Picarro **Caddy** Interface

Quick Start Guide

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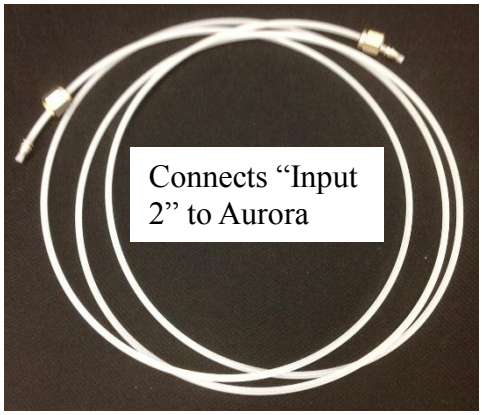
The Caddy Interface Quick Start Guide

The Caddy is an interface that connects various analytical front-ends to the Isotopic CO_2 CRDS analyzers.

The Caddy is meant to handle a transient CO_2 pulse from a front-end, broaden it, and split the carrier gas flow rate in an adjustable way to match the flow rate of the CRDS analyzer (~ 25ml/min). The Caddy allows up to two front-ends to connect to it and has an option to flow room air into the CRDS analyzer for the healthy operation of the WaveLength Monitor (WLM) and the system calibration with ambient CO_2 levels.



Input 1 Port: Input 1 is a 5/16” Swagelok fitting located on the front of the Caddy interface that allows a 1/16” tubing to be connected to it. To select this input option to flow into the CRDS analyzer, you need to rotate the black handle of the selection valve to point to the Left handside (SS tubing will be included with the Caddy kit in case the Combustion Module has been purchased as well).
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Input 2 Port: Input 1 is a 7/16” Swagelok fitting located on the front of the Caddy interface that allows a 1/8” tubing to be connected to it. To select this input option to flow into the CRDS analyzer, you need to rotate the black handle of the selection valve to point to the Right handside (polymer tubing will be included with the Caddy kit).

Room Air Port: When the CRDS system is idle with no analyses intended to be run with either of the connected front-ends, it is highly recommended to flow room air into the CRDS analyzer by rotating the black handle of the selection valve located on the front of the Caddy interface to point upwards.

Note: Pointing the black handle of the selection valve downwards will block the CRDS analyzer inlet and prevent any flow from flowing into the analyzer.

Output to CRDS Port: The “Output to CRDS” port is a 9/16” Swagelok fitting that needs to be connected to the CRDS analyzer 9/16” inlet port to enable the gas flow from the front-end to reach the CRDS analyzer. The ¼” connecting tubing shown below is provided with the Caddy interface.

Open-Split Port and Metering Valve: The metering valve located on the left handside of the Caddy interface is intended to adjust the split flow from either front-end at the time when the specific input port is selected via the selection valve. To adjust the split flow, attach flowmeter to the open split port located right behind the metering valve and adjust the metering valve accordingly to allow ~25ml/min to the CRDS. For instance, if the selected front-end is putting out 100ml/min, you should then adjust the split flow vent to release 75ml/min, allowing only 25ml/min to flow into the CRDS analyzer.

Carrier Gas Options: The Isotopic CO_2 CRDS analyzer can handle a variety of carrier gases flowing through the Caddy interface.

1. Nitrogen Carrier Gas: To use the N_2 as a carrier gas, no modifications are needed on the Caddy side. However, **make sure to use the appropriate operation mode on the CRDS analyzer** by making a selection from the drop-down menu of the "Picarro Mode Switcher". The "Picarro Mode Switcher" icon is located on the desktop. Double-click on it to launch it.

2. Zero-Air Carrier Gas: To use Zero-Air as a carrier gas, no modifications are needed on the Caddy side. However, **make sure to use the appropriate operation mode on the CRDS analyzer** by making a selection from the drop-down menu of the "Picarro Mode Switcher". The "Picarro Mode Switcher" icon is located on the desktop. Double-click on it to launch it.

The Caddy interface proper operation will require the use of the Caddy Coordinator software that can be selected after double-clicking on the "**Coordinator Launcher"** icon located on the CRDS analyzer computer desktop. The Caddy coordinator will allow the software to detect CO_2 transient peaks evolving from the front-end and reports the $^{12}CO_2$ in ppm,$^{13}CO_2$ in ppm and the $\delta^{13}C$ (permil) values in addition to the sample description of each sample analyzed.

Please refer to the Picarro Peak Integration Software Supplement below for more details.

