Package ‘multpois’

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Title Analyze Nominal Response Data with the Multinomial-Poisson Trick

Version 0.3.3

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Description Dichotomous responses having two categories can be analyzed with stats::glm() or lme4::glmer() using the family=binomial option. Unfortunately, polytomous responses with three or more unordered categories cannot be analyzed similarly because there is no analogous family=multinomial option. For between-subjects data, nnet::multinom() can address this need, but it cannot handle random factors and therefore cannot handle repeated measures. To address this gap, we transform nominal response data into counts for each categorical alternative. These counts are then analyzed using (mixed) Poisson regression as per Baker (1994) <doi:10.2307/2348134>. Omnibus analyses of variance can be run along with post hoc pairwise comparisons. For users wishing to analyze nominal responses from surveys or experiments, the functions in this package essentially act as though stats::glm() or lme4::glmer() provide a family=multinomial option.

License GPL (>= 2)

URL `https://github.com/wobbrock/multpois/`

BugReports `https://github.com/wobbrock/multpois/issues`

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Contents

`Anova.mp` *ANOVA-style results for a multinomial-Poisson model*

Description

Get ANOVA-style results for a model returned by `glm.mp` or `glmer.mp`. The output table contains chi-square results for the main effects and interactions indicated by the given model.

Usage

```
Anova.mp(model, type = c(3, 2, 1, "III", "II", "I"))
```

Arguments

`model`	A model built by `glm.mp` or `glmer.mp`. (The underlying model will have been built by `glm` or `glmer`, with `family=poisson`.)
`type`	In the case of a Type II or Type III ANOVA, this value will be the `type` parameter passed to `Anova`. In the case of a Type I ANOVA, for models built with `glm.mp`, the `anova.glm` function will be called; for models built with `glmer.mp`, the `anova.merMod` function will be called. The default is 3. See the details for `Anova`.

Details

For Type II or III ANOVAs, the `Anova.mp` function uses `Anova` behind the scenes to produce an ANOVA-style table with chi-square results. For Type I ANOVAs, it uses `anova.glm` or `anova.merMod`, depending on the model.

Users wishing to verify the correctness of these results can compare `Anova` results for dichotomous response models built with `glm` or `glmer` (using `family=binomial`) to `Anova.mp` results for models built with `glm.mp` or `glmer.mp`, respectively. The results should be similar.

Users can also compare `Anova` results for polytomous response models built with `multinom` to `Anova.mp` results for models built with `glm.mp`. Again, the results should be similar.

To date, there is no similarly easy comparison for polytomous response models with repeated measures. This lack of options was a key motivation for developing `glmer.mp` in the first place.

Value

An ANOVA-style table of chi-square results for models built by `glm.mp` or `glmer.mp`. See the return values for `Anova`, `anova.glm`, or `anova.merMod`.

Author(s)

Jacob O. Wobbrock

References

Baker, S.G. (1994). The multinomial-Poisson transformation. *The Statistician 43* (4), pp. 495-504. doi:10.2307/2348134

Chen, Z. and Kuo, L. (2001). A note on the estimation of the multinomial logit model with random effects. *The American Statistician 55* (2), pp. 89-95. `https://www.jstor.org/stable/2685993`

Guimaraes, P. (2004). Understanding the multinomial-Poisson transformation. *The Stata Journal 4* (3), pp. 265-273. `https://www.stata-journal.com/article.html?article=st0069`

Lee, J.Y.L., Green, P.J.,and Ryan, L.M. (2017). On the "Poisson trick" and its extensions for fitting multinomial regression models. *arXiv preprint* available at doi:10.48550/arXiv.1707.08538

See Also

`glm.mp()`, `glm.mp.con()`, `glmer.mp()`, `glmer.mp.con()`, `car::Anova()`, `stats::anova.glm()`, `lme4::anova.merMod()`

