Package ‘VetResearchLMM’

May 7, 2026

Type Package

Title Linear Mixed Models - An Introduction with Applications in Veterinary Research

Version 1.1.0

Description R Codes and Datasets for Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998). Linear Mixed Models. An Introduction with applications in Veterinary Research. International Livestock Research Institute.

Depends R (>= 4.1.0)

Suggests collapse, emmeans, ggplot2, lme4, lmerTest, multcomp, nlme, quarto, report, testthat (>= 3.0.0)

VignetteBuilder quarto

License GPL-2

URL `https://myaseen208.com/VetResearchLMM/`, `https://github.com/myaseen208/VetResearchLMM/`

BugReports `https://github.com/myaseen208/VetResearchLMM/issues`

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NeedsCompilation no

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Repository CRAN

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`VetResearchLMM-package`

VetResearchLMM: Linear Mixed Models for Veterinary Research Examples

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Description

The **VetResearchLMM** package provides the datasets and reproducible R examples that accompany Duchateau, Janssen, and Rowlands (1998), *Linear Mixed Models: An Introduction with Applications in Veterinary Research*. The package is intended for readers who want to reproduce, inspect, and adapt the linear mixed model examples from the book using current R tooling.

Details

The package focuses on small applied veterinary research examples involving fixed effects, random effects, variance components, nested designs, repeated measurements, and basic hypothesis tests for linear mixed models. The package also includes `report_mixed_model()` and `emmeans_mixed_model()`, small helpers that delegate fitted model interpretation and post hoc marginal-mean inference to the optional **report** and **emmeans** packages when they are installed. The main user-facing data objects are the book datasets:

`ex121`	Dose comparison data for packed cell volume.
`ex124`	Herd, drug, and dose packed cell volume data.
`ex125`	Region, drug, and dose split-plot data.
`ex127`	Sire-level weaning weight data.
`ex31`	Designed experiment data for PCV response.
`ex32`	Breed, sire, sex, age, and weaning weight data.
`ex33`	Longitudinal PCV data by animal and breed.

The example help pages reproduce the corresponding analyses with modern R packages such as **lme4**, **lmerTest**, **nlme**, **multcomp**, **collapse**, **ggplot2**, and **emmeans** where those packages are available. Numerical results can differ slightly from the book because the book reports SAS output and modern R packages use their own optimizers, parameterizations, and degrees-of-freedom methods.

A typical workflow is:

1. Load one of the included datasets with `data()`.
2. Inspect the matching example help page, such as `?Examp2.4.2.2`.
3. Fit the fixed effect or mixed model shown in the example.
4. Compare estimates, variance components, and tests with the book.
5. Use `report_mixed_model()` for an optional narrative model report when **report** is installed.
6. Use `emmeans_mixed_model()` for optional estimated marginal means and post hoc comparisons when **emmeans** is installed.
7. Use the package vignettes for chapter-level narrative examples.

Affiliation

School of Mathematical and Statistical Sciences, Clemson University, Clemson, South Carolina, USA.

Vignettes

The Quarto vignettes provide an introduction, methodology overview, chapter/example walkthrough, and plotting guide:

- `vetresearchlmm-introduction`
- `vetresearchlmm-methodology`
- `vetresearchlmm-examples`
- `vetresearchlmm-plotting`

Author(s)

Muhammad Yaseen <myaseen208@gmail.com>

References

Duchateau, L., Janssen, P., and Rowlands, G. J. (1998). *Linear Mixed Models: An Introduction with Applications in Veterinary Research*. International Livestock Research Institute.

See Also

Useful links:

- `https://myaseen208.com/VetResearchLMM/`
- `https://github.com/myaseen208/VetResearchLMM/`
- Report bugs at `https://github.com/myaseen208/VetResearchLMM/issues`

`emmeans_mixed_model` *Estimated Marginal Means for a Fitted Mixed Model*

Description

Compute estimated marginal means or pairwise comparisons for a fitted linear mixed model using the optional **emmeans** package.

Usage

```
emmeans_mixed_model(
  model,
  specs,
  pairwise = FALSE,
  method = "pairwise",
  adjust = "tukey",
  ...
)
```

Arguments

`model`	A fitted model object, typically from `lme4::lmer()`, `lmerTest::lmer()`, or `nlme::lme()`.
`specs`	Specifications for the marginal means, passed to `emmeans::emmeans()`; for example, `~ dose` or `~ dose | Drug`.
`pairwise`	Logical. If `FALSE`, return the estimated marginal means. If `TRUE`, return contrasts computed from those marginal means.
`method`	Contrast method passed to `emmeans::contrast()` when `pairwise = TRUE`. The default is `"pairwise"`.
`adjust`	Multiplicity adjustment passed to `emmeans::contrast()` when `pairwise = TRUE`. The default is `"tukey"`. Use `NULL` to leave the adjustment unspecified.
`...`	Additional arguments passed to `emmeans::emmeans()`.

