Package 'VetResearchLMM'

October 12, 2022

Type Package

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

Version 1.0.0

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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 (>= 3.1)

Imports ggplot2, lme4, nlme, lmerTest, multcomp

License GPL-2

URL https://github.com/MYaseen208/VetResearchLMM

LazyData TRUE

RoxygenNote 6.0.1

Note Department of Mathematics and Statistics, University of Agriculture Faisalabad, Faisalabad-Pakistan.

NeedsCompilation no

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Repository CRAN

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R topics documented:

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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

ex121 is.

Usage

```
data(ex121)
```

Format

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

Details

- herd two treatment 0 and 1
- drug unit of observation or observation ID
- dose is continuous \& may be assumed Gaussian
- PCVDif is the number of "successes"(N and F specify a binomial 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.

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

ex124 is.

Usage

```
data(ex124)
```

Format

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

Details

- herd two treatment 0 and 1
- drug unit of observation or observation ID
- dose is continuous \& may be assumed Gaussian
- PCVDif is the number of "successes"(N and F specify a binomial 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(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

ex125 is.

Usage

```
data(ex125)
```

Format

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

Details

- herd two treatment 0 and 1
- drug unit of observation or observation ID
- dose is continuous \& may be assumed Gaussian
- PCVDif is the number of "successes"(N and F specify a binomial 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

ex127 is.

Usage

```
data(ex127)
```

Format

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

Details

- herd two treatment 0 and 1
- drug unit of observation or observation ID
- dose is continuous \& may be assumed Gaussian
- PCVDif is the number of "successes"(N and F specify a binomial 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(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

ex31 is.

Usage

```
data(ex31)
```

Format

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

Details

- herd Herds of Cattle
- animal_id Animal ID
- PCV1 Packed Cell Volume (PCV) determined at the time of treatment
- PCV2 Packed Cell Volume (PCV) determined at a month later following treatment
- dose Dose of Drugs
- drug Two drugs against trypanosomosis, Berenil and Samorin, are studied

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

ex32 is.

Usage

```
data(ex32)
```

Format

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

Details

- herd two treatment 0 and 1
- drug unit of observation or observation ID
- dose is continuous \& may be assumed Gaussian
- PCVDif is the number of "successes"(N and F specify a binomial 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(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

ex33 is.

Usage

```
data(ex33)
```

Format

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

Details

- herd two treatment 0 and 1
- drug unit of observation or observation ID
- dose is continuous \& may be assumed Gaussian
- PCVDif is the number of "successes"(N and F specify a binomial 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`	*#' @title 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;

library(lme4)
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
  #  , ...
    )
summary(fm1.1)
```

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;


library(lme4)
str(ex125)
```

```
fm2.4 <-
  lme4::lmer(
         formula    = Pcv ~ dose*Drug + (1|Region/Drug)
       , data       = ex125
       , REML       = FALSE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
    #  , weights
    #  , na.action
    #  , offset
       , contrasts  = NULL
       , devFunOnly = FALSE
    #  , ...
       )
summary(fm2.4)
anova(fm2.4)

fm2.5 <-
  lme4::lmer(
         formula    = Pcv ~ dose*Drug + (1|Region/Drug)
       , data       = ex125
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
    #  , weights
    #  , na.action
    #  , offset
       , contrasts  = NULL
       , devFunOnly = FALSE
    #  , ...
       )
summary(fm2.5)
anova(fm2.5)

library(lmerTest)

fm2.6 <-
    lmerTest::lmer(
         formula    = Pcv ~ dose*Drug + (1|Region/Drug)
       , data       = ex125
       , REML       = FALSE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
      # , subset
      # , weights
      # , na.action
      # , offset
       , contrasts  = NULL
```

```
       , devFunOnly = FALSE
      # , ...
       )
summary(fm2.6)
anova(fm2.6)

fm2.7 <-
    lmerTest::lmer(
         formula    = Pcv ~ dose*Drug + (1|Region/Drug)
       , data       = ex125
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
      # , subset
      # , weights
      # , na.action
      # , offset
       , contrasts  = NULL
       , devFunOnly = FALSE
      # , ...
       )
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;

library(lme4)
str(ex127)
fm2.8 <-
  lme4::lmer(
         formula    = Ww~(1|sire)
       , data       = ex127
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
    #  , weights
    #  , na.action
    #  , offset
       , contrasts  = NULL
       , devFunOnly = FALSE
    #  , ...
       )
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;

library(lme4)
str(ex125)

fm2.9 <-
  lme4::lmer(
         formula    = Pcv ~ dose*Drug + (1|Region/Drug)
       , data       = ex125
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
    #  , weights
    #  , na.action
    #  , offset
       , contrasts  = list(dose = "contr.SAS", Drug = "contr.SAS")
       , devFunOnly = FALSE
    #  , ...
       )
 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;

library(lmerTest)
str(ex125)

fm2.10 <-
  lmerTest::lmer(
         formula    = Pcv ~ dose*Drug + (1|Region/Drug)
       , data       = ex125
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
    #  , weights
    #  , na.action
    #  , offset
       , contrasts  = list(dose = "contr.SAS", Drug = "contr.SAS")
       , devFunOnly = FALSE
    #  , ...
       )
summary(fm2.10)
anova(fm2.10)
summary(fm2.10)$vcov
lsmeansLT(model = fm2.10)
```

