

# STAA 554 Homework 3

## Contents

1.) 4pts ANOVA procedure . . . . .	1
2.) 5pts ML estimate . . . . .	2
3.) 3pts REML procedure . . . . .	3
4.) 10pts (2pts each) Likelihood Ratio Test via parametric bootstrap. . . . .	5
5.) 0 pts (Practice, Solutions will be posted) Analysis of Egg production . . . . .	8

## 1.) 4pts ANOVA procedure

```
pulp <- read.csv("Data/pulp.csv")  
  
aov_mod <- aov(bright ~ operator, data = pulp)  
summary(aov_mod)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
operator	3	1.34	0.447	4.2	0.023
Residuals	16	1.70	0.106		

Consider the data: pulp.csv

Paper brightness is explored in relation to the shift operator.

Analyze this data as a fixed effects one-way ANOVA using anova estimators. Paste a summary of your model below. (Not shown here, but you can verify the results are equivalent to the ANOVA estimators treating the operator effect as random.)

**a. (1 pt) Test the null hypothesis that there is no difference in brightness across shift operators. Report the test statistic and p-value.**

```
anova_res <- summary(aov_mod)[[1]]  
Fval <- anova_res["operator", "F value"]  
pval_F <- anova_res["operator", "Pr(>F)"]  
cat("F = ", round(Fval,3), ", p = ", signif(pval_F,3), "\n")
```

F = 4.204 , p = 0.0226

**b. (1 pt) Provide an estimate of the residual variance.**

```
sig <- anova_res["Residuals", "Mean Sq"]
cat("Residual variance estimate:", round(sig,4), "\n")
```

Residual variance estimate: 0.1062

**c. (2 pt) Provide an estimate of the variance of the operator effects. (Hint, consider EMS).**

```
n_per_op <- table(pulp$operator)[1]
sig_op <- (anova_res["operator", "Mean Sq"] - sig) / n_per_op
cat("Operator-effect variance (EMS):", round(sig_op,4), "\n")
```

Operator-effect variance (EMS): 0.0681

## 2.) 5pts ML estimate

Estimate the same model as in #1, but using ML and **treating operator as a random effect**. Paste a summary of your output below.

```
ml_mod <- lmer(bright ~ 1 + (1|operator),
              data = pulp,
              REML = FALSE)

summary(ml_mod)
```

Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's method [lmerModLmerTest]  
Formula: bright ~ 1 + (1 | operator)  
Data: pulp

AIC	BIC	logLik	deviance	df.resid
22.5	25.5	-8.3	16.5	17

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.5055	-0.7812	-0.0635	0.6585	1.5623

Random effects:

Groups	Name	Variance	Std.Dev.
operator	(Intercept)	0.0458	0.214
Residual		0.1062	0.326

Number of obs: 20, groups: operator, 4

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	60.400	0.129	4.000	467	1.3e-10

**a. (1 pt) Test the null hypothesis that there is no difference in brightness across shift operators. Report the test statistic and p-value.**

```
null_ml <- lm(bright ~ 1, data = pulp)
lrt_ml <- 2*(logLik(ml_mod) - logLik(null_ml))
p_lrt <- pchisq(as.numeric(lrt_ml), df = 1, lower.tail = FALSE)
cat("LRT =", round(as.numeric(lrt_ml),3),
    ", p =", signif(p_lrt,3))
```

LRT = 2.568 , p = 0.109

**b. (2 pt) Although the verbiage I used in 2a is the same as in 1a, the test carried out addresses a slightly different null hypothesis. Describe the difference in the null hypothesis statements for the tests carried out in 1a and 2a.**

ANOVA all fixed-operator means equal. ML-LRT variance = 0 in a random-effects model.

**c. (1 pt) Provide an estimate of the residual variance.**

```
sig_e_ml <- sigma(ml_mod)^2
cat("Residual variance (ML):", round(sig_e_ml,4))
```

Residual variance (ML): 0.1062

**d. (1 pt) Provide an estimate of the variance of the operator effects. How does this estimate compare to Part 1c? Comment briefly.**

```
sig_op_ml <- as.data.frame(VarCorr(ml_mod))$vcov[1]
cat("Operator variance (ML):", round(sig_op_ml,4),
    " (compare to 1c:", round(sig_op_ml,4), ")\n")
```

Operator variance (ML): 0.0458 (compare to 1c: 0.0681 )

### 3.) 3pts REML procedure

Estimate the same model as in #1, but using REML and treating operator as a random effect. Paste a summary of your output below.