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Picarro Peak Integration Software Module

Peak Integration Software Supplement

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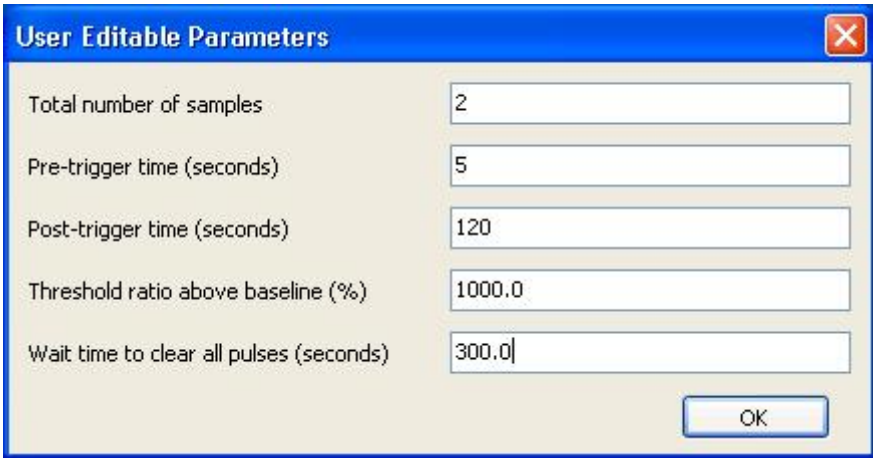
CRDS (Cavity Ring-Down Spectroscopy): Using the PEAK INTEGRATION SOFTWARE

Overview

This supplement to the Picarro CRDS User's Guide is to show how to use the Peak Integration Software to integrate the infrared absorption curve of isotopic carbon dioxide from sample combustion. The CRDS concentration and isotopic measurements can be seen on the CRDS Data Viewer Window. The software provides easy-to-understand detailed measurements, including the concentration of both $^{12}CO_2$ and $^{13}CO_2$, and the isotopic ratio expressed as $\delta^{13}C$ CRDS.

Step 1: After loading your samples into the carousel, double click on the "Coordinator Launcher" icon on the analyzer's desktop.

Step 2: The "Picarro Coordinator Launcher" will appear on your desktop. Click on the drop-down menu and select the "Peak Integration Coordinator," then click on the launch button.



Step 3: The following user interface will then pop up.

This "User Editable Parameters" window can be used to set various parameters for your sample analysis.

1. You can specify the **total number of samples** you plan to analyze.

2. Pre-trigger time and post-trigger time will be pre-populated with values recommended by Picarro. However, they can be modified easily on this window:

   Pre-trigger time: is the time the user sets for the peak integration to be extended prior to when the threshold is reached.. We recommend using "0" initially and adjust as necessary.

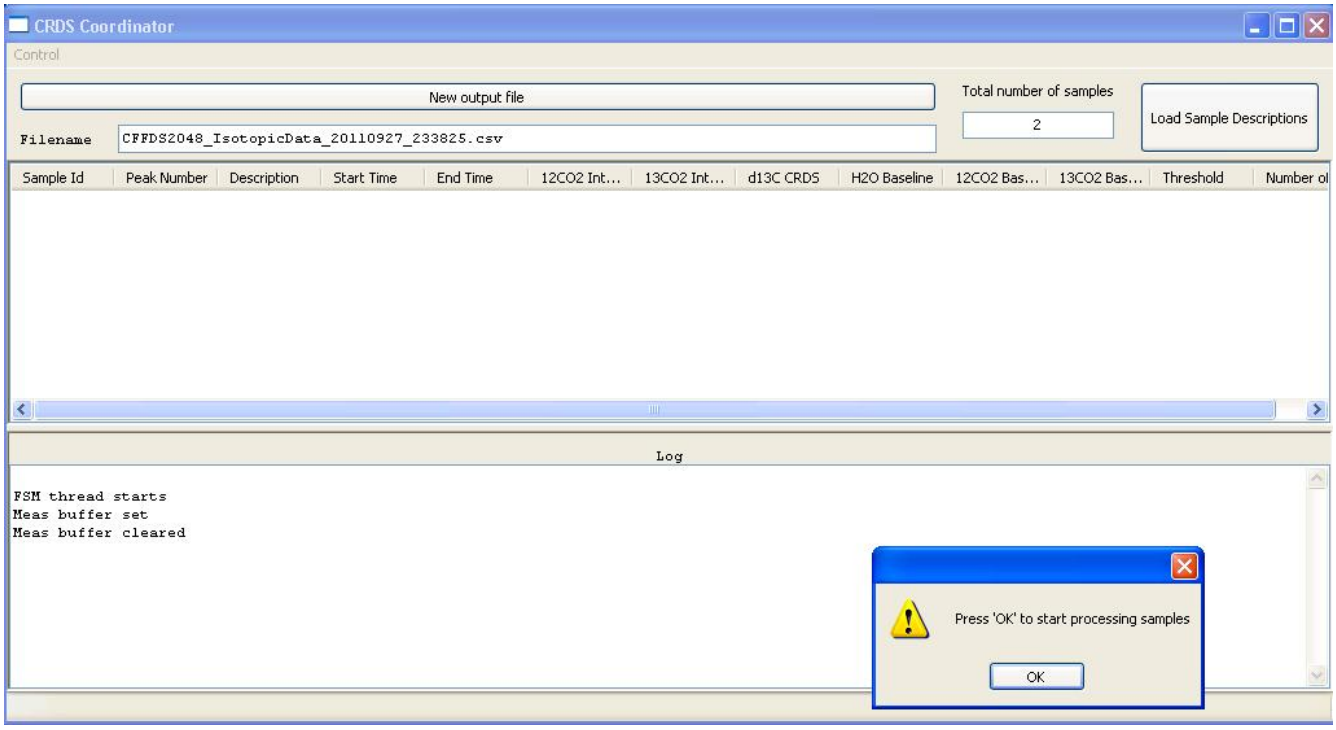
   Post-trigger time: is the timethe user sets for the peak integration to be extend after signal drops below threshold. We recommend using "0" initially and adjusting as necessary.

