

Estimation of genetic differences in environmental variance

Han Mulder



Contents

- Gibbs sampling algorithm
- Iterative BLUP procedure
- Double hierarchical generalized linear models
(Lars Ronnegard (Ronnegard et al., 2010))

Gibbs sampling algorithm

Quantitative genetic model

- Genetic differences in environmental variance

$$P = \mu + A_m + \chi \sqrt{\sigma_E^2} + A_v$$

$$G = \begin{bmatrix} \sigma_{A_m}^2 & r\sigma_{A_m}\sigma_{A_v} \\ r\sigma_{A_m}\sigma_{A_v} & \sigma_{A_v}^2 \end{bmatrix}$$

Statistical model

$$\begin{bmatrix} \mathbf{P} \\ \mathbf{t}(e_p^2) \end{bmatrix} = \begin{bmatrix} \mathbf{X}\mathbf{b}_p \\ \mathbf{X}\mathbf{b}_{te^2} \end{bmatrix} + \begin{bmatrix} \mathbf{Z}\mathbf{u}_p \\ \mathbf{Z}\mathbf{u}_{te^2} \end{bmatrix} + \begin{bmatrix} \mathbf{e}_p \\ \mathbf{e}_{te^2} \end{bmatrix}$$

$$\begin{bmatrix} \mathbf{u}_p \\ \mathbf{u}_{te^2} \end{bmatrix} \sim N(0, \mathbf{A} \otimes \mathbf{G})$$

$$\mathbf{G}_s = \begin{bmatrix} \sigma_{u_p}^2 & r\sigma_{u_p}\sigma_{u_{te^2}} \\ r\sigma_{u_p}\sigma_{u_{te^2}} & \sigma_{u_{te^2}}^2 \end{bmatrix}$$

$$\begin{bmatrix} e_p \\ e_{te^2} \end{bmatrix} \sim N(0, R_i \otimes I)$$

$$R_i = \begin{bmatrix} \sigma_{e_{p,i}}^2 & r\sigma_{e_p}\sigma_{e_{te^2}} \\ r\sigma_{e_p}\sigma_{e_{te^2}} & \sigma_{e_{te^2}}^2 \end{bmatrix}$$

$$\sigma_{e_{p,i}}^2 = \overline{\sigma_{e_p}^2} + f * u_{te^2,i}$$

- Cube root transformation of squared residual
 - = Wilson and Hilferty (1931) transformation of Chi-squared distributed variable to normally distributed variable

- Variance shrinkage parameter
 - Regression of residual variance on $u_{te^2}^2$
 - Background: residual variance \neq environmental variance

Algorithm

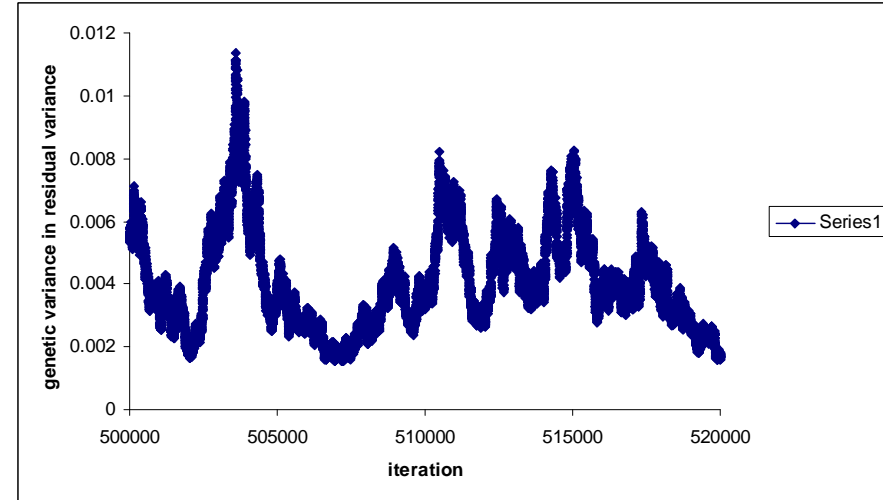
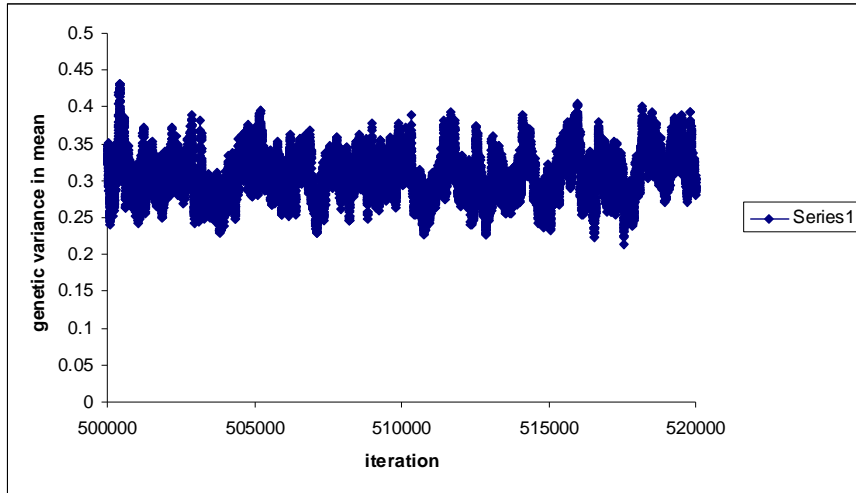
- Run 10000 MCMC cycle with the univariate model on the phenotype only (first row)
- In cycle 10001, use the cube root of the squared residuals of cycle 10000.
- Run bivariate model for 100 cycles.
 - In each Gibbs cycle 20 MH-cycles are performed to update the variance-covariance matrices (important when $r \neq 0$)
 - Use of priors on wishart distribution
- Update the cube root of the squared residuals.
- Continue with 3
- Finished after 500,000 Gibbs cycles

