Model Selection and Variance Components

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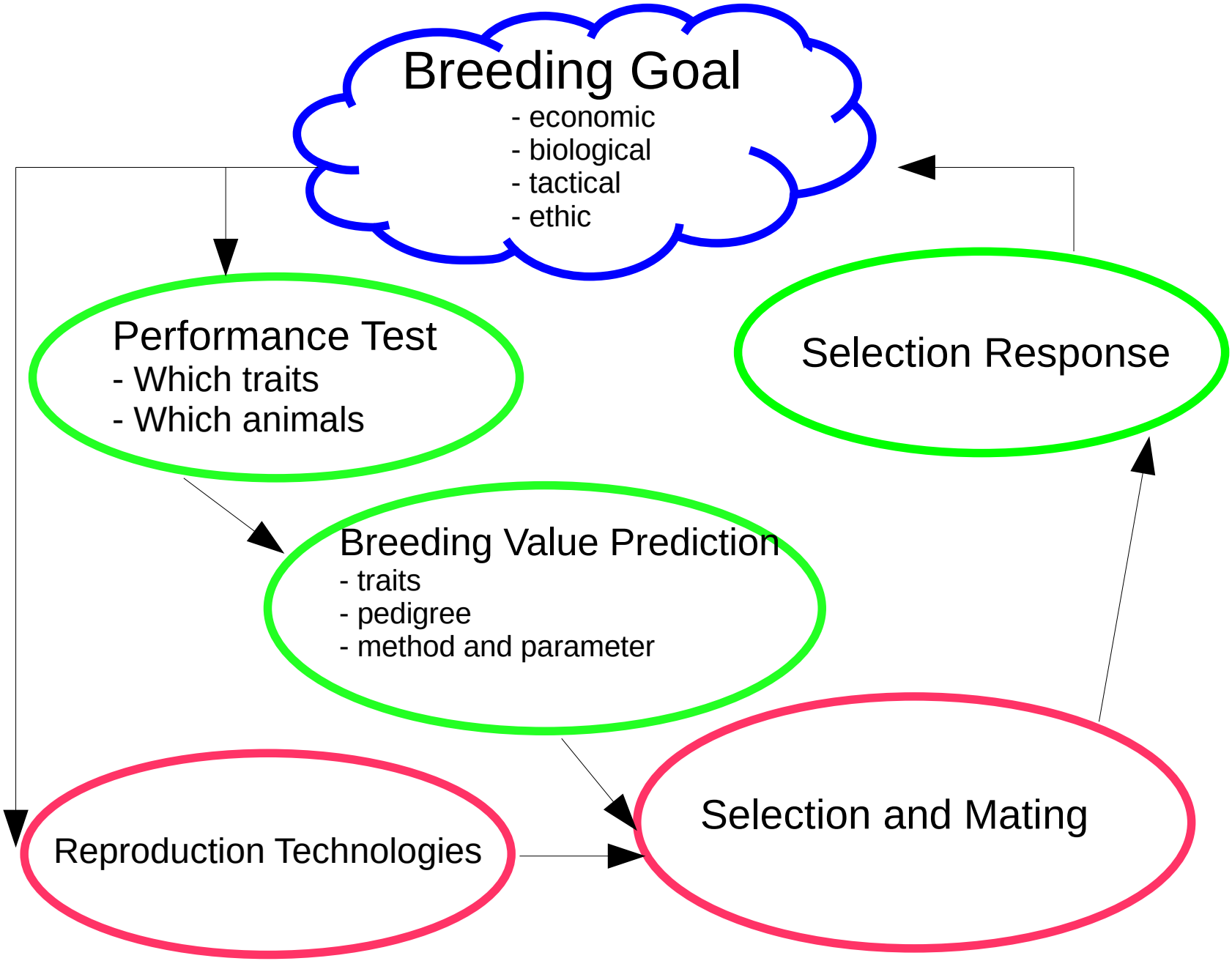
Breeding Programs



New Trait

- New trait to be considered in breeding program
- Why? $\rightarrow$ Trait is of economic importance
- Want to improve average level of trait in a given population
- How is this done?
- What do we have to do?

