Prediction of Breeding Values

Peter von Rohr

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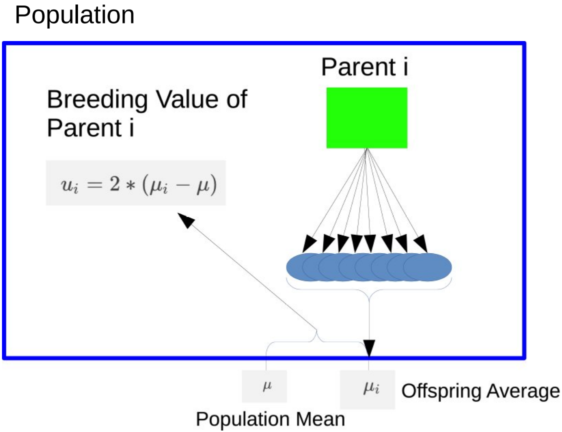
What are breeding values

Definition: two times difference between offspring of a given parent from population mean



Practical Considerations

- Definition of breeding value is based on biological fact that parent passes half of its alleles to offspring
- In practice, definition cannot be used
  - most parents do not have enough offspring
  - breeding values are needed before animals have offspring
  - different environmental factors not considered

Solution

- Use genetic model to predict breeding values based on phenotypic observations
- Genetic model decomposes phenotypic observation (y_i) in different components

$$y_i = \mu + u_i + d_i + i_i + e_i$$

where μ is the general mean, u_i the breeding value, d_i the dominance deviation, i_i the epistasis effect and e_i the random error term.

Solution II

- For predicting breeding values d_i and i_i are often ignored, leading to a simplified version of the genetic model

$$y_i = \mu + u_i + e_i$$

- Expected values and variance-covariance matrix

$$E\left[\begin{array}{c} y_i \\ u_i \\ e_i \end{array}\right] = \left[\begin{array}{c} \mu \\ 0 \\ 0 \end{array}\right]$$

$$var\left[\begin{array}{c} y_i \\ u_i \\ e_i \end{array}\right] = \left[\begin{array}{ccc} \sigma_y^2 & \sigma_u^2 & \sigma_e^2 \\ \sigma_u^2 & \sigma_u^2 & 0 \\ \sigma_e^2 & 0 & \sigma_e^2 \end{array}\right]$$

How to Predict Breeding Values

- Predicted breeding values ($\hat{u}$) are a function of the observed phenotypic data (y)

$\rightarrow \hat{u} = f(y)$

- What should $f()$ look like?
- Goal: Maximize improvement of offspring generation over parents

$\rightarrow$ $\hat{u}$ should be conditional expected value of true breeding value u given y:

$$\hat{u} = E(u|y)$$

Derivation

- Assume: multivariate normality of u and y and $E(u) = 0$, then

$$\begin{aligned}\hat{u} &= E(u|y) = E(u) + cov(u, y^T) * var(y)^{-1} * (y - E(y)) \\ &= E(u|y) = cov(u, y^T) * var(y)^{-1} * (y - E(y))\end{aligned}$$

- $\hat{u}$ consists of two parts

1. $(y - E(y))$: phenotypic observations corrected for environmental effects
2. $cov(u, y^T) * var(y)^{-1}$: weighting factor of corrected observation

Unbiasedness

- Expected value ($E(\hat{u})$)

$$\begin{aligned} E(\hat{u}) &= E(cov(u, y^T) * var(y)^{-1} * (y - E(y))) \\ &= cov(u, y^T) * var(y)^{-1} * E(y - E(y)) \\ &= cov(u, y^T) * var(y)^{-1} * (E(y) - E(y)) = 0 \end{aligned}$$

- With $E(u) = 0$, it follows $E(\hat{u}) = E(u) = 0$

Variance

- $var(\hat{u})$ and $cov(u, \hat{u})$ important for quality of prediction

$$\begin{aligned}
var(\hat{u}) &= var(cov(u, y^T) * var(y)^{-1} * (y - E(y))) \\
&= cov(u, y^T) * var(y)^{-1} * var(y - E(y)) \\
&* var(y)^{-1} * cov(y, u^T) \\
&= cov(u, y^T) * var(y)^{-1} * cov(y, u^T) \\
cov(u, \hat{u}) &= cov(u, (cov(u, y^T) * var(y)^{-1} * (y - E(y)))^T) \\
&= cov(u, (y - E(y))^T) * var(y)^{-1} * cov(y, u^T) \\
&= cov(u, y^T) * var(y)^{-1} * cov(y, u^T) = var(\hat{u})
\end{aligned}$$

Accuracy

- Measured by $r_{u,\hat{u}}$
- Recall $cov(u, \hat{u}) = var(\hat{u})$

$$
\begin{aligned}
r_{u,\hat{u}} &= \frac{cov(u, \hat{u})}{\sqrt{var(u) * var(\hat{u})}} \\
&= \sqrt{\frac{var(\hat{u})}{var(u)}}
\end{aligned}
$$

