# A coefficient of determination ( $R^{2}$ ) for linear mixed models in one go 



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## $R^{2}$ and adjusted $R^{2}$ for linear models (LM)

## Full model

$y=X \beta+e$,
where
$y=$ response vector of length $n$
$\beta=$ fixed effects vector
$X=$ design matrix, and
$e \sim N\left(0, V=I_{n} \sigma_{e}^{2}\right)=$ residual error vector

## $R^{2}$ and adjusted $R^{2}$ for linear models (LM)

## Null model

$y=1_{n} \lambda+e$,
where
$1_{n}=$ a vector of $n$ ones
$\lambda=$ intercept
$e \sim N\left(0, V_{0}=I_{n} \sigma_{e 0}^{2}\right)=$ residual error vector

## $R^{2}$ and adjusted $R^{2}$ for linear models (LM)

## The standard procedure

Error sum of squares for full model:

$$
S S_{\text {error }}^{\text {full }}=y^{T} P_{\beta} y \quad \text { where } \quad P_{\beta}=I_{n}-X\left(X^{T} X\right)^{-} X^{T}
$$

Error sum of squares for null model:

$$
S S_{\text {error }}^{\text {null }}=y^{T} P_{\lambda} y \quad \text { where } \quad P_{\lambda}=I_{n}-n^{-1} 1_{n} 1_{n}^{T}
$$

## $R^{2}$ and adjusted $R^{2}$ for linear models (LM)

## Coefficient of determination $\left(R^{2}\right)$

$$
R^{2}=1-\frac{S S_{\text {error }}^{\text {full }}}{S S_{\text {error }}^{\text {full }}}
$$

Adjusted coefficient of determination ( $R_{a d j}^{2}$ )

$$
R_{\text {adj }}^{2}=1-\frac{(n-1) S S_{\text {error }}^{\text {full }}}{(n-p) S S_{\text {elror }}^{\text {null }}} \quad \text { where } \quad p=\operatorname{rank}(X)
$$

## $R^{2}$ and adjusted $R^{2}$ for linear models (LM)

## Coefficient of determination $\left(R^{2}\right)$

$$
R^{2}=1-\frac{n^{-1} S S_{\text {error }}^{\text {full }}}{n^{-1} S S_{\text {error }}^{\text {null }}}=1-\frac{\hat{\sigma}_{e(M L)}^{2}}{\hat{\sigma}_{e 0(M L)}^{2}}
$$

Adjusted coefficient of determination ( $R_{a d j}^{2}$ )

$$
R_{\text {adj }}^{2}=1-\frac{(n-p)^{-1} S S_{\text {error }}^{\text {full }}}{(n-1)^{-1} S S_{\text {error }}^{\text {null }}}=1-\frac{\hat{\sigma}_{e(\text { REML })}^{2}}{\hat{\sigma}_{e 0(\text { REML })}^{2}}
$$

## $R^{2}$ and adjusted $R^{2}$ for linear models (LM)

## What does $\boldsymbol{R}^{2}$ estimate?

$\Omega_{\beta}=\frac{\Delta \theta\left(V, V_{0}\right)}{\theta\left(V_{0}\right)}$,
where
$\theta(V)=$ total variance implied by the variance-covariance structure $V$
$\Delta \theta\left(V, V_{0}\right)=\theta\left(V_{0}\right)-\theta(V)$
= variance explained by effects added in full model relative to null model

## $R^{2}$ and adjusted $R^{2}$ for linear models (LM)

## For LM

$$
\theta\left(V_{0}\right)=\sigma_{e 0}^{2},
$$

$$
\theta(V)=\sigma_{e}^{2}, \text { and }
$$

$\Delta \theta\left(V, V_{0}\right)=\sigma_{e 0}^{2}-\sigma_{e}^{2}$ and hence

$$
\Omega_{\beta}=\frac{\sigma_{e 0}^{2}-\sigma_{e}^{2}}{\sigma_{e 0}^{2}}=1-\frac{\sigma_{e}^{2}}{\sigma_{e 0}^{2}}
$$

## $R^{2}$ and adjusted $R^{2}$ for linear models (LM)

## Extensions of $\boldsymbol{R}^{\mathbf{2}}$

Generalized linear models (GLM): Zhang (2017)

Linear mixed models (LMM): Edwards et al. (2008), Liu et al. (2008),
Demidenko et al. (2012), Schreck \& Wiesenfarth (2022)

Generalized linear mixed models (GLMM): Nagakawa and Schielzeth (2013),
Jaeger et al. (2017, 2018), Nakagawa et al. (2017),
Stoffel et al. (2017), Ives (2019), Piepho (2019), Zhang (2022)
$\Rightarrow$ No time to review in detail
$\Rightarrow$ None of these seemed general enough \& easy to communicate

## $R^{2}$ and adjusted $R^{2}$ for linear models (LM)

## Methods in Ecology and Evolution

# A general and simple method for obtaining $R^{2}$ from generalized linear mixed-effects models 

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> 6900 citations and counting on SCOPUS!
> Two problems:
(i) covariance among observations ignored
(ii) bias in estimate of variance explained by fixed effects

## The main idea

Data vector

$$
y=\left(y_{1}, y_{2}, \ldots, y_{n}\right)^{T} \text { with }
$$

$$
E(y)=\mu=\left(\mu_{1}, \mu_{2}, \ldots, \mu_{n}\right)^{T} \text { and } \operatorname{var}(y)=V=\left\{v_{i j}\right\}
$$

## Semivariance

$$
s v\left(y_{i}, y_{j}\right)=\frac{1}{2} \operatorname{var}\left(y_{i}-y_{j}\right)=\frac{1}{2}\left(v_{i i}+v_{i j}\right)-v_{i j}
$$

## The main idea

## Average semivariance (ASV)

$$
\theta^{A S V}(V)=\frac{2}{n(n-1)} \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} s v\left(y_{i}, y_{j}\right)=\frac{1}{n-1} \operatorname{trace}\left(V P_{\lambda}\right)
$$

where $P_{\lambda}=I_{n}-n^{-1} 1_{n} 1_{n}^{T}$

This is a discrete version of the double integral given in Webster \& Oliver (2007), which integrates the semivariance over a defined spatial area:

## The main idea

### 4.8 SUPPORT AND KRIGE'S RELATION

Spatial dependence within a finite region has both theoretical and practical consequences, which we now explore.

The variance of $Z(\mathbf{x})$ within a region $R$ of area $|R|$ is the double integral of the variogram:

$$
\begin{equation*}
\sigma_{R}^{2}=\bar{\gamma}(R, R)=\frac{1}{|R|^{2}} \int_{R} \int_{R} \gamma\left(\mathbf{x}-\mathbf{x}^{\prime}\right) \mathrm{d} \mathbf{x} \mathrm{~d} \mathbf{x}^{\prime}, \tag{4.23}
\end{equation*}
$$

where $\mathbf{x}$ and $\mathbf{x}^{\prime}$ sweep independently over $R$. In geostatistics this variance is called the dispersion variance of $Z(\mathbf{x})$ in $R$. Unless the variogram is
(Webster \& Oliver, 2007, Geostatistics for environmental scientists. Wiley, p.61)

## The main idea

- ASV only captures the total variance in the random-effects part.
- Also need to capture the fixed-effects part

To do so, we here use the expected value of $\frac{1}{2}\left(y_{i}-y_{j}\right)^{2}$, which may be denoted as expected semi-squared difference:
$\operatorname{essd}\left(y_{i}, y_{j}\right)=\frac{1}{2} E\left[\left(y_{i}-y_{j}\right)^{2}\right]=\operatorname{ssb}\left(y_{i}, y_{j}\right)+\operatorname{sv}\left(y_{i}, y_{j}\right)$
where
$\operatorname{ssb}\left(y_{i}, y_{j}\right)=\frac{1}{2}\left(\mu_{i}-\mu_{j}\right)^{2}$ is the semi-squared bias

## The main idea

Average semi-squared bias (ASSB):

$$
\theta^{A S S B}(\mu)=\frac{2}{n(n-1)} \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} s s b\left(y_{i}, y_{j}\right)=\frac{1}{n-1} \operatorname{trace}\left(\mu^{T} P_{\lambda} \mu\right)
$$

Average expected semi-squared difference (AESSD):

$$
\theta^{A E S S D}(V, \mu)=\frac{2}{n(n-1)} \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} \operatorname{essd}\left(y_{i}, y_{j}\right)=\theta^{A S S B}(\mu)+\theta^{A S V}(V)
$$

## The main idea

The average expected semi-squared difference, $\theta^{A E S S D}(V, \mu)$, can be related to the sample variance

$$
s_{y}^{2}=\frac{1}{n-1} y^{T} P_{\lambda} y
$$

It follows from results on quadratic forms that

$$
E\left(s_{y}^{2}\right)=\theta^{A E S S D}(V, \mu)
$$

## The LM case

The candidate model can be written as
$y=X \beta+e$
where $e \sim N\left(0, V=I \sigma_{e}^{2}\right)$. The error variance can be unbiasedly estimated by
$\hat{\sigma}_{e}^{2}=\frac{1}{n-p} y^{T} P_{\beta} y$,
where $p=\operatorname{rank}(X)$, and $P_{\beta}=I-X\left(X^{T} X\right)^{-} X^{T}$.

## The LM case

## Average expected semi-squared difference:

$$
\theta^{A E S S D}\left(V=I \sigma_{e}^{2}, \mu=X \beta\right)=\theta^{A S S B}(X \beta)+\theta^{A S V}\left(I \sigma_{e}^{2}\right)
$$

The proposed coefficient of determination:

$$
\Omega_{\beta}=\frac{\theta^{A S S B}(X \beta)}{\theta^{A S S B}(X \beta)+\theta^{A S V}\left(I \sigma_{e}^{2}\right)}
$$

We find that $\theta^{A S V}\left(I \sigma_{e}^{2}\right)=\sigma_{e}^{2}$, which is estimated by
$\hat{\theta}_{L M}^{A S V}\left(I \sigma_{e}^{2}\right)=\hat{\sigma}_{e}^{2}$

## The LM case

Naïve estimator of $\theta^{A S S B}(X \beta)$ :

$$
\begin{aligned}
& \frac{1}{n-1} \hat{\beta}^{T} X^{T} P_{\lambda} X \hat{\beta} \quad \text { with } \quad \hat{\beta}=\left(X^{T} X\right)^{-} X^{T} y \\
& E\left[\frac{1}{n-1} \hat{\beta}^{T} X^{T} P_{\lambda} X \hat{\beta}\right]=\theta^{A S S B}(X \beta)+\frac{1}{n-1} \operatorname{trace}\left[X^{T} P_{\lambda} X \operatorname{var}(\hat{\beta})\right]
\end{aligned}
$$

$\Rightarrow$ unbiased estimator:

$$
\hat{\theta}_{L M}^{A S S B}(X \beta)=\frac{1}{n-1} \hat{\beta}^{T} X^{T} P_{\lambda} X \hat{\beta}-\frac{1}{n-1} \operatorname{trace}\left[X^{T} P_{\lambda} X \operatorname{var}(\hat{\beta})\right]
$$

## The LM case

Putting it all together:

$$
\hat{\theta}_{L M}^{A S S B}(X \beta)+\hat{\theta}_{L M}^{A S V}\left(I \sigma_{e}^{2}\right)=\frac{1}{n-1} \hat{\beta}^{T} X^{T} P_{\lambda} X \hat{\beta}-\frac{\hat{\sigma}_{e}^{2}}{n-1}(p-1)+\hat{\sigma}_{e}^{2}=\hat{\sigma}_{e 0}^{2}
$$

i.e., the estimator of the residual variance under the null model $\Rightarrow$

$$
\hat{\Omega}_{\beta}=\frac{\hat{\theta}_{L M}^{A S S B}(X \beta)}{\hat{\theta}_{L M}^{A S S B}(X \beta)+\hat{\theta}_{L M}^{A S V}\left(I \sigma_{e}^{2}\right)}=1-\frac{\hat{\sigma}_{e}^{2}}{\hat{\sigma}_{e 0}^{2}}
$$

which is identical with the adjusted $R^{2}$ for LM (Draper \& Smith, 1998)

## Extension to linear mixed models (LMM)

A LMM can be written as
$y=X \beta+Z u+e$
with $\operatorname{var}(u)=G, \operatorname{var}(e)=R$ and $\operatorname{cov}(u, e)=0$, such that

$$
\operatorname{var}(y)=V=Z G Z^{T}+R
$$

The fixed effects are estimated by
$\hat{\beta}=\left(X^{T} V^{-1} X\right)^{-} X^{T} V^{-1} y$

## Extension to linear mixed models (LMM)

Average expected semi-squared difference, $\theta^{A E S S D}(V, \mu)$ :

$$
\theta^{A E S S D}(V, X \beta)=\theta^{A S S B}(X \beta)+\theta^{A S V}(V)
$$

Coefficient of determination:

$$
\Omega_{\beta}=\frac{\theta^{A S S B}(X \beta)}{\theta^{A S S B}(X \beta)+\theta^{A S V}(V)}
$$

## Extension to linear mixed models (LMM)

The unbiased estimator of $\theta^{A S S B}(X \beta)$ is
$\hat{\theta}_{L M M}^{\text {ASSB }}(X \beta)=\frac{1}{n-1} \hat{\beta}^{T} X^{T} P_{\lambda} X \hat{\beta}-\frac{1}{n-1} \operatorname{trace}\left[X^{T} P_{\lambda} X \operatorname{var}(\hat{\beta})\right]$
where $\operatorname{var}(\hat{\beta})=\left(X^{T} V^{-1} X\right)^{-}$.

Need to replace $V$ by $\hat{V}$, its residual maximum likelihood (REML) estimator
$\Rightarrow$ consistent

## Extension to linear mixed models (LMM)

Variance explained jointly by random effects $u$ and residual $e$ :

$$
\hat{\theta}_{L M M}^{A S V}(V)=\frac{1}{n-1} \operatorname{trace}\left(P_{\lambda} \hat{V}\right)
$$

Consistent estimator of the coefficient of determination for LMM:

$$
\hat{\Omega}_{\beta}=\frac{\hat{\theta}_{L M M}^{A S S B}(X \beta)}{\hat{\theta}_{L M M}^{A S S B}(X \beta)+\hat{\theta}_{L M M}^{A S V}(V)}
$$

## Extension to linear mixed models (LMM)

Coefficient of determination for the variance explained by random effects:

$$
\Omega_{u}=\frac{\theta^{A S V}\left(Z G Z^{T}\right)}{\theta^{A S S B}(X \beta)+\theta^{A S V}(V)}
$$

This may be motivated by the partition

$$
\theta^{A S V}(V)=\frac{1}{n-1} \operatorname{trace}\left(P_{\lambda} V\right)=\theta^{A S V}\left(Z G Z^{T}\right)+\theta^{A S V}(R)
$$

The estimator of $\theta^{A S V}\left(Z G Z^{T}\right)$ is simply $\theta^{A S V}\left(Z \hat{G} Z^{T}\right)$.

## Extension to linear mixed models (LMM)

The variance explained by both fixed and random effects:

$$
\Omega_{\beta u}=\frac{\theta^{A S S B}(X \beta)+\theta^{A S V}\left(Z G Z^{T}\right)}{\theta^{A S S B}(X \beta)+\theta^{A S V}(V)}
$$

## Extension to linear mixed models (LMM)

Also, $\theta^{A S V}(V)$ can be partitioned according to the component random effects:

$$
Z u=Z_{1} u_{1}+Z_{2} u_{2}
$$

with $\operatorname{var}\left(u_{1}\right)=G_{1}, \operatorname{var}\left(u_{2}\right)=G_{2}$ and $\operatorname{cov}\left(u_{1}, u_{2}\right)=0 \Rightarrow$

$$
\begin{aligned}
\theta^{A S V}(V) & =\frac{1}{n-1} \operatorname{trace}\left(P_{\lambda} V\right) \\
& =\frac{1}{n-1} \operatorname{trace}\left(P_{\lambda} Z_{1} G_{1} Z_{1}^{T}\right)+\frac{1}{n-1} \operatorname{trace}\left(P_{\lambda} Z_{2} G_{2} Z_{2}^{T}\right)+\frac{1}{n-1} \operatorname{trace}\left(P_{\lambda} R\right) \\
& =\theta^{A S V}\left(Z_{1} G_{1} Z_{1}^{T}\right)+\theta^{A S V}\left(Z_{2} G_{2} Z_{2}^{T}\right)+\theta^{A S V}(R)
\end{aligned}
$$

## Extension to generalized linear mixed models (GLMM)

A GLMM has linear predictor

$$
\begin{aligned}
& \eta=X \beta+Z u+f \\
& \operatorname{var}(f)=R_{f}
\end{aligned}
$$

The residual random effect $f$ associated with the $n$ units in the linear predictor is optional and may be added to account for overdispersion.

## Extension to generalized linear mixed models (GLMM)

The observed data have conditional expectation

$$
E(y \mid \eta)=\mu=g^{-1}(\eta)
$$

where $g($.$) is the link function.$

## Extension to generalized linear mixed models (GLMM)

The variance takes the general form
$\operatorname{var}(y \mid \mu)=A_{\mu}^{1 / 2} R A_{\mu}^{1 / 2}$
$A_{\mu}=$ a diagonal matrix with evaluations of the variance function $\operatorname{var}\left(y_{i} \mid \mu_{i}\right)$ on the diagonal
$R=$ a correlation matrix or a covariance matrix if overdispersion needs to be modelled (Wolfinger \& O'Connell, 1993; Stroup, 2015)