Examples

```
library(multpois)

## two between-subjects factors (X1,X2) with polytomous response (Y)
data(bs3, package="multpois")

bs3$PId = factor(bs3$PId)
bs3$Y = factor(bs3$Y)
bs3$X1 = factor(bs3$X1)
bs3$X2 = factor(bs3$X2)
```

```
contrasts(bs3$X1) <- "contr.sum"
contrasts(bs3$X2) <- "contr.sum"

m1 = glm.mp(Y ~ X1*X2, data=bs3)
Anova.mp(m1, type=3)

## two within-subjects factors (X1,X2) with polytomous response (Y)
data(ws3, package="multpois")

ws3$PId = factor(ws3$PId)
ws3$Y = factor(ws3$Y)
ws3$X1 = factor(ws3$X1)
ws3$X2 = factor(ws3$X2)
contrasts(ws3$X1) <- "contr.sum"
contrasts(ws3$X2) <- "contr.sum"

m2 = glmer.mp(Y ~ X1*X2 + (1|PId), data=ws3)
Anova.mp(m2, type=3)
```

`bs2` *Between-subjects 2×2 design with dichotomous response data*

Description

This generic synthetic long-format data set has a dichotomous response `Y` and two factors `X1` and `X2`. The response has categories `{yes, no}`. Factor `X1` has levels `{a, b}`, and factor `X2` has levels `{c, d}`. It also has a `PId` column for a participant identifier. Each participant appears on only one row.

Format

A data frame with 60 observations on the following 4 variables:

PId a participant identifier with levels `"1"` ... `"60"`

X1 a between-subjects factor with levels `"a"`, `"b"`

X2 a between-subjects factor with levels `"c"`, `"d"`

Y a dichotomous response with categories `"yes"`, `"no"`

See Also

See `glm.mp` and `glm.mp.con` for complete examples.

Examples

```
library(multpois)
data(bs2, package="multpois")

bs2$PId = factor(bs2$PId)
bs2$Y = factor(bs2$Y, levels=c("yes","no"))
bs2$X1 = factor(bs2$X1)
bs2$X2 = factor(bs2$X2)
contrasts(bs2$X1) <- "contr.sum"
contrasts(bs2$X2) <- "contr.sum"

m = glm.mp(Y ~ X1*X2, data=bs2)
Anova.mp(m, type=3)
glm.mp.con(m, pairwise ~ X1*X2, adjust="holm")
```

`bs3` *Between-subjects 2×2 design with polytomous response data*

Description

This generic synthetic long-format data set has a polytomous response `Y` and two factors `X1` and `X2`. The response has categories {`yes, no, maybe`}. Factor `X1` has levels {`a, b`}, and factor `X2` has levels {`c, d`}. It also has a `PId` column for a participant identifier. Each participant appears on only one row.

Format

A data frame with 60 observations on the following 4 variables:

PId a participant identifier with levels `"1"` ... `"60"`

X1 a between-subjects factor with levels `"a"`, `"b"`

X2 a between-subjects factor with levels `"c"`, `"d"`

Y a polytomous response with categories `"yes"`, `"no"`, `"maybe"`

See Also

See `glm.mp` and `glm.mp.con` for complete examples.

Examples

```
library(multpois)
data(bs3, package="multpois")

bs3$PId = factor(bs3$PId)
bs3$Y = factor(bs3$Y, levels=c("yes","no","maybe"))
bs3$X1 = factor(bs3$X1)
bs3$X2 = factor(bs3$X2)
```

```
contrasts(bs3$X1) <- "contr.sum"
contrasts(bs3$X2) <- "contr.sum"

m = glm.mp(Y ~ X1*X2, data=bs3)
Anova.mp(m, type=3)
glm.mp.con(m, pairwise ~ X1*X2, adjust="holm")
```

`glm.mp` *Multinomial-Poisson GLM for nominal response data*

Description

This function uses the multinomial-Poisson trick to analyze **nominal response** data using a Poisson generalized linear model (GLM). The nominal response should be a factor with two or more unordered categories. The independent variables should be between-subjects factors and/or numeric predictors.

Usage

```
glm.mp(formula, data, ...)
```

Arguments

`formula`	A formula object in the style of, e.g., `Y ~ X1*X2`, where `X1` and `X2` are factors or predictors. The response `Y` must be of type `factor`. See the `formula` entry for `glm`.
`data`	A data frame in long-format. See the `data` entry for `glm`.
`...`	Additional arguments to be passed to `glm`. Generally, these are unnecessary but are provided for advanced users. They must not pass `formula`, `data`, or `family` arguments. See `glm` for valid arguments.

Details

This function should be used for nominal response data with only between-subjects factors or predictors. In essence, it provides for the equivalent of `glm` with `family=multinomial`, were that option to exist. (That option does not exist, but `multinom` serves the same purpose.)