- Reliability (“Bestimmtheitsmass”): $B = r^2_{u,\hat{u}}$

Prediction Error Variance (PEV)

- Variability of prediction error: $u - \hat{u}$

$$\begin{aligned} var(u - \hat{u}) &= var(u) - 2cov(u, \hat{u}) + var(\hat{u}) = var(u) - var(\hat{u}) \\ &= var(u) * \left[1 - \frac{var(\hat{u})}{var(u)}\right] \\ &= var(u) * \left[1 - r^2_{u,\hat{u}}\right] \end{aligned}$$

- Obtained from coefficient matrix of mixed model equations
- Used to compute reliability

Conditional Density

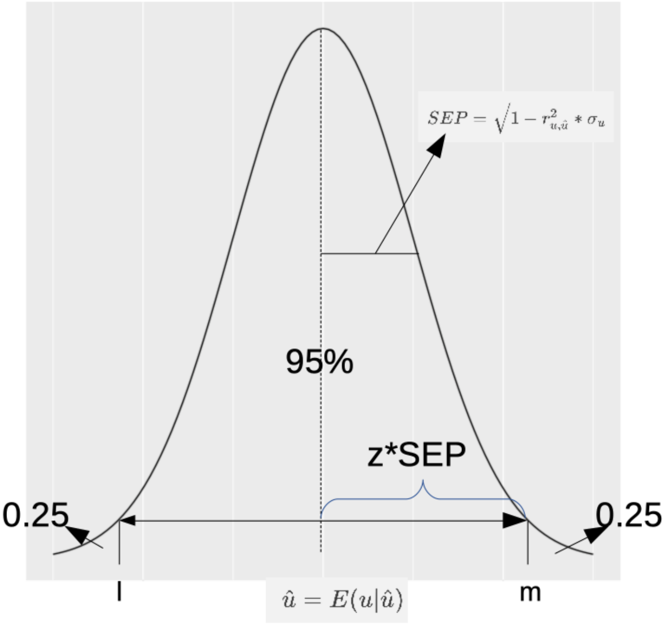
- Assessment of risk when using animals with predicted breeding values with different reliabilities quantified by $f(u|\hat{u})$
- Multivariate normal density with mean $E(u|\hat{u})$ and variance $var(u|\hat{u})$

$$
\begin{aligned}
E(u|\hat{u}) &= E(u) + cov(u, \hat{u}^T) * var(\hat{u})^{-1} * (\hat{u} - E(\hat{u})) = \hat{u} \\
var(u|\hat{u}) &= var(u) - cov(u, \hat{u}^T) * var(\hat{u})^{-1} * cov(\hat{u}, u^T) \\
&= var(u) * \left[1 - \frac{cov(u, \hat{u}^T)^2}{var(u) * var(\hat{u})}\right] \\
&= var(u) * \left[1 - r^2_{u,\hat{u}}\right]
\end{aligned}
$$

Confidence Intervals (CI)

- Assume an error level α, this results in $100 * (1 - \alpha)$%-CI
- Typical values of α 0.05 or 0.01
- With $\alpha = 0.05$, the 95%-CI gives interval around mean which covers a surface of 0.95

CI-Plot



CI Limits

- lower limit l and upper limit m are given by

$$\begin{aligned} l &= \hat{u} - z * SEP \\ m &= \hat{u} + z * SEP \end{aligned} \tag{1}$$

- z corresponds to quantile value to cover a surface of $(1 - \alpha)$
- Use R-function `qnorm()` to get value of z

Linear Mixed Effects Model

- Use more realistic model for prediction of breeding values

$$y = Xb + Zu + e$$

where

y	vector of length n with observations
b	vector of length p with fixed effects
u	vector of length q with random breeding values
e	vector of length n with random error terms
X	$n \times p$ incidence matrix
Z	$n \times q$ incidence matrix

Expected Values and Variances

$$E\begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \end{bmatrix}$$

$$var\begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} ZGZ^T + R & ZG & 0 \\ GZ^T & G & 0 \\ 0 & 0 & R \end{bmatrix}$$

Solutions

- Same as for simple model

$$\hat{u} = E(u|y) = GZ^T V^{-1}(y - X\hat{b})$$

with

$$\hat{b} = (X^T V^{-1} X)^{-} X^T V^{-1} y$$

corresponding to the general least squares solution of b

Problem

- Solution for $\hat{u}$ contains V^{-1} which is large and difficult to compute
- Use mixed model equations

$$\begin{bmatrix} X^T R^{-1} X & X^T R^{-1} Z \\ Z^T R^{-1} X & Z^T R^{-1} Z + G^{-1} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X^T R^{-1} y \\ Z^T R^{-1} y \end{bmatrix}$$

Sire Model

$$y = Xb + Zs + e$$

where s is a vector of length q_s with all sire effects.

$$var(s) = A_s * \sigma_s^2$$

where A_s: numerator relationship considering only sires

Animal Model

$$y = Xb + Za + e$$

where a is a vector of length q_a containing the breeding values

$$var(a) = A\sigma_a^2$$

where A is the numerator relationship matrix