

Solution to Exercise 4.4 (Version 1, 22/09/14)

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Exercise 4.4 (Data: courtesy J. Pell, Rothamsted Research)

An experiment investigated the effect of conidia density on transmission of a fungus that attacks aphids. Cadavers of aphids killed by the fungus, and from which the fungus was releasing spores, were placed on bean plants at three densities (A = 1, B = 5 or C = 10 cadavers per plant) to give different doses of fungal conidia. The densities were allocated to individual bean plants as a CRD with six replicates. Twenty uninfected live aphids were placed on each plant with one ladybird which was allowed to forage to facilitate transfer of conidia between the cadavers and the live aphids. For each plant the proportion of aphids that became infected after seven days was recorded and transformed to the logit scale for analysis (see Chapter 6). The unit numbers (*DPlant*), treatment allocations (factor *Density*) and transformed responses (variate *LogitP*) are in file TRANSMISSION.DAT.

- Write down the null and alternative hypotheses associated with this experiment.
- Obtain the ANOVA table. Is there any evidence that the density of fungal conidia affects the rate of transmission of the fungus to the aphids?
- Plot the predicted means for each density with the LSD. What does this plot suggest?
- State your conclusions from this analysis.

(We re-visit these data in Exercise 5.2.)

Data 4.4 (TRANSMISSION.DAT)

Logit-transformed proportions (LogitP) of aphids infected from the experiment to investigate the transmission of fungal infection by ladybirds:

Plant	Density	LogitP	Plant	Density	LogitP
1	C	-0.65	10	B	-0.30
2	A	-1.61	11	A	-1.42
3	B	-0.12	12	A	-0.65
4	C	0.51	13	C	0.74
5	B	-1.27	14	C	1.19
6	B	-1.61	15	A	-1.89
7	C	-0.10	16	B	0.34
8	C	0.11	17	B	-0.48
9	A	-0.34	18	A	-0.90

Solution 4.4

a) The null hypothesis is that the population means for the logit-transformed proportion of infected aphids are equal across the different initial densities of conidia. We can write a simple model for this data as

$$\text{Logit}P_{jk} = \text{Density}_j + e_{jk} ,$$

where $\text{Logit}P_{jk}$ is the logit-transformed proportion of infected aphids from the k th replicate of the j th density, with density groups labelled as $j=1$ for group A, $j=2$ for group B and $j=3$ for group C. Density_j is the (unknown) population mean for the j th density and e_{jk} is the deviation from the group population mean for the k th replicate of the j th density. We can then write the null hypothesis as

$$H_0: \text{Density}_1 = \text{Density}_2 = \text{Density}_3 .$$

The alternative hypothesis, H_1 , is that the population means for the different conidial densities are not all equal.

b) Details of the types of calculation required to produce the ANOVA table can be found in Solution 4.2. Here we present the ANOVA table produced by statistical software (see the programs for this exercise) in Table S4.4.1. Note that there are $N = 18$ observations in total, consisting of $t = 3$ treatments (densities) which are each replicated $n = 6$ times.

Table S4.4.1 ANOVA table for logit-transformed proportions of aphids infected with different initial conidial densities (factor Density).

Source of variation	df	Sum of squares	Mean square	Variance ratio	P
Density	2	6.2748	3.1374	7.119	0.007
Residual	15	6.6109	0.4407		
Total	17	12.8857			

The observed significance level associated with the variance ratio, $F=7.119$ with 2 numerator df and 15 denominator df, is $P = 0.007$. Hence we reject the null hypothesis and conclude that there is strong evidence that the population means for the different initial densities of fungal conidia are not all equal.

c) The predicted means (i.e. the estimated treatment population means) are equal to the group sample means and are shown in Table S4.4.2. The SED between treatments requires the estimate of background variation from the ResMS, $s^2 = 0.4407$, and the replication of each treatment, $n = 6$, to calculate

$$\text{SED} = \sqrt{\frac{2s^2}{n}} = \sqrt{\frac{2 \times 0.4407}{6}} = 0.3833 ,$$

and, using $t_{15}^{[0.025]} = 2.131$,

$$\text{LSD} = t_{15}^{[0.025]} \times \text{SED} = 2.131 \times 0.3833 = 0.8170 .$$

Table S4.4.2 Estimated population means (logit-transformed proportion) for density treatments (A, B and C), with estimated standard error of differences (SED, df=15) and least significant difference (LSD, df = 15).

