

17. Example SAS Commands for Analysis of a Classic Split-Plot Experiment

options nocenter nonumber nodate ls=80; *FORMAT SCREEN OUTPUT*

proc import datafile="c:\Data\SimulatedSplitPlotData.txt"
dbms=TAB replace out=d; *READ TAB-DELIMITED TEXT FILE*
run; *INTO SAS DATASET d*

proc print data=d (obs=14); *PRINT FIRST 14 Rows OF d*
run; *TO SCREEN*

ods listing close; *TURN OFF OUTPUT TO SCREEN*
options orientation=landscape;
ods pdf *WRITE OUTPUT TO*
file="c:\sasoutput.pdf" notoc; *A PDF FILE*

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proc mixed;

DEFINE $E(y)$

$$E(y_{ijk}) = \mu + \alpha_i + \beta_j + \gamma_{ij} = \mu_{ij}$$

class block geno fert;

model y=geno fert geno*fert / ddfm=satterthwaite;

DENOMINATOR DEGREES OF FREEDOM
METHOD

random block block*geno;

$$b_1, b_2, b_3, b_4 \stackrel{iid}{\sim} N(0, \sigma_b^2) \rightarrow w_1, \dots, w_{12} \stackrel{iid}{\sim} N(0, \sigma_w^2)$$

estimate 'geno 1' ESTIMATE MARGINAL MEAN FOR GENOTYPE 1

intercept 4 geno 4 0 0 fert 1 1 1 1

geno*fert 1 1 1 1 0 0 0 0 0 0 0 0 / divisor=4 cl;

$$\bar{\mu}_{1.} = (\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14}) / 4 = \frac{1}{4} \sum_{j=1}^4 (\mu + \alpha_1 + \beta_j + \gamma_{1j})$$

$$= \frac{4\mu + 4\alpha_1 + \beta_1 + \beta_2 + \beta_3 + \beta_4 + \gamma_{11} + \gamma_{12} + \gamma_{13} + \gamma_{14}}{4}$$

$$= \mu + \alpha_1 + \bar{\beta}_{.} + \bar{\gamma}_{1.}$$

$$\bar{\mu}_1 - \bar{\mu}_2 = \frac{1}{4} \sum_{j=1}^4 (\mu + \alpha_1 + \beta_j + \gamma_{1j}) - \frac{1}{4} \sum_{j=1}^4 (\mu + \alpha_2 + \beta_j + \gamma_{2j})$$

$$\text{estimate 'geno 1 - geno 2'} = \frac{1}{4} \sum_{j=1}^4 (\alpha_1 - \alpha_2 + \gamma_{1j} - \gamma_{2j})$$

geno 4 -4 0

geno*fert 1 1 1 1 -1 -1 -1 -1 0 0 0 0 / divisor=4 cl;

$$\frac{4\alpha_1 - 4\alpha_2 + \gamma_{11} + \gamma_{12} + \gamma_{13} + \gamma_{14} - \gamma_{21} - \gamma_{22} - \gamma_{23} - \gamma_{24}}{4}$$

$$= \alpha_1 - \alpha_2 + \bar{\gamma}_1 - \bar{\gamma}_2$$

estimate 'geno 1 - geno 2 with no fertilizer'

geno 1 -1 0 geno*fert 1 0 0 0 -1 0 0 0 0 0 0 0 / cl;

run;

$$\begin{aligned} \mu_{11} - \mu_{21} &= \mu + \alpha_1 + \beta_1 + \gamma_{11} - (\mu + \alpha_2 + \beta_1 + \gamma_{21}) \\ &= \alpha_1 - \alpha_2 + \gamma_{11} - \gamma_{21} \end{aligned}$$

The SAS System

The Mixed Procedure

Model Information	
Data Set	WORK.D
Dependent Variable	y
Covariance Structure	Variance Components
Estimation Method	REML
Residual Variance Method	Profile
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Satterthwaite

Class Level Information		
Class	Levels	Values
block	4	1 2 3 4
geno	3	1 2 3
fert	4	0 50 100 150

Dimensions	
Covariance Parameters	3
Columns in X	20
Columns in Z	16
Subjects	1
Max Obs per Subject	48

Number of Observations	
Number of Observations Read	48
Number of Observations Used	48
Number of Observations Not Used	0

MATCHES OUR DATA WITH GENOTYPES
A, B, AND C → 1, 2, AND 3, RESPECTIVELY

$\sigma_b^2, \sigma_w^2, \sigma_e^2$

$\mu, \alpha_1, \alpha_2, \alpha_3, \beta_1, \beta_2, \beta_3, \beta_4, \gamma_{11}, \gamma_{12}, \dots, \gamma_{34}$

$b_1, b_2, b_3, b_4, w_1, \dots, w_{12}$

DON'T WORRY ABOUT THIS FOR NOW. REASON WILL BECOME CLEAR WHEN WE DISCUSS REPEATED MEASURES ANALYSIS.

$n = 48$ (4 BLOCKS X 3 GENOTYPES X 4 FERTILIZER AMOUNTS)

The SAS System

The Mixed Procedure

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	314.54790074	
1	1	275.05625945	0.00000000

Convergence criteria met.

