
	SKILLS CENTER MODULE METHODS TASK ANSWER SHEET	A BIOFIZZ  PRODUCTON
Name: Iona Kelly	Module: Pipette Calibration	Student ID: XXXXXXXXXX
Date: 5/14/25		Class: MCDB 1234/3456

NOTES:

- You must use this form to submit your MMT as a word doc.
- Paste images, screen shots etc, from your MMT into this document
- Include Module title from the website
- In the space below, please copy/paste EACH MMT question and complete each prompt in full sentences with clean and clearly labelled data.
- Do not attach any data or responses that are not directly relevant to answering each individual MMT
- Please make sure to follow the [rubric](#) guidelines. **Universal module prompts** (those that are general to all modules) are indicated in bold font.
- Conclusions are required for EACH MMT. Please summarize the data used to draw conclusions. Discuss how the findings can be applied or relate to real-life scenarios. Clearly address the hypothesis, including discussing any sources of errors that might have influenced the results.

MMT QUESTIONS/ANSWERS

Planning/Organization)

This lab exercise involved using a pipette to measure volumes of water at increasing increments and utilizing this data to determine the accuracy of the pipette. This works because 1g of water is approximately 1ml (when you account for temperature using the Z factor) and so you are able to use the measured mass to derive the measured volume and then compare that to your expected volume. The importance of measuring different amounts is that it allows you to check the accuracy through the full range of the pipette. It is expected that the pipette will be slightly inaccurate, but if the amount of inaccuracy varies a lot between trials that might indicate user error.

Materials and Methods)

1. Calculate the increments necessary to increase the volume ten times and span from the maximum volume to 10% of the maximum volume for a P20, P200, and P1000 pipette

A handwritten table on graph paper showing the volume increments for three different pipettes: P20, P200, and P1000. The table is organized into three columns, one for each pipette. The rows are numbered 1 through 10, representing the volume in microliters (µL) for each pipette. The P20 column shows increments from 2 µL to 20 µL. The P200 column shows increments from 20 µL to 200 µL. The P1000 column shows increments from 100 µL to 1000 µL.

	<u>P20</u>	<u>P200</u>	<u>P1000</u>
1	2 µL	20 µL	100 µL
2	4 µL	40 µL	200 µL
3	6 µL	60 µL	300 µL
4	8 µL	80 µL	400 µL
5	10 µL	100 µL	500 µL
6	12 µL	120 µL	600 µL
7	14 µL	140 µL	700 µL
8	16 µL	160 µL	800 µL
9	18 µL	180 µL	900 µL
10	20 µL	200 µL	1000 µL

2. Make three tables, one for each size of pipette that includes each of the ten volume increments and a space to record measured mass for each
3. Set up a weigh boat on a scale measuring grams and tare it
4. Retrieve a beaker of water and measure its temperature with a thermometer
5. Choose a pipette, attach a disposable tip securely, and calibrate it to its maximum volume
6. Aspirate and dispense the full volume three times to adjust the temperature of the pipette and tip to match the water
7. Then calibrate the pipette to each of the calculated volumes on your table, aspirate the water, dispense it into the weigh boat, record the mass, and tare the scale again
8. Repeat steps 5 through 7 for each of the three differently sized pipettes
9. Calculate the volume of each trial from the recorded mass based on $1 \text{ g H}_2\text{O} = 1 \text{ mL H}_2\text{O}$

10. Identify the Z factor based on the recorded temperature and multiply each mass measurement by it to account for temperature variations

7	137.3 mg	Z factor / accounts for temp → $Z = 1.0033$ at 22°C	P20 Dispensed Volume 1) $1.4 \mu\text{L} \cdot Z = 1.4 \mu\text{L}$ 2) $3.2 \mu\text{L} \cdot Z = 3.2 \mu\text{L}$ 3) $5.2 \mu\text{L} \cdot Z = 5.2 \mu\text{L}$ 4) $7.4 \mu\text{L} \cdot Z = 7.4 \mu\text{L}$ 5) $8.9 \mu\text{L} \cdot Z = 8.9 \mu\text{L}$ 6) $11.2 \mu\text{L} \cdot Z = 11.2 \mu\text{L}$ 7) $13.2 \mu\text{L} \cdot Z = 13.2 \mu\text{L}$ 8) $15.3 \mu\text{L} \cdot Z = 15.4 \mu\text{L}$ 9) $17.2 \mu\text{L} \cdot Z = 17.3 \mu\text{L}$ 10) $18.9 \mu\text{L} \cdot Z = 19.0 \mu\text{L}$
6	118.1 mg		
5	97.4 mg		
4	78.4 mg		
3	58.5 mg		
2	38.8 mg		
1	19.6 mg		

