Lab 1 – BLUPF90 family of programs
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Estimation of breeding values and Variance components

1. Read documentation for BLUPF90 program in the wiki:
    http://nce.ads.uga.edu/wiki/doku.php

2. Data and parameter files for the following exercises are in this link:
    http://nce.ads.uga.edu/wiki/doku.php?id=course_materials_-
    _moscow_russia_2019

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.

    a) Open exmr99s1 and identify the key words required by blupf90.
        How many effects in this model?
        What is the second effect in the model?
        What is the third effect in the model?
        How many animals in the pedigree?

    b) Assuming that variance components are known, use **blupf90** to estimate
        breeding values using the parameter file exmr99s1 for a single-trait model and
        exmr99s for a three-trait model. Check solutions file and identify each column.

    c) For the single trait model, add an option to compute standard error (SE) of
        EBV. Based on SE, accuracy for EBV of animal i can be calculated as:
        $$Acc_i = sqrt(1 - PEV_i/VarA), \text{ where } PEV_i = SE_i \text{ x } SE_i$$

    d) Estimate variance components by **remlf90** and **airemlf90** using the parameter
        file exmr99s1. Record the number of rounds and approximate computing time.

    e) Extend the model to 2 traits by adding the observations in column 4
        (parameter file exmr99s2).

    f) Repeat the computations for both models using AIREMLF90. How much
        slower is REMLF90 and how longer are the computations in the two-trait case?

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

OPTIONAL

4. 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.

5. 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.

More test examples can be found in the BLUPF90 manual:
http://nce.ads.uga.edu/wiki/lib/exe/fetch.php?media=blupf90_all7.pdf