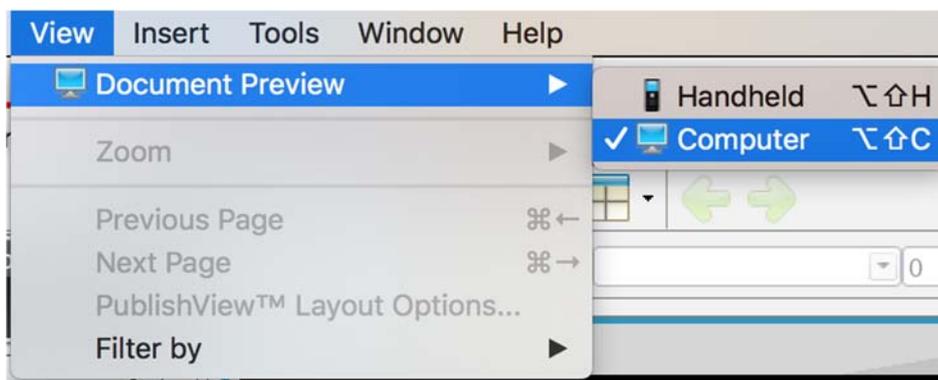


APPENDIX 4

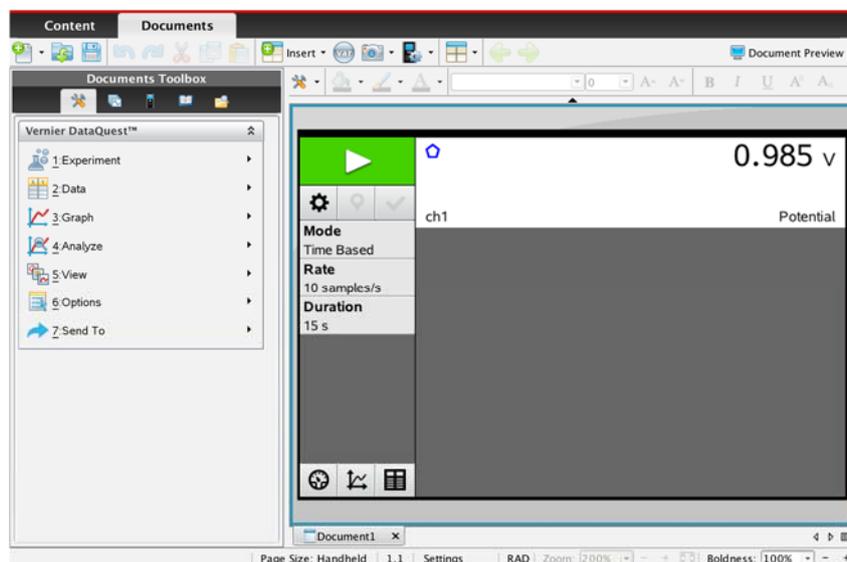
Ti-Nspire

4.1. Collecting data with the data logging Lab Cradle interface connected to a calculator with the TI-Nspire CX Software.

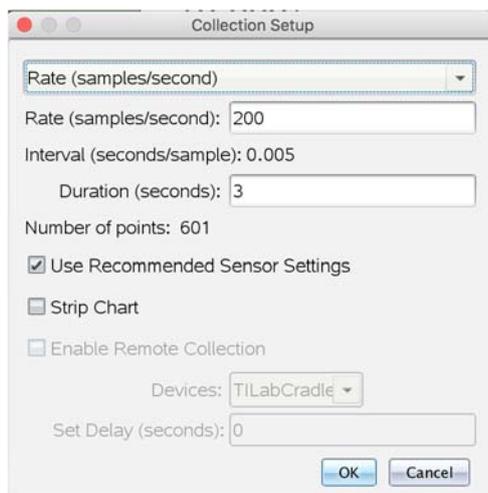
1. In the computer launch the application TI-Nspire CX. Choose the option “Trial Version”
2. In order to view the document in the computer mode make the following selection:



3. Connect the sensor/ sensors to the Lab Cradle
4. Connect the Lab Cradle to the computer using a mini USB to USB cable.
5. The program automatically detects the sensor/ sensors, showing you the following interface:

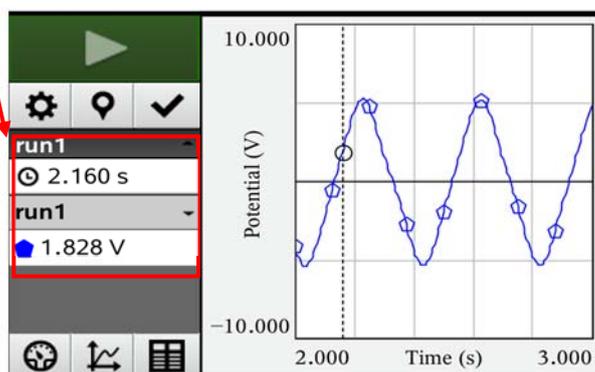


6. To adjust the sampling rate and define the acquisition duration by clicking on  and making your choices:



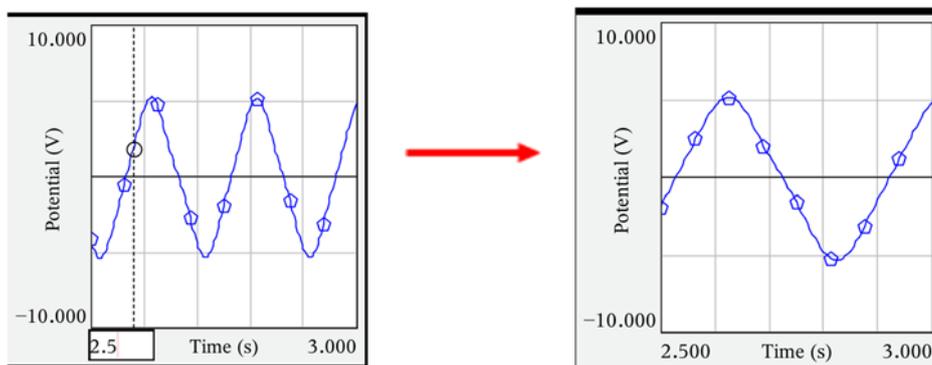
Note that if the sampling rate is too low your plots will not have sufficient points.

7. To start the collection click on 
8. The collected data can be visualized in a meter by selecting , in a graph by selecting  or in a table .
9. Save your document choosing the “Save” or “Save as” option in the menu “File” or by clicking on  .
10. You can read data points in a plot by clicking on the graph to position the cursor at the desired point:



You can use the arrow keys to move the cursor.

11. To change the axes limits, write a new value over the current one:



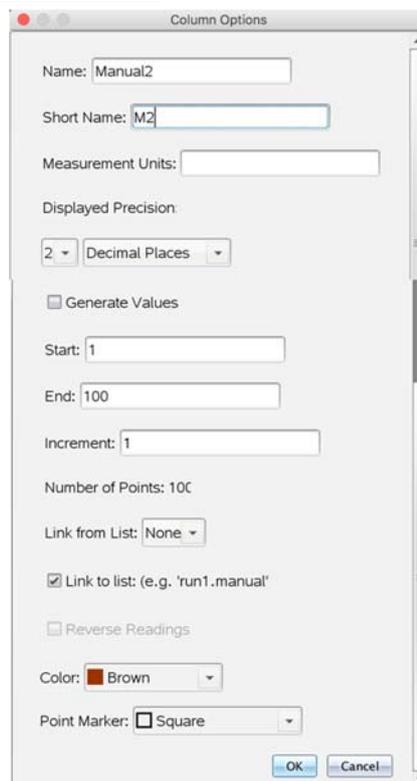
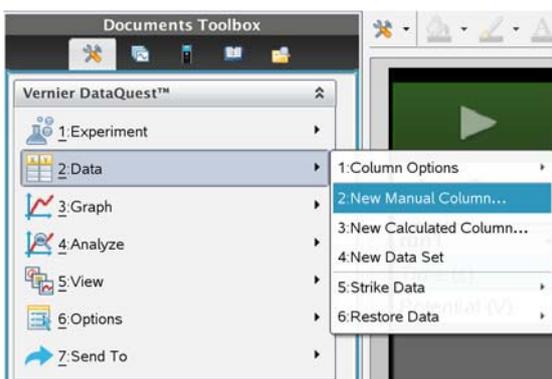
12. You can work out your data by: **appending columns to your table, making calculations with data from existing columns and creating a new column with the results, plotting data from existing columns, making curve fits to your plots, etc.** You can find some examples below.