Simulation

- Simulation according to simplified genetic model
 - No fixed effect yet on mean or environmental variance

- Structured population
 - 5 discrete generations
 - 50 bulls with each 40 daughters, bulls are sired by 10 randomly selected bull-sires
 - No selection

Results



- Mixing better for mean model than for residual variance model
- Effective sample size is around 100-200 for varav when using 400,000 iterations (500,000 and 100,000 burn-in)

Results

Effect of varav

Varied parameter	$\sigma_{a_m}^2$						
	True	mean	median	SD within	SD across	5%	95%
$\sigma_{A_v}^2$	0.3	0.294	0.294	0.023	0.020	0.257	0.332
0.00		0.279	0.279	0.024	0.025	0.241	0.318
0.05		0.256	0.256	0.025	0.028	0.216	0.298
0.10							
	r_a						
0.00	0	0.034	0.035	0.160	0.093	-0.230	0.299
0.05		-0.002	-0.003	0.143	0.130	-0.238	0.234
0.10		-0.003	-0.003	0.113	0.119	-0.190	0.183
	$\sigma_{A_v}^2$						
	Cube root						
0.00	0.00E+00	1.76E-03	1.69E-03	5.01E-04	1.08E-04	1.08E-03	2.69E-03
0.05	7.30E-03	2.68E-03	2.58E-03	8.08E-04	3.80E-04	1.55E-03	4.16E-03
0.10	2.01E-02	5.38E-03	5.25E-03	1.46E-03	1.00E-03	3.27E-03	7.92E-03

Results

Effect van heritability

Varied parameter	σ_{am}^2								
	σ_{am}^2	true	mean	median	SD within	SD across	5%	95%	
	0.1	= σ_{am}^2	0.098	0.097	0.013	0.009	0.076	0.121	
	0.3		0.279	0.279	0.024	0.025	0.241	0.318	
	0.5		0.479	0.479	0.028	0.031	0.433	0.525	
			r_a						
	0.1	0	0.018	0.019	0.146	0.123	-0.223	0.258	
	0.3		-0.002	-0.003	0.143	0.130	-0.238	0.234	
	0.5		-0.008	-0.008	0.139	0.102	-0.236	0.221	
		Cube root	σ_{Av}^2						
	0.1	4.59E-03	3.58E-03	3.45E-03	1.08E-03	6.69E-04	2.05E-03	5.55E-03	
	0.3	7.30E-03	2.68E-03	2.58E-03	8.08E-04	3.80E-04	1.55E-03	4.16E-03	
	0.5	1.54E-02	2.08E-03	2.00E-03	5.95E-04	2.73E-04	1.26E-03	3.18E-03	

Results

Effect van rg

Varied parameter	$\sigma_{a_m}^2$							
	r_A	true	mean	median	SD within	SD across	5%	95%
0	0.3	0.279	0.279	0.024	0.025	0.241	0.318	
0.25		0.291	0.290	0.024	0.028	0.252	0.330	
0.5		0.280	0.279	0.024	0.022	0.242	0.319	
0.75		0.299	0.299	0.025	0.024	0.260	0.342	
		r_a						
0	= r_A	-0.002	-0.003	0.143	0.130	-0.238	0.234	
0.25		0.211	0.214	0.136	0.101	-0.018	0.431	
0.5		0.350	0.355	0.126	0.136	0.136	0.549	
0.75		0.571	0.578	0.101	0.056	0.394	0.723	
		Cube root $\sigma_{A_v}^2$						
0	7.30E-03	2.68E-03	2.58E-03	8.08E-04	3.80E-04	1.55E-03	4.16E-03	
0.25		2.73E-03	2.63E-03	8.10E-04	4.43E-04	1.60E-03	4.22E-03	
0.5		2.91E-03	2.80E-03	8.41E-04	4.23E-04	1.75E-03	4.43E-03	
0.75		3.21E-03	3.13E-03	7.89E-04	4.15E-04	2.06E-03	4.63E-03	

Discussion

- Effect of priors is quite large
- With non-normal distributed environmental effects (t or X^2) you may pick up as genetic variation in environmental variance
- With homogeneous residual variance you find slightly less varav, but model is much more stable

Thank you for your attention

© Wageningen UR

