

Using `lm` with `asremlPlus` for the Ladybird example from Welham et al. (2014)

Chris Brien

15 September, 2026

Introduction

This vignette shows how to use `asremlPlus` (Brien, 2026a), and `dae` (Brien, 2026b), for exploring and presenting predictions (estimated marginal means: EMMs) from a linear mixed model analysis, the predictions having been produced using `lmerTest` (Kuznetsova et al., 2017), `lm` and `emmeans` (Lenth, 2025). Here, `asremlPlus`, `dae`, `lmerTest` and `emmeans` are packages for the R Statistical Computing environment (R Core Team, 2026) and `lm` is available from `stats` and is included in R.

The context is a three-factor factorial experiment on ladybirds (Welham et al., 2014, Example 8.2) that aims to answer the question “Will ladybirds transfer fungus to aphids on plants?” The experiment consists of 2 runs of 36 containers, each with a plant and aphids. There are three factors that results in 12 treatments: Host plant (beans, trefoil), infected Cadavers (5, 10, 20), Ladybird (-, +). These are randomized to the containers within a run so that each is replicated 3 times within a run. The response to be analysed is the logit of the proportion of live aphids that were infected.

Initialize

```
library(knitr)
opts_chunk$set("tidy" = FALSE, comment = NA)
suppressMessages(library(lmerTest))
packageVersion("lmerTest")
```

```
## [1] '3.2.1'
```

```
suppressMessages(library(emmeans))
packageVersion("emmeans")
```

```
## [1] '2.0.3'
```

```
suppressMessages(library(asremlPlus))
packageVersion("asremlPlus")
```

```
## [1] '4.4.65'
```

```
suppressMessages(library(dae))
packageVersion("dae")
```

```
## [1] '3.2.35'
```

```
options(width = 95, show.signif.stars = FALSE)
```

Get data available in asremlPlus

```
data("Ladybird.dat")
```

Do an ANOVA of logits

```
Ladybird.aov <- aov(logitP ~ Host*Cadavers*Ladybird + Error(Run/Plant),
                    data=Ladybird.dat)
summary(Ladybird.aov)
```

```
Error: Run
      Df Sum Sq Mean Sq F value Pr(>F)
Residuals  1 0.06766 0.06766

Error: Run:Plant
      Df Sum Sq Mean Sq F value Pr(>F)
Host      1 13.599  13.599  59.172 1.82e-10
Cadavers  2 17.027   8.514  37.044 3.78e-11
Ladybird  1 11.091  11.091  48.257 3.33e-09
Host:Cadavers  2  0.308   0.154   0.670  0.5158
Host:Ladybird  1  0.228   0.228   0.992  0.3234
Cadavers:Ladybird  2  1.735   0.867   3.774  0.0287
Host:Cadavers:Ladybird  2  0.200   0.100   0.435  0.6493
Residuals    59 13.560   0.230
```

The anova table gives the F-tests for the three-factor effects and interactions. Note the **Residuals Mean Sq** value for Run:Plant of 0.230. Also, it is clear that the Run component is negative, given that the **Residuals Mean Sq** value for Run is less than that for Run:Plant; it is $(0.06766 - 0.230) / 36$). From the table it is seen that the only significant interaction is Cadavers:Ladybird and that the Host main effect is significant.

Use lmerTest and lm to analyse the logits

Mixed model analysis of logits

```
m1.lmer <- lmerTest::lmer(logitP ~ Host*Cadavers*Ladybird + (1|Run),
                          data=Ladybird.dat)
```

boundary (singular) fit: see help('isSingular')

```
summary(m1.lmer)
```

Linear mixed model fit by REML. t-tests use Satterthwaite's method [`'lmerModLmerTest'`]

Formula: `logitP ~ Host * Cadavers * Ladybird + (1 | Run)`

Data: `Ladybird.dat`

REML criterion at convergence: 102.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.9633	-0.5217	0.1360	0.5789	2.1896

Random effects:

Groups	Name	Variance	Std.Dev.
Run	(Intercept)	0.0000	0.0000
Residual		0.2271	0.4766

Number of obs: 72, groups: Run, 2

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.603097	0.194560	60.000000	-8.240	1.91e-11
Hosttrefoil	-0.870675	0.275149	60.000000	-3.164	0.00244
Cadavers10	0.564771	0.275149	60.000000	2.053	0.04448
Cadavers20	0.919229	0.275149	60.000000	3.341	0.00144
Ladybird+	0.547710	0.275149	60.000000	1.991	0.05109
Hosttrefoil:Cadavers10	-0.212735	0.389120	60.000000	-0.547	0.58661
Hosttrefoil:Cadavers20	-0.120410	0.389120	60.000000	-0.309	0.75806
Hosttrefoil:Ladybird+	0.073153	0.389120	60.000000	0.188	0.85151
Cadavers10:Ladybird+	-0.040048	0.389120	60.000000	-0.103	0.91837
Cadavers20:Ladybird+	0.414204	0.389120	60.000000	1.064	0.29138
Hosttrefoil:Cadavers10:Ladybird+	0.005698	0.550299	60.000000	0.010	0.99177
Hosttrefoil:Cadavers20:Ladybird+	0.449979	0.550299	60.000000	0.818	0.41676

Correlation of Fixed Effects:

	(Intr)	Hsttrf	Cdvr10	Cdvr20	Ldybr+	Hs:C10	Hs:C20	Hst:L+	C10:L+	C20:L+	H:C10:
Hosttrefoil	-0.707										
Cadavers10	-0.707	0.500									
Cadavers20	-0.707	0.500	0.500								
Ladybird+	-0.707	0.500	0.500	0.500							
Hsttrf1:C10	0.500	-0.707	-0.707	-0.354	-0.354						
Hsttrf1:C20	0.500	-0.707	-0.354	-0.707	-0.354	0.500					
Hsttrf1:Ld+	0.500	-0.707	-0.354	-0.354	-0.707	0.500	0.500				
Cdvr10:Ld+	0.500	-0.354	-0.707	-0.354	-0.707	0.500	0.250	0.500			
Cdvr20:Ld+	0.500	-0.354	-0.354	-0.707	-0.707	0.250	0.500	0.500	0.500		
Hstt:C10:L+	-0.354	0.500	0.500	0.250	0.500	-0.707	-0.354	-0.707	-0.707	-0.354	
Hstt:C20:L+	-0.354	0.500	0.250	0.500	0.500	-0.354	-0.707	-0.707	-0.354	-0.707	0.500

optimizer (nloptwrap) convergence code: 0 (OK)

boundary (singular) fit: see help('isSingular')

As expected the Run component is bound at zero, leading to a singular model. This results in a change in the estimate of the residual variance to 0.227. To allow for a negative estimate we will redo the analysis

with `Run` fixed, because with `lme4` (`lmerTest`) one cannot unconstrain the `Run` component to allow it to be negative. As Littell et al. (2006, p.150) say

if you do not set the negative variance component estimate to zero, but allow it to remain negative, you get better control over Type I error and, for cases of negative wholeplot error variance estimates, greater power. Therefore, this is the recommended procedure.

Analyse with Reps fixed using `lm` to make the analysis equivalent to ANOVA

The function `lm` has to be used because there are no random terms; `lme4` cannot be used because it requires at least one random term.

```
m.lm <- lm(logitP ~ Run + Host*Cadavers*Ladybird,
           data=Ladybird.dat)
(aov.tab <- anova(m.lm))
```

Analysis of Variance Table

Response: logitP

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Run	1	0.0677	0.0677	0.2944	0.58946
Host	1	13.5992	13.5992	59.1720	1.815e-10
Cadavers	2	17.0274	8.5137	37.0444	3.784e-11
Ladybird	1	11.0907	11.0907	48.2571	3.329e-09
Host:Cadavers	2	0.3078	0.1539	0.6695	0.51579
Host:Ladybird	1	0.2279	0.2279	0.9916	0.32341
Cadavers:Ladybird	2	1.7349	0.8675	3.7744	0.02867
Host:Cadavers:Ladybird	2	0.1999	0.1000	0.4350	0.64932
Residuals	59	13.5596	0.2298		

Now the `Run:Plant` variance estimate is equal to that for the `Residuals` `Mean Sq` for `Run:Plant` from the anova table.

Obtain the marginality matrix for the fixed terms

The `pstructure` function from the `dae` package (Brien, 2026b) produce the marginality matrix for a formula as a side effect and we take advantage of that to obtain the matrix required here.

```
Ladybird.pstr <- pstructure(formula = ~ Host*Cadavers*Ladybird,
                           data = Ladybird.dat)
(HCL.marg <- marginality(Ladybird.pstr))
```

	Host	Cadavers	Host:Cadavers	Ladybird	Host:Ladybird	Cadavers:Ladybird
Host	1	0	1	0	1	0
Cadavers	0	1	1	0	0	1
Host:Cadavers	0	0	1	0	0	0
Ladybird	0	0	0	1	1	1
Host:Ladybird	0	0	0	0	1	0
Cadavers:Ladybird	0	0	0	0	0	1
Host:Cadavers:Ladybird	0	0	0	0	0	0
Host:Cadavers:Ladybird						

Host	1
Cadavers	1
Host:Cadavers	1
Ladybird	1
Host:Ladybird	1
Cadavers:Ladybird	1
Host:Cadavers:Ladybird	1

This marginality matrix is interpreted by taking a row term and noting that it is marginal to any column term with a one in this row.

Choose marginality-compliant model

```
chosen <- chooseModel(aov.tab, DF = "Df", denDF = 59, p.values = "Pr(>F)" ,
                      terms.marginality =HCL.marg)
(chosen$choose.summary)
```

Sequence of model investigations

	terms	DF	denDF	p	action
1	Host:Cadavers:Ladybird	2	59	0.6493	Nonsignificant
2	Cadavers:Ladybird	2	59	0.0287	Significant
3	Host:Ladybird	1	59	0.3234	Nonsignificant
4	Host:Cadavers	2	59	0.5158	Nonsignificant
5	Host	1	59	0.0000	Significant

```
(chosen$sig.terms)
```

```
[[1]]
[1] "Cadavers:Ladybird"
```

```
[[2]]
[1] "Host"
```

The `chooseModel` function produces a list with components `sig.terms`, a list with the terms in the marginality-compliant model, and `choose.summary`, a data.frame that details the tests performed in choosing the model. Note that `chooseModel` does not test the main effects for Cadavers or Ladybird, because these are marginal to the significant two-factor interaction Cadavers:Ladybird.