For data with repeated measures, use `glmer.mp`, which can take random factors and thus handle correlated responses.

Users wishing to verify the correctness of `glm.mp` should compare `Anova.mp` results to `Anova` results for models built with `glm` using `family=binomial` (for dichotomous responses) or `multinom` (for polytomous responses). The results should be similar if not identical.

Post hoc pairwise comparisons for factors can be conducted with `glm.mp.con`.

Value

A Poisson regression model of type `glm`. See the return value for `glm`.

Author(s)

Jacob O. Wobbrock

References

Baker, S.G. (1994). The multinomial-Poisson transformation. *The Statistician 43* (4), pp. 495-504. doi:10.2307/2348134

Guimaraes, P. (2004). Understanding the multinomial-Poisson transformation. *The Stata Journal 4* (3), pp. 265-273. `https://www.stata-journal.com/article.html?article=st0069`

Lee, J.Y.L., Green, P.J.,and Ryan, L.M. (2017). On the “Poisson trick” and its extensions for fitting multinomial regression models. *arXiv preprint* available at doi:10.48550/arXiv.1707.08538

See Also

`Anova.mp()`, `glm.mp.con()`, `glmer.mp()`, `glmer.mp.con()`, `stats::glm()`, `stats::glm.control()`, `nnet::multinom()`

Examples

```
library(multpois)
library(car)
library(nnet)

## two between-subjects factors (X1,X2) with dichotomous response (Y)
data(bs2, package="multpois")

bs2$PId = factor(bs2$PId)
bs2$Y = factor(bs2$Y)
bs2$X1 = factor(bs2$X1)
bs2$X2 = factor(bs2$X2)
contrasts(bs2$X1) <- "contr.sum"
contrasts(bs2$X2) <- "contr.sum"

m1 = glm(Y ~ X1*X2, data=bs2, family=binomial)
Anova(m1, type=3)

m2 = glm.mp(Y ~ X1*X2, data=bs2) # compare
Anova.mp(m2, type=3)

## two between-subjects factors (X1,X2) with polytomous response (Y)
data(bs3, package="multpois")

bs3$PId = factor(bs3$PId)
bs3$Y = factor(bs3$Y)
bs3$X1 = factor(bs3$X1)
bs3$X2 = factor(bs3$X2)
contrasts(bs3$X1) <- "contr.sum"
contrasts(bs3$X2) <- "contr.sum"

m3 = multinom(Y ~ X1*X2, data=bs3, trace=FALSE)
Anova(m3, type=3)
```

```
m4 = glm.mp(Y ~ X1*X2, data=bs3) # compare
Anova.mp(m4, type=3)
```

`glm.mp.con` *Contrast tests for multinomial-Poisson GLM*

Description

This function conducts *post hoc* pairwise comparisons on generalized linear models (GLMs) built with `glm.mp`. Such models have **nominal response** types, i.e., `factor`s with unordered categories.

Usage

```
glm.mp.con(
  model,
  formula,
 adjust = c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"),
  ...
)
```

Arguments

`model`	A multinomial-Poisson generalized linear model created by `glm.mp`.
`formula`	A formula object in the style of, e.g., `pairwise ~ X1*X2`, where `X1` and `X2` are factors in `model`. The `pairwise` keyword *must* be used on the left-hand side of the formula. See the `specs` entry for `emmeans`.
`adjust`	A string indicating the *p*-value adjustment to use. Defaults to `"holm"`. See the details for `p.adjust`.
`...`	Additional arguments to be passed to `glm`. Generally, these are unnecessary but are provided for advanced users. They must not pass `formula`, `data`, or `family` arguments. See `glm` for valid arguments.

Details

Post hoc pairwise comparisons should be conducted *only* after a statistically significant omnibus test using `Anova.mp`. Comparisons are conducted in the style of `emmeans` but not using this function; rather, the multinomial-Poisson trick is used on the subset of the data relevant to each pairwise comparison.

Users wishing to verify the correctness of `glm.mp.con` should compare its results to `emmeans` results for models built with `glm` using `family=binomial` for dichotomous responses. Factor contrasts should be set to sum-to-zero contrasts (i.e., `"contr.sum"`). The results should be similar.

Value

Pairwise comparisons for all levels indicated by the factors in `formula`.

