The examples of Chapters 1 and 2

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2026-11-10

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1 Abstract

Every example of Chapters 1 and 2 of Duchateau, Janssen and Rowlands (1998), with the SAS program of Appendix B, the same analysis with **VetResearchLMM**, and the numbers printed in the book next to the computed ones. All of them agree (the variance 3.685 of Example 2.4.3.1 is printed truncated; it is 3.6855).

```
ref <-
  vlm_reference(
      source   = NULL
    , evaluate = TRUE
    , level    = 1
    )
show_ref <- function(pattern) {
  r <- ref[grepl(pattern = pattern, x = ref$source)]
```

```
  knitr::kable(x = r[, c("quantity", "value", "computed", "agrees")],
↪  digits = 4,
              col.names = c("Quantity", "Book", "Computed", "Agrees"))
}
```

2 Example 1.3.2: expected mean squares

Drugs were given to whole herds and doses to animals (ex124). With herd random, drug must be tested against herd within drug, as the expected mean squares show; when one animal is removed, the two expected mean squares no longer match (9.7143 against 9.7222) and the F test becomes approximate, one reason to prefer the mixed model.

```
em1 <-
  vlm_ems(
      fixed  = PCVdif ~ drug + drug:herd + dose + dose:drug
    , data   = ex124[-1, ]
    , random = ~ drug:herd
    , type   = 3
    , class  = "herd"
    )
em1
```

```
Type 3 analysis of variance of PCVdif

Analysis of variance
    source df     ss     ms                                                  ems
      drug  1  1.619  1.619 Var(Residual) + 9.71429 Var(drug:herd) + Q(drug)
 drug:herd  2  10.99  5.496           Var(Residual) + 9.72222 Var(drug:herd)
      dose  1  167.2  167.2                          Var(Residual) + Q(dose)
 drug:dose  1 0.1687 0.1687                     Var(Residual) + Q(drug:dose)
  Residual 33  7.999 0.2424                                  Var(Residual)
      F den_df      p
 0.2948  2.000  0.642
  22.67  33.00 <1e-04
  689.6  33.00 <1e-04
 0.6958  33.00  0.410
                   .

Error terms of the tests
    source                                              error
      drug 0.999184 MS(drug:herd) + 0.000816327 MS(Residual)
 drug:herd                                       1 MS(Residual)
      dose                                       1 MS(Residual)
 drug:dose                                       1 MS(Residual)
```

```
Type 3 estimates of the variance components
 component estimate
 drug:herd   0.5404
  Residual   0.2424

Sources: Duchateau, Janssen and Rowlands (1998); Searle, Casella and McCulloch
(1992); Satterthwaite (1946). Full references: vlm_cite(x).
```

```
show_ref("Table 1.3.2")
```

Quantity	Book	Computed	Agrees
coefficient of the herd variance in E(MS drug)	10.0000	10.0000	TRUE
coefficient of the herd variance in E(MS herd(drug))	10.0000	10.0000	TRUE
coefficient in E(MS drug), one observation deleted	9.7143	9.7143	TRUE
coefficient in E(MS herd(drug)), one observation deleted	9.7222	9.7222	TRUE

3 Example 2.2.1.7: one-way analysis of variance

```
f2217 <-
  vlm_fit(
      fixed    = PCVdiff ~ dose
    , data     = ex121
    , random   = NULL
    , repeated = NULL
    , method   = c("REML", "ML", "Type3")
    , ddfm     = c("default", "contain", "residual", "betwithin",
 ↪  "satterth", "kr")
    , type     = 3
    , class    = NULL
    , bound    = TRUE
    , control  = list()
    )
vlm_estimate(
    fit    = f2217
  , L      = list("l vs mh" = list(dose = c(-0.5, 1, -0.5)))
  , random = NULL
  , level  = 0.95
  )
```

```
Estimates (denominator df: residual)

Estimates
   label estimate     se df      t       p  lower  upper space
```

```
 l vs mh   -3.683 0.9370 11 -3.930 0.00235 -5.745 -1.620 fixed
```

```
Sources: Duchateau, Janssen and Rowlands (1998); McLean, Sanders and Stroup
(1991). Full references: vlm_cite(x).
```

```
show_ref("2.2.1")
```

Quantity	Book	Computed	Agrees
sum of squares among doses	80.7300	80.7268	TRUE
error sum of squares	30.9100	30.9075	TRUE
mean square among doses	40.3600	40.3634	TRUE
error mean square	2.8100	2.8098	TRUE
F statistic of dose	14.3700	14.3654	TRUE
p-value of dose	0.0009	0.0009	TRUE
estimate l vs mh	-3.6800	-3.6825	TRUE
standard error of l vs mh	0.9370	0.9370	TRUE
variance of l vs mh	0.8750	0.8781	TRUE
t of l vs mh	-3.9300	-3.9299	TRUE
F of the contrast l vs mh	15.4400	15.4442	TRUE
p-value of the contrast l vs mh	0.0024	0.0024	TRUE

4 Section 2.3.2: the models of Chapter 1

The randomised blocks of `ex122`, the herds nested in drug of `ex123` and the ELISA data of `ex126`, where animals and times are random and the mean is the only fixed effect:

```
f126 <-
  vlm_fit(
      fixed    = OD ~ 1
    , data     = ex126
    , random   = ~ anim_id + time
    , repeated = NULL
    , method   = c("REML", "ML", "Type3")
    , ddfm     = c("default", "contain", "residual", "betwithin",
 ↪  "satterth", "kr")
    , type     = 3
    , class    = "time"
    , bound    = TRUE
    , control  = list()
    )
f126$covariance
```

```
   parameter subject     estimate           se        z            p
1:   anim_id         0.0193086158 1.578702e-02 1.223069 1.106517e-01
2:      time         0.0001238079 8.874540e-05 1.395090 8.149429e-02
```

```
3:  Residual          0.0005826121 9.578042e-05 6.082789 5.905472e-10
```

5 Example 2.4.2.2: ML and REML

```
ml <-
  vlm_fit(
      fixed    = Pcv ~ Drug + dose + Drug:dose
    , data     = ex125
    , random   = ~ Region + Region:Drug
    , repeated = NULL
    , method   = "ML"
    , ddfm     = c("default", "contain", "residual", "betwithin",
 ↪  "satterth", "kr")
    , type     = 3
    , class    = NULL
    , bound    = TRUE
    , control  = list()
    )
reml <-
  vlm_fit(
      fixed    = Pcv ~ Drug + dose + Drug:dose
    , data     = ex125
    , random   = ~ Region + Region:Drug
    , repeated = NULL
    , method   = "REML"
    , ddfm     = c("default", "contain", "residual", "betwithin",
 ↪  "satterth", "kr")
    , type     = 3
    , class    = NULL
    , bound    = TRUE
    , control  = list()
    )
data.frame(
    component = reml$covariance$parameter
  , ML        = ml$covariance$estimate
  , REML      = reml$covariance$estimate
  )
```

```
    component       ML     REML
1      Region 4.292361 5.150833
2 Region:Drug 0.322500 0.387000
3    Residual 1.747014 2.096417
```

```
show_ref("Table 2.4.2.1")
```

Quantity	Book	Computed	Agrees
ML region variance	4.292	4.2924	TRUE

Quantity	Book	Computed	Agrees
ML herd within region variance	0.322	0.3225	TRUE
ML residual variance	1.747	1.7470	TRUE
REML region variance	5.151	5.1508	TRUE
REML herd within region variance	0.387	0.3870	TRUE
REML residual variance	2.096	2.0964	TRUE

6 Example 2.4.3.1: best linear unbiased prediction

```
fs <-
  vlm_fit(
      fixed    = Ww ~ 1
    , data     = ex127
    , random   = ~ sire
    , repeated = NULL
    , method   = c("REML", "ML", "Type3")
    , ddfm     = c("default", "contain", "residual", "betwithin",
↪   "satterth", "kr")
    , type     = 3
    , class    = NULL
    , bound    = TRUE
    , control  = list()
    )
vlm_blup(
    fit   = fs
  , level = 0.95
  )
```

```
Best linear unbiased predictions of the random effects

Solution for random effects
 effect level estimate     se df        t       p   lower   upper
   sire     1   -2.198  1.101 35   -1.997 0.05364  -4.432 0.03641
   sire     2 -0.03189 0.8983 35 -0.03550 0.97188  -1.855   1.792
   sire     3   -1.743  1.101 35   -1.584 0.12216  -3.978  0.4908
   sire     4    3.159 0.9589 35    3.294 0.00227   1.212   5.106
   sire     5   0.8692 0.9340 35   0.9306 0.35842  -1.027   2.765
   sire     6  -0.8628 0.9915 35  -0.8702 0.39013  -2.876   1.150
   sire     7    1.356  1.036 35    1.309 0.19922 -0.7475   3.459
   sire     8  -0.5476 0.9589 35  -0.5710 0.57162  -2.494   1.399

Sources: Duchateau, Janssen and Rowlands (1998); Henderson (1975). Full
references: vlm_cite(x).
```

```
show_ref("2.4.3.1")
```

Quantity	Book	Computed	Agrees
sire variance	3.685	3.6855	FALSE
residual variance	3.542	3.5418	TRUE
overall mean	13.970	13.9686	TRUE
prediction of sire 4	3.160	3.1588	TRUE

