Package ‘emmeans’

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Description Obtain estimated marginal means (EMMs) for many linear, 
generalized linear, and mixed models. Compute contrasts or linear functions of EMMs, 
trends, and comparisons of slopes. Plots and other displays. 
Least-squares means are discussed, and the term `estimated marginal means” 
is suggested, in Searle, Speed, and Milliken (1980) Population marginal means 

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emmeans-package

Description

This package provides methods for obtaining estimated marginal means (EMMs, also known as least-squares means) for factor combinations in a variety of models. Supported models include [generalized linear] models, models for counts, multivariate, multinomial and ordinal responses, survival models, GEEs, and Bayesian models. For the latter, posterior samples of EMMs are provided. The package can compute contrasts or linear combinations of these marginal means with various multiplicity adjustments. One can also estimate and contrast slopes of trend lines. Some graphical displays of these results are provided.

Overview

Vignettes A number of vignettes are provided to help the user get acquainted with the emmeans package and see some examples.

Concept Estimated marginal means (see Searle et al. 1980) are popular for summarizing linear models that include factors. For balanced experimental designs, they are just the marginal means. For unbalanced data, they in essence estimate the marginal means you would have observed that the data arisen from a balanced experiment. Earlier developments regarding these techniques were developed in a least-squares context and are sometimes referred to as “least-squares means”. Since its early development, the concept has expanded far beyond least-squares settings.

Reference grids The implementation in emmeans relies on our own concept of a reference grid, which is an array of factor and predictor levels. Predictions are made on this grid, and estimated marginal means (or EMMs) are defined as averages of these predictions over zero or more dimensions of the grid. The function ref_grid explicitly creates a reference grid that can subsequently be used to obtain least-squares means. The object returned by ref_grid is of class "emmGrid", the same class as is used for estimated marginal means (see below).

Our reference-grid framework expands slightly upon Searle et al.’s definitions of EMMs, in that it is possible to include multiple levels of covariates in the grid.

Models supported As is mentioned in the package description, many types of models are supported by the package. See vignette("models", "emmeans") for full details. Some models may require other packages be installed in order to access all of the available features.

Estimated marginal means The emmeans function computes EMMs given a fitted model (or a previously constructed emmGrid object), using a specification indicating what factors to include. The emtrends function creates the same sort of results for estimating and comparing slopes of fitted lines. Both return an emmGrid object.
Summaries and analysis The *summary.emmGrid* method may be used to display an *emmGrid* object. Special-purpose summaries are available via *confint.emmGrid* and *test.emmGrid*, the latter of which can also do a joint test of several estimates. The user may specify by variables, multiplicity-adjustment methods, confidence levels, etc., and if a transformation or link function is involved, may reverse-transform the results to the response scale.

Contrasts and comparisons The *contrast* method for *emmGrid* objects is used to obtain contrasts among the estimates; several standard contrast families are available such as deviations from the mean, polynomial contrasts, and comparisons with one or more controls. Another *emmGrid* object is returned, which can be summarized or further analyzed. For convenience, a *pairs.emmGrid* method is provided for the case of pairwise comparisons.

Graphs The *plot.emmGrid* method will display side-by-side confidence intervals for the estimates, and/or “comparison arrows” whereby the *P* values of pairwise differences can be observed by how much the arrows overlap. The *emmp* function displays estimates like an interaction plot, multi-paneled if there are by variables. These graphics capabilities require the *lattice* package be installed.

MCMC support When a model is fitted using MCMC methods, the posterior chains(s) of parameter estimates are retained and converted into posterior samples of EMMs or contrasts thereof. These may then be summarized or plotted like any other MCMC results, using tools in, say *coda* or *bayesplot*.

Multcomp interface The *as.glht* function and *glht* method for *emmGrids* provide an interface to the *glht* function in the *multcomp* package, thus providing for more exacting simultaneous estimation or testing. The package also provides an *emm* function that works as an alternative to *mcp* in a call to *glht*.

---

**add_grouping**

*Add a grouping factor*

**Description**

This function adds a grouping factor to an existing reference grid or other *emmGrid* object, such that the levels of an existing factor (call it the reference factor) are mapped to a smaller number of levels of the new grouping factor. The reference factor is then nested in the grouping factor. This facilitates obtaining marginal means of the grouping factor, and contrasts thereof.

**Usage**

```r
add_grouping(object, newname, refname, newlevs)
```

**Arguments**

- **object**: An *emmGrid* object
- **newname**: Character name of grouping factor to add (different from any existing factor in the grid)
- **refname**: Character name of the reference factor
- **newlevs**: Character vector or factor of the same length as that of the levels for *refname*. The grouping factor *newname* will have the unique values of *newlevs* as its levels.
as.emmGrid

Value
A revised emmGrid object having an additional factor named newname, and a new nesting structure
refname %in% newname

Note
By default, the levels of newname will be ordered alphabetically. To dictate a different ordering of
levels, supply newlevs as a factor having its levels in the required order.

Examples
fiber.lm <- lm(strength ~ diameter + machine, data = fiber)
(frg <- ref_grid(fiber.lm))

# Suppose the machines are two different brands
brands <- factor(c("FiberPro", "FiberPro", "Acme"), levels = c("FiberPro", "Acme"))
(gfrg <- add_grouping(frg, "brand", "machine", brands))

emmeans(gfrg, "machine")
emmeans(gfrg, "brand")

as.emmGrid
Convert to and from emmGrid objects

Description
These are useful utility functions for creating a compact version of an emmGrid object that may
be saved and later reconstructed, or for converting old ref.grid or lsmobj objects into emmGrid
objects.

Usage
as.emmGrid(object, ...)

## S3 method for class 'emmGrid'
as.list(x, ...)

Arguments
object Object to be converted to class emmGrid. It may be a list returned by as.list.emmGrid,
or a ref.grid or lsmobj object created by emmeans’s predecessor, the lsmeans package. An error is thrown if object cannot be converted.

... In as.emmGrid, additional arguments passed to update.emmGrid before returning
the object. This argument is ignored in as.list.emmGrid

x An emmGrid object
Details

An emmGrid object is an S4 object, and as such cannot be saved in a text format or saved without a lot of overhead. By using as.list, the essential parts of the object are converted to a list format that can be easily and compactly saved for use, say, in another session or by another user. Providing this list as the arguments for emmobj allows the user to restore a working emmGrid object.

Value

as.emmGrid returns an object of class emmGrid.

as.list.emmGrid returns an object of class list.

See Also

emmobj

Examples

pigs.lm <- lm(log(conc) ~ source + factor(percent), data = pigs)
pigs.sav <- as.list(ref_grid(pigs.lm))

pigs.anew <- as.emmGrid(pigs.sav)
emmeans(pigs.anew, "source")

## Not run:
## Convert an entire workspace saved from an old **lsmeans** session
a.problem <- lsmeans::lsmeans(pigs.lm, "source")
#- Now global env contains at least two ref.grid and lsmobj objects,
#- and the "lsmeans" namespace is loaded
emmeans:::convert_workspace()
class(a.problem)
"lsmeans" %in% loadedNamespaces()
#- It's all better now

## End(Not run)

as.mcmc.emmGrid  

Description

When a model is fitted using Markov chain Monte Carlo (MCMC) methods, its reference grid contains a post.beta slot. These functions transform those posterior samples to posterior samples of EMMs or related contrasts. They can then be summarized or plotted using, e.g., functions in the coda package.
Usage

```r
## S3 method for class 'emmGrid'
as.mcmc(x, names = TRUE, sep.chains = TRUE,
       likelihood, ...)

## S3 method for class 'emmGrid'
as.mcmc.list(x, names = TRUE, ...)
```

Arguments

- `x` An object of class `emmGrid`
- `names` Logical scalar or vector specifying whether variable names are appended to levels in the column labels for the as.mcmc or as.mcmc.list result – e.g., column names of treat A and treat B versus just A and B. When there is more than one variable involved, the elements of names are used cyclically.
- `sep.chains` Logical value. If TRUE, and there is more than one MCMC chain available, an `mcmc.list` object is returned by as.mcmc, with separate EMMs posteriors in each chain.
- `likelihood` Character value or function. If given, simulations are made from the corresponding posterior predictive distribution. If not given, we obtain the posterior distribution of the parameters in object. See Prediction section below.
- `...` arguments passed to other methods

Value

An object of class `mcmc` or `mcmc.list`.

Details

When the object’s post.beta slot is non-trivial, as.mcmc will return an `mcmc` or `mcmc.list` object that can be summarized or plotted using methods in the coda package. In these functions, post.beta is transformed by post-multiplying it by t(linfct), creating a sample from the posterior distribution of LS means. In as.mcmc, if sep.chains is TRUE and there is in fact more than one chain, an `mcmc.list` is returned with each chain’s results. The as.mcmc.list method is guaranteed to return an `mcmc.list`, even if it comprises just one chain.

Prediction

When likelihood is specified, it is used to simulate values from the posterior predictive distribution corresponding to the given likelihood and the posterior distribution of parameter values. Denote the likelihood function as $f(y|\theta, \phi)$, where $y$ is a response, $\theta$ is the parameter estimated in object, and $\phi$ comprises zero or more additional parameters to be specified. If likelihood is a function, that function should take as its first argument a vector of $\theta$ values (each corresponding to one row of object@grid). Any $\phi$ values should be specified as additional named function arguments, and passed to likelihood via . . . . This function should simulate values of $y$.

A few standard likelihoods are available by specifying likelihood as a character value. They are:
"normal" The normal distribution with mean $\theta$ and standard deviation specified by additional argument sigma

"binomial" The binomial distribution with success probability $\theta$, and number of trials specified by trials

"poisson" The Poisson distribution with mean $\theta$ (no additional parameters)

"gamma" The gamma distribution with scale parameter $\theta$ and shape parameter specified by shape

Examples

```r
require("coda")

### A saved reference grid for a mixed logistic model (see lme4::cbpp)
cbpp.rg <- do.call(emmobj,
   readRDS(system.file("extdata", "cbpplist", package = "emmeans")))
# Predictive distribution for herds of size 20
# (perhaps a bias adjustment should be applied; see "sophisticated" vignette)
pred.incidence <- as.mcmc(regrid(cbpp.rg), likelihood = "binomial", trials = 20)
```

auto.noise

### Auto Pollution Filter Noise

**Description**

Three-factor experiment comparing pollution-filter noise for two filters, three sizes of cars, and two sides of the car.

**Usage**

```r
auto.noise
```

**Format**

A data frame with 36 observations on the following 4 variables.

- `noise` Noise level in decibels - a numeric vector.
- `size` The size of the vehicle - an ordered factor with levels S, M, L.
- `type` Type of anti-pollution filter - a factor with levels Std and Octel
- `side` The side of the car where measurement was taken – a factor with levels L and R.

**Details**

The data are from a statement by Texaco, Inc., to the Air and Water Pollution Subcommittee of the Senate Public Works Committee on June 26, 1973. Mr. John McKinley, President of Texaco, cited an automobile filter developed by Associated Octel Company as effective in reducing pollution. However, questions had been raised about the effects of filters on vehicle performance, fuel consumption, exhaust gas back pressure, and silencing. On the last question, he referred to the data included here as evidence that the silencing properties of the Octel filter were at least equal to those of standard silencers.
Source

The dataset was obtained from the Data and Story Library (DASL) at Carnegie-Mellon University. Apparently it has since been removed. The original dataset was altered by assigning meaningful names to the factors and sorting the observations in random order as if this were the run order of the experiment.

Examples

```r
noise.lm <- lm(noise ~ size * type * side, data = auto.noise)

# Interaction plot of predictions
emmip(noise.lm, type ~ size | side)

# Confidence intervals
plot(emmeans(noise.lm, ~ size | side*type))
```

CLD

Extract and display information on all pairwise comparisons of estimated marginal means.

Description

Extract and display information on all pairwise comparisons of estimated marginal means.

Usage

```r
CLD(object, ...)
```

Arguments

- `object` An object of class `emmGrid`
- `...` Arguments passed to `contrast` (for example, an adjust method)

This function uses the Piepho (2004) algorithm (as implemented in the `multcompView` package) to generate a compact letter display of all pairwise comparisons of estimated marginal means. The function obtains (possibly adjusted) P values for all pairwise comparisons of means, using the `contrast` function with method = "pairwise". When a P value exceeds `alpha`, then the two means have at least one letter in common.
CLD details Logical value determining whether detailed information on tests of pairwise comparisons is displayed

sort Logical value determining whether the EMMs are sorted before the comparisons are produced. When TRUE, the results are displayed according to reversed.

by Character value giving the name or names of variables by which separate families of comparisons are tested. If NULL, all means are compared. If missing, the object's by.\texttt{vars} setting, if any, is used.

alpha Numeric value giving the significance level for the comparisons

Letters Character vector of letters to use in the display. Any strings of length greater than 1 are expanded into individual characters

reversed Logical value (passed to \texttt{multcompView::multcompLetters}) If TRUE, the order of use of the letters is reversed. In addition, if both \texttt{sort} and \texttt{reversed} are TRUE, the sort order of results is reversed.

Value

When details == FALSE, an object of class \texttt{summary.ref_grid} (which inherits from \texttt{data.frame}) showing the summary of EMMs with an added column named .\texttt{groups} containing the CLD information. When details == TRUE, a list with the object just described, as well as the summary of the contrast results showing each comparison, its estimate, standard error, t ratio, and adjusted \( P \) value.

Deprecated

The \texttt{CLD} function and methods are deprecated. Compact-letter displays (CLDs) encourage a misleading interpretation of significance testing by visually grouping means whose comparisons have \( P > \alpha \) as though they are equal. However, failing to prove two means are different does not prove that they are the same. In addition, CLDs make a hard distinction between \( P \) values nearly equal to \( \alpha \) but on opposite sides.

Some users may find \texttt{pwpp} to be a useful alternative. It produces a plot showing all \( P \) values for all pairwise comparisons (or other set of comparisons), and can also show one-sided \( P \) values and tests of equivalence or noninferiority. Also, if you insist, \texttt{cld} is still available in the \texttt{multcomp} package, and \texttt{multcomp::cld(emm)} still works.

References


See Also

cld in the \texttt{multcomp} package, for which a courtesy method is provided for \texttt{emmGrid} objects.
Description

These methods provide for follow-up analyses of \texttt{emmGrid} objects: Contrasts, pairwise comparisons, tests, and confidence intervals. They may also be used to compute arbitrary linear functions of predictions or EMMs.

