

## **Basic Operating Instructions for the Hewlett Packard GC/MS System**

*These are instructions for students in Instrumental Analysis Laboratory for basic operations using the HP 5890 GC with HP 5971A MSD and HP Chemstation.  
May 2003*

### **Startup**

The instrument is always on and should not be shut-down.

The icon to open the GC/MS main control panel should be on the desktop. It is called MS Top #1 and looks like a GC/MS. If it is not on the desktop, check in the start menu under 5971-Instument #1. Double click this icon to start the main control panel. I have attached a figure of what this control panel should look like. From this menu you can control all the functions of the instrument.

### **Setting up a Method**

Click 'Methods' to begin setting up a method. This menu has seven options.

1. Load and Run Method: this allows you to load a method that was saved previously and start a run on the GC/MS
2. Edit entire method: this option allows you to change a previously saved method or to edit the default method and save it as a new method.
3. Edit Method Information: this option changes only the information about the method not the parameters
4. Run: if a method has already been loaded but you have not yet run it, this command brings you directly to the screen from which you can start a GC/MS run.
5. Load: Loads a method but does not run it.
6. Print: Prints your method parameters
7. Save: Saves your method parameters

Normally the default method will load automatically. If it does you should see the name of the method in the top blue bar of the main window. Here it appears as DEFAULT.M. If starting a new method for the first time first click 'Load' and choose DEFAULT.M. Now click back into the 'Methods' menu and choose 'Edit entire method.' The first selection box allows you to choose which parts of the method you would like to edit. You can check or uncheck these boxes as you see fit. For basic GC/MS most of these panels will not need to be edited. You can select the default options that come up. For our experiments we need only to concern ourselves with the 'Temperature Information Panel.' Here is where we program into the instrument the temperature gradient. One important point to note here is to make sure that the 'Oven Max' is the same on the control panel on the front of the GC as it is typed into the computer. If it does not match, change temperature on the GC to match the computer; otherwise the system will crash when it tries to load the parameters into the instrument. The remaining panels also have some options but for our purposes we do not need to change those. Once you have finished editing the program will ask you to save your method.

## **Starting a Run**

To begin a run, click on 'Methods' then on 'Load and Run Method.' Select your method from the list and then click OK. A window will pop up called 'Start Run' and should look like the second figure on the attached page. From here you need to type in where you would like to have your file saved. (c:\HPCHEM\1\DATA\filename.D) Max characters for the filename is 8. Remember between runs the computer will not change the name or location of where your file will be saved so you must change it to avoid having your data overwritten. When you have your entire information entered click on 'Run Method.' Do not click on OK. This will only close the menu and you will have to open it again to begin the method. Once you have clicked 'Run Method' the computer will begin to download the parameters into the GC. An injection can be made as soon as both the lights on the front panel of the GC go off. As soon as an injection is made press 'Start' on the main control panel of the GC. The computer will ask you if you would like to override the solvent delay. Choose NO. The run will now begin.

**Always inject 1  $\mu$ L or less of dilute solutions of analyte in volatile solvents.** If you inject  $\mu$ L quantities of concentrated analyte liquid (such as neat kerosene), damage to the MSD may result.

## **Data Analysis**

The program has two ways of analyzing data. From within the program itself from the 'Data Analysis' menu option or on the desktop there is a Stand Alone data analysis. I recommend using the standalone data analysis because the one from within the program will not allow you to analyze data while a run is taking place.

To open a chromatogram click on 'File' then 'Load' and find where you saved your chromatogram and load it. Once the chromatogram is loaded you can move the mouse cursor over the peaks. Clicking and holding the left mouse button allows you to zoom in. To zoom out double click twice in an area with no peaks with the left mouse button or choose 'Draw Chromatogram' from the 'Chromatogram' menu option. To get the MS of a peak place the mouse cursor at the maximum height and double click twice with the right button on the mouse. The mass spectrum will be displayed below. Zooming on the mass spectrum is the same as the chromatogram. Double clicking twice with the right mouse button on a peak in the MS will tell the computer to search the library and try to guess what that fragment might be. Works well for super simple compounds.

Auto-integration can be done from the chromatogram menu and manual integration can be done from the Options menu.

## **Shutdown**

The instrument should be left on and running. **DO NOT SHUT OFF THE INSTRUMENT OR THE CARRIER GAS.** You can shut down the software program on the computer.