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DHGLMF90: A software tool using double hierarchical generalized linear models for estimating the genetic heterogeneity of residual variance

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Motivation

Differences in residual variances among individuals are common

1. Interest in selecting uniform animals expressing consistent responses
2. Modeling heteroskedastic residuals when estimating breeding values
3. Canalisation: Selection to reduce the environmental variability

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Motivation (cont.)

Hierarchical single-trait model

Mean
Trait performance

\+

Dispersion
Variability

A global criterion
Selection for mean and against the variance

Selection index: $(\bar{y} - y_0)^2 + S_y^2$

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Problem

Bayesian methods

- Can estimate heteroskedastic residuals
- Metropolis-Hastings algorithm
- Inference with posterior distribution
- **Slow and inefficient**

Double Hierarchical GLM (DHGLM)

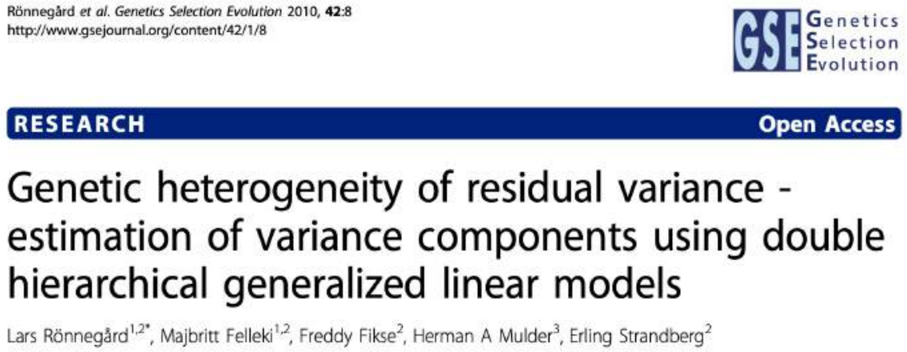
- Lee & Nelder, 2006
- Rönnegård et al., 2010
- No inference with posterior distribution
- **Faster counterpart → Alternative**

Objective

Develop a software named DHGLMF90 to implement DHGLM to estimate heterogeneous residual variances and breeding values

DHGLM

- Similar performance
  - Bayesian methods
  - H-Likelihood
- Bivariate normal-normal model
- Challenges
  - Convergence issues
  - 27/100 replicates failed



Rönnegård *et al. Genetics Selection Evolution* 2010, **42**:8
http://www.gsejournal.org/content/42/1/8

RESEARCH **Open Access**

Genetic heterogeneity of residual variance - estimation of variance components using double hierarchical generalized linear models

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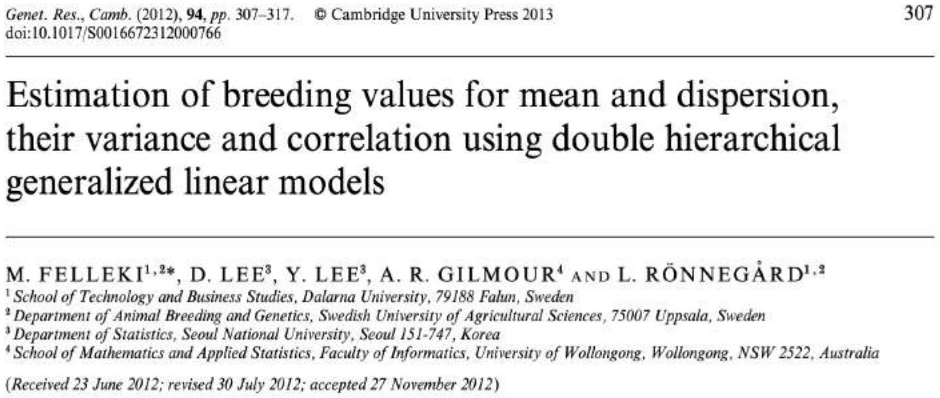

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Estimation of breeding values for mean and dispersion, their variance and correlation using double hierarchical generalized linear models