Background and Context

- Farms/Enterprise use livestock products as base for economic existence
- Improvements of production efficiency improves sustainability
- Short-term:
  - improve management and environment
  - select optimal livestock breed / population for given environment
- Long-term:
  - improve population at genetic level
  - define breeding goal
  - select parents such that offspring are “closer” to goal compared to parents

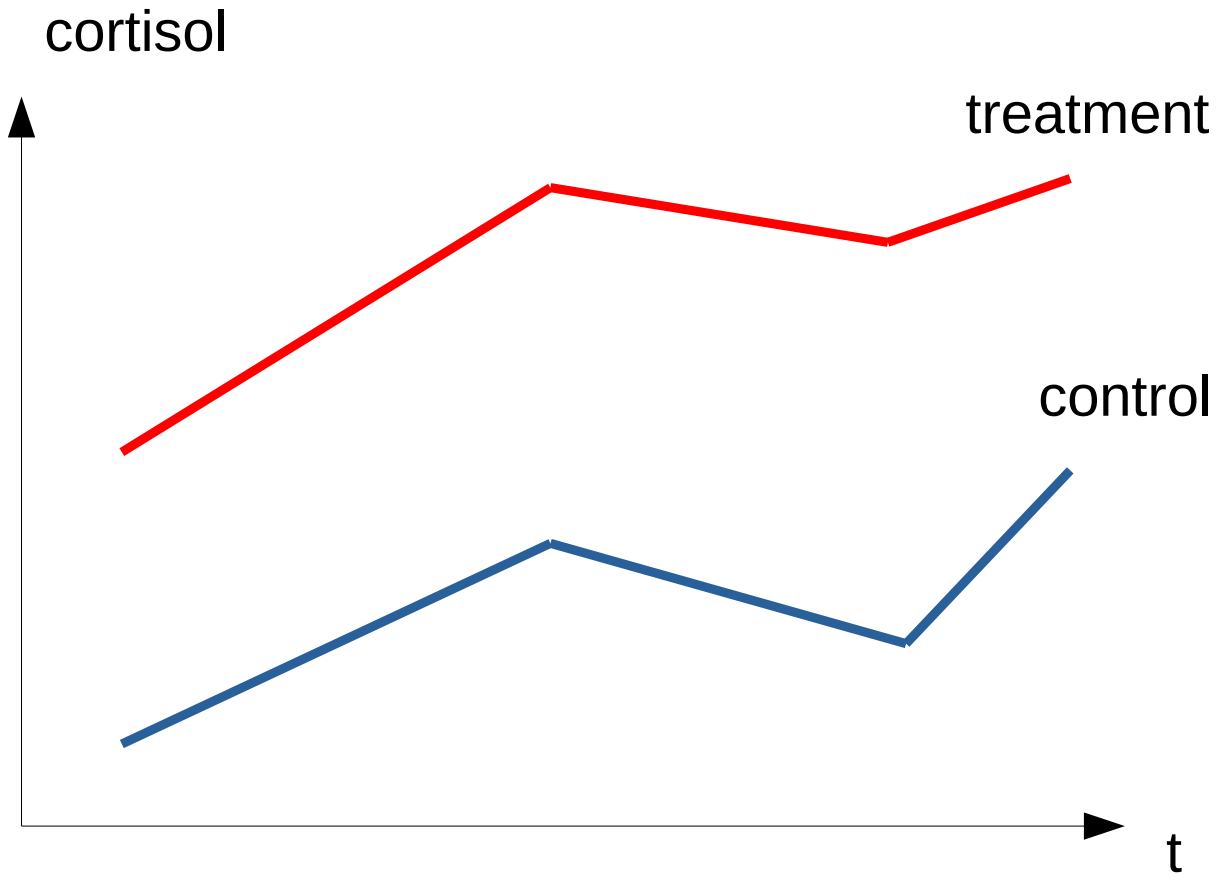
Genetic Improvement

- Genetic improvement happens between parents and offspring
- Parents pass random sample of alleles to offspring
- Goal: select parents that have many "good" alleles to pass to offspring
- How to find parents with "good" alleles without knowing which genes are important?

$\rightarrow$ **Statistical Modeling**

Why Statistical Modelling?

Some people believe, they do not need statistics. For them it is enough to look at a diagram

