Session 38: Free communications in Animal Genetics

EUROPA 2010 - HERAKLION - GREECE - EAAP - FEZ - EVT - ΕΑΖ 61

EAAP 2010

61st Annual Meeting of the European Association for Animal Production

AUGUST 23rd-27th, 2010 - HERAKLION, CRETE ISLAND, GREECE

Fine decomposition of the inbreeding and the coancestry coefficients by using the tabular method

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POLITÉCNICA
Ingeniamos el futuro

- **Effective population size**

$Ne=1/2\,\Delta F$ or $Ne=1/2\,\Delta f$

is the most important parameter describing the evolution of genetic diversity

But it is used mainly for predictive purposes

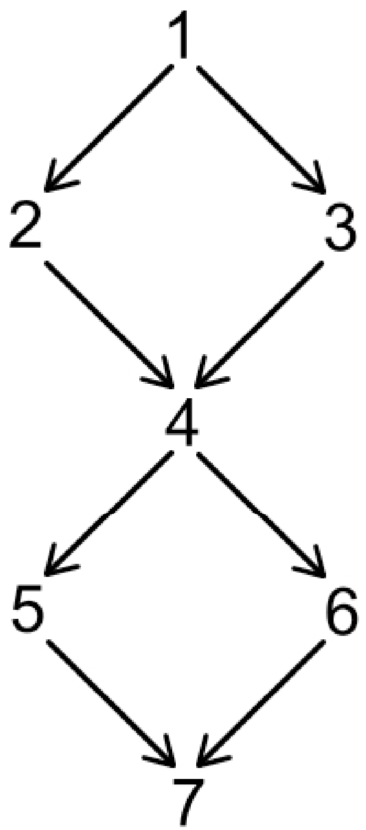
- On the othe hand,

When analysing **a realized genealogy** the main concept is the **contributions from an ancestor to descendents**: ***the proportion of all distinct genealogical pathways that travel from an ancestor to a group of descendents***

There are several ways of approaching the topic

A) Nodal common ancestors decomposition

Wright's (1922) consists in determining the common ancestors from which the same copy of the gene have been received