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Algorithm

Iteratively calculates variance components and leverages for a bivariate model

Initialize weights $\Sigma^{-1} = \begin{bmatrix} \boldsymbol{\phi}^{-1} & \mathbf{0} \\ \mathbf{0} & \mathrm{diag}(\frac{1-q}{2}) \end{bmatrix}$ and working variables Z_d

Fit correlation structure $\mathbf{G} \otimes \mathbf{A}$ between a and a_d, but y and Z_d conditional uncorrelated

Update σ^2, e and q, and thereby Z_d and $\mathrm{diag}((1-q)/2)$ in $\boldsymbol{\Sigma}^{-1}$

Repeat step 2

Update $\boldsymbol{\phi}^{-1}$ and update $\boldsymbol{\Sigma}^{-1}$

Reweighted
least squares
Algorithm (IRWLS)

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Improving the algorithm

$$H = \begin{bmatrix} X^T \boldsymbol{\phi}^{-1} X & X^T \boldsymbol{\phi}^{-1} Z \\ Z^T \boldsymbol{\phi}^{-1} X & Z^T \boldsymbol{\phi}^{-1} Z + \frac{1}{(1-\rho^2)\sigma_a^2} A^{-1} \end{bmatrix}$$

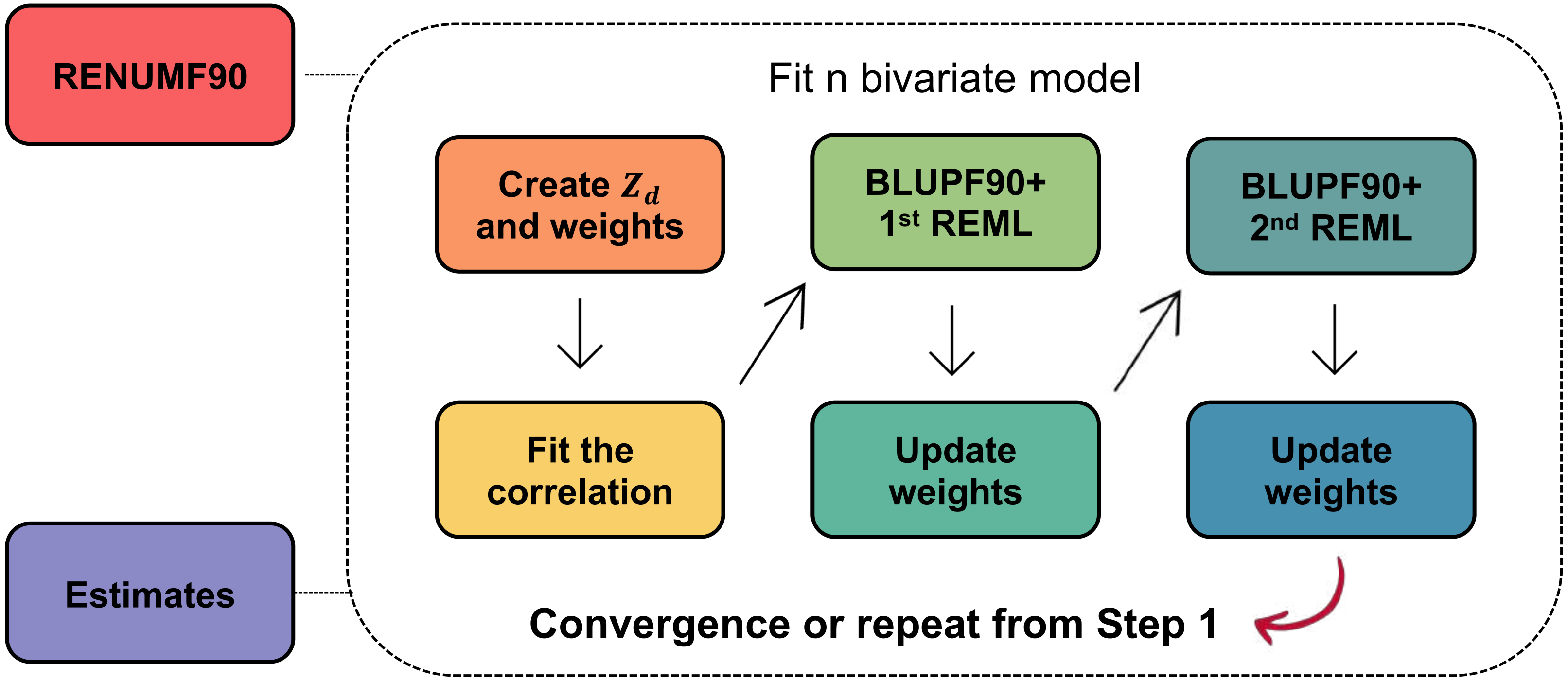
Leverages

Felleki et al., (2012)

