Lab 1 – BLUPF90 family program.

Prepared by I. Aguilar & D. Lourenco

BLUPF90 – Estimation of breeding values and reliabilities

1. Documentation for BLUPF90 program in the wiki: <http://nce.ads.uga.edu/wiki/doku.php> and also in blupf90.pdf file.
2. Using the following example (from Mrode and Thompson, 2005 -*Linear Models for Predicting Animal Breeding Value*)

Create data, pedigree and parameter to run **renumf90** and then run **blupf90** to obtain solutions and reliabilities.

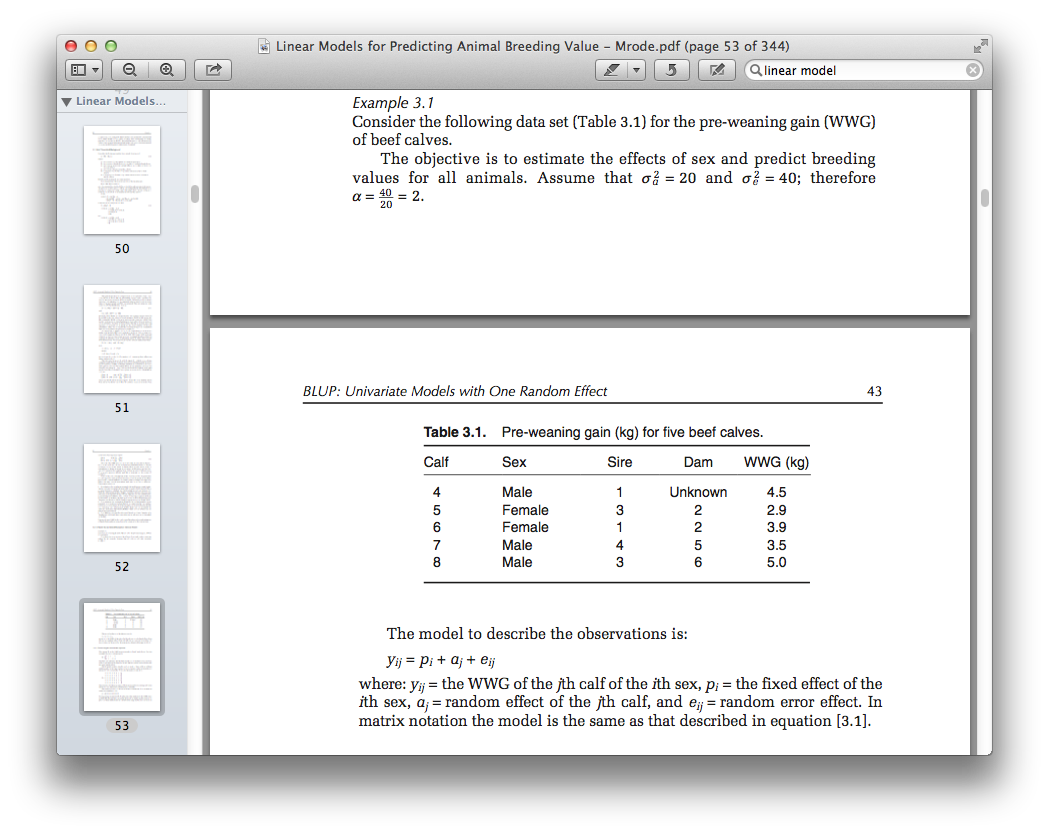
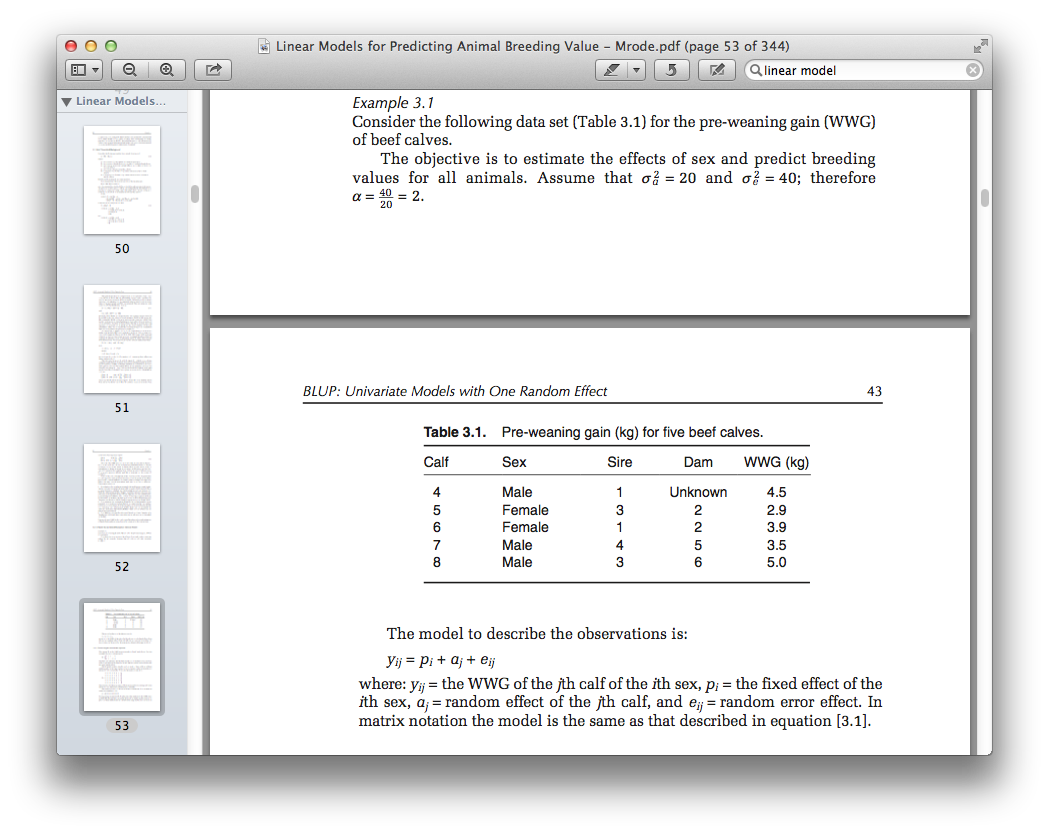
Reliability for animal i can be calculated as:

Reli = 1 – PEVi/VarA

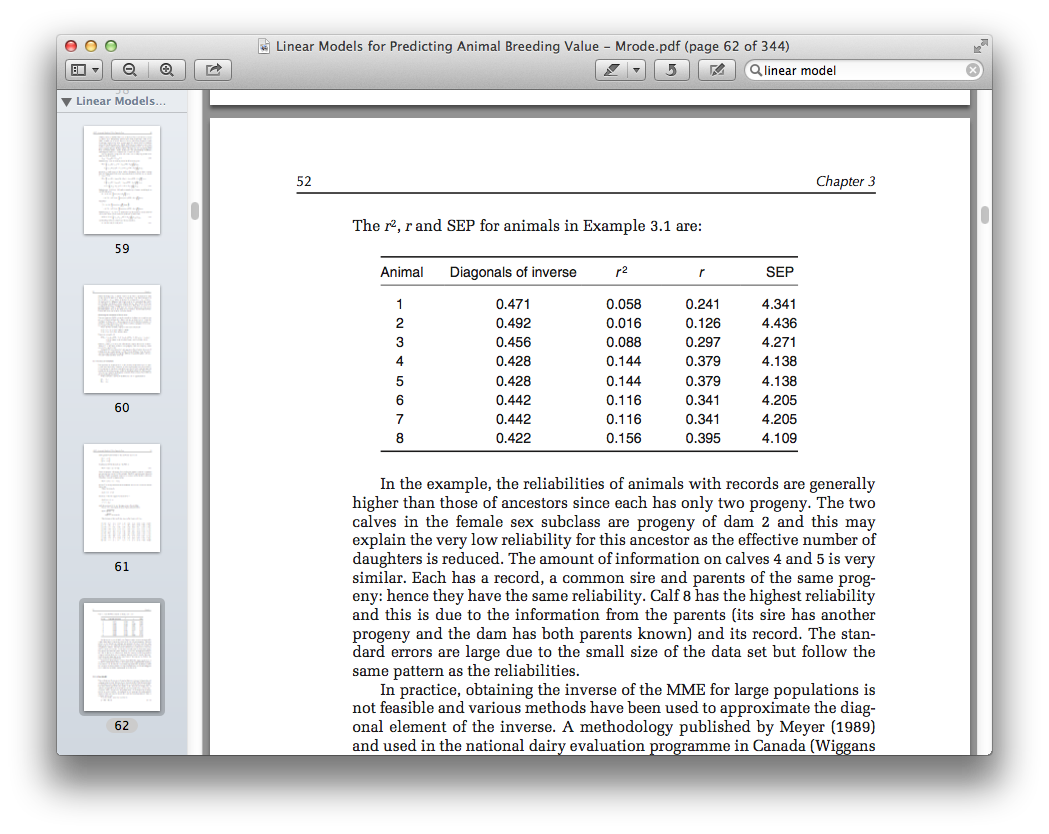
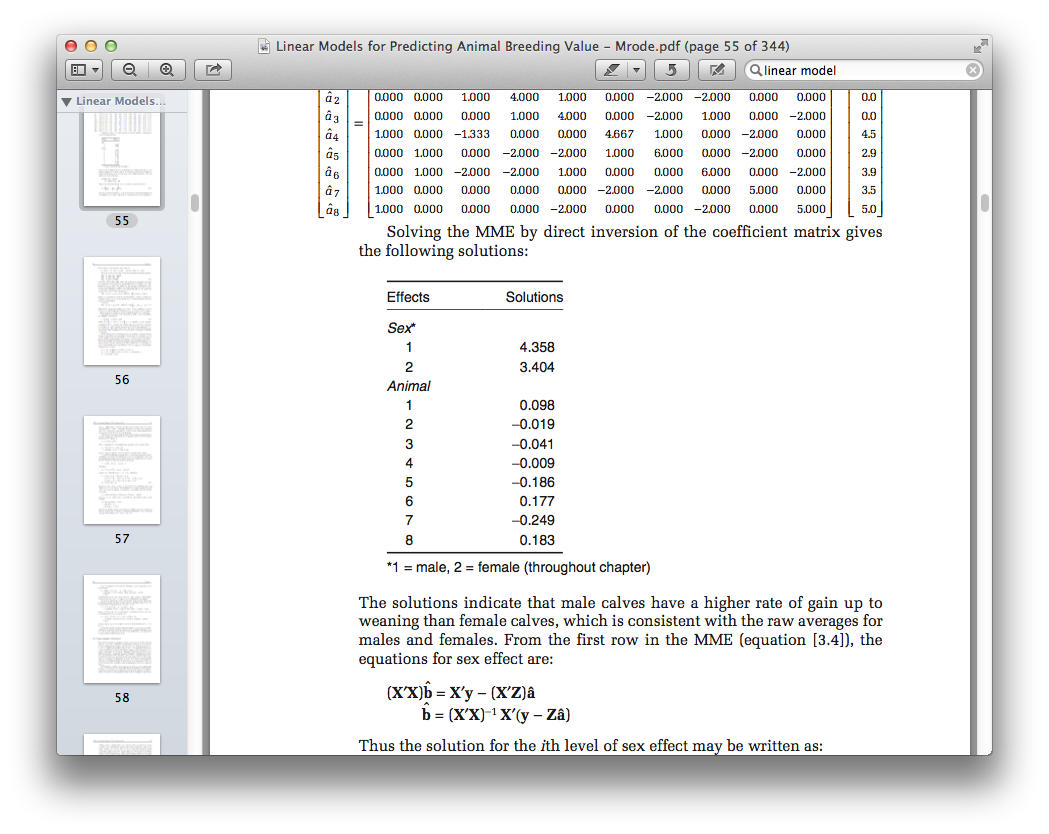
Where:

PEV is the prediction error variance (S.E. = sqrt(PEV))

VarA is the additive genetic variance

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The solutions from the example are:



Variance components estimation

1. Read documentation for REMLF90 program in the wiki: <http://nce.ads.uga.edu/wiki/doku.php> and also in remlf90.pdf file.
2. Parameter files for these exercises are in directory /home/course/courseadmin/course/lab1
3. Files with \*99 contain data for up to 14 traits. Parameter file exmr99s1 uses these files for a single-trait model, exmr99s2 uses for a two-trait model, and exmr99s for a three-trait model.

Calculate estimates of variance components by **remlf90** and **airemlf90** using the parameter file exmr99s1.

Record the number of rounds and CPU time.

Using the command “*time echo renf90.par | remlf90 | tee reml.log”* The CPU time will be printed after to program stop.

Extend the model to 2 traits by adding the observations in column 4 (parameter file exmr99s2). Repeat the computations for AIREMLF90 only. How much slower is REMLF90 and how longer are the computations in the two-trait case?

With AIREMLF90 add option to get SE for heritability and genetic correlations. Look at wiki to add OPTIONS.

1. Run gibbs2f90 for the single trait example; use the number of samples 1000 and burn-in 0. Run postgibbsf90 with burn-in of 0; try burn-in of 200. For graphical output, postgibbsf90 requires a plotting package GNUPLOT and X Windows (e.g., as provided by X emulation packages: Xming).
2. Estimate breeding values using gibbs2f90. Initial values should be replaced by posterior means. Check the manual to find the correct option to get EBV and SE. Use 1000 samples and burn-in of 200.

OPTIONAL

1. Random regression models using renumf90 and blupf90

Parameter, data and pedigree files (renrr.par, datrr.leg, pedrr) for this exercise are in directory

/home/course/courseadmin/course/lab1/

This data is for a random regression model using Legendre polynomials from example 7.2 of Mrode and Thompson, 2005 - *Linear Models for Predicting Animal Breeding Value*, Example 7. Look the parameter file and identify components of renumf90 parameter file. Run blupf90 to obtain solutions.