Repeated measures analysis with R

Summary for experienced R users

The `lmer` function from the `lme4` package has a syntax like `lm`.

Add something like `+ (1|subject)` to the model for the random subject effect.

To get p-values, use the `car` package.

Avoid the `lmerTest` package.

For balanced designs, `Anova(dichotic, test="F")`

For unbalanced designs,

Set contrasts on the factors like this:
```r
contrasts(Time) = contr.sum(5)
And BlueModel = lmer(Beck ~ Time*Drug*Treatment + (1|Subject))
And Anova(BlueModel, test="F", type="III")
```

Or

```r
BlueModel = lmer(Beck ~ Time*Drug*Treatment + (1|Subject),
                 contrasts = list(Time="contr.sum", Drug="contr.sum",
                                  Treatment="contr.sum"))
And Anova(BlueModel, test="F", type="III")
```

# Install packages if necessary. Only need to do this once.
# install.packages("lme4")
# install.packages("car")
# Load packages -- do this every time
library(lme4)  # For the lmer function
library(car)   # For F and Wald tests with p-values

The `glmer` function from the `lme4` package has a syntax like `glm`.

```r
hoops = glmer(Hit ~ Spot*Hand + (1 | Subject), family=binomial)
Anova(hoops, type="III")
```
> # Hand-ear dichotic listening study
> # Install packages if necessary. Only need to do this once.
> # install.packages("lme4")
> # install.packages("car")
> # Load packages -- do this every time
> library(lme4)  # For lmer function

Loading required package: Matrix
> library(car)  # For F-tests, likelihood ratio and Wald chi-squared tests
> # Read data into a data frame
> dichotic = read.table("http://www.utstat.toronto.edu/~brunner/data/legal/HandEar.data.txt")
> head(dichotic)  # Look at the first few lines.

subject handed   ear rtime
1       1   Left  Left   330
2       1   Left Right   327
3       1   Left  Both   303
4       2   Left Left   294
5       2   Left Right   339
6       2   Left  Both   315
> attach(dichotic)  # Make variable names available
>
> # Sample sizes
> table(handed,ear)

<table>
<thead>
<tr>
<th></th>
<th>Both</th>
<th>Left</th>
<th>Right</th>
</tr>
</thead>
<tbody>
<tr>
<td>Left</td>
<td>20</td>
<td>20</td>
<td>20</td>
</tr>
<tr>
<td>Right</td>
<td>20</td>
<td>20</td>
<td>20</td>
</tr>
</tbody>
</table>

> # Treatment means
> aggregate(rtime,by=list(ear,handed),FUN=mean)  # First changes fastest

     Group.1 Group.2      x
1     Both    Left 317.90
2     Left    Left 326.60
3      Right    Left 332.80
4     Both    Right 315.10
5     Left    Right 324.65
6     Right    Right 320.85

> # Two-way table of means
> LeftHanded = meantable[1:3,3]; RightHanded = meantable[4:6,3]
> TwoWay = rbind(LeftHanded,RightHanded)
> colnames(TwoWay) = c("BothEars","LeftEar","RightEar")
> TwoWay

<table>
<thead>
<tr>
<th>BothEars</th>
<th>LeftEar</th>
<th>RightEar</th>
</tr>
</thead>
<tbody>
<tr>
<td>LeftHanded</td>
<td>317.9</td>
<td>326.6</td>
</tr>
<tr>
<td>RightHanded</td>
<td>315.1</td>
<td>324.65</td>
</tr>
</tbody>
</table>

> # Marginal means
> aggregate(rtime,by=list(handed),FUN=mean)

     Group.1   x
1    Left 325.77
2   Right 320.20

> aggregate(rtime,by=list(ear),FUN=mean)