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;

library(lme4)
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
  #  , ...
    )
 summary(fm2.11)

 fm2.12 <-
  lmerTest::lmer(
         formula    = Pcv ~ dose*Drug + (1|Region/Drug)
       , data       = ex125
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
    #  , weights
    #  , na.action
    #  , offset
       , contrasts  = list(dose = "contr.SAS", Drug = "contr.SAS")
       , devFunOnly = FALSE
    #  , ...
       )
 summary(fm2.12)
 anova(object = fm2.12, ddf = "Satterthwaite")

library(multcomp)
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(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;

 library(lme4)
 str(ex125)
 ex125$Region1 <- factor(ex125$Region)
  fm2.13 <-
  lmerTest::lmer(
         formula    = Pcv ~ dose*Drug + (1|Region/Drug)
```

```
      , data       = ex125
      , REML       = TRUE
      , control    = lmerControl()
      , start      = NULL
      , verbose    = 0L
   #  , subset
   #  , weights
   #  , na.action
   #  , offset
      , contrasts  = list(dose = "contr.SAS", Drug = "contr.SAS")
      , devFunOnly = FALSE
   #  , ...
      )
 summary(fm2.13)

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

Contrasts2
summary(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;

 library(lmerTest)
 str(ex125)
 ex125$Region1 <- factor(ex125$Region)
 fm2.14 <-
  lmerTest::lmer(
         formula    = Pcv ~ dose*Drug + (1|Region/Drug)
       , data       = ex125
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
    #  , weights
    #  , na.action
    #  , offset
       , contrasts  = list(dose = "contr.SAS", Drug = "contr.SAS")
       , devFunOnly = FALSE
    #  , ...
      )
 summary(fm2.14)
 anova(object = fm2.14, ddf = "Satterthwaite")

 library(multcomp)
 Contrasts3 <-
           matrix(c(
                    0, 0, -1, -0.5
                   )
                , ncol = 4
                , byrow = TRUE
                , dimnames = list(
                   c("C1")
                 , rownames(summary(fm2.14)$coef)
                )
               )
```

```
 Contrasts3
 summary(glht(fm2.14, linfct=Contrasts3))

if(packageVersion("lmerTest") >= "3.0")
   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;
```

```
library(lmerTest)
str(ex31)
ex31$drug1 <- factor(ex31$drug)
ex31$dose1 <- factor(ex31$dose)
ex31$herd1 <- factor(ex31$herd)

fm3.1 <-
 lmerTest::lmer(
        formula    = PCV2 ~ drug1 + dose1:drug1 + (1|herd1:drug1)
      , data       = ex31
      , REML       = TRUE
      , control    = lmerControl()
      , start      = NULL
      , verbose    = 0L
   #  , subset
   #  , weights
   #  , na.action
   #  , offset
      , contrasts  = list(dose1 = "contr.SAS", drug1 = "contr.SAS")
      , devFunOnly = FALSE
   #  , ...
      )
summary(fm3.1)
anova(object = fm3.1, ddf = "Satterthwaite")
lsmeansLT(model = fm3.1, test.effs = "dose1:drug1")

#-------------------------------------------------------------
## 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;

library(lmerTest)
str(ex31)
ex31$drug1 <- factor(ex31$drug)
ex31$dose1 <- factor(ex31$dose)
ex31$herd1 <- factor(ex31$herd)

fm3.2 <-
 lmerTest::lmer(
        formula    = PCV2 ~ PCV1 + drug1 + dose1:drug1 + (1|herd1:drug1)
      , data       = ex31
      , REML       = TRUE
      , control    = lmerControl()
      , start      = NULL
      , verbose    = 0L
   #  , subset
   #  , weights
   #  , na.action
   #  , offset
```

```
       , contrasts  = list(dose1 = "contr.SAS", drug1 = "contr.SAS")
       , devFunOnly = FALSE
    #  , ...
       )
 summary(fm3.2)
 anova(object = fm3.2, ddf = "Satterthwaite")
 lsmeansLT(model = fm3.2, test.effs = "herd1:drug1")

