Sveriges lantbruksuniversitet
Swedish University of Agricultural Sciences

Randomized block trials with spatial correlation

Workshop in Mixed Models
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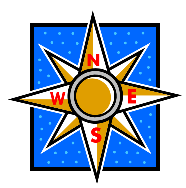
Johannes Forkman, Field Research Unit, SLU

Reseeding and extra fertilization in spring barley

Treatment
A: No extra N
B: 30 kg extra N
C: 60 kg extra N
D: Reseeding, no extra N
E: Reseeding + 30 kg extra N
F: Reseeding + 60 kg extra N
G: Reseeding + 90 kg extra N

Example from Anders Ericsson,
Swedish Rural Economy and Agricultural Societies, HS Konsult

Design



- Four replicates
- Altogether 28 plots in a single row
- Seven treatments (A-G)

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28
C	A	G	D	E	F	B	G	E	B	C	A	F	D	B	A	G	E	D	F	C	E	A	C	F	G	B	D

Randomized complete block analysis

Yield = Treatment + Block + E

Fixed effects of Treatment

Random effects of Block and E

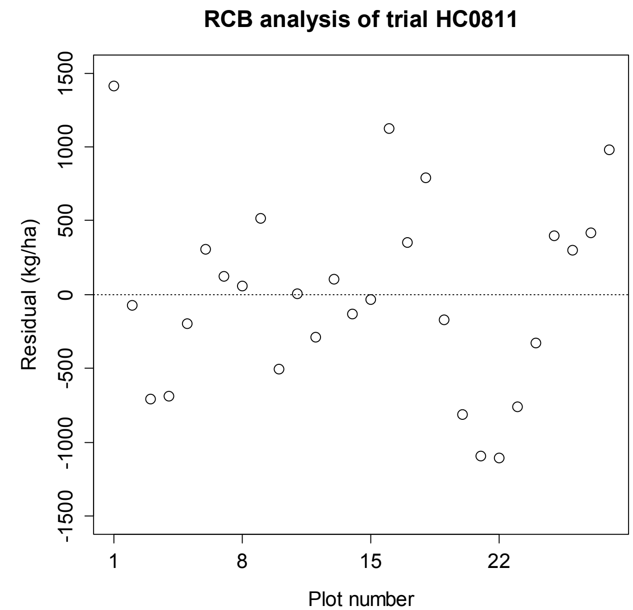
The errors (E) are normally distributed and **independent**

RCB analysis

Trial HC0811

	Degrees of freedom			
	Num	Den.	F	P
Treatment	6	21	1,18	0,352

The block variance was estimated to 0



Systematic error

- The plots differ, so
- If we subjectively decide to investigate A on some plots and B on some other plots, then
- We do not compare the treatments on equal terms, and
- There will be a systematic error in the comparison of A and B.

Randomization is important!

- Randomization justifies the assumption of independent errors
- Randomization is strongly recommended
- Nevertheless, it is possible to take spatial correlation into account

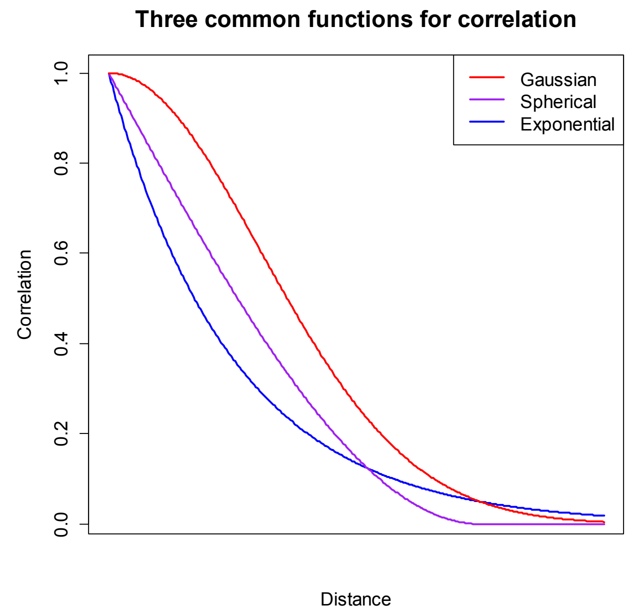
Model with spatial correlation

Yield = Treatment + Block + E

Fixed effects of Treatment

Random effects of Block and E

Errors (E) are normally distributed and **correlated**



How to choose correlation function?

The Akaike information criterion

$$AIC = -2L + 2p$$

AIC should be as small as possible!

