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

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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 respose to be analysed is the logit of the proportion of live aphids that were infected.

Initialize

```
library(asreml)
```

```
## Loading required package: Matrix
```

```
library(asremlPlus)
library(dae)
```

```
## Loading required package: ggplot2
```

```
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 Jan 27 22:34:25 2020
##           LogLik        Sigma2     DF     wall    cpu
##  1       3.07130      0.226239     60 22:34:25    0.0 (1 restrained)
##  2       3.64260      0.226912     60 22:34:25    0.0 (1 restrained)
##  3       3.71250      0.227106     60 22:34:25    0.0 (1 restrained)
##  4       3.71721      0.227121     60 22:34:25    0.0 (1 restrained)
##  5       3.71751      0.227122     60 22:34:25    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 Jan 27 22:34:26 2020
##           LogLik        Sigma2     DF     wall    cpu
##  1       3.07130      0.226239     60 22:34:26    0.0 (1 restrained)
##  2       3.64260      0.226912     60 22:34:26    0.0 (1 restrained)
##  3       3.80283      0.227454     60 22:34:26    0.0 (1 restrained)
##  4       3.83949      0.233418     60 22:34:26    0.0
##  5       3.95568      0.230971     60 22:34:26    0.0
##  6       3.97333      0.230035     60 22:34:26    0.0
##  7       3.97405      0.229835     60 22:34:26    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")
```

```
##
##
##   Sequence of model terms whose status in the model has been investigated
##
##
##
## ####  Table of hypothesis tests performed
##
##                     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. 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 ot 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, caclulate 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,
```

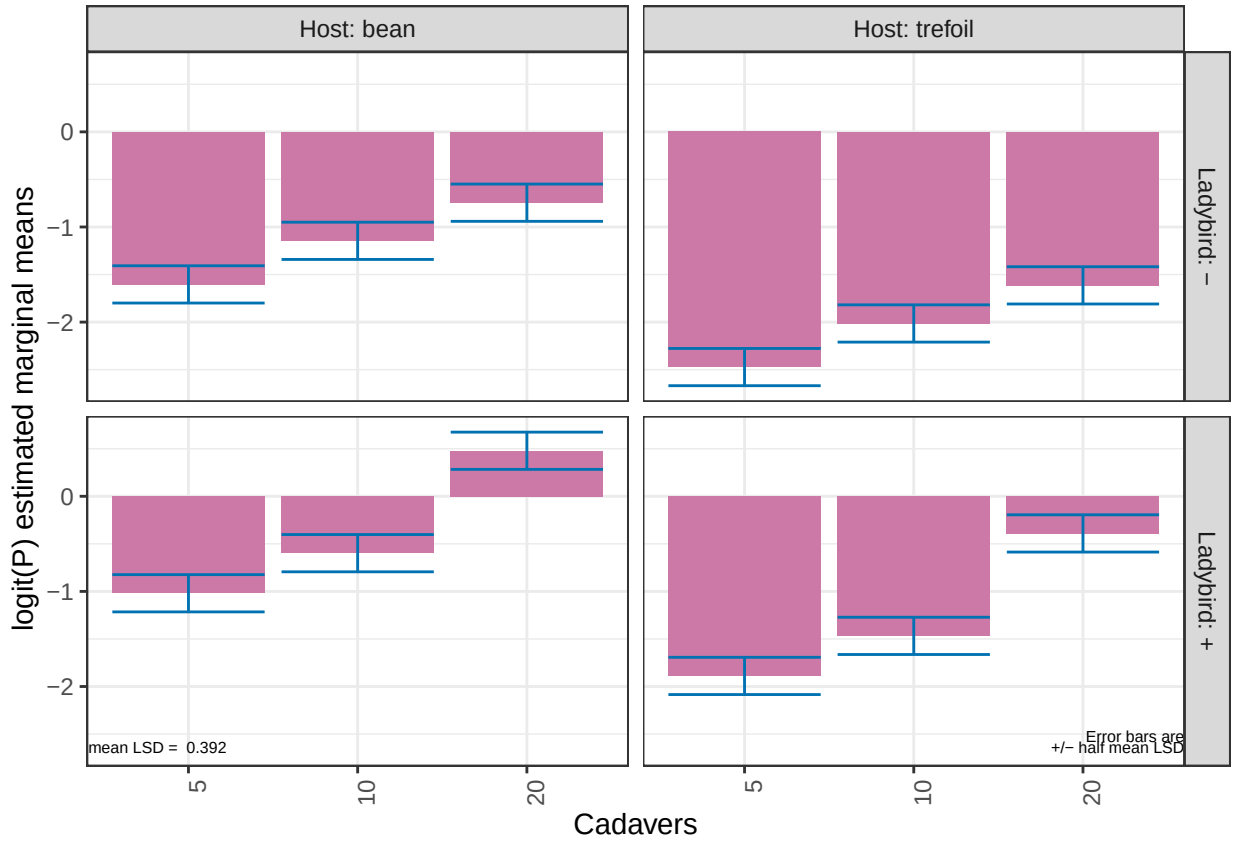
```
                      error.intervals = "halfLeast",
                      meanLSD.type = "factor.combination", LSDby = "Host",
                      tables = "predictions")
```

```
##
##
## #### 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)))
```

