NST IA Elementary Mathematics for Biologists **Statistics Examination Handout**

1. Symbols

Descriptive Statistics

Statistic	Population	Sample (estimating population)
Mean	μ	$\bar{x}$
Standard Deviation	σ_x	s
Variance	σ_x^2	s^2

Hypothesis testing

Null Hypothesis	H_0	Alternative Hypothesis	H_1
Probability (given H_0)	p	Significance Level	α
Chance of a Type I error	$\boldsymbol{\alpha}$	Chance of a Type II error	$\boldsymbol{\beta}$

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2. Formulae

Variance & standard deviation

$$s_x^{\ 2} = \frac{\sum\left(x-\bar{x}\right)^2}{N-1} = \frac{\sum x^2 - \left(\sum x\right)^2 / N}{N-1}$$

Standardised score
(‘number of standard deviations above the mean’)

$$z = \frac{x-\mu}{\sigma_x}$$

Standard error of the mean
(‘standard deviation of the sampling distribution of the mean’)

$$s_{\bar{x}} = \frac{s_x}{\sqrt{n}}$$

Student’s t-statistic

$$t = \frac{\left(\bar{x}-\mu\right)}{s_{\bar{x}}}$$

Pearson’s Chi-Squared

$$\chi^2 = \sum\frac{(O-E)^2}{E}$$

3. Step by step recipes for tests

t-tests

A t statistic is a **mean** divided by a **standard error**.

Confidence intervals

$$\mu \approx \bar{x} \pm t\left(s_{\bar{x}}\right) = \bar{x} \pm t\left(\frac{s_x}{\sqrt{N}}\right)$$

1. Look up the critical value of t for N-1 degrees of freedom, for the relevant α level
   a. 90% confidence intervals: use the α = 0.05 one-tailed value.
   b. 95% confidence intervals: use the α = 0.05 two-tailed value.
   c. 99% confidence intervals: use the α = 0.01 two-tailed value.

2. Estimate the standard error of the mean for the sample:
   a. Calculate the standard deviation estimate from the sample
   b. Divide this by the square root of N

3. Calculate t x the standard error of the mean (result of step 1 x result of step 2)

4. The confidence intervals are the result of step 3 above and below the mean of the sample.

One sample t-test

$$t = \frac{\left(\bar{x} - \mu\right)}{s_{\bar{x}}} = \frac{\left(\bar{x} - \mu\right)}{s_x / \sqrt{N}}$$

1. Calculate the mean of the sample

2. Calculate the difference between this and the expected (test) value μ

3. Estimate the standard error of the mean for the sample:
   a. Calculate the standard deviation estimate from the sample
   b. Divide this by the square root of N

4. Divide the difference by the standard error of the mean (result of 2 / result of 3). This is your t score.

5. If the size (ignoring the sign) of the t score is larger than the critical value for **N-1 degrees of freedom**, the mean of the sample is significantly different from μ.

<u>Related samples *t*-test</u>

$$t = \frac{\left(\bar{d} - 0\right)}{s_{\bar{d}}} = \frac{\bar{d}}{s_d / \sqrt{N}}$$

1. Calculate a difference score **d** = score1 – score 2 for each subject

2. Calculate the mean of the difference scores.

3. Estimate the standard error of the mean difference score:
   a. Calculate the standard deviation of the difference scores
   b. Divide this by the square root of N

4. Divide the mean difference score by the standard error of the mean difference score (result of step2 / result of step 3). This is your *t* score.

5. If the size (ignoring the sign) of the *t* score is larger than the critical value for N-1 degrees of freedom, the means of the two related samples are significantly different.

[This is just a one-sample t-test, on the difference scores, comparing the mean difference score with zero]

<u>Unrelated samples t-test:</u> [equal N]*

$$t = \frac{\bar{x}_1 - \bar{x}_2}{s_{\left(\bar{x}_1 - \bar{x}_2\right)}} = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\dfrac{s_1^{\,2} + s_2^{\,2}}{N}}}$$

1. Calculate the means for the two samples.

2. Calculate the difference between the two means.

3. Estimate the standard error of this difference:
   a. Calculate the variance of sample 1 (this is the standard deviation of sample 1 squared)
   b. Calculate the variance of sample 2
   c. Add the two variances together
   d. Divide the sum of the variances by N (the number in each sample)
   e. Take the square root of this value. This is the 'standard error of the difference between the means'.