Details

Estimated marginal means, also called least-squares means, summarize model predictions for factor levels after accounting for the fitted model structure. They are useful after mixed model fitting because fixed-effect coefficients are often expressed relative to contrast coding, while marginal means and their contrasts are closer to the scientific comparisons shown in the book examples.

This helper complements `report_mixed_model()`. Use `report_mixed_model()` for narrative model interpretation and `emmeans_mixed_model()` for post hoc inference, estimated marginal means, and pairwise comparisons.

The helper keeps **emmeans** optional. It does not refit the model or change the estimates; it delegates marginal-mean calculations to `emmeans::emmeans()` and, when requested, contrasts to `emmeans::contrast()`.

Value

An `emmGrid` object from **emmeans**. With `pairwise = FALSE`, this contains estimated marginal means. With `pairwise = TRUE`, this contains the requested contrasts.

References

Lenth, R. V. (2024). **emmeans**: Estimated Marginal Means, aka Least-Squares Means. R package. See `utils::citation("emmeans")`.

Duchateau, L., Janssen, P., and Rowlands, G. J. (1998). *Linear Mixed Models: An Introduction with Applications in Veterinary Research*. International Livestock Research Institute.

See Also

`report_mixed_model()`, `emmeans::emmeans()`, `emmeans::contrast()`.

Examples

```
if (requireNamespace("lme4", quietly = TRUE) &&
    requireNamespace("emmeans", quietly = TRUE)) {
  data(ex125, package = "VetResearchLMM")
  fit <- lme4::lmer(
    Pcv ~ dose * Drug + (1 | Region / Drug),
    data = ex125,
    REML = TRUE
  )

  emmeans_mixed_model(fit, ~ dose | Drug, lmer.df = "asymptotic")
  emmeans_mixed_model(
    fit,
    ~ dose | Drug,
    pairwise = TRUE,
    lmer.df = "asymptotic"
  )
}
```

`ex121` *ex121 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Packed cell volume data for the dose comparison in Example 1.2.1.

Usage

```
data(ex121)
```

Format

A `data.frame` with 14 rows and 5 variables:

animals Animal identifier within dose group.

dose Dose group with levels `H`, `L`, and `M`.

PCV1 Packed cell volume measured at treatment.

PCV2 Packed cell volume measured after treatment.

PCVdiff Difference between post-treatment and baseline packed cell volume.

Author(s)

1. Muhammad Yaseen (`<myaseen208@gmail.com>`)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

Examples

```
data(ex121)
```

`ex124` *ex124 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Packed cell volume response data by herd, drug, and dose.

Usage

```
data(ex124)
```

Format

A `data.frame` with 40 rows and 4 variables:

herd Herd identifier.

drug Drug administered, Berenil or Samorin.

dose Dose group, high (`h`) or low (`l`).

PCVdif Change in packed cell volume after treatment.

Author(s)

1. Muhammad Yaseen (`<myaseen208@gmail.com>`)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`Examp1.3.2`

Examples

```
data(ex124)
```

`ex125` *ex125 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Packed cell volume response data by region, drug, and dose.

Usage

```
data(ex125)
```

Format

A `data.frame` with 24 rows and 4 variables:

Region Region identifier.

Drug Drug administered, Berenil or Samorin.

dose Dose group, high (`h`) or low (`l`).

Pcv Packed cell volume response.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`Examp1.3.2`

Examples

```
data(ex125)
```

`ex127` *ex127 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Weaning weight observations grouped by sire.

Usage

```
data(ex127)
```

Format

A `data.frame` with 43 rows and 2 variables:

sire Sire identifier.

Ww Weaning weight.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research*. International Livestock Research Institute.

See Also

`Examp1.3.2`

Examples

```
data(ex127)
```

`ex31` *ex31 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Packed cell volume data for two trypanosomosis drugs.

Usage

```
data(ex31)
```

Format

A `data.frame` with 38 rows and 6 variables:

herd Herd identifier.

animal_id Animal identifier.

PCV1 Packed cell volume measured at treatment.

PCV2 Packed cell volume measured one month after treatment.

dose Dose level.

drug Drug administered, Berenil or Samorin.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`Examp1.3.2`

Examples

```
data(ex31)
```

`ex32` *ex32 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Weaning weight data by breed, sire, sex, and age.

Usage

```
data(ex32)
```

Format

A `data.frame` with 65 rows and 5 variables:

breed Breed identifier.

sire_id Sire identifier nested within breed.

sex Sex of the animal, female (`F`) or male (`M`).

agew Age at weighing.

Ww Weaning weight.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`Examp1.3.2`

Examples

```
data(ex32)
```

`ex33` *ex33 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Longitudinal packed cell volume data by animal, breed, and time.

Usage

```
data(ex33)
```

Format

A `data.frame` with 168 rows and 4 variables:

animal_id Animal identifier.

breed Breed group.

time Time of packed cell volume measurement.

