Operation Manual for the TA Instruments TGA Q-500:

Temperature Range: Room Temperature – 1000°C
Sample Weight: 10 mg – 1 g
Platinum Sample Pans are supplied by the lab.

1. If the TGA Q-500 experimental view is not showing, click on Q-500 on the bottom of the computer screen. On the experimental view page, open the **NOTES** tab and check the gas selection and flow rate.

2. **Gas Selection**: The balance gas is ALWAYS inert (Nitrogen or Argon) but you may select the sample gas, You may choose argon, nitrogen, oxygen, or air. Other gases are available upon request. Gas selection is made by clicking the arrow next to **SAMPLE**.

3. If the gas you want is not available in the pull-down menu you may find it using the following procedure: At the top of the screen click on **TOOLS**, then select **INSTRUMENT PREFERENCES**. Click on the **MFC** tab and select the gas you want.

4. The correct flow rate is 40 ml/min for the balance and 60 ml/min for the furnace.

5. Platinum pans are available and must be cleaned prior to use. You may run up to 16 samples at a time though you will have to request additional pans to do so. The pans are cleaned in the front room of the lab. A Q-tip is wet with acetone and run around the inside of the pan. The Bunsen burner is used to burn off excess residue. The procedure is repeated until the pan is sufficiently clean. A re-shaping tool is available if the pan is bent too far out of shape.

6. The clean pans are placed on the auto-sampler taking care to line up the welded hangers with the slots on the base of the autosampler. Click on the tare icon 

on the top of the screen and then select the pan/pans that need to be tared. Taring will begin automatically and continue until all the pans are weighed. The pan weight will be automatically subtracted from the sample weight.

7. When taring is complete you may load your samples using 10-20 mg of sample. You may use more or less sample. The most important thing is that the sample should fit within the pan and should be as flat as possible.

8. Click on the **SUMMARY** tab on the computer screen to input sample information. **SAMPLE NAME** and **PAN #** are self-explanatory. Your data will be saved in a data file. You must make a new folder. To do so, click on the icon next to **DATA FILE NAME** (looks like the pages of an open book). Click on the UP icon until you find **DATA**, then click on the **NEW FOLDER** icon. Name the folder (your name), click to open it and then enter your sample name. Your data will be automatically saved in your folder as the "data name.001". The numbering will automatically increase (.002, etc) if you do not change the sample name with each new sample.
9. Click on the **PROCEDURE** tab to write your method. To the left hand side of the screen there is a heading **SEQUENCE**. Select the **PAGE** icon to clear the current sequence. It will ask you if you want to save it…select **NO**. Now click on the **EDITOR** command in the center of the screen. Again select the **PAGE** icon to clear the current method. To write a method, double click the options to the right. Start with **GAS SELECTION** and then choose **1** (inert) or **2** (air or oxygen). Double click **RAMP** and fill in the ramp rate (generally 5, 10, or 20°C/min) to a final temperature. The maximum temperature allowed is 1000°C. Generally, 600°C-800°C is enough to completely degrade a polymer. You may hold the instrument isothermal at any temperature for any length of time. You may also switch the gases during a run, also at any temperature. End your method with **DATA STORAGE OFF** followed by **EQUILIBRATE at 60°C**. This will cool the furnace down without collecting data. The instrument is set to cool for an additional 10-15 minutes after the sample is unloaded. When you are done inputting information, click on the next tab.

10. Click on the **NOTES** tab. You have already selected your gases that you will use, but you need to put your name next to "**OPERATOR**".

11. Now click on the **APPLY** command at the bottom of the screen.

12. If you have more than one pan, click **APPEND** and go back to the **SUMMARY** tab to input the next sample. You must change your sample name, data file name and pan number (it automatically advances to the next pan #). You may change your procedure at this time or leave it the same. When you are done, click **APPLY** (if you are finished) or **APPEND** if you have more samples.

13. To begin the sequence, click on the **GREEN** arrow at the top of the screen. All runs in the sequence will run and be saved automatically.

14. You may stop a sequence using the red buttons on the top of the screen. You may modify your procedure at any time by clicking on **EXPERIMENTAL** and then **MODIFY PROCEDURE**. You may change conditions as well as add or delete steps from here.

15. You may observe real-time data in Universal Analysis. Open UA from the bottom of the screen by clicking on **UNIVERSAL ANALYSIS**. Open the data files and find your sample. It will open and continue to update the data as it runs. Data is automatically saved at the end of the run.

16. See Laura for help with data analysis and interpretation.