$$C = \begin{bmatrix} X^T \boldsymbol{\phi}^{-1} X & 0 & X^T \boldsymbol{\phi}^{-1} Z & 0 \\ 0 & X_d^T \operatorname{diag}(\frac{1-q}{2}) X_d & 0 & X_d^T \operatorname{diag}\left(\frac{1-q}{2}\right) Z \\ Z^T \boldsymbol{\phi}^{-1} X & 0 & Z^T \boldsymbol{\phi}^{-1} Z + \frac{1}{(1-\rho^2)\sigma_a^2} A^{-1} & -\frac{\rho}{(1-\rho^2)\sqrt{\sigma_a^2 \sigma_{a_d}^2}} A^{-1} \\ 0 & Z^T \operatorname{diag}(\frac{1-q}{2}) X_d & -\frac{\rho}{(1-\rho^2)\sqrt{\sigma_a^2 \sigma_{a_d}^2}} A^{-1} & Z^T \operatorname{diag}\left(\frac{1-q}{2}\right) Z + \frac{1}{(1-\rho^2)\sigma_{a_d}^2} A^{-1} \end{bmatrix}$$

DHGLMF90 flowchart

DHGLMF90 uses BLUPF90+ to estimate variance components using REML



RENUMF90

Fit n bivariate model

Create Z_d and weights

Fit the correlation

BLUPF90+ 1st REML

Update weights

BLUPF90+ 2nd REML

Update weights

Convergence or repeat from Step 1

Estimates

Renumber the data

Initialize weights $\boldsymbol{\Sigma}^{-1}$ and Z_d

Fit the correlation $\mathbf{G} \otimes \mathbf{A}$ for a/a_d

REML for the mean part

Update σ_a^2, Zd and $\mathrm{diag}((1-q)/2)$

REML for the dispersion part

Update $\sigma_{a_d}^2$, $\boldsymbol{\phi}^{-1}$ and weights $\boldsymbol{\Sigma}^{-1}$

VCE + EBV + Residuals

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Data sets

	Data 1	Data 2
Trait	Pigs littler size	Daily feed intake
Animals in the pedigree	51	5460
Records	306	109680
Effects	Additive + PE	Additive + PE