## Extension to generalized linear mixed models (GLMM)

## Challenge with GLMMs

- The random model terms occur both on the linear predictor scale (via the random effects $Z u$ ) and on the observed scale (via the conditional distribution of $y$ for given value of the linear predictor $\eta$ )
- In defining a coefficient of determination, a choice needs to be made as to the scale on which variance is to be assessed
- In either case, the variance occurring on the one scale needs to be projected onto the other scale in order to have a common scale on which to define the coefficient of determination $\Rightarrow$ I am projecting onto the linear predictor scale


## Extension to generalized linear mixed models (GLMM)

Extending the linear predictor for the projection:

$$
\eta_{h}=X \beta+Z u+f+h
$$

$\operatorname{var}(h)=R_{h}$
$h=$ auxiliary residual term to take up the projection of the residual from the original scale (Nakagawa \& Schielzeth, 2013)
$V_{h}=Z G Z^{T}+R_{f}+R_{h}$

## Extension to generalized linear mixed models (GLMM)

Use the Taylor-series expansion approach of Foulley et al. (1987) to project the residual variance from the original scale onto $h$ on the linear predictor scale:
$R_{h}=D_{\eta}^{-1} A_{\mu}^{1 / 2} R A_{\mu}^{1 / 2} D_{\eta}^{-1}$
where $D_{\eta}=\operatorname{diag}\left[\partial g^{-1}(\eta) / \partial \eta\right]$
$\Rightarrow$ Particularly easy to compute when model is fitted using pseudo-likelihood (Wolfinger \& O'Connell, 1993)

## Extension to generalized linear mixed models (GLMM)

Table: Values of diagonal elements of $D_{\eta}$ and $A_{\mu}$ for a few examples ( $m=$ sample size of binomial distribution).

| Link function | $D_{\eta}$ | Distribution | $A_{\mu}$ |
| :--- | :--- | :--- | :--- |
| Logit | $m \mu(1-\mu)$ | Binomial | $m \mu(1-\mu)$ |
| Probit $^{\S}$ | $m \varphi(\eta)$ | Binomial | $m \mu(1-\mu)$ |
| Complementary log-log | $m \exp [\eta-\exp (\eta)]$ | Binomial | $m \mu(1-\mu)$ |
| Log | $\mu$ | Poisson | $\mu$ |

$\S \varphi($.$) is the probability density function of the standard normal distribution$

## Extension to generalized linear mixed models (GLMM)

Exact results for the binary distribution (binomial distribution with $m=1$ ):

| Link function | Implied c.d.f. | Variance of $h_{i}$ |
| :--- | :--- | :--- |
| Logit | standard logistic | $\operatorname{var}\left(h_{i}\right)=\pi^{2} / 3$ |
| Probit | standard normal | $\operatorname{var}\left(h_{i}\right)=1$ |
| Complementary log-log | standard extreme value | $\operatorname{var}\left(h_{i}\right)=\pi^{2} / 6$ |

## Example 1

- Beetle larvae sampled from 12 populations (Nakagawa and Schielzeth, 2013)
- Within each population, larvae obtained from two microhabitats
- Larvae distinguished as male and female
- Sexed pupae were reared in containers, each holding eight animals

There are three responses:
(i) body length (Gaussian distribution)
(ii) frequency of two male colour morphs (binary distribution)
(iii) the number of eggs laid by each female (Poisson distribution)

## Example 1

## Linear predictor

Fixed effects: habitat
Random effects: population and container

## Distribution, link function and unit variance

Morph frequency:
$\Rightarrow$ binomial, logit link, $\operatorname{var}\left(h_{i}\right)=\pi^{2} / 3$ and $\operatorname{cov}\left(h_{i}, h_{j}\right)=0(i \neq j)$
Egg counts:
$\Rightarrow$ Poisson, log link, $\operatorname{var}\left(h_{i}\right)=\mu_{i}^{-1}$ and $\operatorname{cov}\left(h_{i}, h_{j}\right)=0(i \neq j)$