4. Divide the difference between the means (result of step 2) by the standard error of the difference between the means (result of step 3). This is your *t* score.

5. If the size (ignoring the sign) of the *t* score is larger than the critical value for **2(N-1) degrees of freedom**, the means of the two unrelated samples are significantly different.

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* If the Ns if the two samples are different, a different procedure must be followed for calculating the standard error of the difference between the means (you will not have to do one of these calculations on this course). The calculations in Step 3 are replaced by the following equation:

$$s_{\left(\bar{x}_1 - \bar{x}_2\right)} = \sqrt{\frac{\left(N_1 - 1\right)s_1^{\,2} + \left(N_2 - 1\right)s_2^{\,2}}{N_1 + N_2 - 2}\left(\frac{1}{N_1} + \frac{1}{N_2}\right)}$$

Pearson's Chi-Squared test

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$

The chi-squared test is used to determine whether the observed pattern of data is significantly different from the pattern predicted by H_0.

General Procedure

1. Draw up a table of the categories into which observations could fall.
   a. Note: If you are investigating the relationship between two variables, then one variable should be the rows of the table, and another the columns. See below.

2. Note the number of observations (O) which fall into each category

3. Calculate the Expected value (E) for each category. How you do this will depend upon H_0, i.e. upon which question you are asking. See below.

4. Calculate χ^2 from the table:
   a. For each cell calculate the difference between the Observed and Expected values (O-E). Square this difference.
   b. Divide the squared difference by the Expected value (E).
   c. Add together the result of (b) for each cell. This is your χ^2 score.

5. Calculate your degrees of freedom (df)*:
   a. If your categories form a table with more than one row & column, df = (Rows-1)x (Columns-1)
   b. If your categories do not form a table then df = Categories-1

6. If your χ^2 is larger than the critical value (with the same df), then the data differs from the pattern predicted by the null hypothesis.

Calculation of Expected values

Goodness of Fit tests

Does the data fit the expected pattern? For example, are 50% of undergraduate science students female? Are equal numbers of granules found in each type of cell?

1. Calculate the total number of observations in the data. Call this value N.

2. Calculate the proportion of observations that would be *expected* to fall into each category, for the 'expected pattern'. Call this value *P* for each category.

3. The Expected value for each category is N x *P*

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* Sometimes when doing a more complicated chi-squared test, you need to calculate certain parameters (e.g. the mean) of your observations in order to get the Expected values. In these cases, we loose a degree of freedom for each parameter we have to calculate. You will not need to do this kind of test in this course.

<u>Contingency, or 2-way relationship tests</u>
Does one variable affect another? For example, are female students less likely to smoke? Are certain species of an animal more likely to have tumours?

1. Each 'category' of the first variable will be one row of the table. Each category of the second variable will be a column of the table.
   E.g. Rows = Wombat, Rabbit, Squirrel
   Columns = Tumours, No Tumours

2. Calculate the total for each row and column (e.g. the total number of squirrels).

3. Calculate the overall (grand) total of all observations.

4. The expected value for each cell in the table is:
   E = (row total)x(column total) / grand total

Special conditions for the validity of χ^2

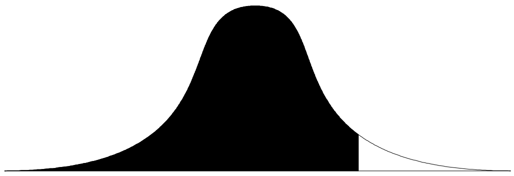
1. All expected values must be greater than one, and should be above 5.

2. All observations must fall into one and only one class (this means that you must use **all** observations taken exactly **once** in your calculation).

3. The observations must all be 'equally independent'. This is important when you have observations that come in 'groups'. For example, if you have N_1 observations from one source (e.g. one plant, animal or person) N_2 from a second, N_3 from a third and so on, you **cannot** lump them all together as a set of (N_1+N_2+N_3+…) observations and apply a single χ^2 test. You have to do separate tests for each set of observations.

