

Testing for Lack of Fit in Blocked and Split-Plot Designs

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(joint work with Steven Gilmour)

Outline

- Completely randomized designs
 - Pure error estimation
 - Full treatment model
- Blocked experiments
 - Block-treatment model
 - SAS and other software packages
- Split-plot experiments
 - Block-treatment model
 - Follow-up tests
- Split-split-plot experiments
- Discussion

Lack-of-fit test

- Textbooks emphasize the importance of lack-of-fit testing when fitting response surface models
- The test separates lack of fit from pure error and requires replicated design points or treatments
- The test is quite standard and certain software packages report it when
 - replicates are detected
 - the number of distinct design points exceeds the number of model parameters

Hypotheses tested

Null hypothesis:

our model including main effects, two-factor interactions, ... is adequate

Alternative hypothesis:

the model including main effects, two-factor interactions, ... is not adequate

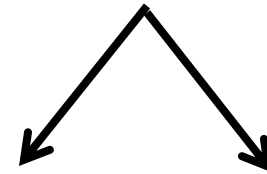
Lack-of-fit test

- Compares two models:
 - a model with as many parameters as treatments in the design
 - a simpler model with only main effects, two-factor interactions, ...
- The former model is the best possible model
- The only thing that that model cannot explain is the true random variation
- It allows us to obtain an unbiased, pure error estimate of the error variance

Decomposition of sum of squares

$$\text{SSTO} = \text{SSR} + \text{SSE}$$

$(n-1) \qquad (p-1) \qquad (n-p)$



$$\text{SSPE} + \text{SSLOF}$$

$(n-m) \qquad (m-p)$

n = number of runs
 p = number of model parameters
 m = number of different treatments in the design

How to get the SSPE?

- Textbooks use the following calculation:

$$SSPE = \sum_{i=1}^m \sum_{j=1}^{n_i} (Y_{ij} - \bar{Y}_i)^2$$

where m is the number of distinct treatments and n_i is the number of occurrences of treatment i

- Alternative approach is to fit the so-called full treatment model and record the SSE from that analysis (which is a one-way ANOVA)

The treatments

Data Yield Maximization Experiment Shipley Chapter 5 With Indication Treatments - JMP Pro

File Edit Tables Rows Cols DOE Analyze Graph SAS Tools Add-Ins View Window Help

Design Custom Design
Criterion D Optimal
Model
Moments Matrix
Design Matrix
Constraint
DOE Dialog
Overlay Plot
Fit Model

Columns (4/0)
Treatment
Time *
Temperature *

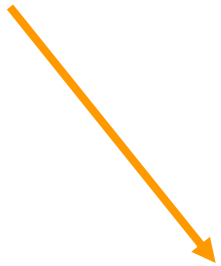
Rows
All rows 15
Selected 4
Excluded 0
Hidden 0
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	Treatment	Time	Temperature	Yield
1	1	580	528	55.9
2	2	360	529	46.7
3	3	480	525	46.8
4	4	720	523	52.8
5	5	360	545	62.1
6	6	660	520	45.7
7	3	480	525	46.6
8	7	420	550	52.6
9	8	360	536	57.8
10	9	454	539	61.9
11	10	720	520	47.7
12	11	630	531	60.0
13	2	360	529	46.8
14	12	510	542	59.4
15	13	360	550	57.3

evaluations done

Full treatment model

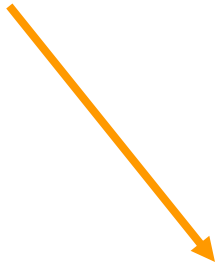
$$Y_{ij} = \mu + \tau_i + \varepsilon_{ij}$$



**response of
observation j
with treatment i**

Full treatment model

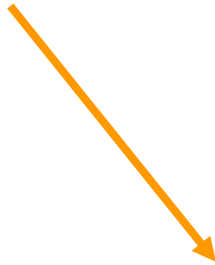
$$Y_{ij} = \mu + \tau_i + \varepsilon_{ij}$$



mean

Full treatment model

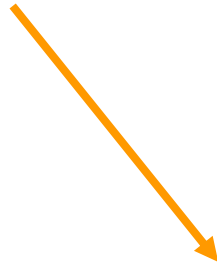
$$Y_{ij} = \mu + \tau_i + \varepsilon_{ij}$$