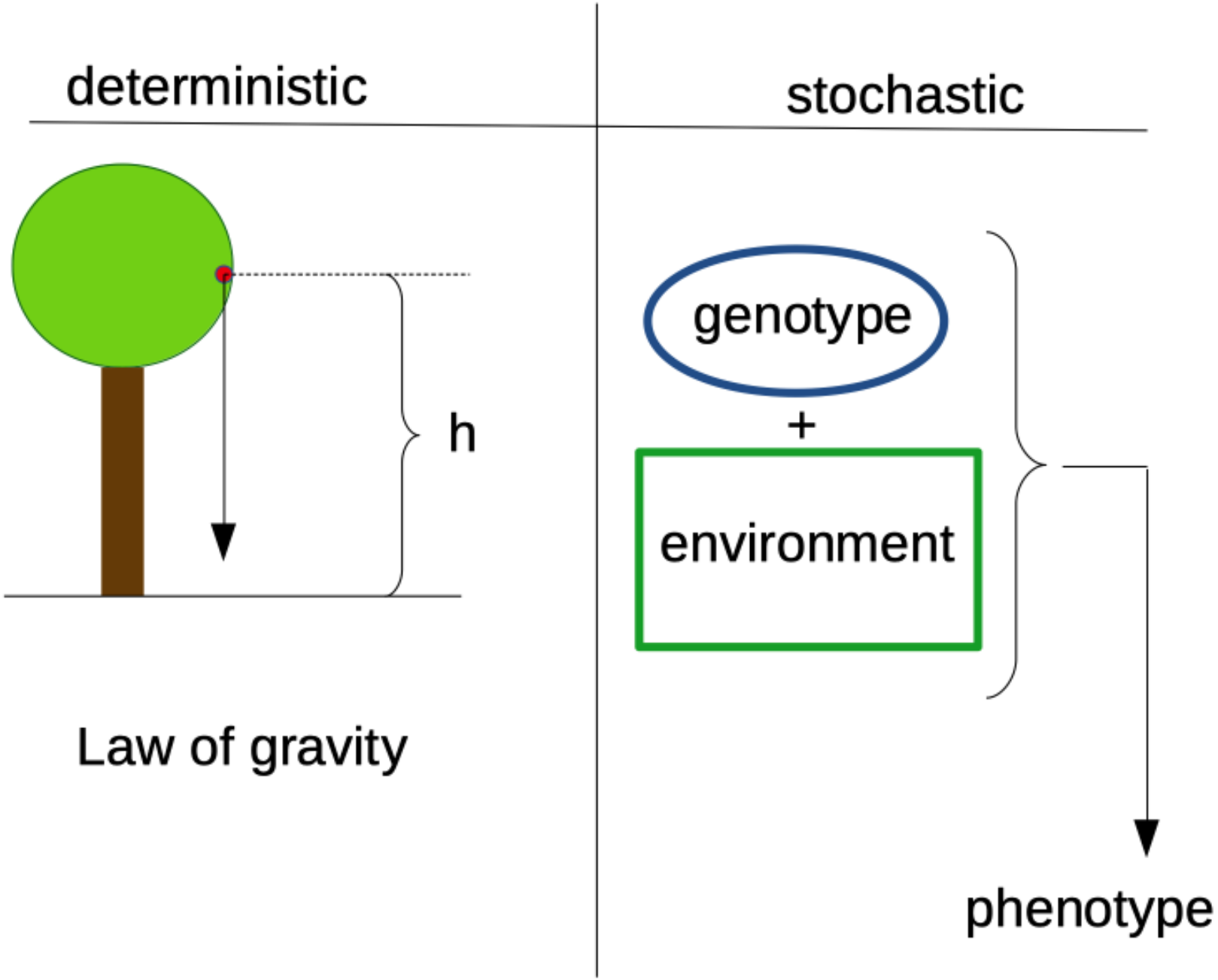


Statistical Modelling Because . . .

Two types of dependencies between physical quantities

1. deterministic
2. stochastic

Deterministic Versus Stochastic



Statistical Model

- stochastic systems contains many sources of uncertainty
- statistical models can handle uncertainty
- components of a statistical model
  - response variable y
  - predictor variables $x_1, x_2, \ldots, x_k$
  - error term e
  - function $m(x)$

How Does A Statistical Model Work?

- predictor variables $x_1, x_2, \ldots, x_k$ are transformed by function $m(x)$ to explain the response variable y
- uncertainty is captured by error term.
- as a formula, for observation i

$$y_i = m(x_i) + e_i$$

Which function $m(x)$?

- class of functions that can be used as $m(x)$ is infinitely large
- restrict to linear functions of predictor variables

Which predictor variables?

- Question, about which predictor variables to use is answered by model selection