PCV Packed cell volume response.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`Examp1.3.2`

Examples

```
data(ex33)
```

`Examp1.3.2` *Examp1.3.2 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Examp1.3.2 is used for inspecting probability distribution and to define a plausible process through linear models and generalized linear models.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`ex124`

Examples

```
#-------------------------------------------------------------
## Example 1.3.2 p-16
#-------------------------------------------------------------
 # PROC GLM DATA=ex124;
 # CLASS herd dose drug;
 # MODEL PCVdif=drug herd(drug) dose dose*drug;
 # RANDOM herd(drug);
 # RUN;

str(ex124)
summary(ex124)

ex124$herd1 <- factor(ex124$herd)
ex124$drug1 <- factor(ex124$drug)
ex124$dose1 <- factor(ex124$dose)

fm1.1 <-
  aov(
      formula     = PCVdif ~ drug1 + Error(herd1:drug1) + dose1 + dose1:drug1
    , data        = ex124
    , projections = FALSE
    , qr          = TRUE
    , contrasts   = NULL
  #  , ...
```

```
    )
if (requireNamespace("report", quietly = TRUE)) {
  fm1.1 |>
    report::report()
}
summary(fm1.1)
```

`Examp2.2.1.7` *Examp2.2.1.7 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Examp2.2.1.7 is used for inspecting probability distribution and to define a plausible process through linear models and generalized linear models.

Author(s)

1. Muhammad Yaseen (`<myaseen208@gmail.com>`)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`ex124`

Examples

```
#-------------------------------------------------------------
## Example 2.2.1.7 p-42
#-------------------------------------------------------------
 # PROC GLM DATA=ex121;
 # CLASS dose;
 # MODEL PCVdif=dose;
 # ESTIMATE 'l vs mh' dose -0.5 1 -0.5;
 # CONTRAST 'l vs mh' dose -0.5 1 -0.5;
 # RUN;

str(ex121)
fm2.1 <-
 aov(
     formula     = PCVdiff ~ dose
   , data        = ex121
   , projections = FALSE
   , qr          = TRUE
```

```
    , contrasts   = NULL
 #  , ...
    )
if (requireNamespace("report", quietly = TRUE)) {
  fm2.1 |>
    report::report()
}
summary(fm2.1)
anova(fm2.1)

LvsMHConc <-
         matrix(
             data    = c(-0.5, 1, -0.5)
           , nrow    = length(levels(ex121$dose))
           , byrow   = FALSE
           , dimnames = list(
                             c(levels(ex121$dose))
                           , c("Low vs Mediam and Hight")
                           )
         )

contrasts(ex121$dose) <- LvsMHConc
fm2.2 <-
 aov(
     formula     = PCVdiff ~ dose
   , data        = ex121
   , projections = FALSE
   , qr          = TRUE
   , contrasts   = NULL
 #  , ...
   )
if (requireNamespace("report", quietly = TRUE)) {
  fm2.2 |>
    report::report()
}
summary(fm2.2, split = list(dose = list("Low vs Mediam and Hight" = 1)))

fm2.3 <-
     lm(
          formula     = PCVdiff ~ dose
        , data        = ex121
     #  , subset
     #  , weights
     #  , na.action
        , method      = "qr"
        , model       = TRUE
        , x           = FALSE
        , y           = FALSE
        , qr          = TRUE
        , singular.ok = TRUE
        , contrasts   = NULL
     #  , offset
     #  , ...
```

```
    )
if (requireNamespace("report", quietly = TRUE)) {
  fm2.3 |>
    report::report()
}
if (requireNamespace("emmeans", quietly = TRUE)) {
  emm2.3 <- emmeans::emmeans(fm2.3, ~ dose)
  print(emm2.3)
  print(emmeans::contrast(
    emm2.3,
    method = list(low_vs_medium_high = c(-0.5, 1, -0.5))
  ))
}
summary(fm2.3)
anova(fm2.3)
# multcomp::glht(
#      model       = fm2.3
#    , linfct      = LvsMHConc
#    , alternative = "two.sided" # c("two.sided", "less", "greater")
#    , rhs         = 0
#    )
```

`Examp2.4.2.2` *Examp2.4.2.2 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Examp2.4.2.2 is used for inspecting probability distribution and to define a plausible process through linear models and generalized linear models.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

ex124

Examples

```
#-------------------------------------------------------------
## Example 2.4.2.2 p-64
#-------------------------------------------------------------
# PROC MIXED DATA=ex125 METHOD=ML;
# CLASS drug dose region;
# MODEL pcv=drug dose drug*dose;
# RANDOM region drug*region;
# RUN;
#
# PROC MIXED DATA=ex125 METHOD=REML;
# CLASS drug dose region;
# MODEL pcv=drug dose drug*dose;
# RANDOM region drug*region;
# RUN;



str(ex125)
if (requireNamespace("lme4", quietly = TRUE)) {
  fm2.4 <-
    lme4::lmer(
           formula    = Pcv ~ dose * Drug + (1 | Region / Drug)
         , data       = ex125
         , REML       = FALSE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = NULL
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm2.4 |>
      report::report()
  }
  summary(fm2.4)
  anova(fm2.4)

  fm2.5 <-
    lme4::lmer(
           formula    = Pcv ~ dose * Drug + (1 | Region / Drug)
         , data       = ex125
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = NULL
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm2.5 |>
      report::report()
```

```
  }
  summary(fm2.5)
  anova(fm2.5)
}

if (requireNamespace("lme4", quietly = TRUE) &&
    requireNamespace("lmerTest", quietly = TRUE)) {
  fm2.6 <-
    lmerTest::lmer(
           formula    = Pcv ~ dose * Drug + (1 | Region / Drug)
         , data       = ex125
         , REML       = FALSE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = NULL
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm2.6 |>
      report::report()
  }
  summary(fm2.6)
  anova(fm2.6)

  fm2.7 <-
    lmerTest::lmer(
           formula    = Pcv ~ dose * Drug + (1 | Region / Drug)
         , data       = ex125
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = NULL
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm2.7 |>
      report::report()
  }
  summary(fm2.7)
  anova(fm2.7)
}
```

