

16. SAS Analysis of Split-Plot Experiments

Field Split-Plot Experiment

Field

Block 1	Genotype C				Genotype A				Genotype B			
	0	100	150	50	50	100	150	0	150	100	50	0
Block 2	Genotype B				Genotype A				Genotype C			
	150	100	50	0	0	50	150	100	100	50	150	0
Block 3	Genotype A				Genotype B				Genotype C			
	100	50	0	150	0	100	150	50	50	100	150	0
Block 4	Genotype B				Genotype C				Genotype A			
	0	50	100	150	150	100	50	0	50	150	100	0

Read Data

READ TAB-DELIMITED
TEXT FILE INTO SAS
DATASET CALLED Field.

```
proc import datafile='C:\Data\FieldSplitPlotData.txt'  
    dbms=TAB replace out=Field;  
run;
```

```
proc print data=Field (obs=14);  
run;
```

PRINT FIRST 14
Rows of Field
To Output

The SAS System

Obs	block	geno	fert	y
1	1	1	0	148.7
2	1	1	50	150.4
3	1	1	100	166.7
4	1	1	150	156.5
5	1	2	0	162.5
6	1	2	50	168.6
7	1	2	100	180.2
8	1	2	150	181.1
9	1	3	0	144.5
10	1	3	50	177.3
11	1	3	100	188.1
12	1	3	150	199.1
13	2	1	0	114.2
14	2	1	50	131.5

Fit Linear Mixed-Effects Model

```
proc mixed data=Field;  
  class block geno fert;
```

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

```
  random block block*geno;
```

SPECIFY $X\beta$

SPECIFY $Z\underline{u}$

SET DENOMINATOR
DEGREES OF FREEDOM
METHOD TO SATTERTHWAITE

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

$$b_1, b_2, b_3, b_4 \stackrel{iid}{\sim} N(0, \sigma_b^2)$$

$$w_{ik} \stackrel{iid}{\sim} N(0, \sigma_w^2)$$

The SAS System

The Mixed Procedure

Model Information	
Data Set	WORK.FIELDEXP
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

WE WILL LEARN
ABOUT REML
SOON.

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

1=A, 2=B, 3=C

The SAS System

The Mixed Procedure

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

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

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

$$b_1, b_2, b_3, b_4, w_{11}, \dots, w_{34}$$

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

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

Convergence criteria met.

The SAS System

The Mixed Procedure

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

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

$$\begin{aligned} \lambda^2 \\ \sigma_b^2 \\ \lambda^2 \\ \sigma_w^2 \\ \lambda^2 \\ \sigma_e^2 \end{aligned}$$

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

$$H_0: \bar{\mu}_{1.} = \bar{\mu}_{2.} = \bar{\mu}_{3.}$$

$$H_0: \bar{\mu}_{.1} = \bar{\mu}_{.2} = \bar{\mu}_{.3} = \bar{\mu}_{.4}$$

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

Example Estimate Statements

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

intercept 4 geno 4 0 0 fert 1 1 1 1 $= \mu + \alpha_1 + \bar{\beta}_{.} + \bar{\gamma}_{1.}$

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

$$(\mu + \alpha_1 + \bar{\beta}_{.} + \bar{\gamma}_{1.}) - (\mu + \alpha_2 + \bar{\beta}_{.} + \bar{\gamma}_{2.}) = \alpha_1 - \alpha_2 + \bar{\gamma}_{1.} - \bar{\gamma}_{2.}$$

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;

$$(\mu + \alpha_1 + \beta_1 + \gamma_{11}) - (\mu + \alpha_2 + \beta_1 + \gamma_{21}) = \alpha_1 - \alpha_2 + \gamma_{11} - \gamma_{21}$$

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;

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

SATTERTHWAITE
METHOD USED
WHEN NEEDED

Refit Model with Fixed Block Effects

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

```
proc mixed data=Field;  
  class block geno fert;  
  model y=block geno fert geno*fert / ddfm=satterthwaite;  
  random block*geno;
```

$$w_{ik} \overset{iid}{\sim} N(0, \sigma_w^2)$$

The SAS System

The Mixed Procedure

Model Information	
Data Set	WORK.FIELDEXP
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

The SAS System

The Mixed Procedure

Dimensions	
Covariance Parameters	2
Columns in X	24
Columns in Z	12
Subjects	1
Max Obs per Subject	48

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

$$\mu, b_1, b_2, b_3, b_4, \alpha_1, \alpha_2, \alpha_3, \beta_1, \beta_2, \beta_3, \beta_4$$

$$\gamma_{11}, \dots, \gamma_{34}$$

$$w_{11}, \dots, w_{34}$$

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

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

Convergence criteria met.