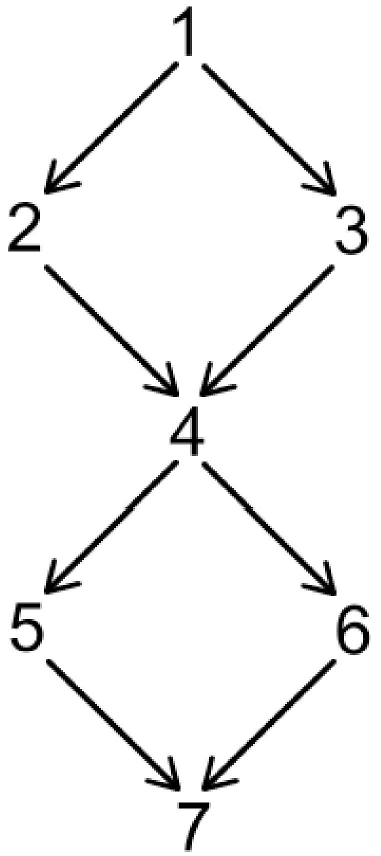
Decomposition of f_7

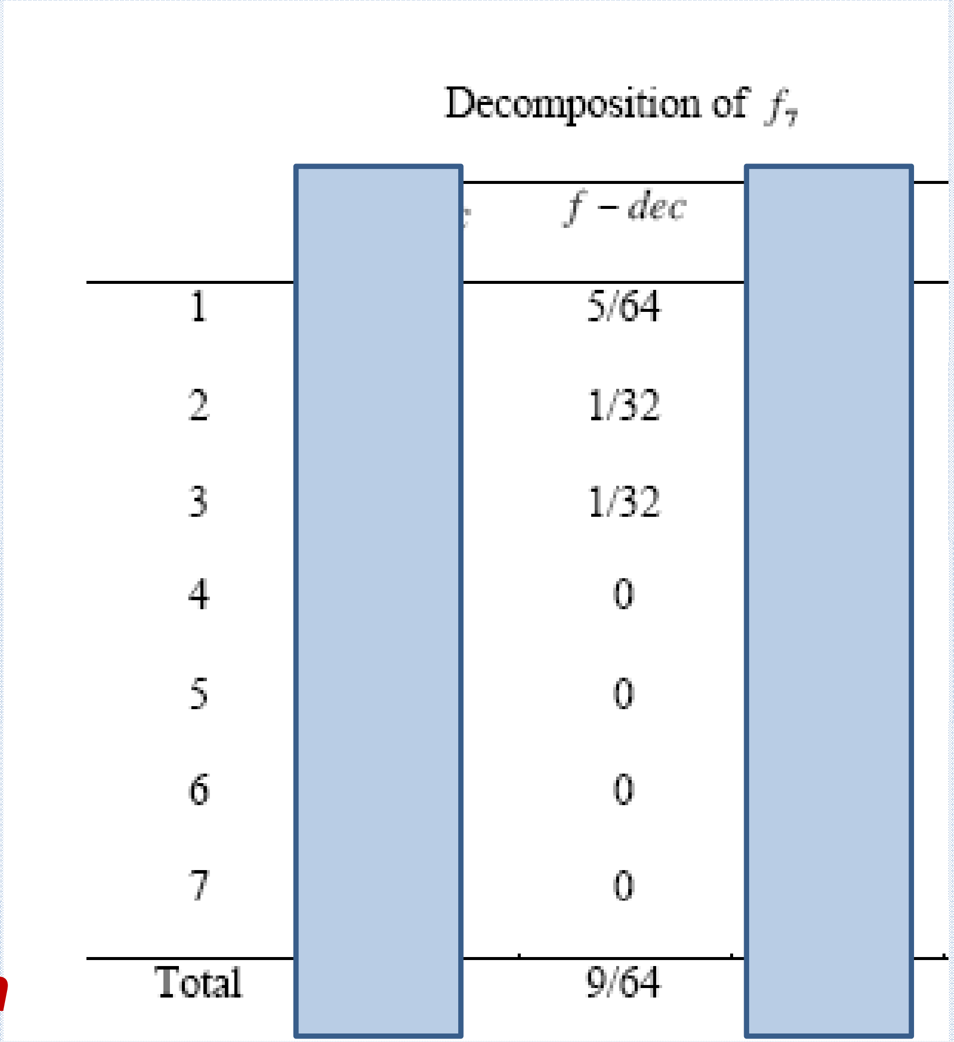
	$n - dec$
1	1/64
2	0
3	0
4	1/8
5	0
6	0
7	0
Total	9/64

n - dec is the nodal decomposition

B) Partial founder decomposition

Consists in determining the partial inbreeding and coancestry atributed to each founder (Lacy, 1996)