Form formula for selected model

```
chosen.mod <- paste(unlist(chosen$sig.terms), collapse = " + ")
(chosen.mod <- as.formula(paste("~", chosen.mod)))
```

```
~Cadavers:Ladybird + Host
```

Form predictions that conform to the chosen model

Use `emmeans` to get the predictions and associated statistics for the full model.

```
HCL.emm <- emmeans::emmeans(m1.lmer, specs = ~ Host:Cadavers:Ladybird)
HCL.preds <- summary(HCL.emm)
den.df <- min(HCL.preds$df)
HCL.vcov <- vcov(HCL.emm)
```

Setting the `specs` argument to `Host:Ladybird:Cadavers` requests predictions for all combinations of the three factors.

Modify `HCL.preds` to be compatible with a `predictions.frame`

Basically, this is an exercise in renaming the columns in the `data.frame` containing the predictions.

```
names(HCL.preds)
```

```
[1] "Host"          "Cadavers" "Ladybird" "emmean"      "SE"          "df"          "lower.CL" "upper.CL"
```

```
HCL.preds <- as.predictions.frame(HCL.preds, predictions = "emmean",
                                  se = "SE", interval.type = "CI",
                                  interval.names = c("lower.CL", "upper.CL"))
```

```
names(HCL.preds)
```

```
[1] "Host"          "Cadavers"          "Ladybird"
[4] "predicted.value" "standard.error"     "df"
[7] "lower.Confidence.limit" "upper.Confidence.limit" "est.status"
```

Form an `alldiffs` object with predictions obtained with `emmeans`

```
HCL.diffs <- allDifferences(predictions = HCL.preds, classify = "Host:Ladybird:Cadavers",
                           vcov = HCL.vcov, tdf = den.df)
```

The functions `allDifferences` is used to form the `alldiffs.obj` that contains a `predictions` component, along with components related to pairwise comparisons. The `predictions` component contains upper and lower confidence limits produced by `emmeans`. The `tdf` is supplied so that it can be used to get the degrees of freedom for the *t*-value to be used in calculating the error intervals.

Transform the prediction to conform to chosen model

The `linTransform` function is used to obtain estimated marginal means (EMMs) that conform to the chosen model. Because we would prefer error intervals based on $\pm 0.5LSD$, the `error.intervals` argument has been set to `"halfLeast"`, the `LSDtype` argument to `"factor.combination"` and the `LSDby` argument to `"Host"` so that the average LSD will be calculated for each `Host`. This necessary because, under the chosen model, the LSDs differ between `Hosts`. It results in `lower.halfLeastSignificant.limit` and `upper.halfLeastSignificant.limit` replacing the limits based on the confidence intervals in the `predictions` component of the resulting `alldiffs` object.

```
diffs <- linTransform(HCL.diffs, linear.transformation = ~Cadavers:Ladybird + Host,
  error.intervals = "halfLeast",
  LSDtype = "factor.combination", LSDby = "Host",
  tables = "predictions")
```

Joining with 'by = join_by(fac.comb)'
 Joining with 'by = join_by(Host)'

Predictions for transform(s) from Host:Ladybird:Cadavers

The original predictions, obtained as described below, have been linearly transformed to form estimated marginal means.

	Host	Ladybird	Cadavers	predicted.value	standard.error	df
1	bean	-	5	-1.6038338	0.1485977	47.2
2	bean	-	10	-1.1454308	0.1485977	47.2
3	bean	-	20	-0.7448097	0.1485977	47.2
4	bean	+	5	-1.0195475	0.1485977	47.2
5	bean	+	10	-0.5983440	0.1485977	47.2
6	bean	+	20	0.4786704	0.1485977	47.2
7	trefoil	-	5	-2.4730339	0.1485977	47.2
8	trefoil	-	10	-2.0146309	0.1485977	47.2
9	trefoil	-	20	-1.6140098	0.1485977	47.2
10	trefoil	+	5	-1.8887476	0.1485977	47.2
11	trefoil	+	10	-1.4675441	0.1485977	47.2
12	trefoil	+	20	-0.3905297	0.1485977	47.2

	upper.halfLeastSignificant.limit	lower.halfLeastSignificant.limit	est.status
1	-1.4081535	-1.7995140	Estimable
2	-0.9497506	-1.3411111	Estimable
3	-0.5491295	-0.9404900	Estimable
4	-0.8238673	-1.2152278	Estimable
5	-0.4026637	-0.7940242	Estimable
6	0.6743507	0.2829901	Estimable
7	-2.2773537	-2.6687142	Estimable
8	-1.8189507	-2.2103112	Estimable
9	-1.4183296	-1.8096901	Estimable
10	-1.6930674	-2.0844279	Estimable
11	-1.2718638	-1.6632243	Estimable
12	-0.1948495	-0.5862100	Estimable

LSD values

minimum LSD = 0.3913605 0.3913605

mean LSD = 0.3913605 0.3913605

maximum LSD = 0.3913605 0.3913605

(sed range / mean sed = 2.45e-14 2.41e-14)

The above LSD values can only be used to compare pairs of EMMs for the same Host.

Explore the LSDs

To investigate the errors that would result from using the overall LSDs as opposed to the LSDs computed for each Host, the `exploreLSDs`, `pickLSDstatistics` and `plotLSDerrors` functions are used, firstly with the default value of "overall" for `LSDtype` and finally with the `LSDtype` set to "factor.combination" and `LSDby` to "Host".

