Chromeleon software orientation
Upon opening of **Chromeleon** shortcut, a blue screen should appear (called **control panel**). If this does not occur, the green circled shortcut will open this screen. To ensure that the PC can control the operation of the ICS-2100, make sure the **connected box** (red circle) is checked. From this screen you can monitor all the hardware settings (pump, injector, column temperature, detector, and eluent concentration). If any of these need to be changed click on the settings box in the bottom right corner. Once, the connected box is checked, click on the **browser shortcut** (orange circle).
Browser display screen, the red box is the separation program files for particular analytes, the orange box is the sample protocol, and the green box is the file location for saved information. Find your folder in the green box and under your folder should have sequence folders (blue folders). A few sequence folders should be templates, while others will be saved data. Choose a sequence template and add the number of samples in the orange box required by using the right button on the mouse. There are numerous headers in the orange box. Name is the sample ID, type is to determine unknowns or standards, Pos is the auto sampler location, Program is the separation program from the red box, method is a peak labeling tool, status comments on sample condition, date/time states time of analysis, dil factor is a correction value if you previously diluted your sample. After your program is set, click on Batch. Once a separation is complete, return to the browser page and double click on a sample.
Labeling Peaks and Creating Calibration Curves

After double clicking on a sample this screen should appear, the **green box** is the chromatogram and the **red box** the raw numbers. Click on view and select **QNT Editor** or simply press on the shortcut (black circle). This will display a split screen view.
QNT Editor Page should be displayed. The green box is the chromatogram, the blue box is the calibration curve for a certain peak, and the red box is the integration software. Ensure the **General tab** (orange circle) is selected. Nothing needs to be changed on this page except the units (red circle) to ppm, mM, etc.). Lastly, click on the **Detection tab** (black circle).
The **Detection** page allows automatic integration of peaks. The Ret Time heading is used to notify the software where to start the command on the chromatogram. The first modification should be done to **Minimum Area** (red circle). This is a threshold value for the minimum area need for the software to identify as a peak (eliminate background noise). Typically set to 0.1 but can be modified to fit the chromatogram. The second modification is the integration style (black circle). Current set to Valley-to-Valley. Once the software identifies all the peaks, you can modify the integration to your liking with the mouse. Lastly, click on the **Peak Table** tab on the bottom of the screen.
Peak Table display is where a sequence folder can be modified (the blue folder within the directory). Depending on your chromatogram, you may have more than 8 peaks. Peak name heading can be modified to the analyte identification. Ret. Time heading cannot be changed, but window (typically 0.03 min) allows the retention time of the analyte to vary between chromatograms, allowing the software to identify peaks in other samples. Lastly, click on the Amount Table tab on the bottom of the screen.
Amount table display is shown here. If you labeled the samples as standards (on browser page) the amount headings should. To change the calibration curve on the right you need to modify the amount headings for each standard you created. If the amount headings do not appear, go back to the browser page and change the type from unknown to standard. Come back to this page and a pop-up menu should occur, click on the pull-down tab and selected name.
Calibration display is shown here. The use of this page is to remove any oddities that may have occurred due to an interruption during the run. For example, if you wanted to remove the second standard for a peak because it co-elutes with another peak, then click on the check mark to remove it from the calibration curve.
To view a single chromatogram, simply click on the sample in the browser page. If you want to compare numerous chromatograms, highlight the selected chromatograms and right-click on the selection. Go to compare and select either ECD (detection) or pressure to view the pressure throughout the run.
Display of chromatogram comparison page. In theory, the chromatograms should be nearly the same, if not it could be due to a pressure problem (as shown here).
To create a report (pdf or xls), first select the samples you want the report created for. Right-click on those selected files and go to batch report.
Batch report windows will pop-up. Deselect the printout function and make sure all of the desired outputs are checked within the box. Click on **export** to select type of file to save.
Upon clicking on export, another pop-up will open. First check the desired output file type from the formats given. Then, select location (browse icon) to determine where to save your file (your own folder or flash drive).
From the pop-up browse menu, select your save location. When done, click on ok.
Double check to make sure all report outputs desired are checked in the export wizard window, and then click ok. And then click ok on the batch report window.
A batch report window will appear showing a downloading stream. When completed click on ok.
Return to the desktop and find your save location to open the downloaded report.