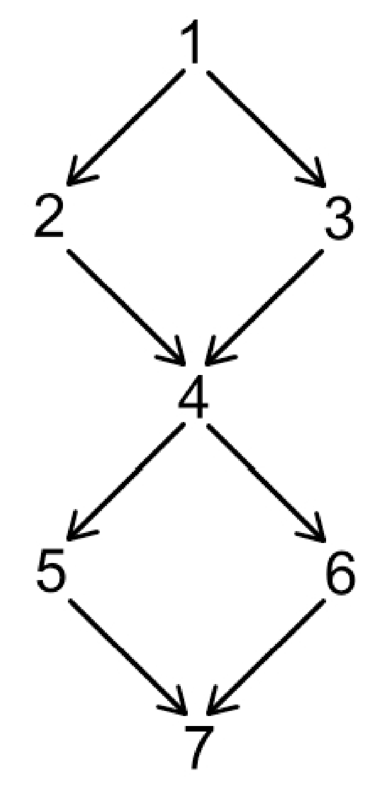
Decomposition of f_7

	$f-dec$
1	5/64
2	1/32
3	1/32
4	0
5	0
6	0
7	0
Total	9/64

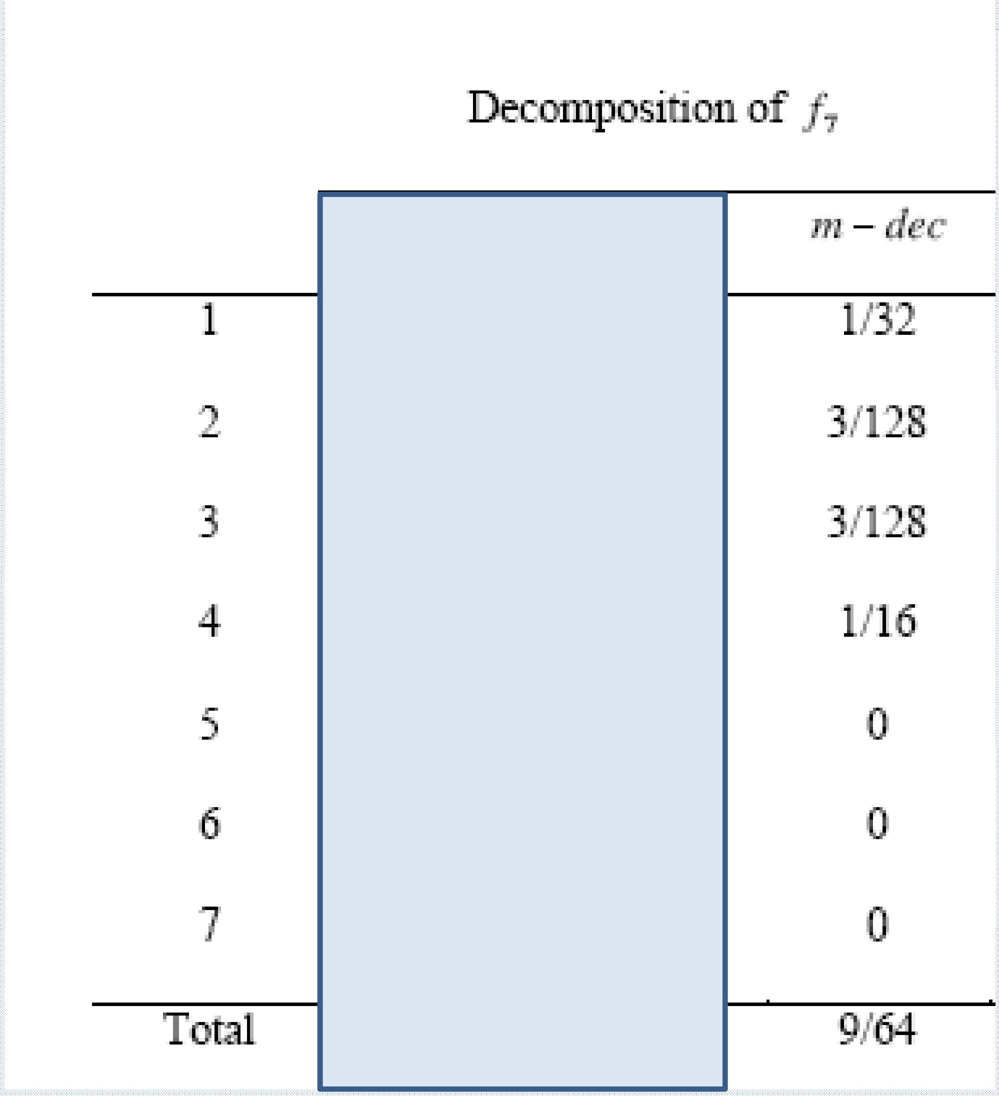
f- dec is the partial founder decomposition

C) Mendelian decomposition

Consists in decompoing the inbreeding and coancestry in several parts attributable to both founders and non-founders (Caballero and Toro, 2002)

