

# Guide and reference manual for use of CoeFR

A program for calculating coefficients of inbreeding and relationship of animals

October 4, 2017  
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## 1. Development

'CoeFR' is software for calculating coefficients of inbreeding and relationship of animals in a (large) population. 'CoeFRre' is the English version of 'CoeFR'. The original is 'CoeF' developed on August 1, 2000. The latest version is 3.7, which is shown on the third line in the source program file. 'CoeFRre' is written in standard FORTRAN90/95. The algorithm for calculating coefficients of inbreeding is based on Meuwissen and Luo (Genet. Sel. Evol., 1992). The user has to prepare a 'Pedigree file' for calculating coefficients of inbreeding before running the program. The user also has to prepare a 'Relationship file' if the user wants to calculate coefficients of relationship between animals in two groups. After preparing the file(s), the user can easily run 'CoeFRre'. The user can rewrite a part of the program and compile it if necessary. The source file is 'CoeFRre.for' and the executive file is 'CoeFRre.exe'.

## 2. Preparation

### 2.1 Pedigree file

The file should be in free format (i.e., spaces or commas between all valuables). The 'Pedigree file' must have three columns of effective data: Animal ID, sire ID, and dam ID. Optionally, the fourth column (usually not necessary) holds the status of the coefficients of inbreeding. Each ID has to be:

1) Animal ID is any positive integer and not more than 18 digits ( $2^{64}-1 \approx 9.22 \times 10^{18}$ ).

2) Sire ID and dam ID are any integers and not more than 18 digits.

If ID is larger than 18 digits, or include characters, ID must be recoded prior to running 'CoeFRre'.

3) If sire ID or dam ID is missing, the missing parent ID must be coded as a 0 or a unique number other than 0.

4) The order of animal ID in the 'Pedigree file' is unrestricted. But the calculating time is faster if sire ID and dam ID as animal ID position before their progeny ID.

An example 'Pedigree file' is shown below:

1	0	0
2	0	0
3	0	0
4	0	0
5	0	0
6	0	0
11	1	3
12	1	4
13	1	4
14	2	5
15	2	5
16	2	6
21	11	16
22	11	16
23	11	13
24	12	14
25	12	15

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26	12	15
31	21	24
32	21	25
33	21	25
34	22	23
35	22	26
36	22	26
41	32	33
42	32	33
43	32	34
46	31	36
45	31	35
44	31	36
56	42	44
55	42	43
58	41	46
59	41	45
57	42	44
60	41	44

## 2.2 Relationship file (Optional file)

If the user wants to calculate coefficients of relationship between animals, the 'Relationship file' has to be prepared before running. The file should be in free format. In the first line, write the numbers of animals in the first and the second groups between which the user wants to calculate the coefficients of relationship in the 'Pedigree file'. For example, the groups may be male and female animals in the last generation. From the second row, the animal ID has to be as below:

1) Write animal ID in each line in the first group.

2) Write animal ID in each line in the second group after following the last animal ID in the first group.

The animal ID in the 'Relationship file' must be in the 'Pedigree file'. If not, only coefficients of inbreeding can be calculated. If there is the same ID in the first and second groups, the coefficient of relationship is 1.0.

An example 'Relationship file' is shown below:

Relationship file (test. r   s)	
1	6
	41
	56
	55
	58
	59
	57
	60

In this case, only ID-41 is in the first group and the coefficients of relationship between ID-41 and the other six animals will be calculated.

## 3. Restrictions

The main restriction of 'CoeFRe' is the maximum number of animals analyzed. The provisional number is 20,000,000 although the number depends on the performance of the computer. If the user wants to change the number of animals to be analyzed, rewrite the number in the parameter statement in the

source program, 'CoeFR.for', and then recompile it. However, 20,000,000 animals should be sufficient in most cases.

#### 4. User interface

If the user runs 'CoeFR', the program asks several questions. An example Q&A is as follows:

```
Name of pedigree file.  
test.ped  
Choice of treatment when animals in the base have the same parent ID. (1-2)  
1. Ignore the relationship between these animals.  
2. Consider the relationship between these animals.  
1 → CoeFR recognizes that the same parent ID of the base animals are different animals.  
Choice of order in output file of inbreeding coefficients. (1-3)'  
1. Order of animals in pedigree file.  
2. Order of animals by age.  
3. Both files (1 and 2).  
1  
Name of output file for inbreeding coefficient.  
test.out1  
Do you want coefficients of relationship? (Y/N)  
Y  
Name of file for coefficients of relationship.  
test.rls  
Name of output file for coefficients of relationship.  
test.out2
```

The computation starts after the user has finished inputting the correct answers. If the answer has a slight error, the program shows the error message and repeats the question. But if it is a fatal error, the program shows the error message and stops automatically.

#### 5. Output

The results are outputted in the file(s) given the name in Q&A. Previous examples ('test.out1' and 'test.out2') are as follows:

##### Output of coefficients of inbreeding (test.out1)

1	0	0	0.000000
2	0	0	0.000000
3	0	0	0.000000
4	0	0	0.000000
5	0	0	0.000000
6	0	0	0.000000
11	1	3	0.000000
12	1	4	0.000000
13	1	4	0.000000
14	2	5	0.000000
15	2	5	0.000000
16	2	6	0.000000

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21	11	16	0.000000
22	11	16	0.000000
23	11	13	0.125000
24	12	14	0.000000
25	12	15	0.000000
26	12	15	0.000000
31	21	24	0.062500
32	21	25	0.062500
33	21	25	0.062500
34	22	23	0.156250
35	22	26	0.062500
36	22	26	0.062500
41	32	33	0.281250
42	32	33	0.281250
43	32	34	0.140625
46	31	36	0.140625
45	31	35	0.140625
44	31	36	0.140625
56	42	44	0.179688
55	42	43	0.273438
58	41	46	0.179688
59	41	45	0.179688
57	42	44	0.179688
60	41	44	0.179688

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Output of coefficients of relationship (test. out2)

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41	56	0.476597
41	55	0.532113
41	58	0.667235
41	59	0.667235
41	57	0.476597
41	60	0.667235

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## 6. Reference

The program 'CoeFRe' is free for research purposes. The author does not offer any guarantee for this program. The user must show the reference if writing any paper, report, etc. based on research using 'CoeFRe'. For the time being, the reference is "Satoh, M., A program for computing inbreeding coefficients from large data sets. *Japanese Journal of Swine Science*. Vol.37 No.3 p.122-126. (2000)".

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