The `exploreLSDs` function produces tables of statistics for the LSDs computed for the settings of the `LSDtype` and `LSDby`; the settings of these arguments does not have to match those used in producing the `alldiffs` object. For `LSDtype` set to "overall", a single LSD statistic is computed that is based on the standard errors of all pairwise differences. To ascertain the errors that arise from using this LSD value for determining, for all pairwise comparisons, whether a comparison is significant, `exploreLSDs` compares the results using the LSD value with the p -values in the `p.differences` component of the `alldiffs` object. For `LSDtype` set to "factor.combination" and `LSDby` to "Host", the LSD statistics are calculated from standard errors of the pairwise differences for each Host. Examination of the `sed` component of `diffs` reveals that there are only three different values for the standard errors of pairwise differences and, hence, only three unique values for the LSD. Of the statistics shown, there is no single value that will not result in errors.

Here are the tables of the numbers of false positive and negative error in using the values of the various LSD statistics for determining the significance of the 66 pairwise comparisons of the 12 predictions.

```
exploreLSDs(diffs, LSDtype = "overall")
```

```
#### Statistics calculated from LSD values
```

	c	min	quant10	quant25	mean	median	quant75	quant90	max
1 66	0.2259521	0.3913605	0.3913605	0.4087627	0.3913605	0.4519042	0.4519042	0.4519042	

```
#### False positives resulting from the use of various LSD statistics
```

	c	min	quant10	quant25	mean	median	quant75	quant90	max
false.pos	66	6	2	2	2	2	0	0	0

```
#### False negatives resulting from the use of various LSD statistics
```

	c	min	quant10	quant25	mean	median	quant75	quant90	max
false.neg	66	0	0	0	0	0	0	0	0

The function `findLSDminerrors` can be used to find a value of the LSD that minimizes the number of false positive (negative) errors i.e. declaring a pairwise difference to be significant (not significant) when it is not significant (significant). The function has an argument `false.pos.wt` that specifies how many false negatives are equivalent to one false positive; the default for `false.pos.wt` is 10, which is a conservative approach because it greatly favours false negatives over false positives.

```
(findLSDminerrors(diffs))
```

	LSD	false.pos	false.neg	false.criterion
overall	0.4486447	0	0	0

```
(minLSDpos <- findLSDminerrors(diffs, false.pos.wt = 1))
```

```

      LSD false.pos false.neg false.criterion
overall 0.4486447      0      0      0

```

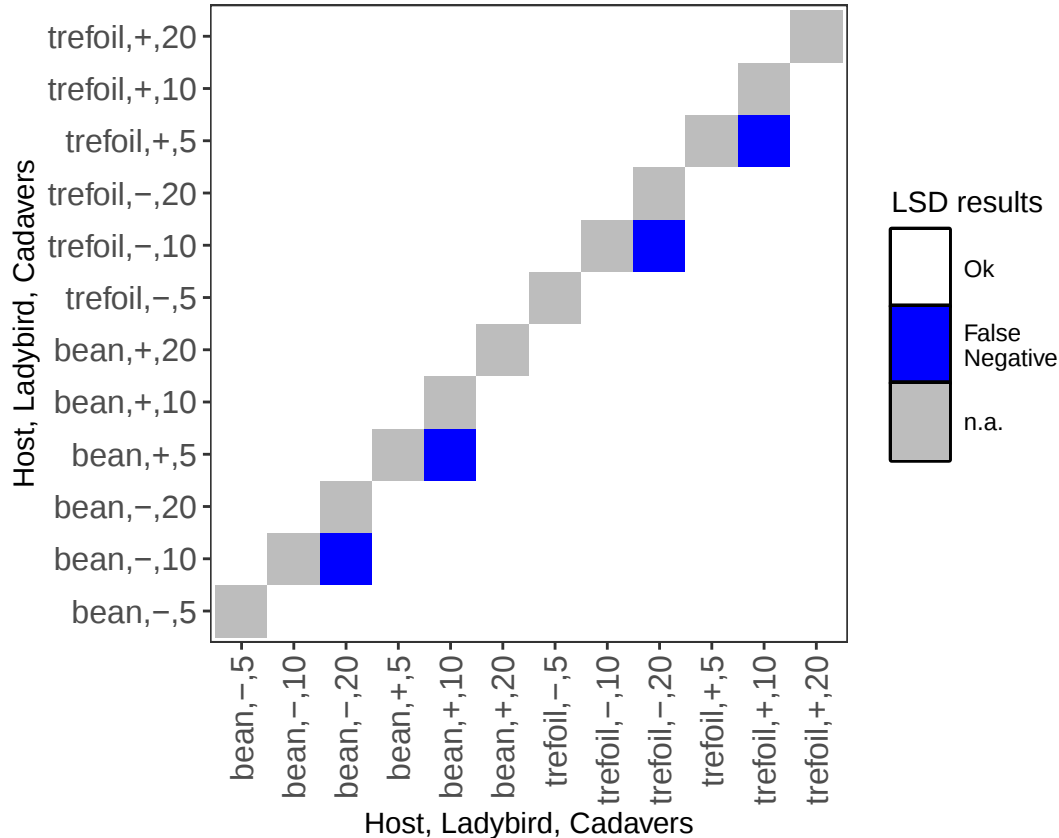
The smallest value of the LSD that results in the minimum weighted sum of the false positives and negatives is 0.4489466 when the weight is 10 and is 0.354983 when the weight is one. These values result in 4 false negatives and 2 false positives respectively.