     Group.1   x
1    Both 316.50
2     Left 325.63
3     Right 326.83
```r
> # Plot the means
> Means = meantable[,3] # All the rows, column 3
> lhand = Means[1:3]; rhand = Means[4:6]
> Ear = c(1:3,1:3)
> # Invisible points at first, x axis points at 1,2,3; see help(plot)
> plot(Ear,Means,pch=" ",xaxp=c(1,3,2),
>     xlab="Ear Receiving Signal: 1=Both, 2=Left, 3=Right",
>     ylab="Mean Reaction Time")
> title("Reaction Time")
> points(1:3,lhand,col='red',pch=15) # Red squares
> points(1:3,rhand,col='blue',pch=19) # Blue circles
> lines(1:3,lhand,lty=1,col='red'); lines(1:3,rhand,lty=3,col='blue')
> # Annotate the plot
> x1 = c(1.1,1.6); y1 = c(332,332); lines(x1,y1,lty=1,col='red')
> points(1.35,332,col='red',pch=15)
> x2 = c(1.1,1.6); y2 = c(331,331); lines(x2,y2,lty=3,col='blue')
> points(1.35,331,col='blue',pch=19)
> text(1.80,332,'Left Handed',col='red')
> text(1.82,331,'Right Handed',col='blue')
```

![Reaction Time Graph](attachment:image.png)

Ear Receiving Signal: 1=Both, 2=Left, 3=Right
> # Naive fixed effects analysis
> anova(lm(rtime ~ handed*ear))

Analysis of Variance Table

Response: rtime

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>handed</td>
<td>1</td>
<td>930</td>
<td>929.63</td>
<td>1.8556</td>
<td>0.17582</td>
</tr>
<tr>
<td>ear</td>
<td>2</td>
<td>2551</td>
<td>1275.41</td>
<td>2.5458</td>
<td>0.08286</td>
</tr>
<tr>
<td>handed:ear</td>
<td>2</td>
<td>615</td>
<td>307.41</td>
<td>0.6136</td>
<td>0.54317</td>
</tr>
<tr>
<td>Residuals</td>
<td>114</td>
<td>57113</td>
<td>500.99</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> # Repeated measures with a mixed model
> dichotic = lmer(rtime ~ handed*ear + (1 | subject))
> Anova(dichotic, test="F") # F tests (from car package)

Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)

Response: rtime

<table>
<thead>
<tr>
<th></th>
<th>F</th>
<th>Df</th>
<th>Df.res</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>handed</td>
<td>0.9706</td>
<td>1</td>
<td>38</td>
<td>0.33075</td>
</tr>
<tr>
<td>ear</td>
<td>4.6787</td>
<td>2</td>
<td>76</td>
<td>0.01213 *</td>
</tr>
<tr>
<td>handed:ear</td>
<td>1.1277</td>
<td>2</td>
<td>76</td>
<td>0.32914</td>
</tr>
</tbody>
</table>

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> # Multiple comparisons: Which marginal means are different?
>
> # The combination variable HandEar will have 6 values
> n = length(rtime); n
[1] 120
> HandEar = character(n) # A character-valued variable of length n
> for(j in 1:n) HandEar[j] = paste(handed[j],ear[j],sep='')
> HandEar = factor(HandEar) # Maybe would be interpreted as a factor anyway
> head(data.frame(handed,ear,HandEar))

<table>
<thead>
<tr>
<th>handed</th>
<th>ear</th>
<th>HandEar</th>
</tr>
</thead>
<tbody>
<tr>
<td>Left</td>
<td>Left</td>
<td>LeftLeft</td>
</tr>
<tr>
<td>Left</td>
<td>Right</td>
<td>LeftRight</td>
</tr>
<tr>
<td>Left</td>
<td>Both</td>
<td>LeftBoth</td>
</tr>
<tr>
<td>Left</td>
<td>Left</td>
<td>LeftLeft</td>
</tr>
<tr>
<td>Left</td>
<td>Right</td>
<td>LeftRight</td>
</tr>
<tr>
<td>Left</td>
<td>Both</td>
<td>LeftBoth</td>
</tr>
</tbody>
</table>

