

# On the usage of the `pbkrtest` package

Søren Højsgaard and Ulrich Halekoh

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## 1 Introduction

The `shoes` data is a list of two vectors, giving the wear of shoes of materials A and B for one foot each of ten boys.

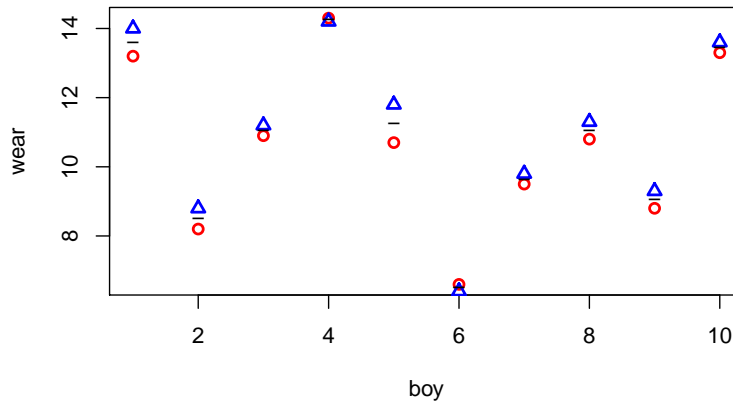
```
R> data(shoes, package="MASS")
R> shoes
```

```
$A
 [1] 13.2  8.2 10.9 14.3 10.7  6.6  9.5 10.8  8.8 13.3
```

```
$B
 [1] 14.0  8.8 11.2 14.2 11.8  6.4  9.8 11.3  9.3 13.6
```

A plot clearly reveals that boys wear their shoes differently.

```
R> plot(A~1, data=shoes, col="red", lwd=2, pch=1, ylab="wear", xlab="boy")
R> points(B~1, data=shoes, col="blue", lwd=2, pch=2)
R> points(I((A+B)/2)~1, data=shoes, pch="-", lwd=2)
```



One option for testing the effect of materials is to make a paired  $t$ -test. The following forms are equivalent:

```
R> r1<-t.test(shoes$A, shoes$B, paired=T)
R> r2<-t.test(shoes$A-shoes$B)
R> r1
```

Paired t-test

```
data: shoes$A and shoes$B
t = -3.3489, df = 9, p-value = 0.008539
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.6869539 -0.1330461
sample estimates:
mean of the differences
 -0.41
```

To work with data in a mixed model setting we create a dataframe, and for later use we also create an imbalanced version of data:

```
R> boy <- rep(1:10,2)
R> boyf<- factor(letters[boy])
R> mat <- factor(c(rep("A", 10), rep("B",10)))
R> ## Balanced data:
R> shoe.b <- data.frame(wear=unlist(shoes), boy=boy, boyf=boyf, mat=mat)
R> head(shoe.b)
```

```
   wear boy boyf mat
A1 13.2  1    a   A
A2  8.2  2    b   A
A3 10.9  3    c   A
A4 14.3  4    d   A
A5 10.7  5    e   A
A6  6.6  6    f   A
```

```
R> ## Imbalanced data; delete (boy=1, mat=1) and (boy=2, mat=b)
R> shoe.i <- shoe.b[-c(1,12),]
```

We fit models to the two datasets:

```
R> lmm1.b <- lmer( wear ~ mat + (1|boyf), data=shoe.b )
R> lmm0.b <- update( lmm1.b, ~/. - mat)
R> lmm1.i <- lmer( wear ~ mat + (1|boyf), data=shoe.i )
R> lmm0.i <- update(lmm1.i, ~/. - mat)
```

The asymptotic likelihood ratio test shows stronger significance than the  $t$ -test:

```
R> anova( lmm1.b, lmm0.b, test="Chisq" ) ## Balanced data
```

Data: shoe.b

Models:

```
lmm0.b: wear ~ (1 | boyf)
```

```
lmm1.b: wear ~ mat + (1 | boyf)
```

	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
lmm0.b	3	67.909	70.896	-30.955	61.909				
lmm1.b	4	61.817	65.800	-26.909	53.817	8.092		1	0.004446 **

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
R> anova( lmm1.i, lmm0.i, test="Chisq" ) ## Imbalanced data
```

Data: shoe.i

Models:

```
lmm0.i: wear ~ (1 | boyf)
```

```
lmm1.i: wear ~ mat + (1 | boyf)
```

	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
lmm0.i	3	63.869	66.540	-28.934	57.869				
lmm1.i	4	60.777	64.339	-26.389	52.777	5.092		1	0.02404 *

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## 2 Kenward–Roger approach

The Kenward–Roger approximation is exact for the balanced data in the sense that it produces the same result as the paired  $t$ -test.

```
R> ( kr.b<-KRmodcomp(lmm1.b, lmm0.b) )
```

F-test with Kenward–Roger approximation; computing time: 0.23 sec.