Author(s)

Jacob O. Wobbrock

References

Baker, S.G. (1994). The multinomial-Poisson transformation. *The Statistician 43* (4), pp. 495-504. doi:10.2307/2348134

Guimaraes, P. (2004). Understanding the multinomial-Poisson transformation. *The Stata Journal 4* (3), pp. 265-273. `https://www.stata-journal.com/article.html?article=st0069`

Lee, J.Y.L., Green, P.J.,and Ryan, L.M. (2017). On the "Poisson trick" and its extensions for fitting multinomial regression models. *arXiv preprint* available at doi:10.48550/arXiv.1707.08538

See Also

`Anova.mp()`, `glm.mp()`, `glmer.mp()`, `glmer.mp.con()`, `stats::glm()`, `stats::glm.control()`, `emmeans::emmeans()`

Examples

```
library(multpois)
library(car)
library(nnet)
library(emmeans)

## two between-subjects factors (X1,X2) with dichotomous response (Y)
data(bs2, package="multpois")

bs2$PId = factor(bs2$PId)
bs2$Y = factor(bs2$Y)
bs2$X1 = factor(bs2$X1)
bs2$X2 = factor(bs2$X2)
contrasts(bs2$X1) <- "contr.sum"
contrasts(bs2$X2) <- "contr.sum"

m1 = glm(Y ~ X1*X2, data=bs2, family=binomial)
Anova(m1, type=3)
emmeans(m1, pairwise ~ X1*X2, adjust="holm")

m2 = glm.mp(Y ~ X1*X2, data=bs2)
Anova.mp(m2, type=3)
glm.mp.con(m2, pairwise ~ X1*X2, adjust="holm") # compare

## two between-subjects factors (X1,X2) with polytomous response (Y)
data(bs3, package="multpois")

bs3$PId = factor(bs3$PId)
bs3$Y = factor(bs3$Y)
bs3$X1 = factor(bs3$X1)
bs3$X2 = factor(bs3$X2)
contrasts(bs3$X1) <- "contr.sum"
contrasts(bs3$X2) <- "contr.sum"
```

```
m3 = multinom(Y ~ X1*X2, data=bs3, trace=FALSE)
Anova(m3, type=3)
emmeans::test(
  contrast(emmeans(m3, ~ X1*X2 | Y, mode="latent"), method="pairwise", ref=1),
  joint=TRUE, by="contrast"
)

m4 = glm.mp(Y ~ X1*X2, data=bs3)
Anova.mp(m4, type=3)
glm.mp.con(m4, pairwise ~ X1*X2, adjust="holm") # compare
```

`glmer.mp` *Multinomial-Poisson GLMM for nominal response data*

Description

This function uses the multinomial-Poisson trick to analyze **nominal response** data using a Poisson generalized linear mixed model (GLMM). The nominal response should be a factor with two or more unordered categories. The independent variables should have at least one within-subjects factor or numeric predictor. There also must be a repeated subject identifier to be used as a random factor.

Usage

```
glmer.mp(formula, data, ...)
```

Arguments

`formula`	A formula object in the style of, e.g., `Y ~ X1*X2 + (1|PId)`, where `X1` and `X2` are factors or predictors and `PId` is a factor serving as a subject identifier. The response `Y` must be of type `factor`. See the `formula` entry for `glmer`.
`data`	A data frame in long-format. See the `data` entry for `glmer`.
`...`	Additional arguments to be passed to `glmer`. Most often, these additional arguments are used to specify alternate optimizers. (See **Note**, below.) These additional arguments must not pass `formula`, `data`, or `family` arguments. See `glmer` for valid arguments.

Details

This function should be used for nominal response data with repeated measures. In essence, it provides for the equivalent of `glmer` with `family=multinomial`, were that option to exist. (That option does not exist, which was a key motivation for developing this function.)

For polytomous response data with only between-subjects factors, use `glm.mp` or `multinom`.

Users wishing to verify the correctness of `glmer.mp` should compare its `Anova.mp` results to `Anova` results for models built with `glmer` using `family=binomial` for dichotomous responses. The results should be similar.

Post hoc pairwise comparisons for factors can be conducted with `glmer.mp.con`.

Value

A mixed-effects Poisson regression model of type `merMod`, specifically of *subclass* `glmerMod`. See the return value for `glmer`.

Note

It is not uncommon to receive a `boundary (singular) fit` message. This message can often be ignored provided the test output looks sensible.

