

## SGRMate: for maximizing genetic gain and controlling inbreeding



**Brazilian Agricultural Research Corporation  
Embrapa Goats & Sheep  
Ministry of Agriculture, Livestock and Food Supply**

## **DOCUMENTOS 144**

# SGRMate: for maximizing genetic gain and controlling inbreeding

*Raimundo Nonato Braga Lôbo*

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**Embrapa Goats & Sheep**  
Fazenda Três Lagoas, Estrada Sobral/  
Groaíras, Km 4 Caixa Postal: 71  
CEP: 62010-970 - Sobral, CE  
Fone: (88) 3112-7400  
www.embrapa.br  
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## Author

### **Raimundo Nonato Braga Lôbo**

Veterinarian, Doctor of Animal Sciences, researcher at Embrapa Goats & Sheep, Sobral, CE, Brazil.

## Presentation

Genetic evaluations in animal breeding are essential for identifying superior individuals, who can be selected to compose the next generation. The indication of sires and dams of proven genetic value improves the efficiency of production systems. On the other hand, the use of few animals in the selection process can increase the inbreeding of the herds, which can reduce the animals' vigor and reduce future genetic variability. Additionally, with the availability of genetic value from several animals, the decision of how to combine these parents for the possibility of greater genetic gain is not such a simple task. Imagine having to combine 20 sires with 300 dams, who should be mated with whom?

The availability of a tool to carry out this work has a great impact, as it reduces time for decision and adds greater prediction of success to the process. The SGRMate was developed for this purpose, to help producers, breeders and scientists in the design of matings that maximize genetic gain and minimize the impacts of inbreeding on the herds under their supervision.

This “Série Embrapa – Documentos” presents a practical guide for the correct use of the SGRMate software.

*Marco Aurélio Delmondes Bomfim*  
Head of Embrapa Goats & Sheep

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## Introduction

Mating methods and selection are the two tools to promote the genetic improvement of herds. Mating methods refer to combinations of parents with greater proximity (inbreeding) or greater genetic distance (crossbreeding). Selection is characterized by the choice of genetically superior animals for a given selection criterion or index, associated with their respective reproductive intensity. Then, it is necessary to form reproductive pairs, that is, direct each male to a specific group of females.

Detailed mating planning should be a routine among breeders, as the genetic progress of the herd depends on the ability to select the best sires to mate with the best dams. However, this is a complex task due to several factors, such as: possible severe phenotypic defects in females, search for progeny homogeneity, presence of different selection objectives, availability and price of the semen or of the sire and the need to maintain genetic variability.

The indiscriminate use of few sires can lead to an increase in the inbreeding coefficient of herds, increasing homozygosity in some loci, which can favor the appearance of diseases caused by recessive alleles. In addition, there is the possibility of inbreeding depression, which is a decrease in the performance of animals, especially in low heritability traits (reproductive and adaptive).

The importance and complexity of forming the reproductive pairs that will generate the next progeny is evident. Thus, it is necessary to use programs (algorithms) to assist in decision making, in order to maximize genetic gains and preserve genetic diversity. SGRMate, which use linear programming as methodology, was developed with this purpose. Montenegro et al. (2019) compared it with other systems that use other methodologies: Gencont (Optimal Genetic Contribution and Lagrange multipliers; Meuwissen, 2012), Mate Selection (Evolutionary differential; Kinghorn, 2000), using a random mating as reference. The authors concluded that SGRmate maintained lowest levels of inbreeding due to higher number of sires selected and equal proportionality in combination of the pairs, and was more efficient in maintaining the genetic diversity of small-closed populations.

The aim of this manuscript is present how to use SGRMate.

## Installing and using multiatr

SGRMate was compiled for Windows© (32 and 64 bits). After getting the executable file, it can be placed in any directory preferred by the user. No need for any additional installation.

Open the prompt of command (CMD; in Windows© search field type cmd) and goes to the directory where the software is. As an example, if the software is in the C:\SGRMATE directory, type at the command prompt 'cd C:\SGRMATE' and hit the enter key.

Thus, type SGRMate and hit enter key starting the software. The sequence that follows indicates the questions that the SGRMate will ask to develop the assessment.

PEDIGREE FILE NAME (1)

FILE MUST HAVE THREE COLUMNS: ANIMAL, SIRE AND DAM

The user must indicate the name of the file that contains the pedigree of the animals under evaluation. This file must be in the same directory as the software or, if it is in another directory, indicate the full path where it is, along with its name. This file must contain three columns, with animal, sire and dam, in this sequence. It must have the codes ordered, with the codes of sire and dam being inferior to that of the animal.

FILE NAME WITH SIRES INFORMATION

THIS FILE MUST HAVE TWO COLUMNS: (2)

CODE (SAME AS THE PEDIGREE FILE) AND GENETIC VALUE

Indicate the path (if the file is not in the same directory as the SGRMate) and the file name with the codes of the sires to be combined, followed by their genetic value (or Expected Progeny Differences - EPD).

