

Setting Up Dual Tower injections for Dual GC (7890) Detector Data in Environmental Mode Mass Hunter Acquisition B.07.01

This document is to help setup dual tower injections for dual GC Signals while configured in Environmental mode. This analysis is designed to allow the same sample to be analyzed by both GC Detectors. The technique we are describing involves simultaneous injection of two aliquots of the same sample simultaneously into two columns or one aliquot to be injected on both columns. The resulting signals may be stored in the same data directory (linked), or in separate data directories (unlinked). In this document we will explore the various ways in which 2 signals can be combined as linked or unlinked files.

Note: There is a related technique in which injection is on a single column with the effluent being split between the two GC detectors. While we will not be discussing this here, the data organization is still the same.

Linked data is a term used where both GC signals are stored in the same *.D data folder. In Data Analysis, when you load linked data, both GC signals are loaded and displayed. This is why the term “Linked” is used. If the user wishes to see only one signal of the GC data, then they need to be able to unlink the various signals.

Unlinked data is a term used when both GC detector data signals are acquired, but are stored in different directories. When you load unlinked data, you would see only one of the GC signals stored in that file. To see the rest of the data, you would have to load the second file. When acquiring this type of data, the front GC Signal (front inlet) will be in the data directory specified in sequencing. The back GC signal (back inlet) will be in a directory with the same name as the front GC Signal (front inlet) however with a “.sec” extension. (Example: if the front GC Signal (front inlet) was in a directory named “mydata”, then the back GC signal (back inlet) would be in a directory named “mydata.sec”.) Both front GC signal and back GC signal will have unique data file names that were specified in the sample log table. You can also specify in the Keyword String field, on the Unlinked sequence line, the directory you would like the back detector saved to.

Let’s start to look at how to setup the method and the sequence for the different types of acquisition modes.

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1. Acquiring Both GC Signal data Linked and or Unlinked together.

When configuring the instrument, you must not configure any MS (select “None” for the MS Instrument), or certain options in the sequence will not be present. Configure a GC only.

First we must set the method to use both towers. This can be done by editing the Inlet/InjectionsType located below the Instrument menu item in Instrument Control. We must set the Injection Location to dual, then just Okay button on the screen. Please refer to Figure 1.