A set of collected data table looks like this:

run1		
	Time	Potential
1	0	1.592
2	0.002	1.615
3	0.004	1.637
4	0.006	1.648
5	0.008	1.660
6	0.010	1.665
7	0.012	1.676
8	0.014	1.682
9	0.016	1.682
10	0.018	1.688
11	0.020	1.693
12	0.022	1.693
13	0.024	1.699

13. Append columns to the table to:

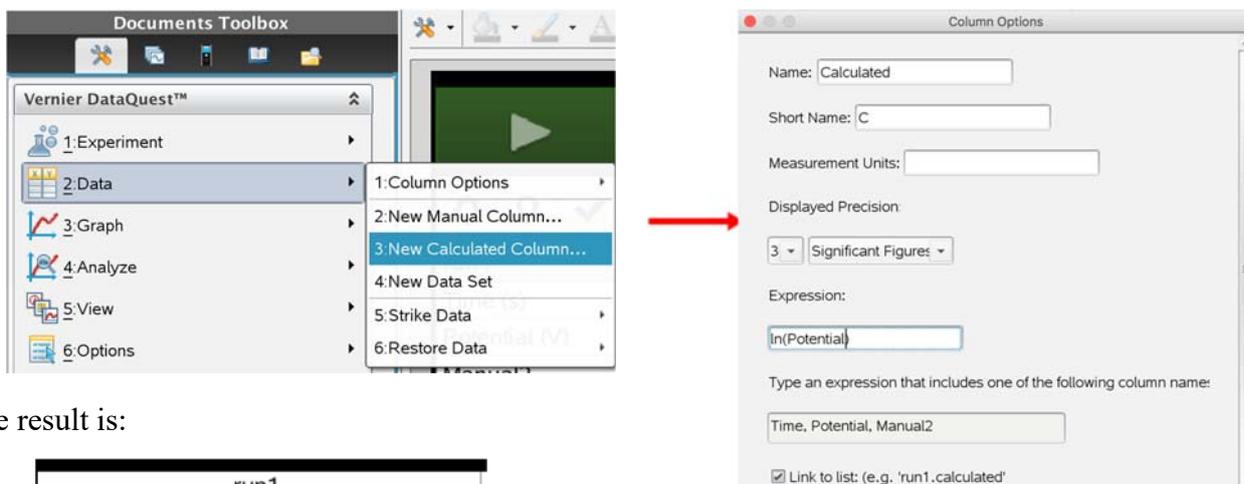
- fill manually



Then you can fill manually the new column:

run1			
	Time	Potential	Manual2
1	0	1.592	1.00
2	0.002	1.615	2.00
3	0.004	1.637	3.00
4	0.006	1.648	
5	0.008	1.660	
6	0.010	1.665	

14. Calculate data from existing columns (in the example the \ln function is applied to the numbers in the column named “Potential” and the results are listed in a new column named “Calculated”)