Sometimes, `glmer.mp` can fail to converge. Convergence issues can often be remedied by changing the optimizer or its control parameters. For example, the following code uses the `bobyqa` optimizer and increases the maximum number of function evaluations to 100,000:

`m = glmer.mp(Y ~ X + (1|PId), data=df, control=glmerControl(optimizer="bobyqa", optCtrl=list(maxfun=1e+0`

Other available `optimizer` strings besides `"bobyqa"` include `"nloptwrap"`, `"nlminbwrap"`, and `"Nelder_Mead"`. Additional optimizers are available via the `optimx` library by passing `"optimx"` to `optimizer` and `method="name"` in the `optCtrl` parameter list. Eligible *name*s include `"nlm"`, `"BFGS"`, and `"L-BFGS-B"`, among others. See the `optimizer` argument in `glmerControl` and the details for `optimx` for more information.

Author(s)

Jacob O. Wobbrock

References

Baker, S.G. (1994). The multinomial-Poisson transformation. *The Statistician 43* (4), pp. 495-504. doi:10.2307/2348134

Chen, Z. and Kuo, L. (2001). A note on the estimation of the multinomial logit model with random effects. *The American Statistician 55* (2), pp. 89-95. `https://www.jstor.org/stable/2685993`

Guimaraes, P. (2004). Understanding the multinomial-Poisson transformation. *The Stata Journal 4* (3), pp. 265-273. `https://www.stata-journal.com/article.html?article=st0069`

Lee, J.Y.L., Green, P.J.,and Ryan, L.M. (2017). On the "Poisson trick" and its extensions for fitting multinomial regression models. *arXiv preprint* available at doi:10.48550/arXiv.1707.08538

See Also

`Anova.mp()`, `glmer.mp.con()`, `glm.mp()`, `glm.mp.con()`, `lme4::glmer()`, `lme4::glmerControl()`

Examples

```
library(multpois)
library(car)
library(lme4)
library(lmerTest)

## two within-subjects factors (x1,X2) with dichotomous response (Y)
data(ws2, package="multpois")

ws2$PId = factor(ws2$PId)
```

```
ws2$Y = factor(ws2$Y)
ws2$X1 = factor(ws2$X1)
ws2$X2 = factor(ws2$X2)
contrasts(ws2$X1) <- "contr.sum"
contrasts(ws2$X2) <- "contr.sum"

m1 = glmer(Y ~ X1*X2 + (1|PId), data=ws2, family=binomial)
Anova(m1, type=3)

m2 = glmer.mp(Y ~ X1*X2 + (1|PId), data=ws2) # compare
Anova.mp(m2, type=3)

## two within-subjects factors (x1,X2) with polytomous response (Y)
data(ws3, package="multpois")

ws3$PId = factor(ws3$PId)
ws3$Y = factor(ws3$Y)
ws3$X1 = factor(ws3$X1)
ws3$X2 = factor(ws3$X2)
contrasts(ws3$X1) <- "contr.sum"
contrasts(ws3$X2) <- "contr.sum"

m3 = glmer.mp(Y ~ X1*X2 + (1|PId), data=ws3)
Anova.mp(m3, type=3)
```

`glmer.mp.con` *Contrast tests for multinomial-Poisson GLMM*

Description

This function conducts *post hoc* pairwise comparisons on generalized linear mixed models (GLMMs) built with `glmer.mp`. Such models have **nominal response** types, i.e., `factor`s with unordered categories.

Usage

```
glmer.mp.con(
  model,
  formula,
 adjust = c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"),
  ...
)
```

Arguments

`model`	A multinomial-Poisson generalized linear mixed model created by `glmer.mp`.
`formula`	A formula object in the style of, e.g., `pairwise ~ X1*X2`, where `X1` and `X2` are factors in `model`. The `pairwise` keyword *must* be used on the left-hand side of the formula. See the `specs` entry for `emmeans`.

`adjust`	A string indicating the *p*-value adjustment to use. Defaults to `"holm"`. See the details for `p.adjust`.
`...`	Additional arguments to be passed to `glmer`. Most often, these additional arguments are used to specify alternate optimizers. (See **Note**, below.) These additional arguments must not pass `formula`, `data`, or `family` arguments. See `glmer` for valid arguments.

Details

Post hoc pairwise comparisons should be conducted *only* after a statistically significant omnibus test using `Anova.mp`. Comparisons are conducted in the style of `emmeans` but not using this function; rather, the multinomial-Poisson trick is used on the subset of the data relevant to each pairwise comparison.