**effect of
treatment i**

Full treatment model

$$Y_{ij} = \mu + \tau_i + \varepsilon_{ij}$$



**random error of
observation j
with treatment i**

Full treatment model

$$Y_{ij} = \mu + \tau_i + \varepsilon_{ij}$$

- This model has as many parameters as there are treatments in the design
- Therefore, it captures all the systematic variation in the response (i.e., variation due to the fact that we used different treatments)
- The error term therefore only captures pure random variation

Estimation

- We can estimate this model in various ways
 - There are easy formulas based on mean responses (which is what we teach)
 - We can use least squares (which is what software packages do)
- To obtain the pure error estimate of the error variance, we can use
 - the mean squared error of the full treatment model
 - restricted maximum likelihood (REML) applied to the full treatment model

Generalizing the pure error estimation?

- It is not clear how to generalize the MSE approach in the event the experiment is not completely randomized
 - Multiple variance components need to be estimated
 - A pure error estimate will be required for each variance component
 - The designs with randomization restrictions may be unbalanced, non-orthogonal, ...
- Restricted maximum likelihood (REML) is a technique that is generally applicable to estimate one or more variance components for all sorts of designs ...

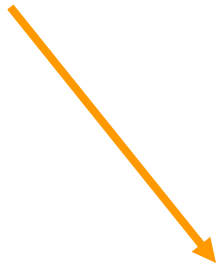
BLOCKED EXPERIMENTS

Pure error in blocked experiments

- Gilmour & Trinca (2000) explain that the pure error can be obtained from the full treatment model augmented with additive block effects
- The assumption that the block effects are additive is a traditional one
 - Hinkelmann & Kempthorne (2008) say it is intrinsic to analyses of experimental data
 - All the work on blocking (fractional) factorial and response surface designs makes the same assumption
 - Software packages make the assumption too

Block-treatment model

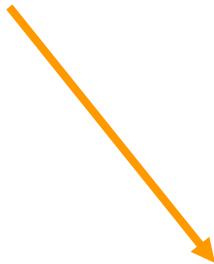
$$Y_{kl(i)} = \mu + \tau_i + \gamma_k + \varepsilon_{kl}$$



**response of
observation l in
block k involving
treatment i**

Block-treatment model

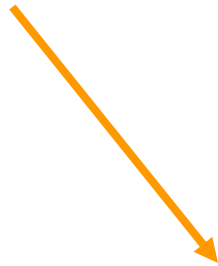
$$Y_{kl(i)} = \mu + \tau_i + \gamma_k + \varepsilon_{kl}$$



mean

Block-treatment model

$$Y_{kl(i)} = \mu + \tau_i + \gamma_k + \varepsilon_{kl}$$



**effect of
treatment i**

Block-treatment model

$$Y_{kl(i)} = \mu + \tau_i + \gamma_k + \varepsilon_{kl}$$

effect of block k

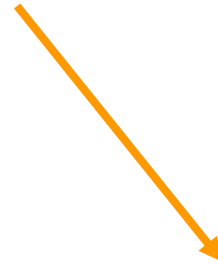
**unknown
fixed effect**

**random block
effect**

i.i.d. $N(0, \sigma_\gamma^2)$

Block-treatment model

$$Y_{kl(i)} = \mu + \tau_i + \gamma_k + \varepsilon_{kl}$$



**random error of
observation l in
block k**

i.i.d. $N(0, \sigma_\varepsilon^2)$

Lack-of-fit test

- Gilmour & Trinca (2000) discuss the case of fixed block effects
- Khuri (1992) discussed a lack-of-fit test for the case of random block effects:
 - Galvanized steel experiment, involving 12 blocks, 2 factors, 9 different treatments and 144 runs
 - He obtained a p-value of 0.225 for the lack of fit test (91 numerator df, 10 denominator df)
 - He used only replicated center points to obtain pure error estimates
 - Our lack-of-fit test also consider the replicates of the other treatments and produces a p-value of 0.0301 (3 numerator df, 98.8 denominator df)