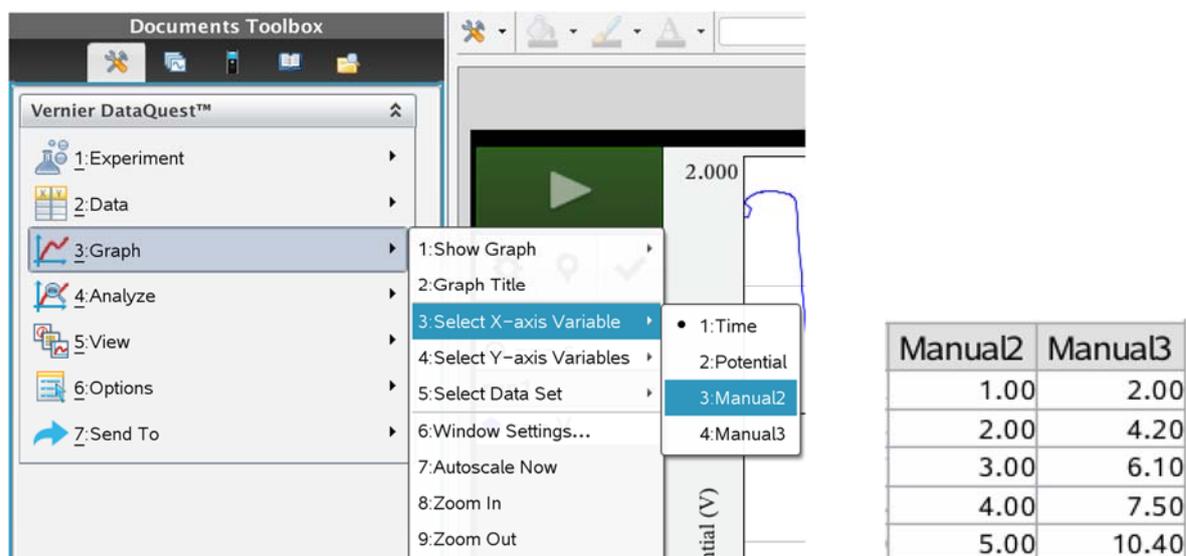


The result is:

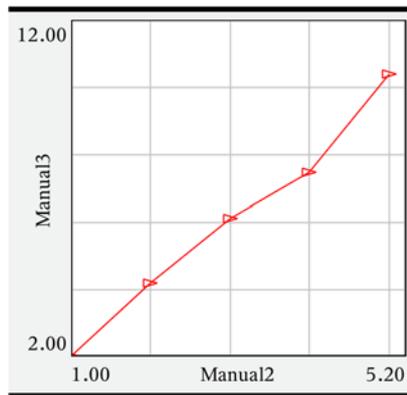
run1				
	Time	Potential	Manual2	C
1	0	1.592	1.00	0.465
2	0.002	1.615	2.00	0.479
3	0.004	1.637	3.00	0.493
4	0.006	1.648	4.00	0.500
5	0.008	1.660		0.507
