DSA 8070 R Session 7: Repeated Measures Analysis

Whitney

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Dog Experiment

```
dat <- read.table("dog1.txt")
temp <- array(dim = c(144, 4))
temp[, 1] <- rep(dat$V1, 4)
temp[, 2] <- rep(dat$V2, 4)
temp[, 3] <- rep(c(1, 5, 9, 13), each = 36)
temp[, 4] <- c(dat$V3, dat$V4, dat$V5, dat$V6)
dat2 <- data.frame(temp)
names(dat2) <- c("Treatment", "Dog_id", "Time", "Response")
dat2$Treatment <- as.factor(dat2$Treatment)
dat2$Dog_id <- as.factor(dat2$Dog_id)
dat2$Time <- as.factor(dat2$Time)
```

Split-plot ANOVA

```
# computing the cell means (by treatment and time combinations)
tapply(dat2$Response, list(dat2$Treatment, dat2$Time), mean)
```

```
##          1        5        9       13
## 1 4.111111 4.400000 5.066667 4.722222
## 2 3.600000 4.200000 4.500000 4.225000
## 3 3.644444 4.011111 3.977778 4.044444
## 4 3.540000 3.620000 3.660000 3.460000
```

```
# interaction plot
par(las = 1, mgp = c(2.2, 1, 0), mar = c(3.6, 3.6, 0.8, 0.6))
with(dat2, interaction.plot(x.factor = Time, trace.factor = Treatment,
                            response = Response, col = 1:4, lwd = 1.5))
# Split-plot anova
library(lmerTest)
```

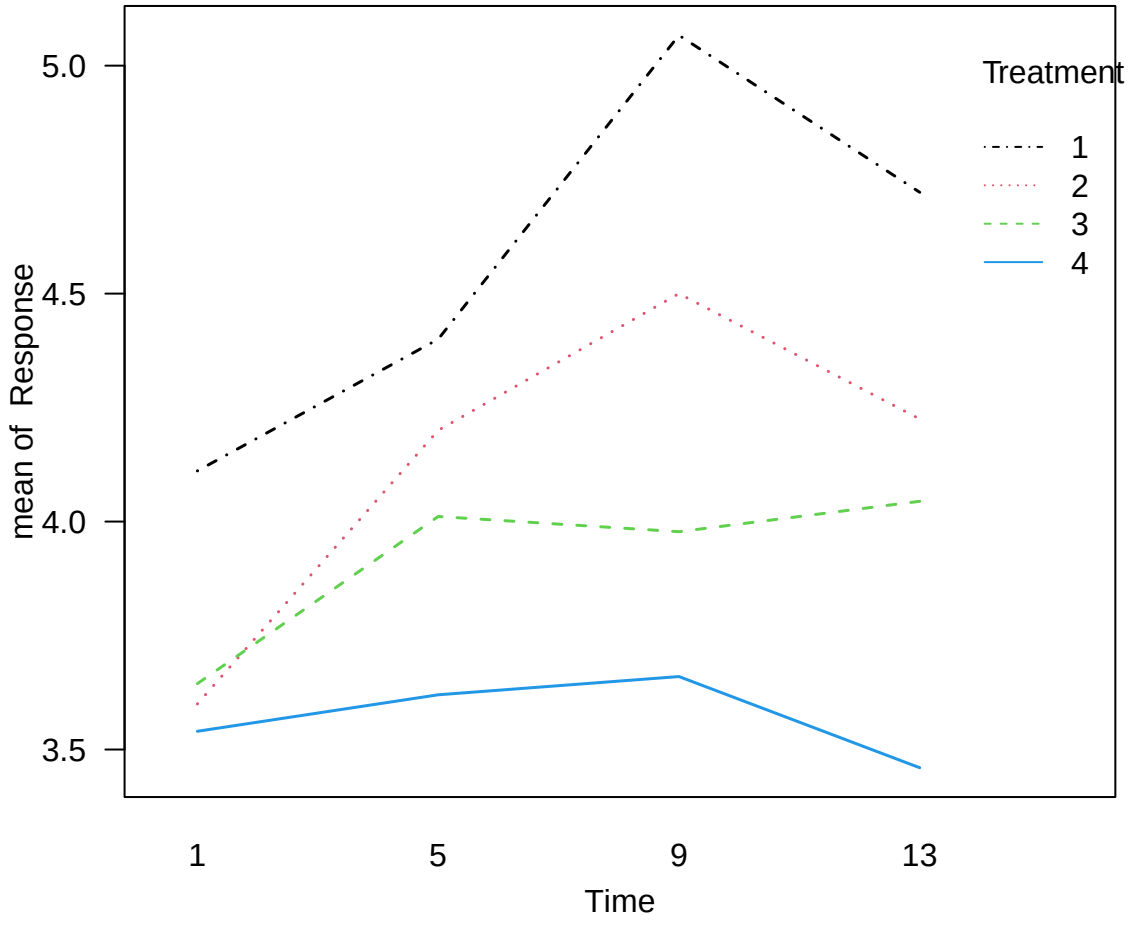
```
## Loading required package: lme4

## Loading required package: Matrix

##
## Attaching package: 'lmerTest'

## The following object is masked from 'package:lme4':
##
##     lmer

## The following object is masked from 'package:stats':
##
##     step
```




```
fit <- lmer(Response ~ Treatment * Time + (1 | Dog_id), data = dat2)
fit
```

```
## Linear mixed model fit by REML ['lmerModLmerTest']
## Formula: Response ~ Treatment * Time + (1 | Dog_id)
##    Data: dat2
## REML criterion at convergence: 239.8063
```

```
## Random effects:
##  Groups   Name        Std.Dev.
##  Dog_id   (Intercept) 0.4798
##  Residual             0.4306
## Number of obs: 144, groups:  Dog_id, 36
## Fixed Effects:
##       (Intercept)         Treatment2         Treatment3         Treatment4
##           4.11111            -0.51111           -0.46667           -0.57111
##             Time5              Time9             Time13   Treatment2:Time5
##           0.28889            0.95556            0.61111            0.31111
##  Treatment3:Time5   Treatment4:Time5   Treatment2:Time9   Treatment3:Time9
##           0.07778           -0.20889           -0.05556           -0.62222
##  Treatment4:Time9  Treatment2:Time13  Treatment3:Time13  Treatment4:Time13
##          -0.83556            0.01389           -0.21111           -0.69111
```

```
anova(fit)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## Treatment      3.3396 1.11319     3    32  6.0038  0.002297 **
## Time           6.2043 2.06811     3    96 11.1540 2.404e-06 ***
## Treatment:Time 3.4397 0.38219     9    96  2.0613  0.040573 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

MANOVA

