Applications of graph theory for verify the family relationship for genetic evaluations through the Animal Model

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Abstract

Animal genetic improvement is an usual method for increasing the productivity of the herd. Therefore, selecting animals that are potentially better than their peers and/or contemporary is important because the descendants of these animals will have enhanced characteristics. Genetic evaluations are used in animal genetic improvement programs to predict the potential genetic value of the animals and their PTAs (predicted transmitting abilities); however, to obtain good results, one needs as much information as possible about the individuals, their relatives, and their ancestors to get the most accurate data. The Animal Model is a computational implementation of genetic evaluations which considers significantly the information about the kinship of animals. The Animal Model considers the data of each evaluated animal, as well as other animals that have the same relationship to it. Some of its best-known instances, such as MTDFREML, require recoding identification of all animals that are in the database, recoding them from the fathers, then the mothers, and finally the sons. By recoding animals in this way, it is possible to identify and, when appropriate, correct any existing irregularities in the set of data, such as the same identification being used for different animals, which can also cause the inconsistency of an animal being its own ancestor. Thus, a graph can be built, considering (i) the individuals and their family relationships as vertexes and edges, respectively, and (ii) the graph concepts and directed graph, the path, circuit, and cycle, and the connected/disconnected graphs and strongly connected graphs. Because the database might be extensive, one should generate many connected graphs, or better, a graph with connected components that resemble kinship trees between animals. The connected components are checked and in the observation of a cycle - a strongly connected sub-graph - it means that some individual of this sub-graph is its own ancestor. Supported by: CAPES, CNPq, Embrapa, Embrapa Dairy Cattle, FAPEMIG and UFJF.