## Example 1

Table: Coefficients of determination (\%) the beetle data in Nakagawa \& Schielzeth (2013)

| Trait | Variance parameter estimation method | Coefficients of determination (\%) |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Approach of this paper |  |  | Piepho (2019) ${ }^{\text {§ }}$ |  |  | \%Nakagawa \& Schielzeth (2013) |  |
|  |  | $\Omega_{\beta}$ | $\Omega_{u}$ | $\Omega_{\beta u}$ | $\Omega_{\beta}$ | $\Omega_{u}$ | $\Omega_{\beta u}$ | $R_{\text {GLMM }(m)}^{2}$ | $R_{G L M M(c)}^{2}$ |
| Body length | REML | 40.09 | 33.30 | 73.39 | 40.09 | 33.30 | 73.39 | 39.16 | 74.09 |
| Egg count | Pseudolikelihood | 8.72 | \& 43.45 | 52.17 | 5.78 | ${ }^{\text {\& }} 44.85$ | 50.63 |  |  |
| Egg count | Laplace | 9.13 | ${ }^{\text {\& }} 41.80$ | 50.93 | \$7.21 | s, ${ }^{8} 42.68$ | s 49.89 | 9.76 | ${ }^{2} 57.23$ |
| Colour morph | Laplace | 7.46 | 21.99 | 29.46 | -3.77 | 24.67 | 20.89 | 7.77 | 31.13 |

## Example 2

## Beitler \& Landis (1985)

- clinical trial with two treatments (control versus intervention)
- eight clinics, 273 patients
- clinics are regarded as a random sample from a larger target population
- Linear predictor:
fixed effect: treatment
random effects: clinic + clinic.treatment
- binomial count $y_{i}$ of the number of patients responding favourably out of the
total number of patients $m_{i}$ allocated to a treatment in a given clinic
- logit, probit and complementary log-log link
- Gaussian quadrature


## Example 2

## Patient-level analysis

The rows of the relevant vector and matrices $\left(\eta, X, Z, R_{h}, V_{h}\right)$ need to be expanded from the binomial model for grouped data $\left(y_{i}, m_{i}\right)$ with 16 clinic $\times$ treatment combinations, to represent the binary patient-level response $y_{i j}$.
$\Rightarrow$ binary inflation

## Example 2

Binomial link function

| Logit |  | Probit |  | Complementary log-log |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Estimate | s.e. | Estimate | s.e. | Estimate | s.e. |


| Fixed effects: |  |  |  |  |  |
| :--- | ---: | ---: | ---: | ---: | ---: |
|  |  |  |  |  |  |
| Intercept | -0.4574 | 0.5529 | -0.2638 | 0.3190 | -0.8568 |
| treatment (control) | -0.7460 | 0.3247 | -0.4434 | 0.1897 | -0.4906 |
|  |  |  |  |  |  |
| Variance components: | , |  |  |  |  |
| Clinic | 1.9632 | 1.1973 | 0.6614 | 0.3900 | 1.1293 |
| Clinic $\times$ treatment | 0.01102 | 0.1593 | 0.003433 | 0.05692 | - |
|  |  |  |  |  |  |
| Information criteria: |  |  |  |  | 81.27 |
|  | 82.07 |  | 82.31 | 81.51 |  |

## Example 2

Coefficient of determination (\%):
Binomial link function

| Level: | Logit |  | Probit |  | Complementary log-log |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Group§ | Patient | Group§ | Patient | Group§ | Patient |
| $\Omega_{\beta}$ | 4.66 | 2.23 | 5.03 | 2.52 | 3.44 | 1.86 |
| $\Omega_{u}$ | 71.34 | 32.76 | 72.84 | 34.92 | 69.21 | 35.87 |
| $\Omega_{\beta u}$ | 75.99 | 34.99 | 77.87 | 37.44 | 72.66 | 37.74 |

## Example 3

## Gilmour et al. (1987)

- deformities in the feet of 2,513 lambs
- scored in three ordered categories, denoted as K1, K2 and K3
- lambs represent 34 sires
- Linear predictor:
random effect: sire
fixed effects: four contrasts denoted as YR (year), B1, B2 and B3 (breeds)
- binomial model with a probit link, merging either K2 \& K3 or K1 \& K2
- multinomial, cumulative probits (threshold model)


## Example 3



## Example 3

Coefficient of determination (\%):

|  | Binomial model |  |  |  | Multinomial model (proportional odds) |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | K1 vs. K2 \& K3 |  | K1 \& K2 vs. K3 |  | Sire $\S, \$$ |  | Lamb ${ }^{\text {S }}$ |
|  | Sire ${ }^{\text {® }}$ | Lamb ${ }^{\text {® }}$ | Sire ${ }^{\text {S }}$ | Lamb ${ }^{\text {§ }}$ | $\begin{gathered} \text { K1 vs. } \\ \text { K2 \& K3 } \end{gathered}$ | $\begin{array}{r} \mathrm{K} 1 \& \mathrm{~K} 2 \\ \text { vs. K3 } \end{array}$ |  |
| $\Omega_{\beta}$ | 50.06 | 5.54 | 59.54 | 20.19 | 54.19 | 40.83 | 6.75 |
| $\Omega_{u}$ | 32.72 | 4.34 | 9.06 | 3.09 | 29.69 | 22.37 | 4.18 |
| $\Omega_{\beta u}$ | 82.78 | 9.88 | 68.60 | 23.28 | 83.89 | 63.20 | 10.93 |