Khuri's 1992 data

Treatment	Factor		Block											
	x_1	x_2	1	2	3	4	5	6	7	8	9	10	11	12
1	-1	-1	1226	1075	1172	1213	1282	1142	1281	1305	1091	1281	1305	1207
2	0	-1	1898	1790	1804	1961	1940	1699	1833	1774	1588	1992	2011	1742
3	2	-1	2142	1843	2061	2184	2095	1935	2116	2133	1913	2213	2192	1995
4	-1	0	1472	1121	1506	1606	1572	1608	1502	1580	1343	1691	1584	1486
5	0	0	2010	2175	2279	2450	2291	2374	2417	2393	2205	2142	2052	2339
5	0	0	1882			2355					2268		2032	
5	0	0	1915			2420					2103		2190	
5	0	0	2106			2240								
6	2	0	2352	2274	2168	2298	2147	2413	2430	2440	2093	2208	2201	2216
7	-1	1	1491	1691	1707	1882	1741	1846	1645	1688	1582	1692	1744	1751
8	0	1	2078	2513	2392	2531	2366	2392	2392	2413	2392	2488	2392	2390
9	2	1	2531	2588	2617	2609	2431	2408	2517	2604	2477	2601	2588	2572

Lack-of-fit test

- We can remove the lack of fit by adding a linear-by-quadratic interaction term to the model
- The p-value then becomes 0.0708 (2 numerator df, 99.1 denominator df)
- R^2 increases from 0.9125 to 0.9147 only
- The pure error estimate for σ_ε^2 was substantially lower when using the block-treatment model

How to achieve that ?

- Response surface model with block effects

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\gamma} + \boldsymbol{\varepsilon}$$

- Block-treatment model

$$\mathbf{Y} = \mathbf{X}_t\boldsymbol{\tau} + \mathbf{Z}\boldsymbol{\gamma} + \boldsymbol{\varepsilon}$$

How to achieve that ?

- Response surface model with block effects

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\gamma} + \boldsymbol{\varepsilon}$$

- Block-treatment model

$$\begin{aligned}\mathbf{Y} &= \mathbf{X}_t\boldsymbol{\tau} + \mathbf{Z}\boldsymbol{\gamma} + \boldsymbol{\varepsilon} \\ &= \mathbf{X}\boldsymbol{\beta} + \mathbf{X}_L\mathbf{L}\boldsymbol{\tau} + \mathbf{Z}\boldsymbol{\gamma} + \boldsymbol{\varepsilon}\end{aligned}$$

- $\mathbf{L}\boldsymbol{\tau}$ represents higher-order terms not included in the response surface model
- We need an F-test for $\mathbf{L}\boldsymbol{\tau} = 0$

How to achieve this ?

- One approach that should work in any software
 - Add a sufficient number of higher-order terms to the model so it has as many terms as the block treatment model
 - Ensure the added effects are estimable
 - Use an F-test to check whether at least one of these effects is significantly different from zero (requires Satterthwaite & Kenward-Roger approach)
- In SAS proc mixed, it is very easy to perform the test

How to achieve this ?

- One approach that should work in any software
 - Add a sufficient number of higher-order terms to the model so it has as many terms as the block treatment model
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 - Use an F-test to check whether at least one of these effects is significantly different from zero (requires Satterthwaite & Kenward-Roger approach)
- In SAS proc mixed, it is very easy to perform the test (because it reports type III tests for the added value of explanatory variables by default)

SAS program

```
data steel;
input block treatment x1 x2 y;
datalines;
1 1 -1 -1 1226
1 2 0 -1 1898
...
12 8 0 1 2390
12 9 2 1 2572;
proc mixed;
class block treatment;
model y = x1 x2 x1*x2 x1*x1 x2*x2 treatment/
ddfm=kr solution;
random block / solution;
run;
```