```
large : wear ~ mat + (1 | boyf)
```

```
small : wear ~ (1 | boyf)
```

	stat	ndf	ddf	F.scaling	p.value
Ftest	11.215	1.000	9.000	1	0.008539 **

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
R> summary( kr.b )
```

F-test with Kenward–Roger approximation; computing time: 0.23 sec.

```
large : wear ~ mat + (1 | boyf)
```

```
small : wear ~ (1 | boyf)
```

	stat	ndf	ddf	F.scaling	p.value
Ftest	11.215	1.000	9.000	1	0.008539 **

```

FtestU 11.215  1.000  9.000          0.008539 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Relevant information can be retrieved with
R> getKR(kr.b, "ddf")

[1] 9

For the imbalanced data we get
R> ( kr.i<-KRmodcomp(lmm1.i, lmm0.i) )

F-test with Kenward-Roger approximation; computing time: 0.06 sec.
large : wear ~ mat + (1 | boyf)
small : wear ~ (1 | boyf)
      stat      ndf      ddf F.scaling p.value
Ftest 5.9893 1.0000 7.0219          1 0.04418 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Notice that this result is similar to but not identical to the paired t-test when
the two relevant boys are removed:
R> shoes2 <- list(A=shoes$A[-(1:2)], B=shoes$B[-(1:2)])
R> t.test(shoes2$A, shoes2$B, paired=T)

      Paired t-test

data:  shoes2$A and shoes2$B
t = -2.3878, df = 7, p-value = 0.04832
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.671721705 -0.003278295
sample estimates:
mean of the differences
      -0.3375

```

### 3 Parametric bootstrap

Parametric bootstrap provides an alternative but many simulations are often needed to provide credible results (also many more than shown here; in this connection it can be useful to exploit that computings can be made en parallel, see the documentation):

```

R> ( pb.b <- PBmodcomp(lmm1.b, lmm0.b, nsim=500) )

Parametric bootstrap test; time: 14.65 sec; samples: 500 extremes: 7;
large : wear ~ mat + (1 | boyf)
small : wear ~ (1 | boyf)
      stat df  p.value
LRT    8.1197  1 0.004379 **
PBtest 8.1197   0.015968 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

R> summary( pb.b )

Parametric bootstrap test; time: 14.65 sec; samples: 500 extremes: 7;
large : wear ~ mat + (1 | boyf)
small : wear ~ (1 | boyf)
      stat      df      ddf p.value
PBtest  8.1197
Gamma   8.1197
Bartlett 6.8113 1.0000
F        8.1197 1.0000 12.411 0.014217 *
LRT      8.1197 1.0000
0.004379 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

For the imbalanced data, the result is similar to the result from the paired t
test.

R> ( pb.i<-PBmodcomp(lmm1.i, lmm0.i, nsim=500) )

Parametric bootstrap test; time: 14.43 sec; samples: 500 extremes: 19;
large : wear ~ mat + (1 | boyf)
small : wear ~ (1 | boyf)
      stat df p.value
LRT     5.1151  1 0.02372 *
PBtest  5.1151  0.03992 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

R> summary( pb.i )

Parametric bootstrap test; time: 14.43 sec; samples: 500 extremes: 19;
large : wear ~ mat + (1 | boyf)
small : wear ~ (1 | boyf)
      stat      df      ddf p.value
PBtest  5.1151
Gamma   5.1151
Bartlett 4.1039 1.0000
F        5.1151 1.0000 10.117 0.04694 *
LRT      5.1151 1.0000
0.02372 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

## A Matrices for random effects

The matrices involved in the random effects can be obtained with

```

R> shoe3 <- subset(shoe.b, boy<=5)
R> shoe3 <- shoe3[order(shoe3$boy), ]
R> lmm1 <- lmer( wear ~ mat + (1|boyf), data=shoe3 )
R> str( SG <- get_SigmaG( lmm1 ), max=2)

List of 3
 $ Sigma :Formal class 'dgCMatrix' [package "Matrix"] with 6 slots
 $ G     :List of 2

```

```

..$ :Formal class 'dgCMatrix' [package "Matrix"] with 6 slots
..$ :Formal class 'dgCMatrix' [package "Matrix"] with 6 slots
$ n.ggamma: int 2
R> round( SG$Sigma*10 )
10 x 10 sparse Matrix of class "dgCMatrix"

[1,] 53 52 . . . . .
[2,] 52 53 . . . . .
[3,] . . 53 52 . . . . .
[4,] . . 52 53 . . . . .
[5,] . . . . 53 52 . . . . .
[6,] . . . . 52 53 . . . . .
[7,] . . . . . 53 52 . . . . .
[8,] . . . . . 52 53 . . . . .
[9,] . . . . . . . 53 52 . . . . .
[10,] . . . . . . . 52 53 . . . . .

R> SG$G
[[1]]
10 x 10 sparse Matrix of class "dgCMatrix"

[1,] 1 1 . . . . .
[2,] 1 1 . . . . .
[3,] . . 1 1 . . . . .
[4,] . . 1 1 . . . . .
[5,] . . . . 1 1 . . . . .
[6,] . . . . 1 1 . . . . .
[7,] . . . . . 1 1 . . . . .
[8,] . . . . . 1 1 . . . . .
[9,] . . . . . . . 1 1 . . . . .
[10,] . . . . . . . 1 1 . . . . .

[[2]]
10 x 10 sparse Matrix of class "dgCMatrix"

[1,] 1 . . . . .
[2,] . 1 . . . . .
[3,] . . 1 . . . . .
[4,] . . . 1 . . . . .
[5,] . . . . 1 . . . . .
[6,] . . . . . 1 . . . . .
[7,] . . . . . . 1 . . . . .
[8,] . . . . . . . 1 . . . . .
[9,] . . . . . . . . 1 . . . . .
[10,] . . . . . . . . . 1 . . . . .

```