Users wishing to verify the correctness of `glmer.mp.con` should compare its results to `emmeans` results for models built with `glmer` using `family=binomial` for dichotomous responses. Factor contrasts should be set to sum-to-zero contrasts (i.e., `"contr.sum"`). The results should be similar.

Value

Pairwise comparisons for all levels indicated by the factors in `formula`.

Note

It is not uncommon to receive `boundary (singular) fit` messages. These messages can often be ignored provided the test output looks sensible.

Sometimes, `glmer.mp.con` can fail to converge. Convergence issues can often be remedied by changing the optimizer or its control parameters. For example, the following code uses the `bobyqa` optimizer and increases the maximum number of function evaluations to 100,000:

```
glmer.mp.con(m, pairwise ~ X1*X2, adjust="holm", control=glmerControl(optimizer="bobyqa",
optCtrl=list(maxfun=1e+05)))
```

Other available `optimizer` strings besides `"bobyqa"` include `"nloptwrap"`, `"nlminbwrap"`, and `"Nelder_Mead"`. Additional optimizers are available via the `optimx` library by passing `"optimx"` to `optimizer` and `method="name"` in the `optCtrl` parameter list. Eligible *name*s include `"nlm"`, `"BFGS"`, and `"L-BFGS-B"`, among others. See the `optimizer` argument in `glmerControl` and the details for `optimx` for more information.

Author(s)

Jacob O. Wobbrock

References

Baker, S.G. (1994). The multinomial-Poisson transformation. *The Statistician 43* (4), pp. 495-504. doi:10.2307/2348134

Chen, Z. and Kuo, L. (2001). A note on the estimation of the multinomial logit model with random effects. *The American Statistician 55* (2), pp. 89-95. `https://www.jstor.org/stable/2685993`

Guimaraes, P. (2004). Understanding the multinomial-Poisson transformation. *The Stata Journal 4* (3), pp. 265-273. `https://www.stata-journal.com/article.html?article=st0069`

Lee, J.Y.L., Green, P.J.,and Ryan, L.M. (2017). On the “Poisson trick” and its extensions for fitting multinomial regression models. *arXiv preprint* available at doi:10.48550/arXiv.1707.08538

See Also

`Anova.mp()`, `glmer.mp()`, `glm.mp()`, `glm.mp.con()`, `lme4::glmer()`, `lme4::glmerControl()`, `emmeans::emmeans()`

Examples

```
library(multpois)
library(car)
library(lme4)
library(lmerTest)
library(emmeans)

## two within-subjects factors (x1,X2) with dichotomous response (Y)
data(ws2, package="multpois")

ws2$PId = factor(ws2$PId)
ws2$Y = factor(ws2$Y)
ws2$X1 = factor(ws2$X1)
ws2$X2 = factor(ws2$X2)
contrasts(ws2$X1) <- "contr.sum"
contrasts(ws2$X2) <- "contr.sum"

m1 = glmer(Y ~ X1*X2 + (1|PId), data=ws2, family=binomial)
Anova(m1, type=3)
emmeans(m1, pairwise ~ X1*X2, adjust="holm")

m2 = glmer.mp(Y ~ X1*X2 + (1|PId), data=ws2)
Anova.mp(m2, type=3)
glmer.mp.con(m2, pairwise ~ X1*X2, adjust="holm") # compare


## two within-subjects factors (x1,X2) with polytomous response (Y)
data(ws3, package="multpois")

ws3$PId = factor(ws3$PId)
ws3$Y = factor(ws3$Y)
ws3$X1 = factor(ws3$X1)
ws3$X2 = factor(ws3$X2)
contrasts(ws3$X1) <- "contr.sum"
contrasts(ws3$X2) <- "contr.sum"

m3 = glmer.mp(Y ~ X1*X2 + (1|PId), data=ws3)
Anova.mp(m3, type=3)
glmer.mp.con(m3, pairwise ~ X1*X2, adjust="holm")
```

`icecream` *Mixed factorial 2×2 design with polytomous response data*

Description

This synthetic long-format data set represents a survey of 40 respondents about their favorite ice cream flavors. Twenty of the respondents were adults and 20 were children. They were asked four times over the course of a year, once in the middle of each season (fall, winter, spring, summer), for their favorite ice cream flavor in that season.