SAS output

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
x1	0	.	.	.
x2	0	.	.	.
x1*x2	0	.	.	.
x1*x1	0	.	.	.
x2*x2	0	.	.	.
treat	3	98.9	3.10	0.0301

Fit Model - JMP Pro

Model Specification

Select Columns

- 8 Columns
 - x1
 - x2
 - y1
 - block
 - treat
 - y
 - Pred Formula y**
 - Pred Formula y 2

Pick Role Variables

Y: **y** *optional*

Weight: *optional numeric*

Freq: *optional numeric*

Validation: *optional*

By: *optional*

Personality: Standard Least Squares

Emphasis: Minimal Report

Method: REML (Recommended)

Unbounded Variance Components
 Estimate Only Variance Components

Help Run

Recall Keep dialog open

Remove

Construct Model Effects

Add Cross Nest Macros

Degree: 2

Attributes Transform

No Intercept

- x1& RS
- x2& RS
- x1*x1
- x1*x2
- x2*x2
- block& Random
- x1*x1*x2
- x2*x2*x1
- x2*x2*x1*x1

Custom Test

LOF test

Parameter			
Intercept	0	0	0
x1	0	0	0
x2	0	0	0
x1*x1	0	0	0
x1*x2	0	0	0
x2*x2	0	0	0
x1*x1*x2	1	0	0
x2*x2*x1	0	1	0
x2*x2*x1*x1	0	0	1
block[1]	0	0	0
block[2]	0	0	0
block[3]	0	0	0
block[4]	0	0	0
block[5]	0	0	0
block[6]	0	0	0
block[7]	0	0	0
block[8]	0	0	0
block[9]	0	0	0
block[10]	0	0	0
block[11]	0	0	0
block[12]	0	0	0
=	0	0	0

Value	-18.33333333	-14.08231751	41.679539729
Std Error	13.835351864	31.043567768	21.713775735
t Ratio	-1.325107848	-0.453630769	1.9194975686
DFDen	98.550603772	99.059872464	99.583082277
Prob> t	0.1881994732	0.6510868304	0.057783693

Numerator DF	3
DFDen	98.911681468
F Ratio	3.1032353335
Prob > F	0.0300758582

Discussion

- SAS allows a quick and easy lack-of-fit test
- Just like for completely randomized designs, we do not have to think about which could be the missing terms
- Thinking about what terms could be missing is something you only want to do when you know there is a significant lack of fit
- So, it would be great packages other than SAS could make the test available

SPLIT-PLOT EXPERIMENTS

Split-plot experiments

- We can again use the block-treatment model, and the same approaches in SAS and other software packages

Block-treatment model (split-plot data)

$$Y_{kl(i)} = \mu + \tau_i + \gamma_k + \varepsilon_{kl}$$

effect of whole plot k

~~unknown
fixed effect~~

random whole
plot effect

i.i.d. $N(0, \sigma_\gamma^2)$

Split-plot experiments

- We can again use the block-treatment model, and the same approaches in SAS and other software packages
- This generalizes the approach of Vining, Kowalski & Montgomery (2005):
 - They discuss a ceramic pipe experiment with 12 whole plots, 2 hard-to-change factors and 2 easy-to-change factors
 - Their design involves replicated whole plots and whole plots involving one treatment
 - This way, they can easily calculate pure error estimates based on sample variances