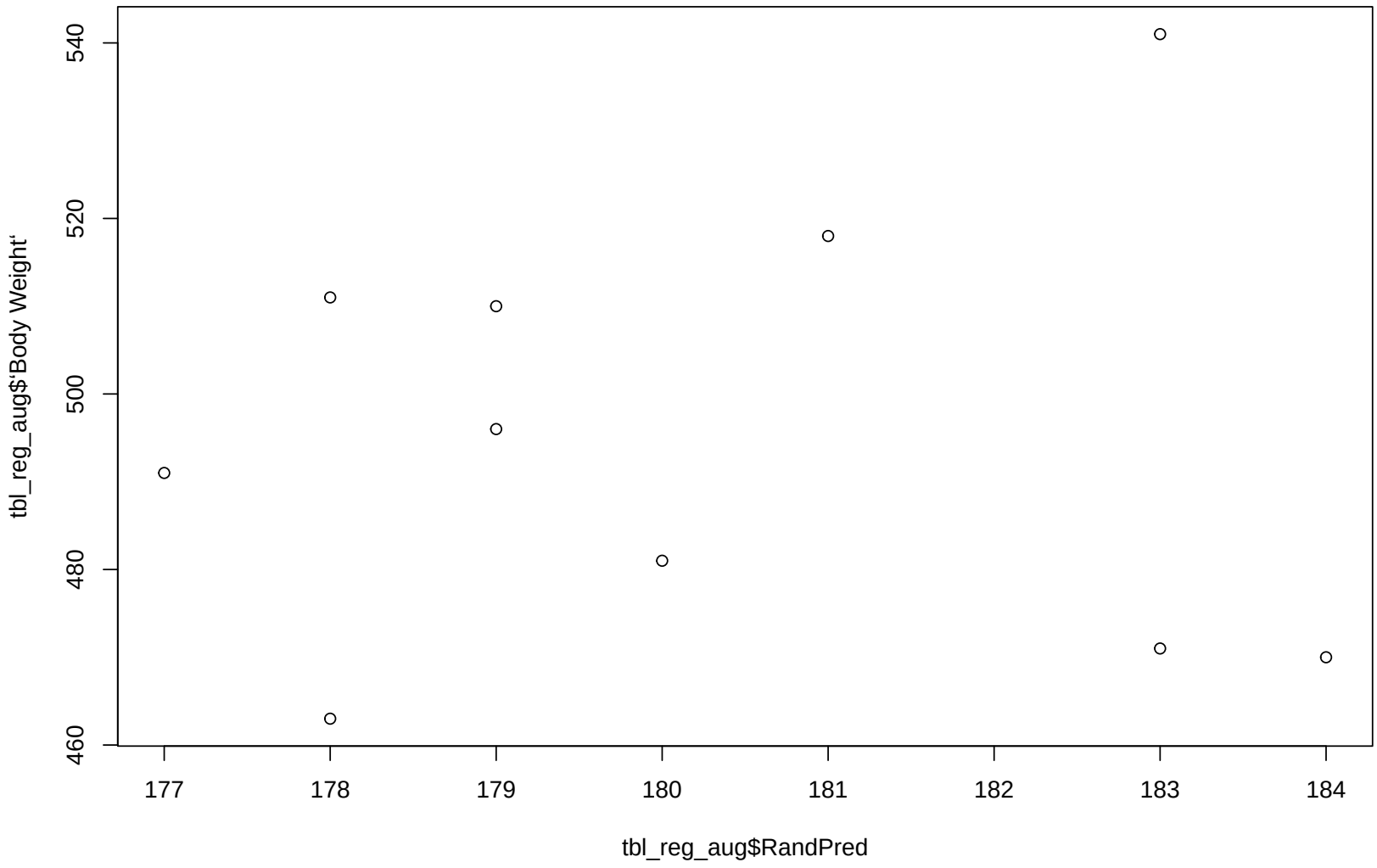
Why Model Selection

- Many predictor variables are available
- Are all of them `relevant`?
- What is the meaning of `relevant` in this context?