`Examp2.4.3.1`	*Examp2.4.3.1 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research*. International Livestock Research Institute.*

Description

Examp2.4.3.1 is used for inspecting probability distribution and to define a plausible process through linear models and generalized linear models.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`ex124`

Examples

```
#-------------------------------------------------------------
## Example 2.4.3.1 p-66
#-------------------------------------------------------------
 # PROC MIXED DATA=ex127;
 # CLASS sire;
 # MODEL ww=;
 # RANDOM sire/solution;
 # RUN;

str(ex127)
if (requireNamespace("lme4", quietly = TRUE)) {
  fm2.8 <-
    lme4::lmer(
           formula    = Ww ~ (1 | sire)
         , data       = ex127
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = NULL
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm2.8 |>
      report::report()
  }
  summary(fm2.8)
  lme4::fixef(fm2.8)
  lme4::ranef(fm2.8)
}
```

`Examp2.5.1.1` *Examp2.5.1.1 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Examp2.5.1.1 is used for inspecting probability distribution and to define a plausible process through linear models and generalized linear models.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`ex124`

Examples

```
#-------------------------------------------------------------
## Example 2.5.1.1 p-67
#-------------------------------------------------------------
 # PROC MIXED DATA=ex125;
 # CLASS drug dose region;
 # MODEL pcv=drug dose drug*dose / solution covb;
 # RANDOM region drug*region;
 # RUN;

str(ex125)
if (requireNamespace("lme4", quietly = TRUE)) {
  fm2.9 <-
    lme4::lmer(
           formula    = Pcv ~ dose * Drug + (1 | Region / Drug)
         , data       = ex125
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = list(dose = "contr.SAS", Drug = "contr.SAS")
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm2.9 |>
```

```
      report::report()
    }
    if (requireNamespace("emmeans", quietly = TRUE)) {
      emm2.9 <- emmeans::emmeans(fm2.9, ~ dose | Drug, lmer.df = "asymptotic")
      print(emm2.9)
      print(emmeans::contrast(emm2.9, method = "pairwise"))
    }
    summary(fm2.9)
    anova(fm2.9)
    summary(fm2.9)$vcov
  }
```

`Examp2.5.2.1` *Examp2.5.2.1 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Examp2.5.2.1 is used for inspecting probability distribution and to define a plausible process through linear models and generalized linear models.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

ex124

Examples

```
#-------------------------------------------------------------
## Example 2.5.2.1 p-68
#-------------------------------------------------------------
 # PROC MIXED DATA=ex125;
 # CLASS drug dose region;
 # MODEL pcv=drug dose drug*dose / solution covb;
 # RANDOM region drug*region;
 # LSMEANS drug*dose;
 # RUN;

str(ex125)
```

```
if (requireNamespace("lme4", quietly = TRUE) &&
    requireNamespace("lmerTest", quietly = TRUE)) {
  fm2.10 <-
    lmerTest::lmer(
           formula    = Pcv ~ dose * Drug + (1 | Region / Drug)
         , data       = ex125
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = list(dose = "contr.SAS", Drug = "contr.SAS")
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm2.10 |>
      report::report()
  }
  if (requireNamespace("emmeans", quietly = TRUE)) {
    emm2.10 <- emmeans::emmeans(fm2.10, ~ dose | Drug, lmer.df = "asymptotic")
    print(emm2.10)
    print(emmeans::contrast(emm2.10, method = "pairwise"))
  }
  summary(fm2.10)
  anova(fm2.10)
  summary(fm2.10)$vcov
}
```

`Examp2.5.3.1` *Examp2.5.3.1 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Examp2.5.3.1 is used for inspecting probability distribution and to define a plausible process through linear models and generalized linear models.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`ex124`