WP	Treatment	x_1	x_2	x_3	x_4	y	WP	Treatment	x_1	x_2	x_3	x_4	y
1	1	-1	-1	-1	-1	80.40	7	10	0	-1	0	0	80.07
1	2	-1	-1	-1	1	89.91	7	10	0	-1	0	0	80.79
1	3	-1	-1	1	-1	71.88	7	10	0	-1	0	0	80.20
1	4	-1	-1	1	1	76.87	7	10	0	-1	0	0	79.95
2	17	1	-1	-1	-1	87.48	8	16	0	1	0	0	68.98
2	18	1	-1	-1	1	90.84	8	16	0	1	0	0	68.64
2	19	1	-1	1	-1	84.49	8	16	0	1	0	0	69.24
2	20	1	-1	1	1	83.61	8	16	0	1	0	0	69.20
3	6	-1	1	-1	-1	62.99	9	11	0	0	-1	0	78.56
3	7	-1	1	-1	1	79.91	9	12	0	0	0	-1	74.59
3	8	-1	1	1	-1	49.95	9	14	0	0	0	1	82.52
3	9	-1	1	1	1	63.23	9	15	0	0	1	0	68.63
4	22	1	1	-1	-1	73.06	10	13	0	0	0	0	74.86
4	23	1	1	-1	1	84.45	10	13	0	0	0	0	74.22
4	24	1	1	1	-1	66.13	10	13	0	0	0	0	74.06
4	25	1	1	1	1	73.29	10	13	0	0	0	0	74.82
5	5	-1	0	0	0	71.87	11	13	0	0	0	0	73.60
5	5	-1	0	0	0	71.53	11	13	0	0	0	0	73.59
5	5	-1	0	0	0	72.08	11	13	0	0	0	0	73.34
5	5	-1	0	0	0	71.58	11	13	0	0	0	0	73.76
6	21	1	0	0	0	82.34	12	13	0	0	0	0	75.52
6	21	1	0	0	0	82.20	12	13	0	0	0	0	74.74
6	21	1	0	0	0	81.85	12	13	0	0	0	0	75.00
6	21	1	0	0	0	81.85	12	13	0	0	0	0	74.90

Ceramic pipe example

- Applying REML to the block-treatment model gives the same pure error estimates as Vining, Kowalski & Montgomery (2005)
- REML works for many more designs than the approach of Vining, Kowalski & Montgomery (2005), especially for more efficient designs with less replication
- Our lack-of-fit test produces a p-value of 0.4499 (10 numerator df, 6.96 denominator df)
- So, there is no significant lack-of-fit

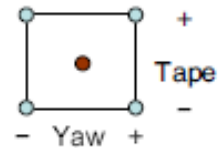
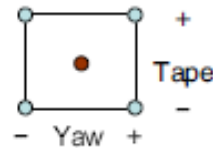
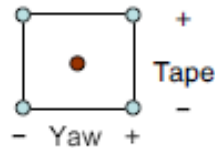
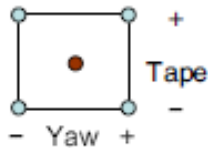
Wind tunnel example

- Simpson, Kowalski & Landman (2004) discuss a 45-run split-plot experiment with 9 whole plots of 5 runs
- There are two hard-to-change and two easy-to-change factors
- There were 25 treatments, 20 of which were duplicated
 - 4 whole plots were replicated completely
 - there was no replication within the whole plots
- Here, the approach of Vining, Kowalski & Montgomery (2005) does not work

Wind tunnel example

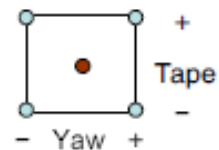
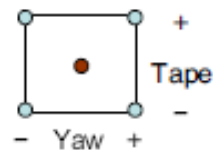
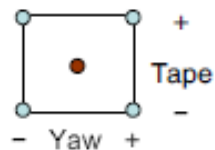
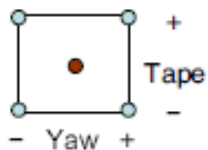
Rep 1

Front RH - Rear RH -	Front RH + Rear RH -	Front RH - Rear RH +	Front RH + Rear RH +
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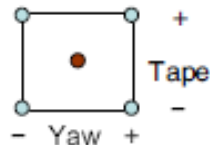


Rep 2

Front RH - Rear RH -	Front RH + Rear RH -	Front RH - Rear RH +	Front RH + Rear RH +
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Front RH 0 Rear RH 0



Wind tunnel example

- For two responses (lift at rear, lift/drag ratio), there was a significant lack of fit
- Removing the lack of fit required all three-factor interactions and some other higher-order terms
- The R^2 values increased slightly to 99%
- Transformations of the response did not help
- We believe the lack of fit may be due to the rounding used for the responses in the paper
- The pure error estimates of σ_γ and σ_ε have the same order of magnitude as the rounding error