FILE NAME WITH DAMS INFORMATION (3)

## CODE (SAME AS THE PEDIGREE FILE) AND GENETIC VALUE

Indicate the path (if the file is not in the same directory as the SGRMate) and the file name with the codes of the dams to be combined, followed by their genetic value (or Expected Progeny Differences - EPD). It is noteworthy that the sire and dam codes must be the same contained in the pedigree file.

## ENTER THE MAXIMUM AVERAGE VALUE FOR ENDOGAMY OF MATINGS (4)

Indicate the maximum value for the average of the allowed inbreeding coefficient for the combination to be obtained between all sires and dams. This percentage value should be indicated as a decimal (e.g., 0.08 for 8%).

It is suggested to know the current average inbreeding coefficient of the herd, since a high restriction may not indicate any combination that meets it. For example, if the average inbreeding of the herd is 10%, using a value higher than this may make a compatible combination unfeasible.

## ENTER THE MAXIMUM AVERAGE VALUE FOR ENDOGAMY FOR A GIVEN MATING (5)

Indicate the maximum value for the average of the allowed inbreeding coefficient for a specific mating. For example, if the user does not want the combination between a father and a daughter, this value must be below 25%. This percentage value should be indicated as a decimal (e.g., 0.25).

After that, the SGRMate will estimate the ideal combination that meets the data and criteria informed. The result is printed in the output.txt file. It is noteworthy that not necessarily all sires and dams can be nominated, as the system will search for the best solution that meets the criteria. There is also a possibility that the system will not find this combination, so that the user must reduce the constraints in the search for this solution. Thus, it is important that the evaluator has a good knowledge of the herd he/she manages to achieve his objectives with parsimony.

It is observed that the use of the SGRMate is simple and practical, and the user only needs to have the necessary information properly (Figure 1).

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                                SGRMate

                                MATING COMBINATION THAT MAXIMIZE THE
                                GENETIC GAIN AND CONTROL INBREEDING

                                v.1.0
                                Build 20161004

                                Authorship: RAIMUNDO NONATO BRAGA LOBO
EMPRESA BRASILEIRA DE PESQUISA AGROPECUARIA - EMBRAPA
*****
PEDIGREE FILE NAME
FILE MUST HAVE THREE COLUMNS: ANIMAL, SIRE AND DAM
ped_teste_ex1.txt

FILE NAME WITH SIRES INFORMATION
THIS FILE MUST HAVE TWO COLUMNS:
CODE (SAME AS THE PEDIGREE FILE) AND GENETIC VALUE
macho_ex1.txt
FILE NAME WITH DAMS INFORMATION
CODE (SAME AS THE PEDIGREE FILE) AND GENETIC VALUE
femea_ex1.txt
ENTER THE MAXIMUM AVERAGE VALUE FOR ENDOGAMY OF          MATINGS
.08
ENTER THE MAXIMUM AVERAGE VALUE FOR ENDOGAMY FOR A      GIVEN MATING
.20

```

**Figure 1.** Image of command prompt with an analysis with SGRMate

## Final considerations

SGRMate is an easy-to-use algorithm that makes an important contribution to animal production systems, especially in situations of small-closed herds, and unavailability of financial resources, such as the conditions of participatory Community Based Breeding Programs (CBBPs).

Its contribution to the search for greater genetic gain in populations, controlling the loss of genetic diversity, will allow for sustainable rural development.

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## Appendix

Simple example of SGRMate

1) Pedigree file (ped\_teste\_ex1.txt)

1 0 0

2 0 0

3 1 2

4 1 2

5 3 4

6 3 0

7 3 6

8 5 4

9 1 6

10 1 4

2) File of Sires (macho\_ex1.txt)

1 .45

3 -.2

5 .01

3) File of Dams (femea\_ex1.txt)

2 .2

4 -.1

8 .05

10 -.04

\*\*\*\*\*

SGRMate

MATING COMBINATION THAT MAXIMIZES THE  
GENETIC GAIN AND CONTROL INBREEDING

v.1.0

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Authorship:

Brazilian Agricultural Research Corporation - EMBRAPA

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PEDIGREE FILE NAME

FILE MUST HAVE THREE COLUMNS: ANIMAL, SIRE AND DAM

ped\_teste\_ex1.txt

FILE NAME WITH SIRES INFORMATION

THIS FILE MUST HAVE TWO COLUMNS:

CODE (SAME AS THE PEDIGREE FILE) AND GENETIC VALUE

macho\_ex1.txt

FILE NAME WITH DAMS INFORMATION

CODE (SAME AS THE PEDIGREE FILE) AND GENETIC VALUE

femea\_ex1.txt

ENTER THE MAXIMUM AVERAGE VALUE FOR ENDOGAMY OF MATINGS

.08

ENTER THE MAXIMUM AVERAGE VALUE FOR ENDOGAMY FOR A  
GIVEN MATING

.20

## 4) Output file (output.txt)

1	10
---	----

1	8
---	---

5	4
---	---

5	2
---	---



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