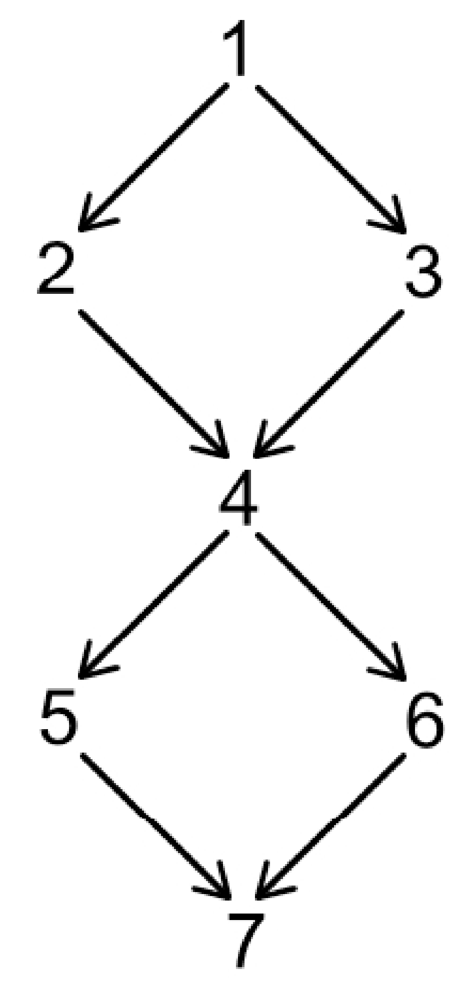


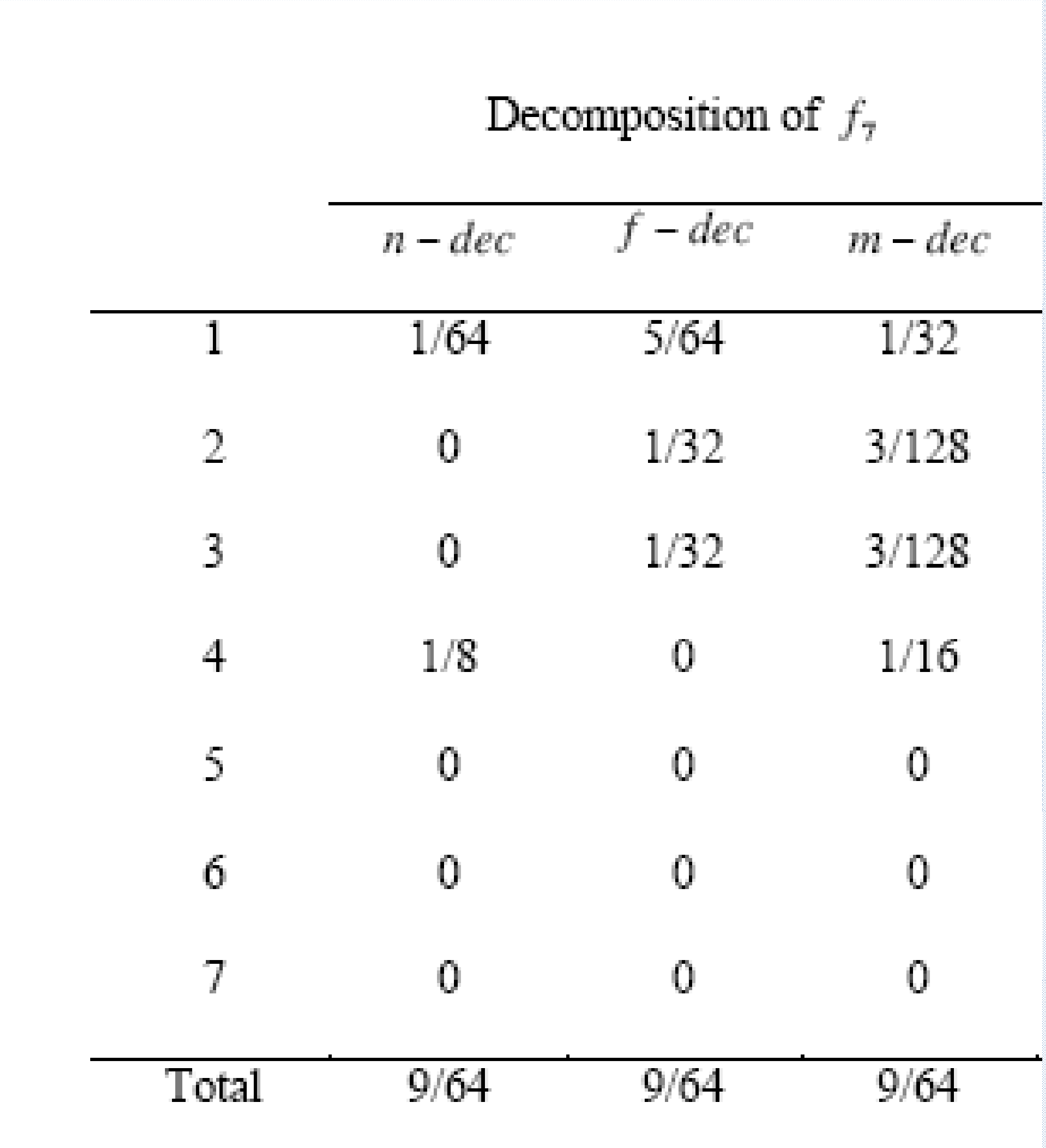
m- dec is the Mendelian decomposition



Decomposition of f_7

		$m - dec$
1		1/32
2		3/128
3		3/128
4		1/16
5		0
6		0
7		0
Total		9/64



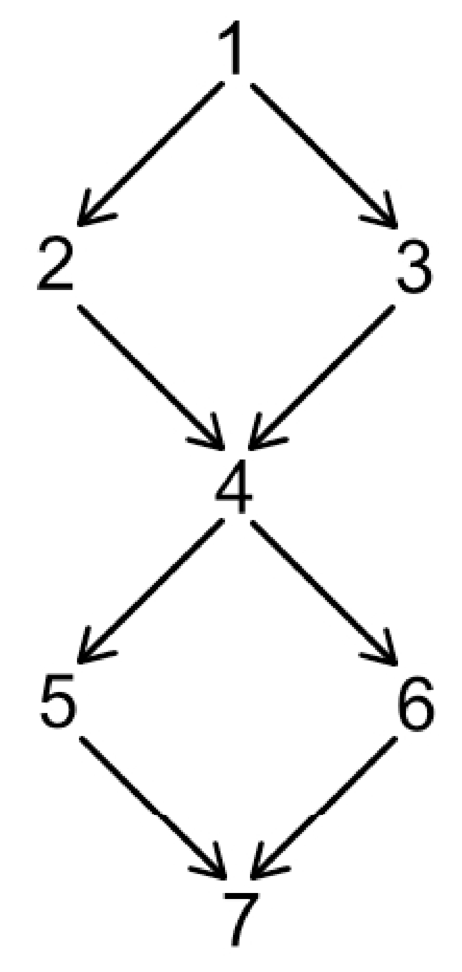


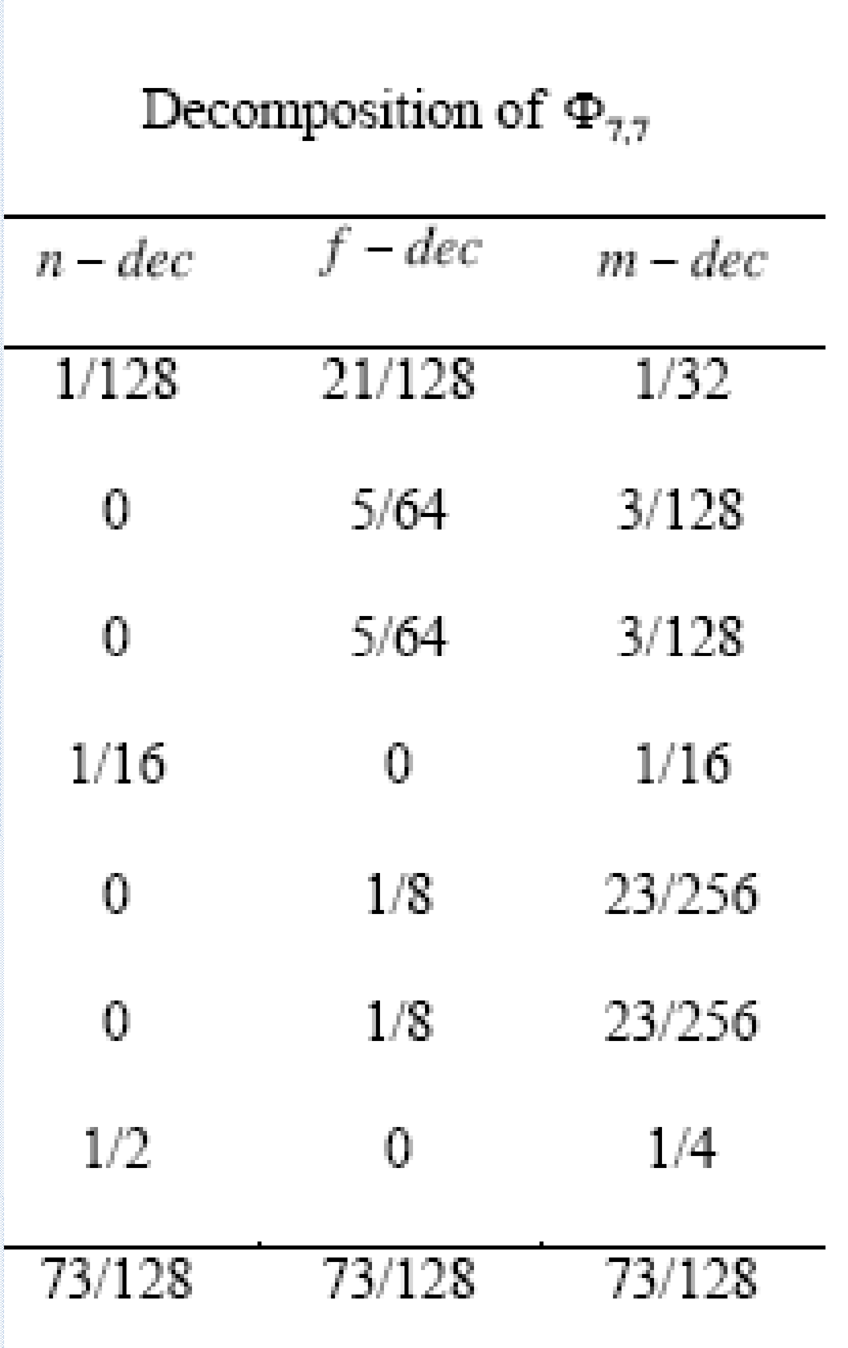
	Decomposition of f_7		
	$n-dec$	$f-dec$	$m-dec$
1	1/64	5/64	1/32
2	0	1/32	3/128
3	0	1/32	3/128
4	1/8	0	1/16
5	0	0	0
6	0	0	0
7	0	0	0
Total	9/64	9/64	9/64

***n - dec is the nodal* decomposition**

f- dec is the founder decomposition

***m- dec is the Mendelian* decomposition**





Decomposition of $\Phi_{7,7}$

$n - dec$	$f - dec$	$m - dec$
1/128	21/128	1/32
0	5/64	3/128
0	5/64	3/128
1/16	0	1/16
0	1/8	23/256
0	1/8	23/256
1/2	0	1/4
73/128	73/128	73/128

n - dec is the nodal decomposition
f- dec is the founder decomposition
m- dec is the Mendelian decomposition

Recent developments

A) Nodal common ancestors decomposition

- Wright (1922) uses a path method but **COLLEAU and SARGOLZAEI (2008)** have provided a **Tabular implementation of Wright's method**

- The nodal based decomposition and the Mendelian decomposition are closely related by a simple transformation (**COLLEAU and SARGOLZAEI, 2008)**

- The nodal based decomposition can be utilized to measuring the retrospective efficiency of a breeding programme (**COLLEAU and SARGOLZAEI, 2008)**