The SAS System

The Mixed Procedure

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

σ_w^2

σ_e^2

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
WERE RANDOM FOR OUR
BALANCED DESIGN

Example Estimate Statements

estimate 'geno 1' $\mu + \bar{b}_{.} + \alpha_1 + \bar{\beta}_{.} + \bar{\gamma}_{1.}$

```
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;
```

estimate 'geno 1 - geno 2' $\alpha_1 - \alpha_2 + \bar{\gamma}_{1.} - \bar{\gamma}_{2.}$

```
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;  
run;
```

$\alpha_1 - \alpha_2 + \gamma_{11} - \gamma_{21}$

SATTERTHWAITE NO LONGER NEEDED HERE

The SAS System

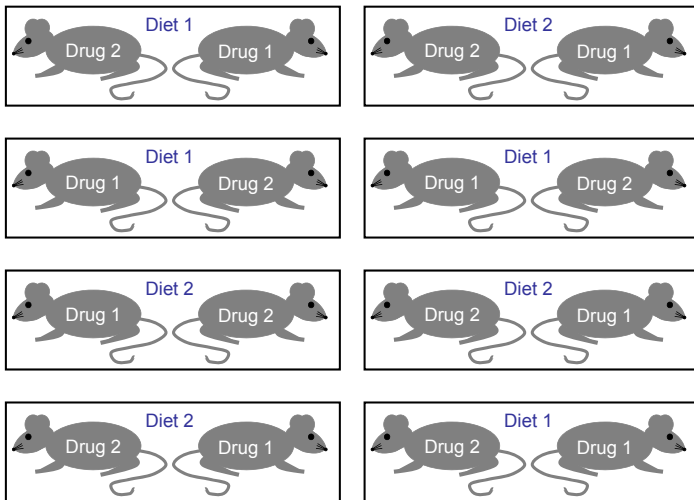
The Mixed Procedure

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
WERE RANDOM
FOR OUR BALANCED
DESIGN

THIS CONFIDENCE
INTERVAL MUCH
NARROWER NOW THAT
BLOCK EFFECTS
ARE MODELED
AS FIXED.

Diet and Drug Split-Plot Experiment



Read Data

```
proc import datafile='C:\Data\DietDrugSplitPlotData.txt'  
    dbms=TAB replace out=DietDrug;  
run;  
  
proc print data=DietDrug;  
run;
```

The SAS System

Obs	litter	diet	drug	y
1	1	1	2	18.8
2	1	1	1	10.3
3	2	2	2	14.5
4	2	2	1	18.5
5	3	1	1	16.8
6	3	1	2	27.2
7	4	1	1	11.5
8	4	1	2	20.5
9	5	2	1	11.9
10	5	2	2	11.3
11	6	2	2	16.4
12	6	2	1	17.6
13	7	2	2	15.4
14	7	2	1	18
15	8	1	2	26.8
16	8	1	1	15.7

Fit Linear Mixed-Effects Model

```
proc mixed data=DietDrug;  
  class litter diet drug;  
  model y=diet drug diet*drug / ddfm=satterthwaite;  
  random litter(diet);
```

The SAS System

The Mixed Procedure

Model Information	
Data Set	WORK.DIETDRUG
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
litter	8	1 2 3 4 5 6 7 8
diet	2	1 2
drug	2	1 2

The SAS System

The Mixed Procedure

Dimensions	
Covariance Parameters	2
Columns in X	9
Columns in Z	8
Subjects	1
Max Obs per Subject	16

Number of Observations	
Number of Observations Read	16
Number of Observations Used	16
Number of Observations Not Used	0

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	68.07389478	
1	1	57.36070457	0.00000000

Convergence criteria met.

The SAS System

The Mixed Procedure

Covariance Parameter Estimates	
Cov Parm	Estimate
litter(diet)	9.7871
Residual	0.9408

Fit Statistics	
-2 Res Log Likelihood	57.4
AIC (Smaller is Better)	61.4
AICC (Smaller is Better)	62.7
BIC (Smaller is Better)	61.5

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
diet	1	6	1.75	0.2335
drug	1	6	62.20	0.0002
diet*drug	1	6	149.25	<.0001

Estimating Marginal Means, Means, and Contrasts

```
lsmeans diet drug diet*drug;
```

```
estimate 'diet 1 - diet 2' diet 2 -2  
        diet*drug 1 1 -1 -1 / divisor=2;
```

```
estimate 'drug 1 - drug 2' drug 2 -2  
        diet*drug 1 -1 1 -1 / divisor=2;
```


More Estimate Statements

```
estimate 'diet 1 - diet 2 for drug 2' diet 1 -1  
                                         diet*drug 0 1 0 -1;
```

```
estimate 'drug 1 - drug 2 for diet 2' drug 1 -1  
                                         diet*drug 0 0 1 -1;  
  
run;
```

The SAS System

The Mixed Procedure

Estimates					
Label	Estimate	Standard Error	DF	t Value	Pr > t
diet 1 - diet 2	3.0000	2.2647	6	1.32	0.2335
drug 1 - drug 2	-3.8250	0.4850	6	-7.89	0.0002
diet 1 - diet 2 for drug 2	8.9250	2.3160	6.55	3.85	0.0071
drug 1 - drug 2 for diet 2	2.1000	0.6859	6	3.06	0.0222

Least Squares Means							
Effect	diet	drug	Estimate	Standard Error	DF	t Value	Pr > t
diet	1		18.4500	1.6014	6	11.52	<.0001
diet	2		15.4500	1.6014	6	9.65	<.0001
drug		1	15.0375	1.1580	6.55	12.99	<.0001
drug		2	18.8625	1.1580	6.55	16.29	<.0001
diet*drug	1	1	13.5750	1.6377	6.55	8.29	0.0001
diet*drug	1	2	23.3250	1.6377	6.55	14.24	<.0001
diet*drug	2	1	16.5000	1.6377	6.55	10.08	<.0001
diet*drug	2	2	14.4000	1.6377	6.55	8.79	<.0001