3. The **"Threshold ratio above baseline"** is a fixed value in ppm for triggering a peak. We recommend that you use 70ppm initial and adjust as necessary.

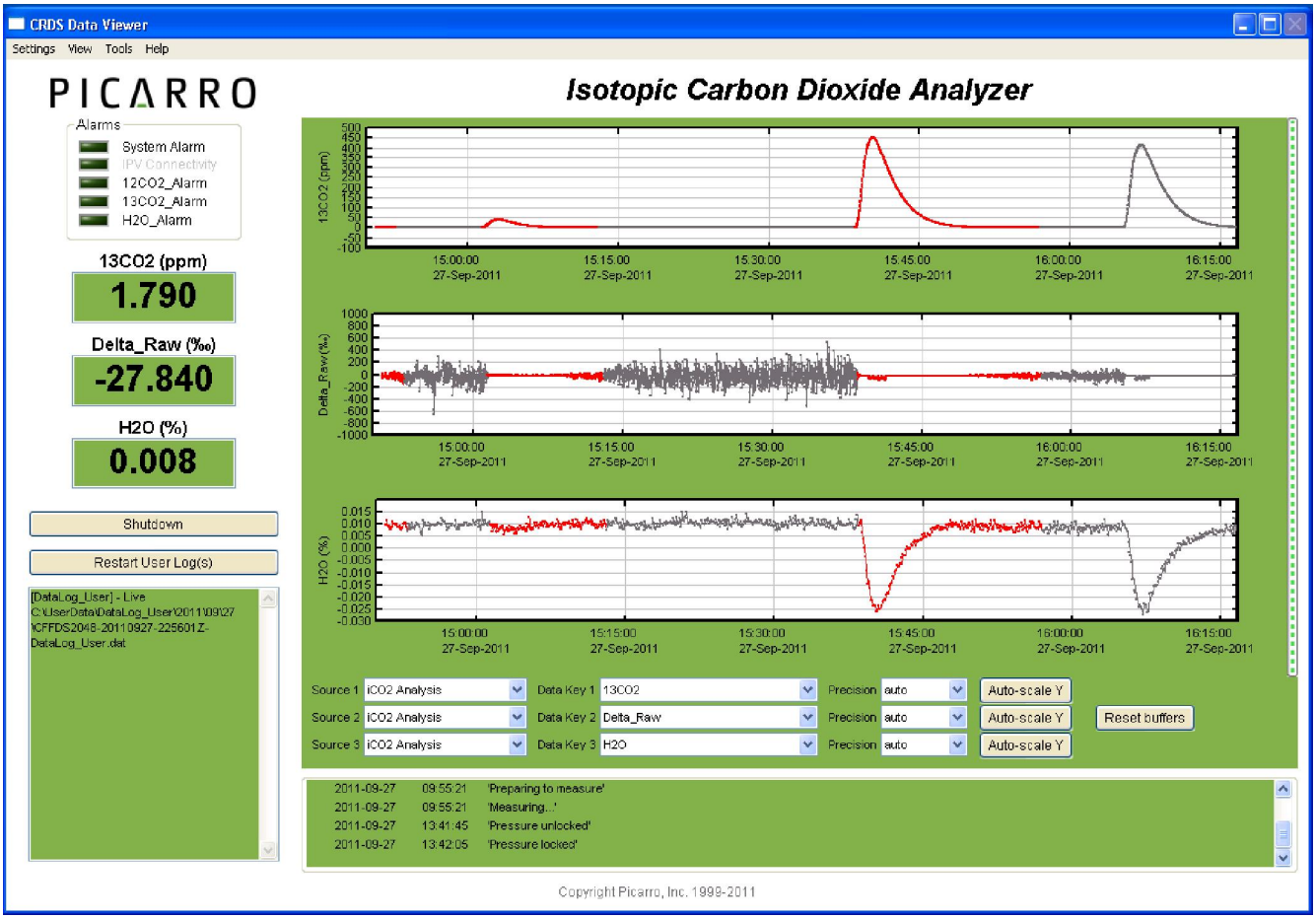
4. Lastly, the **"Wait time to clear all pulses"** is the time that your CRDS will wait before it will attempt to trigger the next sample analysis.