To see which of the two pairwise comparisons will be falsely identified as being significant when the LSD value is set to minimum LSD, the LSDs stored in the `alldiffs` object need to be recalculated to be based on this LSD value. Then plot the errors or save the return values obtained using the function `plotLSDerrors`. The plot below shows that the two pairs whose differences are incorrectly identified as significant have the same level of the Ladybird factor, but differ in both of the levels for the Host and Cadaver factors.

```

diffs.overall <- recalcLSD(diffs, LSDtype = "supplied", LSDsupplied = minLSDpos["LSD"])
plotLSDerrors(diffs.overall)

```



This raises the question of whether the minimum LSD should be used. There are at least four alternatives: (i) use it without restriction, on the basis that it can be concluded that using it is unlikely to result in seriously flawed conclusions; (ii) use it with the restriction that it only be applied to assess pairwise comparisons that have the same Host or the same Cadaver treatment; (iii) investigate the use of the minimum LSD with only false negative errors; and (iv) rather than use an overall LSD value, use LSD values computed from the LSDs within each Host level.

Because `LSDtype` was set to `"factor.combination"` and `LSDby` to `"Host"` in forming the object `diffs`, the LSDs for alternative (iv) are stored in the `LSD` component of the object `diffs`. Printing out the LSD

component will summarize how those LSD values perform. Otherwise, the following call to `exploreLSDs` will display the properties of the LSDs for various LSD statistics:

```
exploreLSDs(diffs, LSDtype = "factor.combination", LSDby = "Host")
```

The following shows the contents of the LSD component of `diffs`:

```
(diffs$LSD)
```

	c	minLSD	meanLSD	maxLSD	assignedLSD	accuracyLSD	falsePos	falseNeg
bean	15	0.3913605	0.3913605	0.3913605	0.3913605	1.886492e-14	0	0
trefoil	15	0.3913605	0.3913605	0.3913605	0.3913605	1.843939e-14	0	0

Because the minimum and maximum LSD values are equal, it follows that there is only one value of the LSD for all pairwise comparisons within each Host level and it happens that the values for the two Hosts are also equal. The table shows that zero false positive and negative errors will result from the use of the value of 0.39 for the 30 within-Host comparisons. Thus, using `findLSDminerrors(diffs, LSDtype = "factor.combinations", LSDby = "Host")` to select the minimum LSDs would only confirm what is already obvious.

Plot the predictions

```
titl <- str2expression("logit~(italic(P))")
names(titl) <- "logitP"
plotPredictions(diffs$predictions, y = "predicted.value",
  y.title = titl,
  classify = "Host:Ladybird:Cadavers",
  error.intervals = "halfLeast", interval.annotate = FALSE,
  ggplotFuncs = list(facet_grid(Ladybird ~ Host,
    labeller = label_both)))
```

The function `plotPredictions` uses `ggplot` to produce the plot and the `ggplotFuncs` argument allows the addition of `ggplot` functions to modify the plot. In this case, the `facet.grid` function is respecified to include `prepender` functions that modify the labels of the facets to include the factor names. Note the statement in the legend of Figure 1 that restricts the use of the error bars to determining the significance of differences for the pairwise comparisons of EMMs for the same Host.

```
plotPvalues(diffs, factors.per.grid = 1, show.sig = TRUE)
```

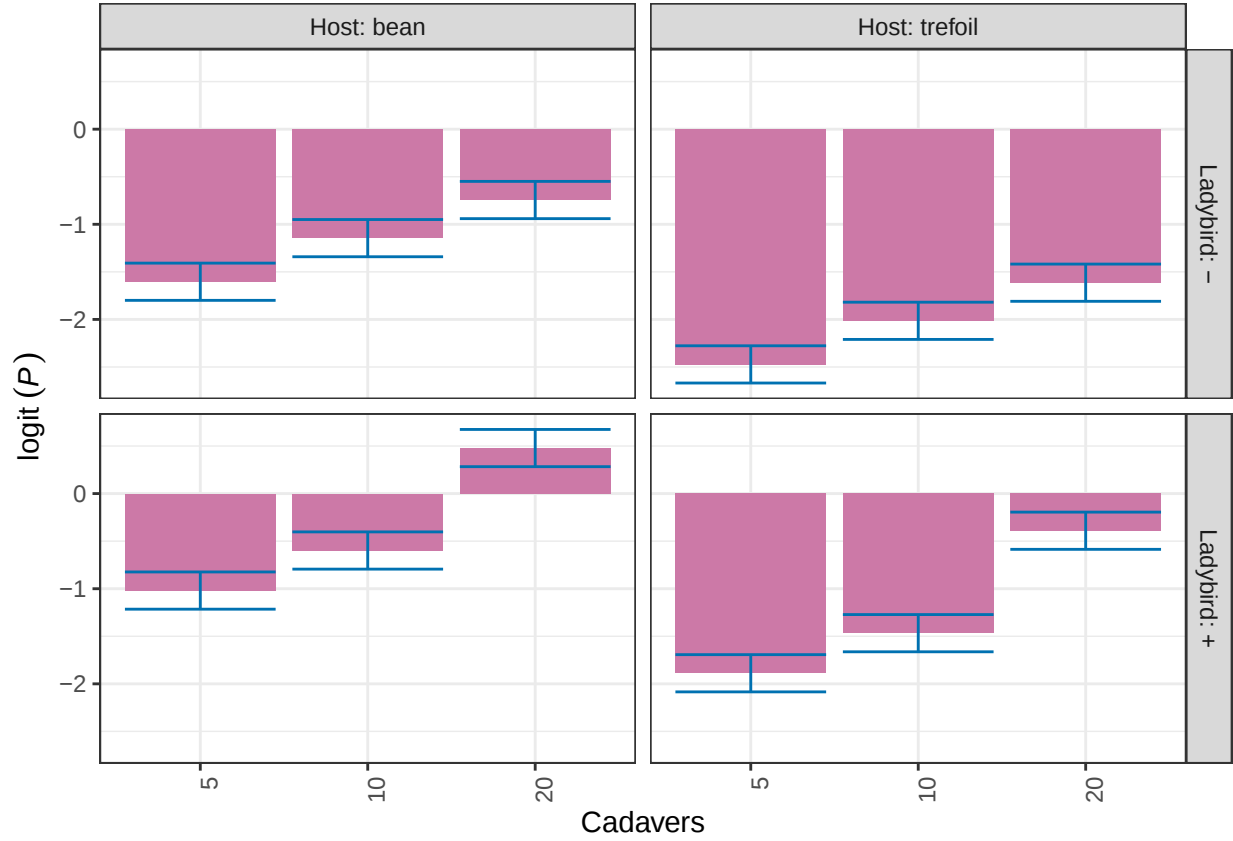


Figure 1. Estimated marginal means (EMMs) for $\text{logit}(P)$, where P is the proportion of live aphids that were infected, for two Hosts, two Ladybird levels and three Cadaver levels. Error bars are an EMM $\pm$ half-LSD (5%). The two EMMs for the same Host are significantly different ($p \leq 0.05$) if their error bars do not overlap.

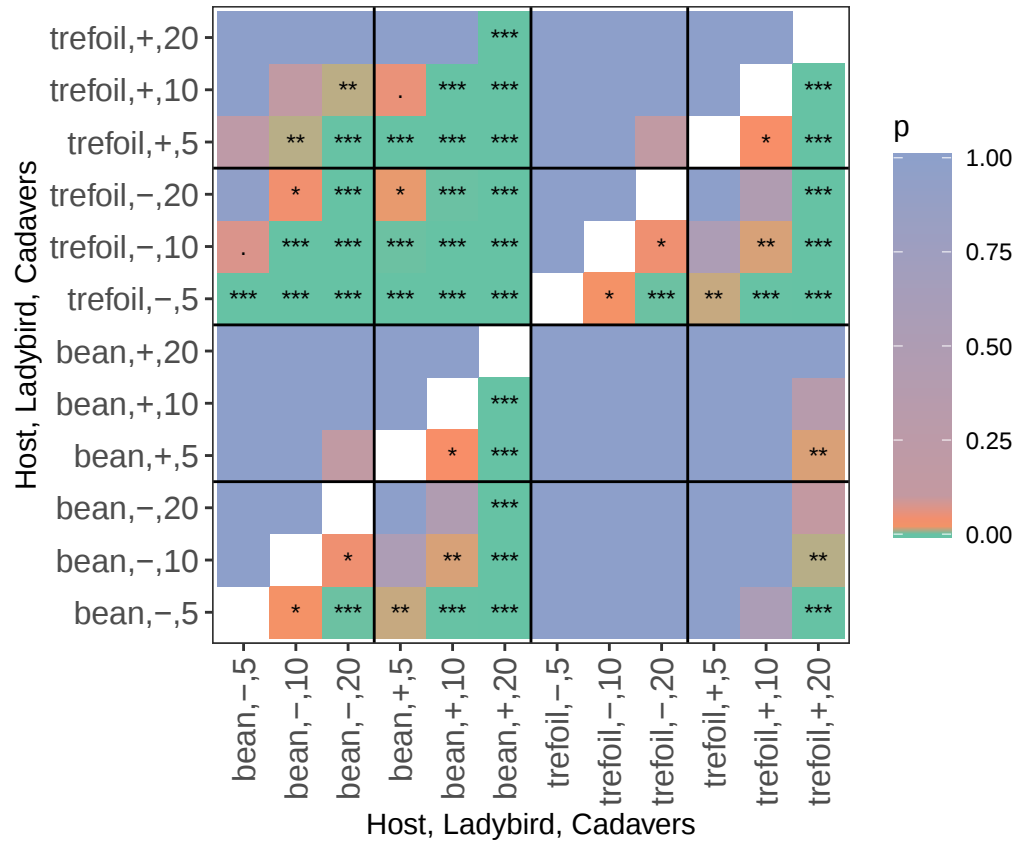


Figure 2. The p -values for each of the pairwise comparisons of the estimated marginal means for $\text{logit}(P)$, where P is the proportion of live aphids that were infected, for two Hosts, two Ladybird levels and three Cadaver levels

```
options(width = 90)
diffs$differences
```

