Session 53

milagros.garcia@toulouse.inra.fr

Comparisons of three models for canalising selection or genetic robustness

M. Garcia

I. David, H. Garreau, N. Ibañez-Escriche, J. Mallard,
J.P Masson, D. Pommeret, C. Robert-Granié

L. Bodin

Introduction

- Two quantitative genetic models
  - SanCristobal et al. (1998)
  - Mulder et al. (2007)

- New features
  - A new model
  - Comparison of three existing models
  - A software that implements these models

General model

Homoscedastic linear mixed model:

$$y_{ij} = \mu_{ij} + u_i + \varepsilon_{ij}^{*} \quad \text{with} \quad \varepsilon_{ij}^{*} \sim N(0, \sigma^2)$$

$$y_{ij} = \mu_{ij} + u_i + \sigma\varepsilon_{ij} \quad \text{with} \quad \varepsilon_{ij} \sim N(0,1)$$

μ : *fixed effects*

u : *genetic effects*

General model

Homoscedastic linear mixed model:

$$y_{ij} = \mu_{ij} + u_i + \varepsilon_{ij}^{*} \quad \text{with} \quad \varepsilon_{ij}^{*} \sim N(0, \sigma^2)$$

$$y_{ij} = \mu_{ij} + u_i + \sigma\varepsilon_{ij} \quad \text{with} \quad \varepsilon_{ij} \sim N(0,1)$$

μ : *fixed effects*

u : *genetic effects*

Heteroscedastic linear mixed model:

$$y_{ij} = \mu_{ij} + u_i + \sigma_{ij}\varepsilon_{ij}$$

$$y_{ij} = \mu_{ij} + u_i + f(\eta_{ij}, v_i)\varepsilon_{ij}$$

η : *fixed effects*

v : *genetic effects*

Different modelisations of $\sigma_{ij} = f(\eta_{ij}, v_i)$

- SanCristobal et al. 1998

$$\sigma_{ij} = \exp^{\left(\frac{\eta_{ij}+v_i}{2}\right)} \varepsilon_{ij} \qquad \text{Exp}$$

- Mulder et al. 2007

$$\sigma_{ij} = \sqrt{\eta_{ij} + v_i}\ \varepsilon_{ij} \qquad \text{Sqr}$$

- Garcia et al. 2009 (working progress)

$$\sigma_{ij} = (\eta_{ij} + v_i)\varepsilon_{ij} \qquad \text{Lin}$$

Simulated data

2000 related animals (5 generations, 1600 animals with records)
3 repeated records

	Mean	Variance
Fixed effects	$F1, F2$	$F1, F3$
Permanent effect	$\sigma^2_p = 10$	$\sigma^2_{\tilde{p}} = 0.5$
Genetic effect	$\sigma^2_u = 20$	$\sigma^2_v = 0.3$
Genetic correlation	$\rho = -0.6 \; ; \; 0 \; ; \; 0.3$	

Simulated data using each of the three models

Estimation parameters crossing models

Comparison criteria : estimated values, std, DIC

Simulation Results (estimated values)

each data with its model

	Simulated value	Estimated value
σ_u^2	19.83	18.268 ; 20.526
σ_v^2	0.2972	0.249 ; 0.318
ρ	0.2915	0.277 ; 0.338

Simulation Results (standard deviation)

each data with its model

	Standard deviation of estimated value		
	Exp	Sqr	Lin
σ_u^2	1.553	1.361	0.368
σ_v^2	0.065	0.023	0.022
ρ	0.080	0.135	0.044

Simulation Results (standard deviation)

each data with its model

	Standard deviation of estimated value		
	Exp	Sqr	Lin
σ_u^2	1.553	1.361	0.368
σ_v^2	0.065	0.023	0.022
ρ	0.080	0.135	0.044

Simulation Results (DIC)

Data / Model	Exp	Sqr	Lin
Exp	19183		
Sqr	20322		
Lin	18294		

Simulation Results (DIC)

Data / Model	Exp	Sqr	Lin
Exp	19183	10471	
Sqr	20322	10461	
Lin	18294	10463	

Simulation Results (DIC)

Data / Model	Exp	Sqr	Lin
Exp	19183	10471	13536
Sqr	20322	10461	14930
Lin	18294	10463	12938

