General calculator use, functions, and tips

※ all instructions in this guide are for TI-84 Plus
but most graphing calculators will have similar inputs and functions

Clearing all RAM from calculator ※ Required before all calculator exams

↳ 2nd [+] (mem) "7: Reset..." "1: All RAM" "2: Reset" → show "RAM Cleared" screen to proctor

convert decimal to fraction

↳ math "1: ▶Frac"

convert fraction to decimal

↳ math "2: ▶Dec"

convert normal value to scientific notation

↳ mode "SCI" 2nd mode (quit) enter

convert scientific notation to normal value

↳ mode "NORMAL" 2nd mode (quit) enter

store values into memory

↳ sto→ alpha choose any letter, ex: math (A)

retrieve values from memory

↳ alpha chosen letter, ex: math (A)

writing in scientific notation, ex: 6.02×10^{23}

↳ 6.02 2nd , (EE) 23 enter

correcting mistakes instead of re-inputting, ex: $(56-62)^2$ should be $(56-64)^2$

↳ 2nd enter (entry) ◁ edit 2 to 4 enter

only round values at the very end to avoid rounding errors

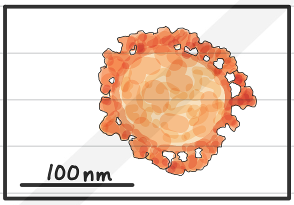
before entering data into lists, clear list data to prevent accidentally leaving-in previous values

↳ 2nd [+] (mem) "4: ClrAllLists" enter

A2.2 Converting measured, actual, and magnified values from micrographs

number of times larger a specimen appears ← magnification (Mag) = $\frac{\text{measured size of image (M)}}{\text{actual size of specimen (A)}}$ → (M) measured / (A) in reality

ex:



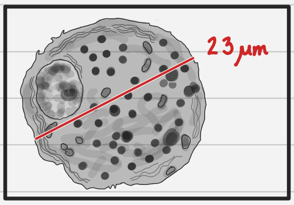
Determine the magnification (given scale bar)

① measure scale bar with ruler → 25mm

② convert into the units given: $25\text{mm} \times 10^6 = 2.5 \times 10^7 \text{nm}$

③ calculate using 'Mag MA': $Mag = \frac{M}{A} = \frac{2.5 \times 10^7 \text{nm}}{100 \text{nm}} = 250000\times$

ex:



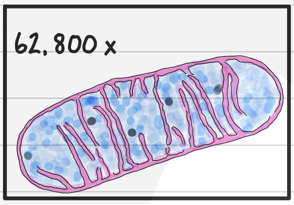
Determine the magnification (given actual size)

① measure length with ruler → 41 mm

② convert into the units given: $41 \text{mm} \times 10^3 = 4.1 \times 10^4 \mu m$

③ calculate using 'Mag MA': $Mag = \frac{M}{A} = \frac{4.1 \times 10^4 \mu m}{23 \mu m} = 1800\times$

ex:



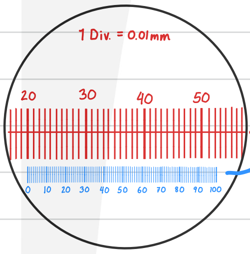
Determine the actual length (given magnification)

① measure length with ruler → 94mm

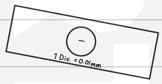
② convert to appropriate units: $94\text{mm} \times 10^3 = 9.4 \times 10 \mu m$

③ calculate using 'Mag MA': $A = \frac{M}{Mag} = \frac{9.4 \times 10^4 \mu m}{62{,}800} = 1.5 \mu m$

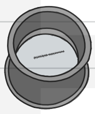
A2.2 Calibrating eyepiece graticule



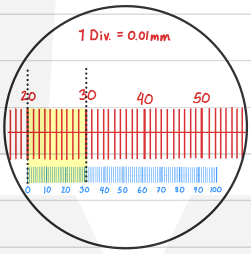
Stage micrometer: slide with divided scale marked on its surface



eyepiece graticule: graduated scale placed inside eyepiece lens.



ex: Determine the value of each increment of eyepiece graticule below



① align graticule with stage micrometer

② count how many divisions on the graticule correspond to a set number of micrometer divisions

③ calculate value of one graticule division

in 10 stage micrometer divisions there are 31 graticule divisions

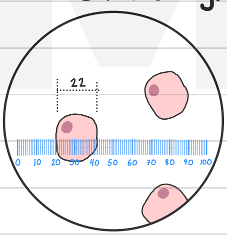
10 : 31

10(0.01mm) : 31 divisions

0.1 / 31 : 1 division

∴ 0.0032 mm or 3.2 μm = 1 division

ex: use calibrated graticule to determine actual length of cell



cell length = 22 units

graticule division = 3.2 μm

$22 \times 3.2 \mu m = 70.4 \mu m$

※ calibration needs to be done for each objective lens i.e. for each magnification

A2.2 Creating a scale bar for a drawing given graticule scale

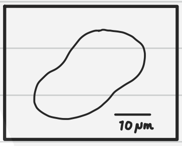
ex: graticule unit = 25 μm

1. measure length of specimen using graticule
2. convert length to μm
3. calculate length as 20% of specimen length
4. draw specimen and measure length of drawing
5. calculate length of scale bar
6. draw line for scale bar 20% the length of drawing

length of specimen = 2.1 graticule units

$2.1 \times 25\,\mu m = 52.5\,\mu m$

$20\% = 10.5\,\mu m = \sim 10\,\mu m$



l drawing = 96 mm

$$\frac{10\,\mu m}{52.5\,\mu m} = \frac{x}{96\,mm} = 18.3\,mm$$

bar 18.3 mm represents 10 μm

A4.2 Calculating biodiversity using Simpson's reciprocal index

Simpson's reciprocal index calculates biodiversity, by accounting for both species richness and species evenness

↳ species richness: number of different species present in an area

↳ species evenness: relative abundance of the different species present in an area

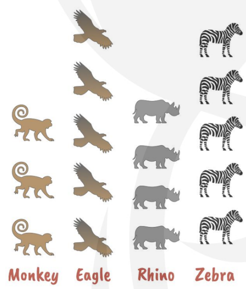
$$\text{Diversity index } (D) = \frac{N(N-1)}{\sum n(n-1)}$$

N = total number of organisms of all species

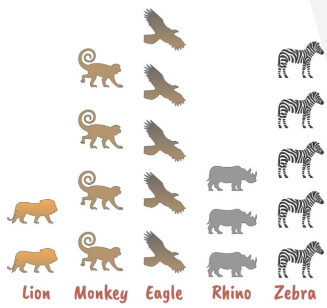
n = number of individuals of a particular species

ex: determine which community, A or B has a higher biodiversity

A.



B:



species	n	n(n-1)
monkey	3	6
eagle	5	20
rhino	4	12
zebra	5	20
TOTAL	17	58

species	n	n(n-1)
lion	2	2
monkey	4	12
eagle	5	20
rhino	3	6
zebra	5	20
TOTAL	19	60

$$D = \frac{17(17-1)}{58} = 4.69$$

$$D = \frac{19(19-1)}{60} = 5.70$$

∴ community B has higher species diversity

B1.1 Convert between SI units

← multiply (value gets larger)

divide (value gets smaller) →

sci notation	10^{-9}	10^{-6}	10^{-3}	10^{-2}	10^{3}	10^{6}
SI prefixes	nano	micro	milli	centi	kilo	mega
symbol	n	μ	m	c	k	M

ex: 0.025 km is how many micrometers?

