Variance Components Estimation

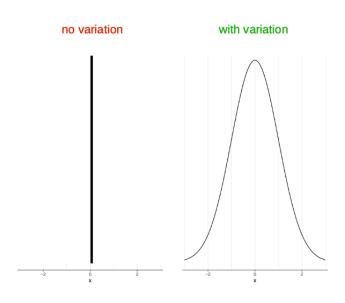
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Genetic Variation

- Requirement for trait to be considered in breeding goal
- Breeding means improvement of next generation via selection and mating
- Only genetic (additive) components are passed to offspring
- Selection should be based on genetic component of trait
- Selection only possible with genetic variation
- \rightarrow genetic variation indicates how good characteristics are passed from parents to offspring
- \rightarrow measured by **heritability** $h^2 = \frac{\sigma_a^2}{\sigma_p^2}$

Two Traits



Problems

- Genetic components cannot be observed or measured
- Must be estimated from data
- Data are mostly phenotypic
- \rightarrow topic of variance components estimation
 - Model based, that means connection between phenotypic measure and genetic component are based on certain model

$$p = g + e$$

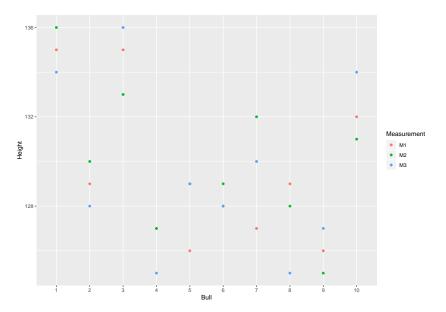
with cov(g, e) = 0

▶ **Goal**: separate variation due to $g\left(\sigma_a^2\right)$ from phenotypic variation

Example of Variance Components Separation

- Estimation of repeatability
- Given repeated measurements of same trait at the same animal
- Repeatability means variation of measurements at the same animal is smaller than variation between measurements at different animals

Repeatability Plot



Model

$$y_{ij} = \mu + t_i + \epsilon_{ij}$$

where

measurement j of animal iУij expected value of y μ deviation of y_{ii} from μ attributed to animal iti

measurement error

 ϵ_{ii}

Estimation Of Variance Components

- $E(t_i) = 0$
- $\sigma_t^2 = E(t_i^2)$: variance component of total variance (σ_y^2) which can be attributed to the t-effects
- $ightharpoonup E(\epsilon_{ij}) = 0$
- $\sigma_{\epsilon}^2 = E(\epsilon_{ij}^2)$: variance component attributed to ϵ -effects
- Repeatability w defined as:

$$w = \frac{\sigma_t^2}{\sigma_t^2 + \sigma_\epsilon^2}$$

 \rightarrow estimate of σ_t^2 needed

Analysis Of Variance (ANOVA)

Effect	df	Sum Sq	Mean Sq	E(Mean Sq)
Bull (t)	r-1	SSQ(t)	SSQ(t)/(r-1)	$\sigma_{\epsilon}^2 + n * \sigma_t^2$
Residual (ϵ)	N-r	$SSQ(\epsilon)$	$SSQ(\epsilon)/(N-r)$	σ^2_ϵ

where

$$SSQ(t) = \left[\frac{1}{n} \sum_{i=1}^{r} \left(\sum_{j=1}^{n} y_{ij}\right)^{2}\right] - \left(\sum_{i=1}^{r} \sum_{j=1}^{n} y_{ij}\right)^{2} / N$$
$$SSQ(\epsilon) = \sum_{i=1}^{r} \sum_{j=1}^{n} y_{ij}^{2} - \left[\frac{1}{n} \sum_{i=1}^{r} \left(\sum_{j=1}^{n} y_{ij}\right)^{2}\right]$$

Zahlenbeispiel

```
## Df Sum Sq Mean Sq F value Pr(>F)
## Bull 9 286.7 31.85 13.85 8.74e-07 ***
## Residuals 20 46.0 2.30
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

Setting expected values of Mean $\,\mathrm{Sq}$ equal to estimates of variance components

$$\hat{\sigma}_{\epsilon}^2 = 2.3 \text{ and } \hat{\sigma}_{t}^2 = \frac{31.85 - 2.3}{3} = 9.85$$

Repeatability

$$\hat{w} = \frac{\hat{\sigma}_t^2}{\hat{\sigma}_t^2 + \hat{\sigma}_\epsilon^2} = 0.81$$

Same Strategy for Sire Model

► Sire model is a mixed linear effects model with sire effects s as random components

$$y = Xb + Zs + e$$

- ▶ In case where sires are not related, $var(s) = I * \sigma_s^2$
- ▶ From σ_s^2 , we get genetic additive variance as $\sigma_a^2 = 4 * \sigma_s^2$

ANOVA

Effect	Degrees of Freedom	Sum Sq	Mean Sq	E(Mean Sq)
Sire $(s b)$	r-1	SSQ(s b)	SSQ(s b)/(r-1)	$\sigma_e^2 + k * \sigma_s^2$
Residual (e)	N-r	SSQ(e)	SSQ(e)/(N-r)	σ_e^2

with

$$k = \frac{1}{r-1} \left[N - \frac{\sum_{i=1}^{r} n_i^2}{N} \right]$$

Maximum Likelihood (ML)

Likelihood

$$L(\theta) = f(y|\theta)$$

Normal distribution

$$L(\theta) = (2\pi)^{-1/2n} \sigma^{-n} |H|^{-1/2} * exp \left\{ -\frac{1}{2\sigma^2} (y - Xb)^T H^{-1} (y - Xb) \right\}$$

with
$$var(y) = H * \sigma^2$$
 and $\theta^T = \begin{bmatrix} b & \sigma^2 \end{bmatrix}$

Maximisation of Likelihood

- ▶ Set $\lambda = logL$
- ightharpoonup Compute partial derivatives of λ with respect to all unknowns

$$\frac{\partial \lambda}{\partial b}$$

$$\frac{\partial \lambda}{\partial \sigma^2}$$

- Set partial derivatives to 0 and solve for unknowns
- Use solutions as estimates

Restricted Maximum Likelihood (REML)

- ▶ Problem with ML: estimate of σ^2 depends on $b \to \text{undesirable}$
- ▶ Do transformations Sy and Qy
- 1. The matrix S has rank n-t and the matrix Q has rank t
- 2. The result of the two transformations are independent, that means cov(Sy, Qy) = 0 which is met when $SHQ^T = 0$
- 3. The matrix S is chosen such that E(Sy) = 0 which means SX = 0
- 4. The matrix QX is of rank t, so that every linear function of the elements of Qy estimate a linear function of b.

REML II

From (i) and (ii) it follows that the likelihood L of y is the product of the likelihoods of Sy (L*) and Qy (L**) that means

$$\lambda = \lambda * + \lambda * *$$

lackbox Variance components are estimated from $\lambda*$ which will then be independent of b