GENE638 – Exam 1

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Nelore-Angus F2 pedigree and data:

ID	SIRE	DAM	GENDER	HERD	NEW BORN CANNON BONE LEGHT (mm)
A	0	0	M	1	302
B	0	0	M	2	275
C	A	0	F	1	279
D	A	0	F	3	250
E	B	C	F	2	285
F	B	D	M	3	278

1. Using the Henderson's methodology for directly building A^{-1} and the above pedigree information.

    (a) Calculate A^{-1}

$$A^{-1} = \begin{bmatrix} 1.67 & 0.00 & -0.67 & -0.67 & 0.00 & 0.00 \\ 0.00 & 2.00 & 0.50 & 0.50 & -1.00 & -1.00 \\ -0.67 & 0.50 & 1.83 & 0.00 & -1.00 & 0.00 \\ -0.67 & 0.50 & 0.00 & 1.83 & 0.00 & -1.00 \\ 0.00 & -1.00 & -1.00 & 0.00 & 2.00 & 0.00 \\ 0.00 & -1.00 & 0.00 & -1.00 & 0.00 & 2.00 \end{bmatrix}$$

    (b) Prove that it is the inverse of the NMR

$$\begin{bmatrix} 1.67 & 0.00 & -0.67 & -0.67 & 0.00 & 0.00 \\ 0.00 & 2.00 & 0.50 & 0.50 & -1.00 & -1.00 \\ -0.67 & 0.50 & 1.83 & 0.00 & -1.00 & 0.00 \\ -0.67 & 0.50 & 0.00 & 1.83 & 0.00 & -1.00 \\ 0.00 & -1.00 & -1.00 & 0.00 & 2.00 & 0.00 \\ 0.00 & -1.00 & 0.00 & -1.00 & 0.00 & 2.00 \end{bmatrix} \times \begin{bmatrix} 1.00 & 0.00 & 0.50 & 0.50 & 0.25 & 0.25 \\ 0.00 & 1.00 & 0.00 & 0.00 & 0.50 & 0.50 \\ 0.50 & 0.00 & 1.00 & 0.25 & 0.50 & 0.12 \\ 0.50 & 0.00 & 0.25 & 1.00 & 0.12 & 0.50 \\ 0.25 & 0.50 & 0.50 & 0.12 & 1.00 & 0.31 \\ 0.25 & 0.50 & 0.12 & 0.50 & 0.31 & 1.00 \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

$$\begin{bmatrix} 1.00 & 0.00 & 0.50 & 0.50 & 0.25 & 0.25 \\ 0.00 & 1.00 & 0.00 & 0.00 & 0.50 & 0.50 \\ 0.50 & 0.00 & 1.00 & 0.25 & 0.50 & 0.12 \\ 0.50 & 0.00 & 0.25 & 1.00 & 0.12 & 0.50 \\ 0.25 & 0.50 & 0.50 & 0.12 & 1.00 & 0.31 \\ 0.25 & 0.50 & 0.12 & 0.50 & 0.31 & 1.00 \end{bmatrix} \times \begin{bmatrix} 1.67 & 0.00 & -0.67 & -0.67 & 0.00 & 0.00 \\ 0.00 & 2.00 & 0.50 & 0.50 & -1.00 & -1.00 \\ -0.67 & 0.50 & 1.83 & 0.00 & -1.00 & 0.00 \\ -0.67 & 0.50 & 0.00 & 1.83 & 0.00 & -1.00 \\ 0.00 & -1.00 & -1.00 & 0.00 & 2.00 & 0.00 \\ 0.00 & -1.00 & 0.00 & -1.00 & 0.00 & 2.00 \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

2. The model for analyses of cannon bone length recorded at birth in calves: $\underline{y} = X\underline{\beta} + Z\underline{u} + \underline{e}$ with $h^2 = \frac{\sigma_a^2}{\sigma_p^2}$ and $\lambda = \frac{\sigma_e^2}{\sigma_a^2} = 1.75$. Using that information:

    (a) Set up the Mixed Model Equations (MME)

$$\begin{bmatrix} 302 \\ 275 \\ 279 \\ 250 \\ 285 \\ 278 \end{bmatrix} = \begin{bmatrix} 1 & 1 & 0 & 1 & 0 & 0 \\ 1 & 1 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 0 & 0 & 1 \end{bmatrix} \times \begin{bmatrix} \mu \\ G_M \\ G_F \\ H_1 \\ H_2 \\ H_3 \end{bmatrix} + \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \times \begin{bmatrix} u_A \\ u_B \\ u_C \\ u_D \\ u_E \\ u_F \end{bmatrix} + \begin{bmatrix} e_A \\ e_B \\ e_C \\ e_D \\ e_E \\ e_F \end{bmatrix}$$

$$
\begin{bmatrix}
6.00 & 3.00 & 3.00 & 2.00 & 2.00 & 2.00 & 1.00 & 1.00 & 1.00 & 1.00 & 1.00 & 1.00 \\
3.00 & 3.00 & 0.00 & 1.00 & 1.00 & 1.00 & 1.00 & 1.00 & 0.00 & 0.00 & 0.00 & 1.00 \\
3.00 & 0.00 & 3.00 & 1.00 & 1.00 & 1.00 & 0.00 & 0.00 & 1.00 & 1.00 & 1.00 & 0.00 \\
2.00 & 1.00 & 1.00 & 2.00 & 0.00 & 0.00 & 1.00 & 0.00 & 1.00 & 0.00 & 0.00 & 0.00 \\
2.00 & 1.00 & 1.00 & 0.00 & 2.00 & 0.00 & 0.00 & 1.00 & 0.00 & 0.00 & 1.00 & 0.00 \\
2.00 & 1.00 & 1.00 & 0.00 & 0.00 & 2.00 & 0.00 & 0.00 & 0.00 & 1.00 & 0.00 & 1.00 \\
1.00 & 1.00 & 0.00 & 1.00 & 0.00 & 0.00 & 3.92 & 0.00 & -1.17 & -1.17 & 0.00 & 0.00 \\
1.00 & 1.00 & 0.00 & 0.00 & 1.00 & 0.00 & 0.00 & 4.50 & 0.88 & 0.88 & -1.75 & -1.75 \\
1.00 & 0.00 & 1.00 & 1.00 & 0.00 & 0.00 & -1.17 & 0.88 & 4.21 & 0.00 & -1.75 & 0.00 \\
1.00 & 0.00 & 1.00 & 0.00 & 0.00 & 1.00 & -1.17 & 0.88 & 0.00 & 4.21 & 0.00 & -1.75 \\
1.00 & 0.00 & 1.00 & 0.00 & 1.00 & 0.00 & 0.00 & -1.75 & -1.75 & 0.00 & 4.50 & 0.00 \\
1.00 & 1.00 & 0.00 & 0.00 & 0.00 & 1.00 & 0.00 & -1.75 & 0.00 & -1.75 & 0.00 & 4.50
\end{bmatrix}
\times
\begin{bmatrix}
\mu \\ G_M \\ G_F \\ H_1 \\ H_2 \\ H_3 \\ u_A \\ u_B \\ u_C \\ u_D \\ u_E \\ u_F
\end{bmatrix}
=
\begin{bmatrix}
1669 \\ 855 \\ 814 \\ 581 \\ 560 \\ 528 \\ 302 \\ 275 \\ 279 \\ 250 \\ 285 \\ 278
\end{bmatrix}
$$

3. What is the narrow sense heritability (h^2) that corresponds to this value of λ?

$$\lambda = \frac{1 - h^2}{h^2}$$
$$1.75 = \frac{1 - h^2}{h^2}$$
$$1.75h^2 = 1 - h^2$$
$$1.75h^2 + h^2 = 1$$
$$2.75h^2 = 1$$
$$h^2 = \frac{1}{2.75}$$
$$h^2 = 0.36$$