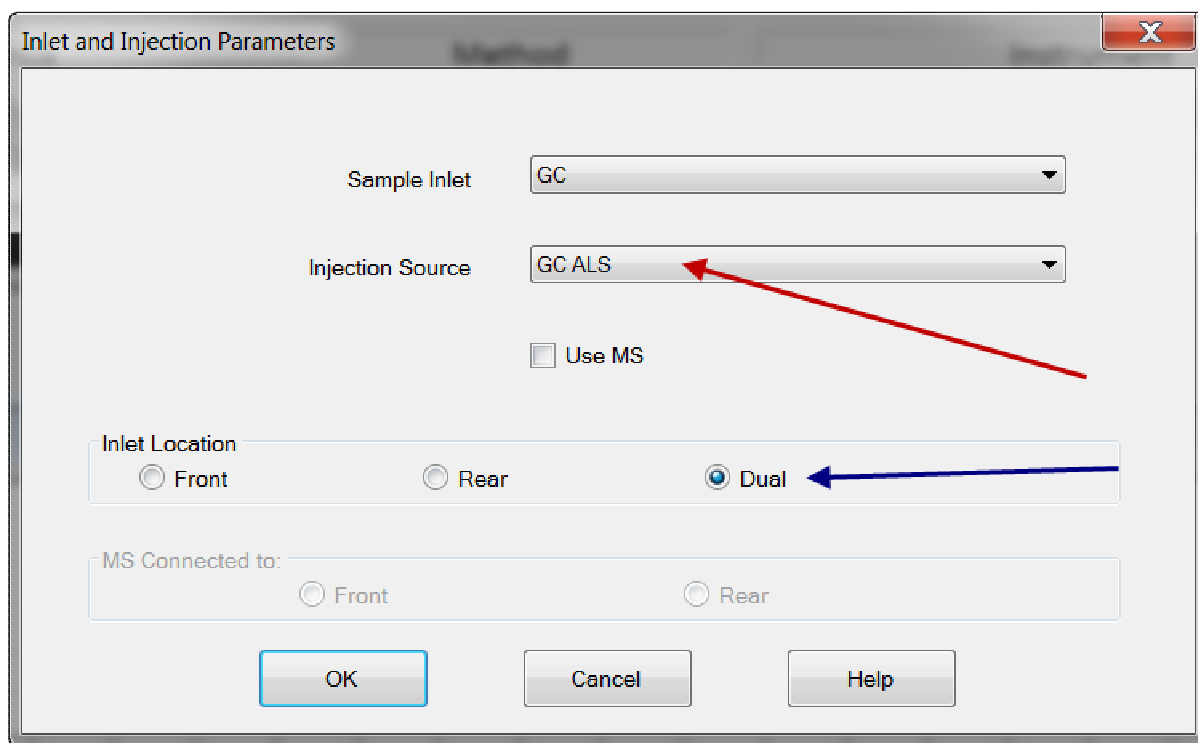


Figure 1

After setting these parameters, we need to setup the signals to be stored for the GC; this is accomplished by going to the menu item Instrument and then GC Edit

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Parameters. Please refer to Figure 2. Note that in our example, we are using “Front Signal (FID)” and “Back Signal (TCD)” as the source of our GC data. In reality, you would set the source to be the actual GC detectors.

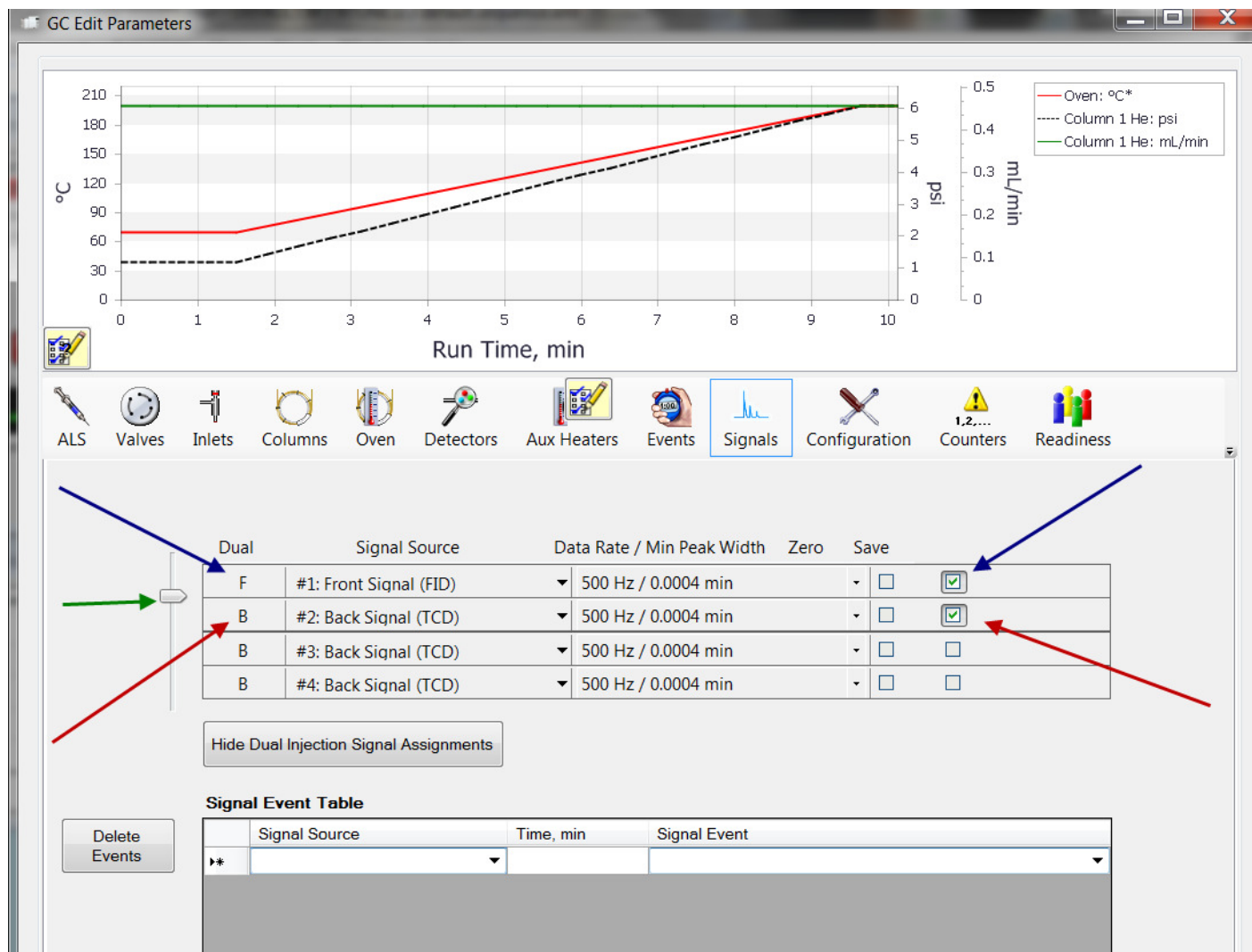


Figure 2

Now in Figure 2, you can set the method to Save Data for 1 GC detector (blue arrow) or you can set it to Save Data for the second detector (red arrow), or you can set it to save both. Now the slider bar (green arrow) on the left hand side needs to be set accordingly. If only acquiring just one signal then the bar would be raised to the top, but if acquiring dual GC signals it must be placed on the line between the first line (F) and second line (B).

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Once we have setup the method completely and saved, we can proceed to setup our sequence. We will be discussing how to setup dual GC signal mode acquisition in multiple configurations:

Linked Dual GC Signal 2 aliquots

Unlinked Dual GC Signals 2 aliquots

Linked Dual GC Signals 1 aliquot

This is done by using keywords in the sequence. Keywords are commands that the sequencing is programmed to recognize and use to perform key functions. The Keywords we will be using in our sequence table are...

Stagger

Unlinked

We also we be displaying differing column in the sequence editor.

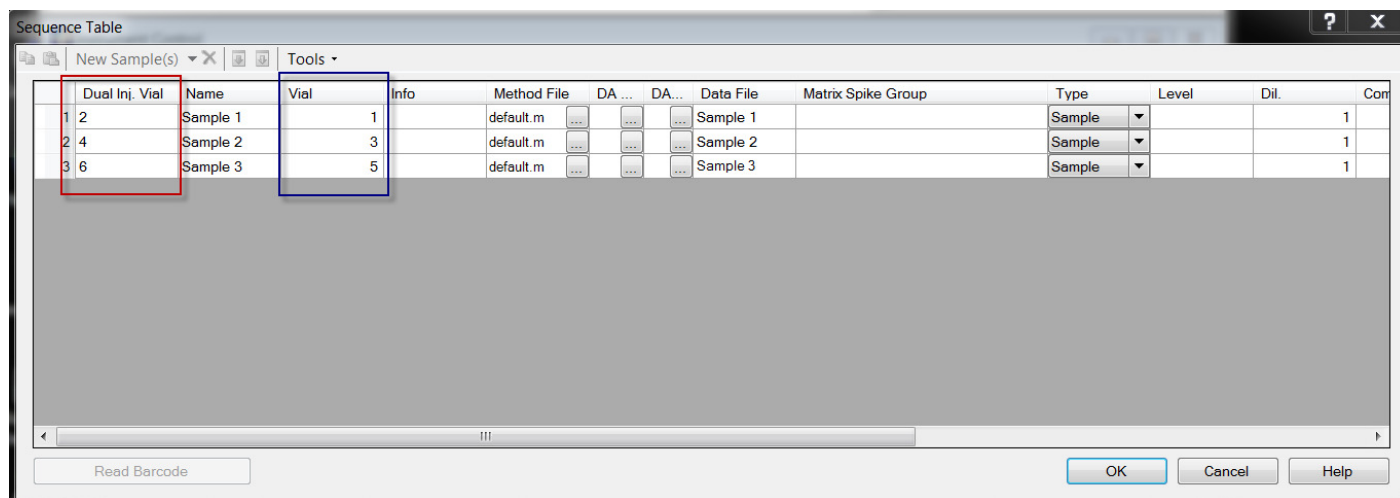
Rear Sample

Dual Inj. Vial

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A. Linked Dual GC Signal 2 aliquots