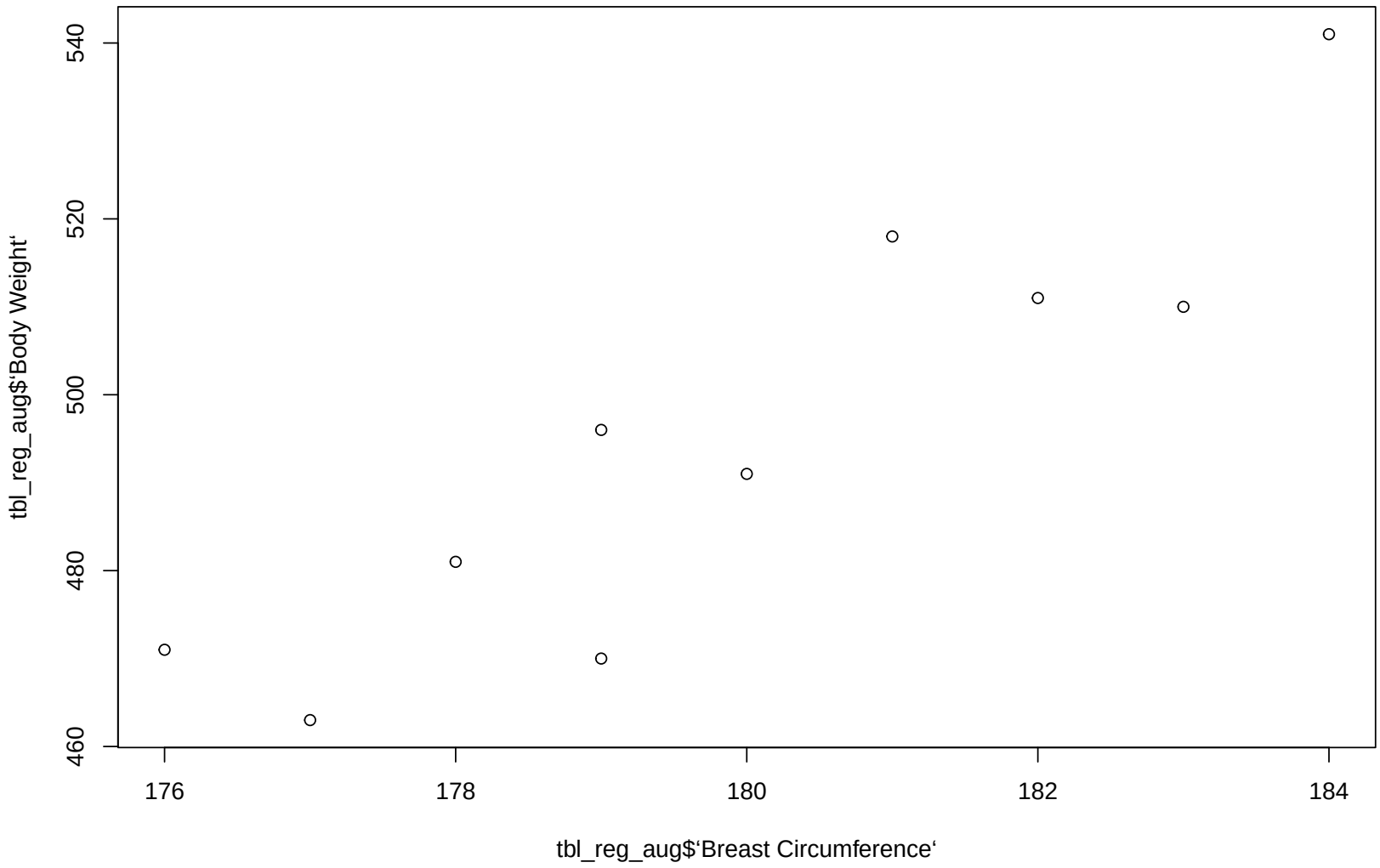
Example Dataset

Animal	Breast Circumference	Body Weight	RandPred
1	176	471	183
2	177	463	178
3	178	481	180
4	179	470	184
5	179	496	179
6	180	491	177
7	181	518	181
8	182	511	178
9	183	510	179
10	184	541	183

No Relevance of Predictors



Relevance of Predictors



Fitting a Regression Model

```
##
## Call:
## lm(formula = `Body Weight` ~ RandPred, data = tbl_reg_aug)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -31.519 -22.335  -1.019  16.154  44.933
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 439.3918   648.8442   0.677    0.517
## RandPred      0.3097     3.6004   0.086    0.934
##
## Residual standard error: 26.36 on 8 degrees of freedom
## Multiple R-squared:  0.0009241,  Adjusted R-squared:  -0.124
## F-statistic: 0.007399 on 1 and 8 DF,  p-value: 0.9336
```

Fitting a Regression Model II

```
##
## Call:
## lm(formula = `Body Weight` ~ `Breast Circumference`, data = tbl_reg_aug)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.3941  -6.5525  -0.0673   9.3707  13.2594
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -1065.115    255.483  -4.169 0.003126 **
## `Breast Circumference`      8.673      1.420   6.108 0.000287 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.08 on 8 degrees of freedom
## Multiple R-squared:  0.8234, Adjusted R-squared:  0.8014
## F-statistic: 37.31 on 1 and 8 DF,  p-value: 0.000287
```

Multiple Regression

```
##
## Call:
## lm(formula = `Body Weight` ~ `Breast Circumference` + RandPred,
##     data = tbl_reg_aug)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.2680  -4.6036   0.8467   7.8715  12.6091
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -1209.2233   403.0958  -3.000 0.019947 *
## `Breast Circumference`      8.7084     1.4955   5.823 0.000648 ***
## RandPred                    0.7646     1.5941   0.480 0.646094
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.66 on 7 degrees of freedom
## Multiple R-squared:  0.829,  Adjusted R-squared:  0.7802
## F-statistic: 16.97 on 2 and 7 DF,  p-value: 0.002066
```

Which model is better?

Why not taking all predictors?