Usage

\begin{verbatim}
contrast(object, ...)  
\end{verbatim}

### S3 method for class 'emmGrid'

\begin{verbatim}
contrast(object, method = "eff", interaction = FALSE,  
by, offset = NULL, name = "contrast",  
options = get_emm_option("contrast"), type, adjust, simple,  
combine = FALSE, ...)
\end{verbatim}

### S3 method for class 'emmGrid'

\begin{verbatim}
pairs(x, reverse = FALSE, ...)
\end{verbatim}

### S3 method for class 'emmGrid'

\begin{verbatim}
coef(object, ...)
\end{verbatim}

Arguments

- \textbf{object}: An object of class \texttt{emmGrid}
- \textbf{...}: Additional arguments passed to other methods
- \textbf{method}: Character value giving the root name of a contrast method (e.g. "pairwise" – see \texttt{emmme-functions}). Alternatively, a named \texttt{list} of coefficients (for a contrast or linear function) that must each conform to the number of results in each by group. In a multi-factor situation, the factor levels are combined and treated like a single factor.
- \textbf{interaction}: Character vector or logical value. If this is specified, \texttt{method} is ignored. See the “Interaction contrasts” section below for details.
- \textbf{by}: Character names of variable(s) to be used for “by” groups. The contrasts or joint tests will be evaluated separately for each combination of these variables. If \texttt{object} was created with by groups, those are used unless overridden. Use \texttt{by} = \texttt{NULL} to use no by groups at all.
- \textbf{offset}: Numeric vector of the same length as each by group. These values are added to their respective linear estimates. (It is ignored when interaction is specified.)
- \textbf{name}: Character name to use to override the default label for contrasts used in table headings or subsequent contrasts of the returned object.
options  If non-NULL, a named list of arguments to pass to update.emmGrid, just after the object is constructed.

type    Character: prediction type (e.g., "response") – added to options

adjust  Character: adjustment method (e.g., "bonferroni") – added to options

simple  Character vector or list: Specify the factor(s) **not** in by, or a list thereof. See the section below on simple contrasts.

combine Logical value that determines what is returned when simple is a list. See the section on simple contrasts.

x       An emmGrid object

reverse Logical value - determines whether to use "pairwise" (if TRUE) or "revpairwise" (if FALSE).

Value

contrast and pairs return an object of class emmGrid. Its grid will correspond to the levels of the contrasts and any by variables. The exception is that an emm_list object is returned if simple is a list and complete is FALSE.

does a data frame containing the object's grid, along with columns named c.1, c.2,... containing the contrast coefficients. If

Pairs method

The call pairs(object) is equivalent to contrast(object, method = "pairwise"); and pairs(object, reverse = TRUE) is the same as contrast(object, method = "revpairwise").

Interaction contrasts

When interaction is specified, interaction contrasts are computed: Contrasts are generated for each factor separately, one at a time; and these contrasts are applied to the object (the first time around) or to the previous result (subsequently). (Any factors specified in by are skipped.) The final result comprises contrasts of contrasts, or, equivalently, products of contrasts for the factors involved. Processing is done in the order of appearance in object@levels. With interaction = TRUE, method (if specified as character) is used for each contrast. If interaction is a character vector, the elements specify the respective contrast method(s); they are recycled as needed.

Simple contrasts

simple is essentially the complement of by: When simple is a character vector, by is set to all the factors in the grid **except** those in simple. If simple is a list, each element is used in turn as simple, and assembled in an "emm_list". To generate all simple main effects, use simple = "each" (this works unless there actually is a factor named "each"). Note that a non-missing simple will cause by to be ignored.

Ordinarily, when simple is a list or "each", the return value is an emm_list object with each entry in correspondence with the entries of simple. However, with combine = TRUE, the elements are all combined into one family of contrasts in a single emmGrid object using rbind.emmGrid. In that case, the adjust argument sets the adjustment method for the combined set of contrasts.
Note

When object has a nesting structure (this can be seen via \texttt{str(object)}), then any grouping factors involved are forced into service as by variables, and the contrasts are thus computed separately in each nest. This in turn may lead to an irregular grid in the returned \texttt{emmGrid} object, which may not be valid for subsequent \texttt{emmeans} calls.

Examples

\begin{verbatim}
warp.lm <- lm(breaks ~ wool*tension, data = warpbreaks)
warp.emm <- emmeans(warp.lm, ~ tension | wool)
contrast(warp.emm, "poly")  # inherits 'by = "wool"' from warp.emm
pairs(warp.emm)  # ditto
contrast(warp.emm, "eff", by = NULL)  # contrasts of the 6 factor combs
pairs(warp.emm, simple = "wool")  # same as pairs(warp.emm, by = "tension")

# Do all "simple" comparisons, combined into one family
pairs(warp.emm, simple = "each", combine = TRUE)

## Not run:
## Note that the following are NOT the same:
contrast(warp.emm, simple = c("wool", "tension"))
contrast(warp.emm, simple = list("wool", "tension"))
## The first generates contrasts for combinations of wool and tension
## (same as by = NULL)
## The second generates contrasts for wool by tension, and for
## tension by wool, respectively.

## End(Not run)

# An interaction contrast for tension:wool
tw.emm <- contrast(warp.emm, interaction = c("poly", "consec"), by = NULL)
tw.emm  # see the estimates
coef(tw.emm)  # see the contrast coefficients
\end{verbatim}

Description

Functions with an extension of \texttt{.emmc} provide for named contrast families. One of the standard ones documented here may be used, or the user may write such a function.

Usage

\begin{verbatim}
pairwise.emmc(levs, exclude = integer(0), include, ...)

revpairwise.emmc(levs, exclude = integer(0), include, ...)
\end{verbatim}
tukey.emmc(levs, reverse = FALSE, ...)  
poly.emmc(levs, max.degree = min(6, k - 1), ...)  
trt.vs.ctrl.emmc(levs, ref = 1, reverse = FALSE, 
              exclude = integer(0), include, ...)  
trt.vs.ctrl1.emmc(levs, ref = 1, ...)  
trt.vs.ctrlk.emmc(levs, ref = length(levs), ...)  
dunnett.emmc(levs, ref = 1, ...)  
eff.emmc(levs, exclude = integer(0), include, ...)  
del.eff.emmc(levs, exclude = integer(0), include, ...)  
consec.emmc(levs, reverse = FALSE, exclude = integer(0), include, ...)  
mean_chg.emmc(levs, reverse = FALSE, exclude = integer(0), include, ...)  

Arguments

levs          Vector of factor levels  
exclude       integer vector of indices, or character vector of levels to exclude from consideration. These levels will receive weight 0 in all contrasts. Character levels must exactly match elements of levs.  
include       integer or character vector of levels to include (the complement of exclude). An error will result if the user specifies both exclude and include.  
...            Additional arguments, passed to related methods as appropriate  
reverse       Logical value to determine the direction of comparisons  
max.degree    Integer specifying the maximum degree of polynomial contrasts  
ref           Integer(s) or character(s) specifying which level(s) to use as the reference. Character values must exactly match elements of levs.  

Details

Each standard contrast family has a default multiple-testing adjustment as noted below. These adjustments are often only approximate; for a more exacting adjustment, use the interfaces provided to glht in the multcomp package.

pairwise.emmc, revpairwise.emmc, and tukey.emmc generate contrasts for all pairwise comparisons among estimated marginal means at the levels in levs. The distinction is in which direction they are subtracted. For factor levels A, B, C, D, pairwise.emmc generates the comparisons A-B, A-C, A-D, B-C, B-D, and C-D, whereas revpairwise.emmc generates B-A, C-A, C-B, D-A, D-B, and D-C. tukey.emmc invokes pairwise.emmc or revpairwise.emmc depending on reverse. The
default multiplicity adjustment method is "tukey", which is only approximate when the standard errors differ.

poly.emmc generates orthogonal polynomial contrasts, assuming equally-spaced factor levels. These are derived from the poly function, but an ad hoc algorithm is used to scale them to integer coefficients that are (usually) the same as in published tables of orthogonal polynomial contrasts. The default multiplicity adjustment method is "none".

trt.vs.ctrl1.emmc and its relatives generate contrasts for comparing one level (or the average over specified levels) with each of the other levels. The argument ref should be the index(es) (not the labels) of the reference level(s). trt.vs.ctrl1.emmc is the same as trt.vs.ctrl1.emmc with a reference value of 1, and trt.vs.ctrlk.emmc is the same as trt.vs.ctrl1 with a reference value of length(levs). dunnett.emmc is the same as trt.vs.ctrl1. The default multiplicity adjustment method is "dunnettx", a close approximation to the Dunnett adjustment. Note in all of these functions, it is illegal to have any overlap between the ref levels and the exclude levels. If any is found, an error is thrown.

consec.emmc and mean_chg.emmc are useful for contrasting treatments that occur in sequence. For a factor with levels A, B, C, D, E, consec.emmc generates the comparisons B-A, C-B, and D-C, while mean_chg.emmc generates the contrasts (B+C+D)/3 - A, (C+D)/2 - (A+B)/2, and D - (A+B+C)/3. With reverse = TRUE, these differences go in the opposite direction.

eff.emmc and del.eff.emmc generate contrasts that compare each level with the average over all levels (in eff.emmc) or over all other levels (in del.eff.emmc). These differ only in how they are scaled. For a set of k EMMs, del.eff.emmc gives weight 1 to one EMM and weight -1/(k-1) to the others, while eff.emmc gives weights (k-1)/k and -1/k respectively, as in subtracting the overall EMM from each EMM. The default multiplicity adjustment method is "fdr". This is a Bonferroni-based method and is slightly conservative; see p.adjust.

Value
A data.frame, each column containing contrast coefficients for levs. The "desc" attribute is used to label the results in emmeans, and the "adjust" attribute gives the default adjustment method for multiplicity.

Note
Caution is needed in cases where the user alters the ordering of results (e.g., using the the "[...]") operator), because the contrasts generated depend on the order of the levels provided. For example, suppose trt.vs.ctrl11 contrasts are applied to two by groups with levels ordered (Ctrl, T1, T2) and (T1, T2, Ctrl) respectively, then the contrasts generated will be for (T1 - Ctrl, T2 - Ctrl) in the first group and (T2 - T1, Ctrl - T1) in the second group, because the first level in each group is used as the reference level.

Examples
warp.lm <- lm(breaks ~ wool*tension, data = warpbreaks)
warp.emm <- emmeans(warp.lm, ~ tension | wool)
contrast(warp.emm, "poly")
contrast(warp.emm, "trt.vs.ctrl", ref = "M")

# Compare only low and high tensions
# Note pairs(emm, ...) calls contrast(emm, "pairwise", ...)
pairs(warp.emm, exclude = 2)
# (same results using exclude = "M" or include = c("L","H") or include = c(1,3))

### Setting up a custom contrast function
helmert.emmc <- function(levs, ...) {
  M <- as.data.frame(contr.helmert(levs))
  names(M) <- paste(levs[-1], "vs earlier")
  attr(M, "desc") <- "Helmert contrasts"
  M
}
contrast(warp.emm, "helmert")
## Not run:
# See what is used for polynomial contrasts with 6 levels
emmeans:::poly.emmc(1:6)
## End(Not run)

---

**emm**

**Support for multcomp::glht**

**Description**

These functions and methods provide an interface between emmeans and the multcomp::glht function for simultaneous inference provided by the multcomp package.

**Usage**

```r
emm(...)
as.glht(object, ...)
```

## S3 method for class 'emmGrid'
as.glht(object, ...)

**Arguments**

- `...` In emm, the specs, by, and contr arguments you would normally supply to emmeans. Only specs is required. Otherwise, arguments that are passed to other methods.
- `object` An object of class emmGrid or emm_list

**Details**

emm is meant to be called only from "glht" as its second (linfct) argument. It works similarly to multcomp::mcp, except with specs (and optionally by and contr arguments) provided as in a call to emmeans.
emmeans

Value

emmeans returns an object of an intermediate class for which there is a multcomp::glht method.
as.glht returns an object of class glht or glht_list according to whether object is of class
emmGrid or emm_list. See Details below for more on glht_lists.

Details

A glht_list object is simply a list of glht objects. It is created as needed – for example, when
there is a by variable. Appropriate convenience methods coef, confint, plot, summary, and vcov
are provided, which simply apply the corresponding glht methods to each member.

Note

The multivariate-t routines used by glht require that all estimates in the family have the same
integer degrees of freedom. In cases where that is not true, a message is displayed that shows what
df is used. The user may override this via the df argument.

Examples

if(require(multcomp)) { # --- multcomp must be installed
  warp.lm <- lm(breaks ~ wool*tension, data = warpbreaks)
  # Using 'emm'
  summary(glht(warp.lm, emm(pairwise ~ tension | wool)))

  # Same, but using an existing 'emmeans' result
  warp.emm <- emmeans(warp.lm, ~ tension | wool)
  summary(as.glht(pairs(warp.emm)))

  # Same contrasts, but treat as one family
  summary(as.glht(pairs(warp.emm), by = NULL))
}

--- was tested only if multcomp is installed

emmeans

Estimated marginal means (Least-squares means)

Description

Compute estimated marginal means (EMMs) for specified factors or factor combinations in a linear
model; and optionally, comparisons or contrasts among them. EMMs are also known as least-
squares means.

Usage

emmeans(object, specs, by = NULL, fac.reduce = function(coefs)
  apply(coefs, 2, mean), contr, options = get_emm_option("emmeans"),
  weights, offset, trend, ...)
Arguments

- **object**: An object of class `emmGrid`; or a fitted model object that is supported, such as the result of a call to `lm` or `lmer`. Many fitted-model objects are supported; see `vignette("models", "emmeans")` for details.

- **specs**: A character vector specifying the names of the predictors over which EMMs are desired. `specs` may also be a formula or a list (optionally named) of valid `specs`. Use of formulas is described in the Overview section below.

- **by**: A character vector specifying the names of predictors to condition on.

- **fac.reduce**: A function that combines the rows of a matrix into a single vector. This implements the “marginal averaging” aspect of EMMs. The default is the mean of the rows. Typically if it is overridden, it would be some kind of weighted mean of the rows. If `fac.reduce` is nonlinear, bizarre results are likely, and EMMs will not be interpretable. **NOTE**: If the `weights` argument is non-missing, `fac.reduce` is ignored.

- **contr**: A character value or list specifying contrasts to be added. See `contrast`. **NOTE**: `contr` is ignored when `specs` is a formula.

- **options**: If non-NULL, a named list of arguments to pass to `update.emmGrid`, just after the object is constructed.

- **weights**: Character value, numeric vector, or numeric matrix specifying weights to use in averaging predictions. See “Weights” section below.

- **offset**: Numeric vector or scalar. If specified, this adds an offset to the predictions, or overrides any offset in the model or its reference grid. If a vector of length differing from the number of rows in the result, it is subsetted or cyclically recycled.

- **trend**: This is now deprecated. Use `emtrends` instead.

- **...**: This is used only when object is not already a “emmGrid” object, these arguments are passed to `ref_grid`. Common examples are at, cov.reduce, data, codetype, transform, df, nesting, and vcov. Model-type-specific options (see `vignette("models", "emmeans")`), commonly mode, may be used here as well. In addition, if the model formula contains references to variables that are not predictors, you must provide a `params` argument with a list of their names.

