

Using asreml and asremlPlus for the Ladybird example from Welham et al. (2014)

Chris Brien

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Introduction

This vignette shows how to use `asremlPlus` (Brien, 2020a), and `dae` (Brien, 2020b), for exploring and presenting predictions from a linear mixed model analysis, the predictions having been produced using `asreml` (Butler et al., 2018). Here, `asremlPlus`, `dae` and `asreml` are packages for the R Statistical Computing environment (R Core Team, 2020).

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(asreml))
packageVersion("asreml")

## [1] '4.1.0.122'

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

## [1] '4.2.17'

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

## [1] '3.1.23'

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 asreml to analyse the logits

Mixed model analysis of logits

```
m <- asreml(logitP ~ Host*Cadavers*Ladybird,
            random = ~ Run,
            residual = ~ Run:Plant,
            data = Ladybird.dat)
```

Model fitted using the gamma parameterization.

ASReml 4.1.0 Mon Mar 16 09:24:18 2020

| | LogLik | Sigma2 | DF | wall | cpu |
|---|---------|----------|----|----------|--------------------|
| 1 | 3.07130 | 0.226239 | 60 | 09:24:18 | 0.0 (1 restrained) |
| 2 | 3.64260 | 0.226912 | 60 | 09:24:18 | 0.0 (1 restrained) |
| 3 | 3.71250 | 0.227106 | 60 | 09:24:18 | 0.0 (1 restrained) |
| 4 | 3.71721 | 0.227121 | 60 | 09:24:18 | 0.0 (1 restrained) |
| 5 | 3.71751 | 0.227122 | 60 | 09:24:18 | 0.0 (1 restrained) |

Warning in asreml(logitP ~ Host * Cadavers * Ladybird, random = ~Run, residual = ~Run:Plant, :
Some components changed by more than 1% on the last iteration.

```
summary(m)$varcomp
```

| | component | std.error | z.ratio | bound | %ch |
|-------------|--------------|------------|----------|-------|------|
| Run | 2.298309e-08 | NA | NA | B | 93.7 |
| Run:Plant!R | 2.271216e-01 | 0.04156985 | 5.463612 | P | 0.0 |

As expected the Run component is bound (B) at approximately zero. This results in a change in the estimate of the residual variance to 0.227. To allow for a negative estimate we will unconstrain the Run component.

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.

Unconstrain Reps to make the analysis equivalent to ANOVA

```
m <- setvarianceterms(m$call, terms = "Run", bounds = "U")
```

Model fitted using the gamma parameterization.

ASReml 4.1.0 Mon Mar 16 09:24:18 2020

| | LogLik | Sigma2 | DF | wall | cpu |
|---|---------|----------|----|----------|--------------------|
| 1 | 3.07130 | 0.226239 | 60 | 09:24:18 | 0.0 (1 restrained) |
| 2 | 3.64260 | 0.226912 | 60 | 09:24:18 | 0.0 (1 restrained) |
| 3 | 3.80283 | 0.227454 | 60 | 09:24:18 | 0.0 (1 restrained) |
| 4 | 3.83949 | 0.233418 | 60 | 09:24:18 | 0.0 |
| 5 | 3.95568 | 0.230971 | 60 | 09:24:18 | 0.0 |
| 6 | 3.97333 | 0.230035 | 60 | 09:24:18 | 0.0 |
| 7 | 3.97405 | 0.229835 | 60 | 09:24:18 | 0.0 |

```
summary(m)$varcomp
```

| | component | std.error | z.ratio | bound | %ch |
|-------------|--------------|-------------|-----------|-------|-----|
| Run | -0.004504789 | 0.002896281 | -1.555370 | U | 0.1 |
| Run:Plant!R | 0.229834648 | 0.042316936 | 5.431269 | P | 0.0 |

Now the Run component is negative and the Run:Plant variance estimate is now equal to that for the Residuals Mean Sq for Run:Plant from the anova table.

Set up an asrtests object

```
current.asrt <- as.asrtests(m)
```

Calculating denominator DF

```
print(current.asrt, which = "pseudoanova")
```

Pseudo-anova table for fixed terms

Wald tests for fixed effects.

Response: logitP

| | Df | denDF | F.inc | Pr |
|------------------------|----|-------|---------|--------|
| (Intercept) | 1 | 1 | 1550.00 | 0.0162 |
| Host | 1 | 59 | 59.17 | 0.0000 |
| Cadavers | 2 | 59 | 37.04 | 0.0000 |
| Ladybird | 1 | 59 | 48.26 | 0.0000 |
| Host:Cadavers | 2 | 59 | 0.67 | 0.5158 |
| Host:Ladybird | 1 | 59 | 0.99 | 0.3234 |
| Cadavers:Ladybird | 2 | 59 | 3.77 | 0.0287 |
| Host:Cadavers:Ladybird | 2 | 59 | 0.44 | 0.6493 |

The `asrtests` object contains a `wald.tab` component which can be printed by specifying that the `pseudoanova` is printed. The F -values for the fixed terms in this table are the same as those in the anova table.