P1000 Dispensed Volume		P200 Dispensed Volume	
1) 110.2 μL	2) 38.9 μL	1) 19.7 μL	2) 38.9 μL
3) 311.6 μL	3) 58.7 μL	3) 58.7 μL	3) 58.7 μL
4) 410.1 μL	4) 78.7 μL	4) 78.7 μL	4) 78.7 μL
5) 501.1 μL	5) 97.7 μL	5) 97.7 μL	5) 97.7 μL
6) 600.0 μL	6) 118.5 μL	6) 118.5 μL	6) 118.5 μL
7) 700.0 μL	7) 137.8 μL	7) 137.8 μL	7) 137.8 μL
8) 797.1 μL	8) 157.9 μL	8) 157.9 μL	8) 157.9 μL
9) 901.8 μL	9) 178.6 μL	9) 178.6 μL	9) 178.6 μL
10) 998.8 μL	10) 197.3 μL	10) 197.3 μL	10) 197.3 μL

← same process

Remember to record temp

See SOP for troubleshooting tips

← same process

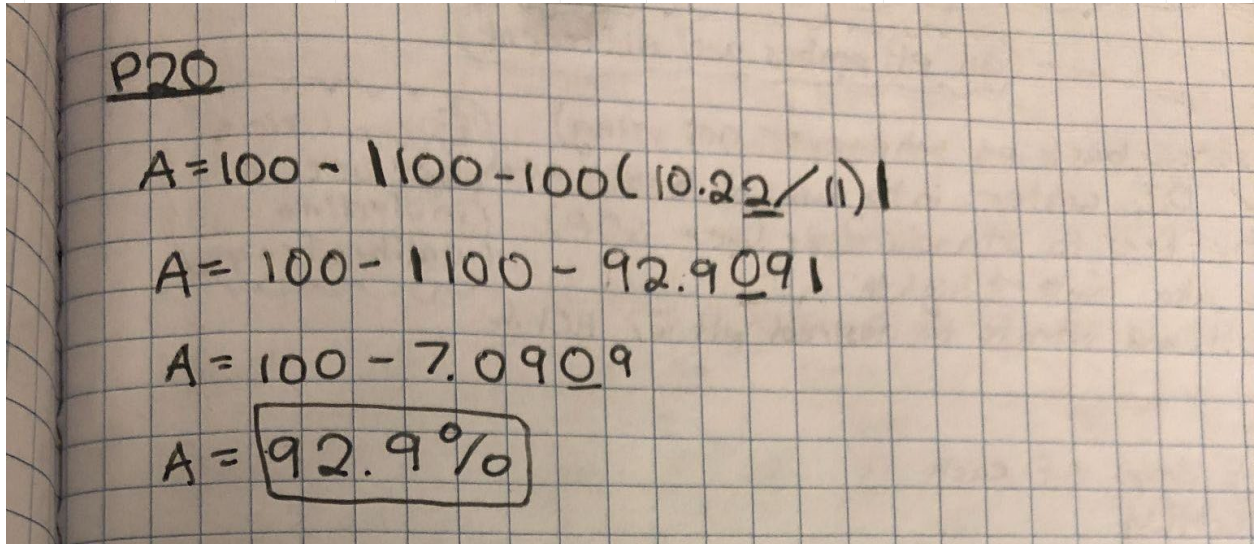
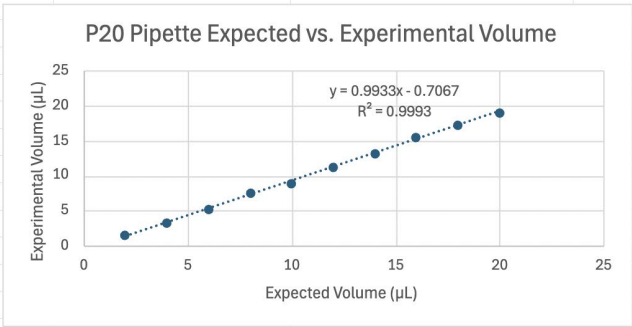
11. Create a data table in excel spreadsheets for each pipette
12. Input the expected volume and experimental volume for each trial (after accounting for the Z factor) into the tables
13. Insert a scatter plot using the data tables and label the x-axis with expected volume and the y-axis with experimental volume
14. Calculate the average of experimental volume and expected volume for each set of 10 trials
15. Use $A = 100 - \text{abs}[100 - 100 \cdot (V_{\text{ave}} / V_{\text{ave}})]$ to calculate A values