Details

Users should also consult the documentation for `ref_grid`, because many important options for EMMs are implemented there, via the `...` argument.

Value

When `specs` is a character vector or one-sided formula, an object of class "emmGrid". A number of methods are provided for further analysis, including `summary.emmGrid`, `confint.emmGrid`, `test.emmGrid`, `contrast.emmGrid`, `pairs.emmGrid`, and `CLD.emmGrid`. When `specs` is a list or a formula having a left-hand side, the return value is an `emm_list` object, which is simply a list of `emmGrid` objects.
Overview

Estimated marginal means or EMMs (sometimes called least-squares means) are predictions from a linear model over a reference grid; or marginal averages thereof. The ref_grid function identifies/creates the reference grid upon which emmeans is based.

For those who prefer the terms “least-squares means” or “predicted marginal means”, functions lsmeans and pmmeans are provided as wrappers. See wrappers.

If specs is a formula, it should be of the form ~ specs, ~ specs | by, contr ~ specs, or contr ~ specs | by. The formula is parsed and the variables therein are used as the arguments specs, by, and contr as indicated. The left-hand side is optional, but if specified it should be the name of a contrast family (e.g., pairwise). Operators like * or : are needed in the formula to delineate names, but otherwise are ignored.

In the special case where the mean (or weighted mean) of all the predictions is desired, specify specs as ~ 1 or "1".

A number of standard contrast families are provided. They can be identified as functions having names ending in .emmc – see the documentation for emmc-functions for details – including how to write your own .emmc function for custom contrasts.

Weights

If weights is a vector, its length must equal the number of predictions to be averaged to obtain each EMM. If a matrix, each row of the matrix is used in turn, wrapping back to the first row as needed. When in doubt about what is being averaged (or how many), first call emmeans with weights = "show.levels".

If weights is a string, it should partially match one of the following:

"equal" Use an equally weighted average.
"proportional" Weight in proportion to the frequencies (in the original data) of the factor combinations that are averaged over.
"outer" Weight in proportion to each individual factor’s marginal frequencies. Thus, the weights for a combination of factors are the outer product of the one-factor margins
"cells" Weight according to the frequencies of the cells being averaged.
"flat" Give equal weight to all cells with data, and ignore empty cells.
"show.levels" This is a convenience feature for understanding what is being averaged over. Instead of a table of EMMs, this causes the function to return a table showing the levels that are averaged over, in the order that they appear.

Outer weights are like the ‘expected’ counts in a chi-square test of independence, and will yield the same results as those obtained by proportional averaging with one factor at a time. All except "cells" uses the same set of weights for each mean. In a model where the predicted values are the cell means, cell weights will yield the raw averages of the data for the factors involved. Using "flat" is similar to "cells", except nonempty cells are weighted equally and empty cells are ignored.
Offsets

Unlike in ref_grid, an offset need not be scalar. If not enough values are supplied, they are cyclically recycled. For a vector of offsets, it is important to understand that the ordering of results goes with the first name in specs varying fastest. If there are any by factors, those vary slower than all the primary ones, but the first by variable varies the fastest within that hierarchy. See the examples.

See Also

ref_grid, contrast, vignette("models", "emmeans")

Examples

warp.lm <- lm(breaks ~ wool * tension, data = warpbreaks)
emmeans (warp.lm, ~ wool | tension)
# or equivalently emmeans(warp.lm, "wool", by = "tension")

emmeans (warp.lm, poly ~ tension | wool)

## Not run:
### Offsets: Consider a silly example:
emmeans(warp.lm, ~ tension | wool, offset = c(17, 23, 47)) @ grid
# note that offsets are recycled so that each level of tension receives
# the same offset for each wool.
# But using the same offsets with ~ wool | tension will probably not
# be what you want because the ordering of combinations is different.

## End(Not run)
grid data.frame. Contains the combinations of the variables that define the reference grid. In addition, there is an auxiliary column named ".wgt." holding the observed frequencies or weights for each factor combination (excluding covariates). If the model has one or more offset() calls, there is an another auxiliary column named ".offset.". Auxiliary columns are not considered part of the reference grid. (However, any variables included in offset calls are in the reference grid.)

levels list. Each entry is a character vector with the distinct levels of each variable in the reference grid. Note that grid is obtained by applying the function expand.grid to this list.

matlevs list. Like levels but has the levels of any matrices in the original dataset. Matrix columns are always concatenated and treated as a single variable for purposes of the reference grid.

linfct matrix. Each row consists of the linear function of the regression coefficients for predicting its corresponding element of the reference grid. The rows of this matrix go in one-to-one correspondence with the rows of grid, and the columns with elements of bhat.

bhat numeric. The regression coefficients. If there is a multivariate response, the matrix of coefficients is flattened to a single vector, and linfct and V redefined appropriately. Important: bhat must include any NA values produced as a result of collinearity in the predictors. These are taken care of later in the estimability check.

nbasis matrix. The basis for the non-estimable functions of the regression coefficients. Every EMM will correspond to a linear combination of rows of linfct, and that result must be orthogonal to all the columns of nbasis in order to be estimable. If everything is estimable, nbasis should be a 1 x 1 matrix of NA.

V matrix. The symmetric variance-covariance matrix of bhat.

dffun function having two arguments. dffun(k, dfargs) should return the degrees of freedom for the linear function sum(k*bhat), or NA if unavailable.

dfargs list. Used to hold any additional information needed by dffun.

misc list. Additional information used by methods. These include at least the following: estName (the label for the estimates of linear functions), and the default values of infer, level, and adjust to be used in the summary.emmGrid method. Elements in this slot may be modified if desired using the update.emmGrid method.

post.beta matrix. A sample from the posterior distribution of the regression coefficients, if MCMC methods were used; or a 1 x 1 matrix of NA otherwise. When it is non-trivial, the as.mcmc.emmGrid method returns post.beta %*% t(linfct), which is a sample from the posterior distribution of the EMMs.

Methods

All methods for these objects are S3 methods except for show. They include [.emmGrid, as.glht.emmGrid, as.mcmc.emmGrid, as.mcmc.list.emmGrid (see coda), cld.emmGrid (see multcomp), coef.emmGrid, confint.emmGrid, contrast.emmGrid, pairs.emmGrid, plot.emmGrid, predict.emmGrid, print.emmGrid, rbind.emmGrid, show.emmGrid, str.emmGrid, summary.emmGrid, test.emmGrid, update.emmGrid, vcov.emmGrid, and xtable.emmGrid.
**Description**

Creates an interaction plot of EMMs based on a fitted model and a simple formula specification.

**Usage**

```r
emmip(object, formula, ...)  
```

```r  
# Default S3 method:  
emmip(object, formula, type, CIs = FALSE,  
PIs = FALSE, engine = get_emm_option("graphics.engine"), pch = c(1,  
2, 6, 7, 9, 10, 15:20), lty = 1, col = NULL, plotit = TRUE, ...)  
```

**Arguments**

- `object`: An object of class `emmGrid`, or a fitted model of a class supported by the `emmeans` package.
- `formula`: Formula of the form `trace.factors ~ x.factors | by.factors`. The EMMs are plotted against `x.factor` for each level of `trace.factors`. `by.factors` is optional, but if present, it determines separate panels. Each element of this formula may be a single factor in the model, or a combination of factors using the `*` operator.
- `...`: Additional arguments passed to `emmeans` (when `object` is not already an `emmGrid` object), `predict.emmGrid`, `ggplot`, or `xyplot`.
- `type`: As in `predict.emmGrid`, this determines whether we want to inverse-transform the predictions (type = "response") or not (any other choice). The default is "link", unless the "predict.type" option is in force; see `emm_options`.
- `CIs`: Logical value. If TRUE, confidence intervals (or HPD intervals for Bayesian models) are added to the plot (works only with engine = "ggplot").
- `PIs`: Logical value. If TRUE, prediction intervals are added to the plot (works only with engine = "ggplot"). If both CIs and PIs are TRUE, the prediction intervals will be somewhat longer, lighter, and thinner than the confidence intervals. Additional parameters to `predict.emmGrid` (e.g., sigma) may be passed via .... For Bayesian models, PIs require frequentist = TRUE and a value for sigma.
- `engine`: Character value matching "ggplot" (default) or "lattice". The graphics engine to be used to produce the plot. These require, respectively, the `ggplot2` or `lattice` package to be installed.
- `pch`: The plotting characters to use for each group (i.e., levels of `trace.factors`). They are recycled as needed.
- `lty`: The line types to use for each group. Recycled as needed.
The colors to use for each group, recycled as needed. If not specified, the default trellis colors are used.

Logical value. If TRUE, the plot is displayed. Otherwise, one may use the "lattice" attribute of the returned object and print it, perhaps after additional manipulation.

If plotit = FALSE, a data.frame (actually, a summary_emm object) with the table of EMMs that would be plotted. The variables plotted are named xvar and yvar, and the trace factor is named tvar. This data frame has an added "labs" attribute containing the labels xlab, ylab, and tlab for these respective variables. The confidence limits are also included, renamed LCL and UCL.

If plotit = TRUE, the function returns an object of class "ggplot" or a "trellis", depending on engine.

If object is a fitted model, emmeans is called with an appropriate specification to obtain estimated marginal means for each combination of the factors present in formula (in addition, any arguments in ... that match at, trend, cov.reduce, or fac.reduce are passed to emmeans). Otherwise, if object is an emmGrid object, its first element is used, and it must contain one estimate for each combination of the factors present in formula.

Conceptually, this function is equivalent to interaction.plot where the summarization function is thought to return the EMMs.

See Also

emmeans, interaction.plot

Examples

#--- Three-factor example
noise.lm = lm(noise ~ size * type * side, data = auto.noise)

# Separate interaction plots of size by type, for each side
emmip(noise.lm, type ~ size | side)

# One interaction plot, using combinations of size and side as the x factor
# ... with added confidence intervals
emmmip(noise.lm, type ~ side * size, CIs = TRUE)

# One interaction plot using combinations of type and side as the trace factor
emmip(noise.lm, type * side ~ size)

# Individual traces in panels
emmmip(noise.lm, ~ size | type * side)
**emmaobj**

*Construct an emmGrid object from scratch*

**Description**

This allows the user to incorporate results obtained by some analysis into an emmGrid object, enabling the use of emmGrid methods to perform related follow-up analyses.

**Usage**

```r
emmaobj(bhat, V, levels, linfct, df = NA, dffun, dfargs = list(),
         post.beta = matrix(NA), ...)
```

**Arguments**

- `bhat` Numeric. Vector of regression coefficients
- `V` Square matrix. Covariance matrix of `bhat`
- `levels` Named list or vector. Levels of factor(s) that define the estimates defined by `linfct`. If not a list, we assume one factor named "level"
- `linfct` Matrix. Linear functions of `bhat` for each combination of `levels`
- `df` Numeric value or function with arguments `(x, dfargs)`. If a number, that is used for the degrees of freedom. If a function, it should return the degrees of freedom for `sum(x*bhat)`, with any additional parameters in `dfargs`.
- `dffun` Overrides `df` if specified. This is a convenience to match the slot names of the returned object.
- `dfargs` List containing arguments for `df`. This is ignored if `df` is numeric.
- `post.beta` Matrix whose columns comprise a sample from the posterior distribution of the regression coefficients (so that typically, the column averages will be `bhat`). A 1 x 1 matrix of `NA` indicates that such a sample is unavailable.
- `...` Arguments passed to `update.emmGrid`

**Details**

The arguments must be conformable. This includes that the length of `bhat`, the number of columns of `linfct`, and the number of columns of `post.beta` must all be equal. And that the product of lengths in `levels` must be equal to the number of rows of `linfct`. The grid slot of the returned object is generated by `expand.grid` using `levels` as its arguments. So the rows of `linfct` should be in corresponding order.

The functions `qdrg` and `emmaobj` are close cousins, in that they both produce emmGrid objects. When starting with summary statistics for an existing grid, `emmaobj` is more useful, while `qdrg` is more useful when starting from an unsupported fitted model.

**Value**

An emmGrid object
See Also

qdrg, an alternative that is useful when starting with a fitted model not supported in emmeans.

Examples

# Given summary statistics for 4 cells in a 2 x 2 layout, obtain
# marginal means and comparisons thereof. Assume heteroscedasticity
# and use the Satterthwaite method
levels <- list(trt = c("A", "B"), dose = c("high", "low"))
ybar <- c(57.6, 43.2, 88.9, 69.8)
s <- c(12.1, 19.5, 22.8, 43.2)
n <- c(44, 11, 37, 24)
se2 = s^2 / n
Satt.df <- function(x, dfargs)
  sum(x * dfargs$v)^2 / sum((x * dfargs$v)^2 / (dfargs$n - 1))
expt.rg <- emmobj(bhat = ybar, V = diag(se2),
  levels = levels, linfct = diag(c(1, 1, 1, 1)),
  df = Satt.df, dfargs = list(v = se2, n = n), estName = "mean")
plot(expt.rg)
  ( trt.emm <- emmeans(expt.rg, "trt") )
  ( dose.emm <- emmeans(expt.rg, "dose") )
  rbind(pairs(trt.emm), pairs(dose.emm), adjust = "mvt")

emmeans

The emm_list class

Description

An emm_list object is simply a list of emmGrid objects. Such a list is returned, for example, by
emmeans with a two-sided formula or a list as its specs argument.

Details

Methods for emm_list objects include summary, CLD, coef, confint, contrast, pairs, plot, print, and test. These are all the same as those methods for emmGrid objects, with an additional
which argument (integer) to specify which members of the list to use. The default is which =
seq_along(object); i.e., the method is applied to every member of the emm_list object. The
exception is plot, where only the which[1]th element is plotted.

As an example, to summarize a single member – say the second one – of an emm_list, one
may use summary(object, which = 2), but it is probably preferable to directly summarize it
using summary(object[[2]]).
Set or change emmeans options

Description

Use `emm_options` to set or change various options that are used in the `emmeans` package. These options are set separately for different contexts in which `emmGrid` objects are created, in a named list of option lists.

Usage

```r
emm_options(...)
```

```r
get_emm_option(x, default = emm_defaults[[x]])
```

Arguments

- `...`: Option names and values (see Details)
- `x`: Character value - the name of an option to be queried
- `default`: Value to return if `x` is not found

Format

An object of class `list` of length 16.

