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;
```

```
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;
```

```
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;
run;
```

```
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;
```

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

The SAS System

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 SAS System

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

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

The SAS System

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

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