	Dual Inj. Vial	Name	Vial	Info	Method File	DA ...	DA...	Data File	Matrix Spike Group	Type	Level	Dil.	Con
1	2	Sample 1	1		default.m	Sample 1		Sample			1
2	4	Sample 2	3		default.m	Sample 2		Sample			1
3	6	Sample 3	5		default.m	Sample 3		Sample			1

Figure 4

The column labeled Dual Inj. Vial (red box), is the vial number for the rear tower. The Vial column (blue box) is the vial number for the front tower. (See Figure 4).

When we run the sequence, if we specified “Mydata” as the subdirectory in which to store our data files, we would end up with the following structures

D:\Masshunter\gcms\1\data\Mydata\

Sample 1.d

Sample 2.d

Sample 3.d

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Each of these data files contains the GC signals from both GC detectors. When you load Sample 1.d, you automatically see both signals.

B. Unlinked Dual GC Signals, 2 aliquots

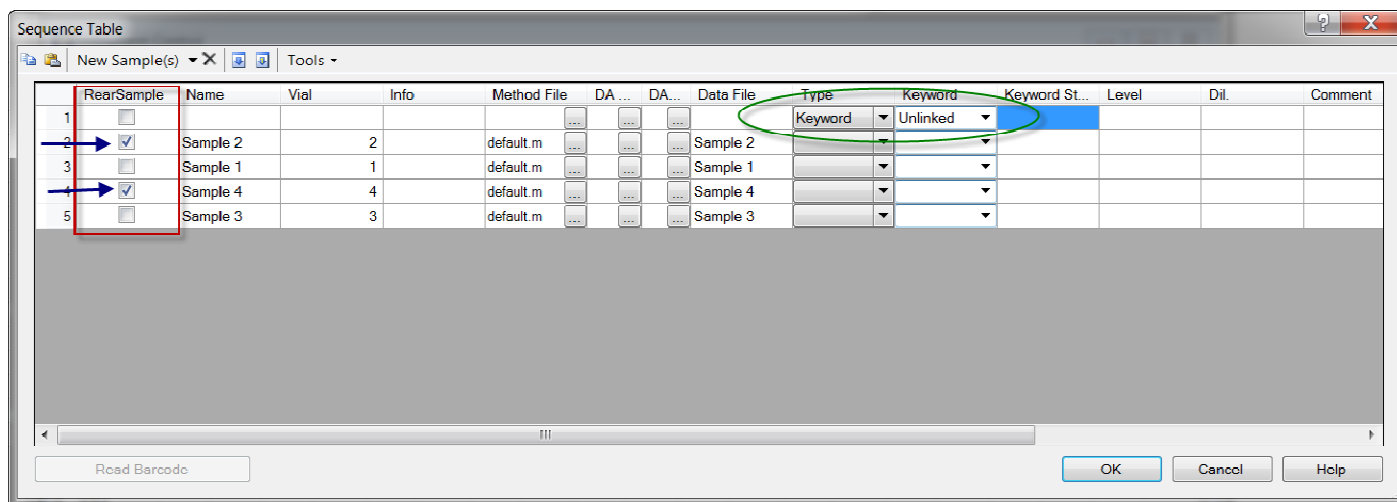


Figure 5

In this sequence we use a keyword “Unlinked” we also display the RearSample column (red box), and then we check the box if it is a rear sample (blue arrows). A rear sample will always be entered before a sample.

