

HANDLING CHROMATOGRAM STORAGE IN THE VISTA II GCC

INTRODUCTION

The Vista II GCC has a total memory address space of one megabyte. Approximately half of that space is dedicated to the firmware and RMX operating system. The other half megabyte is used for operating information, analysis data, dual ported RAM for the VistaNET communications, static memory space, and chromatogram storage.

The average GCC with a typical application, before starting to save chromatograms, has about 350 Kilobytes of memory. The GCC keeps a certain amount of RAM to process post-analysis results and to build E2PROM images for saving to static memory. To minimize the amount of memory required for chromatogram storage, the GCC performs data compression on chromatogram information. Data compression adds a level of complexity that makes it impossible to determine exactly how much memory is required to save a chromatogram. This is because the efficiency of the compression is linked to the shape of the chromatogram: more peaks = more memory, more noise = more memory.

Due to the limitations listed above the GCC can run low on memory. The GCC will alarm when the memory goes below 20% (i.e., 70 Kb). This usually happens on GCCs that have long cycle times coupled with multiple streams. To make the best use of the memory available, configuration options have been installed in the GCC that allow the user to:

- configure which streams are saved
- determine under what conditions to save the data on the streams
- determine the resolutions of the saved data (points per second)
- release memory

DEFINING WHICH STREAMS ARE SAVED

1. From the front panel of the GCC press the F1 (Commands) soft key.
2. On the COMMANDS screen cursor to CHROMATOGRAM STORAGE (see Figure 1) and then press the F4 (Define Saved and Release) soft key.

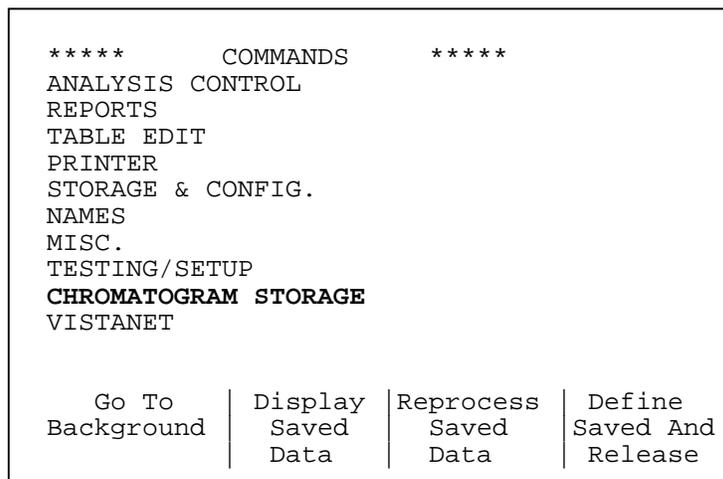


Figure 1

- On the Define Save/Release screen (see Figure 2) cursor to AUTO SAVE/RELEASE and then press the F2 (Execute the Command) soft key.

```

***** Define Save/Release *****
MANUAL SAVE
MANUAL RELEASE
AUTO SAVE/RELEASE
POINTS PER SECOND TO SAVE

Escape | Execute |
        | The     |
        | Command|

```

Figure 2

- From the Automatically Save Analyses screen (see Figure 3) you can configure the chromatograms that are saved for each stream by selecting **Yes**.

```

**** Automatically Save Analyses ****
          Save This Type

Stream  Cal   Bench  Last  Alarm  Alarm
Mask
01      No   No     Yes   Yes    65535
02      No   No     Yes   Yes    65535
03      No   No     Yes   Yes    65535
04      No   No     Yes   Yes    65535
05      No   No     Yes   Yes    65535
06      No   No     Yes   Yes    65535
07      No   No     Yes   Yes    65535
08      No   No     Yes   Yes    65535

Exit   |           |           | Expand
        |           |           | Alarm
        |           |           | Mask

```

Figure 3

When a **Yes** is placed in either the **Cal** or **Bench** column, the GCC will save a chromatogram for the stream whenever the analyzer runs a calibration or benchmark on that stream. Before marking **Yes** in the column for a benchmark or calibration stream, make sure that it is defined in the method. You cannot store a benchmark or calibration chromatogram unless it was defined in the method. The **Last** column informs the GCC to save the last chromatogram on the stream. The **Alarm** column informs the GCC to save the chromatogram only when the alarm mask is found to be true. The **Alarm Mask** column displays the alarm mask to be applied to the stream. This option allows the user to save chromatograms only when certain alarms have occurred in the GCC.

It is possible to place **Yes** in all four of the option columns. The GCC would then save four chromatograms on one stream: one for calibration, one for benchmark, one for the last regular analysis, and one for the last regular analysis that meets the conditions of the alarm mask.

It is important to be careful in configuring this screen. You do not want the GCC to store chromatograms you will never need, as this wastes valuable memory. In storing chromatograms you need to ask, "For what will I be using the stored chromatograms?" Some applications will only need the last chromatogram and the benchmark or calibration run stored once a day (or other period chosen). This allows you to compare the last analysis run with the last benchmark or calibration run. Other applications will only require looking at the chromatogram when the unit goes into alarm, to use as a troubleshooting tool. Still other applications may only be concerned with storing the last calibration run. Remember this configuration is easy to change, to enable you to make changes at any time.