How to set a good wait time between pulses: Depends on the application, 8000.0 sec for now should work well. The wait time should be longer than any wait time between any two eluting peaks or longer than the time it takes for the first peak to elute from the LC column (whichever is longer).

5. After you've typed in your desired measurements, click "OK" to confirm.



Step 4: The following windows will pop up next. Before clicking "OK" to start processing your samples, please check to make sure that your samples are ready for combustion in the carousal on top of the CRDS.



Step 5: After clicking “OK”, the following "Isotopic Carbon Dioxide Analyzer” GUI will pop up on your desktop. The GUI above shows graphs after two sample analysis by a CRDS.

Description of the Figure

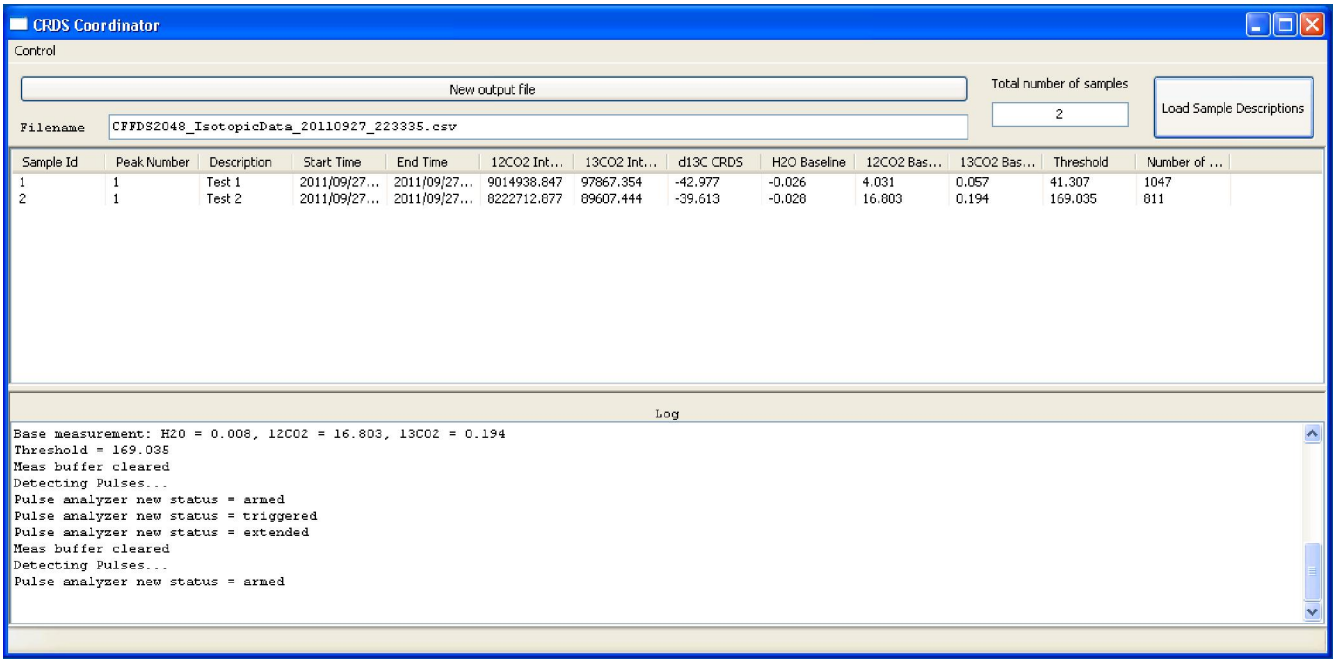
The **top graph** shows two large pulses, each pulse representing infrared absorption of one sample. You will notice that one of the pulses is highlighted in red. The **curve highlighted in red** represents the area that will be integrated to calculate the concentration of a specific gas type (e.g 12 CO_2) by the Peak Integration Software. The highlight in red includes the pre-triggered, the triggered, and the post triggered phases.

Before each pre-triggered phase, base measurements and combustion of sample occur. After each post triggered phase, there is a wait time to clear all pulses before another trigger.

On the top graph, you see a small bump highlighted in red in front of two large pulses. This is a failed case of trigger that never went through due to threshold never having been reached.

In the lowest graph (percentage of water present), you also see a plunge into the negative

zone in the Y-axis. This is an artifact from the combustion, and should be ignored.



