

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

Chris Brien

26 October, 2023

## Introduction

This vignette shows how to use `asremlPlus` (Brien, 2023a), and `dae` (Brien, 2023b), for exploring and presenting predictions from a linear mixed model analysis, the predictions having been produced using `lmerTest` (Kuznetsova et al., 2017), `lm` and `emmeans` (Lenth, 2023). Here, `asremlPlus`, `dae`, `lmerTest` and `emmeans` are packages for the R Statistical Computing environment (R Core Team, 2023) 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 (-, +). Ther 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] '3.1.3'

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

## [1] '1.8.8'

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

## [1] '4.4.17'

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

## [1] '3.2.19'

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, 2023b) 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             | 0                 |
| Cadavers               | 0    | 1        |               | 1        | 0             | 1                 |
| Host:Cadavers          | 0    | 0        | 1             | 0        | 0             | 0                 |
| Ladybird               | 0    | 0        |               | 0        | 1             | 1                 |
| Host:Ladybird          | 0    | 0        |               | 0        | 0             | 1                 |
| Cadavers:Ladybird      | 0    | 0        |               | 0        | 0             | 0                 |
| Host:Cadavers:Ladybird | 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 (emm) 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

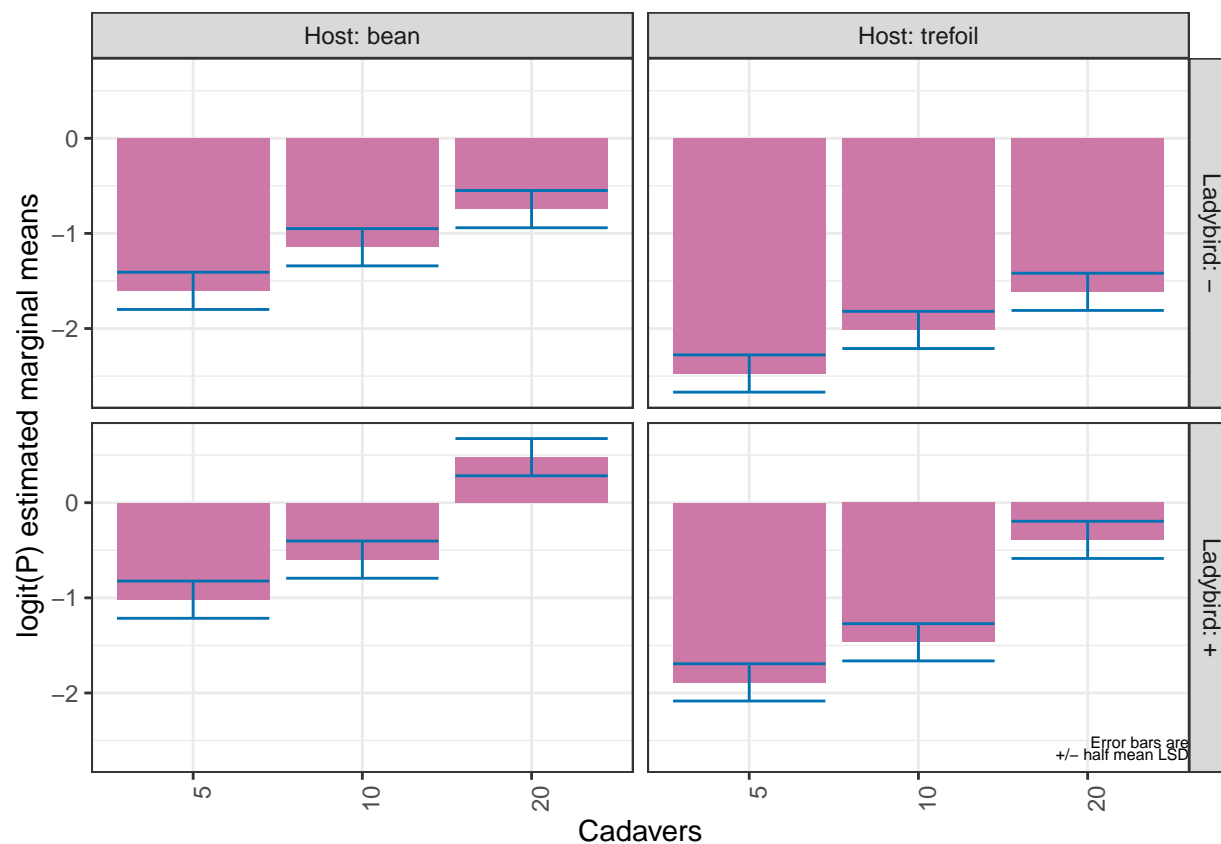
maximum LSD = 0.3913605 0.3913605

(sed range / mean sed = 3.49e-14 3.45e-14 )