POINTS PER SECOND

Another useful option in the GCC for conserving memory is the Points Per Second option in the Define Save/Release screen.

1. From the Define Save/Release screen cursor to POINTS PER SECOND TO SAVE and then press the F2 (Execute the Command) soft key.
2. When the Points Per Second To Save screen appears (see Figure 4), you can insert the time resolution in points per second in which the chromatogram is to be stored.

The range of the resolution is 1 to 32. If it is set to 1 the GCC will average all 32 points that it collects in a second and store only one point. If it is set to 32 the GCC will store all points as read from the detector. (NOTE: If you are reprocessing chromatograms you must save 32 points per second). A setting between 4 and 16 will do for most applications. If you encounter chromatogram storage problems the first options to try is to reduce the number of points per second saved. If you have a short analysis with a large number of peaks, you may want to consider increasing the number of points per second to save to give the best resolution possible.

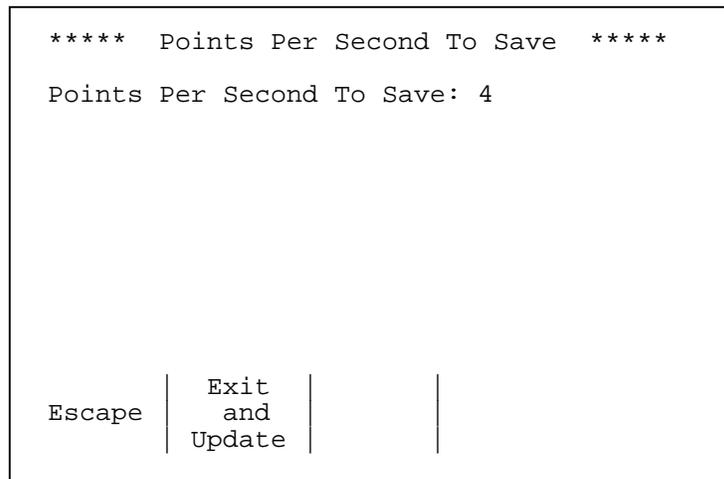


Figure 4

3. When you have entered the desired setting, press the F2 (Exit and Update) soft key to save the new setting, or press the F1 (Escape) soft key to retain the original setting.

RETURNING MEMORY

As stated in the introduction the GCC will post an alarm whenever its free memory goes below 20%. If this occurs you need to consider changing some of the options listed in DEFINING WHICH STREAMS ARE SAVED and POINTS PER SECOND. After you change either the streams saved or the points per second saved, then you should return all the memory used to save chromatograms back to the operating system. This enables you to start the collection process again to see if the changes made to the configuration have the desired effect. Before you release memory you should save any chromatograms that you wish to keep by using the GCCRUI to load these chromatograms into the PC and store them to the disk in the PC. To return memory to the operating system manually:

1. From the Define/Release screen (see Figure 2) cursor to MANUAL RELEASE and then press the F2 (Execute the Command) soft key to display the Manually Release Analysis screen (see Figure 5).
2. To release an individual chromatogram, select the type of analysis to be released, select the stream number, and then press the F2 (Manually Release Analysis) soft key to release memory used to save that individual chromatogram.
3. To release the memory used to save all chromatograms, press the F3 (Release All Analyses) soft key.
4. To return all the memory to the operating system (RMX) after releasing analyses, press the F4 (Return Free Memory) soft key.

```
***** Manually Release Analysis *****  
  
Type: Cal Bench Last In Out Typ  
Stream 1  
  
Escape | Manually | Release | Return  
        | Release  | All     | Free  
        | Analysis | Analyses | Memory
```

Figure 5

MANUAL SAVE

By selecting this option you can transfer chromatograms from one type to another type or from one stream to another stream. This becomes useful in situations where a chromatogram from the process stream is representative of a good or bad run. You can save this chromatogram as a **typ** (typical) or an **out** (out of alarm). You can then call up either one of these chromatograms in the future and compare it to the last chromatogram saved or to an alarm chromatogram. Using this in conjunction with the Manual Release Analysis Screen allows you to return memory of unwanted chromatograms while keeping other chromatograms for future reference. To perform a manual save:

1. From the Define/Release screen (see Figure 2) cursor to Manual Save and then press the F2 (Execute the Command) soft key to display the Manually Save Analysis screen (see Figure 6).

```
***** Manually Save Analysis *****
Make A Copy Of:
  Cal Bench Last In Out Typ
Stream: 1

And Save As:
  Cal Bench Last In Out Typ
Stream: 1

Escape | Manually | |
       | Save    | |
       | Analysis| |
```

Figure 6

2. Select the analysis type and stream number of the analysis to be saved.
3. Select the analysis type and stream number to be given to the saved analysis.
4. Press the F2 (Manually Save Analysis) soft key to save the analysis for future reference, or press the F1 (Escape) soft key to exit without saving the analysis.