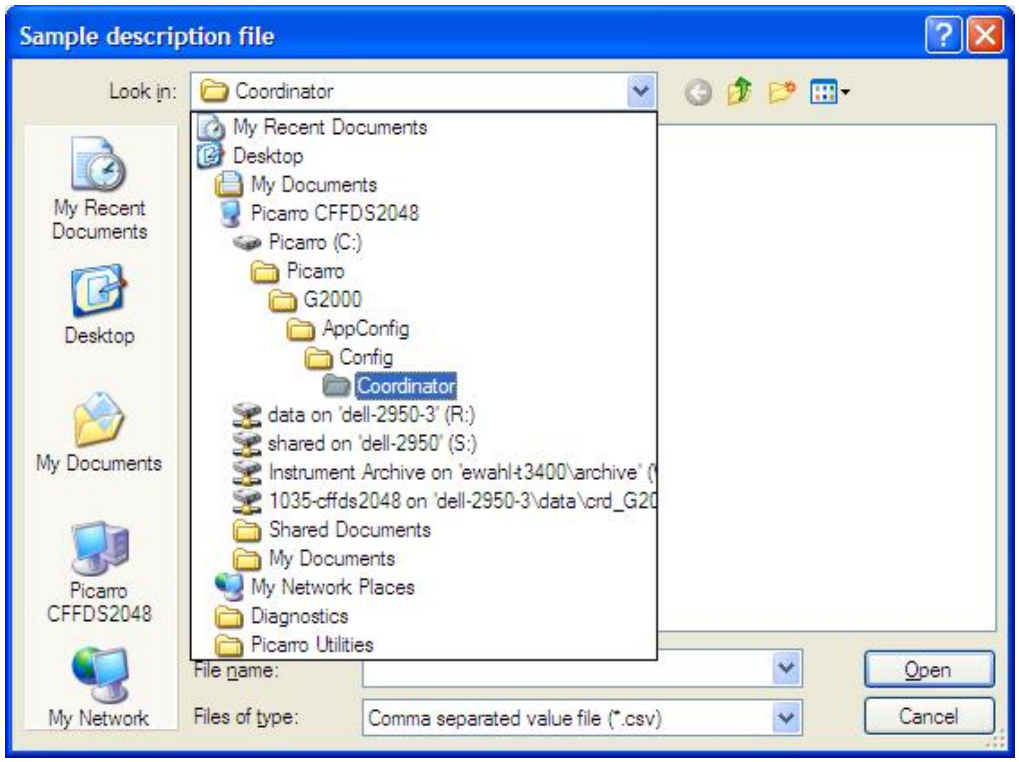
Step 6: The "CRDS Coordinator" window can be seen on analyzer's desktop at the same time as the "Isotopic Carbon Dioxide Analyzer" window. The "Peak Integration Software" will automatically upload your data into this "CRDS Coordinator" window. Click on the "Load Sample Descriptions" to add a description for each sample.

Description of the Figure

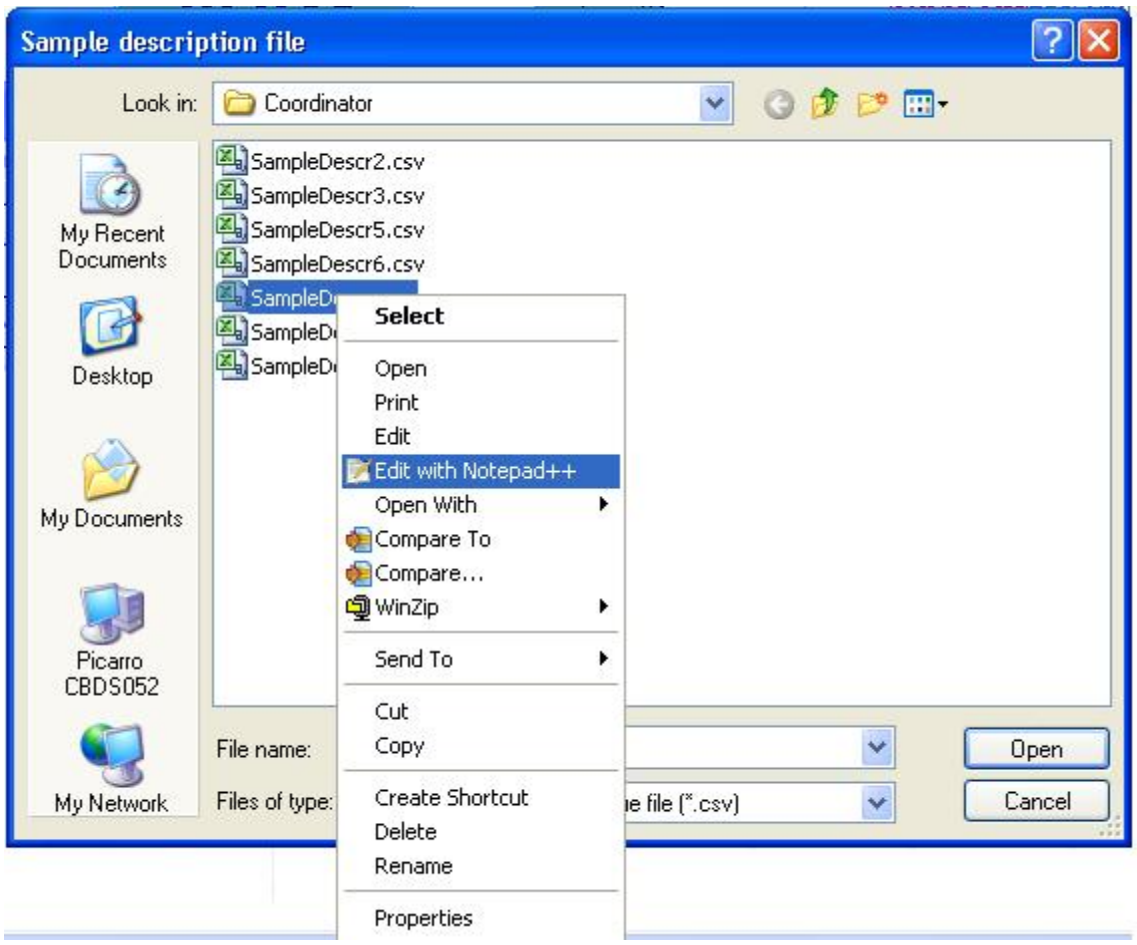
The CRDS Coordinator window shows detailed measurements made for each sample run. Below describes each column.

