

4.0 LINEAR MODEL APPROACH

4.1 The Model

This approach was proposed by **Schaeffer (1984)**. Its goals are to evaluate dairy sires from progeny test evaluations from one or more populations and to estimate genetic differences among populations. The linear model is:

$$y = Xc + ZQg + Zs + e$$

where

y = vector of average daughter deviations from all fixed effects within country, i.e. "deregressed" transmitting abilities

c = vector of effects due to country of proof

g = vector of effects due to country of birth, year of birth and breed composition of bull

s = vector of sire transmitting abilities

e = vector of errors of evaluations

X, Z = design matrices

Q = matrix that defines groups of sires

$$E \begin{bmatrix} s \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

$$V \begin{bmatrix} s \\ c \end{bmatrix} = \begin{bmatrix} A\sigma_s^2 & 0 \\ 0 & D\sigma_e^2 \end{bmatrix}$$

σ_s^2 is assumed constant across all sires

σ_e^2 could vary for each population

D is a diagonal matrix with elements n^{-1}

A is a matrix of additive genetic relationships among all sires.

4.2 General requirements

1. The transmitting abilities from the different populations need to be predicted by BLUP or another method with a clearly defined base (e.g. MCC).
2. All transmitting abilities from one country included in the analysis need to be expressed relative to the same base.

4.3 Assumptions

1. All transmitting abilities are expressed for the same trait in the same unit of measurement. Transformation to the same scale (e.g. kg, mature equivalent) needs to be done. The assumption is violated, e.g., in the case of single trait analysis in one population and multitrait analysis in another population.

2. The covariances among elements of $\mathbf{e}$ are equal to zero.
Even in an unbiased method without the relationship matrix this is not true, but to properly account for the error structure, all data from each country would be needed (the inverse of the mixed model equations).
3. Heterosis and interactions between genotype and country of proof do not exist.
This can be assumed to be true from present knowledge.
4. Sires are mated at random.
Non random mating should be corrected for by the sire evaluation procedures within each country.
5. No preferential treatment of daughters of particular sires.
This assumption may be violated for daughters of imported sires. The exclusion of these records would eliminate most of the links between populations.

4.4 Data needed for each country

1. Transmitting abilities for **all** AI-bulls in as many generations as possible must be included in the analysis. Only then can genetic differences between AI-populations be estimated.
2. The ratio σ_e^2 / σ_s^2 must be known.

4.5 Information required on an individual bull

1. Unique identification across populations
2. Year of birth
3. Country of birth, breed composition
4. Identification of sire and maternal grand-sire
5. Estimated transmitting abilities for each trait after appropriate transformation
6. Actual and effective number of daughters per trait
7. Group constants.

4.6 Remarks on the usefulness of available data

The model assumes that daughter averages can be reconstructed by deregressing the estimated transmitting abilities. The deregressing has to be done within groups and the group effects should be known. This corresponds to $\mathbf{P}_{Bj}^*$ in method 4 of chapter 3.

If the relationship matrix is used, the group effects do not exist or they are small and do not reflect the generation averages. Instead of using group effects, the average breeding value within generation (or other group definition) could be computed and subtracted before the deregressing. Then the group solutions are not needed.

Another effect of using the relationship matrix is that the number of daughters does not reflect the accuracy of the proof entirely.

4.7 Possible examples for an application

4.7.1 Brown breeds in Central Europe and the USA

Populations to include are: Austria (A), Baden - Wuerttemberg (BW), Bavaria (BY), Switzerland (CH) and USA (US). Exchange of semen exists from the USA to Europe where the same bulls are used in several countries.

	A	BW	BY	CH	US
Method of sire evaluation ¹	MT ²	Rep	ST	ST	MCC
Number of bulls evaluated per year (NS and AI) only AI	130	100	150	500 70	

¹ MT = multiple trait BLUP

ST = single trait BLUP

Rep = repeatability model BLUP

MCC = modified contemporary comparison

² on an experimental basis

Bull sires with proven sons in more than one population:

A and BY: 20 sires

A and CH: 12 sires

BY and CH: 10 sires

4.7.2 Red breeds in Scandinavia and Germany

Populations to include are NRF (Norway), FAY (Finland), SRB (Sweden) and Angler (Germany).

Exchange of semen exists between

NRF - SRB in both directions

NRF - FAY in both directions

FAY - SRB one way exchange

SRB - Angler one way exchange

Bull calves of FAY and Angler have been imported to Sweden. The semen exchange is limited just to get sons from each bull sire, so the number of daughters for each of them is small.

	NRF	SRB	FAY	Angler ³
Method of sire evaluation ¹	ST	ST	ST	ST ²
Number of bulls evaluated per year, only AI	130	180	175	20

¹ ST = single trait BLUP

² on an experimental basis

³ progeny test result in Sweden 1987