Obtain the marginality matrix for the fixed terms

The `pstructure` function from the `dae` package (Brien, 2020) 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)
print(HCL.marg)
```

| | 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(current.asrt, terms.marginality = HCL.marg)
```

```
Calculating denominator DF
Calculating denominator DF
Calculating denominator DF
Calculating denominator DF
Calculating denominator DF
```

```
current.asrt <- chosen$asrtests.obj
print(current.asrt, which = "test", omit.columns = c("AIC", "BIC"))
```

```
#### 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 `asrtests.obj`, the `asrtests` object resulting from the model selection. In particular, the `asrtests` object contains a `test.summary` that details the tests performed in choosing the model; the AIC and BIC columns are omitted from `test.summary` because their inclusion has not been requested. 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
```

Obtain predictions under the chosen model and form an `alldiffs` object

```
diffs <- predictPlus(current.asrt$asreml.obj,  
                     classify = "Host:Ladybird:Cadavers",  
                     linear.transformation = ~Cadavers:Ladybird + Host,  
                     wald.tab = current.asrt$wald.tab,  
                     error.intervals = "halfLeast",  
                     meanLSD.type = "factor.combination", LSDby = "Host",  
                     tables = "predictions")
```

```
#### Predictions for logitP transform(s) from Host:Ladybird:Cadavers
```

Notes:

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

- The predictions are obtained by averaging across the `hypertable` calculated from model terms constructed solely from factors in the averaging and `classify` sets.
- Use 'average' to move ignored factors into the averaging set.
- The ignored set: Run

| | Host | Ladybird | Cadavers | predicted.value | standard.error | upper.halfLeastSignificant.limit |
|---|---------|----------|----------|-----------------|----------------|----------------------------------|
| 1 | bean | - | 5 | -1.6038338 | 0.1417454 | -1.4080222 |
| 2 | bean | - | 10 | -1.1454308 | 0.1417454 | -0.9496192 |
| 3 | bean | - | 20 | -0.7448097 | 0.1417454 | -0.5489981 |
| 4 | bean | + | 5 | -1.0195475 | 0.1417454 | -0.8237359 |
| 5 | bean | + | 10 | -0.5983440 | 0.1417454 | -0.4025323 |
| 6 | bean | + | 20 | 0.4786704 | 0.1417454 | 0.6744820 |
| 7 | trefoil | - | 5 | -2.4730339 | 0.1417454 | -2.2772223 |

| | | | | | | |
|----|---------|---|----|------------|-----------|------------|
| 8 | trefoil | - | 10 | -2.0146309 | 0.1417454 | -1.8188193 |
| 9 | trefoil | - | 20 | -1.6140098 | 0.1417454 | -1.4181982 |
| 10 | trefoil | + | 5 | -1.8887476 | 0.1417454 | -1.6929360 |
| 11 | trefoil | + | 10 | -1.4675441 | 0.1417454 | -1.2717325 |
| 12 | trefoil | + | 20 | -0.3905297 | 0.1417454 | -0.1947181 |

| | lower.halfLeastSignificant.limit | est.status |
|----|----------------------------------|------------|
| 1 | -1.7996454 | Estimable |
| 2 | -1.3412425 | Estimable |
| 3 | -0.9406214 | Estimable |
| 4 | -1.2153592 | Estimable |
| 5 | -0.7941556 | Estimable |
| 6 | 0.2828588 | Estimable |
| 7 | -2.6688455 | Estimable |
| 8 | -2.2104426 | Estimable |
| 9 | -1.8098215 | Estimable |
| 10 | -2.0845593 | Estimable |
| 11 | -1.6633557 | Estimable |
| 12 | -0.5863414 | Estimable |

LSD values

minimum LSD = 0.3916233 0.3916233

mean LSD = 0.3916233 0.3916233

maximum LSD = 0.3916233 0.3916233

(sed range / mean sed = 7.09e-16 5.67e-16)

Setting the `terms` argument to `Host:Ladybird:Cadavers` requests predictions for all combinations of the three factors and the `linear.transformation` argument is used to obtain estimated marginal means (emm) that conform to the chosen model. The `wald.tab` is supplied so that it can be used to get the degrees of freedom for the *t*-value to be used in calculating the LSD; the degrees of freedom of the source for the `terms` argument will be used. The `error.intervals` argument has been set to `"halfLeast"`, the `meanLSD.type` 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` being added to the `predictions` component of the `alldiffs` object.

Or, calculate predictions to check first and then transform to conform to chosen model

```
diffs.full <- predictPlus(current.asrt$asreml.obj,
  classify = "Host:Ladybird:Cadavers",
  wald.tab = current.asrt$wald.tab,
  tables = "none", Vmatrix = TRUE)

diffs <- linTransform(diffs.full, linear.transformation = ~Cadavers:Ladybird + Host,
  wald.tab = current.asrt$wald.tab,
  error.intervals = "halfLeast",
  meanLSD.type = "factor.combination", LSDby = "Host",
  tables = "predictions")
```

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

Notes:

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

- The predictions are obtained by averaging across the hypertable calculated from model terms constructed solely from factors in the averaging and classify sets.
- Use 'average' to move ignored factors into the averaging set.
- The ignored set: Run

| | Host | Ladybird | Cadavers | predicted.value | standard.error | upper.halfLeastSignificant.limit |
|----|---------|----------|----------|----------------------------------|----------------|----------------------------------|
| 1 | bean | - | 5 | -1.6038338 | 0.1417454 | -1.4080222 |
| 2 | bean | - | 10 | -1.1454308 | 0.1417454 | -0.9496192 |
| 3 | bean | - | 20 | -0.7448097 | 0.1417454 | -0.5489981 |
| 4 | bean | + | 5 | -1.0195475 | 0.1417454 | -0.8237359 |
| 5 | bean | + | 10 | -0.5983440 | 0.1417454 | -0.4025323 |
| 6 | bean | + | 20 | 0.4786704 | 0.1417454 | 0.6744820 |
| 7 | trefoil | - | 5 | -2.4730339 | 0.1417454 | -2.2772223 |
| 8 | trefoil | - | 10 | -2.0146309 | 0.1417454 | -1.8188193 |
| 9 | trefoil | - | 20 | -1.6140098 | 0.1417454 | -1.4181982 |
| 10 | trefoil | + | 5 | -1.8887476 | 0.1417454 | -1.6929360 |
| 11 | trefoil | + | 10 | -1.4675441 | 0.1417454 | -1.2717325 |
| 12 | trefoil | + | 20 | -0.3905297 | 0.1417454 | -0.1947181 |
| | | | | lower.halfLeastSignificant.limit | est.status | |
| 1 | | | | -1.7996454 | Estimable | |
| 2 | | | | -1.3412425 | Estimable | |
| 3 | | | | -0.9406214 | Estimable | |
| 4 | | | | -1.2153592 | Estimable | |
| 5 | | | | -0.7941556 | Estimable | |
| 6 | | | | 0.2828588 | Estimable | |
| 7 | | | | -2.6688455 | Estimable | |
| 8 | | | | -2.2104426 | Estimable | |
| 9 | | | | -1.8098215 | Estimable | |
| 10 | | | | -2.0845593 | Estimable | |
| 11 | | | | -1.6633557 | Estimable | |
| 12 | | | | -0.5863414 | Estimable | |

LSD values

minimum LSD = 0.3916233 0.3916233

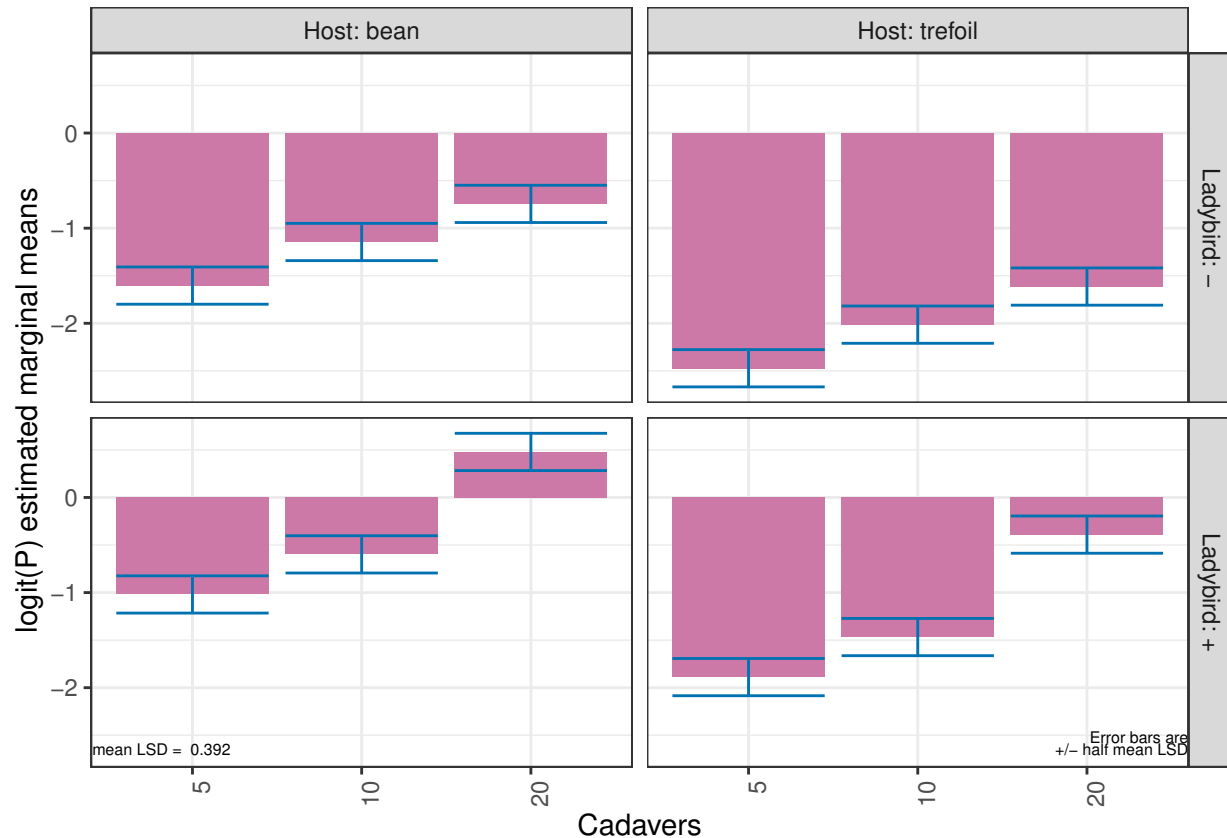
mean LSD = 0.3916233 0.3916233

maximum LSD = 0.3916233 0.3916233

(sed range / mean sed = 7.09e-16 5.67e-16)

Plot the predictions

```
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)))
```



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

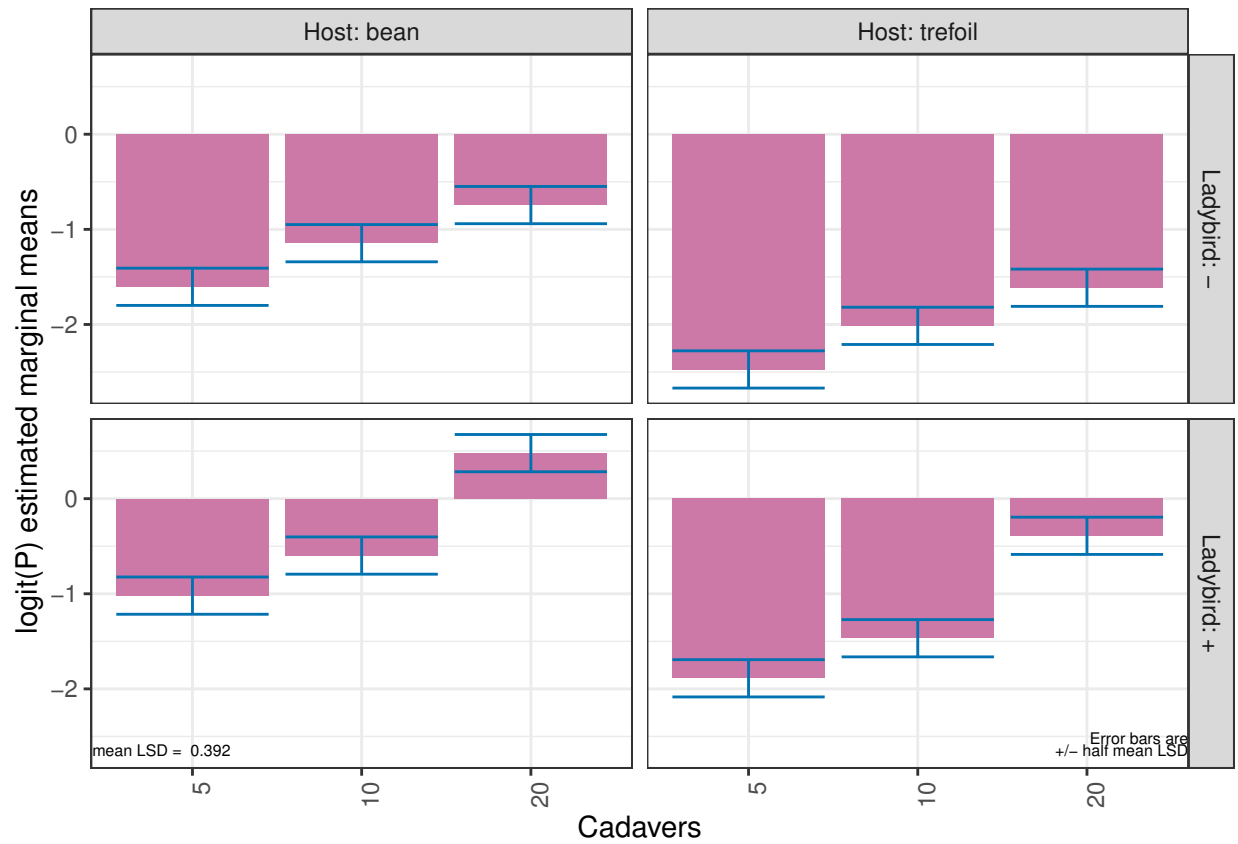
Get and plot the predictions with a single function call

The `predictPresent` function combines the functionality of `predictPlus` and `plotPredictions`, as demonstrated now. Also, the use of `plotPvalues` to plot the pairwise p -values is displayed. The `predictPresent` function has the capability of producing `alldiffs` objects for multiple `terms` and these are stored in a list each of which is named for the term whose `alldiffs` object it stores. Thus, the term has to be specified in referencing components of `diffs`.

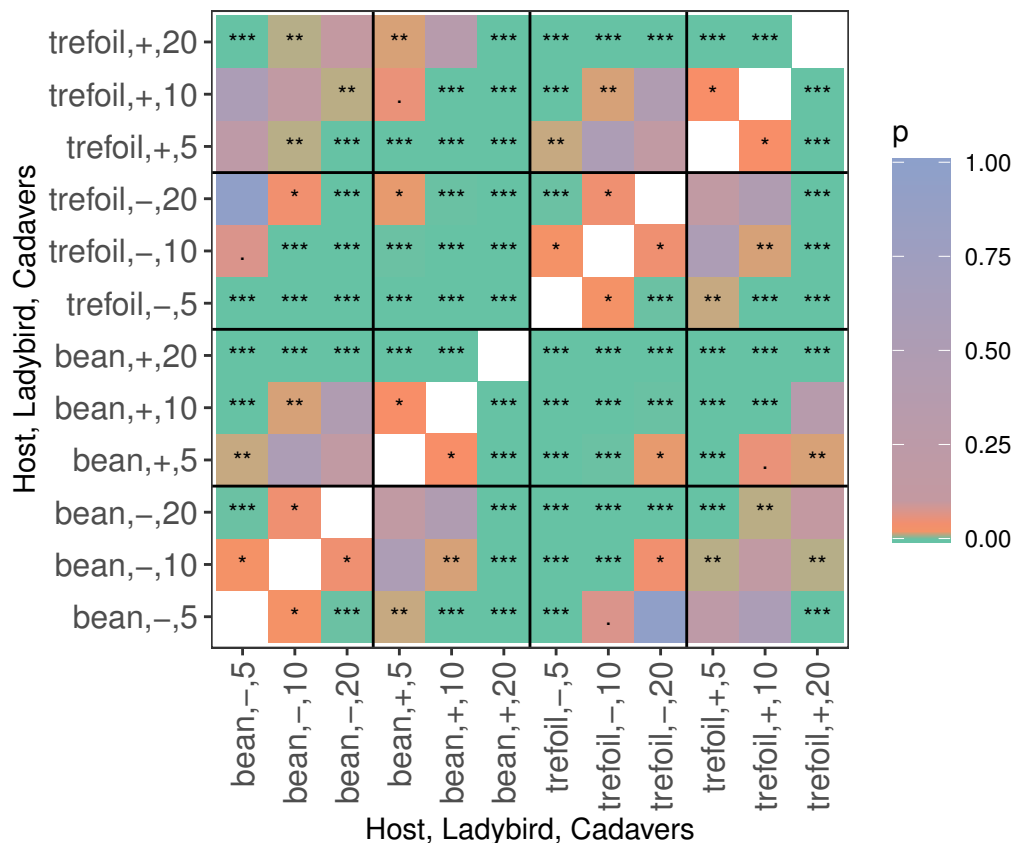
```
titl <- "logit(P) estimated marginal means"
names(titl) <- "logitP"
diffs <- predictPresent(current.asrt$asreml.obj,
  terms = "Host:Ladybird:Cadavers",
```



```
linear.transformation = ~Cadavers:Ladybird + Host,
titles = titl,
wald.tab = current.asrt$wald.tab,
error.intervals = "halfLeast",
meanLSD.type = "factor.combination", LSDby = "Host",
tables = "none",
ggplotFuncs = list(facet_grid(Ladybird ~ Host,
                             labeller = label_both)))
```



```
plotPvalues(diffs$Host.Ladybird.Cadavers, factors.per.grid = 1, show.sig = TRUE)
```



```
options(width = 90)
```

```
diffs$Host.Ladybird.Cadavers$differences
```

| | bean,-,5 | bean,-,10 | bean,-,20 | bean,+,5 | bean,+,10 | bean,+,20 |
|--------------|-------------|------------|-------------|------------|------------|------------|
| bean,-,5 | 0.0000000 | -0.4584030 | -0.8590241 | -0.5842863 | -1.0054898 | -2.0825042 |
| bean,-,10 | 0.45840297 | 0.0000000 | -0.4006211 | -0.1258833 | -0.5470869 | -1.6241012 |
| bean,-,20 | 0.85902408 | 0.4006211 | 0.0000000 | 0.2747378 | -0.1464657 | -1.2234801 |
| bean,+,5 | 0.58428627 | 0.1258833 | -0.2747378 | 0.0000000 | -0.4212036 | -1.4982179 |
| bean,+,10 | 1.00548982 | 0.5470869 | 0.1464657 | 0.4212036 | 0.0000000 | -1.0770144 |
| bean,+,20 | 2.08250420 | 1.6241012 | 1.2234801 | 1.4982179 | 1.0770144 | 0.0000000 |
| trefoil,-,5 | -0.86920012 | -1.3276031 | -1.7282242 | -1.4534864 | -1.8746899 | -2.9517043 |
| trefoil,-,10 | -0.41079715 | -0.8692001 | -1.2698212 | -0.9950834 | -1.4162870 | -2.4933014 |
| trefoil,-,20 | -0.01017604 | -0.4685790 | -0.8692001 | -0.5944623 | -1.0156659 | -2.0926802 |
| trefoil,+,5 | -0.28491385 | -0.7433168 | -1.1439379 | -0.8692001 | -1.2904037 | -2.3674180 |
| trefoil,+,10 | 0.13628970 | -0.3221133 | -0.7227344 | -0.4479966 | -0.8692001 | -1.9462145 |
| trefoil,+,20 | 1.21330408 | 0.7549011 | 0.3542800 | 0.6290178 | 0.2078143 | -0.8692001 |
| trefoil,-,5 | 0.8692001 | 0.4107972 | 0.01017604 | 0.2849139 | -0.1362897 | -1.2133041 |
| trefoil,-,10 | 1.3276031 | 0.8692001 | 0.46857901 | 0.7433168 | 0.3221133 | -0.7549011 |
| trefoil,-,20 | 1.7282242 | 1.2698212 | 0.86920012 | 1.1439379 | 0.7227344 | -0.3542800 |
| trefoil,+,5 | 1.4534864 | 0.9950834 | 0.59446231 | 0.8692001 | 0.4479966 | -0.6290178 |
| trefoil,+,10 | 1.8746899 | 1.4162870 | 1.01566586 | 1.2904037 | 0.8692001 | -0.2078143 |
| trefoil,+,20 | 2.9517043 | 2.4933014 | 2.09268024 | 2.3674180 | 1.9462145 | 0.8692001 |
| trefoil,-,5 | 0.0000000 | -0.4584030 | -0.85902408 | -0.5842863 | -1.0054898 | -2.0825042 |
| trefoil,-,10 | 0.4584030 | 0.0000000 | -0.40062111 | -0.1258833 | -0.5470869 | -1.6241012 |
| trefoil,-,20 | 0.8590241 | 0.4006211 | 0.00000000 | 0.2747378 | -0.1464657 | -1.2234801 |

```

trefoil,+,5    0.5842863    0.1258833   -0.27473781    0.0000000    -0.4212036    -1.4982179
trefoil,+,10   1.0054898    0.5470869    0.14646574    0.4212036    0.0000000    -1.0770144
trefoil,+,20   2.0825042    1.6241012    1.22348012    1.4982179    1.0770144    0.0000000

```

```

options(width = 90)
print(diffs$Host.Ladybird.Cadavers$sed)

```

```

      bean,-,5 bean,-,10 bean,-,20  bean,+,5 bean,+,10 bean,+,20 trefoil,-,5
bean,-,5      NA 0.1957142 0.1957142 0.1957142 0.1957142 0.1957142 0.1129957
bean,-,10    0.1957142      NA 0.1957142 0.1957142 0.1957142 0.1957142 0.2259913
bean,-,20    0.1957142 0.1957142      NA 0.1957142 0.1957142 0.1957142 0.2259913
bean,+,5     0.1957142 0.1957142 0.1957142      NA 0.1957142 0.1957142 0.2259913
bean,+,10    0.1957142 0.1957142 0.1957142 0.1957142      NA 0.1957142 0.2259913
bean,+,20    0.1957142 0.1957142 0.1957142 0.1957142 0.1957142      NA 0.2259913
trefoil,-,5  0.1129957 0.2259913 0.2259913 0.2259913 0.2259913 0.2259913      NA
trefoil,-,10 0.2259913 0.1129957 0.2259913 0.2259913 0.2259913 0.2259913 0.1957142
trefoil,-,20 0.2259913 0.2259913 0.1129957 0.2259913 0.2259913 0.2259913 0.1957142
trefoil,+,5  0.2259913 0.2259913 0.2259913 0.1129957 0.2259913 0.2259913 0.1957142
trefoil,+,10 0.2259913 0.2259913 0.2259913 0.2259913 0.1129957 0.2259913 0.1957142
trefoil,+,20 0.2259913 0.2259913 0.2259913 0.2259913 0.2259913 0.1129957 0.1957142
      trefoil,-,10 trefoil,-,20 trefoil,+,5 trefoil,+,10 trefoil,+,20
bean,-,5      0.2259913    0.2259913    0.2259913    0.2259913    0.2259913
bean,-,10     0.1129957    0.2259913    0.2259913    0.2259913    0.2259913
bean,-,20     0.2259913    0.1129957    0.2259913    0.2259913    0.2259913
bean,+,5      0.2259913    0.2259913    0.1129957    0.2259913    0.2259913
bean,+,10     0.2259913    0.2259913    0.2259913    0.1129957    0.2259913
bean,+,20     0.2259913    0.2259913    0.2259913    0.2259913    0.1129957
trefoil,-,5   0.1957142    0.1957142    0.1957142    0.1957142    0.1957142
trefoil,-,10      NA      0.1957142    0.1957142    0.1957142    0.1957142
trefoil,-,20   0.1957142      NA      0.1957142    0.1957142    0.1957142
trefoil,+,5   0.1957142    0.1957142      NA      0.1957142    0.1957142
trefoil,+,10   0.1957142    0.1957142    0.1957142      NA      0.1957142
trefoil,+,20   0.1957142    0.1957142    0.1957142    0.1957142      NA

```

Perform the analysis with just 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.

```

ns.terms <- current.asrt$test.summary$terms[current.asrt$test.summary$action == "Nonsignificant"]
red.asrt <- changeTerms(current.asrt, dropFixed = paste(ns.terms, collapse = "+"))

```

Calculating denominator DF

Calculating denominator DF

```
summary(red.asrt$asreml.obj)$varcomp
```

```

      component  std.error  z.ratio bound %ch
Run            -0.004327123 0.002802858 -1.543825    U 0.8
Run:Plant!R    0.223431515 0.039503521  5.655990    P 0.0

```

```
print(red.asrt, which = "pseudoanova")
```

```
#### Pseudo-anova table for fixed terms
```

Wald tests for fixed effects.

Response: logitP

| | Df | denDF | F.inc | Pr |
|-------------------|----|-------|---------|--------|
| (Intercept) | 1 | 1 | 1550.00 | 0.0162 |
| Host | 1 | 64 | 60.88 | 0.0000 |
| Cadavers | 2 | 64 | 38.12 | 0.0000 |
| Ladybird | 1 | 64 | 49.65 | 0.0000 |
| Cadavers:Ladybird | 2 | 64 | 3.88 | 0.0256 |

```
diffs.red <- predictPlus(red.asrt$asreml.obj,
  classify = "Host:Ladybird:Cadavers",
  wald.tab = current.asrt$wald.tab,
  error.intervals = "halfLeast",
  meanLSD.type = "factor.combination", LSDby = "Host",
  tables = "predictions")
```

Predictions for logitP from Host:Ladybird:Cadavers

Notes:

- The predictions are obtained by averaging across the hypertable calculated from model terms constructed solely from factors in the averaging and classify sets.
- Use 'average' to move ignored factors into the averaging set.
- The ignored set: Run

| | Host | Ladybird | Cadavers | predicted.value | standard.error |
|----|---------|----------|----------|-----------------|----------------|
| 1 | bean | - | 5 | -1.6038338 | 0.1398332 |
| 2 | bean | - | 10 | -1.1454308 | 0.1398332 |
| 3 | bean | - | 20 | -0.7448097 | 0.1398332 |
| 4 | bean | + | 5 | -1.0195475 | 0.1398332 |
| 5 | bean | + | 10 | -0.5983440 | 0.1398332 |
| 6 | bean | + | 20 | 0.4786704 | 0.1398332 |
| 7 | trefoil | - | 5 | -2.4730339 | 0.1398332 |
| 8 | trefoil | - | 10 | -2.0146309 | 0.1398332 |
| 9 | trefoil | - | 20 | -1.6140098 | 0.1398332 |
| 10 | trefoil | + | 5 | -1.8887476 | 0.1398332 |
| 11 | trefoil | + | 10 | -1.4675441 | 0.1398332 |
| 12 | trefoil | + | 20 | -0.3905297 | 0.1398332 |

| | upper.halfLeastSignificant.limit | lower.halfLeastSignificant.limit | est.status |
|----|----------------------------------|----------------------------------|------------|
| 1 | -1.4107942 | -1.7968734 | Estimable |
| 2 | -0.9523913 | -1.3384704 | Estimable |
| 3 | -0.5517702 | -0.9378493 | Estimable |
| 4 | -0.8265080 | -1.2125871 | Estimable |
| 5 | -0.4053044 | -0.7913835 | Estimable |
| 6 | 0.6717100 | 0.2856308 | Estimable |
| 7 | -2.2799944 | -2.6660735 | Estimable |
| 8 | -1.8215914 | -2.2076705 | Estimable |
| 9 | -1.4209703 | -1.8070494 | Estimable |
| 10 | -1.6957081 | -2.0817872 | Estimable |
| 11 | -1.2745045 | -1.6605837 | Estimable |

