

Analysis of the Cigarette Butts in Nests Dataset

We have the data that shows on the number of cigarette butts and parasites in the nest. The sample is of 60 nests among 2 host species.

We remove the observations which have the significant large residuals in our model. One of the outliers is on 12 row of the nest (residual=1.577). It is HOSP that has the nest content of chicks, butt weight of 2.14, number of mites 73. Another outlier is on 56 row of the nest (residual= -2.592). It is HOFI that has the nest content of eggs, butt weight of 4.46, number of mites 1. The table of figure 1 in the paper is wrong because it only used first 42 rows of the nest without a reason.

And the author told us his regression is done on a log-scale but we find it is under anti-log scale. We made a new regression without the 2 outliers.

$\log(\text{Number.of.mites}) = \text{SpeciesF} + \text{Nest.contentF} + \text{SpeciesF} * \text{Nest.contentF} + \text{Butts.weight}$

The result is presented in table 1. We found that **NO** evidence that the number of mites varies among nest content (p-value=0.55) and among the interactions between species & nest content (p-value=0.15). However, there are evidence that the number of mites varies between species (p-value=0.04) after we eliminate the outliers. For being HOFI, the number of log (mites) increase by 0.19 (the coefficient) compared to being HOSP. And there are strong evidence that the number of mites varies with different butt weights. For every increased gram of butts, the number of log(mites) decreases by 0.2(the coefficient).

Table 1: the result of our new model without outliers

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	433.97	1	937.1831	< 2.2e-16 ***
SpeciesF	2.04	1	4.4093	0.04102 *
Nest.contentF	0.56	2	0.6002	0.55279
Butts.weight	28.64	1	61.8407	3.538e-10 ***
SpeciesF:Nest.contentF	1.86	2	2.0038	0.14594
Residuals	22.23	48		