When we run the sequence, if we specified “Mydata” as the subdirectory in which to store our data files, we would end up with the following structures.

D:\Masshunter\gcms\1\data\Mydata\

Sample 1.d

Sample 3.d (This first group contains only front GC Signal)

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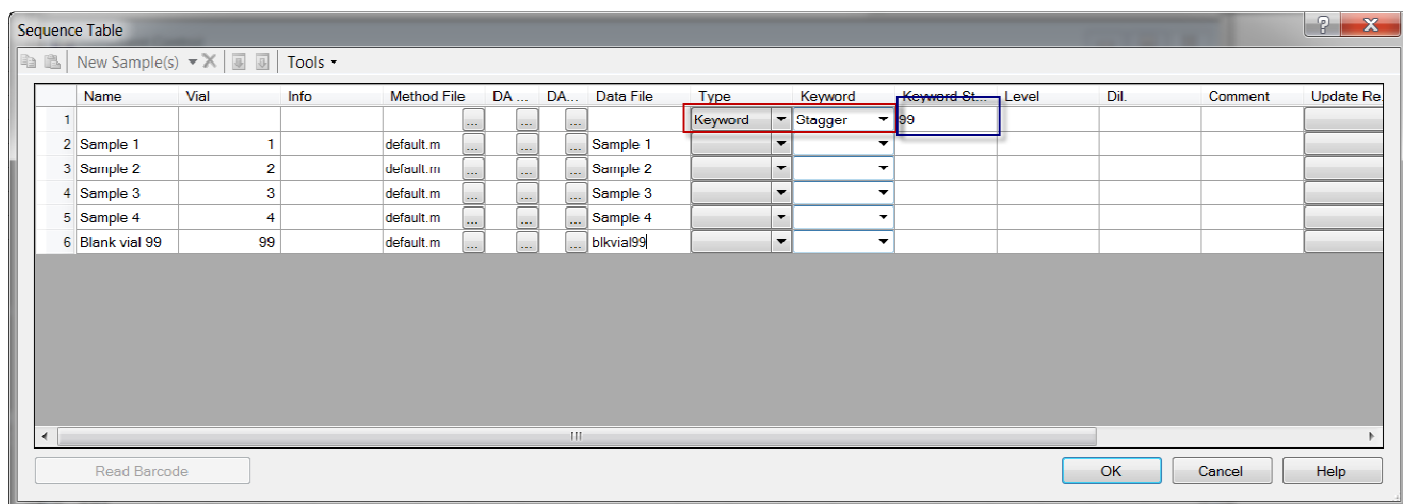
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D:\Masshunter\gcms\1\data\Mydata.sec

Sample 2.d

Sample 4.d (This second group contains back GC Signal)

D. Linked Dual GC Signals 1 aliquot



	Name	Vial	Info	Method File	DA ...	DA...	Data File	Type	Keyword	Keyword-St...	Level	Dil.	Comment	Update Re
1					Keyword	Stagger	99				
2	Sample 1	1		default.m	Sample 1							
3	Sample 2	2		default.m	Sample 2							
4	Sample 3	3		default.m	Sample 3							
5	Sample 4	4		default.m	Sample 4							
6	Blank vial 99	99		default.m	blkvial99							

Figure 7

In this example we are using the keyword Stagger (red box), this is to tell the autosampler where the blank vial (blank solvent vial number is entered in the keyword string field blue box) is in the autosampler tray. In this situation only 1 aliquot of sample is needed.

Before the first injection happens, the blank solvent vial will be placed in the back tower and the first sample will be placed in the front tower. The second injection of the sequence, the software will put the sample 1 in back tower and the sample 2 in front tower. It will then continue this “staggered” mode until all vials have been

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injected on both towers. In this mode there is no way to unlink the signals. This mode is usually used for dual column quantitation. When we run the sequence, if we specified "Mydata" as the subdirectory in which to store our data files, we would end up with the following structures.

D:\Masshunter\gcms\1\data\Mydata\

Sample 1.d

Sample 2.d

Sample 3.d

Sample 4.d

Each data file contains the data from both columns.

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