4. Why does the rank of the coefficient matrix not equal the order of the matrix? *Because the rank of a matrix is defined as (a) the maximum number of linearly independent column vectors in the matrix or (b) the maximum number of linearly independent row vectors in the matrix. In this case, G_F and H_3 are not independent rows/columns reducing the rank from 12 to 10.*

5. Find a generalized inverse of the coefficient matrix. Probe that it is a generalized inverse.

$$
C^- =
\begin{bmatrix}
1.11 & -0.41 & 0.00 & -0.70 & -0.79 & 0.00 & -0.20 & -0.06 & -0.22 & -0.46 & -0.18 & -0.35 \\
-0.41 & 0.91 & 0.00 & -0.15 & -0.00 & 0.00 & -0.01 & -0.19 & 0.21 & 0.07 & 0.10 & -0.16 \\
0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 \\
-0.70 & -0.15 & 0.00 & 1.53 & 0.74 & 0.00 & -0.21 & 0.14 & -0.32 & 0.21 & -0.08 & 0.32 \\
-0.79 & -0.00 & 0.00 & 0.74 & 1.56 & 0.00 & 0.11 & -0.27 & -0.02 & 0.36 & -0.28 & 0.21 \\
0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 & 0.00 \\
-0.20 & -0.01 & 0.00 & -0.21 & 0.11 & 0.00 & 0.52 & 0.03 & 0.30 & 0.25 & 0.15 & 0.16 \\
-0.06 & -0.19 & 0.00 & 0.14 & -0.27 & 0.00 & 0.03 & 0.55 & -0.01 & 0.02 & 0.28 & 0.28 \\
-0.22 & 0.21 & 0.00 & -0.32 & -0.02 & 0.00 & 0.30 & -0.01 & 0.56 & 0.16 & 0.27 & 0.06 \\
-0.46 & 0.07 & 0.00 & 0.21 & 0.36 & 0.00 & 0.25 & 0.02 & 0.16 & 0.54 & 0.09 & 0.30 \\
-0.18 & 0.10 & 0.00 & -0.08 & -0.28 & 0.00 & 0.15 & 0.28 & 0.27 & 0.09 & 0.54 & 0.16 \\
-0.35 & -0.16 & 0.00 & 0.32 & 0.21 & 0.00 & 0.16 & 0.28 & 0.06 & 0.30 & 0.16 & 0.56
\end{bmatrix}
$$

```
> round(Cminus %*% C)

    mu Gm Gf H1 H2 H3 A B C D E F
mu   1  0  1  0  0  1 0 0 0 0 0 0
Gm   0  1 -1  0  0  0 0 0 0 0 0 0
Gf   0  0  0  0  0  0 0 0 0 0 0 0
H1   0  0  0  1  0 -1 0 0 0 0 0 0
H2   0  0  0  0  1 -1 0 0 0 0 0 0
H3   0  0  0  0  0  0 0 0 0 0 0 0
A    0  0  0  0  0  0 1 0 0 0 0 0
```

```
B   0  0  0  0  0   0 0 1 0 0 0 0
C   0  0  0  0  0   0 0 0 1 0 0 0
D   0  0  0  0  0   0 0 0 0 1 0 0
E   0  0  0  0  0   0 0 0 0 0 1 0
F   0  0  0  0  0   0 0 0 0 0 0 1
```

```
> round(C %*% Cminus %*% C,2)
```