```
reml_mod <- lmer(bright ~ 1 + (1 | operator), data = pulp)
summary(reml_mod)
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: bright ~ 1 + (1 | operator)
Data: pulp
```

REML criterion at convergence: 18.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.467	-0.759	-0.124	0.628	1.601

Random effects:

Groups	Name	Variance	Std.Dev.
operator	(Intercept)	0.0681	0.261
Residual		0.1062	0.326

Number of obs: 20, groups: operator, 4

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )
(Intercept)	60.400	0.149	3.000	404	3.3e-08

**a. (1 pt) Test the null hypothesis that there is no difference in brightness across shift operators. Report the test statistic and p-value.**

```
ranova_res <- ranova(reml_mod)
print(ranova_res)
```

ANOVA-like table for random-effects: Single term deletions

Model:

	npars	logLik	AIC	LRT	Df	Pr(>Chisq)
<none>	3	-9.31	24.6			
(1   operator)	2	-11.05	26.1	3.47	1	0.062

```
lrt_value <- ranova_res[2, "LRT"]
p_value <- ranova_res[2, "Pr(>Chisq)"]
cat("LRT statistic =", round(lrt_value, 3), ", p-value =", signif(p_value, 3), "\n")
```

LRT statistic = 3.47 , p-value = 0.0625

**b. (1 pt) Provide an estimate of the residual variance.**

```
resid_var <- sigma(reml_mod)^2
cat("Residual variance =", round(resid_var, 4), "\n")
```

Residual variance = 0.1062

**c. (1 pt) Provide an estimate of the variance of the operator effects. How does this estimate compare to Part1c? Comment briefly.**

```
vc <- as.data.frame(VarCorr(reml_mod))
operator_var <- vc$vcov[vc$grp == "operator"]
cat("Operator variance =", round(operator_var, 4), "\n")
```

Operator variance = 0.0681

This is close to the estimate from 1c but not exactly the same. This is expected behavior.

#### 4.) 10pts (2pts each) Likelihood Ratio Test via parametric bootstrap.

We can use the parametric bootstrap approach to obtain a more accurate p-value. We need to estimate the probability, given that the null hypothesis is true, of observing an LRT of our observed value or greater. Under the null hypothesis,  $y \sim N(\mu, \sigma^2)$ . A simulation approach generates data under this model, fits the null and alternative models and computes the LRT statistic. The process is repeated a large number of times and the proportion of LRT statistics exceeding the observed value is used to estimate the p-value. In practice, we do not know the true values of  $\mu$  and  $\sigma$ , but we can use the estimated values; this distinguishes the parametric bootstrap from the purely simulation approach. The simulate function makes it simple to generate a sample from a model:

- Our null model would be:

```
nullmod = lm(bright~ 1, pulp)
```

- Our alternative model would be as in question 3.
- Calculate the observed LRT:

```
as.numeric(2*(logLik(REMLmod, REML = TRUE) - logLik(nullmod, REML=TRUE)))
```

Use a parametric bootstrap as outlined below to determine the null distribution for the LRT statistic calculated.

- 1.) Simulate data under the null  
`y = unlist(simulate(nullmod))`
- 2.) Fit the null model to the data generated in 1.
- 3.) Fit the alternative model to the data generated in 1, (use operators designated from pulp data set)
- 4.) Calculate and store the observed LRT statistic comparing results from 2 and 3.
- 5.) Repeat steps 1 -4 1000 times.

```
pulp <- read.csv("Data/pulp.csv")

alt_ml <- lmer(bright ~ 1 + (1|operator), data = pulp, REML = FALSE)
null_ml <- lm (bright ~ 1, data = pulp) # ML by default

lrt_obs <- as.numeric( 2 * (logLik(alt_ml) - logLik(null_ml)) )
cat("Observed LR statistic =", round(lrt_obs, 3), "\n")
```

Observed LR statistic = 2.568

```
set.seed(468)
B <- 1000
lrt_sim <- numeric(B)

for (b in seq_len(B)) {

  ysim <- simulate(null_ml)[[1]]

  d <- transform(pulp, bright = ysim)