- Additional parameters must be estimated from data
- Predictive power decreased with too many predictors (cannot be shown for this data set, because too few data points)
- Bias-variance trade-off

Bias-variance trade-off

- Assume, we are looking for optimum prediction

$$s_i = \sum_{r=1}^{q} \hat{\beta}_{j_r} x_{ij_r}$$

with q relevant predictor variables

- Average mean squared error of prediction s_i

$$MSE = n^{-1} \sum_{i=1}^{n} E\left[(m(x_i) - s_i)^2\right]$$

where $m(.)$ denotes the linear function of the unknown true model.

Bias-variance trade-off II

- MSE can be split into two parts

$$MSE = n^{-1} \sum_{i=1}^{n} \left(E\left[s_i\right] - m(x_i) \right)^2 + n^{-1} \sum_{i=1}^{n} var(s_i)$$

where $n^{-1} \sum_{i=1}^{n} \left(E\left[s_i\right] - m(x_i) \right)^2$ is called the squared **bias**

- Increasing q leads to reduced bias but increased variance ($var(s_i)$)
- Hence, find s_i such that MSE is minimal
- Problem: cannot compute MSE because $m(.)$ is not known

$\rightarrow$ estimate MSE

Mallows C_p statistic

- For a given model $\mathcal{M}$, $SSE(\mathcal{M})$ stands for the residual sum of squares.
- MSE can be estimated as

$$\widehat{MSE} = n^{-1} SSE(\mathcal{M}) - \hat{\sigma}^2 + 2\hat{\sigma}^2 |\mathcal{M}|/n$$

where $\hat{\sigma}^2$ is the estimate of the error variance of the full model, $SSE(\mathcal{M})$ is the residual sum of squares of the model $\mathcal{M}$, n is the number of observations and $|\mathcal{M}|$ stands for the number of predictors in $\mathcal{M}$

$$C_p(\mathcal{M}) = \frac{SSE(\mathcal{M})}{\hat{\sigma}^2} - n + 2|\mathcal{M}|$$

Searching The Best Model

- Exhaustive search over all sub-models might be too expensive
- For p predictors there are $2^p - 1$ sub-models
- With $p = 16$, we get 6.5535×10^4 sub-models

$\rightarrow$ step-wise approaches

Forward Selection

1. Start with smallest sub-model $\mathcal{M}_0$ as current model
2. Include predictor that reduces SSE the most to current model
3. Repeat step 2 until all predictors are chosen

$\rightarrow$ results in sequence $\mathcal{M}_0 \subseteq \mathcal{M}_1 \subseteq \mathcal{M}_2 \subseteq \ldots$ of sub-models

4. Out of sequence of sub-models choose the one with minimal C_p

Backward Selection

1. Start with full model $\mathcal{M}_0$ as the current model
2. Exclude predictor variable that increases SSE the least from current model
3. Repeat step 2 until all predictors are excluded (except for intercept)

$\rightarrow$ results in sequence $\mathcal{M}_0 \supseteq \mathcal{M}_1 \supseteq \mathcal{M}_2 \supseteq \ldots$ of sub-models

4. Out of sequence choose the one with minimal C_p

Considerations

- Whenever possible, choose **backward** selection, because it leads to better results
- If $p \geq n$, only forward is possible, but then consider LASSO

Alternative Selection Criteria

- AIC or BIC, requires distributional assumptions.
- AIC is implemented in `MASS::stepAIC()`
- Adjusted R^2 is a measure of goodness of fit, but sometimes is not conclusive when comparing two models
- Try in exercise

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

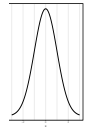
$\rightarrow$ genetic variation indicates how good characteristics are passed from parents to offspring