1. **Sample Id**: Identification number for each trial.
2. **Peak Number:** Number of pulses for each sample analysis - Typically one for each sample.
3. **Description**: Name given for each trial.
4. **StartTime**: Date and time at the start of a sample run.
5. **EndTime**: Date and time at the end of a sample run.
6. **$^{12}CO_2$ Integration**: Concentration of $^{12}CO_2$ in a sample.
7. **$^{13}CO_2$ Integration**: Concentration of $^{13}CO_2$ in a sample.
8. **$\delta^{13}C$ CRDS:** Ratio of stable isotopes ^{13}C and ^{12}C in parts permil in a sample.
    a. **$\delta^{13}C$ CRDS** = ((($^{13}C/^{12}C$)Sample/($^{13}C/^{12}C$)Standard) – 1) × 1000%
9. **H_2O Baseline**: Water that was present before a sample run.
10. **$^{12}CO_2$ Baseline**: $^{12}CO_2$ that was present before a sample run.
11. **$^{13}CO_2$ Baseline:** $^{13}CO_2$ that was present before a sample run.
12. **Threshold**: Point where a trigger happens.
13. **Number of Data Points**: Number of measurements taken during one sample run to

make up a curve.



Step 7: To enter the description of the samples being analyzed, you need to create a "SampleDescr.csv" file. To do so, please go to your "Picarro Hard Disk Drive(C:)" under "Computer". The figure above shows the chain of directories which you can follow to find your "SampleDescr.csv" file.



Step 8: Right-click on "SampleDescr.csv" file, and select "Edit with Notepad++".