> table(HandEar) # Sample sizes

<table>
<thead>
<tr>
<th>HandEar</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>LeftBoth</td>
<td>20</td>
</tr>
<tr>
<td>LeftLeft</td>
<td>20</td>
</tr>
<tr>
<td>LeftRight</td>
<td>20</td>
</tr>
<tr>
<td>RightBoth</td>
<td>20</td>
</tr>
<tr>
<td>RightLeft</td>
<td>20</td>
</tr>
<tr>
<td>RightRight</td>
<td>20</td>
</tr>
</tbody>
</table>

> # Want a table of means in a similar format.
> meantable # Again

<table>
<thead>
<tr>
<th>Ear</th>
<th>Handed</th>
<th>Mean</th>
<th>RT</th>
</tr>
</thead>
<tbody>
<tr>
<td>Both</td>
<td>Left</td>
<td>317.90</td>
<td></td>
</tr>
<tr>
<td>Left</td>
<td>Left</td>
<td>326.60</td>
<td></td>
</tr>
<tr>
<td>Right</td>
<td>Left</td>
<td>332.80</td>
<td></td>
</tr>
<tr>
<td>Both</td>
<td>Right</td>
<td>315.10</td>
<td></td>
</tr>
<tr>
<td>Left</td>
<td>Right</td>
<td>324.65</td>
<td></td>
</tr>
<tr>
<td>Right</td>
<td>Right</td>
<td>320.85</td>
<td></td>
</tr>
</tbody>
</table>

> ComboMeans = meantable[,3] # All the rows, 3d column
> names(ComboMeans) = sort(unique(HandEar)); ComboMeans

<table>
<thead>
<tr>
<th>HandEar</th>
<th>ComboMeans</th>
</tr>
</thead>
<tbody>
<tr>
<td>LeftBoth</td>
<td>317.90</td>
</tr>
<tr>
<td>LeftLeft</td>
<td>326.60</td>
</tr>
<tr>
<td>LeftRight</td>
<td>332.80</td>
</tr>
<tr>
<td>RightBoth</td>
<td>315.10</td>
</tr>
<tr>
<td>RightLeft</td>
<td>324.65</td>
</tr>
<tr>
<td>RightRight</td>
<td>320.85</td>
</tr>
</tbody>
</table>
> # For a no-intercept model on a combination variable, the regression coefficients are the treatment combination means. Details omitted.
> # Fit a no-intercept model
> ComboModel = lmer(rtime ~ 0 + HandEar + (1 | subject))
> # Contrast matrix for testing Ear, just as a check
> CM1 = rbind(c(1, -1, 0, 1, -1, 0), # Both - Left
> + c(0, 1, -1, 0, 1, -1)) # Left - Right
> colnames(CM1) = sort(unique(HandEar)) # Makes it easier to look at
> CM1
> LeftBoth LeftLeft LeftRight RightBoth RightLeft RightRight
> [1,] 1 -1 0 1 -1 0
> [2,] 0 1 -1 0 1 -1
> linearHypothesis(ComboModel,CM1,test="F") # Compare F = 4.6787

Linear hypothesis test

Hypothesis:
HandEarLeftBoth - HandEarLeftLeft + HandEarRightBoth - HandEarRightLeft = 0
HandEarLeftLeft - HandEarLeftRight + HandEarRightLeft - HandEarRightRight = 0

Model 1: restricted model
Model 2: rtime ~ 0 + HandEar + (1 | subject)

<table>
<thead>
<tr>
<th>Res.Df</th>
<th>Df</th>
<th>F</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>78</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>76</td>
<td>4.6787</td>
<td>0.01213*</td>
</tr>
</tbody>
</table>

---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ‘ 1
# Now 3 pairwise comparisons of marginal means for ear.
# Use a Bonferroni correction, meaning compare p-value to
# 0.05 divided by the number of tests: 0.05/3 = 0.01666667

```r
bothVSleft = c(1, -1, 0, 1, -1, 0)
linearHypothesis(ComboModel, bothVSleft, test="F")
```