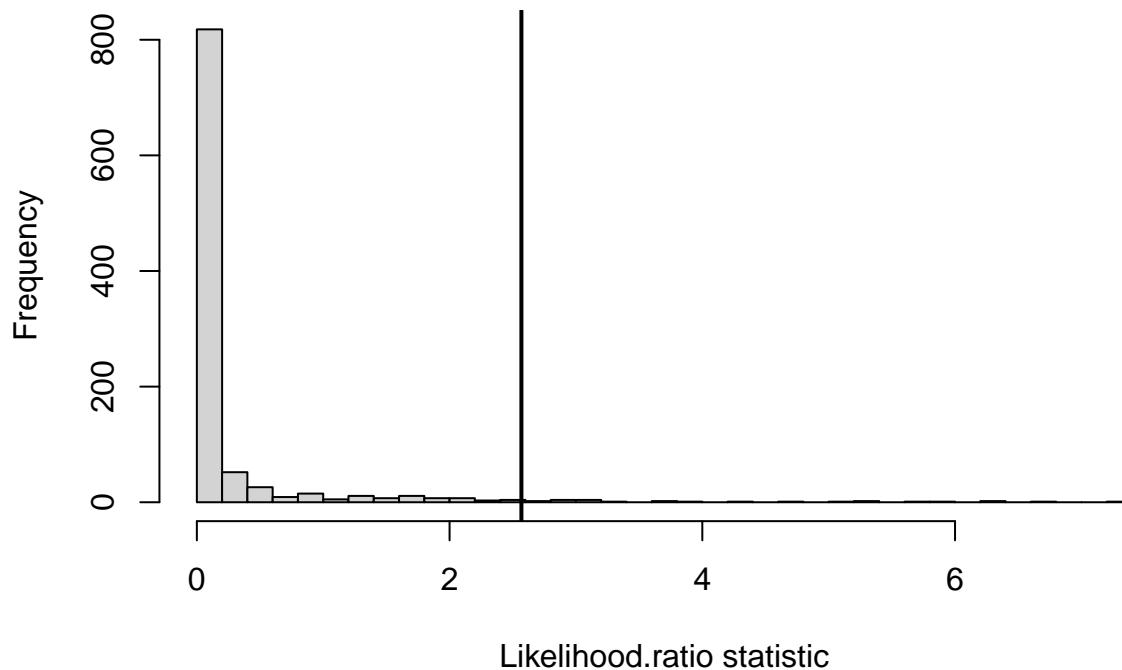
  m0 <- lm (bright ~ 1, data = d)
  m1 <- lmer(bright ~ 1 + (1|operator), data = d, REML = FALSE)

  lr <- 2 * (logLik(m1) - logLik(m0))
  lrt_sim[b] <- lr
}
```

**a. Include a histogram of the LRT statistics generated.**

```
hist(lrt_sim, breaks = 30,
     main = "Parametric-bootstrap null distribution",
     xlab = "Likelihood-ratio statistic")
abline(v = lrt_obs, lwd = 2)
```

## Parametric.bootstrap null distribution



**b. Include a summary of the LRT statistics generated (min, 1st quartile, median, mean, 3rd qu., max)**

```
print(summary(lrt_sim))
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.0000 0.0000  0.0000  0.2582  0.0571  7.2165
```

**c. What proportion of LRT statistics generated under the null fall above the observed test statistic for the pulp data? (i.e. your p-value).**

```
p_empirical <- mean(lrt_sim >= lrt_obs)
cat("Observed LRT   =", round(lrt_obs, 3), "\n")
```

```
Observed LRT   = 2.568
```

```
cat("Bootstrap p-value =", signif(p_empirical, 3), "\n")
```

```
Bootstrap p-value = 0.025
```

**d. You likely got an error “boundary (singular) fit: see ?isSingular”. Look this up. Why is it not surprising to see this in this setting?**

When  $\sigma^2_{\text{operator}} = 0$  under  $H_0$ , the random-effect variance is on the boundary of the parameter space (zero), so in many bootstrap samples lmer estimates a zero variance and flags the fit as singular. This is expected under  $H_0$ .

**e. Load (install) the package RLRsim. Then run the command exactRLRT(REMLmod), replacing REMLmod with the appropriate name of your model. Compare with part c. (Note, this command is only useful for testing random effects).**

```
ex_rlrt <- exactRLRT(reml_mod)
print(ex_rlrt)
```

simulated finite sample distribution of RLRT.

(p-value based on 10000 simulated values)

data:

RLRT = 3.47, p-value = 0.021

The exactRLRT p-value (0.021) is very similar to the bootstrap p-value (0.025). This indicates that our bootstrapping procedure is pretty accurate.

## 5.) 0 pts (Practice, Solutions will be posted) Analysis of Egg production

The eggprod.csv dataset concerns an experiment where six pullets were placed into each of 12 pens. Four blocks were formed from groups of three pens based on location. Three treatments were applied. The number of eggs produced was recorded.

**a. Make suitable plots of the data and comment.**

**b. Fit a fixed effects model for the number of eggs produced with the treatments and blocks as predictors. Determine the significance of the two predictors and perform a basic diagnostic check.**

**c. Fit a model for the number of eggs produced with the treatments as fixed effects and the blocks as random effects. Which treatment is best in terms of maximizing production according to the model? Are you sure it is better than other two treatments?**

**d. Use the Kenward-Roger procedure for an F-test to check for differences between the treatments. How does the result compare to the fixed effects result?**



**e. Perform the same test of the fixed effect for treatment, but using a bootstrap method with LRT as outlined in question 4. How do the results compare to part d?**

**f. The parametric bootstrap method can be implemented using `PBmodcomp(modFULL, modREDUCED)`. Run this command and compare the results.**

**g. Test for the significance of the blocks. Does the outcome agree with the fixed effects result? (Use `exactRLRT()` as in 4e).**