Details

Currently, the following main list entries are supported:

- `ref_grid`: A named list of defaults for objects created by `ref_grid`. This could affect other objects as well. For example, if `emmeans` is called with a fitted model object, it calls `ref_grid` and this option will affect the resulting `emmGrid` object.
- `emmeans`: A named list of defaults for objects created by `emmeans` or `emtrends`.
- `contrast`: A named list of defaults for objects created by `contrast.emmGrid` or `pairs.emmGrid`.
- `summary`: A named list of defaults used by the methods `summary.emmGrid`, `predict.emmGrid`, `test.emmGrid`, `confint.emmGrid`, and `emmip`. The only option that can affect the latter four is "predict.method".
- `graphics.engine`: A character value matching `c("ggplot", "lattice")`, setting the default engine to use in `emmip` and `plot.emmGrid`. Defaults to "ggplot".
- `msg.interaction`: A logical value controlling whether or not a message is displayed when `emmeans` averages over a factor involved in an interaction. It is probably not appropriate to do this, unless the interaction is weak. Defaults to TRUE.
msg.nesting  A logical value controlling whether or not to display a message when a nesting structure is auto-detected. The existence of such a structure affects computations of EMMs. Sometimes, a nesting structure is falsely detected – namely when a user has omitted some main effects but included them in interactions. This does not change the model fit, but it produces a different parameterization that is picked up when the reference grid is constructed. Defaults to TRUE.

simplify.names  A logical value controlling whether to simplify (when possible) names in the model formula that refer to datasets – for example, should we simplify a predictor name like "data$trt" to just "trt"? Defaults to TRUE.

opt.digits  A logical value controlling the precision with which summaries are printed. If TRUE (default), the number of digits displayed is just enough to reasonably distinguish estimates from the ends of their confidence intervals; but always at least 3 digits. If FALSE, the system value getOption("digits") is used.

back.bias.adj  A logical value controlling whether we try to adjust bias when back-transforming. If FALSE, we use naive back transformation. If TRUE and sigma is available, a second-order adjustment is applied to estimate the mean on the response scale.

Some other options have more specific purposes:

estble.tol  Tolerance for determining estimability in rank-deficient cases. If absent, the value in emm_defaults$estble.tol is used.

save.ref_grid  Logical value of TRUE if you wish the latest reference grid created to be saved in .Last.ref_grid

Options for \texttt{lmer4::lmerMod} models  Options lmer.df, disable.pbkrtest, pbkrtest.limit, disable.lmerTest, and lmerTest.limit options affect how degrees of freedom are computed for lmerMod objects produced by the \texttt{lme4} package. See that section of the "models" vignette for details.

Value

\texttt{emm_options} returns the current options (same as the result of \texttt{getOption("emmeans")}) – invisibly, unless called with no arguments.

\texttt{get_emm_option} returns the currently stored option for \texttt{x}, or its default value if not found.

See Also

\texttt{update.emmGrid}

Examples

\begin{verbatim}
## Not run:
emmeans_options(ref_grid = list(level = .90),
contrasts = list(infer = c(TRUE,FALSE)),
estble.tol = 1e-6)
# Sets default confidence level to .90 for objects created by ref.grid
# AS WELL AS emmeans called with a model object (since it creates a
# reference grid). In addition, when we call 'contrast', 'pairs', etc.,
# confidence intervals rather than tests are displayed by default.

## End(Not run)
\end{verbatim}
# Not run:
emtrends(disable.pbkrtest = TRUE)
# This forces use of asymptotic methods for lmerMod objects.
# Set to FALSE or NULL to re-enable using pbkrtest.

## End(Not run)

# See tolerance being used for determining estimability
get_emm_option("estble.tol")

---

emtrends  
*Estimated marginal means of linear trends*

**Description**

The `emtrends` function is useful when a fitted model involves a numerical predictor \( x \) interacting with another predictor \( a \) (typically a factor). Such models specify that \( x \) has a different trend depending on \( a \); thus, it may be of interest to estimate and compare those trends. Analogous to the `emmeans` setting, we construct a reference grid of these predicted trends, and then possibly average them over some of the predictors in the grid.

**Usage**

```r
df <- data.frame(x = 1:10, a = gl(2, 5), y = rnorm(10))
model <- lmer(y ~ x + a + x:a + (1 | a), data = df)
emtrends(model, specs = "x:a", var = "x", delta.var = 0.01 * rng, data = df)
```

**Arguments**

- `model`  
  A supported model object (not a reference grid)

- `specs`  
  Specifications for what marginal trends are desired – as in `emmeans`

- `var`  
  Character value giving the name of a variable with respect to which a difference quotient of the linear predictors is computed. In order for this to be useful, `var` should be a numeric predictor that interacts with at least one factor in `specs`. Then instead of computing EMMs, we compute and compare the slopes of the `var` trend over levels of the specified other predictor(s). As in EMMs, marginal averages are computed for the predictors in `specs` and by. See also the “Generalizations” section below.

- `delta.var`  
  The value of \( h \) to use in forming the difference quotient \( (f(x + h) - f(x))/h \). Changing it (especially changing its sign) may be necessary to avoid numerical problems such as logs of negative numbers. The default value is 1/100 of the range of `var` over the dataset.

- `data`  
  As in `ref_grid`, you may use this argument to supply the dataset used in fitting the model, for situations where it is not possible to reconstruct the data. Otherwise, leave it missing.
transform  If object has a response transformation or link function, then specifying `transform = "response"` will cause `emtrends` to calculate the trends after back-transforming to the response scale. This is done using the chain rule, and standard errors are estimated via the delta method. With `transform = "none"` (the default), the trends are calculated on the scale of the linear predictor, without back-transforming it. This argument works similarly to the `transform` argument in `ref_grid`, in that the returned object is re-gridded to the new scale (see also `regrid`).

Additional arguments passed to other methods or to `ref_grid`.

Value

An `emmGrid` or `emm_list` object, according to `specs`. See `emmeans` for more details on when a list is returned.

Generalizations

Instead of a single predictor, the user may specify some monotone function of one variable, e.g., `var = "log(dose)"`. If so, the chain rule is applied. Note that, in this example, if `model` contains `log(dose)` as a predictor, we will be comparing the slopes estimated by that model, whereas specifying `var = "dose"` would perform a transformation of those slopes, making the predicted trends vary depending on `dose`.

See Also

`link(emmeans), ref_grid`

Examples

```r
fiber.lm <- lm(strength ~ diameter*machine, data=fiber)
# Obtain slopes for each machine ...
( fiber.emt <- emtrends(fiber.lm, "machine", var = "diameter") )
# ... and pairwise comparisons thereof
pairs(fiber.emt)

# Suppose we want trends relative to sqrt(diameter)...
emtrends(fiber.lm, ~ machine | diameter, var = "sqrt(diameter)",
at = list(diameter = c(20, 30)))
```

Description

This documents the methods that `ref_grid` calls. A user or package developer may add `emmeans` support for a model class by writing `recover_data` and `emm_basis` methods for that class.
Usage

recover_data(object, ...)  
## S3 method for class 'call'
recover_data(object, trms, na.action, data = NULL, 
params = NULL, ...)  

emem_basis(object, trms, xlev, grid, ...)  
.recover_data(object, ...)  
.emm_basis(object, trms, xlev, grid, ...)  
.emm_register(classes, pkgname)

Arguments

object An object of the same class as is supported by a new method.
... Additional parameters that may be supported by the method.
trms The terms component of object (typically with the response deleted, e.g. via delete.response)
na.action Integer vector of indices of observations to ignore; or NULL if none
data Data frame. Usually, this is NULL. However, if non-null, this is used in place of the reconstructed dataset. It must have all of the predictors used in the model, and any factor levels must match those used in fitting the model.
params Character vector giving the names of any variables in the model formula that are not predictors. An example would be a variable knots specifying the knots to use in a spline model.
xlev Named list of factor levels (excluding ones coerced to factors in the model formula)
grid A data.frame (provided by ref_grid) containing the predictor settings needed in the reference grid
classes Character names of one or more classes to be registered. The package must contain the functions recover_data.foo and emm_basis.foo for each class foo listed in classes.
pkgname Character name of package providing the methods (usually should be the second argument of .onLoad)

Value

The recover_data method must return a data.frame containing all the variables that appear as predictors in the model, and attributes "call", "terms", "predictors", and "responses". (recover_data.call will provide these attributes.)

The emm_basis method should return a list with the following elements:
X The matrix of linear functions over grid, having the same number of rows as grid and the number of columns equal to the length of bhat.

bhat The vector of regression coefficients for fixed effects. This should include any NAs that result from rank deficiencies.

nbasis A matrix whose columns form a basis for non-estimable functions of beta, or a 1x1 matrix of NA if there is no rank deficiency.

V The estimated covariance matrix of bhat.

dffun A function of \((k, dfargs)\) that returns the degrees of freedom associated with \(\text{sum}(k \times \text{bhat})\).

dfargs A list containing additional arguments needed for dffun.

recover_data and emm_basis are hidden exported versions of recover_data and emm_basis, respectively. They run in emmeans’s namespace, thus providing access to all existing methods.

Details

To create a reference grid, the ref_grid function needs to reconstruct the data used in fitting the model, and then obtain a matrix of linear functions of the regression coefficients for a given grid of predictor values. These tasks are performed by calls to recover_data and emm_basis respectively. A vignette giving details and examples is available via vignette("xtending", "emmeans")

To extend emmeans’s support to additional model types, one need only write S3 methods for these two functions. The existing methods serve as helpful guidance for writing new ones. Most of the work for recover_data can be done by its method for class "call", providing the terms component and na.action data as additional arguments. Writing an emm_basis method is more involved, but the existing methods (e.g., emmeans:::emm_basis.lm) can serve as models. Certain recover_data and emm_basis methods are exported from emmeans. (To find out, do methods("recover_data").) If your object is based on another model-fitting object, it may be that all that is needed is to call one of these exported methods and perhaps make modifications to the results. Contact the developer if you need others of these exported.

If the model has a multivariate response, bhat needs to be “flattened” into a single vector, and X and V must be constructed consistently.

In models where a non-full-rank result is possible (often, you can tell by seeing if there is a singular.ok argument in the model-fitting function), summary.emmGrid and its relatives check the estimability of each prediction, using the nonest.basis function in the estimability package.

The models already supported are detailed in the "models" vignette. Some packages may provide additional emmeans support for its object classes.

Communication between methods

If the recover_data method generates information needed by emm_basis, that information may be incorporated by creating a “misc” attribute in the returned recovered data. That information is then passed as the misc argument when ref_grid calls emm_basis.
Optional hooks

Some models may need something other than standard linear estimates and standard errors. If so, custom functions may be pointed to via the items `misc$estHook`, `misc$vcovHook` and `misc$postGridHook`. If just the name of the hook function is provided as a character string, then it is retrieved using `get`.

The `estHook` function should have arguments `'(object,do.se,tol,...)'` where `object` is the `emmGrid` object, `do.se` is a logical flag for whether to return the standard error, and `tol` is the tolerance for assessing estimability. It should return a matrix with 3 columns: the estimates, standard errors (NA when `do.se==FALSE`), and degrees of freedom (NA for asymptotic). The number of rows should be the same as `object@linfct`. The `vcovHook` function should have arguments `'(object,tol,...)'` as described. It should return the covariance matrix for the estimates. Finally, `postGridHook`, if present, is called at the very end of `ref_grid`; it takes one argument, the constructed object, and should return a suitably modified `emmGrid` object.

Registering S3 methods for a model class

The `.emm_register` function is provided as a convenience to conditionally register your S3 methods for a model class, `recover_data.foo` and `emm_basis.foo`, where `foo` is the class name. Your package should implement an `.onLoad` function and call `.emm_register` if `emmeans` is installed. See the example.

Note

Without an explicit `data` argument, `recover_data` returns the current version of the dataset. If the dataset has changed since the model was fitted, then this will not be the data used to fit the model. It is especially important to know this in simulation studies where the data are randomly generated or permuted, and in cases where several datasets are processed in one step (e.g., using `dplyr`). In those cases, users should be careful to provide the actual data used to fit the model in the `data` argument.

See Also

Vignette on extending emmeans

Examples

```r
## Not run:
#--- If your package provides recover_data and emm_grid methods for class 'mymod',
#--- put something like this in your package code -- say in zzz.R:
.onLoad = function(libname, pkpname) {
  if (requireNamespace("emmeans", quietly = TRUE))
    emmeans::.emm_register("mymod", pkpname)
}

## End(Not run)
```
**Description**

This is an unbalanced analysis-of-covariance example, where one covariate is affected by a factor. Feeder calves from various herds enter a feedlot, where they are fed one of three diets. The weight of the animal at entry is the covariate, and the weight at slaughter is the response.

**Usage**

`feedlot`

**Format**

A data frame with 67 observations and 4 variables:

- `herd`: a factor with levels 9 16 3 32 24 31 19 36 34 35 33, designating the herd that a feeder calf came from.
- `diet`: a factor with levels Low Medium High: the energy level of the diet given the animal.
- `swt`: a numeric vector: the weight of the animal at slaughter.
- `ewt`: a numeric vector: the weight of the animal at entry to the feedlot.

**Details**

The data arise from a Western Regional Research Project conducted at New Mexico State University. Calves born in 1975 in commercial herds entered a feedlot as yearlings. Both diets and herds are of interest as factors. The covariate, ewt, is thought to be dependent on herd due to different genetic backgrounds, breeding history, etc. The levels of herd ordered to similarity of genetic background.

Note: There are some empty cells in the cross-classification of herd and diet.

**Source**


**Examples**

```r
feedlot.lm <- lm(swt ~ ewt + herd*diet, data = feedlot)

# Obtain EMMs with a separate reference value of ewt for each herd. This reproduces the last part of Table 2 in the reference
emmeans(feedlot.lm, ~ diet | herd, cov.reduce = ewt ~ herd)
```
fiber  

Fiber data

Description

Fiber data from Montgomery Design (8th ed.), p.656 (Table 15.10). Useful as a simple analysis-of-covariance example.

Usage

fiber

Format

A data frame with 15 observations and 3 variables:

machine  a factor with levels A B C. This is the primary factor of interest.
strength  a numeric vector. The response variable.
diameter  a numeric vector. A covariate.

Details

The goal of the experiment is to compare the mean breaking strength of fibers produced by the three machines. When testing this, the technician also measured the diameter of each fiber, and this measurement may be used as a concomitant variable to improve precision of the estimates.

Source


Examples

fiber.lm <- lm(strength ~ diameter + machine, data=fiber)
ref_grid(fiber.lm)

# Covariate-adjusted means and comparisons
df_equality(fiber.lm, pairwise ~ machine)
hpd.summary

Summarize an emmGrid from a Bayesian model

Description

This function computes point estimates and HPD intervals for each factor combination in object@emmGrid. While this function may be called independently, it is called automatically by the S3 method summary.emmGrid when the object is based on a Bayesian model. (Note: the level argument, or its default, is passed as prob).

Usage

hpd.summary(object, prob, by, type, point.est = median, bias.adjust = get_emm_option("back.bias.adj"), sigma, ...)