1. find the difference between km and μm — $km = 10^3$ $\mu m = 10^{-6}$, $3-(-6) = 10^9$ → multiply
2. use dimensional analysis — $0.025\ \cancel{km} \times \frac{10^9\ \mu m}{1\ \cancel{km}} = \boxed{2.5 \times 10^7\ \mu m}$

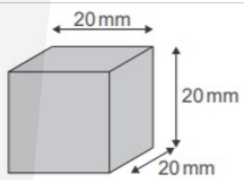
ex: 22.3 nm is how many centimeters?

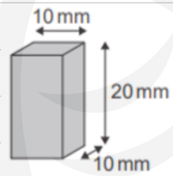
1. find the difference between nm and cm — $nm = 10^{-9}$ $cm = 10^{-2}$, $-9-(-2) = 10^{-7}$ → divide
2. use dimensional analysis — $22.3\ \cancel{nm} \times \frac{1\ cm}{10^7\ \cancel{nm}} = \boxed{2.23 \times 10^{-6}\ cm}$

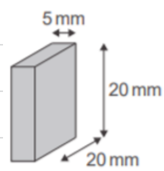
B2.3 Surface area to volume ratios

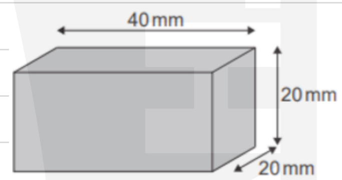
Cells can be modeled as simple shapes, such as cubes or rectangular prisms to investigates how ratios change with increasing side lengths. Surface area : volume ratio is positively correlated with rate of cell membrane exchange.

ex: which of the following cells would have the greatest rate of diffusion across its membrane?









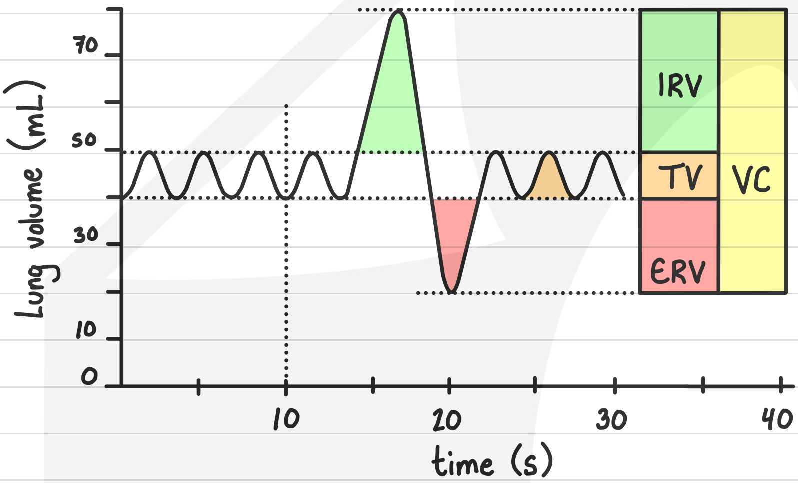
SA = 6(20×20)	SA = 4(20×10) + 2(10×10)	SA = 4(5×20) + 2(20×20)	SA = 4(40×20) + 2(20×20)
2400 cm^2	1000 cm^2	1200 cm^2	4000 cm^2
Vol = 20 × 20 × 20	Vol = 20 × 10 × 10	Vol = 20 × 20 × 5	Vol = 40 × 20 × 20
8000 cm^3	2000 cm^3	2000 cm^3	16000 cm^3
SA/vol = 0.3	SA/vol = 0.5	SA/vol = 0.6	SA/vol = 0.25
SA:vol = 3:10	SA:vol = 1:2	SA:vol = **3:5**	SA:vol = 1:4

※ convert decimal to ratio on calculator:

0.6 math "1: ▸ Frac" = $\frac{3}{5}$ = 3 : 5

B3.1 Measurement of lung volumes

Spirometery: test of lung function including lung volumes and ventilation rate



graph analysis:

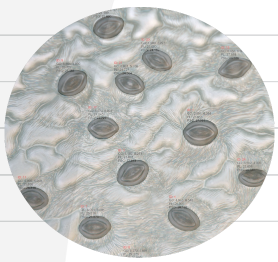
Tidal volume (TV) = 10 mL
Inspiratory reserve volume (IRV) = 30 mL
Expiratory reserve volume (ERV) = 20 mL
Vital capacity (VC) = 10 + 30 + 20 = 60 mL

ventilation rate = 3 breaths / 10s
= 0.3 breaths / s
= 18 breaths / min

B3.1 Determine stomatal density

Stomatal density = number of stomata per unit area (mm^{-2} or μm^{-2}) of a leaf surface

ex: a leaf casting was performed and the following micrograph produced. Stage micrometer calculates the diameter of the field of view at 400x magnification to be 0.46mm. Calculate Stomatal density



① Calculate radius of FOV — $r = d/2 = 0.46mm / 2 = 0.23mm$
② Calculate F.O.V. area — F.O.V. area $= \pi r^2 = \pi (0.23mm)^2 = 0.1662\ mm^2$
③ Calculate Stomatal density — total stomata / area $= 12 / 0.1662\ mm^2$
$= 72$ stomata per mm

B3.1 Calculate rate of transpiration using potometry ~ extra; not explicitly required

rate of transpiration = the volume of water lost by a plant via transpiration over time

ex: a plant's transpiration rate was investigated using a potometer. In 5 minutes, the air bubble moved 3.2 mm through a 3mm diameter capillary tube. Calculate its rate of transpiration per minute.

① Calculate radius — $r = d/2 = 3mm/2 = 1.5\ mm$
② Calculate rate of transpiration — transpiration rate $= \dfrac{\text{volume water } (mm^3)}{\text{time (min)}}$

$$= \frac{\pi r^2 d}{t} = \frac{\pi (1.5mm)^2 (3.2\ mm)}{5\ min} = 4.5\ mm^3\ min^{-1}$$

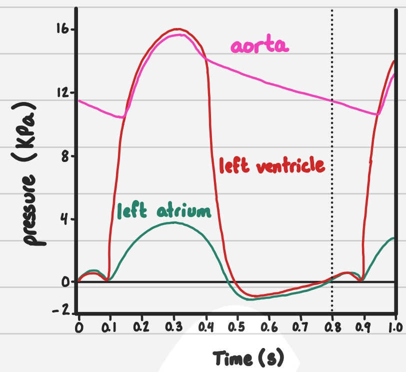
B3.2 Measurement of pulse rates

pulse rate : frequency of pulses which equates to heart beats
typically measured per minute (bpm or beats per minute)

ex: A student measured their pulse after an exercise. They counted 21 beats in 10 seconds. Calculate bpm

$$\frac{21 \text{ beats}}{10 \cancel{s}} \times \frac{60 \cancel{s}}{1 \text{ min}} = 126 \text{ bpm}$$

ex: graph shows changes in pressure in different parts of the heart over a period of one second. Calculate bpm



one complete cycle takes 0.8s

$$\frac{1 \text{ heart beat}}{0.8 \cancel{s}} \times \frac{60 \cancel{s}}{1 \text{ min}} = 75 \text{ bpm}$$