FOLLOW-UP LACK-OF-FIT TESTS

Follow-up tests

- Our lack-of-fit test does not distinguish between whole-plot effects, sub-plot effects and whole-plot-by-sub-plot interactions (it is an omnibus test)
- A follow-up test treating the effects of the whole plots as fixed results in a lack-of-fit test for sub-plot effects and whole-plot-by-sub-plot interactions
- If the result is negative, we know that the lack of fit exclusively involves hard-to-change factors

SPLIT-SPLIT-PLOT EXPERIMENTS

Split-split-plot experiments

- The lack-of-fit test discussed can be generalized to cope with split-split-plot, strip-plot, ... experiments
- The same goes for the follow-up test
- We demonstrate this using a split-split-plot design from Trinca & Gilmour (2017)
 - 12 whole plots
 - 24 sub-plots
 - 48 runs
- 29 distinct treatments, 19 of which are duplicated

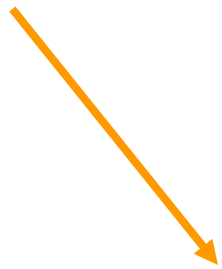
WP	SP	Treat-								y	WP	SP	Treat-							
		ment	x_1	x_2	x_3	x_4	x_5	x_6	ment				x_1	x_2	x_3	x_4	x_5	x_6	y	
1	1	1	-1	-1	-1	-1	-1	-1	96.9	7	13	34	1	-1	-1	-1	-1	1	96.7	
1	1	4	-1	-1	-1	-1	1	1	93.8	7	13	35	1	-1	-1	-1	1	-1	97.1	
1	2	10	-1	-1	1	-1	-1	1	88.7	7	14	41	1	-1	1	-1	-1	-1	138.8	
1	2	15	-1	-1	1	1	1	-1	93.5	7	14	47	1	-1	1	1	1	-1	109.5	
2	3	1	-1	-1	-1	-1	-1	-1	96.5	8	15	34	1	-1	-1	-1	-1	1	91.2	
2	3	4	-1	-1	-1	-1	1	1	90.8	8	15	37	1	-1	-1	1	-1	-1	79.8	
2	4	12	-1	-1	1	-1	1	1	84.8	8	16	41	1	-1	1	-1	-1	-1	129.1	
2	4	14	-1	-1	1	1	-1	1	93.3	8	16	48	1	-1	1	1	1	1	100.3	
3	5	3	-1	-1	-1	-1	1	-1	96.0	9	17	35	1	-1	-1	-1	1	-1	94.2	
3	5	8	-1	-1	-1	1	1	1	104.8	9	17	37	1	-1	-1	1	-1	-1	82.4	
3	6	12	-1	-1	1	-1	1	1	86.5	9	18	47	1	-1	1	1	1	-1	104.3	
3	6	14	-1	-1	1	1	-1	1	93.5	9	18	48	1	-1	1	1	1	1	101.8	
4	7	22	-1	1	-1	1	-1	1	97.6	10	19	49	1	1	-1	-1	-1	-1	92.6	
4	7	23	-1	1	-1	1	1	-1	98.8	10	19	56	1	1	-1	1	1	1	98.7	
4	8	26	-1	1	1	-1	-1	1	121.4	10	20	60	1	1	1	-1	1	1	101.8	
4	8	29	-1	1	1	1	-1	-1	116.1	10	20	62	1	1	1	1	-1	1	103.4	
5	9	20	-1	1	-1	-1	1	1	91.2	11	21	54	1	1	-1	1	-1	1	98.0	
5	9	22	-1	1	-1	1	-1	1	91.3	11	21	56	1	1	-1	1	1	1	95.3	
5	10	27	-1	1	1	-1	1	-1	115.2	11	22	58	1	1	1	-1	-1	1	100.3	
5	10	29	-1	1	1	1	-1	-1	107.1	11	22	63	1	1	1	1	1	-1	99.3	
6	11	20	-1	1	-1	-1	1	1	92.7	12	23	60	1	1	1	-1	1	1	102.9	
6	11	23	-1	1	-1	1	1	-1	93.9	12	23	62	1	1	1	1	-1	1	106.6	
6	12	25	-1	1	1	-1	-1	-1	121.2	12	24	49	1	1	-1	-1	-1	-1	96.4	
6	12	32	-1	1	1	1	1	1	110.6	12	24	54	1	1	-1	1	-1	1	104.0	