```
out <- manova(cbind(V3, V4, V5, V6) ~ as.factor(V1), data = dat)
summary(out, test = "Wilks")
```

```
##               Df   Wilks approx F num Df den Df  Pr(>F)
## as.factor(V1)  3 0.48452    2.022     12 77.018 0.03316 *
## Residuals     32
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(out)
```

```
##               Df Pillai approx F num Df den Df  Pr(>F)
## as.factor(V1)  3 0.5978   1.9286     12     93 0.04048 *
## Residuals     32
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Mixed Model with AR(1) temporal correlation structure

```
library(nlme)
```

```
##
## Attaching package: 'nlme'

## The following object is masked from 'package:lme4':
##
##     lmList
```

```
fit1 = gls(Response ~ Treatment * Time,
           correlation = corCompSymm(form = ~ 1 | Dog_id), data = dat2)
fit1
```

```
## Generalized least squares fit by REML
##   Model: Response ~ Treatment * Time
##   Data: dat2
##   Log-restricted-likelihood: -119.9032
##
## Coefficients:
##       (Intercept)        Treatment2        Treatment3        Treatment4
##         4.11111111       -0.51111111       -0.46666667       -0.57111111
##             Time5             Time9            Time13  Treatment2:Time5
##         0.28888889        0.95555556        0.61111111        0.31111111
##  Treatment3:Time5  Treatment4:Time5  Treatment2:Time9  Treatment3:Time9
##         0.07777778       -0.20888889       -0.05555556       -0.62222222
##  Treatment4:Time9 Treatment2:Time13 Treatment3:Time13 Treatment4:Time13
##        -0.83555556        0.01388889       -0.21111111       -0.69111111
##
## Correlation Structure: Compound symmetry
##  Formula: ~1 | Dog_id
##  Parameter estimate(s):
##       Rho
## 0.5538616
## Degrees of freedom: 144 total; 128 residual
## Residual standard error: 0.6446676
```

```
fit2 = gls(Response ~ Treatment * Time,
           correlation = corAR1(form = ~ 1 | Dog_id), data = dat2)
fit2
```

```
## Generalized least squares fit by REML
##   Model: Response ~ Treatment * Time
##   Data: dat2
##   Log-restricted-likelihood: -120.7906
##
## Coefficients:
##       (Intercept)        Treatment2        Treatment3        Treatment4
##         4.11111111       -0.51111111       -0.46666667       -0.57111111
##             Time5             Time9            Time13  Treatment2:Time5
##         0.28888889        0.95555556        0.61111111        0.31111111
##  Treatment3:Time5  Treatment4:Time5  Treatment2:Time9  Treatment3:Time9
##         0.07777778       -0.20888889       -0.05555556       -0.62222222
##  Treatment4:Time9 Treatment2:Time13 Treatment3:Time13 Treatment4:Time13
##        -0.83555556        0.01388889       -0.21111111       -0.69111111
##
```

```
## Correlation Structure: AR(1)
##  Formula: ~1 | Dog_id
##  Parameter estimate(s):
##       Phi
## 0.5928708
## Degrees of freedom: 144 total; 128 residual
## Residual standard error: 0.6376364
```

```
anova(fit1, fit2)
```

```
##      Model df      AIC      BIC    logLik
## fit1     1 18 275.8063 327.1429 -119.9032
## fit2     2 18 277.5811 328.9177 -120.7906
```