Arguments

object an emmGrid object having a non-missing post.beta slot
prob numeric probability content for HPD intervals (note: when not specified, the current level option is used; see emm_options)
by factors to use as by variables
type prediction type as in summary.emmGrid
point.est function to use to compute the point estimates from the posterior sample for each grid point
bias.adjust Logical value for whether to adjust for bias in back-transforming (type = "response"). This requires a value of sigma to exist in the object or be specified.
sigma Error SD assumed for bias correction (when type = "response"). If not specified, object@misc$sigma is used, and an error is thrown if it is not found. Note: sigma may be a vector, as long as it conforms to the number of observations in the posterior sample.
...

Value

an object of class summary_emm

See Also

summary.emmGrid
Examples

```r
if(require("coda")) {
  # Create an emmGrid object from a system file
  cbpp.rg <- do.call(emmobj,
    readRDS(system.file("extdata", "cbpplist", package = "emmeans")))
  hpd.summary(emmeans(cbpp.rg, "period"))
}
```

### joint_tests

**Compute joint tests of the terms in a model**

**Description**

This function produces an analysis-of-variance-like table based on linear functions of predictors in a model or emmGrid object. Specifically, the function constructs, for each combination of factors (or covariates reduced to two or more levels), a set of (interaction) contrasts via `contrast`, and then tests them using `test` with `joint = TRUE`. Optionally, one or more of the predictors may be used as by variable(s), so that separate tables of tests are produced for each combination of them.

**Usage**

```r
joint_tests(object, by = NULL, show0df = FALSE, ...)
```

**Arguments**

- `object`: a fitted model or an emmGrid. If a fitted model, it is replaced by `ref_grid(object, cov.reduce = range,...)`
- `by`: character names of by variables. Separate sets of tests are run for each combination of these.
- `show0df`: logical value; if TRUE, results with zero numerator degrees of freedom are displayed, if FALSE they are skipped
- `...`: additional arguments passed to `ref_grid` and `emmeans`

**Details**

In models with only factors, no covariates, we believe these tests correspond to “type III” tests a la SAS, as long as equal-weighted averaging is used and there are no estimability issues. When covariates are present and interact with factors, the results depend on how the covariate is handled in constructing the reference grid. See the example at the end of this documentation. The point that one must always remember is that `joint_tests` always tests contrasts among EMMs, in the context of the reference grid, whereas type III tests are tests of model coefficients – which may or may not have anything to do with EMMs or contrasts.

**Value**

A summary_emm object (same as is produced by `summary.emmGrid`). All effects for which there are no estimable contrasts are omitted from the results.
ismeans

Wrappers for alternative naming of EMMs

See Also
test

Examples

```r
pigs.lm <- lm(log(conc) ~ source * factor(percent), data = pigs)
joint_tests(pigs.lm)            ## will be same as type III ANOVA
joint_tests(pigs.lm, weights = "outer") ## differently weighted
joint_tests(pigs.lm, by = "source")     ## separate joint tests of 'percent'

### Comparisons with type III tests

```r
# These two models have identical fitted values and residuals)

Joint_tests(toy.fac)

# ref grid uses mean(female) = 0.4
Joint_tests(toy.cov, cov.reduce = FALSE)  # ref grid uses female = c(0, 1)
Joint_tests(toy.cov, at = list(female = c(-1, 1)))  # center on intercept

# -- Compare with SAS output -- female as factor --

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>treat</td>
<td>1</td>
<td>488.8928571</td>
<td>488.8928571</td>
<td>404.60</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>female</td>
<td>1</td>
<td>78.8928571</td>
<td>78.8928571</td>
<td>65.29</td>
<td>0.0002</td>
</tr>
<tr>
<td>treat*female</td>
<td>1</td>
<td>1.7500000</td>
<td>1.7500000</td>
<td>1.45</td>
<td>0.2741</td>
</tr>
</tbody>
</table>

# -- Compare with SAS output -- female as covariate --

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Type III SS</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>treat</td>
<td>1</td>
<td>252.0833333</td>
<td>252.0833333</td>
<td>208.62</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>female</td>
<td>1</td>
<td>78.8928571</td>
<td>78.8928571</td>
<td>65.29</td>
<td>0.0002</td>
</tr>
<tr>
<td>female*treat</td>
<td>1</td>
<td>1.7500000</td>
<td>1.7500000</td>
<td>1.45</td>
<td>0.2741</td>
</tr>
</tbody>
</table>
```

Description

These are wrappers for emmeans and related functions to provide backward compatibility, or for users who may prefer to use other terminology than “estimated marginal means” – namely “least-squares means” or “predicted marginal means”.

See Also
test
Usage

lsmeans(...)

pmmeans(...)

lstrends(...)

pmtrends(...)

lsmip(...)

pmmip(...)

lsm(...)

pmm(...)

lsmobj(...)

pmmobj(...)

lsm.options(...)

get.lsm.option(x, default = emm_defaults[[x]])

Arguments

... Arguments passed to the corresponding emxxxx function

x Character name of desired option

default default value to return if x not found

Details

For each function with lsxxxx or pmxxxx in its name, the same function named emxxxx is called. Any estimator names or list items beginning with “em” are replaced with “ls” or “pm” before the results are returned.

Value

The result of the call to emxxxx, suitably modified.

get.lsm.option and lsm.options remap options from and to corresponding options in the lsmeans options system.

See Also

emmeans, emtrends, emmip, emm, emmobj, emm_options, get_emm_option
make.tran

Examples

```r
pigs.lm <- lm(log(conc) ~ source + factor(percent), data = pigs)
lsmeans(pigs.lm, "source")
```

make.tran (Response-transformation extensions)

Description

The make.tran function creates the needed information to perform transformations of the response variable, including inverting the transformation and estimating variances of back-transformed predictions via the delta method. make.tran is similar to make.link, but it covers additional transformations. The result can be used as an environment in which the model is fitted, or as the tran argument in update.emmGrid (when the given transformation was already applied in an existing model).

Usage

```r
make.tran(type = c("genlog", "power", "boxcox", "sympower", "asin.sqrt"),
            param = 1)
```

Arguments

- **type**: The name of the transformation. See Details.
- **param**: Numeric parameter needed for the transformation. Optionally, it may be a vector of two numeric values; the second element specifies an alternative base or origin for certain transformations. See Details.

Details

The functions emmeans, ref.grid, and related ones automatically detect response transformations that are recognized by examining the model formula. These are `log`, `log2`, `log10`, `sqrt`, `logit`, `probit`, `cauchit`, `cloglog`; as well as (for a response variable `y`) `asin(sqrt(y))`, `asinh(sqrt(y))`, and `sqrt(y) + sqrt(y+1)`. In addition, any constant multiple of these (e.g., `2*sqrt(y)`) is auto-detected and appropriately scaled (see also the tran.mult argument in update.emmGrid).

A few additional character strings may be supplied as the tran argument in update.emmGrid: "identity", "1/mu^2", "inverse", "reciprocal", "asin.sqrt", and "asinh.sqrt".

More general transformations may be provided as a list of functions and supplied as the tran argument as documented in update.emmGrid. The make.tran function returns a suitable list of functions for several popular transformations. Besides being usable with update, the user may use this list as an enclosing environment in fitting the model itself, in which case the transformation is auto-detected when the special name `linkfun` (the transformation itself) is used as the response transformation in the call. See the examples below.

Most of the transformations available in "make.tran" require a parameter, specified in `param`; in the following discussion, we use `p` to denote this parameter, and `y` to denote the response variable. The type argument specifies the following transformations:
"genlog" Generalized logarithmic transformation: \( \log(y + p) \), where \( y > -p \)

"power" Power transformation: \( y^p \), where \( y > 0 \). When \( p = 0 \), "log" is used instead

"boxcox" The Box-Cox transformation (unscaled by the geometric mean): \( (y^p - 1)/p \), where \( y > 0 \). When \( p = 0 \), \( \log(y) \) is used.

"sympower" A symmetrized power transformation on the whole real line: \( abs(y)^p \times \text{sign}(y) \). There are no restrictions on \( y \), but we require \( p > 0 \) in order for the transformation to be monotone and continuous.

"asin.sqrt" Arcsin-square-root transformation: \( \sin^{-1}(y/p)^{1/2} \). Typically, the parameter \( p \) is equal to 1 for a fraction, or 100 for a percentage.

The user may include a second element in \( \text{param} \) to specify an alternative origin (other than zero) for the "power", "boxcox", or "sympower" transformations. For example, 'type = "power", param = c(1.5,4)' specifies the transformation \( (y^4 - 1.5) \). In the "genpower" transformation, a second \( \text{param} \) element may be used to specify a base other than the default natural logarithm. For example, 'type = "genlog", param = c(.5,10)' specifies the \( \log_{10}(y + 5) \) transformation.

For purposes of back-transformation, the 'sqrt(y) + sqrt(y+1)' transformation is treated exactly the same way as '2*sqrt(y)', because both are regarded as estimates of \( 2\sqrt{\mu} \).

Value

A list having at least the same elements as those returned by \texttt{make.link}. The \texttt{linkfun} component is the transformation itself.

Note

We modify certain \texttt{make.link} results in transformations where there is a restriction on valid prediction values, so that reasonable inverse predictions are obtained, no matter what. For example, if a sqrt transformation was used but a predicted value is negative, the inverse transformation is zero rather than the square of the prediction. A side effect of this is that it is possible for one or both confidence limits, or even a standard error, to be zero.

Examples

# Fit a model using an oddball transformation:
bctran <- make.tran("boxcox", 0.368)
warp.bc <- with(bctran,  
  lm(linkfun(breaks) ~ wool * tension, data = warpbreaks))

# Obtain back-transformed LS means:
emmeans(warp.bc, ~ tension | wool, type = "response")

## Not run:
# An existing model 'mod' was fitted with a log(y + 1) transformation...
mod.rg <- update(ref_grid(mod), tran = make.tran("genlog", 1))
emmeans(mod.rg, "treatment")

## End(Not run)
MOats

Oats data in multivariate form

Description

This is the Oats dataset provided in the nlme package, but it is rearranged as one multivariate observation per plot.

Usage

MOats

Format

A data frame with 18 observations and 3 variables

Variety  a factor with levels Golden Rain, Marvellous, Victory
Block  an ordered factor with levels VI < V < III < IV < II < I
yield  a matrix with 4 columns, giving the yields with nitrogen concentrations of 0, .2, .4, and .6.

Details

These data arise from a split-plot experiment reported by Yates (1935) and used as an example in Pinheiro and Bates (2000) and other texts. Six blocks were divided into three whole plots, randomly assigned to the three varieties of oats. The whole plots were each divided into 4 split plots and randomized to the four concentrations of nitrogen.

Source

The dataset Oats in the nlme package.

References


Examples

MOats.lm <- lm (yield ~ Block + Variety, data = MOats)
MOats.rg <- ref_grid (MOats.lm, mult.name = "nitro")
emmeans(MOats.rg, ~ nitro | Variety)
**Models supported in emmeans**

**Description**

Documentation for models has been moved to a vignette. To access it, use `vignette("models", "emmeans")`.

**neuralgia**

**Neuralgia data**

**Description**

These data arise from a study of analgesic effects of treatments of elderly patients who have neuralgia. Two treatments and a placebo are compared. The response variable is whether the patient reported pain or not. Researchers recorded the age and gender of 60 patients along with the duration of complaint before the treatment began.

**Usage**

```r
euralgia
```

**Format**

A data frame with 60 observations and 5 variables:

- **Treatment**  Factor with 3 levels A, B, and P. The latter is placebo
- **Sex**  Factor with two levels F and M
- **Age**  Numeric covariate – patient’s age in years
- **Duration**  Numeric covariate – duration of the condition before beginning treatment
- **Pain**  Binary response factor with levels No and Yes

**Source**


**Examples**

```r
# Model and analysis shown in the SAS report:
neuralgia.glm <- glm(Pain ~ Treatment * Sex + Age, family = binomial(),
data = neuralgia)
pairs(emmeans(neuralgia.glm, ~ Treatment, at = list(Sex = "F")),
     reverse = TRUE, type = "response", adjust = "bonferroni")
```
Description

This observational dataset involves three factors, but where several factor combinations are missing. It is used as a case study in Milliken and Johnson, Chapter 17, p.202. (You may also find it in the second edition, p.278.)

Usage

nutrition

Format

A data frame with 107 observations and 4 variables:

- `age` a factor with levels 1, 2, 3, 4. Mother’s age group.
- `group` a factor with levels FoodStamps, NoAid. Whether or not the family receives food stamp assistance.
- `race` a factor with levels Black, Hispanic, White. Mother’s race.
- `gain` a numeric vector (the response variable). Gain score (posttest minus pretest) on knowledge of nutrition.

Details

A survey was conducted by home economists “to study how much lower-socioeconomic-level mothers knew about nutrition and to judge the effect of a training program designed to increase their knowledge of nutrition.” This is a messy dataset with several empty cells.

Source


Examples

```r
nutr.aov <- aov(gain ~ (group + age + race)^2, data = nutrition)

# Summarize predictions for age group 3
nutr.emm <- emmeans(nutr.aov, ~ race * group, at = list(age="3"))

emmip(nutr.emm, race ~ group)

# Hispanics seem exceptional; but this doesn’t test out due to very sparse data
CLD(nutr.emm, by = "group")
CLD(nutr.emm, by = "race")
```
Description

This example dataset on sales of oranges has two factors, two covariates, and two responses. There is one observation per factor combination.

Usage

oranges

Format

A data frame with 36 observations and 6 variables:

store   a factor with levels 1 2 3 4 5 6. The store that was observed.
day    a factor with levels 1 2 3 4 5 6. The day the observation was taken (same for each store).
price1 a numeric vector. Price of variety 1.
price2 a numeric vector. Price of variety 2.
sales1 a numeric vector. Sales (per customer) of variety 1.
sales2 a numeric vector. Sales (per customer) of variety 2.

Source


References


Examples

# Example on p.244 of Littell et al.
oranges.lm <- lm(sales1 ~ price1*day, data = oranges)
emmeans(oranges.lm, "day")

# Example on p.246 of Littell et al.
emmeans(oranges.lm, "day", at = list(price1 = 0))

# A more sensible model to consider, IMHO (see vignette("interactions"))
org.mlm <- lm(cbind(sales1, sales2) ~ price1 * price2 + day + store,
              data = oranges)
**Description**

A two-factor experiment with some observations lost

**Usage**

```r
pigs
```

**Format**

A data frame with 29 observations and 3 variables:

- **source** Source of protein in the diet (factor with 3 levels: fish meal, soybean meal, dried skim milk)
- **percent** Protein percentage in the diet (numeric with 4 values: 9, 12, 15, and 18)
- **conc** Concentration of free plasma leucine, in mcg/ml

**Source**


**Examples**

```r
pigs.lm <- lm(log(conc) ~ source + factor(percent), data = pigs)
emmeans(pigs.lm, "source")
```

**plot.emmGrid**  
*Plot an emmGrid or summary_emm object*

**Description**

Methods are provided to plot EMMs as side-by-side CIs, and optionally to display “comparison arrows” for displaying pairwise comparisons.
Usage

```r
## S3 method for class 'emmGrid'
plot(x, y, type, CIs = TRUE, PIs = FALSE,
     comparisons = FALSE, colors = c("black", "blue", "blue", "red"),
     alpha = 0.05, adjust = "tukey", int.adjust = "none", intervals,
     frequentist, ...)