Examples

```
#-------------------------------------------------------------
## Example 2.5.3.1 p-70
#-------------------------------------------------------------
 # PROC GLM DATA=ex125;
 # CLASS drug dose region;
 # MODEL pcv=region drug region*drug dose drug*dose;
 # RANDOM region drug*region;
 # RUN;


 # PROC MIXED DATA=ex125;
 # CLASS drug dose region;
 # MODEL pcv=drug dose drug*dose / ddfm=satterth;
 # RANDOM region drug*region;
 # ESTIMATE 'drug dif' drug -1 1 drug*dose -0.5 -0.5 0.5 0.5;
 # ESTIMATE 'Samorin mean' INTERCEPT 1 drug 0 1 dose 0.5 0.5
 #                            drug*dose 0 0 0.5 0.5;
 # ESTIMATE 'Samorin HvsL' dose 1 -1 drug*dose 0 0 1 -1;
 # ESTIMATE 'Samorin high' INTERCEPT 1 drug 0 1 dose 1 0
 #                            drug*dose 0 0 1 0;
 # RUN;

str(ex125)
ex125$Region1 <- factor(ex125$Region)
fm2.11 <-
  aov(
      formula     = Pcv ~ Region1 + Drug + Error(Drug:Region1) + dose + dose:Drug
    , data        = ex125
    , projections = FALSE
    , qr          = TRUE
    , contrasts   = NULL
    )
if (requireNamespace("report", quietly = TRUE)) {
  fm2.11 |>
    report::report()
}
summary(fm2.11)

if (requireNamespace("lme4", quietly = TRUE) &&
    requireNamespace("lmerTest", quietly = TRUE)) {
  fm2.12 <-
    lmerTest::lmer(
           formula    = Pcv ~ dose * Drug + (1 | Region / Drug)
         , data       = ex125
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = list(dose = "contr.SAS", Drug = "contr.SAS")
         , devFunOnly = FALSE
         )
```

```
  if (requireNamespace("report", quietly = TRUE)) {
    fm2.12 |>
      report::report()
  }
  if (requireNamespace("emmeans", quietly = TRUE)) {
    emm2.12 <- emmeans::emmeans(fm2.12, ~ dose | Drug, lmer.df = "asymptotic")
    print(emm2.12)
    print(emmeans::contrast(emm2.12, method = "pairwise"))
  }
  summary(fm2.12)
  anova(object = fm2.12, ddf = "Satterthwaite")

  if (requireNamespace("multcomp", quietly = TRUE)) {
    Contrasts1 <-
      matrix(
        c(1, 0.5, 0, 0, 0, 0, -1, -0.5, 1, 1, 0, 0, 0, 1, 0, 0),
        ncol = 4,
        byrow = TRUE,
        dimnames = list(
          c("C1", "C2", "C3", "C4"),
          rownames(summary(fm2.12)$coef)
        )
      )
    Contrasts1
    summary(multcomp::glht(fm2.12, linfct = Contrasts1))
  }
}
```

`Examp2.5.4.1` *Examp2.5.4.1 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Examp2.5.4.1 is used for inspecting probability distribution and to define a plausible process through linear models and generalized linear models.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research*. International Livestock Research Institute.

See Also

`ex124`

Examples

```
#-------------------------------------------------------------
## Example 2.5.4.1 p-74
#-------------------------------------------------------------
 # PROC MIXED DATA=ex125;
 # CLASS drug dose region;
 # MODEL pcv=drug dose drug*dose / ddfm=satterth;
 # RANDOM region drug*region;
 # ESTIMATE 'Samorin mean' INTERCEPT 1 drug 0 1 dose 0.5 0.5
 #                             drug*dose 0 0 0.5 0.5;
 # RUN;

 # PROC GLM DATA=ex125;
 # CLASS drug dose region;
 # MODEL pcv=region drug region*drug dose drug*dose;
 # ESTIMATE 'Samorin mean' INTERCEPT 1 drug 0 1 dose 0.5 0.5
 #                             drug*dose 0 0 0.5 0.5;
 # RUN;

str(ex125)
ex125$Region1 <- factor(ex125$Region)
if (requireNamespace("lme4", quietly = TRUE) &&
    requireNamespace("lmerTest", quietly = TRUE)) {
  fm2.13 <-
    lmerTest::lmer(
           formula    = Pcv ~ dose * Drug + (1 | Region / Drug)
         , data       = ex125
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = list(dose = "contr.SAS", Drug = "contr.SAS")
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm2.13 |>
      report::report()
  }
  if (requireNamespace("emmeans", quietly = TRUE)) {
    emm2.13 <- emmeans::emmeans(fm2.13, ~ dose | Drug, lmer.df = "asymptotic")
    print(emm2.13)
    print(emmeans::contrast(emm2.13, method = "pairwise"))
  }
  summary(fm2.13)

  if (requireNamespace("multcomp", quietly = TRUE)) {
    Contrasts2 <-
      matrix(
        c(1, 0.5, 0, 0),
        ncol = 4,
        byrow = TRUE,
        dimnames = list(c("C5"), rownames(summary(fm2.13)$coef))
```

```
      )
    Contrasts2
    summary(multcomp::glht(fm2.13, linfct = Contrasts2))
  }
}
```

Examp2.6.1	*Examp2.6.1 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Examp2.6.1 is used for inspecting probability distribution and to define a plausible process through linear models and generalized linear models.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`ex124`