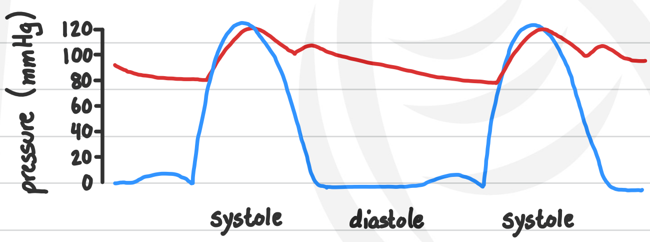
※ reading this type of graph is AHL

B3.2 Measurement of blood pressure AHL

blood pressure: pressure exerted on arterial (aortic) walls, typically expressed as the maximum over minimum

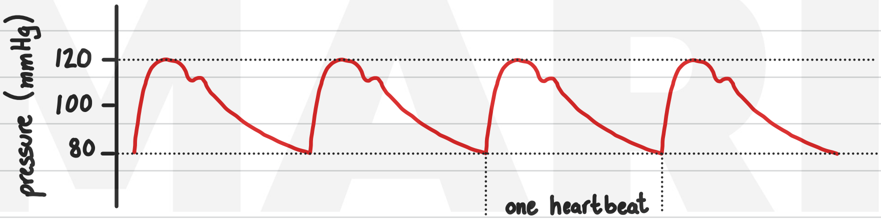
blood pressure = $\frac{\text{systolic}}{\text{diastolic}}$
systolic → arterial blood pressure is at its maximum, during systole
diastolic → arterial blood pressure is at its minimum, during diastole

ex:



systolic blood pressure (120mmHg)
diastolic blood pressure (80mmHg)

ex:

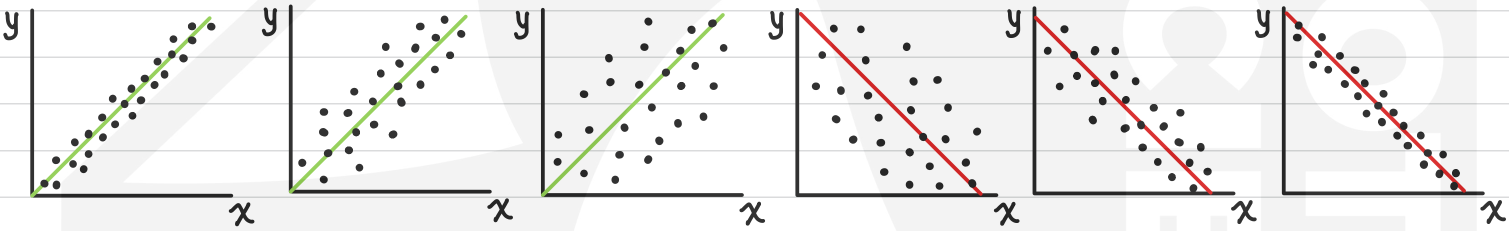


systolic blood pressure (120mmHg)
diastolic blood pressure (80mmHg)

B3.2 Correlation coefficient interpretation

Correlation coefficient (r): quantifies correlation and the strength of a <u>linear</u> relationship between two variables

↳ positive = positive correlation and vice-versa ↳ 1 and -1 = perfect correlation ↳ 0 = no correlation



$0.5 < r < 1$	$0.3 < r < 0.5$	$0 < r < 0.3$	$-0.3 < r < 0$	$-0.5 < r < -0.3$	$-1 < r < -0.5$
strong +	moderate +	weak +	weak -	moderate -	strong -

※ just because two variables are correlated, even strongly, does not prove a causal link

↳ there may be a causal link but further studies investigating this is required

ex: positive correlation between CO_2 and temperature. Further studies confirmed CO_2 absorbs infrared radiation - causal

↳ there may be a third factor (common-cause variable) that causes both variables

ex: positive correlation between ice cream sales and pool drownings. Heat waves are likely causing both

↳ the relationship may be purely coincidental and simply correlate by chance

ex: link to many ridiculous examples

B4.1 Transects and Kite diagrams

Transects are used to measure change in species abundance along an environmental gradient

↳ continuous line transect: every individual touching tape measure is recorded

↳ interrupted line transect: every individual touching tape measure at regular interval is recorded

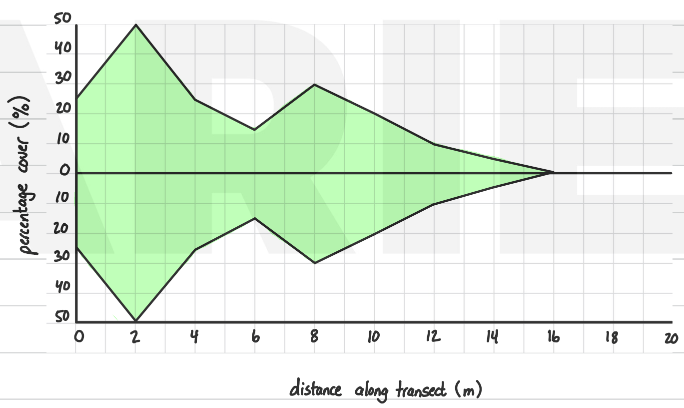
↳ continuous belt transect: individuals within quadrats placed end-to-end is recorded

↳ interrupted belt transect: individuals within quadrats placed at regular interval is recorded

Kite diagram: visually displays species distribution and abundance

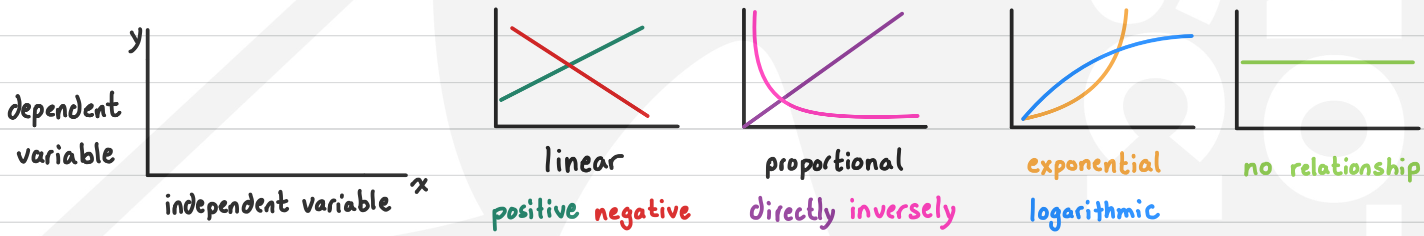
ex: average percentage cover of alpine plant along transect

Distance/ + 2m	Mosses
0.0	50
2.0	100
4.0	50
6.0	30
8.0	60
10.0	40
12.0	20
14.0	10
16.0	0
18.0	0
20.0	0



C1.1 Interpret relationships in graphs

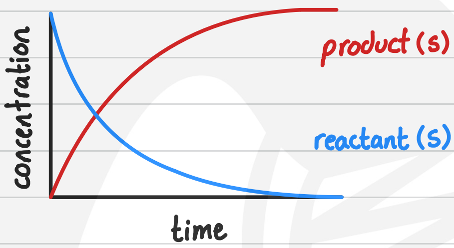
When plotting a scatter plot between 2 continuous variables, the type of relationship can be visualized



C1.1 Determining enzyme-catalyzed reaction rates

rate of a chemical reaction can be measured as either change in reactant or product over time