Data Analysis & Discussion)

[Excel Spreadsheet with Data](#)

P20 Pipette

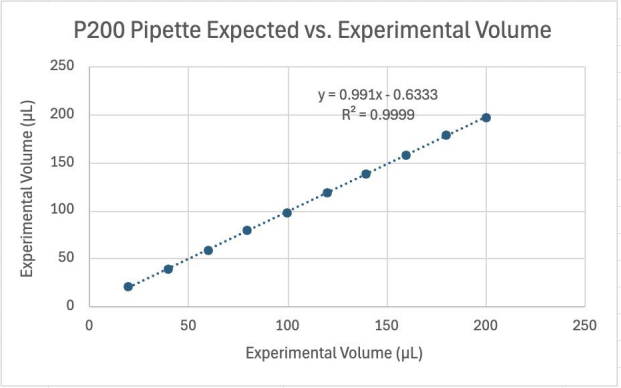
Trial	Expected Volume (μL)	Experimental Volume (μL)	Expected Value Average (μL)	Experimental Volume Average (μL)
1	2	1.4	11	10.22
2	4	3.2		
3	6	5.2		
4	8	7.4		
5	10	8.9		
6	12	11.2		
7	14	13.2		
8	16	15.4		
9	18	17.3		
10	20	19		

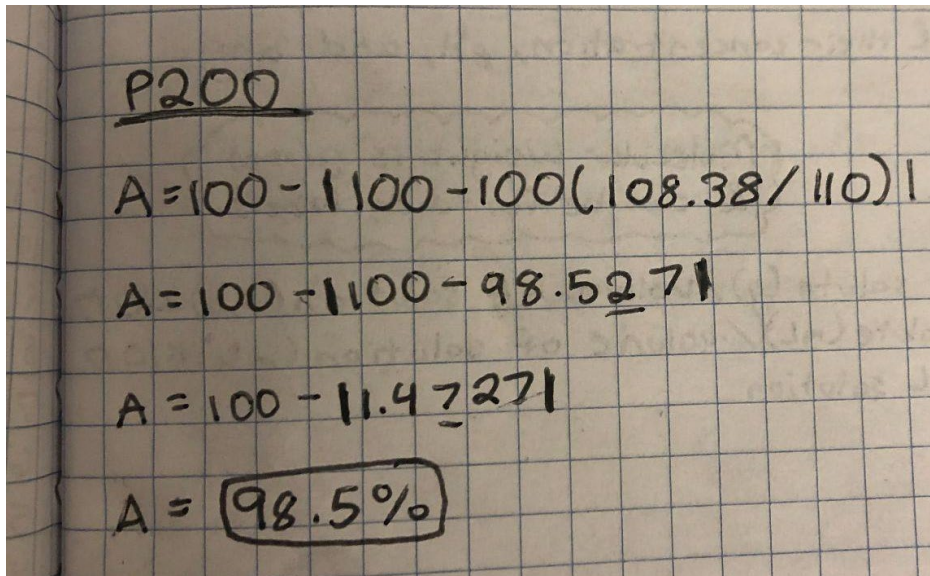


I found that the P20 pipette is 92.9% accurate and has an R² value of 0.9993. The measured volumes were lower than the expected volumes for the entire range.