$\rightarrow$ measured by **heritability** $h^2 = \frac{\sigma_a^2}{\sigma_p^2}$

Two Traits

no variation

with variation



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

$$p = g + e$$

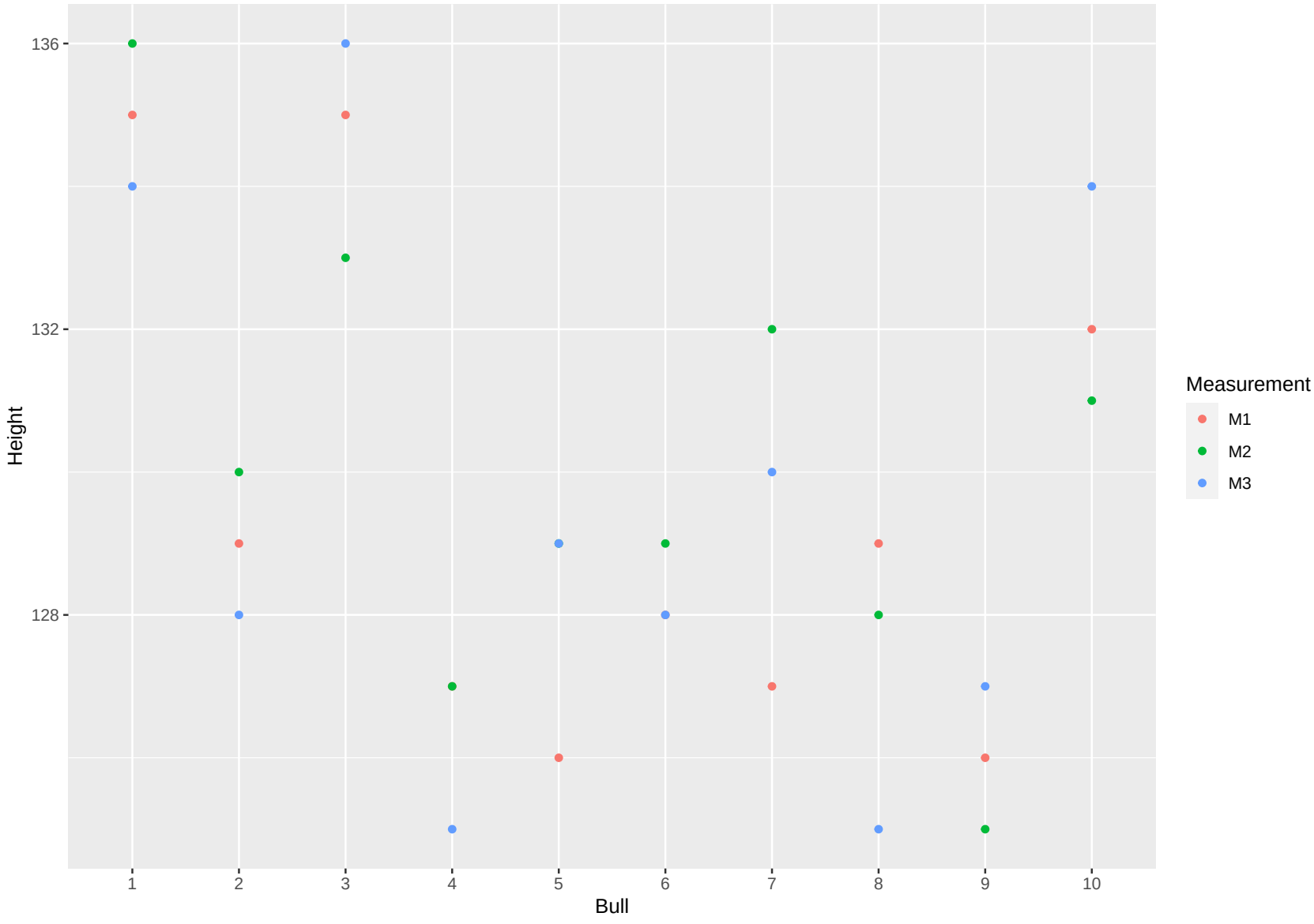
with $cov(g, e) = 0$

- **Goal**: separate variation due to g (σ_a^2) 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

y_{ij}	measurement j of animal i
μ	expected value of y
t_i	deviation of y_{ij} from μ attributed to animal i
ϵ_{ij}	measurement error

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
- $E(\epsilon_{ij}) = 0$
- $\sigma_\epsilon^2 = E(\epsilon_{ij}^2)$: variance component attributed to ϵ-effects
- $\sigma_y^2 = \sigma_t^2 + \sigma_\epsilon^2$
- 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_ϵ^2

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 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Setting expected values of `Mean 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 $\theta^T = \begin{bmatrix} b & \sigma^2 \end{bmatrix}$

Maximization of Likelihood

- Set $\lambda = logL$
- 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 $b \rightarrow$ undesirable
- Do transformations Sy and Qy

(i) The matrix S has rank $n - t$ and the matrix Q has rank t

(ii) The result of the two transformations are independent, that means $cov(Sy, Qy) = 0$ which is met when $SHQ^T = 0$

(iii) The matrix S is chosen such that $E(Sy) = 0$ which means $SX = 0$

(iv) 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

$$\lambda = \lambda^* + \lambda^{**}$$

- Variance components are estimated from λ^* which will then be independent of b

Bayesian Estimation

- Proposed already in the 80's
- Full implementation only in 1993
- Requirements:
  - cheap computing and
  - good pseudo-random number generators
- Bayesian estimation is based on conditional posterior distribution of unknowns given the knowns
- Conditional posterior distribution is computed from prior distribution of unknowns times the likelihood

Model

- Univariate Gaussian linear mixed model

$$y = Xb + Zu + e$$

where

y	vector of observations (length n)
b	vector of fixed effects (length p)
u	vector of random breeding values (length q)
e	vector of random residuals (length n)
X	$n \times p$ design matrix linking fixed effects to observations
Z	$n \times q$ design matrix linking breeding values to observations

Likelihood

- Data generating distribution

$$y|b, u, \sigma_e^2 \sim \mathcal{N}(Xb + Zu, I * \sigma_e^2)$$

where I is a $n \times n$ identity matrix and σ_e^2 is the variance of the random residuals.

