

# Package ‘multpois’

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**Title** Analyze Nominal Response Data with the Multinomial-Poisson Trick

**Version** 0.2.0

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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](https://doi.org/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()` had a `family=multinomial` option.

**License** GPL (>= 2)

**URL** <https://github.com/wobbrock/multpois/>

**BugReports** <https://github.com/wobbrock/multpois/issues>

**Depends** R (>= 2.10)

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|          |  |
|----------|--|
| Anova.mp | <i>Get ANOVA-style results for a multinomial-Poisson model</i> |
|----------|--|

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## 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

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

## 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`.

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 generally match, or be very 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 generally match, or be very similar.

There is no similarly easy comparison for polytomous response models with repeated measures. The 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](https://doi.org/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](https://doi.org/10.48550/arXiv.1707.08538)

## See Also

`glm.mp()`, `glm.mp.con()`, `glmer.mp()`, `glmer.mp.con()`, `car::Anova()`

## Examples

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

bs3$PIId = factor(bs3$PIId)
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)

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

ws3$PIId = factor(ws3$PIId)
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|PIId), data=ws3)
Anova.mp(m2, type=3)

```

---

bs2

*Between-subjects 2x2 design with dichotomous response*


---

### Description

This generic synthetic dataset 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  $PIId$  column for participant identifier. Each participant is on only one row.

### Format

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

**PIId** a subject identifier with levels "1" ... "40"

**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

```

data(bs2, package="multpois")

bs2$PIId = factor(bs2$PIId)
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"

```

```
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 2x2 design with polytomous response***Description**

This generic synthetic dataset 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  $PIId$  column for participant identifier. Each participant is on only one row.

**Format**

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

**PIId** a subject 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", and "maybe"

**See Also**

See [glm.mp](#) and [glm.mp.con](#) for complete examples.

**Examples**

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

bs3$PIId = factor(bs3$PIId)
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"

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

---

`glm.mp`*Build a 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

|                      |   |
|----------------------|---|
| <code>formula</code> | A formula object in the style of, e.g., $Y \sim X1 * X2$ , where $X1$ and $X2$ are factors or predictors. The response $Y$ must be of type factor. See the formula entry for <a href="#">glm</a> .  |
| <code>data</code>    | A data frame in long-format. See the data entry for <a href="#">glm</a> .   |
| <code>...</code>     | Additional arguments to be passed to <a href="#">glm</a> . Generally, these are unnecessary but are provided for advanced users. They should not specify formula, data, or family arguments. See <a href="#">glm</a> 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 its [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 generally match, or be very similar.

### 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\(\)](#), [nnet::multinom\(\)](#)

## Examples

```
library(car)
library(nnet)

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

bs2$PIId = factor(bs2$PIId)
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)

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

bs3$PIId = factor(bs3$PIId)
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)
```

## 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., factors 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 <a href="#">glm.mp</a> .  |
| formula | A formula object in the style of, e.g., <code>pairwise ~ X1*X2</code> , where X1 and X2 are factors in model. The <code>pairwise</code> keyword <b>must</b> be used on the left-hand side of the formula. See the specs entry for <a href="#">emmeans</a> . |
| adjust  | A string indicating the <i>p</i> -value adjustment to use. Defaults to "holm". See the Details section for <a href="#">p.adjust</a> .   |
| ...     | Additional arguments to be passed to <a href="#">glm</a> . Generally, these are unnecessary but are provided for advanced users. They should not specify formula, data, or family arguments. See <a href="#">glm</a> 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 a 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. 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](https://doi.org/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](https://doi.org/10.48550/arXiv.1707.08538)

## See Also

[Anova.mp\(\)](#), [glm.mp\(\)](#), [glmer.mp\(\)](#), [glmer.mp.con\(\)](#), [emmeans::emmeans\(\)](#)

## Examples

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

## 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

## 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)
e0 = emmeans(m3, ~ X1*X2 | Y, mode="latent")
c0 = contrast(e0, method="pairwise", ref=1)
test(c0, 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

*Build a 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., $Y \sim X1*X2 + (1 PIId)$ , where $X1$ and $X2$ are factors or predictors and $PIId$ is a factor serving as a subject identifier. The response $Y$ must be of type factor. See the formula entry for <a href="#">glmer</a> . |
| data    | A data frame in long-format. See the data entry for <a href="#">glmer</a> .  |
| ...     | Additional arguments to be passed to <a href="#">glmer</a> . Generally, these are unnecessary but are provided for advanced users. They should not specify formula, data, or family arguments. See <a href="#">glmer</a> 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 generally match, or be very similar.