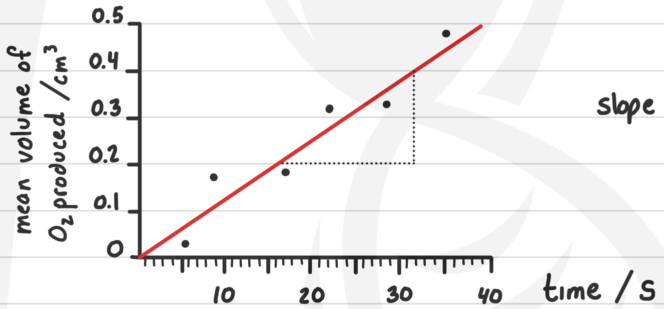
↳ rate of reaction can be calculated by determining the slope of the curve



$$\text{slope} = \frac{\Delta y}{\Delta x} = \frac{\Delta \text{ product}}{\Delta \text{ time}} \text{ or } \frac{\Delta \text{ reactant}}{\Delta \text{ time}}$$

greater / Steeper slope ⟶ greater rate and vice-versa

ex: Calculate the rate of reaction of the following reaction $2H_2O_2 \xrightarrow{\text{catalase}} 2H_2O + O_{2\,(g)}$



$$\text{slope} = \frac{\Delta y}{\Delta x} = \frac{\Delta\ O_2 \text{ production } (cm^3)}{\Delta \text{ time (s)}}$$

$$= \frac{0.4cm^3 - 0.2cm^3}{32s - 17s} = 0.013\ cm^3 s^{-1}$$

C1.2 Calculate rate of respiration using respirometer

ex: rate of respiration of germinating peas was investigated using a respirometer. In 3 minutes, the air bubble moved 10 mm through a 4 mm diameter manometer tube. Calculate its rate of respiration per minute.

① Calculate radius $r = d/2 = 4\text{ mm}/2 = 2\text{ mm}$

② Calculate rate of respiration transpiration rate $= \dfrac{\text{volume } O_2\ (mm^3)}{\text{time (min)}}$

$$= \frac{\pi r^2 d}{t} = \frac{\pi (2mm)^2 (10\ mm)}{3\ min} = 41.9\ mm^3 min^{-1}$$

C1.3 Creating action spectra from rates of photosynthesis

rate of photosynthesis can be determined through change in oxygen production over time or change in carbon dioxide consumption over time

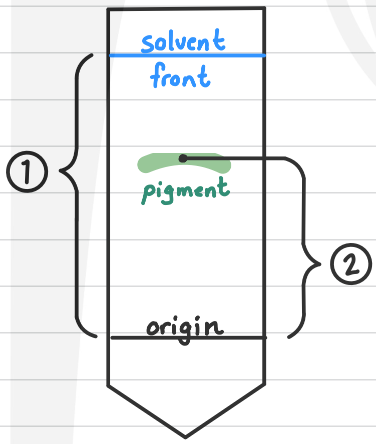
↳ action spectrum: graph plotting the relative efficiency of photosynthesis or photosynthetic rate vs wavelength of light (nm)

highest rate at these wavelengths suggests high absorbance of light ∴ more photosynthesis

lowest rate at these wavelengths suggests low absorbance of light ∴ less photosynthesis

C1.3 Calculate R_f value from results of chromatography

Chromatography : technique used to separate components of a mixture, whereby separated parts (pigments) can be identified



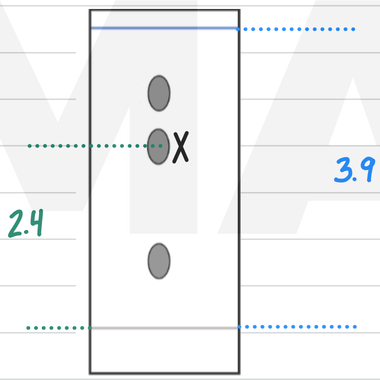
1. Using a ruler, measure the distance from origin to solvent front
2. For pigment : measure the distance from origin to ~ the center of the pigment (distance moved by pigment)
3. Calculate the retention factor

$$R_f = \frac{\text{distance moved by pigment}}{\text{distance moved by solvent}}$$

※ value between 0-1

4. Compare calculated R_f value to known R_f values to deduce pigment identity

ex: deduce the identity of pigment X using chromatogram below. Bottom line is baseline and top is solvent front



$$R_f = \frac{2.4 \text{ units}^*}{3.9 \text{ units}} = 0.62$$

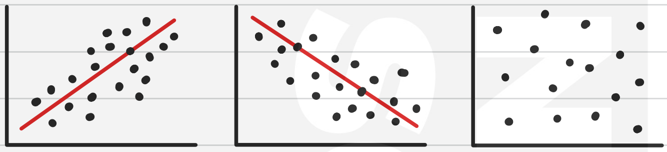
∴ likely pigment X is chlorophyll-a

pigment	R_f
carotene	0.95
xanthophyll	0.71
chlorophyll-a	0.65
chlorophyll-b	0.45

*measured on iPad but scale doesn't matter

C2.2 Negative and positive correlations and coefficient of determination (r^2)

Correlation : statistical test for degree of association between two variables. Can be positive or negative



※ B3.2 for information on Correlation coefficient (r)

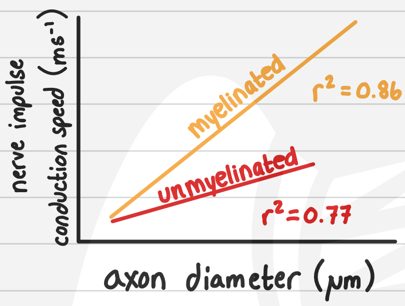
↳ linear regression : straight line that represents relationship between dependent (y) and independent (x) variable

coefficient of determination (r^2) indicates what percentage of the variation in the dependent variable (y) is explained by the variation in the independent variable (x) i.e. how close each data point fits a regression line.

↳ r^2 quantifies how much better a regression line fits the data relative to the mean

ex: $r^2 = 0.81$ ⟶ there is 81% less variation around a line than the mean
⟶ 81% of the variation in y is explained by variation in x, 19% by other factors
⟶ the x/y relationship accounts for 81% of the total variation

ex:



- positive correlation between impulse conduction speed and axon diameter
- for myelinated axons, 86% of the variation in speed is predicted by variation in axon diameter. 14% of the variation in speed is predicted by other factors
- for unmyelinated axons, 77% of the variation in speed is predicted by variation in axon diameter. 23% of the variation in speed is predicted by other factors

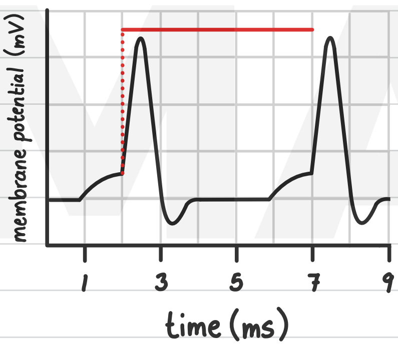
※ r^2 is easier to interpret and can be used to better-explain r

ex: how much better is $r = 0.7$ vs $r = 0.5$?
$r^2 = 0.5$ $\quad$ $r^2 = 0.25$ $\quad$ ∴ $r = 0.7$ is twice as good at accounting for the variation!