Examples

```
#-------------------------------------------------------------
## Example 2.6.1 p-76
#-------------------------------------------------------------
 # PROC MIXED DATA=ex125;
 # CLASS drug dose region;
 # MODEL pcv=drug dose drug*dose / ddfm=satterth;
 # RANDOM region drug*region;
 # CONTRAST 'drug dif' drug -1 1 drug*dose -0.5 -0.5 0.5 0.5;
 # CONTRAST 'all' drug 1 -1 dose 0  0 drug*dose 0.5  0.5 -0.5 -0.5,
 #                drug 0  0 dose 1 -1 drug*dose 0.5 -0.5  0.5 -0.5,
 #                drug 0  0 dose 0  0 drug*dose 0.5 -0.5 -0.5  0.5;
 # RUN;

str(ex125)
ex125$Region1 <- factor(ex125$Region)
if (requireNamespace("lme4", quietly = TRUE) &&
    requireNamespace("lmerTest", quietly = TRUE)) {
```

```
  fm2.14 <-
    lmerTest::lmer(
           formula    = Pcv ~ dose * Drug + (1 | Region / Drug)
         , data       = ex125
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = list(dose = "contr.SAS", Drug = "contr.SAS")
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm2.14 |>
      report::report()
  }
  if (requireNamespace("emmeans", quietly = TRUE)) {
    emm2.14 <- emmeans::emmeans(fm2.14, ~ dose | Drug, lmer.df = "asymptotic")
    print(emm2.14)
    print(emmeans::contrast(emm2.14, method = "pairwise"))
  }
  summary(fm2.14)
  anova(object = fm2.14, ddf = "Satterthwaite")

  Contrasts3 <-
    matrix(
      c(0, 0, -1, -0.5),
      ncol = 4,
      byrow = TRUE,
      dimnames = list(c("C1"), rownames(summary(fm2.14)$coef))
    )
  Contrasts3
  if (requireNamespace("multcomp", quietly = TRUE)) {
    summary(multcomp::glht(fm2.14, linfct = Contrasts3))
  }
  if (utils::packageVersion("lmerTest") >= "3.0") {
    lmerTest::contest(fm2.14, Contrasts3, joint = FALSE)
  }
}
```

`Examp3.1` *Examp3.1 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Examp3.1 is.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`ex124`

Examples

```
#--------------------------------------------------------------
## Example 3.1 Model 1 p-80
#--------------------------------------------------------------
# PROC MIXED DATA=ex31;
# CLASS drug dose herd;
# MODEL PCV2=drug dose(drug)/solution ddfm=satterth;
# RANDOM herd(drug);
# ESTIMATE 'Mean Samorin' intercept 1 drug 0 1 dose(drug) 0 0 1;
# ESTIMATE 'Berenil 2 doses' dose(drug) 1 -1 0;
# ESTIMATE 'Ber vs Sam at dose 1' drug 1 -1 dose(drug) 1 0 -1;
# CONTRAST 'Mean Samorin' intercept 1 drug 0 1 dose(drug) 0 0 1;
# CONTRAST 'Berenil dif 2 doses' dose(drug) 1 -1 0;
# CONTRAST 'Ber vs Sam at dose 1' drug 1 -1 dose(drug) 1 0 -l;
# CONTRAST 'some difference' drug 1 -1 dose(drug) 0.5 0.5 -1,
#           drug 0 0 dose(drug) 1 -1 0;
# LSMEANS dose(drug);
# RUN;

str(ex31)
ex31$herd1 <- factor(ex31$herd)
ex31$drug1 <- factor(ex31$drug)
ex31$dose1 <- factor(ex31$dose)
ex31$ber   <- as.integer(ex31$drug == ”BERENIL”)
ex31$ber1  <- as.integer(ex31$drug == ”BERENIL” & ex31$dose == 1L)
ex31$pcv_ber1 <- ex31$PCV1 * as.integer(ex31$drug == ”BERENIL” & ex31$dose == 1L)
ex31$pcv_ber2 <- ex31$PCV1 * as.integer(ex31$drug == ”BERENIL” & ex31$dose == 2L)

if (requireNamespace(”lme4”, quietly = TRUE) &&
    requireNamespace(”lmerTest”, quietly = TRUE)) {
  fm3.1 <-
    lmerTest::lmer(
           formula    = PCV2 ~ drug1 + dose1:drug1 + (1 | herd1:drug1)
         , data       = ex31
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = list(dose1 = ”contr.SAS”, drug1 = ”contr.SAS”)
```

```
          , devFunOnly = FALSE
          )
  if (requireNamespace("report", quietly = TRUE)) {
    fm3.1 |>
      report::report()
  }
  if (requireNamespace("emmeans", quietly = TRUE)) {
    emm3.1 <- emmeans::emmeans(fm3.1, ~ dose1 | drug1, lmer.df = "asymptotic")
    print(emm3.1)
    print(emmeans::contrast(emm3.1, method = "pairwise"))
  }
  summary(fm3.1)
  anova(object = fm3.1, ddf = "Satterthwaite")

#-------------------------------------------------------------
## Example 3.1 Model 2 p-84
#-------------------------------------------------------------
# PROC MIXED DATA=ex31;
# CLASS drug dose herd;
# MODEL PCV2=PCV1 drug dose(drug)/solution ddfm=satterth;
# RANDOM herd(drug);
# RUN;

  fm3.2 <-
    lmerTest::lmer(
           formula    = PCV2 ~ PCV1 + drug1 + dose1:drug1 + (1 | herd1:drug1)
         , data       = ex31
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = list(dose1 = "contr.SAS", drug1 = "contr.SAS")
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm3.2 |>
      report::report()
  }
  if (requireNamespace("emmeans", quietly = TRUE)) {
    emm3.2 <- emmeans::emmeans(fm3.2, ~ dose1 | drug1, lmer.df = "asymptotic")
    print(emm3.2)
    print(emmeans::contrast(emm3.2, method = "pairwise"))
  }
  summary(fm3.2)
  anova(object = fm3.2, ddf = "Satterthwaite")

#-------------------------------------------------------------
## Example 3.1 Model 3 p-86
#-------------------------------------------------------------
# PROC MIXED DATA=ex31;
# CLASS drug dose herd;
# MODEL PCV2=drug dose(drug) PCV1*dose(drug)/solution ddfm=satterth;
# RANDOM herd(drug);
```

```
# RUN;

  fm3.3 <-
    lmerTest::lmer(
           formula    = PCV2 ~ drug1 + PCV1 * dose1:drug1 + (1 | herd1:drug1)
         , data       = ex31
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = list(dose1 = "contr.SAS", drug1 = "contr.SAS")
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm3.3 |>
      report::report()
  }
  if (requireNamespace("emmeans", quietly = TRUE)) {
    emm3.3 <- emmeans::emmeans(fm3.3, ~ dose1 | drug1, lmer.df = "asymptotic")
    print(emm3.3)
    print(emmeans::contrast(emm3.3, method = "pairwise"))
  }
  summary(fm3.3)
  anova(object = fm3.3, ddf = "Satterthwaite")
}
```

