Directions for downloading GC-MS data on computers in room 230

1. **Log on** to any one of the four computers on the same table with the printer in SCI-230.
2. Starting from the Windows button on the bottom left-hand side of the screen, **type "\\ntm"** in the rectangular white box and hit **Enter**. (Make sure to use the correct 'backslashes' in your search.)
3. From the file folders on the ntm server, navigate to the **Chemistry/211 GC-MS folder**.
4. Locate your data by opening the following folders: **your semester folder**, **your lab day folder**, and **then the desired experiment folder**, for example, 211F12/Tuesday/COMPNUC for the competing nucleophiles experiment.
5. **Drag your data file name folder to the desktop.**
6. **Open the "Data Analysis" program shortcut** on the desktop (or go to all programs/MSD ChemStation/Data Analysis.) Wait for the program to load.
7. From the **File** menu, select **Load Data File**.
8. On the **"Select Data File..."** dialog box, **click "Change Path".** Select **Desktop** in the "Browse for Folder" dialog box. **Click OK**.
9. **Highlight your data file name and click OK**. This will bring your GC to the screen.
10. **If the GC for your sample shows a black background and no peaks, do the following**. Click on the "Edit Colors" icon, which is a rectangle of four colors. From the drop-down menu, choose "Default Theme" and save your choice. (You will only have to do this once. The colors will be saved for the next time you open the program.)
11. From the menu bar, select **Chromatogram** and then select **Percent Report**. To copy your percent report data table into your e-lab, **highlight** your Area Percent Report's data table and **copy (ctrl-C)** and **paste (ctrl-V)** the data table into your e-lab.
12. To copy your GC into your e-lab, select "**Copy Windows...**" from **Tools** in the menu bar. In the Input window, enter "**2**" and click **OK** to copy your GC. Then, **paste (ctrl-V)** your GC into your e-lab.
13. To obtain a mass spectrum of any compound in your GC, put the cursor directly over the middle of the GC peak and **double click with the right mouse button**. [It's recommended that you follow the instructions below for enlarging each GC peak before obtaining its mass spectrum.]

**TO ENLARGE...a section/peak of either the GC or the MS, use the left mouse button to drag a box around the desired area. You must include the tip of the peak and the x-axis scale. To return to the full spectrum, double click with the left mouse button anywhere on the GC or MS.)

14. You will need to remove the masses in your mass spectrum that come from the compounds which make up the baseline in your GC. To do this, **generate the mass spectrum for the GC peak** you are interested in. Then, **generate the mass spectrum of the baseline to the left or right of the GC peak.** Make sure the area you select is completely flat and isn't part of any GC peak. Under **Spectrum**, in the menu bar at the top of the screen, highlight **Subtract**. This will generate the mass spectrum for your compound only. It will remove any masses in your spectrum created by the baseline compounds, such as the solvent that you dissolved your sample in.
15. Only copy the peaks and mass spectra that are of interest to you. To copy either any expanded region of your GC or expanded MS for your e-lab: find **Tools** in the menu bar and select **Copy Window…**. In the Input window, **type 2 for your GC** of the expanded peak or **type 1 for your MS on the screen**. Open the document you want to paste your GC or MS in and under Edit, select Paste or type **ctrl-V**.
16. For the Competing Nucleophiles lab, you should copy the mass spectra of at least 3 peaks of interest on the GC into your e-lab. Two of these spectra should be your 2 expected products. You may also see a peak from unreacted starting material. (Your instructor may modify this assignment.)
17. When finished, go to **File** and select **Exit**.
18. Remember to **log off** when you are finished.