C2.2 Calculating nerve impulses per second from oscilloscope trace AHL

The change in neuron membrane potential during action potential propagation can be measured and visualized with an oscilloscope, producing a trace (mV over time)

ex: How many action potentials are propogated a) per second? b) per minute?



a) $\dfrac{2}{5\cancel{ms}} \times \dfrac{1000\ \cancel{ms}}{s} = 400$ impulses /s

b) $\dfrac{400}{1\cancel{s}} \times \dfrac{60\ \cancel{s}}{min} = 24000$ impulses / min

C3.2 Calculating minimum number of immune individuals for herd immunity ~ extra; not explicitly required

the minimum percentage of the population which should be vaccinated for a given pathogen can be estimated in order for herd immunity to be reached and reduce / halt the spread of the pathogen

critical proportion of population needed to be immune to pathogen $= 1 - \left(\frac{1}{R_0}\right) \times 100$ R_0 = mean number of people infected person infects

ex: measles has an estimated R_0 value between 12-18. Calculate critical proportion range.

$1 - \left(\frac{1}{12}\right) \times 100 = 91.7\%$ $1 - \left(\frac{1}{18}\right) \times 100 = 94.4\%$

∴ Between 91.7% and 94.4% of the population need to be immune from measles in order to reach herd immunity

C3.2 Calculate percentage difference

percentage difference examines the difference between two values as a percentage of their average

↳ used to measure relative size of the difference between two related values

$$\text{percentage difference} = \left(\frac{\text{value A} - \text{value B}}{\text{average of A+B}}\right) \times 100$$

ex: May 15 2021, USA reported 32,534,073 COVID-19 cases and Japan reported 671,841. Calculate % difference

$$\text{percentage difference} = \left[\frac{32{,}534{,}073 - 671{,}841}{\left(\frac{32{,}534{,}073 + 671{,}841}{2}\right)}\right] \times 100$$

= 192% difference in COVID-19 cases on May 15, 2021 between USA and Japan

C3.2 / D4.2 Calculate percentage change

percentage change examines how a final value has changed from an initial value

↳ used to measure whether a quantity has increased or decreased as a percentage

$$\text{percentage change} = \left(\frac{\text{new} - \text{original}}{\text{original}}\right) \times 100$$

ex: USA reported 163,199 COVID-19 cases on April 1 2020 and 578,268 cases on April 15. Calculate % change.

$$\text{percentage change} = \left(\frac{578{,}268 - 163{,}199}{163{,}199}\right) \times 100$$

= 254 % increase in USA COVID-19 cases from April 1-15 2020

※ positive value → increased, negative value → decreased

C4.1 using random quadrat sampling to estimate population size of sessile organisms

the population size for a sessile organism can be estimated by calculating the average frequency of the organism in quadrats placed randomly in a sampling area

$$\text{population estimate} = \frac{(\text{mean count per quadrat})(\text{area of whole site})}{\text{area of one quadrat}}$$

ex: a study was done where the number of dandelions were counted in a meadow. Ten 0.5m × 0.5m quadrats were randomly placed in the meadow. The sampled area of meadow was 10m × 10m.
Calculate the estimated total population size of dandelions in this meadow.

Quadrat number	1	2	3	4	5	6	7	8	9	10
Dandelion count	4	5	2	0	1	5	3	2	5	3

1. Calculate the mean number of dandelions per quadrat — $\bar{x} = 30/3 = 3$
2. Calculate the total area of the quadrats — $0.5m \times 0.5m = 0.25m^2$
3. Calculate the total area of sampled area — $10m \times 10m = 100m^2$
4. Calculate estimate using formula — $\frac{(3 \text{ dandelions})(100m^2)}{0.25m^2} = 1200$

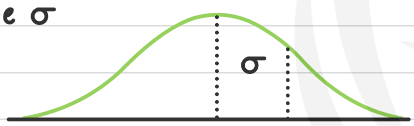
∴ there is an estimated population size of 1200 dandelions in this meadow

C4.1 Calculating and interpreting standard deviation to assess population spread

standard deviation (σ): measure of spread or dispersion of data around mean of dataset

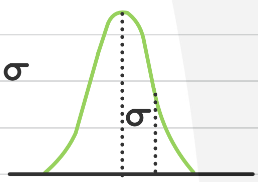
↳ allows an understanding of the distribution of a population

large σ



- ↑ variability
  population may be uneven / clumped

small σ



- ↓ variability
  population more evenly spread out

ex: Calculate the variability surrounding the calculated estimated total population size of dandelions

Calculate standard deviation using calculator

1. stat [EDIT] "1: Edit..." enter
2. enter values under L1 and then quit 2nd mode (quit)
3. stat [CALC] "1: 1-Var Stats" enter
4. "Calculate" enter
5. $S_x = 1.76$

6. calculate total number of quadrats that fit in habitat $\frac{100m^2}{0.25m^2} = 400$
7. multiply S_x by above value
   $1.76 \times 400 = 704$

∴ estimated population size varies by ± 704 dandelions

C4.1 Using Capture-mark-release-recapture and Lincoln Index to estimate population size of motile organisms

the population size for a motile organism can be estimated by using the Capture-mark-release-recapture technique and calculating the Lincoln Index

$$\text{Estimated population size} = \frac{M \times N}{R}$$

M : number of individuals caught and marked initially
N : total number of individuals recaptured
R : number of marked individuals recaptured

ex: In a study, 248 snails were caught in a pond and marked with non-toxic yellow paint on their shells. After 2 weeks, 168 were recaptured, of which 42 were marked yellow. Estimate the snail population

$M = 248$
$N = 168$
$R = 42$

$$\text{Estimated population size} = \frac{248 \times 168}{42} = 992 \text{ snails}$$

C4.1 Use chi-squared test for association between two species

Chi-squared (χ^2) test for association: statistical hypothesis test which examines whether distribution of two species is independent of the other, i.e. associated or not

↳ used to determine if species distribution displays association with one another:
- positive association : species may have mutualistic relationship
- negative association : species may have interspecific competition
- no association : species randomly dispersed, no relationship

$$\chi^2 = \sum \frac{(obs - exp)^2}{exp}$$

observed values is distribution actually recorded
expected values is distribution if random

↳ the calculated χ^2 value is compared to a critical value at a particular α and degree of freedom in order to see if null hypothesis (H_0) is rejected or not

α = the significance value assigned to p value, typically ≥ 0.05
degree of freedom = number of independent values which can be assigned to statistical distribution, here it is 1
null hypothesis (H_0) = there is <u>no</u> significant difference between the distribution of both species i.e. distribution is random and there is <u>no</u> association
p-value = probability of attaining observed effect or larger in the dataset if the null hypothesis is <u>true</u>

↳ if χ^2 > critical value ($p \leq 0.05$) → reject H_0
if χ^2 < critical value ($p \leq 0.05$) → fail to reject H_0

C4.1 Use chi-squared test for association between two species

ex: the presence and/or absence of two species of scallop, King scallop and Queen scallop was recorded in fifty $1m^2$ quadrats on a rocky shore. The following distribution was recorded:

6 both present; 15 King scallop only; 20 Queen scallop only; 9 neither present

How to solve in long-form:

① write null and alternative hypotheses:

H_0 = there is no significant difference between the distribution of both species i.e. distribution is random and there is no association

H_A = there is a significant difference between the distribution of both species i.e. distribution is non-random and there is an association

② Complete table of observed values from given information

Obs		Queen scallop Present	Queen scallop Absent	Total
King scallop	Present	6	15	21
King scallop	Absent	20	9	29
	Total	26	24	50

③ Calculate expected values (i.e. if distribution is random)