Linear hypothesis test

Hypothesis:
HandEarLeftBoth - HandEarLeftLeft + HandEarRightBoth - HandEarRightLeft = 0

Model 1: restricted model
Model 2: rtime ~ 0 + HandEar + (1 | subject)

<table>
<thead>
<tr>
<th>Res.Df</th>
<th>Df</th>
<th>F</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td></td>
<td>6.109</td>
<td>0.01569</td>
</tr>
</tbody>
</table>

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

```r
bothVSright = c(1, 0, -1, 1, 0, -1)
linearHypothesis(ComboModel, bothVSright, test="F")
```

Linear hypothesis test

Hypothesis:
HandEarLeftBoth - HandEarLeftRight + HandEarRightBoth - HandEarRightRight = 0

Model 1: restricted model
Model 2: rtime ~ 0 + HandEar + (1 | subject)

<table>
<thead>
<tr>
<th>Res.Df</th>
<th>Df</th>
<th>F</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td></td>
<td>7.8214</td>
<td>0.006536</td>
</tr>
</tbody>
</table>

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

```r
leftVSright = c(0, 1, -1, 0, 1, -1)
linearHypothesis(ComboModel, leftVSright, test="F")
```

Linear hypothesis test

Hypothesis:
HandEarLeftLeft - HandEarLeftRight + HandEarRightLeft - HandEarRightRight = 0

Model 1: restricted model
Model 2: rtime ~ 0 + HandEar + (1 | subject)