## S3 method for class 'summary_emm'
plot(x, y, horizontal = TRUE, xlab, ylab, layout,
     ...)
```

Arguments

- `x` Object of class `emmGrid` or `summary_emm`
- `y` (Required but ignored)
- `type` Character value specifying the type of prediction desired (matching "linear.predictor", "link", or "response"). See details under `summary.emmGrid`.
- `CIs` Logical value. If `TRUE`, confidence intervals are plotted for each estimate.
- `PIs` Logical value. If `TRUE`, prediction intervals are plotted for each estimate. If object is a Bayesian model, this requires `frequentist = TRUE` and `sigma = (some value)`. Prediction intervals are not available with `engine = "lattice"`.
- `comparisons` Logical value. If `TRUE`, “comparison arrows” are added to the plot, in such a way that the degree to which arrows overlap reflects as much as possible the significance of the comparison of the two estimates. (A warning is issued if this can’t be done.)
- `colors` Character vector of color names to use for estimates, CIs, PIs, and comparison arrows, respectively. CIs and PIs are rendered with some transparency, and colors are recycled if the length is less than four; so all plot elements are visible even if a single color is specified.
- `alpha` The significance level to use in constructing comparison arrows
- `adjust` Character value: Multiplicity adjustment method for comparison arrows only.
- `int.adjust` Character value: Multiplicity adjustment method for the plotted confidence intervals only.
- `intervals` If specified, it is used to set CIs. This is the previous name of CIs and is provided for backward compatibility.
- `frequentist` Logical value. If there is a posterior MCMC sample and frequentist is non-missing and `TRUE`, a frequentist summary is used for obtaining the plot data, rather than the posterior point estimate and HPD intervals. This argument is ignored when it is not a Bayesian model.
- `...` Additional arguments passed to `update.emmGrid`, `predict.emmGrid`, or `dotplot`
- `horizontal` Logical value specifying whether the intervals should be plotted horizontally or vertically
- `xlab` Character label for horizontal axis
- `ylab` Character label for vertical axis
- `layout` Numeric value passed to `dotplot`
Details

If any by variables are in force, the plot is divided into separate panels. These functions use the `dotplot` function, and thus require that the `lattice` package be installed. For "summary_emm" objects, the ... arguments in `plot` are passed only to `dotplot`, whereas for "emmGrid" objects, the object is updated using ... before summarizing and plotting.

In plots with `comparisons = TRUE`, the resulting arrows are only approximate, and in some cases may fail to accurately reflect the pairwise comparisons of the estimates – especially when estimates having large and small standard errors are intermingled in just the wrong way. Note that the maximum and minimum estimates have arrows only in one direction, since there is no need to compare them with anything higher or lower, respectively.

If `adjust` or `int.adjust` are not supplied, they default to the internal `adjust` setting saved in `pairs(x)` and `x` respectively (see `update.emmGrid`).

Examples

```r
warp.lm <- lm(breaks ~ wool * tension, data = warpbreaks)
warp.emm <- emmeans(warp.lm, ~ tension | wool)
plot(warp.emm)
plot(warp.emm, by = NULL, comparisons = TRUE, adjust = "mvt",
     horizontal = FALSE, colors = "darkgreen")
```

**pwpp**

*Pairwise P-value plot*

Description

Constructs a plot of P values associated with pairwise comparisons of estimated marginal means.

Usage

```r
pwpp(emm, method = "pairwise", by, sort = TRUE, values = TRUE,
     rows = ".", xlab, ylab, xsub = "", add.space = 0, ...)
```

Arguments

- **emm**
  - An emmGrid object
- **method**
  - Character or list. Passed to `contrast`, and defines the contrasts to be displayed. Any contrast method may be used, provided that each contrast includes one coefficient of 1, one coefficient of -1, and the rest 0. That is, calling `contrast(object,method)` produces a set of comparisons, each with one estimate minus another estimate.
- **by**
  - Character vector of variable(s) in the grid to condition on. These will create different panels, one for each level or level-combination. Grid factors not in by are the primary factors: whose levels or level combinations are compared pairwise.
sort  Logical value. If TRUE, levels of the factor combinations are ordered by their marginal means. If FALSE, they appear in order based on the existing ordering of the factor levels involved. Note that the levels are ordered the same way in all panels, and in many cases this implies that the means in any particular panel will not be ordered even when sort = TRUE.

values Logical value. If TRUE, the values of the EMMs are included in the plot. When there are several side-by-side panels due to by variable(s), the labels showing values start stealing a lot of space from the plotting area; in those cases, it may be desirable to specify FALSE or use rows so that some panels are vertically stacked.

rows Character vector of which by variable(s) are used to define rows of the panel layout. Those variables in by not included in rows define columns in the array of panels. A "." indicates that only one row is used, so all panels are stacked side-by-side.

xlab Character label to use in place of the default for the P-value axis.

ylab Character label to use in place of the default for the primary-factor axis.

xsub Character label used as caption at the lower right of the plot.

add.space Numeric value to adjust amount of space used for value labels. Positioning of value labels is tricky, and depends on how many panels and the physical size of the plotting region. This parameter allows the user to adjust the position. Changing it by one unit should shift the position by about one character width (right if positive, left if negative).

... Additional arguments passed to contrast and summary.emmGrid

Details

Factor levels (or combinations thereof) are plotted on the vertical scale, and P values are plotted on the horizontal scale. Each P value is plotted twice – at vertical positions corresponding to the levels being compared – and connected by a line segment. Thus, it is easy to visualize which P values are small and large, and which levels are compared. In addition, factor levels are color-coded, and the points and half-line segments appear in the color of the other level. The P-value scale is nonlinear, so as to stretch-out smaller P values and compress larger ones.

If xlab, ylab, and xsub are not provided, reasonable labels are created. xsub is used to note special features; e.g., equivalence thresholds or one-sided tests.

Note

The ggplot2 package must be installed in order for pwpp to work.

Examples

pigs.lm <- lm(log(conc) ~ source * factor(percent), data = pigs)
emm = emmeans(pigs.lm, ~ percent | source)
pwpp(emm)
pwpp(emm, method = "trt.vs.ctrl1", type = "response", side = ">")
Quick and dirty reference grid

Description

This function may make it possible to compute a reference grid for a model object that is otherwise not supported.

Usage

qdrg(formula, data, coef, mcmc, vcov, object, df, subset, weights, contrasts, link, qr, ...)

Arguments

- formula: Formula for the fixed effects
- data: Dataset containing the variables in the model
- coef: Fixed-effect regression coefficients (must conform to formula)
- mcmc: Posterior sample of fixed-effect coefficients
- vcov: Variance-covariance matrix of the fixed effects
- object: Optional model object. If provided, it is used to set certain other arguments, if not specified. See Details.
- df: Error degrees of freedom
- subset: Subset of data used in fitting the model
- weights: Weights used in fitting the model
- contrasts: List of contrasts specified in fitting the model
- link: Link function (character or list) used, if a generalized linear model. (Note: response transformations are auto-detected from formula)
- qr: QR decomposition of the model matrix; needed only if there are NAs in coef.
- ...: Optional arguments passed to ref_grid

Details

If object is specified, it is used to try to obtain certain other arguments, as detailed below. The user should ensure that these defaults will work. The default values for the arguments are as follows:

- formula: Required unless obtainable via formula(object)
- data: Required if variables are not in parent.frame() or obtainable via object$data
- coef: coef(object)
- mcmc: object$sample
- vcov: vcov(object)
- df: Set to Inf if not available in object$df.residual
• subset: NULL (so that all observations in `data` are used)
• contrasts: NULL (so that `getOption("contrasts")` is used)

The functions `qdrg` and `emmobj` are close cousins, in that they both produce `emmGrid` objects. When starting with summary statistics for an existing grid, `emmobj` is more useful, while `qdrg` is more useful when starting from a fitted model.

Value

An `emmGrid` object constructed from the arguments

See Also

`emmobj` for an alternative way to construct an `emmGrid`.

Examples

```r
if(require(coda) && require(lme4)) {
  # Use a stored example having a posterior sample
  # Model is based on the data in lme4::cbpp
  post <- readRDS(system.file("extdata", "cbpplist", package = "emmeans"))$post.beta
  rg1 <- qdrg(~ size + period, data = lme4::cbpp, mcmc = post, link = "logit")
  summary(rg1, type = "response")
}
if (require(biglm)) {
  bigmod <- biglm(log(conc) ~ source + factor(percent), data = pigs)
  rg2 <- qdrg(object = bigmod, data = pigs)
  summary(emmeans(rg2, "source"), type = "response")
}
```

rbind.emmGrid

Combine or subset emmGrid objects

Description

These functions provide methods for `rbind` and `[` that may be used to combine `emmGrid` objects together, or to extract a subset of cases. The primary reason for doing this would be to obtain multiplicity-adjusted results for smaller or larger families of tests or confidence intervals.

Usage

```r
## S3 method for class 'emmGrid'
rbind(..., deparse.level = 1, adjust = "bonferroni")
```

```r
## S3 method for class 'emmGrid'
e1 + e2
```
## S3 method for class 'emmGrid'

x[i, adjust, drop.levels = TRUE, ...]

### Arguments

... In `rbind`, object(s) of class `emmGrid`. In "[", it is ignored.

deparse.level (required but not used)

adjust Character value passed to `update.emmGrid`

e1 An `emmGrid` object

e2 Another `emmGrid` object

x An `emmGrid` object to be subsetted

i Integer vector of indexes

drop.levels Logical value. If TRUE, the "levels" slot in the returned object is updated to hold only the predictor levels that actually occur

### Value

A revised object of class `emmGrid`

The result of `e1 + e2` is the same as `rbind(e1,e2)`

### Note

`rbind` throws an error if there are incompatibilities in the objects’ coefficients, covariance structures, etc. But they are allowed to have different factors; a missing level `.` is added to factors as needed.

### Examples

```r
warp.lm <- lm(breaks ~ wool * tension, data = warpbreaks)
warp.rg <- ref_grid(warp.lm)