	mu	Gm	Gf	H1	H2	H3	A	B	C	D	E	F
mu	6	3	3	2	2	2	1.00	1.00	1.00	1.00	1.00	1.00
Gm	3	3	0	1	1	1	1.00	1.00	0.00	0.00	0.00	1.00
Gf	3	0	3	1	1	1	0.00	0.00	1.00	1.00	1.00	0.00
H1	2	1	1	2	0	0	1.00	0.00	1.00	0.00	0.00	0.00
H2	2	1	1	0	2	0	0.00	1.00	0.00	0.00	1.00	0.00
H3	2	1	1	0	0	2	0.00	0.00	0.00	1.00	0.00	1.00
A	1	1	0	1	0	0	3.92	0.00	-1.17	-1.17	0.00	0.00
B	1	1	0	0	1	0	0.00	4.50	0.87	0.87	-1.75	-1.75
C	1	0	1	1	0	0	-1.17	0.87	4.21	0.00	-1.75	0.00
D	1	0	1	0	0	1	-1.17	0.87	0.00	4.21	0.00	-1.75
E	1	0	1	0	1	0	0.00	-1.75	-1.75	0.00	4.50	0.00
F	1	1	0	0	0	1	0.00	-1.75	0.00	-1.75	0.00	4.50

6. Show that these provide a solution of the MME you developed in question 3: $\hat{\mu} = 256.8636$, $\hat{G}_M = 14.03433$, $\hat{G}_F = 0$, $\hat{H}_1 = 25.89654$, $\hat{H}_2 = 15.68469$, $\hat{H}_3 = 0$, $\hat{u}_A = 0.821931$, $\hat{u}_B = -0.54795$, $\hat{u}_C = 0.623531$, $\hat{u}_D = -0.21257$, $\hat{u}_E = 1.417117$, $\hat{u}_F = 0.451115$

```
> betaHat <- c(256.8636, 14.03433, 0, 25.89654, 15.68469, 0)
> uHat <- c(0.821931, -0.54795, 0.623531, -0.21257, 1.417117, 0.451115)
> print(yHat <- X %*% betaHat + Z %*% uHat)

           [,1]
[1,] 297.6164
[2,] 286.0347
[3,] 283.3837
[4,] 256.6510
[5,] 273.9654
[6,] 271.3490
```

7. What does these solutions estimate? *A set of numerical values in function of G_F and H_3 that satisfies the system of equations.*

```
> sE <- round(Cminus %*% C)
> sE <- paste(colnames(sE),apply(sE,1,function(x){
+   paste(x[x!=0],colnames(sE)[x!=0],sep = "", collapse = "+")
+   }), sep = "=")
> sE <- gsub("\\+\\-","\\-",gsub("1","",gsub("=$","=0",sE)))
> writeLines(sE)

mu=mu+Gf+H3
Gm=Gm-Gf
Gf=0
H=H-H3
H2=H2-H3
```

```
H3=0
A=A
B=B
C=C
D=D
E=E
F=F
```

8. Describe the difference between fixed and random effects *Fixed effects are constant across individuals, for that reason, these effects are computed as average for the given sample sharing a given factor. Meanwhile, random effects vary from one to another individual, for that reason, a unique value is calculated for each independently.*

9. In this model: $y_{ijk} = \mu + H_i + L_j + C_k + e_{ijk}$ in which y_{ijk} is 305-d milk yield of cows, μ is the overal mean, H_i is the fixed effect in the ith herd, L_j is the fixed effect of the jth lactation, C_k is the effect of the kth cow, and e_{ijk} is the residual associated with the ijk^{th} observation.

$$P = A + NA + PE + TE$$

Detail any differences in σ_c^2 when cows are modeled as fixed effects vs when (in separate analyses) they are modeled as random effects. Where would you expect the additive component of phenotype to be under each of those parameterizations? *When cows are modeled as fixed effects, the computed values for each cow are the deviation of that specific cow with respect to another one used as a point of comparison (usually the last one); under this parameterization, the σ_c^2 are underestimated and the portion of the variance not explained will be assigned to the σ_e^2. When cows are modeled as random effects, the computed values for each cow are the deviation of that specific cow with respect to the mean value of all the cows, under this parameterization, the σ_c^2 are optimized to be the maximum and then the σ_e^2 will be minimized.*