMOMLDIMFJA-DPAQBDIFSA-N Non-stereo
10 largest peaks:
43 999 | 55 886 | 57 744 | 105 686 | 386 681 |
107 661 | 95 610 | 81 582 | 91 567 | 41 559 |
Synonyms:
1.Cholest-5-en-3-ol (3β)-; 2.(-)-Cholesterol; 3.Cholest-5-en-3β-ol; 4.Cholesterin; 5.Cholesterol base H; 6.Cholesteryl alcohol; 7.Cordulan; 8.Dusoline; 9.Dusoran; 10.Dythol; 11.Hydrocerin; 12.Kathro; 13.Lanol; 14.Nimco cholesterol base H; 15.Nimco cholesterol base No. 712; 16.Provitamin D; 17.Tegolan; 18.Wool alcohols B. P.; 19.3β-Hydroxycholest-5-ene; 20.5-Cholesten-3β-ol; 21.Cholestrin; 22.Cholestrol; 23.Super hartolan; 24.5,6-Cholesten-3β-ol; 25..DELTA.5-Cholesten-3-β-ol; 26.Cholesterine; 27.Dastar; 28.Fancol CH; 29.Cholest-5-en-3-ol, (3β)- #; 30.Cholest-5-en-3beta-ol; 31.Lidinite; 32.NSC 8798;

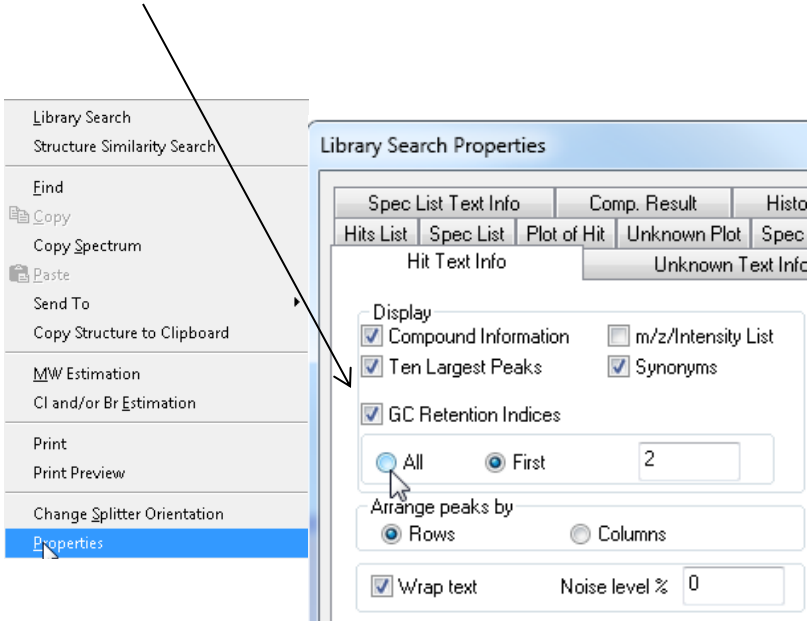
Experimental RI median±deviation [#data]
Semi-standard non-polar: 3087±12 (2)
Standard non-polar: 3052±29 (32)
Estimated non-polar retention index (n-alkane scale):
Value: 2596 iu
Confidence interval (Low reliability): 174(50%) 752(95%) iu

Retention index
1. Value: 3098 iu
Column Type: Capillary
Column Class: Standard non-polar
Active Phase: DB-1
Column Length: 30 m
Carrier Gas: Helium
Column Diameter: 0.25 mm
Phase Thickness: 0.25 um
Data Type: Normal alkane RI
Program Type: Ramp
Start T: 50 C
End T: 250 C
Heat Rate: 10 K/min
Source: Steiger, S.; Haberer, W.; Muller, J.K., **Social environment determines degree of chemical signalling (Supplemented matherials)**, *Biol. Lett.*, *1*(6), **2011**, 822-824.

2. Value: 3098 iu
Column Type: Capillary
Column Class: Semi-standard non-polar
Data Type: Normal alkane RI
Program Type: Ramp
Source: Steiger, S.; Peschke, K.; Francke, W.; Muller, J.K., **The smell of parents: breeding status influences cuticular hydrocarbon pattern in the burying beetle Nicrophorus vespilloides**, *Proc. Roy. Soc. B*, *274*, **2007**, 2211-2220.