# Show only 3 of the 6 cases
summary(warp.rg[c(2,4,5)])

# Do all pairwise comparisons within rows or within columns,
# all considered as one family of tests:
w.t <- pairs(emmeans(warp.rg, ~ wool | tension))
t.w <- pairs(emmeans(warp.rg, ~ tension | wool))
rbind(w.t, t.w, adjust = "mvt")
update(w.t + t.w, adjust = "fdr")  # same as above except for adjustment
```
Create a reference grid from a fitted model

Description

Using a fitted model object, determine a reference grid for which estimated marginal means are defined. The resulting ref_grid object encapsulates all the information needed to calculate EMMs and make inferences on them.

Usage

ref_grid(object, at, cov.reduce = mean, mult.names, mult.levs,
        options = get_emm_option("ref_grid"), data, df, type,
        transform = c("none", "response", "mu", "unlink", "log"), nesting,
        covnest = FALSE, offset, sigma, ...)

Arguments

object An object produced by a supported model-fitting function, such as lm. Many models are supported. See vignette("models", "emmeans").
at Optional named list of levels for the corresponding variables
cov.reduce A function, logical value, or formula; or a named list of these. Each covariate not specified in at is reduced according to these specifications. See the section below on “Using cov.reduce”.
mult.names Character value: the name(s) to give to the pseudo-factor(s) whose levels delineate the elements of a multivariate response. If this is provided, it overrides the default name(s) used for class(object) when it has a multivariate response (e.g., the default is "rep.meas" for "mlm" objects).
mult.levs A named list of levels for the dimensions of a multivariate response. If there is more than one element, the combinations of levels are used, in expand.grid order. The (total) number of levels must match the number of dimensions. If mult.name is specified, this argument is ignored.
options If non-NULL, a named list of arguments to pass to update.emmGrid, just after the object is constructed.
data A data.frame to use to obtain information about the predictors (e.g. factor levels). If missing, then recover_data is used to attempt to reconstruct the data. See the note with recover_data for an important precaution.
df Numeric value. This is equivalent to specifying options(df = df). See update.emmGrid.
type Character value. If provided, this is saved as the "predict.type" setting. See update.emmGrid and the section below on prediction types and transformations.
transform Character value. If other than "none", the reference grid is reconstructed via regrid with the given transform argument. See the section below on prediction types and transformations.
**ref_grid**

- **nesting**: If the model has nested fixed effects, this may be specified here via a character vector or named list specifying the nesting structure. Specifying nesting overrides any nesting structure that is automatically detected. See Details.

- **covnest**: Logical value. If TRUE, covariates having more than one value in the reference grid are included when auto-detecting nesting. Set this to TRUE only if you have covariate values that logically depend on some other factor’s levels.

- **offset**: Numeric scalar value (if a vector, only the first element is used). This may be used to add an offset, or override offsets based on the model. A common usage would be to specify offset = 0 for a Poisson regression model, so that predictions from the reference grid become rates relative to the offset that had been specified in the model.

- **sigma**: Numeric value to use for subsequent predictions or back-transformation bias adjustments. If not specified, we use sigma(object), if available, and NULL otherwise.

- **...**: Optional arguments passed to `emm_basis`, such as vcov. (see Details below) or options for certain models (see vignette("models", "emmeans").

**Details**

To users, the `ref_grid` function itself is important because most of its arguments are in effect arguments of `emmeans` and related functions, in that those functions pass their ... arguments to `ref_grid`.

The reference grid consists of combinations of independent variables over which predictions are made. Estimated marginal means are defined as these predictions, or marginal averages thereof. The grid is determined by first reconstructing the data used in fitting the model (see `recover_data`), or by using the data.frame provided in data. The default reference grid is determined by the observed levels of any factors, the ordered unique values of character-valued predictors, and the results of `cov.reduce` for numeric predictors. These may be overridden using at. See also the section below on recovering/overriding model information.

**Value**

An object of the S4 class "emmGrid" (see `emmGrid-class`). These objects encapsulate everything needed to do calculations and inferences for estimated marginal means, and contain nothing that depends on the model-fitting procedure.

**Using cov.reduce**

`cov.reduce` may be a function, logical value, formula, or a named list of these.

If a single function, it is applied to each covariate.

If logical and TRUE, mean is used. If logical and FALSE, it is equivalent to specifying ‘function(x) sort(unique(x))’, and these values are considered part of the reference grid; thus, it is a handy alternative to specifying these same values in at.

If a formula (which must be two-sided), then a model is fitted to that formula using `lm`; then in the reference grid, its response variable is set to the results of `predict` for that model, with the reference grid as newdata. (This is done after the reference grid is determined.) A formula is appropriate here when you think experimental conditions affect the covariate as well as the response.
If `cov.reduce` is a named list, then the above criteria are used to determine what to do with covariates named in the list. (However, formula elements do not need to be named, as those names are determined from the formulas’ left-hand sides.) Any unresolved covariates are reduced using “mean”.

Any `cov.reduce` specification for a covariate also named in `at` is ignored.

**Interdependent covariates**

Care must be taken when covariate values depend on one another. For example, when a polynomial model was fitted using predictors `x`, `x^2` (equal to `x^2`), and `x^3` (equal to `x^3`), the reference grid will by default set `x^2` and `x^3` to their means, which is inconsistent. The user should instead use the `at` argument to set these to the square and cube of mean(`x`). Better yet, fit the model using a formula involving `poly(x, 3)` or `I(x^2)` and `I(x^3)`; then there is only `x` appearing as a covariate; it will be set to its mean, and the model matrix will have the correct corresponding quadratic and cubic terms.

**Matrix covariates**

Support for covariates that appear in the dataset as matrices is very limited. If the matrix has but one column, it is treated like an ordinary covariate. Otherwise, with more than one column, each column is reduced to a single reference value – the result of applying `cov.reduce` to each column (averaged together if that produces more than one value); you may not specify values in `at`; and they are not treated as variables in the reference grid, except for purposes of obtaining predictions.

**Recovering or overriding model information**

Ability to support a particular class of object depends on the existence of `recover_data` and `emmeans` methods – see extending-emmeans for details. The call `methods("recover_data")` will help identify these.

**Data.** In certain models, (e.g., results of `glmer.nb`), it is not possible to identify the original dataset. In such cases, we can work around this by setting `data` equal to the dataset used in fitting the model, or a suitable subset. Only the complete cases in `data` are used, so it may be necessary to exclude some unused variables. Using `data` can also help save computing, especially when the dataset is large. In any case, `data` must represent all factor levels used in fitting the model. It *cannot* be used as an alternative to `at`. (Note: If there is a pattern of NAs that caused one or more factor levels to be excluded when fitting the model, then `data` should also exclude those levels.)

**Covariance matrix.** By default, the variance-covariance matrix for the fixed effects is obtained from `object`, usually via its `vcov` method. However, the user may override this via a `vcov.` argument, specifying a matrix or a function. If a matrix, it must be square and of the same dimension and parameter order of the fixed effects. If a function, must return a suitable matrix when it is called with `object` as its only argument.

**Nested factors.** Having a nesting structure affects marginal averaging in `emmeans` in that it is done separately for each level (or combination thereof) of the grouping factors. `ref_grid` tries to discern which factors are nested in other factors, but it is not always obvious, and if it misses some, the user must specify this structure via `nesting`; or later using `update.emmGrid`. The nesting argument may be a character vector or a named list. If a list, each name should be the name of a single factor in the grid, and its entry a character vector of the name(s) of its grouping factor(s). `nested` may also be a character value of the form "factor1 %in% (factor2*factor3)"
(the parentheses are optional). If there is more than one such specification, they may be appended separated by commas, or as separate elements of a character vector. For example, these specifications are equivalent: nesting = list(state = "country", city = c("state", "country"), nesting = "state %in% country, city %in% (state*country)", and nesting = c("state %in% country", "city %in% state*country").

In certain unusual cases, a covariate (rather than a factor) may be nested. Support for such situations is limited to the extent that only covariate values that exactly match a value in the dataset is permitted. I recommend supplying a reference dataset in the data argument that contains the desired covariate values for the reference grid; then the nesting will be handled correctly if you specify covnest = TRUE and cov.reduce = FALSE.

**Predictors with subscripts and data-set references**

When the fitted model contains subscripts or explicit references to data sets, the reference grid may optionally be post-processed to simplify the variable names, depending on the simplify.names option (see emm_options), which by default is TRUE. For example, if the model formula is data1$resp ~ data1$trt + data2[[3]] + data2["cov"], the simplified predictor names (for use, e.g., in the specs for emmeans) will be trt, data2[[3]], and cov. Numerical subscripts are not simplified; nor are variables having simplified names that coincide, such as if data2$trt were also in the model.

Please note that this simplification is performed after the reference grid is constructed. Thus, non-simplified names must be used in the at argument (e.g., at = list("data2["cov"] = 2:4).

If you don't want names simplified, use emm_options(simplify.names = FALSE).

**Prediction types and transformations**

There is a subtle difference between specifying `type = "response"` and `transform = "response"`. While the summary statistics for the grid itself are the same, subsequent use in emmeans will yield different results if there is a response transformation or link function. With `type = "response"`, EMMs are computed by averaging together predictions on the linear-predictor scale and then back-transforming to the response scale; while with `transform = "response"`, the predictions are already on the response scale so that the EMMs will be the arithmetic means of those response-scale predictions. To add further to the possibilities, geometric means of the response-scale predictions are obtainable via `transform = "log", type = "response"`.

**Side effect**

The most recent result of ref_grid, whether called directly or indirectly via emmeans, emtrends, or some other function that calls one of these, is saved in the user's environment as .Last.ref_grid. This facilitates checking what reference grid was used, or reusing the same reference grid for further calculations. This automatic saving is enabled by default, but may be disabled via `emm_options(save.ref_grid = FALSE)`, and re-enabled by specifying TRUE.

**See Also**

Reference grids are of class emmGrid, and several methods exist for them – for example summary.emmGrid.

Reference grids are fundamental to emmeans. Supported models are detailed in vignette("models", "emmeans").
regrid

Reconstruct a reference grid with a new transformation or posterior sample

Description

The typical use of this function is to cause EMMs to be computed on a different scale, e.g., the back-transformed scale rather than the linear-predictor scale. In other words, if you want back-transformed results, do you want to average and then back-transform, or back-transform and then average?

Usage

regrid(object, transform = c("response", "mu", "unlink", "log", "none", "pass"), inv.log.lbl = "response", predict.type, bias.adjust = get_emm_option("back.bias.adj"), sigma, N.sim, sim = mvtnorm::rmvnorm, ...)

Arguments

object An object of class emmGrid
**regrid**

transform Character or logical value. If "response" or "mu", the inverse transformation is applied to the estimates in the grid (but if there is both a link function and a response transformation, "mu" back-transforms only the link part); if "log", the results are formulated as if the response had been log-transformed; if "none", predictions thereof are on the same scale as in object, and any internal transformation information is preserved. If transform = "pass", the object is not re-gridded in any way (this may be useful in conjunction with N.sim). For compatibility with past versions, transform may also be logical; TRUE is taken as "response", and FALSE as "none".

inv.log.lbl Character value. This applies only when transform = "log", and is used to label the predictions if subsequently summarized with type = "response".

predict.type Character value. If provided, the returned object is updated with the given type to use by default by summary.emmGrid (see update.emmGrid). This may be useful if, for example, when one specifies transform = "log" but desires summaries to be produced by default on the response scale.

bias.adjust Logical value for whether to adjust for bias in back-transforming (transform = "response"). This requires a value of sigma to exist in the object or be specified.

sigma Error SD assumed for bias correction (when transform = "response" and a transformation is in effect). If not specified, object@misc$sigma is used, and an error is thrown if it is not found.

N.sim Integer value. If specified and object is based on a frequentist model (i.e., does not have a posterior sample), then a fake posterior sample is generated using the function sim.

sim A function of three arguments (no names are assumed). If N.sim is supplied with a frequentist model, this function is called with respective arguments N.sim, object@bhat, and object@V. The default is the multivariate normal distribution.

... Ignored.

Details

The regrid function reparameterizes an existing ref.grid so that its linfct slot is the identity matrix and its bhat slot consists of the estimates at the grid points. If transform is TRUE, the inverse transform is applied to the estimates. Outwardly, when transform = "response", the result of summary.emmGrid after applying regrid is identical to the summary of the original object using ‘type="response"’. But subsequent EMMs or contrasts will be conducted on the new scale – which is the reason this function exists.

In cases where the degrees of freedom depended on the linear function being estimated, the d.f. from the reference grid are saved, and a kind of “containment” method is substituted in the returned object whereby the calculated d.f. for a new linear function will be the minimum d.f. among those having nonzero coefficients. This is kind of an ad hoc method, and it can over-estimate the degrees of freedom in some cases.

This function may also be used to convert a reference grid for a frequentist model to one for a Bayesian model. To do so, specify a value for N.sim and a posterior sample is simulated using the function sim. The grid may be further processed in accordance with the other arguments; or if
transform = "pass", it is simply returned with the only change being the addition of the posterior sample.

Value
An emmGrid object with the requested changes

Note
Another way to use regrid is to supply a transform argument to regrid (either directly of indirectly via emmeans). This is often a simpler approach if the reference grid has not already been constructed.

Examples

pigs.lm <- lm(log(conc) ~ source + factor(percent), data = pigs)
rg <- ref_grid(pigs.lm)

# This will yield EMMs as GEOMETRIC means of concentrations:
(emm1 <- emmeans(rg, "source", type = "response"))
pairs(emm1) ## We obtain RATIOS

# This will yield EMMs as ARITHMETIC means of concentrations:
(emm2 <- emmeans(regrid(rg, transform = "response"), "source"))
pairs(emm2) ## We obtain DIFFERENCES
# Same result, useful if we hadn't already created 'rg'
# emm2 <- emmeans(pigs.lm, "source", transform = "response")

# Simulate a posterior sample
set.seed(2.71828)
rgb <- regrid(rg, N.sim = 200, transform = "pass")
emmeans(rgb, "source", type = "response") ## similar to emm1

Description
Miscellaneous methods for emmGrid objects

Usage

## S3 method for class 'emmGrid'
str(object, ...)

## S3 method for class 'emmGrid'
print(x, ...)

## S3 method for class 'emmGrid'
vcov(object, ...)
Arguments

- **object**: An emmGrid object
- **x**: An emmGrid object

Value

The `vcov` method returns a symmetric matrix of variances and covariances for `predict.emmGrid(object, type = "lp")`

Description

These are the primary methods for obtaining numerical or tabular results from an emmGrid object.

Usage

```r
## S3 method for class 'emmGrid'
summary(object, infer, level, adjust, by, type, df, null,
         delta, side, frequentist,
         bias.adjust = get_emm_option("back.bias.adj"), sigma, ...)

## S3 method for class 'emmGrid'
predict(object, type, interval = c("none", "confidence", "prediction"), level = 0.95,
         bias.adjust = get_emm_option("back.bias.adj"), sigma, ...)