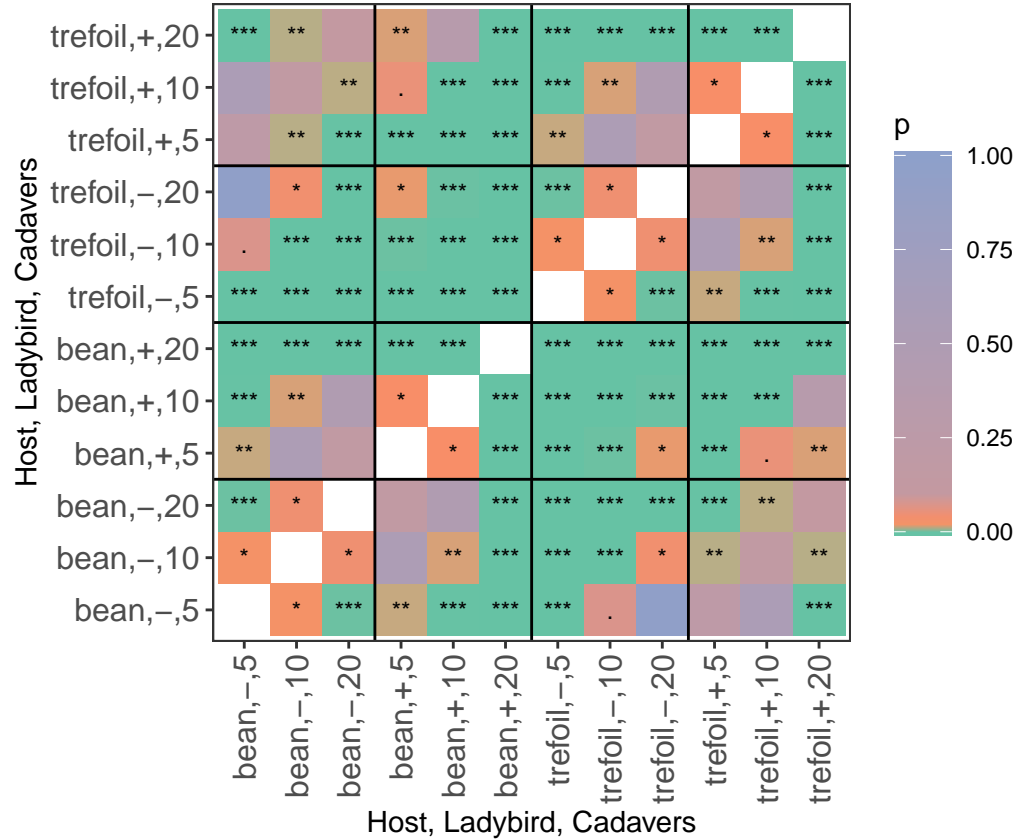
## Plot the predictions

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 error bars in the plots are of  $\pm 0.5LSD$  so that pairs of prediction with nonoverlapping bars are significantly different (Snee, 1981).

```
plotPredictions(diffs$predictions, y = "predicted.value",
  y.title = "logit(P) estimated marginal means",
  classify = "Host:Ladybird:Cadavers",
  error.intervals = "halfLeast",
  ggplotFuncs = list(facet_grid(Ladybird ~ Host,
    labeller = label_both)))
```



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



```
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. (2023a) **asremlPlus**: *Augments ASReml-R in fitting mixed models and packages generally in exploring prediction differences*. Version 4.4.17. <https://cran.r-project.org/package=asremlPlus/> or <http://chris.brien.name/rpackages/>.
- Brien, C. J. (2023b) **dae**: *Functions useful in the design and ANOVA of experiments*. Version 3.2-19. <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., Buerkner, P., Herve, M. J., Jung, M., Love, J., Miguez, F., Riebl, H., & Singmann, H. (2023) **emmeans**: *Estimated Marginal Means, aka Least-Squares Means*. Version 1.8.8. <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 (2023) **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.