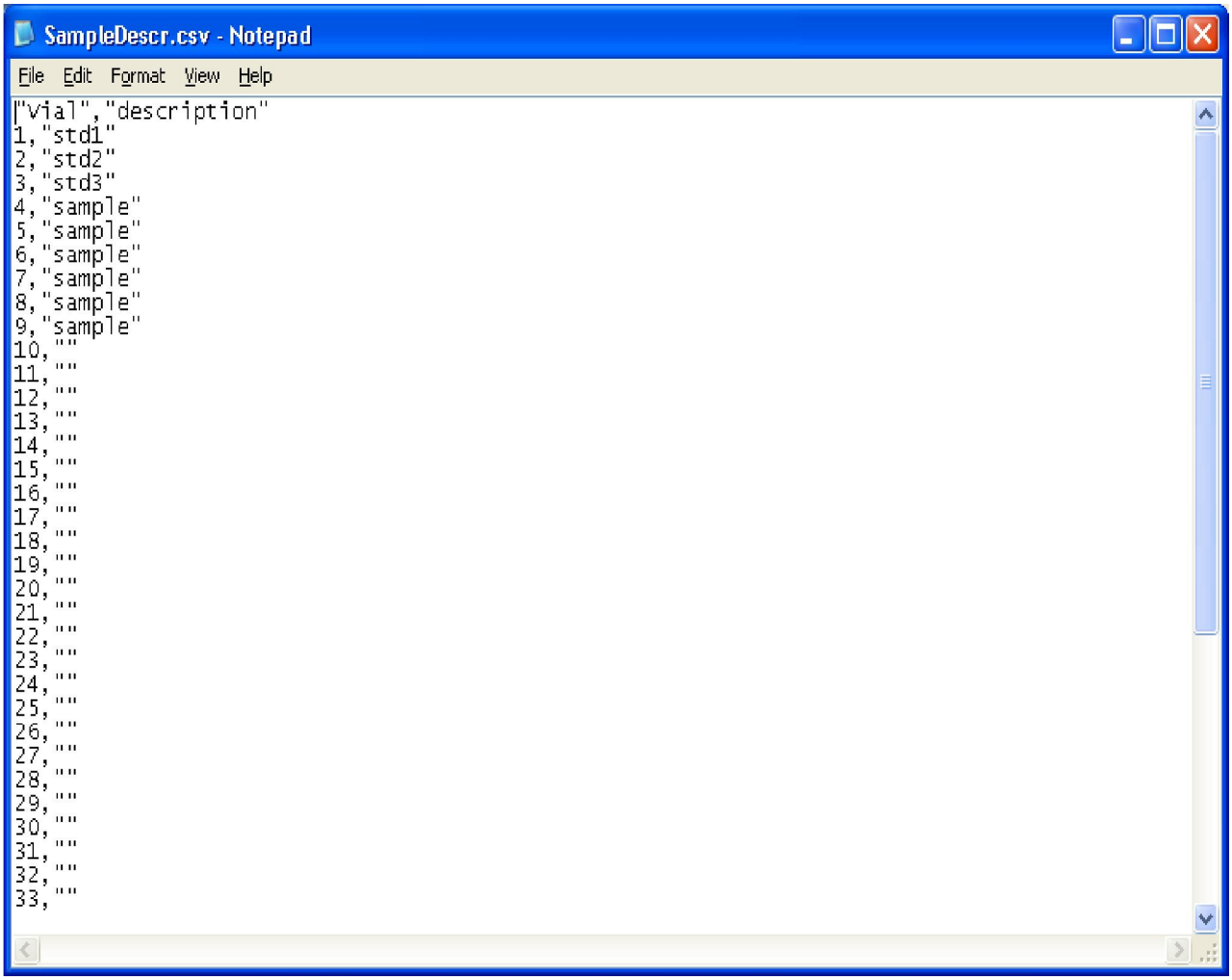
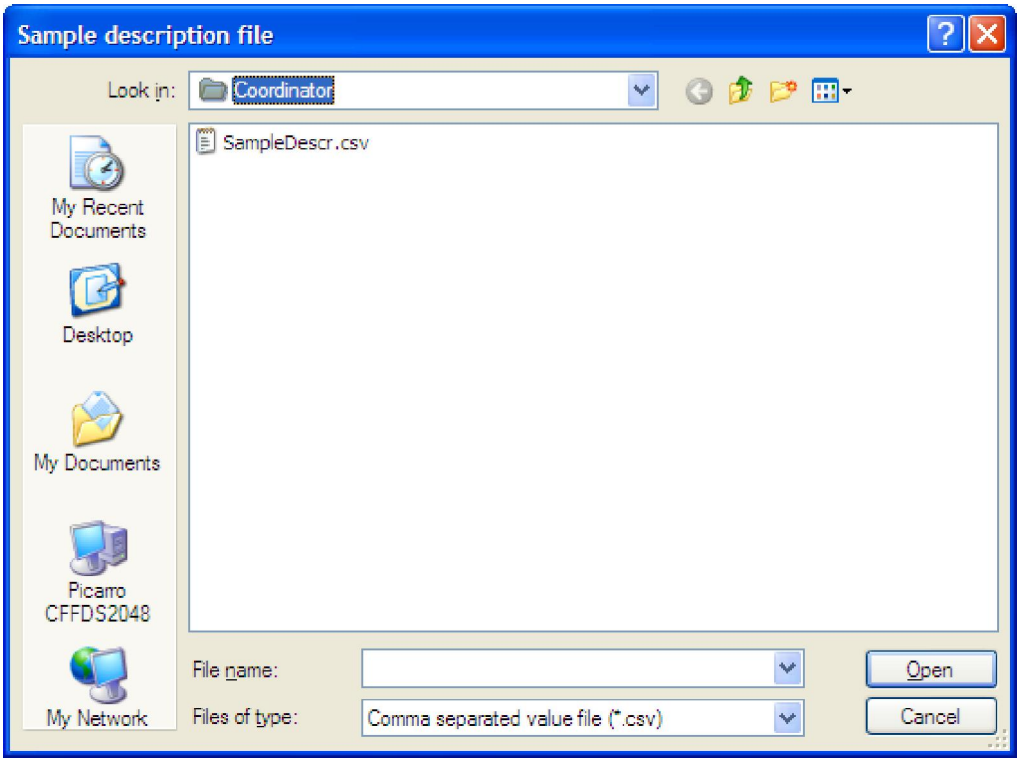