P200 Pipette

Trial	Expected Volume (μL)	Experimental Volume (μL)	Expected Value Average (μL)	Experimental Volume Average (μL)
1	20	19.7	110	108.38
2	40	38.9		
3	60	58.7		
4	80	78.7		
5	100	97.7		
6	120	118.5		
7	140	137.8		
8	160	157.9		
9	180	178.6		
10	200	197.3		

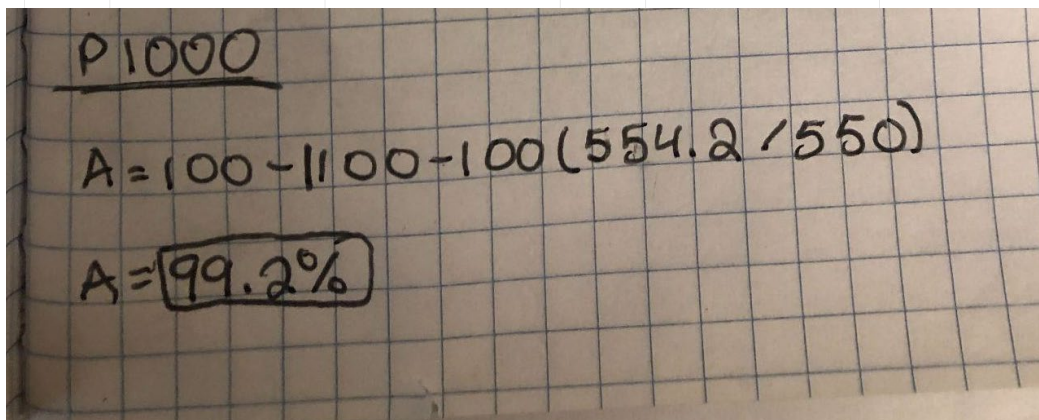
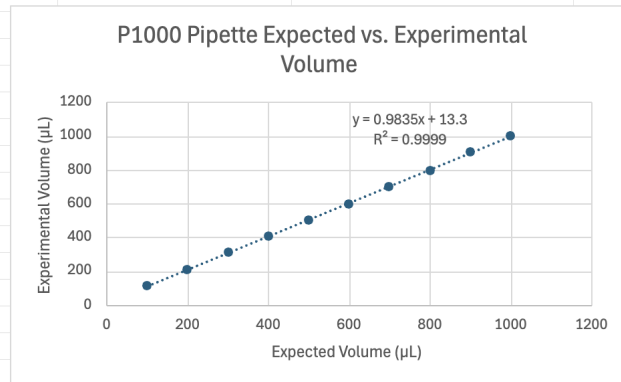




I found that the P200 pipette is 98.5% accurate and has an R² value of 0.9999. The measured volumes were lower than the expected volumes for the entire range.

P1000 Pipette

Trial	Expected Volume (μL)	Experimental Volume (μL)	Expected Value Average (μL)	Experimental Volume Average (μL)
1	100	110.2	550	554.2
2	200	211.3		
3	300	311.6		
4	400	410.1		
5	500	501.1		
6	600	600		
7	700	700		
8	800	797.1		
9	900	901.8		
10	1000	998.8		



I found that the P1000 pipette is 99.2% accurate and has an R² value of 0.9993. The measured volumes were lower than the expected volumes for the volumes >800µL, precise for 700-600µL, and higher than the expected volumes for <600µL.

Conclusion)

Through my measurements and analysis I found that the P20 Pipette was significantly inaccurate with an accuracy of 92.9%, the P200 pipette was moderately inaccurate with an accuracy of 98.5%, and the P1000 pipette was relatively accurate with an accuracy of 99.2%. I also found that my R² value was much lower for the P20 pipette than the others which indicates that it is less precise and correlate with human error in using it. This would also make sense since it was the first pipette I collected data for and this is my first time using a pipette. Pipetting is a valuable skill and is used in various experiments and procedures throughout biochemistry and microbiology which is why it is so valuable to learn.

Sources Cited)

Stowell, M., de Vito, M., & Hazlett, Z. (2023). Pipette Calibration. *Skills Center Standard Operating Procedure*. Pages 1-6.

https://skillscenter.colorado.edu/assets/files/IntroLabMeeting_2025_01_22.pdf

Please include the exact wording for each MMT prompt within the module, and answer each in order below:

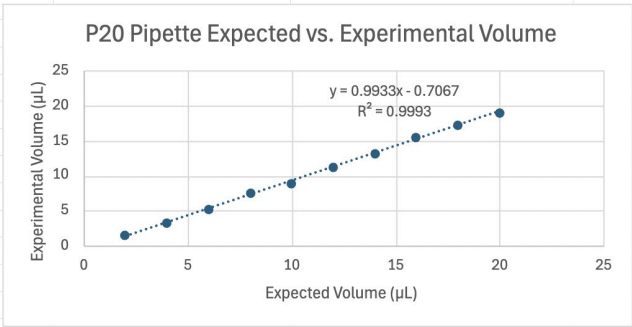
This task will test your ability to make several standard solutions using a laboratory pipette.

