**Appendix 1.**

**Implementation of mixed models equation. Example.**

We have reproduced the example that was explained in the study by Varona et al., (2019) to show the applied methodology, based in the one proposed by García-Cortés et al., (2010). We first obtained the partial inbreeding coefficients for each of the individuals (see Appendix 2 for the implementation in R on how to obtain for each individual). The pedigree consisted of five individuals, linked as follows:

|  |  |  |
| --- | --- | --- |
| Animal | Sire | Dam |
| 1 | 0 | 0 |
| 2 | 0 | 0 |
| 3 | 1 | 2 |
| 4 | 1 | 3 |
| 5 | 4 | 3 |

The resulting partial inbreeding coefficients are:

|  |  |  |
| --- | --- | --- |
| Descendant | Ancestor |  |
| 4 | 1 | 0.2500 |
| 5 | 1 | 0.1875 |
| 5 | 2 | 0.0625 |
| 5 | 3 | 0.1250 |

Results show the animal contributions of the inbreeding in individuals 4 and 5. The partial inbreeding coefficient of individual 4 is 0.2500, obtained from individual 1. For individual 5, the partial inbreeding coefficient is 0.375 and is obtained from individuals 1 (0.1875), 2 (0.0625) and 3 (0.125).

Following the model:

We obtain the vectors and matrices required for the implementation of the mixed-models equation. Individuals 3,4, and 5 had the phenotypes 113, 87, and 96:

,

,

,

where ,

and .

In addition, the numerator relationship matrix () and the corresponding inverse () are:

, and

,

ending up with the mixed-model equation:

Where , , and are the elements of the inverse of the covariance matrix between the additive and the inbreeding load effects (). Assuming , , , and then:

,

the final equation is:

= ,

and the solutions are: