The examples of Chapter 3

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1 Abstract

Chapter 3 of the book applies the mixed model to a designed experiment with a covariate (Example 3.1), to the estimation of heritability and breeding values (Example 3.2) and to repeated measures with several covariance structures (Example 3.3). The book prints only part of the data of Examples 3.1 and 3.2, so their analyses run but cannot reproduce the printed numbers; the complete data of Example 3.3 reproduce every printed number.

```
ref <-
  vlm_reference(
      source   = "Example 3"
    , evaluate = TRUE
    , level    = 1
    )
```

2 Example 3.1: doses nested in drug, with a covariate

```
m1 <-
  vlm_fit(
      fixed    = PCV2 ~ drug + drug:dose
    , data     = ex31
```

```
    , random   = ~ drug:herd
    , repeated = NULL
    , method   = c("REML", "ML", "Type3")
    , ddfm     = "satterth"
    , type     = 3
    , class    = c("herd", "dose")
    , bound    = TRUE
    , control  = list()
    )
m1$tests
```

```
      effect num_df   den_df           F         p
1:      drug      1 10.08194 0.001544608 0.9694174
2: drug:dose      1 31.51959 2.600111652 0.1168256
```

```
vlm_estimate(
    fit    = m1
  , L      = list(
       "Mean Samorin"         = list(Intercept = 1, drug = c(0, 1),
        ↪  "drug:dose" = c(0, 0, 1))
     , "Berenil 2 doses"      = list("drug:dose" = c(1, -1, 0))
     , "Ber vs Sam at dose 1" = list(drug = c(1, -1), "drug:dose" = c(1,
 ↪  0, -1))
     )
  , random = NULL
  , level  = 0.95
  )
```

```
Estimates (denominator df: satterth)

Estimates
                label estimate    se    df       t      p  lower  upper space
         Mean Samorin    24.17 1.038 15.36   23.28 <1e-04  21.96  26.38 broad
      Berenil 2 doses   -2.102 1.303 31.52  -1.612  0.117 -4.758 0.5548 broad
 Ber vs Sam at dose 1   -1.000 1.468 15.36 -0.6811  0.506 -4.123  2.123 broad

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).
```

Model 3 lets each treatment have its own slope on the PCV at treatment, and compares the treatments for an animal with PCV1 = 18:

```
m3 <-
  vlm_fit(
     fixed    = PCV2 ~ drug + drug:dose + PCV1:drug:dose
    , data     = ex31
    , random   = ~ drug:herd
    , repeated = NULL
```

```
    , method   = c("REML", "ML", "Type3")
    , ddfm     = "kr"
    , type     = 3
    , class    = c("herd", "dose")
    , bound    = TRUE
    , control  = list()
    )
vlm_lsmeans(
    fit    = m3
  , specs  = ~ drug:dose
  , at     = list(PCV1 = 18)
  , diff   = FALSE
  , adjust = c("none", "tukey", "bonferroni", "sidak")
  , level  = 0.95
  )
```

```
Least-squares means (denominator df: kr; 95% limits)

Least squares means
    drug dose estimate    se    df     t      p lower upper
 BERENIL    1    24.20 1.987 29.16 12.18 <1e-04 20.14 28.27
 BERENIL    2    24.79 1.174 13.62 21.11 <1e-04 22.27 27.32
 SAMORIN    1    25.26 2.169 26.49 11.64 <1e-04 20.80 29.71

Sources: Duchateau, Janssen and Rowlands (1998); Searle, Speed and Milliken
(1980); Kenward and Roger (1997). Full references: vlm_cite(x).
```

3 Example 3.2: heritability and sire predictions

```
f32 <-
  vlm_fit(
      fixed    = Ww ~ sex + agew + breed
    , data     = ex32
    , random   = ~ breed:sire_id
    , repeated = NULL
    , method   = c("REML", "ML", "Type3")
    , ddfm     = "satterth"
    , type     = 3
    , class    = "breed"
    , bound    = TRUE
    , control  = list()
    )
f32$covariance
```

```
       parameter subject estimate       se        z           p
1: breed:sire_id         0.000000       NA       NA          NA
```

```
2:      Residual         5.447347 1.020382 5.338539 4.684922e-08
```

```
vlm_lsmeans(
    fit    = f32
  , specs  = ~ breed
  , at     = NULL
  , diff   = TRUE
  , adjust = "tukey"
  , level  = 0.95
  )$lsmeans
```

```
   breed  estimate        se df        t            p     lower    upper
1:     1 13.123981 0.6055657 57 21.67227 3.343968e-29 11.911357 14.33661
2:     2 12.396055 0.7201282 57 17.21368 3.012048e-24 10.954023 13.83809
3:     3 10.598945 0.8773799 57 12.08022 2.364957e-17  8.842022 12.35587
4:     4 12.740250 0.6569679 57 19.39250 8.957490e-27 11.424695 14.05581
5:     5  9.722305 0.8625235 57 11.27193 3.896394e-16  7.995131 11.44948
6:     6 10.050959 0.9686565 57 10.37618 9.546083e-15  8.111258 11.99066
```

On this part of the data the sire variance is estimated as zero, so the heritability $h^2 = 4\sigma_s^2/(\sigma_s^2 + \sigma^2)$ is zero; with the complete data the book finds 0.49.

4 Example 3.3: covariance structures for repeated measures

Model 1 (a random animal effect, equivalently compound symmetry), Model 2 (first-order autoregressive errors) and Model 3 (a random intercept and slope per animal):

```
cs <-
  vlm_fit(
      fixed    = PCV ~ breed + breed:time
    , data     = ex33
    , random   = NULL
    , repeated = vlm_repeated(
          type    = c("vc", "cs", "ar1", "sp_pow", "un")[2]
        , subject = ~ animal_id:breed
        , order   = NULL
        )
    , method   = c("REML", "ML", "Type3")
    , ddfm     = c("default", "contain", "residual", "betwithin",
 ↪  "satterth", "kr")
    , type     = 3
    , class    = NULL
    , bound    = TRUE
    , control  = list()
    )
ar <-
```

```
  vlm_fit(
      fixed    = PCV ~ breed + breed:time
    , data     = ex33
    , random   = NULL
    , repeated = vlm_repeated(
          type    = c("vc", "cs", "ar1", "sp_pow", "un")[3]
        , subject = ~ animal_id:breed
        , order   = NULL
        )
    , method   = c("REML", "ML", "Type3")
    , ddfm     = c("default", "contain", "residual", "betwithin",
↪  "satterth", "kr")
    , type     = 3
    , class    = NULL
    , bound    = TRUE
    , control  = list()
    )
rc <-
  vlm_fit(
      fixed    = PCV ~ breed + breed:time
    , data     = ex33
    , random   = vlm_random(
          effects = ~ 1 + time
        , subject = ~ animal_id:breed
        , type    = c("vc", "un")[2]
        )
    , repeated = NULL
    , method   = c("REML", "ML", "Type3")
    , ddfm     = c("default", "contain", "residual", "betwithin",
↪  "satterth", "kr")
    , type     = 3
    , class    = NULL
    , bound    = TRUE
    , control  = list()
    )
rc$covariance
```

```
   parameter         subject     estimate          se         z            p
1:   UN(1,1) animal_id:breed 12.464572630 6.049874059  2.060303 1.968480e-02
2:   UN(2,1) animal_id:breed -0.255121593 0.142828341 -1.786211 7.406506e-02
3:   UN(2,2) animal_id:breed  0.005758072 0.003777797  1.524188 6.373091e-02
4:  Residual                 4.353042151 0.513010930  8.485282 1.075986e-17
```

```
cmp <-
  vlm_compare(
      CS   = cs
    , AR1  = ar
    , RC   = rc
    , test = TRUE
```

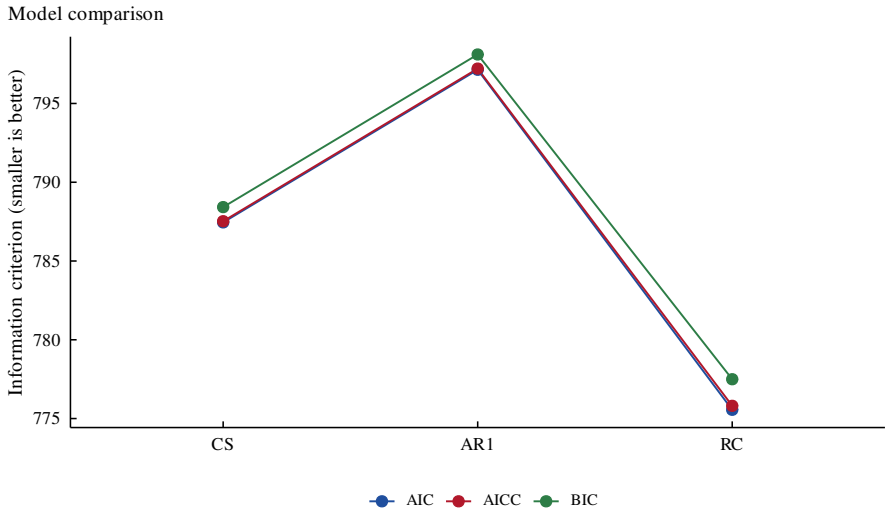
```
    )
cmp
```

```
Comparison of 3 models; smallest AIC: RC

Models
 model method cov_parms   m2ll    AIC   AICC    BIC  chisq df      p p_boundary
    CS   REML         2 783.45 787.45 787.53 788.42      .  .      .          .
   AR1   REML         2 793.14 797.14 797.21 798.11      .  .      .          .
    RC   REML         4 767.56 775.56 775.81 777.50 25.583  2 <1e-04          .

Sources: Duchateau, Janssen and Rowlands (1998); Akaike (1974); Schwarz (1978).
Full references: vlm_cite(x).
```

```
plot(cmp)
```



The book compared Models 1 and 2 only (the restricted log-likelihoods −391.73 and −396.57 favour compound symmetry); the random coefficients model has a much smaller AIC still, as the negative covariance of the intercepts and slopes (animals that start higher fall faster) suggests.

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

Source	Quantity	Book	Computed	Agrees
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	animal variance	5.4780	5.4785	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	residual variance	4.9650	4.9649	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	fixed effect, row 1	35.0600	35.0602	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	standard error, row 1	1.0560	1.0558	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	containment df, row 1	10.0000	10.0000	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	fixed effect, row 2	-0.8420	-0.8420	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	standard error, row 2	1.4930	1.4931	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	containment df, row 2	10.0000	10.0000	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	fixed effect, row 4	-0.4130	-0.4134	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	standard error, row 4	0.0225	0.0225	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	containment df, row 4	154.0000	154.0000	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	fixed effect, row 5	-0.2760	-0.2761	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	standard error, row 5	0.0225	0.0225	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	containment df, row 5	154.0000	154.0000	TRUE

Source	Quantity	Book	Computed	Agrees
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 3	-0.6720	-0.6720	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 4	-2.4970	-2.4967	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 5	-2.3830	-2.3827	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 2	3.0380	3.0379	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 6	0.0324	0.0324	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 1	2.4810	2.4811	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 7	-1.6670	-1.6671	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 8	2.6260	2.6264	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 9	-1.6670	-1.6671	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 10	-0.3720	-0.3723	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 11	-1.7540	-1.7543	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	prediction of animal 12	2.8340	2.8344	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	standard error of prediction	1.0910	1.0912	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	df of the predictions	154.0000	154.0000	TRUE

Source	Quantity	Book	Computed	Agrees
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	-2 restricted log-likelihood, compound symmetry	783.4510	783.4514	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	Akaike's criterion (SAS 6)	-393.7300	-393.7257	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	Schwarz's criterion (SAS 6)	-396.8300	-396.8255	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	null model likelihood ratio chi-square	80.8450	80.8447	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	Type 3 F, row 1	470.0500	470.0533	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	denominator df, row 1	154.0000	154.0000	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	Type 3 F, row 2	0.3200	0.3180	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	denominator df, row 2	10.0000	10.0000	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	Type 3 F, row 3	18.6200	18.6168	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 1	denominator df, row 3	154.0000	154.0000	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 2	AR(1) correlation	0.6210	0.6214	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 2	residual variance	10.1900	10.1898	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 2	-2 restricted log-likelihood	793.1390	793.1394	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 2	Akaike's criterion (SAS 6)	-398.5700	-398.5697	TRUE

Source	Quantity	Book	Computed	Agrees
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 2	Schwarz's criterion (SAS 6)	-401.6704	-401.6696	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 2	null model likelihood ratio chi-square	71.1560	71.1566	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	UN(1,1)	12.4600	12.4646	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	UN(2,1)	-0.2550	-0.2551	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	UN(2,2)	0.0058	0.0058	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	residual variance	4.3530	4.3530	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	standard error of the intercept	1.5010	1.5014	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	standard error of breed BO	2.1230	2.1233	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	standard error of a slope	0.0370	0.0375	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	random intercept of BO241	-1.8360	-1.8358	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	random slope of BO241	0.0563	0.0563	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	standard error of a random intercept	1.6400	1.6376	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	standard error of a random slope	0.0417	0.0417	TRUE
Duchateau, Janssen and Rowlands (1998), Example 3.3, Model 3	df of the predictions	144.0000	144.0000	TRUE