## Example 3

| YR | B 1 | B 2 | B 3 | $\Omega_{\beta}$ | $\Omega_{u}$ | $\Omega_{\beta u}$ | AIC | BIC |
| :--- | :--- | :--- | :--- | ---: | ---: | ---: | ---: | :--- |
|  |  |  |  |  |  |  |  |  |
| - | - | - | - | 0.00 | 11.58 | 11.58 | 3904.63 | 3912.20 |
| + | - | - | - | 9.99 | 11.21 | 3902.56 | 3908.66 |  |
| - | + | - | - | 6.47 | 8.25 | 14.72 | 3897.08 | 3903.19 |
| - | - | + | - | 3.23 | 10.25 | 13.49 | 3903.50 | 3909.60 |
| - | - | - | + | -0.54 | 11.50 | 10.97 | 3906.29 | 3912.39 |
| + | + | - | - | 5.25 | 6.27 | 11.53 | 3891.32 | 3898.95 |
| + | - | + | - | 9.19 | 1.49 | 10.68 | 3902.51 | 3910.14 |
| + | - | - | + | 9.53 | 11.42 | 3903.36 | 3910.99 |  |
| - | + | + | - | 13.57 | 5.35 | 18.92 | 3888.65 | 3896.28 |
| - | + | - | + | 6.45 | 8.14 | 14.59 | 3898.73 | 3906.36 |
| - | - | + | + | 3.45 | 10.06 | 13.51 | 3905.01 | 3912.64 |
| + | + | + | - | 6.26 | 4.58 | 10.84 | 3884.36 | 3893.51 |
| + | + | - | + | 6.10 | 5.83 | 11.93 | 3891.57 | 3900.73 |
| + | - | + | + | 1.70 | 9.06 | 10.76 | 3903.25 | 3912.41 |
| - | + | + | + | 13.60 | 5.17 | 18.76 | 3889.89 | 3899.05 |
| + | + | + | + | 6.75 | 4.18 | 10.92 | 3884.12 | 3894.81 |

## Simulation

## Single covariate

Simulation scenarios for random-coefficient regression as described in Xu (2003).

$$
\begin{aligned}
& y_{i j}=\beta_{0}+u_{0 i}+\left(\beta_{1}+u_{1 i}\right) z_{1 i j}+e_{i j} \\
& \left(i=1, \ldots, n ; j=1, \ldots, n_{i}\right) \text { with } u_{i 0} \sim N\left(0, \tau_{0}^{2}\right), u_{i 1} \sim N\left(0, \tau_{1}^{2}\right) \text { and } e_{i j} \sim N\left(0, \sigma^{2}\right)
\end{aligned}
$$

The covariate values $z_{1 i j}$ were simulated once from a standard normal distribution and this one set of values used in all 1,000 simulation runs for a scenario.

## Simulation

| $\beta_{1}$ | $\tau_{0}$ | $\tau_{1}$ |  | $n=50, n_{i}=5$ |  |  |  |  |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
|  |  |  | $\hat{\Omega}_{\beta}$ | $\hat{\Omega}_{u}$ | $\hat{\Omega}_{\beta u}$ | $\Omega_{\beta}$ | $\Omega_{u}$ | $\Omega_{\beta u}$ |
| 0.7 | 0 | 0 | $0.531(0.036)$ | $0.019(0.021)$ | $0.551(0.040)$ | 0.533 | 0 | 0.533 |
|  | 0 | 0.5 | $0.417(0.072)$ | $0.225(0.057)$ | $0.642(0.056)$ | 0.419 | 0.213 | 0.633 |
|  | 0 | 1 | $0.255(0.093)$ | $0.525(0.083)$ | $0.780(0.045)$ | 0.256 | 0.521 | 0.776 |
|  | 1 | 0 | $0.284(0.042)$ | $0.473(0.065)$ | $0.757(0.036)$ | 0.280 | 0.474 | 0.754 |
|  | 1 | 0.5 | $0.243(0.055)$ | $0.539(0.063)$ | $0.782(0.035)$ | 0.245 | 0.540 | 0.785 |
|  | 1 | 1 | $0.181(0.072)$ | $0.661(0.070)$ | $0.843(0.027)$ | 0.179 | 0.665 | 0.844 |
|  |  |  |  |  |  |  |  |  |
| 0.5 | 1 | 0 | $0.167(0.034)$ | $0.550(0.062)$ | $0.716(0.044)$ | 0.166 | 0.549 | 0.715 |
|  | 1 | 0.5 | $0.141(0.048)$ | $0.611(0.061)$ | $0.752(0.041)$ | 0.142 | 0.613 | 0.756 |
|  | 1 | 1 | $0.097(0.058)$ | $0.729(0.060)$ | $0.825(0.031)$ | 0.100 | 0.729 | 0.829 |

