Name: _____
Date: _____Mod: ____

Genetic Variation Graphing

Part I.

Obtain a measurement of the index (pointer) finger of each person in class. Be sure that you measure the finger from the first knuckle, where the finger meets the hand to the tip of the finger. Complete your measurements in millimeters. Record data for the entire class on the table located below.

Subject	Index Finger Length (mm)	Subject	Index Finger Length (mm)
1		11	
2		12	
3		13	
4		14	
5		15	
6		16	
7		17	
8		18	
9		19	
10		20	

Part II.

Organize the data above into ranges and create a histogram that shows the distribution of index finger length within this class. Use graph paper from the back cabinet or (and this is preferable) Google Sheets.

Part III.

Now you need to find fifty of the same biological items, easy examples this time of year might be pine needles, peanuts, grapes, house plant leaves (from the same plant or type of plant), fresh produce (take a trip to the grocery store ask the produce manager before you start to be sure it is okay). You need to record one dimension of each of these biological items, so for example if you chose fifty apples (same type of apple) then you need to measure the height, width, or circumference but not all three. Record the data that you collect in the table below. Once this is complete organize the data that you recorded into ranges and create a histogram to illustrate the genetic variation that is present in the population that you studied. Keep in mind that if you go to the grocery store to gather data you want to pick a product that is not sorted by size or sold by size. The produce manager or a clerk can help you find produce that will fit the bill.

Object	Length in mm	Object	Length in mm
1		26	
2		27	
3		28	
4		29	
5		30	
6		31	
7		32	
8		33	
9		34	
10		35	
11		36	
12		37	
13		38	
14		39	
15		40	
16		41	
17		42	
18		43	
19		44	
20		45	
21		46	
22		47	
23		48	
24		49	
25		50	

Use the space below to determine the size ranges that you will use on your histogram. Determine the largest and smallest examples from your data table above, subtract the smallest from the largest, this will give you the difference in size between the largest and smallest. Now divide that number by five, this will give you the five ranges that will be present on the X-axis of your histogram.

For example:

I measured fifty peanuts, the largest I measured was 12mm the smallest was 6.1mm. That means that there is a difference of 6mm in length between the largest and the smallest. So:

6.1 / 5 = 1.22 (Which we can round down to 1.2)

So my ranges will be:

6.1mm – 7.2mm, 7.3mm – 8.4mm, 8.5mm-9.6mm, 9.7mm-10.8mm, 10.9mm-12mm

Notice that in the second range I run from 7.3 to 8.4. This is a range of 1.1 millimeters (not 1.2). This is because to get 8.4 you need to start with the top number from the previous range so 7.2 + 1.2 = 8.4. This keeps the ranges the same size and keeps you from having the same measurement in more than one range.