True model

$$\begin{aligned} Y_{ijk} = & 100 + 2x_{1i} + x_{2i} + 6x_{3ij} - x_{4ijk} - x_{5ijk} \\ & - x_{6ijk} - x_{1i}x_{2i} + 3x_{1i}x_{3ij} - 2.5x_{1i}x_{4ijk} \\ & + x_{2i}x_{3ij} + 1.5x_{2i}x_{4ijk} - 2x_{3ij}x_{4ijk} \\ & - 6.5x_{1i}x_{2i}x_{3ij} + 5x_{1i}x_{2i}x_{4ijk} + \delta_i \\ & + \gamma_{ij} + \varepsilon_{ijk} \end{aligned}$$

Block-treatment model (split-split-plot data)

$$Y_{klm(i)} = \mu + \tau_i + \gamma_k + \delta_{kl} + \varepsilon_{klm}$$



**response of
observation m in
sub-plot l of whole
plot k involving
treatment i**

Block-treatment model (split-split-plot data)

$$Y_{klm(i)} = \mu + \tau_i + \gamma_k + \delta_{kl} + \varepsilon_{klm}$$



effect of whole plot k



random whole-plot effect

i.i.d. $N(0, \sigma_\gamma^2)$

Block-treatment model (split-split-plot data)

$$Y_{klm(i)} = \mu + \tau_i + \gamma_k + \delta_{kl} + \varepsilon_{klm}$$

effect of sub-plot l in
whole plot k

random sub-
plot effect

i.i.d. $N(0, \sigma_\delta^2)$

SAS program

```
data splitsplitplot;
input wp sp treat x1-x6 y;
datalines;
1 1 1 -1 -1 -1 -1 -1 -1 96.9
1 1 4 -1 -1 -1 -1 1 1 93.8
. . .
12 24 49 1 1 -1 -1 -1 -1 96.4
12 24 54 1 1 -1 1 -1 1 104.0
;
proc mixed data = splitsplitplot;
class wp sp treat;
model y = x1|x2|x3|x4|x5|x6@2 treat/ ddfm = kr
solution;
random wp sp;
run;
```

SAS program

```
* first follow-up lack-of-fit test with whole-  
plot effects fixed;
```

```
proc mixed data = splitsplitplot;
```

```
class wp sp treat;
```

```
model y2 = wp x1|x2|x3|x4|x5|x6@2 treat /
```

```
ddfm = kr solution;
```

```
random sp;
```

```
run;
```

```
* second follow-up lack-of-fit test with whole-  
plot effects and sub-plot effects fixed;
```

```
proc mixed data = splitsplitplot;
```

```
class wp sp treat;
```

```
model y2 = wp sp x1|x2|x3|x4|x5|x6@2 treat /
```

```
ddfm = kr solution;
```

```
run;
```

Discussion

- I have presented the first lack-of-fit test for blocked and split-plot experiments
- The test can be extended to other multi-stratum experiments
- Follow-up tests can be done to identify in what parts of the model the lack of fit occurs
- The tests should be done by default whenever sufficient replication is present and the number of treatments exceeds the number of terms in the response surface model at hand

Design challenge

- Many optimal designs do not have sufficient replication of the treatments to obtain pure error estimates of all variance components
- Hence, we need design construction methods that give
 - Efficient designs
 - Enough replication for pure error estimation
 - More treatments than parameters in the response surface model considered
- Gilmour & Trinca (2017) and Mylona, Gilmour & Goos (2017) set steps in this direction

Testing for Lack of Fit in Blocked and Split-Plot Designs

Peter Goos

(joint work with Steven Gilmour)