Exp		Queen scallop Present	Queen scallop Absent
King scallop	Present	$\frac{21 \times 26}{50} = 10.92$	$\frac{21 \times 24}{50} = 10.08$
King scallop	Absent	$\frac{29 \times 26}{50} = 15.08$	$\frac{29 \times 24}{50} = 13.92$

$$\frac{\text{row total} \times \text{column total}}{\text{grand total}}$$

④ Calculate $x^2 = \sum \frac{(obs - exp)^2}{exp}$

$$x^2 = \frac{(6 - 10.92)^2}{10.92} + \frac{(15 - 10.08)^2}{10.08} + \frac{(20 - 15.08)^2}{15.08} + \frac{(9 - 13.92)^2}{13.92} = 7.96$$

⑤ Determine degrees of freedom

$$df = (rows - 1)(columns - 1)$$
$$= (2-1)(2-1)$$
$$= 1$$

⑥ Compare x^2 value with critical value of $p = 0.05$ or smaller

Probability level (alpha)

df	0.5	0.10	0.05	0.02	0.01	0.001
1	0.455	2.706	3.841	5.412	6.635	10.827
2	1.386	4.605	5.991	7.824	9.210	13.815
3	2.366	6.251	7.815	9.837	11.345	16.268

⑦ $\because x^2 >$ critical value at $p = 0.01$ ($7.96 > 6.635$), we reject the null hypothesis

$\therefore$ there is a significant difference between the distribution of both species, association is likely

C4.1 Use chi-squared test for association between two species

ex: two species of fir tree are found along the coast of Southern California. These two species are the Grand Fir and Noble Fir. Their distribution patterns were established via quadrat samples:

25 both present; 30 Noble Fir only; 45 Grand Fir only; 50 neither present

How to solve using calculator stat function:

① write null and alternative hypotheses:

H_0 = there is no significant difference between the distribution of both species
i.e. distribution is random and there is no association

H_A = there is a significant difference between the distribution of both species
i.e. distribution is non-random and there is an association

② 2nd, x^{-1} (matrix) [EDIT] "1: [A]" enter

③ MATRIX [A] 2 × 2 enter

④ input observed values in table

$$\begin{bmatrix} 25 & 45 \\ 30 & 50 \end{bmatrix}$$

Species A

B		
	✓ ✓	✓ ×
	× ✓	× ×

⑤ 2nd, mode (quit)

⑥ stat [TEST] "C: χ^2 – Test" enter

⑦ "Calculate" enter

$\chi^2 = 0.051$ $p = 0.82$ $df = 1$

⑧ compare χ^2 value to critical value at $p = 0.05$

Probability level (alpha)

df	0.5	0.10	0.05	0.02	0.01	0.001
1	0.455	2.706	3.841	5.412	6.635	10.827
2	1.386	4.605	5.991	7.824	9.210	13.815
3	2.366	6.251	7.815	9.837	11.345	16.268

∵ χ^2 < critical value at $p = 0.05$ $(0.051 < 3.84)$, we fail to reject the null hypothesis

∴ there is not a significant difference between the distribution of both species, association is not likely

C4.2 Construction of energy pyramids

energy pyramid: illustrates the rate per area at which energy is contained within the biomass of organisms at each trophic level

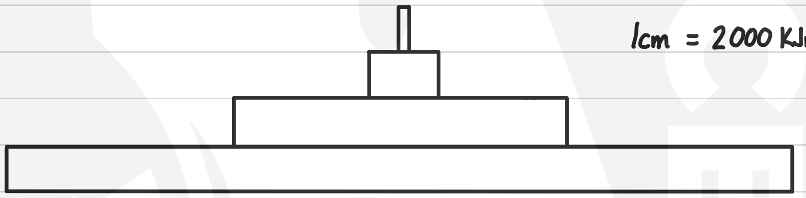
ex: construct a scaled energy pyramid for the following ecosystem:

Pyramid of Energy for a river ecosystem

Tropic level	Energy kJm^{-2}y^{-1}
Tertiary consumers	316
Secondary Consumers	1890
Primary Consumers	8833
Producers	20810

1. choose a scale for bar length ex: 1cm = 2000 KJm^{-2}y^{-1}
2. choose a height for each bar ex: 1cm
3. calculate scaled length of each bar
   - tertiary consumers: 316 / 2000 = 0.158cm
   - secondary consumers: 1890 / 2000 = 0.945cm
   - primary consumers: 8833 / 2000 = 4.4165cm
   - producers: 20810 / 2000 = 10.405cm
4. draw pyramid with each bar centered over each other

tertiary consumers
secondary consumers
primary consumers
producers



1cm = 2000 KJm^{-2}y^{-1}

2000 KJm^{-2}y^{-1}

C4.2 Determining primary and secondary production

Primary production: accumulation of carbon compounds in biomass by autotrophs. ※ units = gm^{-2}yr^{-1}

↳ Gross primary production (GPP): <u>total</u> biomass of carbon compounds made by autotrophs

↳ Net primary production (NPP): biomass of carbon compounds made by autotrophs <u>after losses</u> due to cellular respiration (R) $NPP = GPP - R$

Secondary production: accumulation of carbon compounds in biomass of heterotrophs

↳ Gross secondary production (GSP): <u>total</u> biomass of carbon compounds assimilated by heterotrophs <u>after losses</u> due to defecation GSP = food eaten − feacal loss

↳ Net secondary production (NSP): biomass of carbon compounds assimilated by heterotrophs <u>after losses</u> due to cellular respiration $NSP = GSP - R$

ex: table shows transfers of energy (KJm^{-2}yr^{-1}) in a small community. Calculate net productivity for all trophic levels

Trophic Level	Gross Production	Respiratory Loss	Loss to decomposers
Producers	60724	36120	477
1° Consumer	21762	14700	3072
2° Consumer	714	576	42
3° Consumer	7	4	1
Respiratory loss by decomposers	---	3120	---

$NPP = 60{,}724 - (36{,}120 + 477) = 24127\ KJm^{-2}yr^{-1}$

$NSP_{1°} = 21{,}762 - (14{,}700 + 3072) = 3990\ KJm^{-2}yr^{-1}$

$NSP_{2°} = 714 - (576 + 42) = 96\ KJm^{-2}yr^{-1}$

$NSP_{3°} = 7 - (4 + 1) = 2\ KJm^{-2}yr^{-1}$

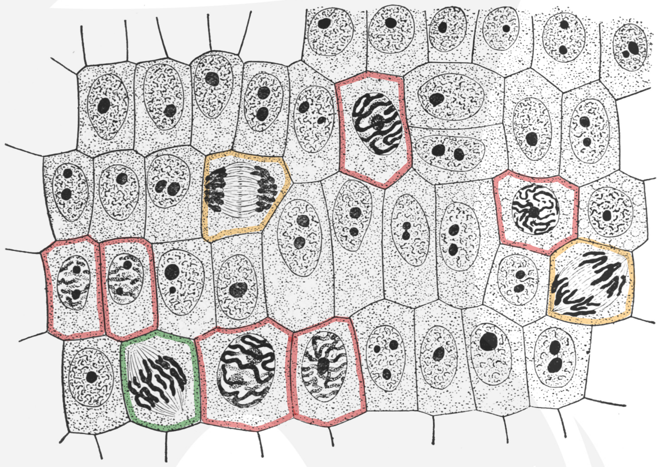
$NSP_{d} = (477 + 3072 + 42 + 1) - 3120 = 472\ KJm^{-2}yr^{-1}$

D2.1 Determine mitotic index AHL

mitotic index is a measure of cellular proliferation. The higher the mitotic index, the greater the proportion of cells undergoing mitosis and cell division.

$$\text{Mitotic index} = \frac{\text{number of cells in mitosis (Prophase + Metaphase + Anaphase + Telophase)}}{\text{total number of cells (Interphase + Mitosis)}}$$

ex: calculate the mitotic index from the micrograph diagram below.



