Mixed models using the SAS® PROC MIXED procedure:

A simulation based approach to assess sample size and resolve a daily biostatistician's dilemma for preclinical trials...

Louise Baschet – Catherine Hessler

SFDS Working Group

- SFDS "Groupe Biopharmacie et Santé"
- Good Preclinical Statistical Practices Working Group
 - L. Baschet, L. Maïofiss, N. Velasquez (Servier)
 - D. Colongo, K. Florin, G. Mathieu, M. Rosé (sanofi aventis R&D)
 - A. De Montfort, C. Hessler *(sanofi pasteur)*
 - E. Houivet (CIT)
 - J. Marsais (Ipsen)
 - C. Phalyvong (SOLADIS)

• • Our context: preclinical research area

- Seen by the biologist
 - Comparison between treatments
 - Limited number of subjects
 - Repeated measures over time
- Seen by the statistician
 - Many experiments related to longitudinal data
 - Small sample size
 - Potentially missing data

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 $\textcircled{} \ensuremath{\mathbb{V}}$ Proc mixed is commonly used

- More suitable than GLM for repeated measures
- Management of missing data
- Better modeling of the correlations between observations
- But
 - Multiple options not well understood to date
 - Choice of the var/cov structure sometimes tricky



- Evaluate the impact of various options in the proc mixed
 - on alpha
 - on power
- Provide sample size evaluation by a simulation program



• • • Studied designs

- Classical and simple experimental design
 - 2 groups (control and treated)
 - Repeated measures over time
- Focus on 4 common response profiles
 - With or without interaction and effect
 - 3 and 10 time points

-	case 0	case 1	case 2	case 3
interaction	0	0	0	Х
treatment	0	Х	Х	Х
time	0	0	Х	Х





Result

Count of significant p-values for :

- Group effect according to interaction
- Interaction
- Time effect



- Simulations under H0
 - α threshold: 10%

No group effect



No interaction effect







No time effect







• Results (1): method



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 - With ML, α is uncontrolled for some very low sample size!





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♦ REML is kept afterwards



• Results (2): variance-covariance matrix



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 - If analyzed with AR(1), α risk is increased for a CS structure



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 - For group effect:
 - If analyzed with AR(1), α risk is increased for a CS structure







- Results (2): variance-covariance matrix
 - For interaction effect:
 - No impact of the matrices for a CS structure



α-level control

- Results (2): variance-covariance matrix
 - For interaction effect:
 - No impact of the matrices for a CS structure
 - If analyzed with CS α risk is increased for a AR(1) structure when ρ is high
 - Conclusions are the same for time effect



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• Without interaction (cases 1 and 2)



- Without interaction (cases 1 and 2)
 - For a data structure AR(1)
 - no impact of the matrices
 - power is higher as ρ is lower



• Without interaction (cases 1 and 2)

- For a data structure AR(1)
 - no impact of the matrices
 - power is higher as ρ is lower
- For a data structure CS
 - AR(1) analysis gives a higher power
 - power is higher as ρ is lower



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- With interaction (case 3)
 - At the middle time-point (T6)



- With interaction (case 3)
 - At the middle time-point (T6)
 - no impact of p and matrices





Impact of the variance-covariance matrix on power for the interaction and time effect

- Interaction effect (case 3)
 - Whatever the data structure is
 - power is higher with CS
 - especially when ρ is high

Impact of the variance-covariance matrix on power for the interaction and time effect

- Interaction effect (case 3)
 - Whatever the data structure is
 - power is higher with CS
 - especially when ρ is high
- Time effect without any interaction (case 2)
 - Whatever the data structure is
 - power is higher with CS
 - especially when p is high



• REML has to be chosen to control the α -risk



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	To control α	To maximize (1-β)
Group effect	CS	AR(1)
Interaction or time effect	AR(1)	CS



- REML has to be chosen to control the α -risk
- It is recommended to choose the matrix according to the primary objective

	To control α	To maximize (1-β)	To estimate n <i>(worst case)</i>
Group effect	CS	AR(1)	CS
Interaction or time effect	AR(1)	CS	AR(1)

Perspectives

- Missing and/or unbalanced data
- Heterogeneous variances
- More than 2 groups and α adjustment
- Time as a continuous variable
- Other types of variance matrix

References

- Linear Mixed Models for Longitudinal Data, Verbeke G., Molenberghs G., Springer Series in Statistics, 2000
- Applied Mixed Models in Medicine, Brown H., Prescott R., Statistics in practice, 1999
- Tutorial in Biostatistics: Modelling covariance structure in the analysis of repeated measures data, Littell R. C. and al., Statistics in Medicine, 2000
- SAS institute, Inc. (1999) SAS/STAT user's Guide, V8. Cary, NC: SAS Institute



Analysed using proc mixed with repeated statement Y_{ijk}=μ + group_i + time_j + groupxtime_{ij} + ε_{ijk} ε ~ iid(0,R)

proc mixed method=&method.;

class group time animal ; model Y = group time group*time / ddfm=satterth; repeated time / subject=animal(group) type=&typvarmixed.;

back



3 times : rejection frequency of time effect



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10 times : rejection frequency of time effect



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Use of AIC / BIC to select the suitable matrix



- Simulations are validated for these two simple structures
- But it is possible to make mistakes is case of low correlation !

Impact of ML and REML on α level (10 times)

1000 simulations

n = 5

			model_simul					
			AR(1)			CS		
			Effect			Effect		
			group	group*time	time	group	group*time	time
mode	l method	ddfm						
AR(1)	ML	Déf(BW)	11.30%	22.80%	22.10%	24.40%	18.50%	18.30%
AR(1)	ML	KR	14.20%	20.10%	19.50%	27.90%	16.30%	16.60%
AR(1)	ML	Satterth	13.20%	23.20%	22.30%	26.70%	18.50%	18.30%
CS	ML	Déf(BW)	13.30%	25.10%	23.60%	12.90%	22.70%	22.30%
CS	ML	KR	13.90%	26.00%	24.20%	14.10%	23.40%	22.90%
CS	ML	Satterth	13.90%	26.00%	24.20%	14.10%	23.40%	22.90%
			$\mathbf{AP}(1)$			CS		
			Effect			Effect		
			Effect			Effect		
			group	group*time	time	group	group*time	time
nodel	method	ddfm						
AR(1)	REML	Déf(BW)	8,10%	11,00%	10,10%	20,30%	8,70%	9,00%
AR(1)	REML	KR	10,00%	8,70%	7,90%	22,20%	6,80%	7,10%
AR(1)	REML	Satterth	8,90%	10,30%	9,50%	21,60%	8,40%	8,70%
CS	REML	Déf(BW)	9,80%	16,10%	14,90%	9,50%	9,90%	10,00%
CS	REML	KR	9,80%	16,10%	14,90%	9,50%	9,90%	10,00%
CS	REML	Satterth	9,80%	16,10%	14,90%	9,50%	9,90%	10,00%