6	0.010	1.665		0.510
7	0.012	1.676		0.517
8	0.014	1.682		0.520
9	0.016	1.682		0.520

15. Plotting data in columns

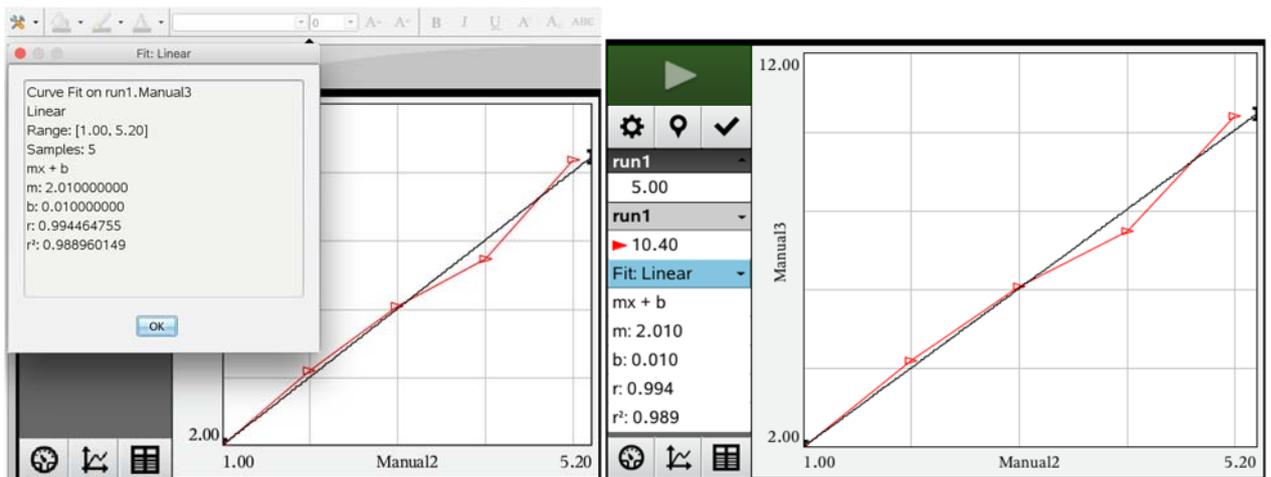
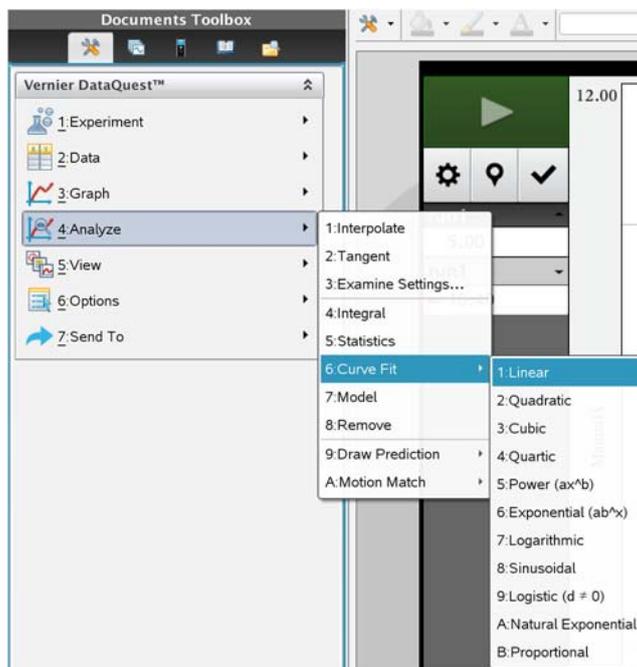
Select  and then select the variables x and y you want to plot:



Manual3 as a function of Manual2 will give:



16. Making curve fits to plots



APPENDIX 5

GLOSSARY

PCR (Polymerase Chain Reaction)*- PCR is an *in vitro* amplification assay of DNA that produces exponentially large amounts of a specific sequence of DNA (template).

PCR amplification requires the presence of at least one DNA template strand, which can be any form of double-stranded DNA (in this case: DNA extracted from mussels).

Specificity comes from the ability to target and amplify a specific segment of DNA out of a complete genome, which is done with adequate primers* (Figure 1).

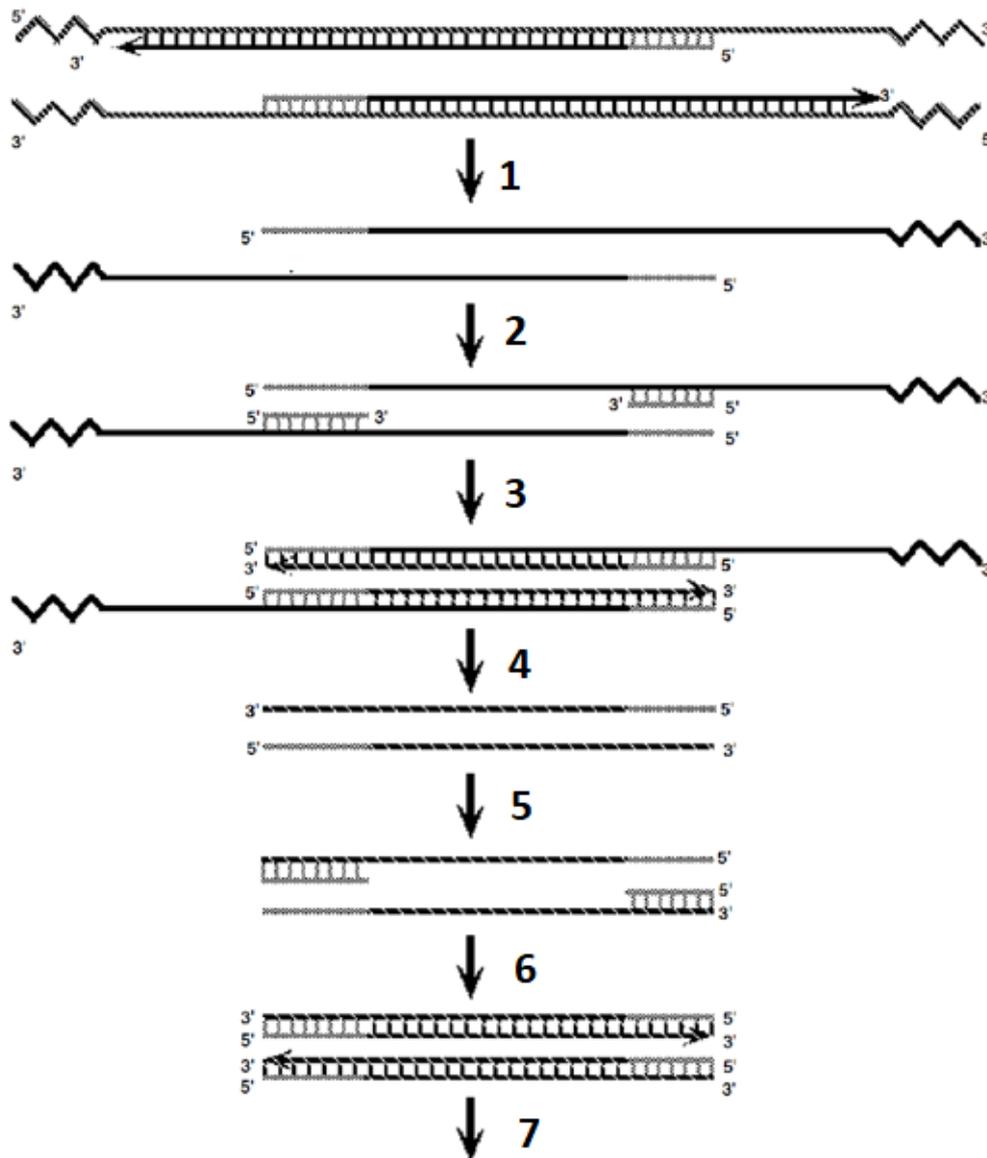


Figure 1 – An example of the amplification of a DNA template by PCR: 1) Denaturation of double strand DNA at high temperatures); 2) Annealing of the primers (hybridization with the complementary sequence); 3) Extension of new complementary DNA strands; 4) Denaturation of double strand DNA at high temperatures); 5) Annealing of the primers; 6) Extension of new complementary DNA strands; 7) Repetition of this reactions for several cycles.

Primers*- are short chains of DNA that are complementary to the DNA template we wish to copy using PCR. Forward primers bind to the downstream (at the 3' end) and reverse primers bind upstream (at the 5' end) of the target region of interest (Figure 2). For a PCR reaction to occur you need to use a suitable pair of forward and reverse primers to generate a specific fragment of DNA (Figure 2).

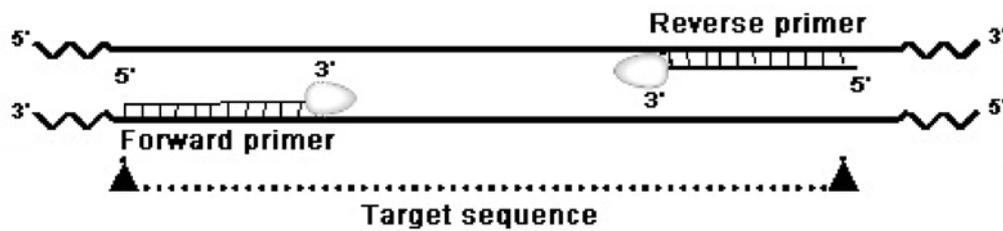


Figure 2 – Forward and reverse primers annealed to a target DNA sequence during PCR.

DNA molecular weight ladder*- Mixture of linear DNA fragments of known molecular weight used to estimate the size in base pairs (bp) of other DNA fragments. Schematic diagram of the expected band sizes of the DNA ladder used in this Task is indicated in Figure 3.