L is the (REML) log likelihood

p is the total number of parameters*) in the model

*) In SAS, p is the total number of variances and covariances
In R, p is the total number of fixed parameters, variances and covariances

Analysis using SAS

```
proc mixed  data = HC0811 ;
    class Block Treatment ;
    model Yield = Treatment / ddfm = kr ;
    random Block ;
    repeated / type = sp(sph)(Plot) subject = intercept ;
    lsmeans Treatment / pdiff adjust = Tukey adjdfe = row ;
run ;
```

Correlation in two dimensions: sp(sph)(x y)

Other structures: sp(exp), sp(gau)

Analysis using R

```
library(nlme)
Model <- lme(Yield ~ Treatment, random = ~ 1 | Block,
          na.action = na.exclude, data = HC0811,
          corr = corSpher(form = ~ Plot))
summary(Model)
anova(Model)
library(multcomp)
summary(glht(Model, linfct = mcp(Led = "Tukey")))
```

Correlation in two dimensions: corSpher(form = ~ x + y)

Other structures: corExp, corGaus

Analysis with spatial correlation

Trial HC0811

	Degrees of freedom			
	Num.	Den.	F	P
Treatment	6	20,8	2,91	0,032

Analysis using the mixed procedure, SAS (Kenward and Roger's method)

Spherical correlation

The block variance was estimated to 0

Both trials
Model without spatial correlation

Yield = Trial + Treatment + Trial×Treatment + Block(Trial) + E

Fixed effects of Trial, Treatment and Trial×Treatment

Random effects of Block(Trial) and E

Errors (E) are normally distributed and **independent**

Analysis without spatial correlation

	Degrees of freedom			
	Num.	Den.	F	P
Trial	1	40	22,65	<,0001
Treatment	6	40	2,37	0,0474
Trial×Treat.	6	40	0,64	0,6999

The block variance was estimated to 0

Model without spatial correlation

Both trials

Treatment	Mean	Tukey
A: No extra N	1479	a
B: 30 kg extra N	1882	a
C: 60 kg extra N	1559	a
D: Reseeding, no extra N	1726	a
E: Reseeding + 30 kg extra N	1871	a
F: Reseeding + 60 kg extra N	2134	a
G: Reseeding + 90 kg extra N	2361	a

Different letters indicate significant differences at level 0.05.

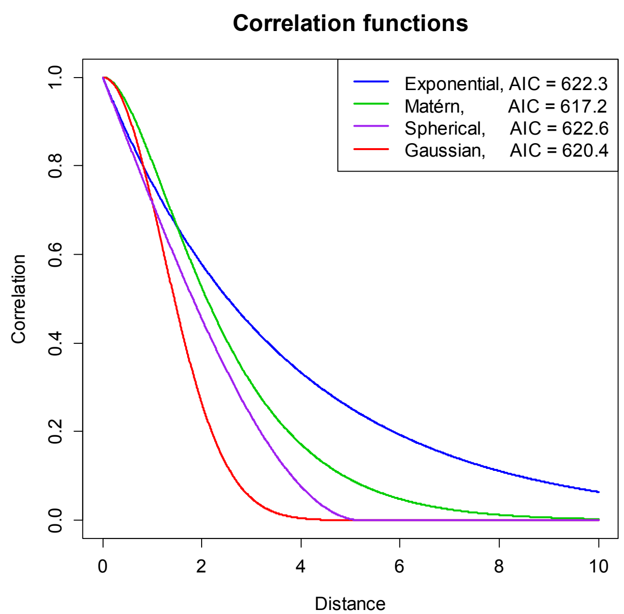
Model with spatial correlation

Yield = Trial + Treatment + Trial×Treatment + Block(Trial) + E

Fixed effects of Trial, Treatment and Trial×Treatment

Random effects of Block(Trial) and E

Errors (E) are normally distributed and **correlated**



Bertil Matérn

Matérn correlation

- Named after Bertil Matérn, professor in mathematical statistics applied to forest sciences, SLU, 1977-1981
- Has a smoothness parameter, v, which determines the shape.
  - $v = 1/2$ gives the exponential structure
  - $v \to \infty$ gives the gaussian structure
- Available in SAS proc mixed

Model with spatial correlation

	Degrees of freedom			
	Num.	Den.	F	P
Trial	1	4.6	5.60	0.069
Treatment	6	18	137.29	< 0.001
Trial×Treat	6	18	0.96	0.481

Analysis using the mixed procedure, SAS (Kenward and Roger's method)

Matérn correlation

The block variance was estimated to 0

Model with spatial correlation

Both trials

Treatment	Mean	Tukey
A: No extra N	1539	d
B: 30 kg extra N	1782	cd
C: 60 kg extra N	1851	bc
D: Reseeding, no extra N	1734	cd
E: Reseeding + 30 kg extra N	2131	ab
F: Reseeding + 60 kg extra N	2266	a
G: Reseeding + 90 kg extra N	2330	a

Different letters indicate significant differences at level 0.05.

Summary

- Randomization justifies the assumption of independent errors.
- In mixed models, errors need not be independent
- Spatial analysis can improve precision

Strategy for spatial analysis

Randomization and blocking is proven good practice

Spatial analysis works well and may improve precision

Strategy

1. Use blocking and randomization
2. Use spatial analysis as an add-on

Müller et al. (2010)