Priors

- Prior distributions must be specified for all unknowns
- Unknowns in our example are: b, u, σ_e^2 and σ_u^2
- Prior distribution for
  - b is flat, i.e. $p(b) \propto c$
  - u Normal distribution as $u|G, \sigma_u^2 \sim N(0, G * \sigma_u^2)$
  - σ_e^2 scaled inverse χ^2:
    $p(\sigma_e^2|\nu_e, s_e^2) \propto (\sigma_e^2)^{-\nu_e/2-1} exp(-\frac{1}{2}\nu_e s_e^2/\sigma_e^2)$
  - σ_u^2 : $p(\sigma_u^2|\nu_u, s_u^2) \propto (\sigma_u^2)^{-\nu_u/2-1} exp(-\frac{1}{2}\nu_u s_u^2/\sigma_u^2)$
- ν_e, ν_s, s_e^2 and s_u^2 are called hyper-parameters and must be determined

Additional Terms

- Let

$$\theta^T = (b^T, u^T) = (\theta_1, \theta_2, \ldots, \theta_N)$$

$$\theta_{-i} = (\theta_1, \theta_2, \ldots, \theta_{i-1}, \theta_{i+1}, \ldots, \theta_N)$$

- Further, let

$$s^T = (s_u^2, s_e^2)$$

and

$$\nu^T = (\nu_u, \nu_e)$$

Joint Posterior Density

The joint posterior distribution can be written as

$$p(\theta, \sigma_u^2, \sigma_e^2 | y, s, \nu) \propto p(\theta) * p(\sigma_u^2 | \nu_u, s_u^2) * p(\sigma_e^2 | \nu_e, s_e^2) * p(y | \theta, \sigma_e^2)$$

Fully Conditional Posterior Densities of θ

- Density of every single unknown component when setting all other components as known

$$\theta_i | y, \theta_{-i}, \sigma_u^2, \sigma_e^2, s, \nu \sim \mathcal{N}(\tilde{\theta}_i, \tilde{v}_i)$$

where $\tilde{\theta}_i = (r_i - \sum_{j=1, j \neq i}^{N} w_{ij}\theta_j)/w_{ii}$ and $\tilde{v}_i = \sigma_e^2/w_{ii}$.

- vector r is the vector of right-hand side of MME
- matrix W is the coefficient matrix of MME

Fully Conditional Posterior Densities of σ_e^2

- scaled inverted chi-square distribution for σ_e^2

$$\sigma_e^2 | y, \theta, \sigma_u^2, s, \nu \sim \tilde{\nu_e} \tilde{s_e}^2 \chi_{\tilde{\nu_e}}^{-2}$$

- Parameters of the above distribution are defined as

$$\tilde{\nu_e} = n + \nu_e$$

and

$$\tilde{s_e}^2 = \left[(y - Xb - Zu)^T (y - Xb - Zu) + \nu_e s_e^2 \right] / \tilde{\nu_e}$$

Fully Conditional Posterior Densities of σ_u^2

- scaled inverted chi-square distribution for σ_u^2

$$\sigma_u^2 | y, \theta, \sigma_e^2, s, \nu \sim \tilde{\nu_u} \tilde{s_u}^2 \chi_{\tilde{\nu_u}}^{-2}$$

- Parameters of the above distribution are defined as

$$\tilde{\nu_u} = q + \nu_u$$

and

$$\tilde{s_u}^2 = \left[u^T G^{-1} u + \nu_u s_u^2 \right] / \tilde{\nu_u}$$

Implementation

- Step 1: set starting values for θ, σ_e^2 and σ_u^2
- Step 2: draw random number for each component θ_i of θ from fully conditional distribution $\mathcal{N}(\tilde{\theta}_i, \tilde{v}_i)$
- Step 3: draw random number for σ_e^2 from $\tilde{\nu}_e \tilde{s}_e^2 \chi_{\tilde{\nu}_e}^{-2}$
- Step 4: draw random number for σ_u^2 from $\tilde{\nu}_u \tilde{s}_u^2 \chi_{\tilde{\nu}_u}^{-2}$
- Repeat steps 2-4 many times and store random numbers
- Step 5: compute means of random numbers to get Bayesian estimates of unknowns θ, σ_e^2 and σ_u^2