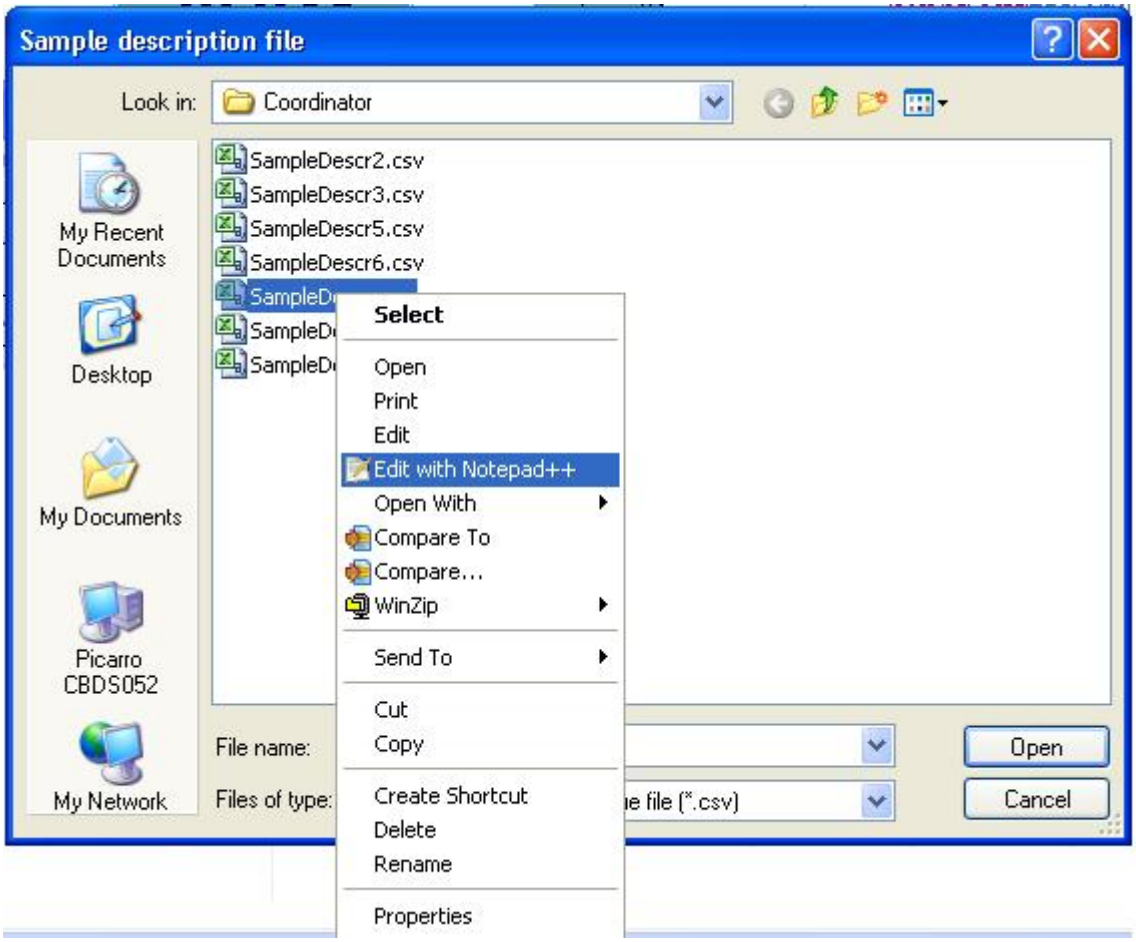
Figure 1: This is an example of a "SampleDescr.csv" file.

Step 9: The sample description needs to be entered between quotation marks, as shown above. "Vial" designates the sample number and it does not require quotation marks. Sample numbers corresponding to empty quotation marks ("") will be entered as a blank in the description column of the coordinator. Once you enter all the sample descriptions, please save the file under the current name or under any other name you choose.

Note: You only need to populate the description corresponding to the total number of samples run. Sample numbers corresponding to empty quotation marks ("") will be entered as a blank in the description column of the coordinator.



Step 10: To load the sample description file, click on the "Load Sample Descriptions" button at the upper right handside of the coordinator window. The window displayed above will pop up. **Double-click** on the "SampleDescr.csv" file and this will load the description corresponding to the sample being analyzed, after the individual sample analysis is finished and its data is reported into the coordinator.



Step 11: You can edit and re-load the sample description file at **any time during analysis** in case the sample descriptions need to be modified. You can edit the description for each sample sequence on this document as long as the sequence is still running and samples are being analyzed. Once the sequence ends, however, the sample description cannot be changed from the coordinator window. If the sample description need to be changed after the sample analysis is finished, the user can introduce those changes directly into the results file.

To edit and re-load the sample description file at **any time during analysis** press the "load sample descriptions" button again, then right-click on the SampleDescr.csv file and select "Edit with Notepad++".

Once the sample description file is open, introduce the edits you desire, save the file and close it, and then double click on its icon in the "Sample description file" open window.

The output results file is generated in .CSV format and is saved in the directory *C:\Picarro\IsotopicData*