Recent developments

B) Partial founder decomposition (LACY et al., 1996)

- **It has been used to detect inbreeding depression heterogeneity attributed to each founder (Rodrigañez et al., 1998; Gulisija et al., 2006; Casellas et al., 2009)**

Recent developments

C) Mendelian decomposition

C. 1. It has been successfully to put in the same framwork genetic response and inbreeding (WOOLLIAMS AND THOMPSON, 1994)

C. 2. It has been use to monitorize the evolution of genetic diversity in a conservation programme *(CABALLERO AND TORO, 2002)*

In a pedigree of M individuals with N_0 founders the average coancestry of a group of individuals is

$$\bar{f} = 0.50 \sum_{i=1}^{N_0} c_i^2 + 0.25 \sum_{i=N_0+1}^{M} c_i^2 \left(1 - \frac{F_{Si} + F_{Di}}{2}\right)$$

Recent developments

$$\bar{f} = 0.50\sum_{i=1}^{N_0} c_i^2 + 0.25\sum_{i=N_0+1}^{M} c_i^2 \left(1 - \frac{F_{Si} + F_{Di}}{2}\right)$$

Effective number of founders of a cohort

$$N_{ef} = \frac{1}{\sum_{i}^{N_0} c_i^2}$$

Effective number of non-founders of a cohort

$$N_{enf} = \frac{1}{\sum_{i=N_0+1}^{M} d_i^2}$$

Number of genome equivalents

$$N_{ge} = \frac{1}{2\bar{f}}$$

$$\frac{1}{2N_{ge}} = \frac{1}{2N_{ef}} + \frac{1}{2N_{enf}}$$

Recent developments

C) Mendelian decomposition

C. 3. It has been successfully used to validate the effectiveness of the different selection decisions (GARCÍA-CORTÉS et al. 2008)

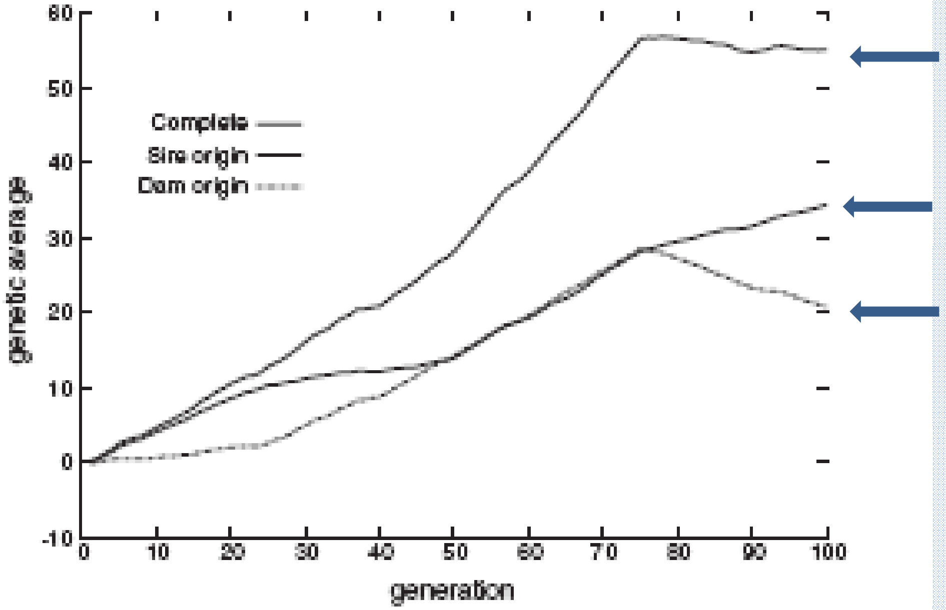


Figure 1 The estimated genetic response of the whole population and the estimated genetic response due to selection of sires and selection of dams. The selection policy varies every 25th generation.