Covariance Parameter Estimates	
Cov Parm	Estimate
block	122.85
block*geno	67.2981
Residual	39.7061

λ^2
 σ_b^2
 λ^2
 σ_w^2
 λ^2
 σ_e^2

Fit Statistics	
-2 Res Log Likelihood	275.1
AIC (Smaller is Better)	281.1
AICC (Smaller is Better)	281.8
BIC (Smaller is Better)	279.2

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
geno	2	6	8.48	0.0179
fert	3	27	73.35	<.0001
geno*fert	6	27	6.54	0.0002

$$H_0: \bar{\mu}_{1.} = \bar{\mu}_{2.} = \bar{\mu}_{3.} \quad (\text{NO GENOTYPE MAIN EFFECTS})$$

$$H_0: \bar{\mu}_{.1} = \bar{\mu}_{.2} = \bar{\mu}_{.3} = \bar{\mu}_{.4} \quad (\text{NO FERT MAIN EFFECTS})$$

$$H_0: \mu_{ij} - \bar{\mu}_{i.} - \bar{\mu}_{.j} + \bar{\mu}_{..} = 0 \quad \forall i, j$$

(NO GENO X FERT INTERACTIONS)

H_0 REJECTED FOR ALL THREE TESTS

SAS AUTOMATICALLY
DOES THESE TESTS CORRECTLY
WHETHER DATA ARE BALANCED OR NOT

The SAS System

The Mixed Procedure

Estimates								
Label	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
geno 1	139.83	7.0725	5.13	19.77	<.0001	0.05	121.78	157.87
geno 1 - geno 2	-24.8812	6.2139	6	-4.00	0.0071	0.05	-40.0861	-9.6764
geno 1 - geno 2 with no fertilizer	-22.5000	7.3145	11.2	-3.08	0.0104	0.05	-38.5725	-6.4275

SAS DOES THESE TESTS CORRECTLY WHETHER DATA ARE BALANCED OR NOT AND USES SATTERTHWAITES APPROXIMATION WHEN NECESSARY.

How Do THINGS CHANGE IF BLOCK EFFECTS ARE FIXED?

```
proc mixed;
```

```
class block geno fert;
```

```
model y=block geno fert geno*fert / ddfm=satterthwaite;
```

```
random block*geno; —————→  $w_1, \dots, w_{12} \stackrel{iid}{\sim} N(0, \sigma_w^2)$ 
```

```
estimate 'geno 1'
```

```
intercept 4 block 1 1 1 1 geno 4 0 0 fert 1 1 1 1
```

```
geno*fert 1 1 1 1 0 0 0 0 0 0 0 0 / divisor=4 cl;
```

$$\bar{\mu}_{1..} = \frac{1}{(4)(4)} \sum_{j=1}^4 \sum_{k=1}^4 (\mu + b_k + \alpha_1 + \beta_j + \gamma_{ij})$$

$$= (16\mu + 4b_1 + 4b_2 + 4b_3 + 4b_4 + 16\alpha_1 + 4\beta_1 + 4\beta_2 + 4\beta_3 + 4\beta_4 + 4\gamma_{11} + 4\gamma_{12} + 4\gamma_{13} + 4\gamma_{14}) / 16$$

```
estimate 'geno 1 - geno 2'
```

```
geno 4 -4 0
```

```
geno*fert 1 1 1 1 -1 -1 -1 -1 0 0 0 0 / divisor=4 cl;
```

```
estimate 'geno 1 - geno 2 with no fertilizer'
```

```
geno 1 -1 0 geno*fert 1 0 0 0 -1 0 0 0 0 0 0 0 / cl;
```

THESE
SAME AS
BEFORE
BECAUSE
BLOCK
EFFECTS
CANCEL
OUT.

```
ods pdf close;
```

```
ods listing;
```

→ STOP WRITING OUTPUT TO PDF FILE

→ START WRITING OUTPUT TO SCREEN

The SAS System

The Mixed Procedure

Model Information	
Data Set	WORK.D
Dependent Variable	y
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Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Satterthwaite

Class Level Information		
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block	4	1 2 3 4
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Dimensions	
Covariance Parameters	2
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Subjects	1
Max Obs per Subject	48

Number of Observations	
Number of Observations Read	48
Number of Observations Used	48
Number of Observations Not Used	0

4 MORE COLUMNS IN X AND 4 FEWER
COLUMNS IN Z BECAUSE b_1, b_2, b_3, b_4
MOVE TO β VECTOR FROM \underline{u} VECTOR

The SAS System

The Mixed Procedure

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	264.34894774	
1	1	250.15263205	0.00000000

Convergence criteria met.

Covariance Parameter Estimates	
Cov Parm	Estimate
block*geno	67.2981
Residual	39.7061

σ^2_w
 σ^2_e

Fit Statistics	
-2 Res Log Likelihood	250.2
AIC (Smaller is Better)	254.2
AICC (Smaller is Better)	254.6
BIC (Smaller is Better)	255.1

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
block	3	6	5.77	0.0335
geno	2	6	8.48	0.0179
fert	3	27	73.35	<.0001
geno*fert	6	27	6.54	0.0002

SAME AS WHEN BLOCK EFFECTS
RANDOM

CONFIDENCE INTERVAL MUCH
NARROWER NOW THAT BLOCK
EFFECTS ARE CONSIDERED TO BE
FIXED.

Estimates								
Label	Estimate	Standard Error	DF	t Value	Pr > t	Alpha	Lower	Upper
geno 1	139.83	4.3939	6	31.82	<.0001	0.05	129.07	150.58
geno 1 - geno 2	-24.8812	6.2139	6	-4.00	0.0071	0.05	-40.0861	-9.6764
geno 1 - geno 2 with no fertilizer	-22.5000	7.3145	11.2	-3.08	0.0104	0.05	-38.5725	-6.4275

SAME AS WHEN BLOCK
EFFECTS RANDOM