This data set has a polytomous response `Pref` and two factors, `Age` and `Season`. The response `Pref` has the unordered categories `{vanilla, chocolate, strawberry}`. Factor `Age` has levels `{adult, child}`. Factor `Season` has levels `{fall, winter, spring, summer}`. It also has a `PId` column for a participant identifier. Each participant identifier is repeated four times, once for each season.

Format

A data frame with 160 observations on the following 4 variables:

PId a participant identifier with levels `"1"` ... `"40"`

Age a between-subjects factor with levels `"adult"`, `"child"`

Season a within-subjects factor with levels `"fall"`, `"winter"`, `"spring"`, `"summer"`

Pref a polytomous response with categories `"vanilla"`, `"chocolate"`, `"strawberry"`

See Also

See `vignette("multpois", package="multpois")` for a complete analysis of this data set.

Examples

```
library(multpois)
data(icecream, package="multpois")

icecream$PId = factor(icecream$PId)
icecream$Pref = factor(icecream$Pref, levels=c("vanilla","chocolate","strawberry"))
icecream$Age = factor(icecream$Age, levels=c("adult","child"))
icecream$Season = factor(icecream$Season, levels=c("fall","winter","spring","summer"))
contrasts(icecream$Age) <- "contr.sum"
contrasts(icecream$Season) <- "contr.sum"

m = glmer.mp(Pref ~ Age*Season + (1|PId), data=icecream)
Anova.mp(m, type=3)
glmer.mp.con(m, pairwise ~ Age*Season, adjust="holm")
```

`ws2` *Within-subjects 2×2 design with dichotomous response data*

Description

This generic synthetic long-format data set has a dichotomous response `Y` and two factors `X1` and `X2`. The response has categories `{yes, no}`. Factor `X1` has levels `{a, b}`, and factor `X2` has levels `{c, d}`. It also has a `PId` column for a participant identifier. Participant identifiers are repeated across rows.

Format

A data frame with 60 observations on the following 4 variables:

PId a participant identifier with levels `"1"` ... `"15"`

X1 a within-subjects factor with levels `"a"`, `"b"`

X2 a within-subjects factor with levels `"c"`, `"d"`

Y a dichotomous response with categories `"yes"`, `"no"`

See Also

See `glmer.mp` and `glmer.mp.con` for complete examples.

Examples

```
library(multpois)
data(ws2, package="multpois")

ws2$PId = factor(ws2$PId)
ws2$Y = factor(ws2$Y, levels=c("yes","no"))
ws2$X1 = factor(ws2$X1)
ws2$X2 = factor(ws2$X2)
contrasts(ws2$X1) <- "contr.sum"
contrasts(ws2$X2) <- "contr.sum"

m = glmer.mp(Y ~ X1*X2 + (1|PId), data=ws2)
Anova.mp(m, type=3)
glmer.mp.con(m, pairwise ~ X1*X2, adjust="holm")
```

`ws3` *Within-subjects 2×2 design with polytomous response data*

Description

This generic synthetic long-format data set has a polytomous response `Y` and two factors `X1` and `X2`. The response has categories `{yes, no, maybe}`. Factor `X1` has levels `{a, b}`, and factor `X2` has levels `{c, d}`. It also has a `PId` column for a participant identifier. Participant identifiers are repeated across rows.

Format

A data frame with 60 observations on the following 4 variables:

PId a participant identifier with levels `"1"` ... `"15"`

X1 a within-subjects factor with levels `"a"`, `"b"`

X2 a within-subjects factor with levels `"c"`, `"d"`

Y a polytomous response with categories `"yes"`, `"no"`, `"maybe"`

See Also

See `glmer.mp` and `glmer.mp.con` for complete examples.

Examples

```
library(multpois)
data(ws3, package="multpois")

ws3$PId = factor(ws3$PId)
ws3$Y = factor(ws3$Y, levels=c("yes","no","maybe"))
ws3$X1 = factor(ws3$X1)
ws3$X2 = factor(ws3$X2)
contrasts(ws3$X1) <- "contr.sum"
contrasts(ws3$X2) <- "contr.sum"

m = glmer.mp(Y ~ X1*X2 + (1|PId), data=ws3)
Anova.mp(m, type=3)
glmer.mp.con(m, pairwise ~ X1*X2, adjust="holm")
```

Index