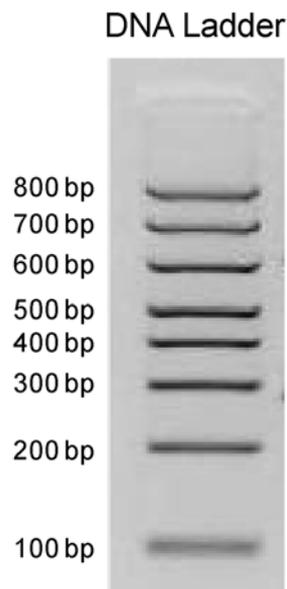


Figure 3 – DNA molecular weight ladder used. DNA bands and their corresponding molecular weight (number of base pairs) are indicated in the figure.

Orange G DNA Loading buffer*- Solution used to prepare DNA samples for loading on agarose gels. It contains a dye (orange) for visual tracking of DNA migration during electrophoresis and glycerol to increase the density of the sample.

APPENDIX 6

Ti-Nspire

3.1. Collecting data with the data logging Lab Cradle interface connected to a calculator with the TI-Nspire CX Software.

1. Connect the calculator to the interface



1 – Calculator

2 – Interface

2. Turn on the calculator.



1 – Switch On/Off

3.2. Instructions for Vernier Colorimeter

The Vernier Colorimeter is designed to determine the concentration of a solution by analysing its colour intensity. The Colorimeter measures the amount of light transmitted through a sample at a user-selectable wavelength.

There are two models: **1** - 2000-2014 model and the **2** - 2014-current model.



Using the Colorimeter

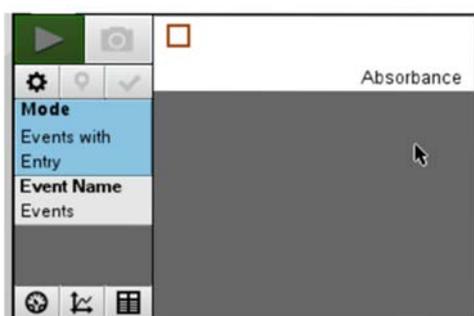
The Colorimeter is easy to use and maintain. Simply connect it to your data collection interface (TI graphing calculator), configure your software (Vernier LabPro®), and you are ready to make measurements. For best results, let the system stabilize at the desired wavelength for 5 minutes prior to calibration or data collection.

General procedure to follow when using the Colorimeter

1. Connect the Colorimeter to the interface in ch1 or ch2 or ch3.
2. Turn on the TI Nspire
3. Use the cursor with the Touchpad and press the icon 



4. The software will identify the colorimeter and load a default data collection setup.



5. Press the < or > button on the Colorimeter to select the correct wavelength setting for your experiment (430 nm, 470 nm, 565 nm, or 635 nm).
6. Calibrate the Colorimeter. **Note:** The Colorimeter needs to be powered about 5 minutes before calibrating. One of the four green wavelength indicator lights will be turned on when it is powered.

- a. Open the Colorimeter lid.
- b. Insert a cuvette with the blank specified in your task. **Important:** Line up one of the *clear* sides of the cuvette with the arrow at the *top* of the cuvette slot. Close the Colorimeter lid.
- c. Next, press the CAL button to begin the calibration process. Release the CAL button when the red LED begins to flash. The absorbance should now be 0.00 or 0.01.
- d. When the LED stops flashing, the calibration is complete and your unit is ready to collect your experimental data.



7. Collecting data.
 - a. Place the cuvette with your sample into the Colorimeter cuvette slot. **Important:** Line up the side of the cuvette with an arrow with the arrow at the *top* of the cuvette slot.
 - b. Read the absorbance value



8. If the Colorimeter does not turn on - no green light - ask your lab assistant for a different cradle.

Lambert-Beer calibration law for Zinc(II) determination for Vernier Colorimeter

Col #	$k (A = k.C)$	Co #	$k (A = k.C)$	Col #	$k (A = k.C)$
1	0.28	13	0.30	27	0.24
2	0.23	14	0.27	28	0.25
3	0.23	15	0.27	29	0.30
4	0.22	16	0.28	30	0.21
5	0.18	17	0.29	31	0.24
6	0.22	19	0.29	32	0.22
7	0.29	20	0.28	33	0.29
8	0.25	21	0.26	34	0.23
9	0.26	22	0.28	35	0.28
10	0.27	23	0.29		
11	0.26	24	0.29		
12	0.25	26	0.26		