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

```
options nocenter nonumber nodate ls=80;

proc import datafile="c:\Data\SimulatedSplitPlotData.txt"
     dbms=TAB replace out=d;
run;

proc print data=d (obs=14);
run;

ods listing close;
options orientation=landscape;
ods pdf
    file="c:\sasoutput.pdf" notoc;
```

Format Screen Output

Read Tab-Delimited Text File Into SAS Dataset d.

Print First 14 Rows of d To Screen.

Turn Off Screen Output.

Write Output To PDF File

No Table of Contents

Define $E(y)$.

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

(α_i: geno, β_j: fert, γ_{ij}: genoxfert)

```
proc mixed;

  class block geno fert;

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

  random block block*geno;
  estimate 'geno 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;
```

ddfm = Denominator Degrees of Freedom Method

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

$w_1, \ldots, w_{12} \overset{iid}{\sim} N(0, \sigma_w^2)$

$$\frac{4\mu + 4\alpha_1 + 0\alpha_2 + 0\alpha_3 + \beta_1 + \beta_2 + \beta_3 + \beta_4 + \gamma_{11} + \gamma_{12} + \gamma_{13} + \gamma_{14}}{4}$$

$$= \mu + \alpha_1 + \bar{\beta}_\cdot + \bar{\gamma}_{1\cdot} = \text{Marginal Mean for Genotype A.} = \bar{\mu}_{1\cdot}$$

```
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;
```

$$\alpha_1 - \alpha_2 + \overline{\gamma}_{1\cdot} - \overline{\gamma}_{2\cdot} = \overline{\mu}_{1\cdot} - \overline{\mu}_{2\cdot}$$

```
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 0 / cl;
run;
```

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

Now See How Results Change When Block Effects Are Modeled As Fixed Instead of Random.

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

ods pdf close;
ods listing;
```

← Stop writing output to PDF file

← Start writing output to screen

The SAS System

The Mixed Procedure

RESULTS FOR RANDOM BLOCK EFFECTS

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

MATCHES OUR DATA

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

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

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

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

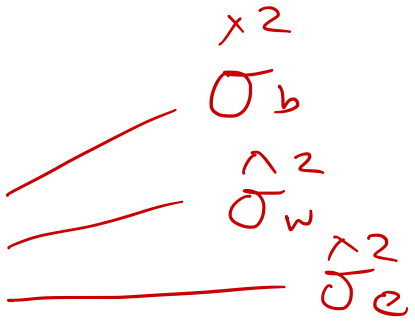
The Mixed Procedure

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.

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

The Mixed Procedure

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

SAS GETS THESE TESTS RIGHT AND USES THE SATTERTHWAITE APPROXIMATION WHEN NECESSARY

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

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	2
Columns in X	24
Columns in Z	12
Subjects	1
Max Obs Per Subject	48

NOW THE RESULTS FOR FIXED BLOCK EFFECTS.

4 MORE COLUMNS IN X FOR THE 4 FIXED BLOCK EFFECTS

ONLY 12 COLUMNS IN Z BECAUSE ONLY THE 12 WHOLE-PLOT EXPERIMENTAL UNIT EFFECTS ARE RANDOM

The Mixed Procedure

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.

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

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

The SAS System

The Mixed Procedure

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

THESE RESULTS EXACTLY THE SAME AS WHEN BLOCK EFFECTS RANDOM

SATTERTHWAITE NOT NEEDED

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 BEFORE

INTERVAL MUCH NARROWER WHEN BLOCKS FIXED COMPARED