Generations 1 to 25: **selection only on the sire side**

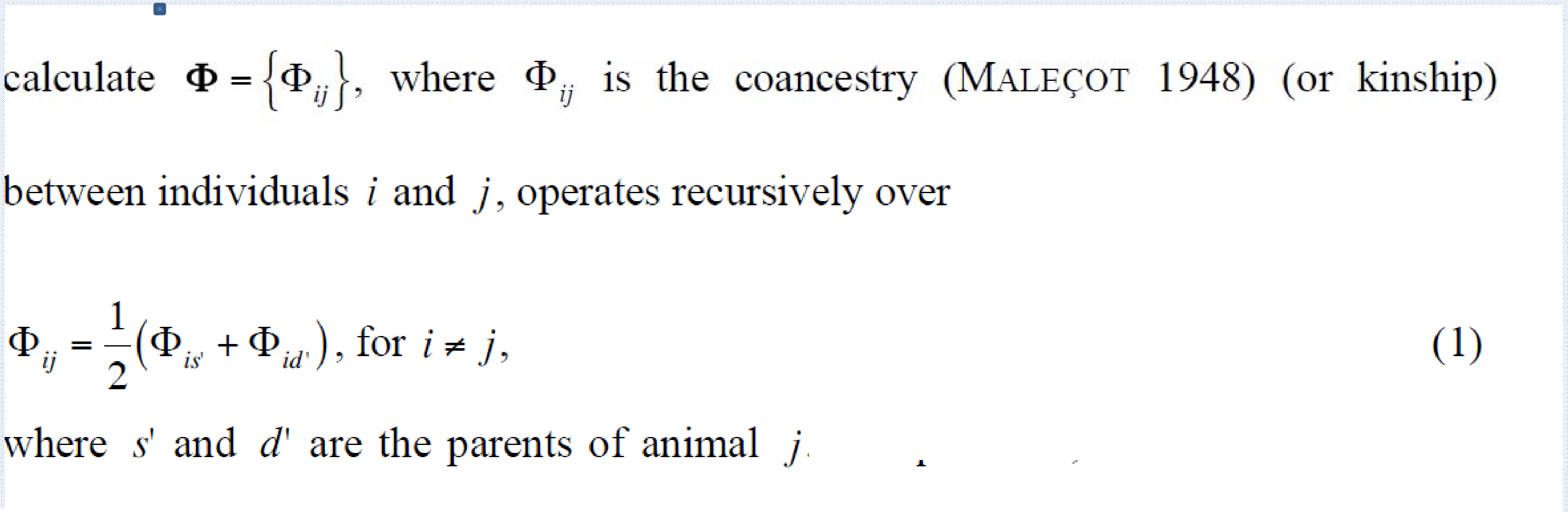
Generations 26 to 50**: selection only on the dam side**

Generations 51 to 75**: selection on males and females simultaneously.**

Generations 76 to 100**: sires and dams were selected in opposite directions**

We have developed a tabular method to do the mendelian decomposition

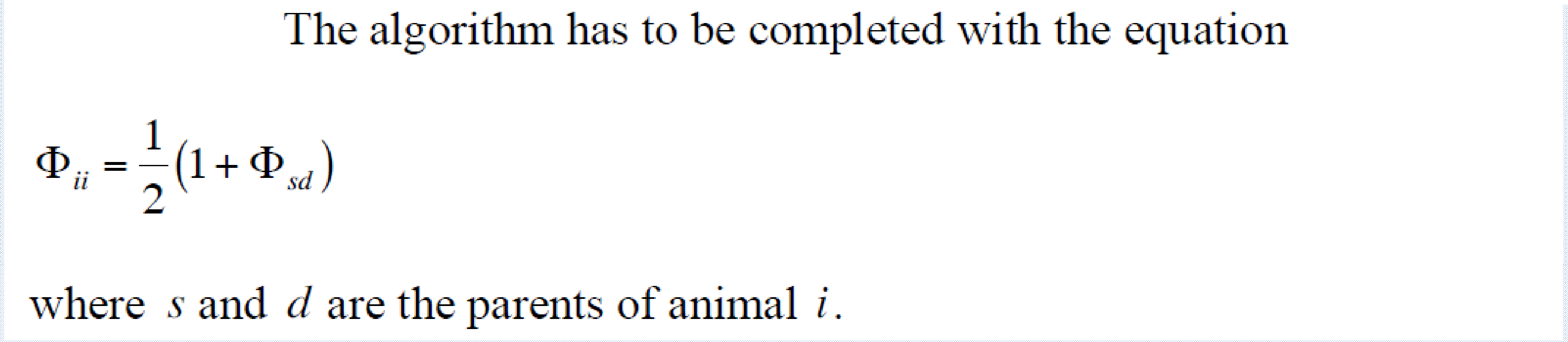
In the classical tabular method:



calculate $\Phi = \{\Phi_{ij}\}$, where Φ_{ij} is the coancestry (MALEÇOT 1948) (or kinship) between individuals i and j, operates recursively over

$$\Phi_{ij} = \frac{1}{2}\left(\Phi_{is'} + \Phi_{id'}\right), \text{ for } i \neq j, \qquad (1)$$

where s' and d' are the parents of animal j.