Real rabbit data

3669 related rabbit does from INRA selection experiment

68712 birth weight records

5 samples (80% for estimation, 20 % for prediction)

	Mean	Variance
Fixed effects	$F1 \ldots F5$	$F1 \ldots F5$
Permanent effect	σ_p^2	$\sigma_{\tilde{p}}^2$
Genetic effect	σ_u^2	σ_v^2
Genetic correlation	ρ	

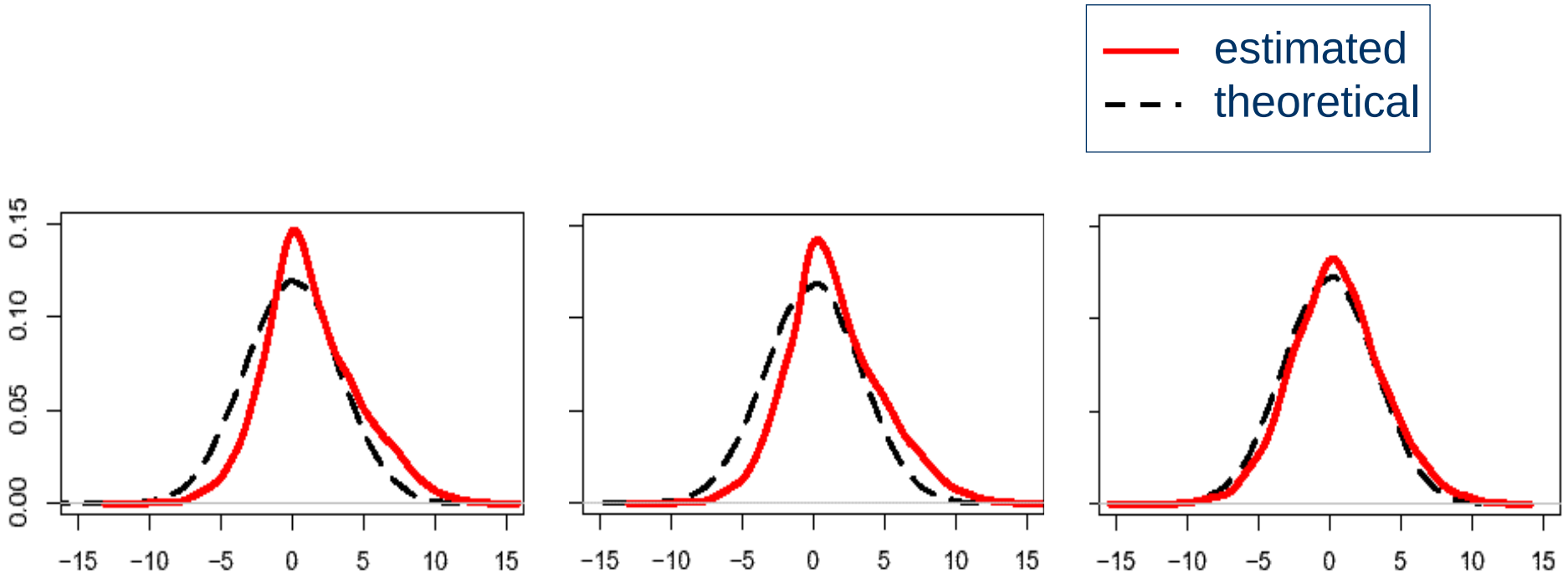
Estimation parameters using each of three models

Comparison criteria : DIC, $\rho(y, \hat{y})$, $Var(y - \hat{y})$

Real data results

		Comparison criteria		
		Exp	Sqr	Lin
estimation	DIC	312145	311372	310463
	$Var(y - \hat{y})$	105.0	104.9	85.7
prediction	$\rho(y, \hat{y})$	0.499	0.499	0.498

Posterior distribution of u



Exp Sqr Lin

A user friendly software : GSEVMM v.4

- Extension from GSEVM (Sorensen D. and Ibañez N.)
- Fortran 90
- Bayesian-MCMC methods
  - Gibbs and Adaptative Metropolis Hasting
- Three possible structural mixed linear models

Conclusions and prospects

- Conclusions
  - Few differences between models
  - DIC values better for Sqr and Lin
  - Lin is an interesting alternative model

- Further works and extensions
  - Comparisons of genetic progress
  - Improvements of GSEVM v4