<table>
<thead>
<tr>
<th>Res.Df</th>
<th>Df</th>
<th>F</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td></td>
<td>0.1056</td>
<td>0.746</td>
</tr>
</tbody>
</table>
```

Page 6 of 12
Baayen, Davidson and Bates (2008)

> # Baayen, Davidson and Bates (2008) Data (Item is a random effect)
> # Reproduce Baayen, Davidson and Bates numbers
> rm(list=ls()); options(scipen=999) # To avoid scientific notation
> # Install packages if necessary. Only need to do this once.
> # install.packages("lme4")
> # install.packages("car")
> # install.packages("tables")
> # Load packages -- do this every time
> library(lme4) # For lmer function
Loading required package: Matrix
> library(car)  # For F-tests, likelihood ratio and Wald chi-squared tests
> library(tables) # For nice-looking tables
Loading required package: Hmisc
Loading required package: lattice
Loading required package: survival
Loading required package: Formula
Loading required package: ggplot2

This data.table install has not detected OpenMP support. It will work but slower in single threaded mode.

Attaching package: ‘Hmisc’

The following objects are masked from ‘package:base’: 

    format.pval, round.POSIXt, trunc.POSIXt, units

> # Read data into a data frame
>
> rt = read.table("BaayenDavidsonBates.Data.txt",header=T)
> rt; attach(rt)
Subject Item Treatment ReactionTime
1  s1  w1   Long        466
2  s1  w2   Long        520
3  s1  w3   Long        502
4  s1  w1   Short       475
5  s1  w2   Short       494
6  s1  w3   Short       490
7  s2  w1   Long        516
8  s2  w2   Long        566
9  s2  w3   Long        577
10 s2  w1  Short        491
11 s2  w2  Short        544
12 s2  w3  Short        526
13 s3  w1   Long        484
14 s3  w2   Long        529
15 s3  w3   Long        539
16 s3  w1  Short        470
17 s3  w2  Short        511
18 s3  w3  Short        528

> table(Treatment, Item) # Sample sizes
Item        Treatment
       Long  w1 w2 w3
   s1       3  3  3
   s2       3  3  3
   s3       3  3  3
> # In the tabular syntax, + means stick it together
> # Row descriptions are on the left of ~
> tabular(Treatment ~ ReactionTime*(mean+sd))

<table>
<thead>
<tr>
<th>ReactionTime</th>
<th>Treatment</th>
<th>mean</th>
<th>sd</th>
</tr>
</thead>
<tbody>
<tr>
<td>Long</td>
<td>522.1</td>
<td>35.91</td>
<td></td>
</tr>
<tr>
<td>Short</td>
<td>503.2</td>
<td>25.41</td>
<td></td>
</tr>
</tbody>
</table>

> tabular(Item ~ ReactionTime*(mean+sd))

<table>
<thead>
<tr>
<th>ReactionTime</th>
<th>Item</th>
<th>mean</th>
<th>sd</th>
</tr>
</thead>
<tbody>
<tr>
<td>w1</td>
<td>483.7</td>
<td>18.29</td>
<td></td>
</tr>
<tr>
<td>w2</td>
<td>527.3</td>
<td>25.33</td>
<td></td>
</tr>
<tr>
<td>w3</td>
<td>527.0</td>
<td>30.46</td>
<td></td>
</tr>
</tbody>
</table>

> # Fit a mixed model: Treatment effect is fixed, Subject and Item are random
> # and independent.
> mixedmod = lmer(ReactionTime ~ Treatment + (1|Item) + (1|Subject) )
> summary(mixedmod)

Linear mixed model fit by REML ['lmerMod']
Formula: ReactionTime ~ Treatment + (1 | Item) + (1 | Subject)

REML criterion at convergence: 141.4

Scaled residuals:
  Min      1Q  Median      3Q     Max
-1.1932 -0.6004 -0.2425  0.4418  1.7307

Random effects:
  Groups   Name        Variance Std.Dev.
  Item     (Intercept) 607.9    24.66
  Subject  (Intercept) 499.4    22.35
  Residual             137.3    11.72
Number of obs: 18, groups:  Item, 3; Subject, 3

Fixed effects:
  Estimate Std. Error t value
(Intercept)     522.111     19.605  26.632
TreatmentShort  -18.889      5.525  -3.419

Correlation of Fixed Effects:
  (Intr) TretmntShrt -0.141

> Anova(mixedmod, test="F")
Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df)

Response: ReactionTime
            Df Df.err Pr(>F)
Treatment 1  12 0.005087 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

>
Unbalanced designs: Beat the Blues study

This R data set contains data from a longitudinal clinical trial of an interactive, multimedia program known as "Beat the Blues" designed to deliver cognitive behavioural therapy to depressed patients via a computer terminal. Patients with depression recruited in primary care were randomised to either the Beating the Blues program, or to "Treatment as Usual" (TAU). The variables are

- **id**: Patient identification code
- **drug**: Did the patient take anti-depressant drugs (No or Yes).
- **length**: The length of the current episode of depression, a factor with values <6m (less than six months) and >6m (more than six months).
- **treatment**: Treatment group, a factor with levels TAU (treatment as usual) and BtheB (Beat the Blues)
- **bdi_pre**: Beck Depression Inventory score before treatment.
- **bdi_2m**: Beck Depression Inventory score after two months
- **bdi_4m**: Beck Depression Inventory score after four months
- **bdi_6m**: Beck Depression Inventory score after six months
- **bdi_8m**: Beck Depression Inventory score after eight months

```r
> # Install packages if necessary. Only need to do this once.
> # install.packages("lme4")
> # install.packages("car")
> # Load packages -- do this every time
> library(lme4)  # For lmer function
Loading required package: Matrix
> library(car)  # For F-tests, likelihood ratio and Wald chi-squared tests
> # install.packages("HSAUR")  # Handbook of Statistical Analyses Using R
> library(HSAUR)
Loading required package: tools
> attach(BtheB); head(BtheB)  # Beat the Blues data