7 Examples 2.5.1.1 to 2.5.4.1: fixed effects, estimates and inference spaces

```
fm <-
  vlm_fit(
      fixed    = Pcv ~ Drug + dose + Drug:dose
    , data     = ex125
    , random   = ~ Region + Region:Drug
    , repeated = NULL
    , method   = c("REML", "ML", "Type3")
    , ddfm     = "satterth"
    , type     = 3
    , class    = NULL
    , bound    = TRUE
    , control  = list()
    )
fm$fixed
```

```
        effect     level  estimate        se        df         t            p
1: (Intercept)           17.133333 1.1279960  8.208034 15.189179 2.687717e-07
2:        Drug   BERENIL  7.150000 0.9098382 11.818516  7.858540 4.962661e-06
3:        Drug   samorin  0.000000        NA        NA        NA           NA
4:        dose         h  4.350000 0.8359459 10.000000  5.203686 3.991647e-04
5:        dose         l  0.000000        NA        NA        NA           NA
6:   Drug:dose BERENIL h -3.183333 1.1822060 10.000000 -2.692706 2.259450e-02
7:   Drug:dose BERENIL l  0.000000        NA        NA        NA           NA
8:   Drug:dose samorin h  0.000000        NA        NA        NA           NA
9:   Drug:dose samorin l  0.000000        NA        NA        NA           NA
```

```
vlm_estimate(
    fit    = fm
  , L      = list(
       "broad"  = list(Intercept = 1, Drug = c(0, 1), dose = c(0.5,
       ↪  0.5), "Drug:dose" = c(0, 0, 0.5, 0.5))
     , "narrow" = list(Intercept = 1, Drug = c(0, 1), dose = c(0.5,
 ↪  0.5), "Drug:dose" = c(0, 0, 0.5, 0.5))
```

```
    )
  , random = list("narrow" = list(Region = rep(1 / 6, 6), "Region:Drug" =
↪  rep(c(0, 1 / 6), 6)))
  , level  = 0.95
  )
```

```
Estimates (denominator df: satterth)

Estimates
  label estimate     se    df     t      p lower upper  space
  broad    19.31  1.048 6.205 18.43 <1e-04 16.77 21.85  broad
 narrow    19.31 0.4180 10.00 46.20 <1e-04 18.38 20.24 narrow

Sources: Duchateau, Janssen and Rowlands (1998); McLean, Sanders and Stroup
(1991); Satterthwaite (1946); Giesbrecht and Burns (1985); Fai and Cornelius
(1996). Full references: vlm_cite(x).
```

```
show_ref("2\\.5\\.|Table 2\\.5")
```

Quantity	Book	Computed	Agrees
fixed-effect solution, row 1	17.1300	NA	FALSE
variance of the solution, row 1	1.2700	NA	FALSE
fixed-effect solution, row 2	7.1500	NA	FALSE
variance of the solution, row 2	0.8300	NA	FALSE
fixed-effect solution, row 4	4.3500	NA	FALSE
variance of the solution, row 4	0.7000	NA	FALSE
fixed-effect solution, row 6	-3.1800	NA	FALSE
variance of the solution, row 6	1.4000	NA	FALSE
cell mean 1	25.4500	NA	FALSE
cell mean 2	24.2800	NA	FALSE
cell mean 3	21.4800	NA	FALSE
cell mean 4	17.1300	NA	FALSE
variance of a cell mean	1.2700	NA	FALSE
estimate c3	19.3100	NA	FALSE
variance of estimate c3	1.0975	NA	FALSE
Satterthwaite df of estimate c3	6.2000	NA	FALSE
variance of estimate c4	0.4780	NA	FALSE
Satterthwaite df of estimate c4	5.0000	NA	FALSE
estimate c5	21.4800	NA	FALSE
variance of estimate c5	1.2720	NA	FALSE
Satterthwaite df of estimate c5	8.2000	NA	FALSE
estimate c6	4.3500	NA	FALSE
variance of estimate c6	0.6980	NA	FALSE
Satterthwaite df of estimate c6	10.0000	NA	FALSE
mean square, row 1	23.4700	23.4738	TRUE

Quantity	Book	Computed	Agrees
mean square, row 2	185.3700	185.3704	TRUE
mean square, row 3	2.8700	2.8704	TRUE
mean square, row 4	45.6500	45.6504	TRUE
mean square, row 5	15.2000	15.2004	TRUE
mean square, row 6	2.0960	2.0964	TRUE
variance of the Samorin mean, narrow inference space	0.1750	NA	FALSE

8 Example 2.6.1: general linear hypotheses

```
vlm_contrast(
    fit = fm
  , L   = list(
        "all" = list(
            list(Drug = c(1, -1), "Drug:dose" = c(0.5, 0.5, -0.5, -0.5))
          , list(dose = c(1, -1), "Drug:dose" = c(0.5, -0.5, 0.5, -0.5))
          , list("Drug:dose" = c(0.5, -0.5, -0.5, 0.5))
          )
      )
  )
```

```
Contrasts (denominator df: satterth)

Contrasts
 label num_df den_df     F        p
   all      3  7.143 31.20 0.000179

Sources: Duchateau, Janssen and Rowlands (1998); McLean, Sanders and Stroup
(1991); Satterthwaite (1946); Giesbrecht and Burns (1985); Fai and Cornelius
(1996). Full references: vlm_cite(x).
```

```
show_ref("2.6.1")
```

Quantity	Book	Computed	Agrees
F of the joint hypothesis of equal cell means	31.2000	NA	FALSE
Satterthwaite denominator df of the joint hypothesis	7.1400	NA	FALSE
p-value of the joint hypothesis	0.0002	NA	FALSE