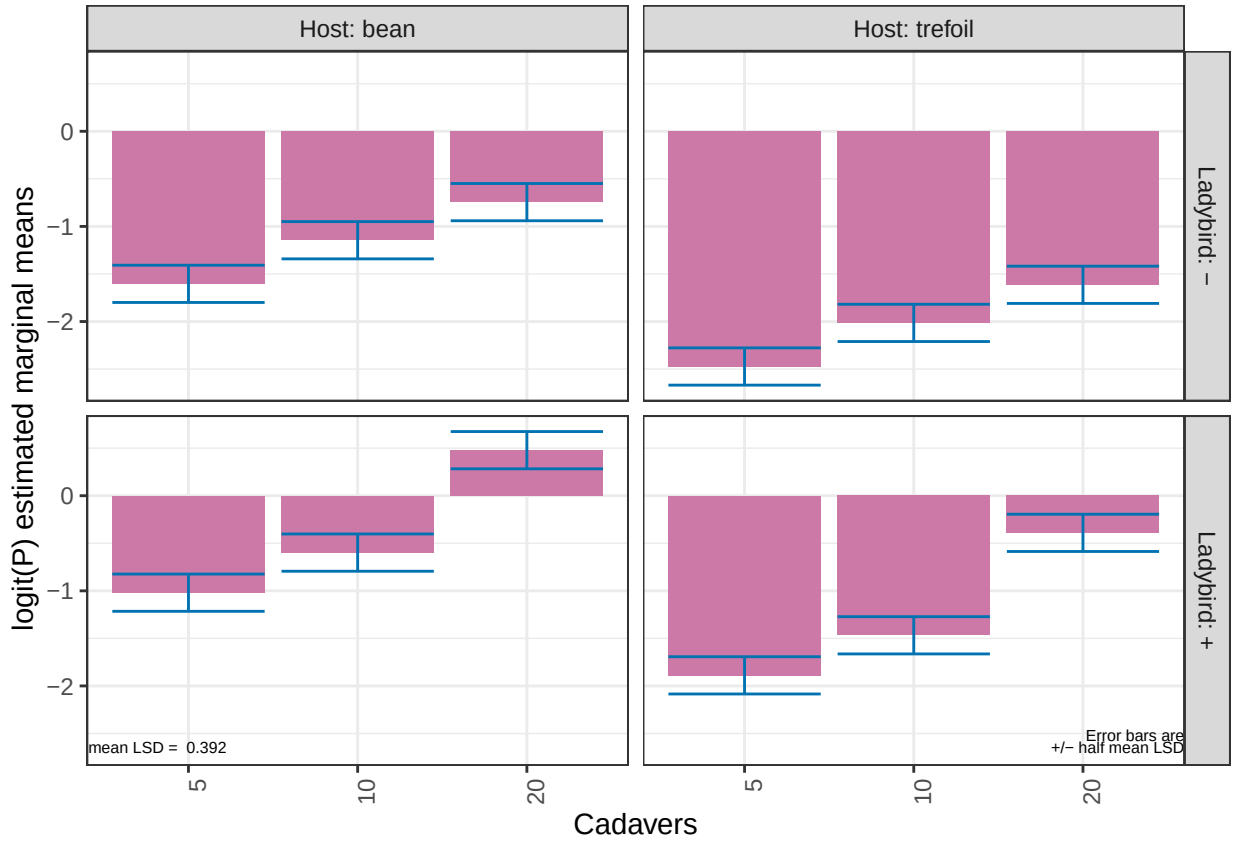


The function `plotPredictions` uses `ggplot` to produce the plot and the `ggplotFuncs` argument allows the addition of `ggplot` functions to modify the plot. In this case, the `facet.grid` function is respecified to include `prepender` functions that modify the labels of the facets to include the factor names. Note the the error bars in the plots are of $\pm 0.5 LSD$ so that pairs of prediction with nonoverlapping bars are significantly different (Snee, 1981).

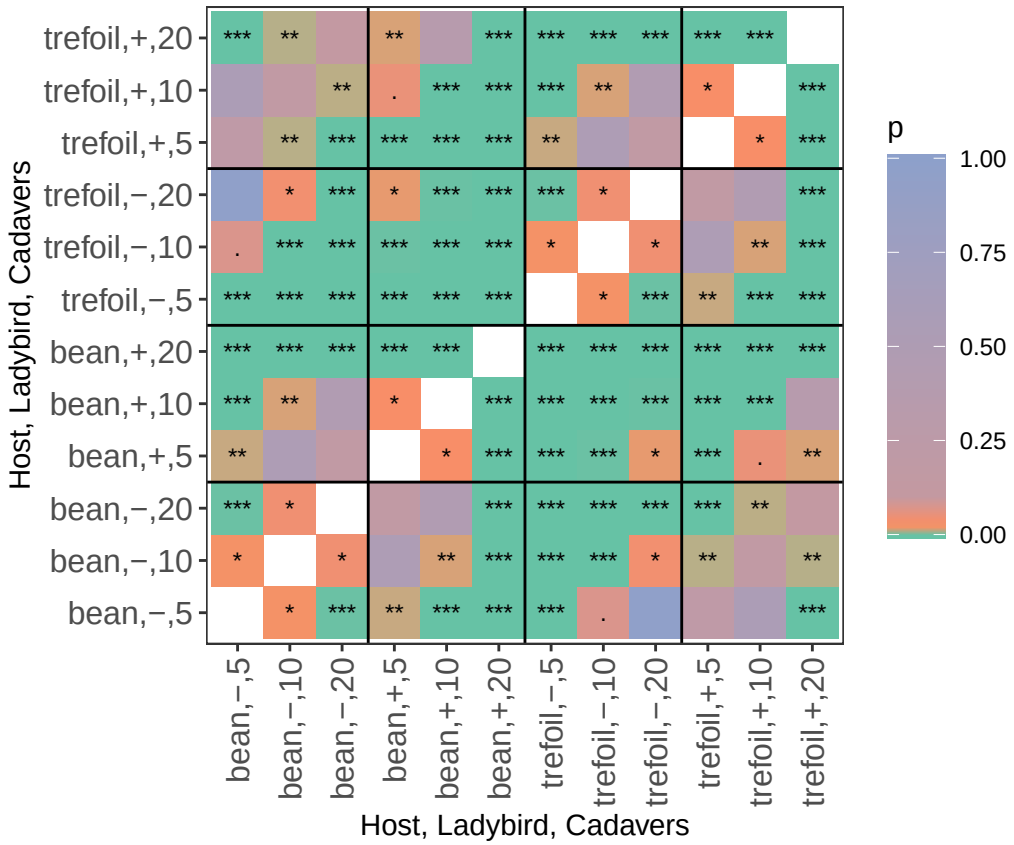
Get and plot the predictions with a single function call

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      0.00000000 -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 trefoil,-,10 trefoil,-,20 trefoil,+,5 trefoil,+,10 trefoil,+,20
## bean,-,5       0.8692001    0.4107972   0.01017604   0.2849139   -0.1362897   -1.2133041
## bean,-,10      1.3276031    0.8692001   0.46857901   0.7433168    0.3221133   -0.7549011
## bean,-,20      1.7282242    1.2698212   0.86920012   1.1439379    0.7227344   -0.3542800
## bean,+,5       1.4534864    0.9950834   0.59446231   0.8692001    0.4479966   -0.6290178
## bean,+,10      1.8746899    1.4162870   1.01566586   1.2904037    0.8692001   -0.2078143
## bean,+,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 etimated 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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