<table>
<thead>
<tr>
<th>drug</th>
<th>length</th>
<th>treatment</th>
<th>bdi.pre</th>
<th>bdi.2m</th>
<th>bdi.4m</th>
<th>bdi.6m</th>
<th>bdi.8m</th>
</tr>
</thead>
<tbody>
<tr>
<td>No</td>
<td>&gt;6m</td>
<td>TAU</td>
<td>29</td>
<td>2</td>
<td>2</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>Yes</td>
<td>&gt;6m</td>
<td>BtheB</td>
<td>32</td>
<td>16</td>
<td>24</td>
<td>17</td>
<td>20</td>
</tr>
<tr>
<td>Yes</td>
<td>&lt;6m</td>
<td>TAU</td>
<td>25</td>
<td>20</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>No</td>
<td>&gt;6m</td>
<td>BtheB</td>
<td>21</td>
<td>17</td>
<td>16</td>
<td>10</td>
<td>9</td>
</tr>
<tr>
<td>Yes</td>
<td>&gt;6m</td>
<td>BtheB</td>
<td>26</td>
<td>23</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>Yes</td>
<td>&lt;6m</td>
<td>BtheB</td>
<td>7</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
> # Format is wrong -- need one line per response for lmer
```
> # Format is wrong -- need one line per response for lmer
> Subject = Drug = Treatment = Beck = Time = NULL
> n = length(drug); n
> [1] 100
> for(j in 1:n)
> + {
> +     Time = c(Time, 0)
> +     Beck = c(Beck, bdi.pre[j])
> +     Subject = c(Subject, j)
> +     Drug = c(Drug, as.character(drug[j]))
> +     Treatment = c(Treatment, as.character(treatment[j]))
> +     }
> Time = c(Time, 2)
> +     Beck = c(Beck, bdi.2m[j])
> +     Subject = c(Subject, j)
> +     Drug = c(Drug, as.character(drug[j]))
> +     Treatment = c(Treatment, as.character(treatment[j]))
> +     }
> Time = c(Time, 4)
> +     Beck = c(Beck, bdi.4m[j])
> +     Subject = c(Subject, j)
> +     Drug = c(Drug, as.character(drug[j]))
> +     Treatment = c(Treatment, as.character(treatment[j]))
> +     }
> Time = c(Time, 6)
> +     Beck = c(Beck, bdi.6m[j])
> +     Subject = c(Subject, j)
> +     Drug = c(Drug, as.character(drug[j]))
> +     Treatment = c(Treatment, as.character(treatment[j]))
> +     }
> Time = c(Time, 8)
> +     Beck = c(Beck, bdi.8m[j])
> +     Subject = c(Subject, j)
> +     Drug = c(Drug, as.character(drug[j]))
> +     Treatment = c(Treatment, as.character(treatment[j]))
> + }
> Time = factor(Time) # Otherwise it's numeric
> blues = data.frame(Subject, Time, Drug, Treatment, Beck)
> dim(blues) # Number of rows and columns
> [1] 500  5
> head(blues)
> Subject Time Drug Treatment Beck
> 1       1    0   No       TAU   29
> 2       1    2   No       TAU    2
> 3       1    4   No       TAU    2
> 4       1    6   No       TAU   NA
> 5       1    8   No       TAU   NA
> 6       2    0   Yes     BtheB  32
> # Sample sizes
> table(Treatment, Time, Drug)
> , , Drug = No
>
<table>
<thead>
<tr>
<th>Treatment</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>BtheB</td>
<td>22</td>
</tr>
<tr>
<td>TAU</td>
<td>34</td>
</tr>
</tbody>
</table>
>
> , , Drug = Yes
>
<table>
<thead>
<tr>
<th>Treatment</th>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>BtheB</td>
<td>30</td>
</tr>
<tr>
<td>TAU</td>
<td>14</td>
</tr>
</tbody>
</table>
>
> table(Treatment, Drug) # Unbalanced

<table>
<thead>
<tr>
