

STATISTICS RECAP – *ask your partner the following questions:*



WHY DO WE USE STATISTICS?

We use statistics to see whether the results from our experiments are significant (statistically significant). That helps us decide whether we have proved the link between the changes we made (IV) and the change/result that occurred (DV)

WHAT DOES THE P VALUE MEAN?

P = the probability that our results came about due to random chance and were not anything to do with our independent variable *i.e. the “null hypothesis” is true (we want to avoid this!)*

WHAT DOES $P < 0.05$ MEAN?

This means that we can be 95% sure that our results are due to the IV and not due to random chance i.e. there is only a 5% probability that these results happened by chance/fluke. The closer to zero, the greater the significance e.g. $p < 0.001$ is a “very highly significant” result

HOW DO WE KNOW OUR RESULTS ARE SIGNIFICANT?

In confidence limits results/means from different conditions are considered to be significant if their confidence limits (on the graph) do not overlap

WHAT DOES THE SIZE OF THE CONFIDENCE LIMIT TELL US?

**LARGE CONFIDENCE LIMIT INDICATES LESS RELIABLE RESULTS THAN A NARROW ONE.
NARROW CFs INDICATE CLUSTERING OF RESULTS.**

WHAT DOES THE SIZE OF OUR STANDARD DEVIATION OF THE MEAN TELL US?

THE LARGER THE STANDARD DEVIATION, THE LESS RELIABLE THE RESULTS

IMPORTANT: Calculating the degrees of freedom

Make sure you know how to calculate the D.F. for each statistical test:

t-test: this is the sum of n_1 and n_2 minus 2. n_1 is the number of results you have from sample one and n_2 is the number of results you have from sample 2. HINT: It is the sum minus “2” as a t-test always compares 2 sample means

Chi-squared test: The degrees of freedom in this case is the number of categories/outcomes minus 1 e.g. in a genetic phenotype ratio from a dihybrid cross of heterozygotes $AaBb \times AaBb$ there would be 4 phenotypic outcomes; therefore $n-1 = 3$

95% confidence limits: The D.F. is determined by the number of repeats/values for each category minus 1 e.g. when comparing rate of growth of a fungus in different pHs then n = the number of measures you took for the fungus at those pHs all added together

COURSEWORK STATS 2014-15

PH AND MEMBRANE PERMEABILITY IN BEETROOT CELLS

Definition of symbols

n = sample size i.e. number of replicates (all results in class, including their repeats)

\bar{x} = sample mean i.e. mean result for each pH

$\hat{\sigma}$ = estimate of the standard deviation

σ^2 = variance

$\hat{\sigma}_{\bar{x}}$ = standard deviation of the mean

\pm = confidence limit

t = t value found at $p=0.05$ at correct degrees of freedom

USING CLASS RESULTS!

NO CALCULATOR TO WORK OUT Standard Deviation of the
Mean?

$$\hat{\sigma}_{\bar{x}}$$

CALCULATE THE VARIANCE

Find difference between each individual value and mean
Square
Sum
Divide by number of values less one

$$\hat{\sigma}^2 = \frac{\sum (x - \bar{x})^2}{(n - 1)}$$

STANDARD DEVIATION OF THE MEAN

Divide variance by number of values
Find square root

$$\hat{\sigma}_{\bar{x}} = \sqrt{\frac{\hat{\sigma}^2}{n}}$$

ON YOUR CALCULATOR: CALCULATE STANDARD DEVIATION OF THE MEAN

$$\hat{\sigma}_{\bar{x}} = \sqrt{\frac{\hat{\sigma}^2}{n}}$$

CONFIDENCE LIMITS

Find t value from table (at $p > 0.05$ and D.F. of $n-1$ (sample size -1))

Multiply t by the standard deviation of the mean

CL is plus and minus each sample mean (each of your pH means)

Plot on graph and read across to estimate statistical significance

$$\bar{x} \pm t (\hat{\sigma}_{\bar{x}})$$

Table 1: Student's t values

d.f.	$p = 0.1$	0.05	0.02	0.01	0.002	0.001
1	6.314	12.706	31.821	63.657	318.31	636.62
2	2.920	4.303	6.965	9.925	22.327	31.598
3	2.353	3.182	4.541	5.841	10.214	12.924
4	2.132	2.776	3.747	4.604	7.173	8.610
5	2.015	2.571	3.365	4.032	5.893	6.869
6	1.943	2.447	3.143	3.707	5.208	5.959
7	1.895	2.365	2.998	3.499	4.785	5.408
8	1.860	2.306	2.896	3.355	4.501	5.041
9	1.833	2.262	2.821	3.250	4.297	4.781
10	1.812	2.228	2.764	3.169	4.144	4.587
11	1.796	2.201	2.718	3.106	4.025	4.437
12	1.782	2.179	2.681	3.055	3.930	4.318
13	1.771	2.160	2.650	3.012	3.852	4.221
14	1.761	2.145	2.624	2.977	3.787	4.140
15	1.753	2.131	2.602	2.947	3.733	4.073
16	1.746	2.120	2.583	2.921	3.686	4.015
17	1.740	2.110	2.567	2.898	3.646	3.965
18	1.734	2.101	2.552	2.878	3.610	3.922
19	1.729	2.093	2.539	2.861	3.579	3.883
20	1.725	2.086	2.528	2.845	3.552	3.850
21	1.721	2.080	2.518	2.831	3.527	3.819
22	1.717	2.074	2.508	2.819	3.505	3.792
23	1.714	2.069	2.500	2.807	3.485	3.767
24	1.711	2.064	2.492	2.797	3.467	3.745