`Examp3.2` *Examp3.2 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Examp3.2 is used for inspecting probability distribution and to define a plausible process through linear models and generalized linear models.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`ex124`

Examples

```
#-------------------------------------------------------------
## Example 3.3 p-88
#-------------------------------------------------------------
# PROC MIXED DATA=ex32;
# CLASS sex sire_id breed;
# MODEL ww = sex agew breed/SOLUTION DDFM=SATTERTH;
# RANDOM sire_id(breed)/SOLUTION;
# LSMEANS breed/ADJUST = TUKEY;
# RUN;

str(ex32)
ex32$sire_id1 <- factor(ex32$sire_id)
ex32$breed1   <- factor(ex32$breed)
if (requireNamespace("lme4", quietly = TRUE) &&
    requireNamespace("lmerTest", quietly = TRUE)) {
  fm3.4 <-
    lmerTest::lmer(
           formula    = Ww ~ sex + agew + breed1 + (1 | sire_id1:breed1)
         , data       = ex32
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = list(sex = "contr.SAS", breed1 = "contr.SAS")
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm3.4 |>
      report::report()
  }
  if (requireNamespace("emmeans", quietly = TRUE)) {
    emm3.4 <- emmeans::emmeans(fm3.4, ~ breed1, lmer.df = "asymptotic")
    print(emm3.4)
    print(emmeans::contrast(emm3.4, method = "pairwise", adjust = "tukey"))
  }
  summary(fm3.4)
  anova(object = fm3.4, ddf = "Satterthwaite")
}
```

`Examp3.3` *Examp3.3 from Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research. *International Livestock Research Institute.*

Description

Examp3.3 is used for inspecting probability distribution and to define a plausible process through linear models and generalized linear models.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Duchateau, L. and Janssen, P. and Rowlands, G. J. (1998).*Linear Mixed Models. An Introduction with applications in Veterinary Research.* International Livestock Research Institute.

