

Test Statistics for model comparison using DMUAI

Nested hypotheses about model parameters can be tested using a likelihood ratio test (LRT) (or differences in log-likelihood). Let L_1 be the maximized the log-likelihood for the “full model”, and let L_0 be the maximized log-likelihood for a “reduced model” of the “full model” obtained by imposing c independent constraints on the parameters. The null hypothesis that the “reduced model” holds can be tested by comparing $2(L_1 - L_0)$ to a suitably chosen percentage point of the chi-square distribution with c degree of freedom. The restricted log-likelihood ratio test (RLRT) is based on the same comparison but with L_1 and L_0 replaced, respectively, by the maximized restricted log-likelihoods for the “full model” and the “reduced model”.

In DMUAI, the restricted log-likelihood is maximized by minimizing -2 times the part of the restricted log-likelihood, which depend on (co)variance components in the model. As long as the fixed part of the models is identical, the significance of the (co)variance components can be tested by a RLRT. To conduct a RLRT, two DMUAI analyses must be performed. One for the “full model” and one for the “reduced model”. The RLRT test statistics is then obtained by subtracting the corresponding values of “Criterion at convergence”.

The following example illustrates how to test whether or not the genetic correlation between direct and maternal effects differ significantly for zero. The data used for this example is the same as used for the “dmuai” test example.

The driver files for the two runs are shown in Table 1.

The full model includes a genetic covariance component between the direct and maternal effect. This is obtained by placing the two random effects in the same random factor (covariance matrix) by the line: 3 1 2 2, in the model section. In total this model includes five (co)-variance components.

The reduced model without the genetic covariance component between direct and maternal effects includes four variance components. The direct and maternal genetic effects are as two uncorrelated random factors (placed in separate covariance matrices) by the model section line: 3 1 2 3. Pedigree variance structures are specified for both the maternal and the direct genetic effect. Here we use the same pedigree file for both effects, but the pedigrees for the maternal (dam) and the direct (animal) effect could have been traced separately and placed in separate files. The PRIOR section has been modified so it now contains 4 (co)variance matrices.

Table 1. “Driver files” for DMUAI analyses of full and reduced models.

Full model	Reduced model
<pre> \$COMMENT Recordings on 2187 growing sheep from field recording. The pedigree file consists of 2729 individuals Trait: birth weight \$ANALYSE 1 1 0 0 \$DATA ASCII (8,6,-99) data_records VARIABLE B_month D_age Litter Sex HY ID DAM L_Dam W_birth W_2mth W_4mth G_0_2 G_0_4 G_2_4 \$MODEL 1 0 1 0 8 1 2 3 4 5 8 7 6 3 1 2 2 0 0 \$VAR_STR 2 PED 2 ASCII pedigree PRIOR 1 1 1 .14 2 1 1 .2 2 1 2 -.1 2 2 2 .2 3 1 1 .3 </pre>	<pre> \$COMMENT Recordings on 2187 growing sheep from field recording. The pedigree file consists of 2729 individuals Trait: birth weight \$ANALYSE 1 1 0 0 \$DATA ASCII (8,6,-99) data_records VARIABLE B_month D_age Litter Sex HY ID DAM L_Dam W_birth W_2mth W_4mth G_0_2 G_0_4 G_2_4 \$MODEL 1 0 1 0 8 1 2 3 4 5 8 7 6 3 1 2 3 0 0 \$VAR_STR 2 PED 2 ASCII pedigree \$VAR_STR 3 PED 2 ASCII pedigree \$PRIOR 1 1 1 .14 2 1 1 .2 3 1 1 .2 4 1 1 .3 </pre>

The analyse with the full model converged after 6 rounds. The criterion was 1323.371494. The estimated correlation between the direct and the maternal genetic effect was -0.37 with a standard error of 0.19.

The analyse with the reduced model converged also after 6 rounds, and the criterion was 1325.749442.

The restricted log-likelihood ratio test for significance of the covariance component between the direct and the maternal genetic effect is therefore:

$$\text{RLRT: } 1325.749442 - 1323.371494 = 2.377948$$

Comparing this value with the chi-square distribution with one (5-4) degree of freedom shows that the genetic correlation between direct and maternal effects is non-significant. This corresponds well with the fact that the estimate from the “full model” is less then 2 times its standard error.