4. Statistical Tables

Areas (probabilities) under a normal distribution

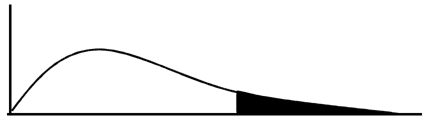


The **left column** gives the **first decimal place** and the top row gives the second decimal place. So the area (probability) corresponding to $Z_1 = 0.23$, for example, is in the row labelled 0.2 and the column headed .03, value = 0.5910).

Z	.00	.01	.02	.03	.04	.05	.06	.07	.08	.09
0.0	.5000	.5040	.5080	.5120	.5160	.5199	.5239	.5279	.5319	.5359
0.1	.5398	.5438	.5478	.5517	.5557	.5596	.5636	.5675	.5714	.5753
0.2	.5793	.5832	.5871	.5910	.5948	.5987	.6026	.6064	.6103	.6141
0.3	.6179	.6217	.6255	.6293	.6331	.6368	.6406	.6443	.6480	.6517
0.4	.6554	.6591	.6628	.6664	.6700	.6736	.6772	.6808	.6844	.6879
0.5	.6915	.6950	.6985	.7019	.7054	.7088	.7123	.7157	.7190	.7224
0.6	.7257	.7291	.7324	.7357	.7389	.7422	.7454	.7486	.7517	.7549
0.7	.7580	.7611	.7642	.7673	.7704	.7734	.7764	.7794	.7823	.7852
0.8	.7881	.7910	.7939	.7967	.7995	.8023	.8051	.8078	.8106	.8133
0.9	.8159	.8186	.8212	.8238	.8264	.8289	.8315	.8340	.8365	.8389
1.0	.8413	.8438	.8461	.8485	.8508	.8531	.8554	.8577	.8599	.8621
1.1	.8643	.8665	.8686	.8708	.8729	.8749	.8770	.8790	.8810	.8830
1.2	.8849	.8869	.8888	.8907	.8925	.8944	.8962	.8980	.8997	.9015
1.3	.9032	.9049	.9066	.9082	.9099	.9115	.9131	.9147	.9162	.9177
1.4	.9192	.9207	.9222	.9236	.9251	.9265	.9279	.9292	.9306	.9319
1.5	.9332	.9345	.9357	.9370	.9382	.9394	.9406	.9418	.9429	.9441
1.6	.9452	.9463	.9474	.9484	.9495	.9505	.9515	.9525	.9535	.9545
1.7	.9554	.9564	.9573	.9582	.9591	.9599	.9608	.9616	.9625	.9633
1.8	.9641	.9649	.9656	.9664	.9671	.9678	.9686	.9693	.9699	.9706
1.9	.9713	.9719	.9726	.9732	.9738	.9744	**.9750**[*]	.9756	.9761	.9767
2.0	.9772	.9778	.9783	.9788	.9793	.9798	.9803	.9808	.9812	.9817
2.1	.9821	.9826	.9830	.9834	.9838	.9842	.9846	.9850	.9854	.9857
2.2	.9861	.9864	.9868	.9871	.9875	.9878	.9881	.9884	.9887	.9890
2.3	.9893	.9896	.9898	.9901	.9904	.9906	.9909	.9911	.9913	.9916
2.4	.9918	.9920	.9922	.9925	.9927	.9929	.9931	.9932	.9934	.9936
2.5	.9938	.9940	.9941	.9943	.9945	.9946	.9948	.9949	.9951	.9952
2.6	.9953	.9955	.9956	.9957	.9959	.9960	.9961	.9962	.9963	.9964
2.7	.9965	.9966	.9967	.9968	.9969	.9970	.9971	.9972	.9973	.9974
2.8	.9974	.9975	.9976	.9977	.9977	.9978	.9979	.9979	.9980	.9981
2.9	.9981	.9982	.9982	.9983	.9984	.9984	.9985	.9985	.9986	.9986
3.0	.9987	.9987	.9987	.9988	.9988	.9989	.9989	.9989	.9990	.9990

[*]This value shows that 0.975 corresponds to Z = 1.96. This means that the probability of sampling $Z > 1.96$ is 0.025 (2.5%). Thus, 95% of values in a Normal population lie approximately between ±2 standard deviations from the mean. This is a useful rule of thumb for judging some statistical significances in Normally distributed scores without using any special tests – if a difference corresponds to a Z score of more than 2, it is probably a significant difference if the score is normally distributed.

Critical Values of χ^2

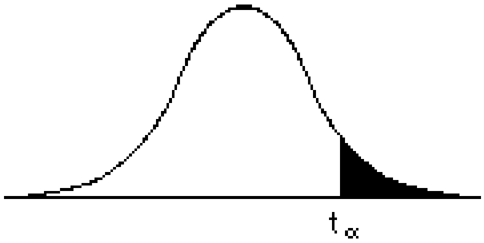


Level of Significance

α	.05	.01	.001
df			
1	3.84	6.64	10.83
2	5.99	9.21	13.82
3	7.82	11.34	16.27
4	9.49	13.28	18.47
5	11.07	15.09	20.52
6	12.59	16.81	22.46
7	14.07	18.48	24.32
8	15.51	20.09	26.12
9	16.92	21.67	27.88
10	18.31	23.21	29.59
11	19.68	24.72	31.26
12	21.03	26.22	32.91
13	22.36	27.69	34.53
14	23.68	29.14	36.12
15	25.00	30.58	37.70
16	26.30	32.00	39.25
17	27.59	33.41	40.79
18	28.87	34.80	42.31
19	30.14	36.19	43.82
20	31.41	37.57	45.32
21	32.67	38.93	46.80
22	33.92	40.29	48.27
23	35.17	41.64	49.73
24	36.42	42.98	51.18
25	37.65	44.31	52.62
26	38.88	45.64	54.05
27	40.11	46.96	55.48
28	41.34	48.28	56.89
29	42.56	49.59	58.30
30	43.77	50.89	59.70
40	55.76	63.69	73.40
50	67.50	76.15	86.66
60	79.08	88.38	99.61
70	90.53	100.42	112.32

If the calculated χ^2 value is greater than or equal to the critical value in the table for the corresponding df and significance level, then we can reject H_o (that the observations occurred with the probabilities described in H_o) and conclude that the data do not fit the model (in a goodness of fit test), or that there **is** some relationship between the 2 category systems (for a contingency test).

Critical Values of t



Level of Significance

1-tailed	**0.05**	(0.025)	**0.01**	(0.005)
2-tailed	(0.10)	**0.05**	(0.02)	**0.01**
df				
1	6.314	12.706	31.821	63.657
2	2.920	4.303	6.965	9.925
3	2.353	3.182	4.541	5.841
4	2.132	2.776	3.747	4.604
5	2.015	2.571	3.365	4.032
6	1.943	2.447	3.143	3.707
7	1.895	2.365	2.998	3.499
8	1.860	2.306	2.896	3.355
9	1.833	2.262	2.821	3.250
10	1.812	2.228	2.764	3.169
11	1.796	2.201	2.718	3.106
12	1.782	2.179	2.681	3.055
13	1.771	2.160	2.650	3.012
14	1.761	2.145	2.624	2.977
15	1.753	2.131	2.602	2.947
16	1.746	2.120	2.583	2.921
17	1.740	2.110	2.567	2.898
18	1.734	2.101	2.552	2.878
19	1.729	2.093	2.539	2.861
20	1.725	2.086	2.528	2.845
21	1.721	2.080	2.518	2.831
22	1.717	2.074	2.508	2.819
23	1.714	2.069	2.500	2.807
24	1.711	2.064	2.492	2.797
25	1.708	2.060	2.485	2.787
26	1.706	2.056	2.479	2.779
27	1.703	2.052	2.473	2.771
28	1.701	2.048	2.467	2.763
29	1.699	2.045	2.462	2.756
∞	1.645	1.960	2.326	2.576

If t is greater than or equal to the critical value in the table for the corresponding df and significance level (and number of 'tails'), then we can reject H_o (that the population means are the same) and conclude that the means are significantly different at that level.