Cells in Prophase	6
Cells in Metaphase	1
Cells in Anaphase	2
Cells in Telophase	0
Total number of cells	40

$$\text{Mitotic index} = \frac{6+1+2+0}{40}$$

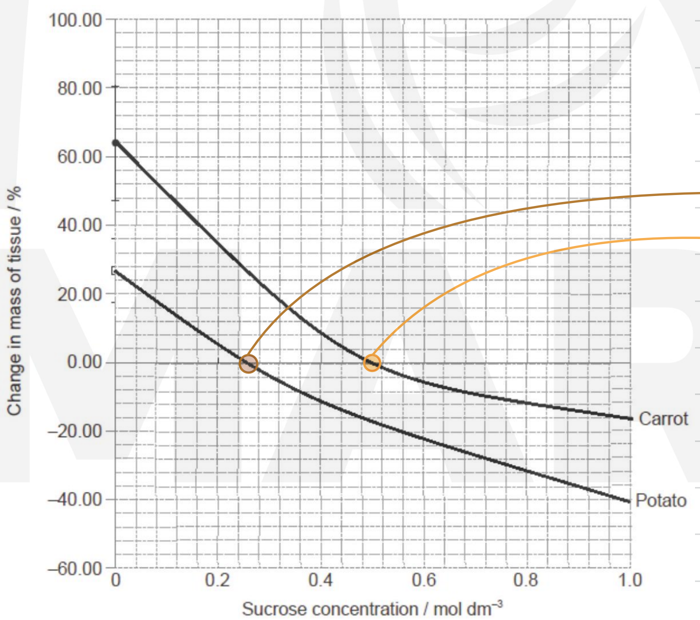
$$= 0.225$$

D2.3 Deduce isotonic solute concentration

isotonic concentration: a solution of equal osmolarity (solute concentration) to another

↳ by immersing a tissue in varying solute concentrations and measuring mass change, its isotonic point can be deduced when there is no change in mass

ex: an experiment was carried out where tissues of carrot and potato were bathed in different sucrose solutions for 24 hours. Results shown on graph below



1) Deduce the isotonic sucrose solution concentration for both carrot and potato tissues.

potato: 0.25 mol dm^{-3}
carrot: 0.50 mol dm^{-3}

2) State the range of concentrations which are hypotonic to carrot tissues

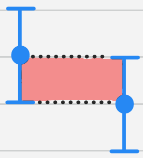
hypotonic solutions are less concentrated than the tissue, thus tissue will gain mass
∴ solutions less than 0.50 mol dm^{-3}

D2.3 Standard deviation, Standard error and error bars

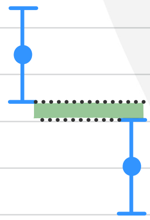
standard deviation (σ): measure of spread or dispersion of data around mean of dataset

standard error (σ_M): how reliably the mean of a sample represents mean of whole population
the larger the sample size (n), the smaller the standard error
※ σ_M typically used if trial sample size > 30

↳ either can be used as error bars on a graph, which represent $\pm 1 \sigma_M$ or σ



overlap suggests there is no difference between both means



no overlap suggests there is a difference between both means

D2.3 Calculating water potential AHL

Water potential (Ψ): potential energy of water per unit volume, measured in KPa or MPa

$$\text{Water potential } (\Psi_w) = \text{Solute potential } (\Psi_s) + \text{pressure potential } (\Psi_p)$$

Solute potential (Ψ_s): reduces Ψ_w

pressure potential (Ψ_p): increases Ψ_w

ex: 1) If a cell's pressure potential is 300 KPa and its solute potential is -450 KPa what is its water potential?

$$\Psi_w = \Psi_s + \Psi_p = 300\text{ KPa} + (-450\text{ KPa}) = -150\text{ KPa}$$

2) the cell from 1) is placed in a beaker of sugar with solute potential of -0.4 MPa.
in which direction will the net flow of water be?

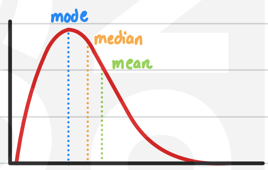
Ψ_p in open container $= 0$, $\therefore \Psi_{w\,(beaker)} = \Psi_{s\,(beaker)}$ $\quad -0.4\,\cancel{MPa} \times \frac{1000\text{ KPa}}{\cancel{MPa}} = -400\text{ KPa}$

$\Psi_{w\,(cell)} > \Psi_{w\,(beaker)}$ $\quad \therefore$ net flow of water is out of cell

D3.2 Calculate measures of central tendency - mean, median, and mode

central tendency: statistical measure that identifies a single value as representative of an entire distribution

- ↳ mean (average): sum of all datapoints divided by number of datapoints in a dataset
- ↳ median (Q_2): middle value of a dataset arranged in order of increasing value
- ↳ mode: most common value in dataset

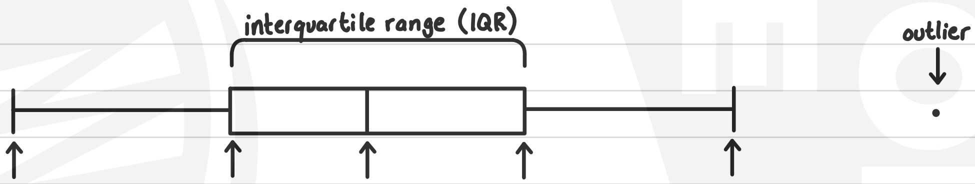


skewed distribution

ex: calculate mean, median, mode for the following dataset: 31, 10, 2, 31, 87, 100, 14, 31, 55, 49

1. [stat] [EDIT] "1: Edit..." [enter]
2. enter values under L1 and then quit [2nd] [mode] (quit)
3. [stat] [CALC] "1: 1-Var Stats" [enter]
4. "Calculate" [enter]
5. $\bar{x}$ (mean) = 41 med (median) = 31
6. [stat] [EDIT] "2: Sort A(" [enter]
7. Sort A([2nd] [1] (L1) [enter]
8. [stat] [EDIT] "1: Edit..." [enter]
9. check for most common value in list
   mode = 31

D3.2 Create box-and-whisker plots to represent continuous data



display on calculator:	minX	Q_1	med	Q_3	maxX
statistical measure:	minimum value	lower quartile	median	upper quartile	maximum value

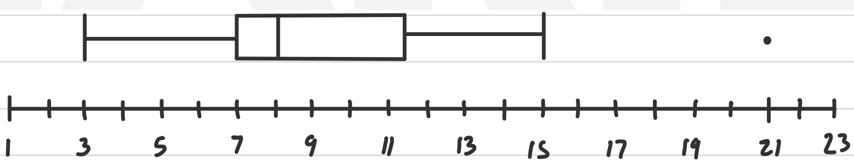
outlier: value that differs significantly from the rest of the dataset (i.e unusually small or large)

↳ lower outlier < Q_1 − 1.5 (IQR) ↳ upper outlier > Q_3 + 1.5 (IQR)

ex: draw a box-and-whisker plot for the following dataset: 3, 21, 12, 7, 10, 7, 8, 8, 11, 7, 3, 15