See Also

`ex124`

Examples

```
#-------------------------------------------------------------
## Example 3.3 Model 1 p-88
#-------------------------------------------------------------
# PROC MIXED DATA=ex33;
# CLASS breed animal_id;
# MODEL pcv = breed breed*time/SOLUTION;
# RANDOM animal_id(breed)/SOLUTION;
# RUN;

str(ex33)
if (requireNamespace("lme4", quietly = TRUE)) {
  fm3.5 <-
    lme4::lmer(
           formula    = PCV ~ breed + breed:time + (1 | animal_id:breed)
         , data       = ex33
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = list(breed = "contr.SAS")
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm3.5 |>
      report::report()
  }
  summary(fm3.5)
  anova(fm3.5)
}

if (requireNamespace("lme4", quietly = TRUE) &&
    requireNamespace("lmerTest", quietly = TRUE)) {
  fm3.6 <-
    lmerTest::lmer(
           formula    = PCV ~ breed + breed:time + (1 | animal_id:breed)
         , data       = ex33
         , REML       = TRUE
         , control    = lme4::lmerControl()
```

```
          , start      = NULL
          , verbose    = 0L
          , contrasts  = list(breed = "contr.SAS")
          , devFunOnly = FALSE
          )
  if (requireNamespace("report", quietly = TRUE)) {
    fm3.6 |>
      report::report()
  }
  if (requireNamespace("emmeans", quietly = TRUE)) {
    trend3.6 <- emmeans::emtrends(fm3.6, ~ breed, var = "time",
                                  lmer.df = "asymptotic")
    print(trend3.6)
    print(emmeans::contrast(trend3.6, method = "pairwise"))
  }
  summary(fm3.6)
  anova(object = fm3.6, ddf = "Satterthwaite")
}

if (requireNamespace("nlme", quietly = TRUE)) {
  fm3.7 <-
    nlme::gls(
          model       = PCV ~ breed + breed:time
        , data        = ex33
        , correlation = nlme::corCompSymm(form = ~ 1 | animal_id / breed)
        , weights     = NULL
        , method      = "REML"
        , na.action   = na.fail
        , control     = list()
        )
  if (requireNamespace("report", quietly = TRUE)) {
    try(report::report(fm3.7), silent = TRUE)
  }
  summary(fm3.7)
  anova(fm3.7)
}

if (requireNamespace("lme4", quietly = TRUE)) {
  fm3.8 <-
    lme4::lmer(
            formula    = PCV ~ time + breed + breed:time + (1 | animal_id:breed)
          , data       = ex33
          , REML       = TRUE
          , control    = lme4::lmerControl()
          , start      = NULL
          , verbose    = 0L
          , contrasts  = list(breed = "contr.SAS")
          , devFunOnly = FALSE
          )
  if (requireNamespace("report", quietly = TRUE)) {
    fm3.8 |>
      report::report()
  }
```

```
  summary(fm3.8)
  anova(fm3.8)
}

if (requireNamespace("lme4", quietly = TRUE) &&
    requireNamespace("lmerTest", quietly = TRUE)) {
  fm3.9 <-
    lmerTest::lmer(
           formula    = PCV ~ time + breed + breed:time + (1 | animal_id:breed)
         , data       = ex33
         , REML       = TRUE
         , control    = lme4::lmerControl()
         , start      = NULL
         , verbose    = 0L
         , contrasts  = list(breed = "contr.SAS")
         , devFunOnly = FALSE
         )
  if (requireNamespace("report", quietly = TRUE)) {
    fm3.9 |>
      report::report()
  }
  if (requireNamespace("emmeans", quietly = TRUE)) {
    trend3.9 <- emmeans::emtrends(fm3.9, ~ breed, var = "time",
                                  lmer.df = "asymptotic")
    print(trend3.9)
    print(emmeans::contrast(trend3.9, method = "pairwise"))
  }
  summary(fm3.9)
  anova(object = fm3.9, ddf = "Satterthwaite", type = 3)
}

if (requireNamespace("nlme", quietly = TRUE)) {
  fm3.10 <-
    nlme::gls(
          model       = PCV ~ breed + breed:time
        , data        = ex33
        , correlation = nlme::corAR1(form = ~ 1 | animal_id / breed)
        , weights     = NULL
        , method      = "REML"
        , na.action   = na.fail
        , control     = list()
        )
  if (requireNamespace("report", quietly = TRUE)) {
    try(report::report(fm3.10), silent = TRUE)
  }
  summary(fm3.10)
  anova(fm3.10)
}
```

`report_mixed_model` *Report a Fitted Mixed Model*

Description

Create an easystats-style narrative report for a fitted linear mixed model.

Usage

```
report_mixed_model(model, ...)
```

Arguments

`model`	A fitted model object, typically from `lme4::lmer()`, `lmerTest::lmer()`, or `nlme::lme()`.
`...`	Additional arguments passed to `report::report()`.

Details

This helper keeps the **report** package optional. It checks that a fitted model was supplied, verifies that **report** is installed, and then delegates the model interpretation to `report::report()`. This provides a stable package-level entry point for readers who want easystats-style interpretation of the fitted mixed models used throughout the book examples.

The helper does not change the fitted model, refit the model, or alter any estimates. It only formats and interprets the model object produced by the modelling package.

Value

A report object returned by `report::report()`.

References

Duchateau, L., Janssen, P., and Rowlands, G. J. (1998). *Linear Mixed Models: An Introduction with Applications in Veterinary Research*. International Livestock Research Institute.

See `utils::citation("report")` for the citation for the optional easystats reporting package.

See Also

`lme4::lmer`, `nlme::lme`.

Examples

```
if (requireNamespace("lme4", quietly = TRUE) &&
    requireNamespace("report", quietly = TRUE)) {
  data(ex127, package = "VetResearchLMM")
  fit <- lme4::lmer(Ww ~ 1 + (1 | sire), data = ex127, REML = TRUE)
  report_mixed_model(fit)
}
```

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