↓

Simulated data

Felleki et al., 2012

Test performance

↓

Real data

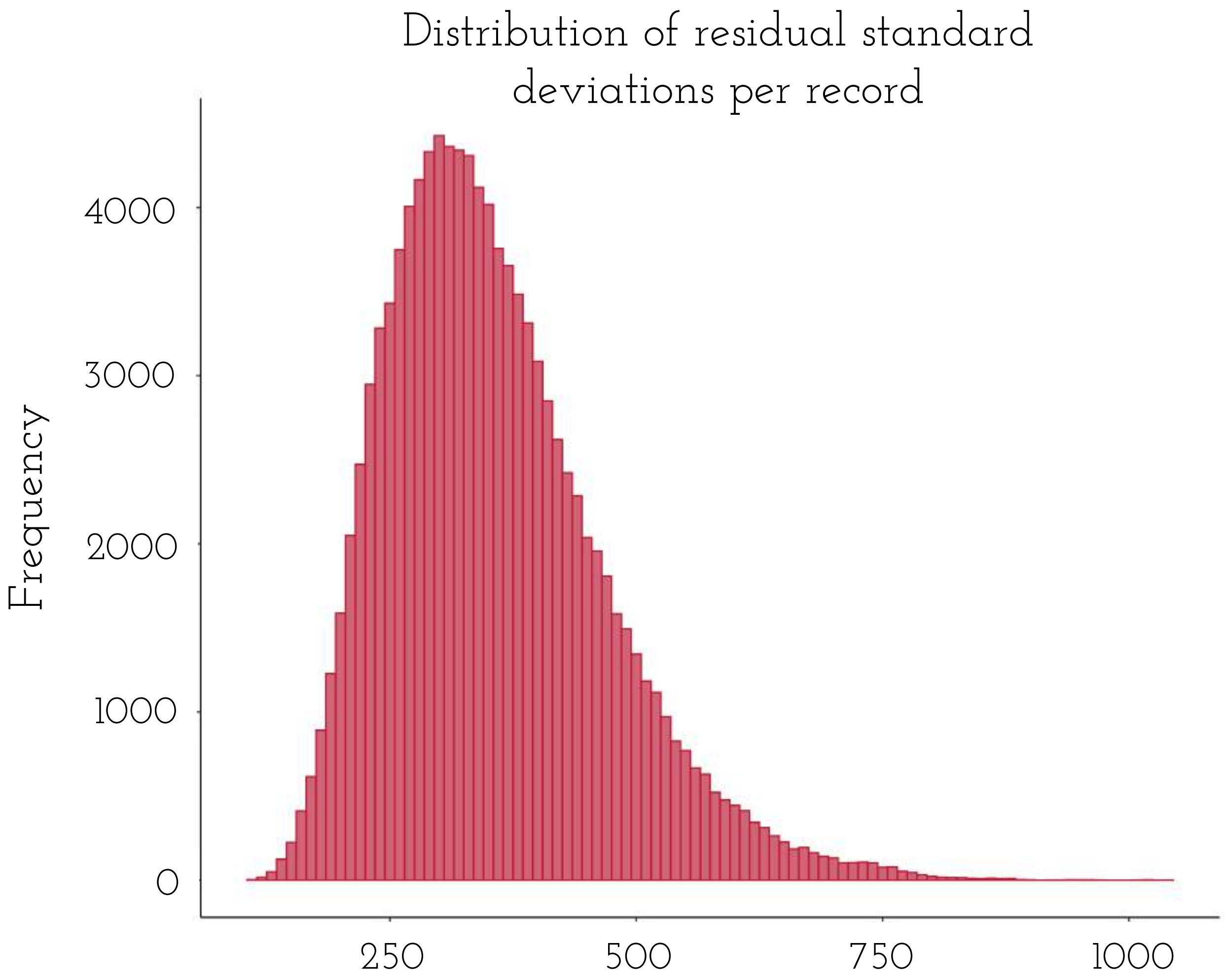
Pietrain pigs

Test method

Data - Results

1. All replicates converged
2. No significant differences

Method	σ_a^2	Convergence
H-Likelihood	1.0	97/100
IRWLS	1.0	74/100
DHGLMF90	1.0	100/100



Computing times

DHGLMF90 converged in order of magnitude faster than Bayesian methods

Method	Data 1	Data 2
DHGLMF90	1 min	10 min
Bayes	15 min	>1 day

X10 computing time **X144 computing time**

Other implementations

- Variance components estimates for Uterine capacity
  - Corr = 0.98
  - Corr = 0.99

Ibáñez-Escriche *et al. (2008; 2024)*

Program	σ_a^2	$\sigma_{a_v}^2$	σ_p^2	$\sigma_{p_v}^2$	r_g	Time
DHGLMF90	0.85 (0.23)	0.23 (0.06)	0.27 (0.12)	0.10 (0.05)	-0.80 (0.08)	~5 min
Bayes	0.81 (0.20)	0.15 (0.05)	0.40 (0.14)	0.03 (0.03)	-0.72 (0.10)	~2.5 h

X30 computing time

- No significant differences

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Challenges

Further developments for the DHGLMF90

1. Extend to multiple-trait models (in progress)
2. Analyzing genomic datasets
3. How to do inference without a posterior distribution?

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Conclusion

DHGLMF90 gives a good approximation

1. Comparable performance with other methodologies
2. Faster convergence
3. Fast to estimate breeding values

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Acknowledgments

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Questions?

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