- 1) Pick a P1000, P200 and P20 to calibrate
- 2) Calibrate the pipettes according to the calibration procedures
- 3) Create a curve on excel for each one of the pipettes, using each of the 10 trials as your data points

Note: Expected Value Average = V_{avg} and Experimental Volume Average = V_{avg}

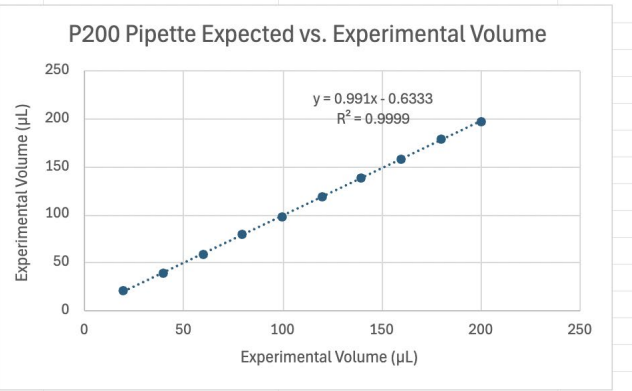
P20

Trial	Expected Volume (μL)	Experimental Volume (μL)	Expected Value Average (μL)	Experimental Volume Average (μL)
1	2	1.4	11	10.22
2	4	3.2		
3	6	5.2		
4	8	7.4		
5	10	8.9		
6	12	11.2		
7	14	13.2		
8	16	15.4		
9	18	17.3		
10	20	19		



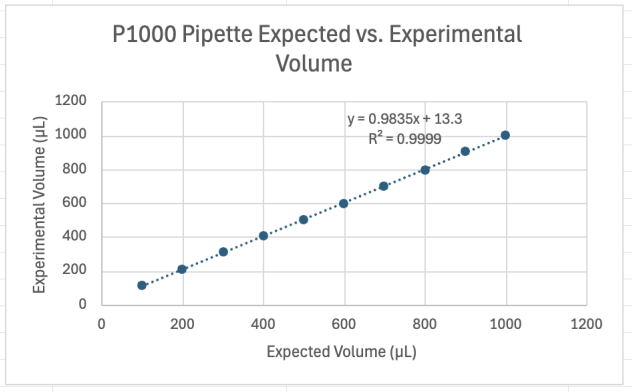
P200

Trial	Expected Volume (μL)	Experimental Volume (μL)	Expected Value Average (μL)	Experimental Volume Average (μL)
1	20	19.7	110	108.38
2	40	38.9		
3	60	58.7		
4	80	78.7		
5	100	97.7		
6	120	118.5		
7	140	137.8		
8	160	157.9		
9	180	178.6		
10	200	197.3		



P1000

Trial	Expected Volume (μL)	Experimental Volume (μL)	Expected Value Average (μL)	Experimental Volume Average (μL)
1	100	110.2	550	554.2
2	200	211.3		
3	300	311.6		
4	400	410.1		
5	500	501.1		
6	600	600		
7	700	700		
8	800	797.1		
9	900	901.8		
10	1000	998.8		



4) Finally, calculate the accuracy for each of the 3 pipettes

P20

$$A = 100 - \frac{1100 - 100(10.22/11)}{1}$$

$$A = 100 - 1100 - 92.9091$$

$$A = 100 - 7.0909$$

$$A = \boxed{92.9\%}$$

P200

$$A = 100 - \frac{1100 - 100(108.38/110)}{1}$$

$$A = 100 - 1100 - 98.5271$$

$$A = 100 - 11.47271$$

$$A = \boxed{98.5\%}$$

P1000

$$A = 100 - \frac{1100 - 100(554.2/550)}{1}$$

$$A = \boxed{99.2\%}$$

5) Described how the A values and R2 values can be used to evaluate the accuracy of the pipette versus the precision of the pipette and pipette operator

- The A value stands for accuracy and it is the percent accuracy of the pipette. This tells you how close your measured values are to what you are expecting.
- The R² value tells you the precision of your trials which represents the variability between trials. The closer it is to 1 the more precise your recorded measurements are.

6) Make sure to provide conclusions and interpretations of the various calculations

7) Send your graphs, calculations, and conclusions to one of the proctors to check your results