3. Value: 3075 iu
Column Type: Capillary

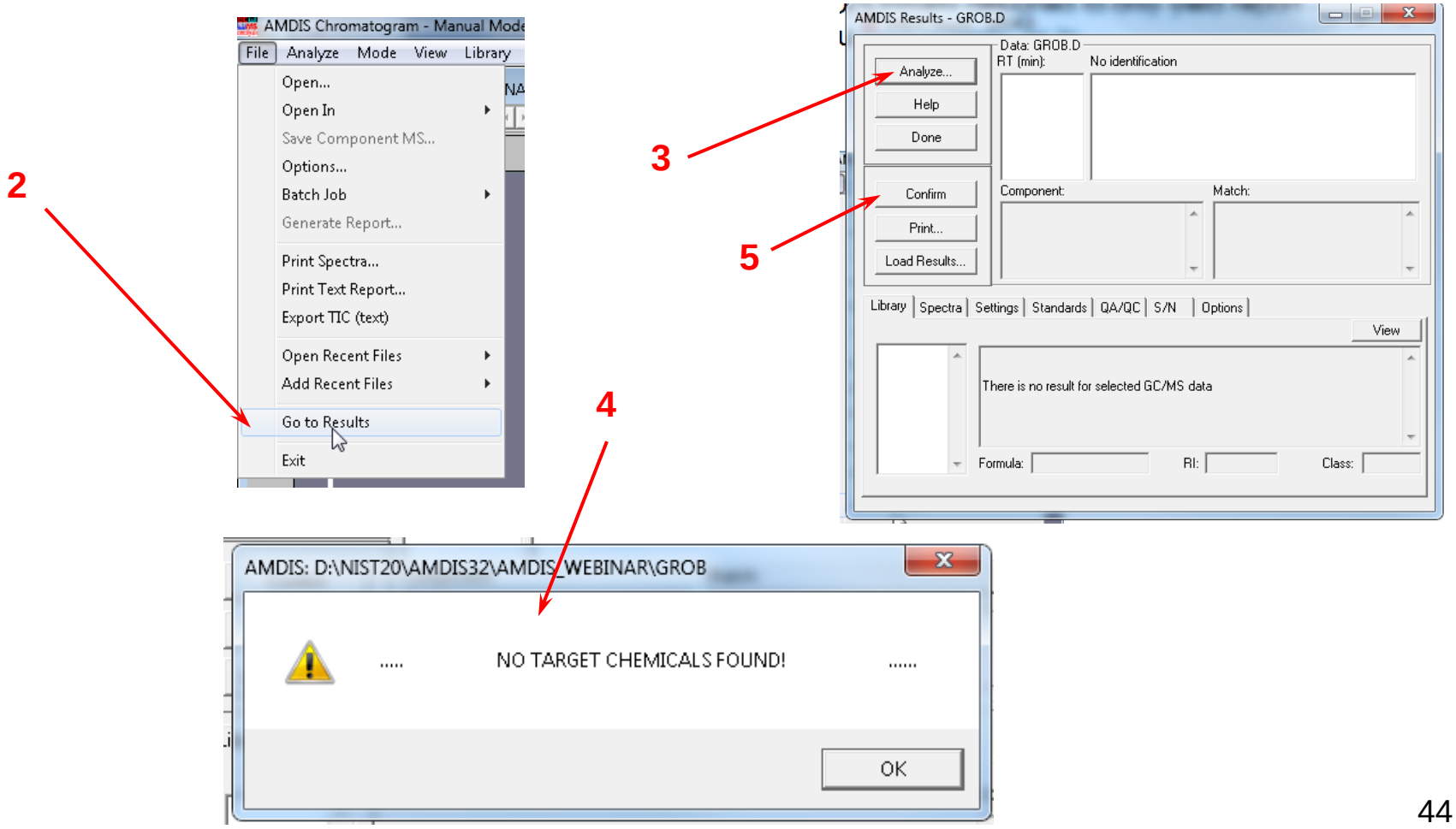
-NIST libraries have Retention/Kovat (RI) indices *
-Converts retention times into ***system-independent*** constants using a hydrocarbon calibration mixture
-RI's ***determined in*** NIST ***AMDIS*** software[3,4,12]
-Limit search, see Library Search Options/RI(GC) tab
-Additional orthogonal information for characterizing compounds
-MS Search results list methods and conditions for determination
-Standard display is top two to avoid "slowing" the display of search results
-Can expand to see **All** for a library entry, display First 0, 1…, or uncheck box to see none



* https://en.wikipedia.org/wiki/Kovats_retention_index

Problem No Chromatogram/Spectrum Window!

1. AMDIS initially designed to only yield report
2. If you inadvertently select “Go to Results”
3. Then “Analyze”
4. You could see “NO TARGET CHEMICALS FOUND!”
5. Select “Confirm” button to return to chromatogram/spectrum window normally used for qualitative analyses



Webinar References (*Internet Links*)

1. *James Little Mass Spectral Resource Website*
2. *NIST Search Software Detailed Manual*
3. *AMDIS Program for Data Processing Detailed Manual*
4. *Basic Instructions for Using AMDIS with NIST Search*
5. *Nightly Automatic Update of Users' Libraries*
6. *Using NIST Search from Instrument Manufacturers' Software*
7. *Chemical Ionization for MW Determination*
8. *Trimethylsilyl Derivatives for GC-MS*
9. *Methyl Ester Derivatives for GC-MS*
10. *SciFinder/ChemSpider and Accurate Mass LC-MS Data for Unknown ID's*
11. *Surfactant Identification*
12. *QuickGuide.rtf Supplied with AMDIS Software Installation for Retention Indices*
13. *New Developments in the Modeling of Ion Fragmentation by MS Interpreter Software*
14. *Enhancements to NIST MS Interpreter for Modeling High Mass Accuracy Tandem Mass Spectra*
15. *An Automated Method for Verifying Structure-Spectral Consistency Based on Ion Thermochemistry*
16. *Combining Fragment-Ion and Neutral-Loss Matching during Mass Spectral Library Searching: A New General Purpose Algorithm Applicable to Illicit Drug Identification*
17. *The Hybrid Search: A Mass Spectral Library Search Method for Discovery of Modifications in Proteomics*
18. *Hybrid Search: A Method for Identifying Metabolites Absent from Tandem Mass Spectrometry Libraries*
19. *Structure Annotation of All Mass Spectra in Untargeted Metabolomics*
20. *Most Current Handouts for Webinar Series, Parts I-V*
21. *Lipid Matrix Ionization Effects in LC-MS*
22. Mass Spectral Similarity Mapping in Hybrid Searches Applied to Fentanyl Analogs
23. User Manual for Wiley Libraries

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