#-------------------------------------------------------------
## 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;

 library(lmerTest)
 str(ex31)
 ex31$drug1 <- factor(ex31$drug)
 ex31$dose1 <- factor(ex31$dose)
 ex31$herd1 <- factor(ex31$herd)

 fm3.3 <-
  lmerTest::lmer(
         formula    = PCV2 ~ drug1 + PCV1*dose1:drug1 + (1|herd1:drug1)
       , data       = ex31
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
    #  , weights
    #  , na.action
    #  , offset
       , contrasts  = list(dose1 = "contr.SAS", drug1 = "contr.SAS")
       , devFunOnly = FALSE
    #  , ...
       )
 summary(fm3.3)
 anova(object = fm3.3, ddf = "Satterthwaite")
 lsmeansLT(model = fm3.3, test.effs = "dose1:drug1")
```

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;

 library(lmerTest)
 str(ex32)
 ex32$sire_id1 <- factor(ex32$sire_id)
 ex32$breed1   <- factor(ex32$breed)

 fm3.4 <-
  lmerTest::lmer(
         formula    = Ww ~ sex + agew + breed1 + (1|sire_id1:breed1)
       , data       = ex32
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
    #  , weights
    #  , na.action
    #  , offset
       , contrasts  = list(sex = "contr.SAS", breed1 = "contr.SAS")
       , devFunOnly = FALSE
    #  , ...
       )
 summary(fm3.4)
 anova(object = fm3.4, ddf = "Satterthwaite")
```

```
lsmeansLT(model = fm3.4)
```

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;

 library(lme4)
 options(contrasts = c(factor = "contr.SAS", ordered = "contr.poly"))
 str(ex33)

 fm3.5 <-
  lme4::lmer(
         formula    = PCV ~ breed + breed:time + (1|animal_id:breed)
       , data       = ex33
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
```

```
   #  , weights
   #  , na.action
   #  , offset
      , contrasts  = list(breed = "contr.SAS")
      , devFunOnly = FALSE
   #  , ...
      )
summary(fm3.5)
anova(fm3.5)

library(lmerTest)
fm3.6 <-
 lmerTest::lmer(
       formula    = PCV ~ breed + breed:time + (1|animal_id:breed)
      , data       = ex33
      , REML       = TRUE
      , control    = lmerControl()
      , start      = NULL
      , verbose    = 0L
   #  , subset
   #  , weights
   #  , na.action
   #  , offset
      , contrasts  = list(breed = "contr.SAS")
      , devFunOnly = FALSE
   #  , ...
      )
summary(fm3.6)
anova(object = fm3.6, ddf = "Satterthwaite")


# PROC MIXED DATA=ex33;
# CLASS breed animal_id;
# MODEL pcv = breed breed*time/SOLUTION;
# REPEATED/TYPE=CS SUB = animal_id(breed) R;
# RUN;


library(nlme)
fm3.7 <-
     nlme::gls(
           model       = PCV ~ breed + breed:time
         , data        = ex33
         , correlation = corCompSymm(, form = ~ 1|animal_id/breed)
         , weights     = NULL
       # , subset      =
         , method      = "REML" # c("REML", "ML")
         , na.action   = na.fail
         , control     = list()
         )
summary(fm3.7)
anova(fm3.7)
```

```
# PROC MIXED DATA=ex33;
# CLASS breed animal_id;
# MODEL pcv = time breed breed*time/SOLUTION;
# RANDOM animal_id(breed)/SOLUTION;
# RUN;

 fm3.8 <-
  lme4::lmer(
         formula    = PCV ~ time + breed + breed:time + (1|animal_id:breed)
       , data       = ex33
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
    #  , weights
    #  , na.action
    #  , offset
       , contrasts  = list(breed = "contr.SAS")
       , devFunOnly = FALSE
    #  , ...
       )
 summary(fm3.8)
 anova(fm3.8)


 fm3.9 <-
  lmerTest::lmer(
         formula    = PCV ~ time + breed + breed:time + (1|animal_id:breed)
       , data       = ex33
       , REML       = TRUE
       , control    = lmerControl()
       , start      = NULL
       , verbose    = 0L
    #  , subset
    #  , weights
    #  , na.action
    #  , offset
       , contrasts  = list(breed = "contr.SAS")
       , devFunOnly = FALSE
    #  , ...
       )
 summary(fm3.9)
 anova(object = fm3.9, ddf = "Satterthwaite", type = 3)


# PROC MIXED DATA=ex33;
# CLASS breed animal_id;
# MODEL pcv = breed breed*time/SOLUTION;
# REPEATED/TYPE=AR(1) SUBJET = animal_id(breed) R;
# RUN;
```

```
library(nlme)
fm3.10 <-
     nlme::gls(
           model       = PCV ~ breed + breed:time
         , data        = ex33
         , correlation = corAR1(, form = ~ 1|animal_id/breed)
         , weights     = NULL
       # , subset      =
         , method      = "REML" # c("REML", "ML")
         , na.action   = na.fail
         , control     = list()
         )
summary(fm3.10)
anova(fm3.10)

# PROC MIXED DATA=ex33;
# CLASS breed animal_id;
# MODEL pcv = breed breed*time/SOLUTION;
# RANDOM INTERCEPT time/TYPE=UN SUBJET = animal_id(breed) SOLUTION;
# RUN;


library(nlme)
# fm3.11 <-
#      nlme::gls(
#            model       = PCV ~ breed + breed:time
#          , data        = ex33
#          , random      = ~1|animal_id/breed
#          , correlation = corAR1(, form = ~ 1|animal_id/breed)
#          , weights     = NULL
#        # , subset      =
#          , method      = "REML" # c("REML", "ML")
#          , na.action   = na.fail
#          , control     = list()
#          )
# summary(fm3.11)
# anova(fm3.11)
```

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