12

-0.1974902

-0.5835693 Estimable

LSD values

minimum LSD = 0.3860791 0.3860791

mean LSD = 0.3860791 0.3860791

maximum LSD = 0.3860791 0.3860791

(sed range / mean sed = 2.44e-15 2.3e-15)

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

| | bean,-,5 | bean,-,10 | bean,-,20 | bean,+,5 | bean,+,10 | bean,+,20 | trefoil,-,5 |
|--------------|--------------|--------------|-------------|--------------|--------------|-----------|-------------|
| bean,-,5 | NA | 0.1929435 | 0.1929435 | 0.1929435 | 0.1929435 | 0.1929435 | 0.1113960 |
| bean,-,10 | 0.1929435 | NA | 0.1929435 | 0.1929435 | 0.1929435 | 0.1929435 | 0.2227920 |
| bean,-,20 | 0.1929435 | 0.1929435 | NA | 0.1929435 | 0.1929435 | 0.1929435 | 0.2227920 |
| bean,+,5 | 0.1929435 | 0.1929435 | 0.1929435 | NA | 0.1929435 | 0.1929435 | 0.2227920 |
| bean,+,10 | 0.1929435 | 0.1929435 | 0.1929435 | 0.1929435 | NA | 0.1929435 | 0.2227920 |
| bean,+,20 | 0.1929435 | 0.1929435 | 0.1929435 | 0.1929435 | 0.1929435 | NA | 0.2227920 |
| trefoil,-,5 | 0.1113960 | 0.2227920 | 0.2227920 | 0.2227920 | 0.2227920 | 0.2227920 | NA |
| trefoil,-,10 | 0.2227920 | 0.1113960 | 0.2227920 | 0.2227920 | 0.2227920 | 0.2227920 | 0.1929435 |
| trefoil,-,20 | 0.2227920 | 0.2227920 | 0.1113960 | 0.2227920 | 0.2227920 | 0.2227920 | 0.1929435 |
| trefoil,+,5 | 0.2227920 | 0.2227920 | 0.2227920 | 0.1113960 | 0.2227920 | 0.2227920 | 0.1929435 |
| trefoil,+,10 | 0.2227920 | 0.2227920 | 0.2227920 | 0.2227920 | 0.1113960 | 0.2227920 | 0.1929435 |
| trefoil,+,20 | 0.2227920 | 0.2227920 | 0.2227920 | 0.2227920 | 0.2227920 | 0.1113960 | 0.1929435 |
| | trefoil,-,10 | trefoil,-,20 | trefoil,+,5 | trefoil,+,10 | trefoil,+,20 | | |
| bean,-,5 | 0.2227920 | 0.2227920 | 0.2227920 | 0.2227920 | 0.2227920 | | |
| bean,-,10 | 0.1113960 | 0.2227920 | 0.2227920 | 0.2227920 | 0.2227920 | | |
| bean,-,20 | 0.2227920 | 0.1113960 | 0.2227920 | 0.2227920 | 0.2227920 | | |
| bean,+,5 | 0.2227920 | 0.2227920 | 0.1113960 | 0.2227920 | 0.2227920 | | |
| bean,+,10 | 0.2227920 | 0.2227920 | 0.2227920 | 0.1113960 | 0.2227920 | | |
| bean,+,20 | 0.2227920 | 0.2227920 | 0.2227920 | 0.2227920 | 0.1113960 | | |
| trefoil,-,5 | 0.1929435 | 0.1929435 | 0.1929435 | 0.1929435 | 0.1929435 | | |
| trefoil,-,10 | NA | 0.1929435 | 0.1929435 | 0.1929435 | 0.1929435 | | |
| trefoil,-,20 | 0.1929435 | NA | 0.1929435 | 0.1929435 | 0.1929435 | | |
| trefoil,+,5 | 0.1929435 | 0.1929435 | NA | 0.1929435 | 0.1929435 | | |
| trefoil,+,10 | 0.1929435 | 0.1929435 | 0.1929435 | NA | 0.1929435 | | |
| trefoil,+,20 | 0.1929435 | 0.1929435 | 0.1929435 | 0.1929435 | NA | | |

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