	bean,-,5	bean,-,10	bean,-,20	bean,+,5	bean,+,10	bean,+,20	trefoil,-,5
bean,-,5	0.0000000	0.0000000	0.0000000	0.0000000	0.0000000	0	0.8692001
bean,-,10	0.4584030	0.0000000	0.0000000	0.0000000	0.0000000	0	1.3276031
bean,-,20	0.8590241	0.4006211	0.0000000	0.2747378	0.0000000	0	1.7282242
bean,+,5	0.5842863	0.1258833	0.0000000	0.0000000	0.0000000	0	1.4534864
bean,+,10	1.0054898	0.5470869	0.1464657	0.4212036	0.0000000	0	1.8746899
bean,+,20	2.0825042	1.6241012	1.2234801	1.4982179	1.0770144	0	2.9517043
trefoil,-,5	0.0000000	0.0000000	0.0000000	0.0000000	0.0000000	0	0.0000000
trefoil,-,10	0.0000000	0.0000000	0.0000000	0.0000000	0.0000000	0	0.4584030
trefoil,-,20	0.0000000	0.0000000	0.0000000	0.0000000	0.0000000	0	0.8590241
trefoil,+,5	0.0000000	0.0000000	0.0000000	0.0000000	0.0000000	0	0.5842863
trefoil,+,10	0.1362897	0.0000000	0.0000000	0.0000000	0.0000000	0	1.0054898
trefoil,+,20	1.2133041	0.7549011	0.3542800	0.6290178	0.2078143	0	2.0825042
	trefoil,-,10	trefoil,-,20	trefoil,+,5	trefoil,+,10	trefoil,+,20		
bean,-,5	0.4107972	0.01017604	0.2849139	0.0000000	0.0000000		
bean,-,10	0.8692001	0.46857901	0.7433168	0.3221133	0.0000000		
bean,-,20	1.2698212	0.86920012	1.1439379	0.7227344	0.0000000		
bean,+,5	0.9950834	0.59446231	0.8692001	0.4479966	0.0000000		
bean,+,10	1.4162870	1.01566586	1.2904037	0.8692001	0.0000000		
bean,+,20	2.4933014	2.09268024	2.3674180	1.9462145	0.8692001		
trefoil,-,5	0.0000000	0.00000000	0.0000000	0.0000000	0.0000000		
trefoil,-,10	0.0000000	0.00000000	0.0000000	0.0000000	0.0000000		
trefoil,-,20	0.4006211	0.00000000	0.2747378	0.0000000	0.0000000		
trefoil,+,5	0.1258833	0.00000000	0.0000000	0.0000000	0.0000000		
trefoil,+,10	0.5470869	0.14646574	0.4212036	0.0000000	0.0000000		
trefoil,+,20	1.6241012	1.22348012	1.4982179	1.0770144	0.0000000		

```
options(width = 90)
print(diffs$sed)
```

	bean,-,5	bean,-,10	bean,-,20	bean,+,5	bean,+,10	bean,+,20	trefoil,-,5
bean,-,5	NA	0.1945600	0.1945600	0.1945600	0.1945600	0.1945600	0.1123293
bean,-,10	0.1945600	NA	0.1945600	0.1945600	0.1945600	0.1945600	0.2246586
bean,-,20	0.1945600	0.1945600	NA	0.1945600	0.1945600	0.1945600	0.2246586
bean,+,5	0.1945600	0.1945600	0.1945600	NA	0.1945600	0.1945600	0.2246586
bean,+,10	0.1945600	0.1945600	0.1945600	0.1945600	NA	0.1945600	0.2246586
bean,+,20	0.1945600	0.1945600	0.1945600	0.1945600	0.1945600	NA	0.2246586
trefoil,-,5	0.1123293	0.2246586	0.2246586	0.2246586	0.2246586	0.2246586	NA
trefoil,-,10	0.2246586	0.1123293	0.2246586	0.2246586	0.2246586	0.2246586	0.1945600
trefoil,-,20	0.2246586	0.2246586	0.1123293	0.2246586	0.2246586	0.2246586	0.1945600
trefoil,+,5	0.2246586	0.2246586	0.2246586	0.1123293	0.2246586	0.2246586	0.1945600
trefoil,+,10	0.2246586	0.2246586	0.2246586	0.2246586	0.1123293	0.2246586	0.1945600
trefoil,+,20	0.2246586	0.2246586	0.2246586	0.2246586	0.2246586	0.1123293	0.1945600
	trefoil,-,10	trefoil,-,20	trefoil,+,5	trefoil,+,10	trefoil,+,20		
bean,-,5	0.2246586	0.2246586	0.2246586	0.2246586	0.2246586		
bean,-,10	0.1123293	0.2246586	0.2246586	0.2246586	0.2246586		
bean,-,20	0.2246586	0.1123293	0.2246586	0.2246586	0.2246586		
bean,+,5	0.2246586	0.2246586	0.1123293	0.2246586	0.2246586		
bean,+,10	0.2246586	0.2246586	0.2246586	0.1123293	0.2246586		
bean,+,20	0.2246586	0.2246586	0.2246586	0.2246586	0.1123293		
trefoil,-,5	0.1945600	0.1945600	0.1945600	0.1945600	0.1945600		
trefoil,-,10	NA	0.1945600	0.1945600	0.1945600	0.1945600		
trefoil,-,20	0.1945600	NA	0.1945600	0.1945600	0.1945600		
trefoil,+,5	0.1945600	0.1945600	NA	0.1945600	0.1945600		
trefoil,+,10	0.1945600	0.1945600	0.1945600	NA	0.1945600		
trefoil,+,20	0.1945600	0.1945600	0.1945600	0.1945600	NA		

Perform the analysis with just the selected model fitted

The model with nonsignificant fixed terms dropped is obtained in order to compare it with the fit when they are retained and the estimated marginal means for the chosen model are obtained.

```
m.sig.lm <- lm(logitP ~ Run + Cadavers*Ladybird + Host,
               data=Ladybird.dat)
(aov.tab <- anova(m.sig.lm))
```

Analysis of Variance Table

Response: logitP

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Run	1	0.0677	0.0677	0.3029	0.58398
Cadavers	2	17.0274	8.5137	38.1160	1.255e-11
Ladybird	1	11.0907	11.0907	49.6531	1.542e-09
Host	1	13.5992	13.5992	60.8836	7.179e-11
Cadavers:Ladybird	2	1.7349	0.8675	3.8836	0.02559
Residuals	64	14.2952	0.2234		

```
HCL.emm <- emmeans::emmeans(m.sig.lm, specs = ~ Host:Cadavers:Ladybird)
HCL.preds <- summary(HCL.emm)
den.df <- min(HCL.preds$df)
HCL.vcov <- vcov(HCL.emm)
HCL.preds <- as.predictions.frame(HCL.preds, predictions = "emmean",
                                  se = "SE", interval.type = "CI",
                                  interval.names = c("lower.CL", "upper.CL"))
diffs.red <- allDifferences(predictions = HCL.preds, classify = "Host:Ladybird:Cadavers",
                             vcov = HCL.vcov, tdf = den.df)
diffs.red <- redoErrorIntervals(diffs, error.intervals = "halfLeast",
                                LSDtype = "factor.combination", LSDby = "Host")
```

Joining with 'by = join_by(fac.comb)'

Joining with 'by = join_by(Host)'

```
options(width = 90)
print(diffs.red$sed)
```

	bean,-,5	bean,-,10	bean,-,20	bean,+,5	bean,+,10	bean,+,20	trefoil,-,5
bean,-,5	NA	0.1945600	0.1945600	0.1945600	0.1945600	0.1945600	0.1123293
bean,-,10	0.1945600	NA	0.1945600	0.1945600	0.1945600	0.1945600	0.2246586
bean,-,20	0.1945600	0.1945600	NA	0.1945600	0.1945600	0.1945600	0.2246586
bean,+,5	0.1945600	0.1945600	0.1945600	NA	0.1945600	0.1945600	0.2246586
bean,+,10	0.1945600	0.1945600	0.1945600	0.1945600	NA	0.1945600	0.2246586
bean,+,20	0.1945600	0.1945600	0.1945600	0.1945600	0.1945600	NA	0.2246586
trefoil,-,5	0.1123293	0.2246586	0.2246586	0.2246586	0.2246586	0.2246586	NA
trefoil,-,10	0.2246586	0.1123293	0.2246586	0.2246586	0.2246586	0.2246586	0.1945600
trefoil,-,20	0.2246586	0.2246586	0.1123293	0.2246586	0.2246586	0.2246586	0.1945600
trefoil,+,5	0.2246586	0.2246586	0.2246586	0.1123293	0.2246586	0.2246586	0.1945600
trefoil,+,10	0.2246586	0.2246586	0.2246586	0.2246586	0.1123293	0.2246586	0.1945600
trefoil,+,20	0.2246586	0.2246586	0.2246586	0.2246586	0.2246586	0.1123293	0.1945600
	trefoil,-,10	trefoil,-,20	trefoil,+,5	trefoil,+,10	trefoil,+,20		

bean,-,5	0.2246586	0.2246586	0.2246586	0.2246586	0.2246586
bean,-,10	0.1123293	0.2246586	0.2246586	0.2246586	0.2246586
bean,-,20	0.2246586	0.1123293	0.2246586	0.2246586	0.2246586
bean,+,5	0.2246586	0.2246586	0.1123293	0.2246586	0.2246586
bean,+,10	0.2246586	0.2246586	0.2246586	0.1123293	0.2246586
bean,+,20	0.2246586	0.2246586	0.2246586	0.2246586	0.1123293
trefoil,-,5	0.1945600	0.1945600	0.1945600	0.1945600	0.1945600
trefoil,-,10	NA	0.1945600	0.1945600	0.1945600	0.1945600
trefoil,-,20	0.1945600	NA	0.1945600	0.1945600	0.1945600
trefoil,+,5	0.1945600	0.1945600	NA	0.1945600	0.1945600
trefoil,+,10	0.1945600	0.1945600	0.1945600	NA	0.1945600
trefoil,+,20	0.1945600	0.1945600	0.1945600	0.1945600	NA

References

- Brien, C. J. (2026a) **asremlPlus**: *Augments ASReml-R in fitting mixed models and packages generally in exploring prediction differences*. Version 4.4.65. <https://cran.r-project.org/package=asremlPlus/> or <http://chris.brien.name/rpackages/>.
- Brien, C. J. (2026b) **dae**: *Functions useful in the design and ANOVA of experiments*. Version 3.2.35. <https://cran.r-project.org/package=dae/> or <http://chris.brien.name/rpackages/>.
- Kuznetsova, A., Brockhoff, P. B. and Christensen, R. H. B. (2017) **lmerTest Package**: Tests in Linear Mixed Effects Models. *Journal of Statistical Software*, **82**, 1–26.
- Lenth, R. V., Banfa, B., Bolker, B., Buerkner, P., Giné-Vázquez, I., Herve, M. J., Jung, M., Love, J., Miguez, F., Piaskowski, J., Riebl, H., & Singmann, H. (2025) **emmeans**: *Estimated Marginal Means, aka Least-Squares Means*. Version 1.11.0. <https://cran.r-project.org/package=emmeans/>.
- Littell, R. C., Milliken, G. A., Stroup, W. W., Wolfinger, R. D., & Schabenberger, O. (2006). *SAS for Mixed Model.* (2nd ed.). Cary, N.C.: SAS Press.
- R Core Team (2026) **R**: *A language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing. <https://www.r-project.org>.
- Snee, R. D. (1981). Graphical Display and Assessment of Means. *Biometrics*, **37**, 835–836.
- Welham, S. J., Gezan, S. A., Clark, S. J., & Mead, A. (2014). *Statistical Methods in Biology: Design and Analysis of Experiments and Regression*. Boca Raton: Chapman and Hall/CRC.