## Value

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

**Note**

It is common to receive a boundary (singular) fit message. This generally can be ignored provided the test output looks sensible. Less commonly, the procedure can fail to converge, which can happen when counts of one or more categories are very small or zero in some conditions. In such cases, any results should be regarded with caution.

**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](https://doi.org/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](https://doi.org/10.48550/arXiv.1707.08538)

**See Also**

[Anova.mp\(\)](#), [glmer.mp.con\(\)](#), [glm.mp\(\)](#), [glm.mp.con\(\)](#), [lme4::glmer\(\)](#)

**Examples**

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

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

ws2$PIId = factor(ws2$PIId)
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|PIId), data=ws2, family=binomial)
Anova(m1, type=3)

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

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

```

ws3$PIid = factor(ws3$PIid)
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|PIid), data=ws3)
Anova.mp(m3, type=3)

```

---

glmer.mp.con

---

*Contrast tests for multinomial-Poisson GLMMs*


---

## 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., factors 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 <a href="#">glmer.mp</a> .   |
| formula | A formula object in the style of, e.g., <code>pairwise ~ X1*X2</code> , where X1 and X2 are factors in model. The <code>pairwise</code> keyword <b>must</b> be used on the left-hand side of the formula. See the <code>specs</code> entry for <a href="#">emmeans</a> . |
| adjust  | A string indicating the <i>p</i> -value adjustment to use. Defaults to "holm". See the <code>Details</code> section for <a href="#">p.adjust</a> .   |
| ...     | Additional arguments to be passed to <a href="#">glmer</a> . Generally, these are unnecessary but are provided for advanced users. They should not specify formula, data, or family arguments. See <a href="#">glmer</a> 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 a 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. The results should be similar.

### Value

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

### Note

It is common to receive boundary (singular) fit messages. These generally can be ignored provided the test outputs look sensible. Less commonly, the procedures can fail to converge, which can happen when counts of one or more categories are very small or zero in some conditions. In such cases, any results should be regarded with caution.

### 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()`, `emmeans::emmeans()`

### Examples

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

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

ws2$PIId = factor(ws2$PIId)
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|PIId), data=ws2, family=binomial)
Anova(m1, type=3)
emmeans(m1, pairwise ~ X1*X2, adjust="holm")

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

## within-subjects factors (x1,x2) with polytomous response (Y)
data(ws3, package="multpois")

ws3$PIId = factor(ws3$PIId)
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|PIId), 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

---

## Description

This synthetic dataset represents a survey of 40 respondents about their favorite ice cream flavor. Twenty of the respondents were adults and 20 were children. They were queried four times over the course of a year, once in the middle of each season (fall, winter, spring, summer).

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

## Format

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

**PIId** a subject 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", "other"

**See Also**

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

**Examples**

```
data(icecream, package="multipois")

icecream$PIId = factor(icecream$PIId)
icecream$Pref = factor(icecream$Pref)
icecream$Age = factor(icecream$Age)
icecream$Season = factor(icecream$Season)
contrasts(icecream$Age) <- "contr.sum"
contrasts(icecream$Season) <- "contr.sum"

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

**Description**

This generic synthetic dataset 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  $PIId$  column for participant identifier. Participant identifiers are repeated across rows.

**Format**

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

**PIId** a subject identifier with levels "1" ... "10"

**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

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

ws2$PIId = factor(ws2$PIId)
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"

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

ws3

*Within-subjects 2x2 design with polytomous response*

## Description

This generic synthetic dataset 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  $PIId$  column for participant identifier. Participant identifiers are repeated across rows.

## Format

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

- PIId** a subject 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

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

ws3$PIId = factor(ws3$PIId)
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"
```



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

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