

Assignment 12

1. Read Readme* in directory thr gibbs1.
 - a) identify subroutines that approximate liabilities and thresholds
 - b) generate the data using program gen_thr.f90.
 - c) estimate parameters using thr gibbs1f90. Compare with assumed values.
 - d) repeat b-c for a number of designs and parameters. How many records are necessary for good estimates with different heritabilities?

Warning: *gen_thr may not work on some systems. where random_number is not treated as an elemental function. In this case, use gen_thr_ibm.f90.*

2. Convert data in exmr99s to result in one trait binary, one with 3 categories, and one linear. Estimate parameters.

Use postgibbsf90 to determine the number of needed samples.

Optional

3. Estimate parameters of 1bc using cblup90reml.f90 (quasi-REML approach).
4. Modify gibbsf90 to a single trait threshold model for binary data. Assume a threshold of 0. Test.

Suggestions: The residual variance needs to be fixed at 1 and not estimated. Subroutine “predict_missing_values” should be modified to sample from the interval $-\infty:0$ for category 1 and $0..\infty$ for category 2.

5. Listen to Shogo’s presentation on renumf90.