<th>Drug</th>
<th>Treatment</th>
</tr>
</thead>
<tbody>
<tr>
<td>BtheB</td>
<td>110</td>
</tr>
<tr>
<td>TAU</td>
<td>170</td>
</tr>
</tbody>
</table>
>
> # For unbalanced designs, set contrasts to contr.sum on all factors and
> # use the type="III" (Type III sums of squares) option on the Anova function.
> # This way, tests of main effects and interactions will correspond to what you
> # would get by testing contrasts on a combination variable, which is usually
> # what you want. Details are definitely omitted.
>
> BlueModel = lmer(Beck ~ Time*Drug*Treatment + (1 | Subject),
+     contrasts = list(Time="contr.sum", Drug="contr.sum", Treatment="contr.sum"))
> Anova(BlueModel, test="F", type="III") # Satterthwaite adjustment to df

Analysis of Deviance Table (Type III Wald F tests with Kenward-Roger df)

<table>
<thead>
<tr>
<th></th>
<th>F</th>
<th>Df</th>
<th>Df.res</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>241.0743</td>
<td>1</td>
<td>99.215</td>
<td>&lt; 2e-16 ***</td>
</tr>
<tr>
<td>Time</td>
<td>37.9453</td>
<td>4</td>
<td>269.910</td>
<td>&lt; 2e-16 ***</td>
</tr>
<tr>
<td>Drug</td>
<td>0.1434</td>
<td>1</td>
<td>99.215</td>
<td>0.70571</td>
</tr>
<tr>
<td>Treatment</td>
<td>3.3556</td>
<td>1</td>
<td>99.215</td>
<td>0.06998</td>
</tr>
<tr>
<td>Time:Drug</td>
<td>3.0517</td>
<td>4</td>
<td>269.910</td>
<td>0.01748 *</td>
</tr>
<tr>
<td>Time:Treatment</td>
<td>0.4104</td>
<td>4</td>
<td>269.910</td>
<td>0.80108</td>
</tr>
<tr>
<td>Drug:Treatment</td>
<td>1.1329</td>
<td>1</td>
<td>99.215</td>
<td>0.28974</td>
</tr>
<tr>
<td>Time:Drug:Treatment</td>
<td>1.8645</td>
<td>4</td>
<td>269.910</td>
<td>0.11693</td>
</tr>
</tbody>
</table>

---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> # This calls for a 2-way table of means
> # install.packages("apaTables")
> library(apaTables) # For 2-way tables of means and Sds

Warning message:
Installed Rcpp (0.12.8) different from Rcpp used to build dplyr (0.12.11).
Please reinstall dplyr to avoid random crashes or undefined behavior.
> apa.2way.table(Drug,Time,Beck,data=blues, show.marginal.means = T)

Means and standard deviations for Beck as a function of a 2(Drug) X 5(Time) design

<table>
<thead>
<tr>
<th>Time</th>
<th>0</th>
<th>2</th>
<th>4</th>
<th>6</th>
<th>8</th>
<th>Marginal</th>
</tr>
</thead>
<tbody>
<tr>
<td>Drug</td>
<td>M</td>
<td>SD</td>
<td>M</td>
<td>SD</td>
<td>M</td>
<td>SD</td>
</tr>
<tr>
<td>No</td>
<td>21.55</td>
<td>8.97</td>
<td>17.69</td>
<td>10.98</td>
<td>15.63</td>
<td>10.78</td>
</tr>
<tr>
<td>Marginal</td>
<td>23.33</td>
<td>10.84</td>
<td>16.92</td>
<td>10.79</td>
<td>14.81</td>
<td>11.82</td>
</tr>
</tbody>
</table>

Note. M and SD represent mean and standard deviation, respectively. Marginal indicates the means and standard deviations pertaining to main effects.

> # I actually edited the table by hand to get rid of the standard deviations

<table>
<thead>
<tr>
<th>Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>Drug</td>
</tr>
<tr>
<td>No</td>
</tr>
<tr>
<td>Yes</td>
</tr>
</tbody>
</table>