Density			SED	LSD
A	B	C		
-1.14	-0.57	0.30	0.383	0.817

These results are summarized in Table S4.4.2. The predicted population means and LSD from Table S4.4.2 are plotted in Figure S4.4.1. In this plot the positions of the treatment groups on the x-axis is equal to the actual cadaver density used (A=1, B=5 and C=10 cadavers). This plot suggests that the mean logit-transformed proportion of infected aphids increases (almost linearly) as a function of density. The LSD indicates there is evidence that the population mean for density C is greater than the population means for both densities A (estimated C–A difference = 1.44) and B (estimated B–A difference = 0.87). However, there is no evidence of differences between the population means for densities A and B.

d) We conclude there is strong evidence ($F_{2,15} = 7.119$, $P = 0.007$) that the initial density of conidia affects the rate of transmission of the fungus to the aphids. There is evidence that the population mean (logit-transformed proportion) for density C (0.30) is greater than those for both densities A (-1.14) and B (-0.57). There is no statistical evidence of differences between the population means for densities A and B. The pattern of the predicted means suggests that the logit-transformed proportion of infection may increase as a linear function of initial density.

The predicted means on the logit scale correspond to proportions of 0.24, 0.36 and 0.57 for treatments A, B and C, respectively. Issues regarding analysis of transformed data and back-transformation of predicted means and confidence intervals are discussed in Chapter 6.

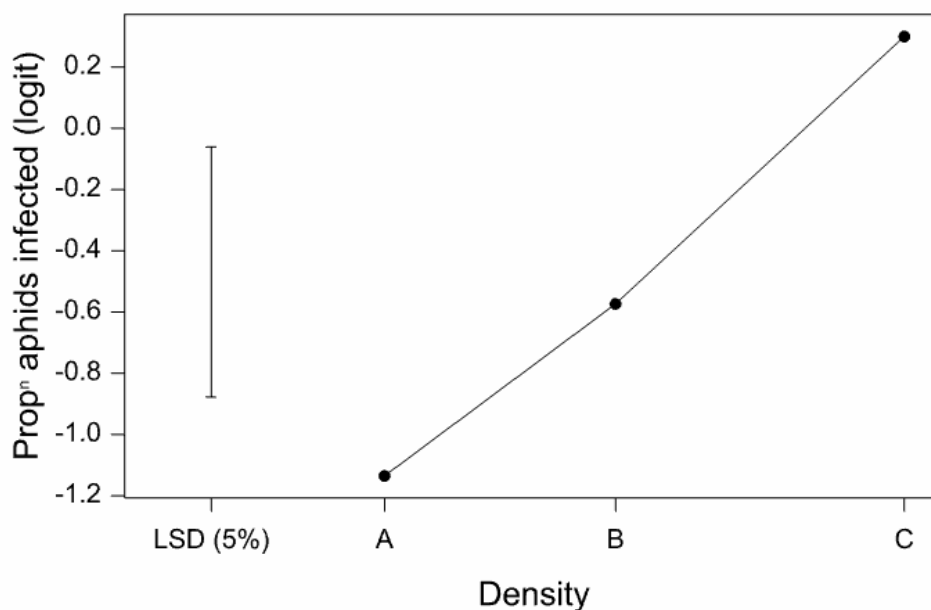


Figure S4.4.1. Predicted means and LSD for logit-transformed proportions of aphids infected with different initial conidial densities (A=1, B=5, C=10 cadavers).