1. [stat] [EDIT] "1: Edit..." [enter]
2. enter values under L1 and then quit [2nd] [mode] (quit)
3. [stat] [CALC] "1: 1-Var Stats" [enter]
4. "Calculate" [enter]
5. IQR = $Q_3 - Q_1$ = 11.5 − 7 = 4.5
6. lower outlier < Q_1 − 1.5 (IQR) = 7 − 1.5 (4.5) = 0.25
   upper outlier > Q_3 + 1.5 (IQR) = 11.5 + 1.5 (4.5) = 18.25 → 21 is outlier ∴ new max = 15
7. draw appropriate scale and draw plot

minX = 3
Q_1 = 7
med = 8
Q_3 = 11.5
maxX = 21



D3.2 Use chi-squared test on data from dihybrid crosses AHL

Chi-squared (χ^2) "goodness of fit" test: assesses if there is a statistically significant difference between observed and predicted values

↳ in genetics, it can be used to assess whether a pair of genes are linked based on the phenotypic ratios from crosses and whether they agree with the predicted Mendelian 9:3:3:1 or 1:1:1:1 ratios or not

※ see C4.1 for more information on χ^2 test and hypothesis testing

ex: the trait for smooth peas (R) is dominant over wrinkled peas (r) and yellow pea colour (Y) is dominant to green (y). A dihybrid cross between a smooth yellow plant, heterozygous at both loci and a wrinkled green plant is performed. The following phenotypic frequencies are observed:

157 Smooth Yellow ; 26 Smooth green ; 23 wrinkled Yellow ; 144 wrinkled green

<u>How to solve in long-form:</u>

① write null and alternative hypotheses:

H_0 = there is <u>no significant difference</u> between the observed and expected frequencies → genes are <u>unlinked</u>

H_A = there is a <u>significant difference</u> between the observed and expected frequencies → genes are <u>linked</u>

② Determine <u>expected ratio</u> of unlinked genes using dihybrid cross

RrYy × rryy

	RY	Ry	rY	ry
ry	RrYy	Rryy	rrYy	rryy

1:1:1:1

③ Calculate <u>expected frequencies</u> (i.e. if Mendelian distribution)

	Smooth Yellow	Smooth green	wrinkled Yellow	wrinkled green	Total
Observed	157	26	23	144	350
Expected	$(350 \times 1/4) = 87.5$	$(350 \times 1/4) = 87.5$	$(350 \times 1/4) = 87.5$	$(350 \times 1/4) = 87.5$	350

④ $$\chi^2 = \sum \frac{(obs - exp)^2}{exp} = \frac{(157-87.5)^2}{87.5} + \frac{(26-87.5)^2}{87.5} + \frac{(23-87.5)^2}{87.5} + \frac{(144-87.5)^2}{87.5} = 182.5$$

⑤ Determine degrees of freedom

$$df = (rows-1)(columns-1)$$
$$= (2-1)(4-1)$$
$$= 3$$

⑥ Compare χ^2 with critical value of $p = 0.05$ or smaller

Probability level (alpha)

df	0.5	0.10	0.05	0.02	0.01	0.001
1	0.455	2.706	3.841	5.412	6.635	10.827
2	1.386	4.605	5.991	7.824	9.210	13.815
3	2.366	6.251	7.815	9.837	11.345	16.268

⑦ ∵ χ^2 > critical value at $p = 0.001$ (182.5 > 16.268), we reject the null hypothesis

∴ there is a significant difference between the observed and expected frequencies

genes are likely linked and do not assort independently

D3.2 Use chi-squared test on data from dihybrid crosses AHL

ex: the trait for smooth peas (R) is dominant over wrinkled peas (r) and yellow pea colour (Y) is dominant to green (y). A dihybrid cross between two yellow smooth peas, heterozygous at both loci is performed. The following phenotypic frequencies are observed:

701 Smooth Yellow ; 204 Smooth green ; 243 wrinkled Yellow ; 68 wrinkled green

How to solve using calculator stat function:

① write null and alternative hypotheses:

H_0 = there is no significant difference between the observed and expected frequencies → genes are unlinked

H_A = there is a significant difference between the observed and expected frequencies → genes are linked

② Determine expected ratio of unlinked genes using dihybrid cross

RrYy × RrYy

	RY	Ry	rY	ry
RY	RRYY	RRYy	RrYY	RrYy
Ry	RRYy	RRyy	RrYy	Rryy
rY	RrYY	RrYy	rrYY	rrYy
ry	RrYy	Rryy	rrYy	rryy

∴ 9:3:3:1

③ Calculate expected frequencies (i.e. if Mendelian distribution)

	Smooth Yellow	Smooth green	wrinkled Yellow	wrinkled green	Total
Observed	701	204	243	68	1216
Expected	$(1246 \times 9/16) = 684$	$(1246 \times 3/16) = 228$	$(1246 \times 3/16) = 228$	$(1246 \times 1/16) = 76$	1216

④ stat [EDIT] "1: Edit..." enter

⑤ enter observed values under L_1 and expected values under L_2 and then quit 2nd mode (quit)

⑥ stat [TEST] "D: χ^2 GOF-Test" enter

⑦ Determine degrees of freedom $df = (rows - 1)(columns - 1) = (2-1)(4-1) = 3$

⑧ "Calculate" enter

$\chi^2 = 4.778$ $p = 0.189$ $df = 3$

⑨ compare χ^2 value to critical value at $p = 0.05$

Probability level (alpha)

df	0.5	0.10	0.05	0.02	0.01	0.001
1	0.455	2.706	3.841	5.412	6.635	10.827
2	1.386	4.605	5.991	7.824	9.210	13.815
3	2.366	6.251	7.815	9.837	11.345	16.268

⑩ ∵ χ^2 < critical value at $p = 0.05$ $(4.78 < 7.815)$, we fail to reject the null hypothesis

∴ there is no significant difference between the observed and expected frequencies

genes are likely unlinked and assort independently

D4.1 Hardy-Weinberg equation and calculations of allele or genotype frequencies AHL

Hardy-Weinberg equations are mathematical expressions that can be used to calculate the allele and genotype frequency of a population at equilibrium, i.e. one that is not evolving

<u>allele frequency</u> $p + q = 1$

p ↑ Dominant allele, q ↑ recessive allele

<u>genotype frequency</u> $p^2 + 2pq + q^2 = 1$

p^2 ↑ Homozygous Dominant, $2pq$ ↑ heterozygous, q^2 ↑ Homozygous recessive

ex: a population of rabbits may be brown (dominant phenotype) or white (recessive phenotype). Trait is controlled by one gene and demonstrates complete dominance. The frequency of the homozygous Dominant genotype is 0.35.
Determine the frequency of heterozygous rabbits and the Dominant and recessive allele.

frequency of B

$p^2 = 0.35$
$p = \sqrt{0.35}$
$= 0.59$

frequency of b

$q = 1 - 0.59$
$= 0.41$

frequency of Bb

$2pq = 2(0.59)(0.41)$
$= 0.48$

ex: a population of birds contain 16 individuals with red tail feathers and 34 with blue tail feathers. Blue tail feathers is dominant over red tail feathers.
Determine the frequency of red and blue alleles and the frequency of homozygous blue birds.

frequency of b

$q^2 = \frac{16}{16+34}$
$= 0.32$
$q = \sqrt{0.32}$
$= 0.57$

frequency of B

$p = 1 - 0.57$
$= 0.43$

frequency of BB

$p^2 = 0.43^2$
$= 0.19$