## Simulation

## Two covariates

$$
y_{i j}=\beta_{0}+u_{0 i}+\left(\beta_{1}+u_{1 i}\right) z_{1 i j}+\left(\beta_{2}+u_{2 i}\right) z_{2 i j}+e_{i j}
$$

where $u_{i 2} \sim N\left(0, \tau_{2}^{2}\right)$

## Simulation

| $\beta_{1}$ | $\beta_{2}$ | $\tau_{1}$ | $\tau_{2}$ |  | $n=50, n_{i}=5$ |  |  |  |  |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
|  |  |  |  | $\hat{\Omega}_{\beta}$ | $\hat{\Omega}_{u}$ | $\hat{\Omega}_{\beta u}$ | $\Omega_{\beta}$ | $\Omega_{u}$ | $\Omega_{\beta u}$ |
| 2 | 2 | 2 | 2 | $0.375(0.063)$ | $0.437(0.061)$ | $0.812(0.032)$ | 0.378 | 0.439 | 0.817 |
| 2 | 1 | 1 | 1 | $0.429(0.053)$ | $0.246(0.054)$ | $0.676(0.047)$ | 0.432 | 0.250 | 0.681 |
| 1 | 1 | 1 | 1 | $0.222(0.054)$ | $0.335(0.067)$ | $0.557(0.063)$ | 0.224 | 0.341 | 0.565 |
| 0.5 | 1 | 1 | 1 | $0.147(0.049)$ | $0.367(0.071)$ | $0.514(0.068)$ | 0.148 | 0.374 | 0.522 |
| 1 | 1 | 0.5 | 1 | $0.246(0.051)$ | $0.268(0.065)$ | $0.514(0.064)$ | 0.248 | 0.272 | 0.520 |
| 0.5 | 0.5 | 1 | 1 | $0.066(0.039)$ | $0.402(0.075)$ | $0.468(0.073)$ | 0.067 | 0.410 | 0.477 |
| 1 | 1 | 0.5 | 0.5 | $0.271(0.047)$ | $0.199(0.060)$ | $0.470(0.062)$ | 0.272 | 0.201 | 0.473 |
| 0.5 | 0.5 | 0.5 | 0.5 | $0.084(0.036)$ | $0.249(0.073)$ | $0.334(0.074)$ | 0.085 | 0.252 | 0.337 |
| 0.5 | 0.5 | 1 | 0.5 | $0.073(0.038)$ | $0.341(0.074)$ | $0.414(0.074)$ | 0.075 | 0.346 | 0.421 |

## Summary

- Average semivariance (ASV) is a natural metric for total variance
- Average semi-squared bias (ASSB) is a natural extension of ASV that also includes fixed effects
- ASV and ASSB account for covariance among observations
- It is important to remove bias in the estimation of ASSB
- A coefficient of determination based on ASSB coincides with the adjusted $R^{2}$ for LM
- Extension to LMM and GLMM is straightforward
- In GLMM, total variance is assessed on the linear predictor scale
- Simulation shows that estimates of variance explained are accurate


## Thanks!

## References

Feldmann, M.J., Piepho, H.P., Bridges, W.C., Knapp, S.J. (2021): Average semivariance yields accurate estimates of the fraction of marker-associated genetic variance and heritability in complex trait analyses. PLoS Genetics 17, e1009762.

Feldmann, M.J., Piepho, H.P., Knapp, S.J. (2022): Average semivariance directly yields accurate estimates of genomic variance of complex, quantitative traits. G3 12(6), jkac080.

Feldmann, M.J., Covarrubias-Pazaran, E., Piepho, H.P. (2023): Complex traits and candidate genes: Estimation of genetic variance components across modes of inheritance. G3 13, jkad148.

Piepho, H.P. (2019): A coefficient of determination $\left(R^{2}\right)$ for generalized linear mixed models. Biometrical Journal 61, 860-872.

Piepho, H.P. (2023): A coefficient of determination $\left(R^{2}\right)$ for linear mixed models in one go. Biometrical Journal 65, 2200290.