## S3 method for class 'emmGrid'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

## S3 method for class 'summary_emm'
x[... as.df = TRUE]

## S3 method for class 'emmGrid'
confint(object, parm, level = 0.95, ...)

test(object, null, ...)
```

```r
## S3 method for class 'emmGrid'
test(object, null = 0, joint = FALSE, verbose = FALSE, rows, by, status = FALSE, ...)
```
Arguments

object
An object of class "emmGrid" (see emmGrid-class)

infer
A vector of one or two logical values. The first determines whether confidence intervals are displayed, and the second determines whether t tests and P values are displayed. If only one value is provided, it is used for both.

level
Numerical value between 0 and 1. Confidence level for confidence intervals, if infer[1] is TRUE.

adjust
Character value naming the method used to adjust p values or confidence limits; or to adjust comparison arrows in plot. See the P-value adjustments section below.

by
Character name(s) of variables to use for grouping into separate tables. This affects the family of tests considered in adjusted P values.

type
Character: type of prediction desired. This only has an effect if there is a known transformation or link function. "response" specifies that the inverse transformation be applied. "mu" (or equivalently, "unlink") is usually the same as "response", but in the case where the model has both a link function and a response transformation, only the link part is back-transformed. Other valid values are "link", "lp", and "linear.predictor"; these are equivalent, and request that results be shown for the linear predictor, with no back-transformation. The default is "link", unless the "predict.type" option is in force; see emm_options, and also the section below on transformations and links.

df
Numeric. If non-missing, a constant number of degrees of freedom to use in constructing confidence intervals and P values (NA specifies asymptotic results).

null
Numeric. Null hypothesis value(s), on the linear-predictor scale, against which estimates are tested. May be a single value used for all, or a numeric vector of length equal to the number of tests in each family (i.e., by group in the displayed table).

delta
Numeric value (on the linear-predictor scale). If zero, ordinary tests of significance are performed. If positive, this specifies a threshold for testing equivalence (using the TOST or two-one-sided-test method), non-inferiority, or non-superiority, depending on side. See Details for how the test statistics are defined.

side
Numeric or character value specifying whether the test is left-tailed (-1, "-", code"<", "left", or "nonsuperiority"); right-tailed (1, "+", ">", "right", or "noninferiority"); or two-sided (0, 2, "+", "two-sided", "both", "equivalence", or "+="). See the special section below for more details.

frequentist
Ignored except if a Bayesian model was fitted. If missing or FALSE, the object is passed to hpd.summary. Otherwise, a logical value of TRUE will have it return a frequentist summary.

bias.adjust
Logical value for whether to adjust for bias in back-transforming (type = "response").

sigma
Error SD assumed for bias correction (when type = "response" and a transformation is in effect), or for constructing prediction intervals. If not specified,
summary.emmGrid

object@misc$sigma is used, and an error is thrown if it is not found. **Note:** sigma may be a vector, as long as it conforms to the number of rows of the reference grid.

... (Not used by summary.emmGrid.) In as.data.frame.emmGrid, confint.emmGrid, predict.emmGrid, and test.emmGrid, these arguments are passed to summary.emmGrid.

**interval**  
Type of interval desired (partial matching is allowed): "none" for no intervals, otherwise confidence or prediction intervals with given arguments, via confint.emmGrid.

**x**  
object of the given class

**row.names**  
passed to as.data.frame

**optional**  
passed to as.data.frame

**as.df**  
Logical value. With x[... ,as.df = TRUE], the result is object is coerced to an ordinary data.frame; otherwise, it is left as a summary_emm object.

**parm**  
(Required argument for confint methods, but not used)

**joint**  
Logical value. If FALSE, the arguments are passed to summary.emmGrid with infer=c(FALSE,TRUE). If joint = TRUE, a joint test of the hypothesis L beta = null is performed, where L is object@linfct and beta is the vector of fixed effects estimated by object@betahat. This will be either an F test or a chi-square (Wald) test depending on whether degrees of freedom are available. See also joint_tests.

**verbose**  
Logical value. If TRUE and joint = TRUE, a table of the effects being tested is printed.

**rows**  
Integer values. The rows of L to be tested in the joint test. If missing, all rows of L are used. If not missing, by variables are ignored.

**status**  
logical. If TRUE, a note column showing status flags (for rank deficiencies and estimability issues) is displayed even when empty. If FALSE, the column is included only if there are such issues.

**Details**

summary.emmGrid is the general function for summarizing emmGrid objects. confint.emmGrid is equivalent to summary.emmGrid with infer = c(TRUE,FALSE). When called with joint = FALSE, test.emmGrid is equivalent to summary.emmGrid with infer = c(FALSE,TRUE).

With joint = TRUE, test.emmGrid calculates the Wald test of the hypothesis linfct %*% bhat = null, where linfct and bhat refer to slots in object (possibly subsetted according to by or rows). An error is thrown if any row of linfct is non-estimable. It is permissible for the rows of linfct to be linearly dependent, as long as null == 0, in which case a reduced set of contrasts is tested. Linear dependence and nonzero null cause an error.

**Value**

summary.emmGrid, confint.emmGrid, and test.emmGrid return an object of class "summary_emm", which is an extension of data.frame but with a special print method that displays it with custom formatting. For models fitted using MCMC methods, the call is diverted to hpd.summary (with prob set to level, if specified); one may alternatively use general MCMC summarization tools with the results of as.mcmc.
predict returns a vector of predictions for each row of object@grid.

The as.data.frame method returns a plain data frame, equivalent to as.data.frame(summary(.)).

Defaults

The misc slot in object contains default values for by, infer, level, adjust, type, null, side, and delta. These defaults vary depending on the code that created the object. The update method may be used to change these defaults. In addition, any options set using ‘emm_options(summary = ...)’ will trump those stored in the object’s misc slot.

Transformations and links

With type = "response", the transformation assumed can be found in ‘object@misc$tran’, and its label, for the summary is in ‘object@misc$inv.lb1’. Any t or z tests are still performed on the scale of the linear predictor, not the inverse-transformed one. Similarly, confidence intervals are computed on the linear-predictor scale, then inverse-transformed.

When bias.adjust is TRUE, then back-transformed estimates are adjusted by adding \(0.5h''(u)\sigma^2\), where \(h\) is the inverse transformation and \(u\) is the linear predictor. This is based on a second-order Taylor expansion. There are better or exact adjustments for certain specific cases, and these may be incorporated in future updates.

P-value adjustments

The adjust argument specifies a multiplicity adjustment for tests or confidence intervals. This adjustment always is applied separately to each table or sub-table that you see in the printed output (see rbind.emmGrid for how to combine tables).

The valid values of adjust are as follows:

"tukey" Uses the Studentized range distribution with the number of means in the family. (Available for two-sided cases only.)

"scheffe" Computes p values from the \(F\) distribution, according to the Scheffe critical value of \(\sqrt{kF(k, d)}\), where \(d\) is the error degrees of freedom and \(k\) is (family size minus 1) for contrasts, and (number of estimates) otherwise. (Available for two-sided cases only.)

"sidak" Makes adjustments as if the estimates were independent (a conservative adjustment in many cases).

"bonferroni" Multiplies p values, or divides significance levels by the number of estimates. This is a conservative adjustment.

"dunnettx" Uses our ownad hoc approximation to the Dunnett distribution for a family of estimates having pairwise correlations of 0.5 (as is true when comparing treatments with a control with equal sample sizes). The accuracy of the approximation improves with the number of simultaneous estimates, and is much faster than "mvt". (Available for two-sided cases only.)

"mvt" Uses the multivariate \(t\) distribution to assess the probability or critical value for the maximum of \(k\) estimates. This method produces the same \(p\) values and intervals as the default summary or confint methods to the results of as.glht. In the context of pairwise comparisons or comparisons with a control, this produces “exact” Tukey or Dunnett adjustments, respectively. However, the algorithm (from the mvtnorm package) uses a Monte Carlo method, so results are not exactly repeatable unless the same random-number seed is used.
(see \texttt{set.seed}). As the family size increases, the required computation time will become noticeable or even intolerable, making the "tukey", "dunnett\texttt{t}x", or others more attractive.

"none" Makes no adjustments to the \( p \) values.

For tests, not confidence intervals, the Bonferroni-inequality-based adjustment methods in \texttt{p.adjust} are also available (currently, these include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", and "none"). If a \texttt{p.adjust.methods} method other than "bonferroni" or "none" is specified for confidence limits, the straight Bonferroni adjustment is used instead. Also, if an adjustment method is not appropriate (e.g., using "tukey" with one-sided tests, or with results that are not pairwise comparisons), a more appropriate method (usually "sidak") is substituted.

In some cases, confidence and \( p \)-value adjustments are only approximate – especially when the degrees of freedom or standard errors vary greatly within the family of tests. The "mvt" method is always the correct one-step adjustment, but it can be very slow. One may use \texttt{as.glht} with methods in the \texttt{multcomp} package to obtain non-conservative multi-step adjustments to tests.

Testing non-superiority, non-inferiority, or equivalence

When \( \delta = 0 \), test statistics are of the usual form ‘(estimate -null)/SE’, or notationally, \( t = (Q - \theta_0)/SE \) where \( Q \) is our estimate of \( \theta \); then left, right, or two-sided \( p \) values are produced.

When \( \delta \) is positive, the test statistic depends on \texttt{side} as follows.

\textbf{Left-sided (nonsuperiority)} \quad H_0 : \theta \geq \theta_0 + \delta \quad \text{versus} \quad H_1 : \theta < \theta_0 + \delta

\[ t = (Q - \theta_0 - \delta)/SE \]

The \( p \) value is the lower-tail probability.

\textbf{Right-sided (noninferiority)} \quad H_0 : \theta \leq \theta_0 - \delta \quad \text{versus} \quad H_1 : \theta > \theta_0 - \delta

\[ t = (Q - \theta_0 + \delta)/SE \]

The \( p \) value is the upper-tail probability.

\textbf{Two-sided (equivalence)} \quad H_0 : |\theta - \theta_0| \geq \delta \quad \text{versus} \quad H_1 : |\theta - \theta_0| < \delta

\[ t = (|Q - \theta_0| - \delta)/SE \]

The \( p \) value is the lower-tail probability.

Non-estimable cases

When the model is rank-deficient, each row \( x \) of \texttt{object}'s \texttt{linfct} slot is checked for estimability. If \( \text{sum}(x*bhat) \) is found to be non-estimable, then the string \texttt{NonEst} is displayed for the estimate, and associated statistics are set to NA. The estimability check is performed using the orthonormal basis \( N \) in the \texttt{nbasis} slot for the null space of the rows of the model matrix. Estimability fails when \(|N x|^2/||x||^2\) exceeds \texttt{tol}, which by default is 1e-8. You may change it via \texttt{emm_options} by setting \texttt{estble.tol} to the desired value.

Warning about potential misuse of \( p \) values

A growing consensus in the statistical and scientific community is that the term “statistical significance” should be completely abandoned, and that criteria such as “\( p < 0.05 \)” never be used to assess the importance of an effect. These practices are just too misleading and prone to abuse. See the “basics” vignette for more discussion.
Note

In doing testing and a transformation and/or link is in force, any null and/or delta values specified must always be on the scale of the linear predictor, regardless of the setting for ‘type’. If type = "response", the null value displayed in the summary table will be back-transformed from the value supplied by the user. But the displayed delta will not be changed, because there (usually) is not a natural way to back-transform it.

The default show method for emmGrid objects (with the exception of newly created reference grids) is print(summary()). Thus, with ordinary usage of emmeans and such, it is unnecessary to call summary unless there is a need to specify other than its default options.

Examples

```r
warp.lm <- lm(breaks ~ wool * tension, data = warpbreaks)
warp.emm <- emmeans(warp.lm, ~ tension | wool)
warp.emm  # implicitly runs 'summary'

confint(warp.emm, by = NULL, level = .90)

# --------------------------------------------------------------
pigs.lm <- lm(log(conc) ~ source + factor(percent), data = pigs)
pigs.emm <- emmeans(pigs.lm, "percent", type = "response")
summary(pigs.emm)  # (inherits type = "response")

# For which percents is EMM non-inferior to 35, based on a 10% threshold?
# Note the test is done on the log scale even though we have type = "response"
test(pigs.emm, null = log(35), delta = log(1.10), side = ">")

test(contrast(pigs.emm, "consec"))

test(contrast(pigs.emm, "consec"), joint = TRUE)
```

update.emmGrid

Update an emmGrid object

Description

Objects of class emmGrid contain several settings that affect such things as what arguments to pass to summary.emmGrid. The update method allows safer management of these settings than by direct modification of its slots.

Usage

```r
## S3 method for class 'emmGrid'
update(object, ..., silent = FALSE)
```
Arguments

- **object**: An `emmGrid` object
- **...**: Options to be set. These must match a list of known options (see Details)
- **silent**: Logical value. If `FALSE` (the default), a message is displayed if any options are not matched. If `TRUE`, no messages are shown.

Value

an updated `emmGrid` object.

Details

The names in ... are partially matched against those that are valid, and if a match is found, it adds or replaces the current setting. The valid names are

- `tran, tran2` (list or character) specifies the transformation which, when inverted, determines the results displayed by `summary.emmGrid`, `predict.emmGrid`, or `emmi` when `type="response"`. The value may be the name of a standard transformation from `make.link` or additional ones supported by name, such as "log2"; or, for a custom transformation, a list containing at least the functions `linkinv` (the inverse of the transformation) and `mu.eta` (the derivative thereof). The `make.tran` function returns such lists for a number of popular transformations. See the help page of `make.tran` for details as well as information on the additional named transformations that are supported. `tran2` is just like `tran` except it is a second transformation (i.e., a response transformation in a generalized linear model).

- `tran.mult` Multiple for `tran`. For example, for the response transformation ‘2*sqrt(y)’ (or ‘sqrt(y) + sqrt(y + 1)’, for that matter), we should have `tran = "sqrt"` and `tran.mult = 2`. If absent, a multiple of 1 is assumed.

- `estName` (character) is the column label used for displaying predictions or EMMs.

- `inv.lbl` (character) is the column label to use for predictions or EMMs when `type="response"`.

- `by.vars` (character vector or NULL) the variables used for grouping in the summary, and also for defining subfamilies in a call to `contrast`.

- `pri.vars` (character vector) are the names of the grid variables that are not in `by.vars`. Thus, the combinations of their levels are used as columns in each table produced by `summary.emmGrid`.

- `alpha` (numeric) is the default significance level for tests, in `summary.emmGrid` as well as `plot.emmGrid` when `CIs = TRUE`. Be cautious that methods that depend on specifying `alpha` are prone to abuse. See the discussion in `vignette("basics", "emmeans")`.

- `adjust` (character) is the default for the `adjust` argument in `summary.emmGrid`.

- `estType` (character) is the type of the estimate. It should match one of ‘c("prediction","contrast","pairs")’. This is used along with “adjust” to determine appropriate adjustments to P values and confidence intervals.

- `famSize` (integer) is the number of means involved in a family of inferences; used in Tukey adjustment.

- `infer` (logical vector of length 2) is the default value of `infer` in `summary.emmGrid`.

- `level` (numeric) is the default confidence level, `level`, in `summary.emmGrid`. Note: You must specify all five letters of ‘level’ to distinguish it from the slot name ‘levels’.
df (numeric) overrides the default degrees of freedom with a specified single value.
null (numeric) null hypothesis for summary or test (taken to be zero if missing).
side (numeric or character) side specification for for summary or test (taken to be zero if missing).
sigma (numeric) Error SD to use in predictions and for bias-adjusted back-transformations
delta (numeric) delta specification for for summary or test (taken to be zero if missing).
predict.type or type (character) sets the default method of displaying predictions in summary.emmGrid,
predict.emmGrid, and emmip. Valid values are "link" (with synonyms "lp" and "linear"), or "response".
avgd.over (character) vector) are the names of the variables whose levels are averaged over in obtaining marginal averages of predictions, i.e., estimated marginal means. Changing this might produce a misleading printout, but setting it to character(0) will suppress the "averaged over" message in the summary.
initMesg (character) is a string that is added to the beginning of any annotations that appear below the summary.emmGrid display.
methDesc (character) is a string that may be used for creating names for a list of emmGrid objects.
nesting (Character or named list) specifies the nesting structure. See “Recovering or overriding model information” in the documentation for ref_grid. The current nesting structure is displayed by str.emmGrid.
levels named list of new levels for the elements of the current emmGrid. The list name(s) are used as new variable names, and if needed, the list is expanded using expand.grid. These results replace current variable names and levels. This specification changes the levels, grid, roles, and misc slots in the updated emmGrid, and resets pri.vars, by.vars, adjust, famSize, avgd.over, and nesting. Note: All six letters of levels is needed in order to distinguish it from level.
(any other slot name) If the name matches an element of slotNames(object) other than levels, that slot is replaced by the supplied value, if it is of the required class (otherwise an error occurs).
The user must be very careful in replacing slots because they are interrelated; for example, the lengths and dimensions of grid, linfct, bhat, and V must conform.

See Also
emm_options

Examples

# Using an already-transformed response:
mypigs <- transform(pigs, logconc = log(pigs$conc))
mypigs.lm <- lm(logconc ~ source + factor(percent), data = mypigs)

# Reference grid that knows about the transformation:
mypigs.rg <- update(ref_grid(mypigs.lm), tran = "log",
predict.type = "response")
emmeans(mypigs.rg, "source")
Using xtable for EMMs

Description

These methods provide support for the xtable package, enabling polished presentations of tabular output from emmeans and other functions.

Usage

## S3 method for class 'Var'

```r
xtable(x, caption = NULL, label = NULL, 
       align = NULL, digits = 4, display = NULL, auto = FALSE, ...)
```

## S3 method for class 'summary_emm'

```r
xtable(x, caption = NULL, label = NULL, 
       align = NULL, digits = 4, display = NULL, auto = FALSE, ...)
```

## S3 method for class 'xtable_emm'

```r
print(x, type = getOption("xtable.type", "latex"), 
      include.rownames = FALSE, sanitize.message.function = footnotesize, 
      ...)```

Arguments

- `x` Object of class emmGrid
- `caption` Passed to xtableList
- `label` Passed to xtableList
- `align` Passed to xtableList
- `digits` Passed to xtableList
- `display` Passed to xtableList
- `auto` Passed to xtableList
- `...` Arguments passed to summary.emmGrid
- `type` Passed to print.xtable
- `include.rownames` Passed to print.xtable
- `sanitize.message.function` Passed to print.xtable

Details

The methods actually use xtableList, because of its ability to display messages such as those for P-value adjustments. These methods return an object of class "xtable_emm" – an extension of "xtableList". Unlike other xtable methods, the number of digits defaults to 4; and degrees of freedom and t ratios are always formatted independently of digits. The print method uses print.xtableList, and any ... arguments are passed there.
Value

The `xtable` methods return an `xtable_emm` object, for which its print method is `print.xtable_emm`.

Examples

```r
pigsint.lm <- lm(log(conc) ~ source * factor(percent), data = pigs)
pigsint.emm <- emmeans(pigsint.lm, ~ percent | source)
xtable::xtable(pigsint.emm, type = "response")
```
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