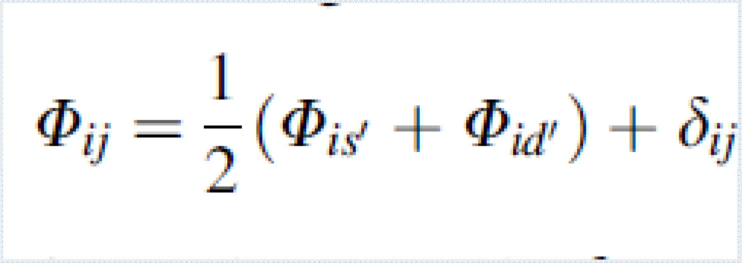


The algorithm has to be completed with the equation

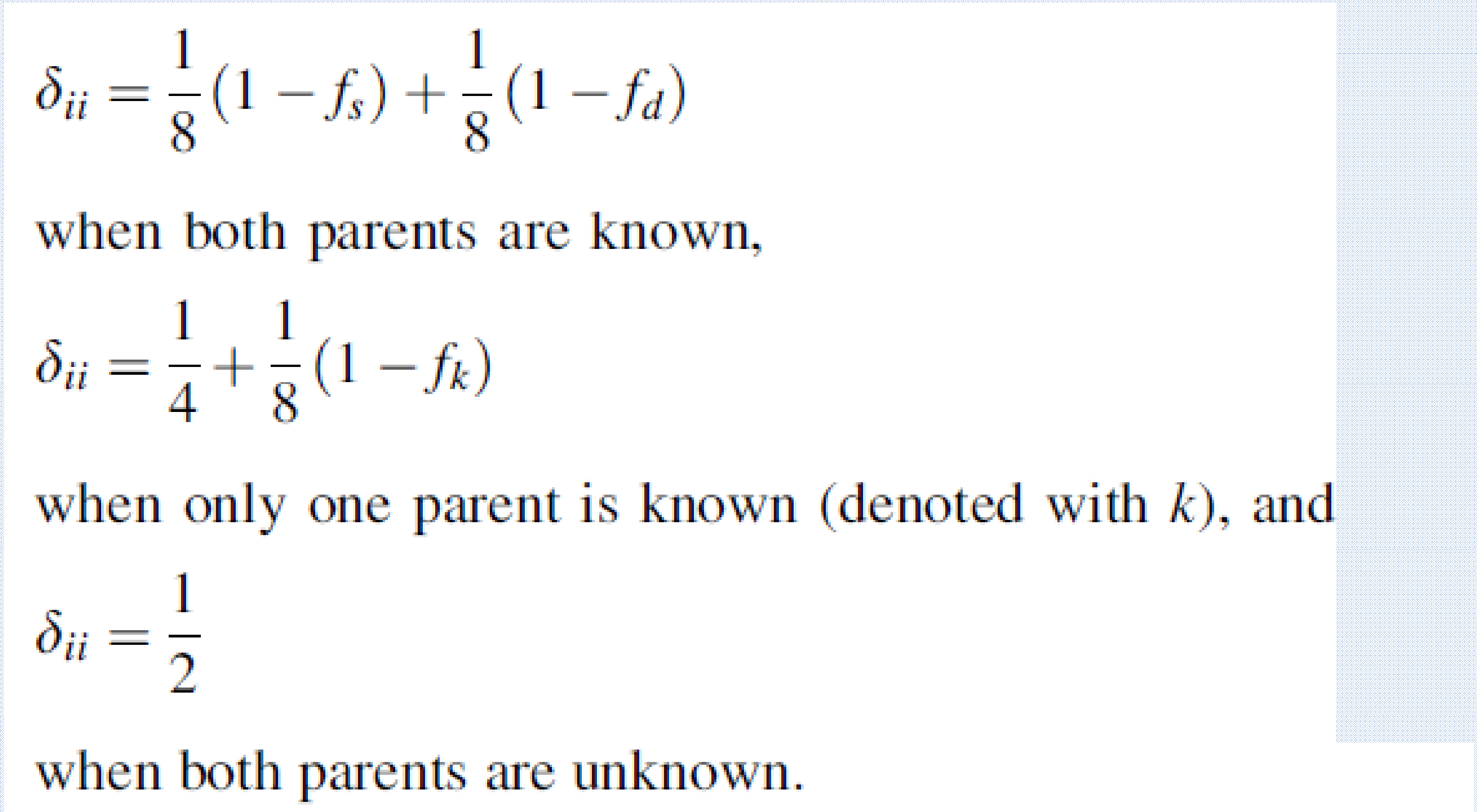
$$\Phi_{ii} = \frac{1}{2}\left(1 + \Phi_{sd}\right)$$

where s and d are the parents of animal i.

Here , we propose to replace the previous equations by



$$\Phi_{ij} = \frac{1}{2}(\Phi_{is'} + \Phi_{id'}) + \delta_{ij}$$



$$\delta_{ii} = \frac{1}{8}(1 - f_s) + \frac{1}{8}(1 - f_d)$$

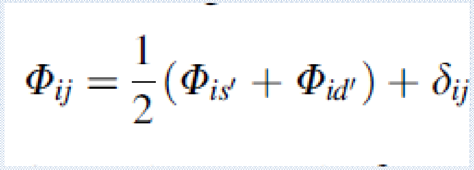
when both parents are known,

$$\delta_{ii} = \frac{1}{4} + \frac{1}{8}(1 - f_k)$$

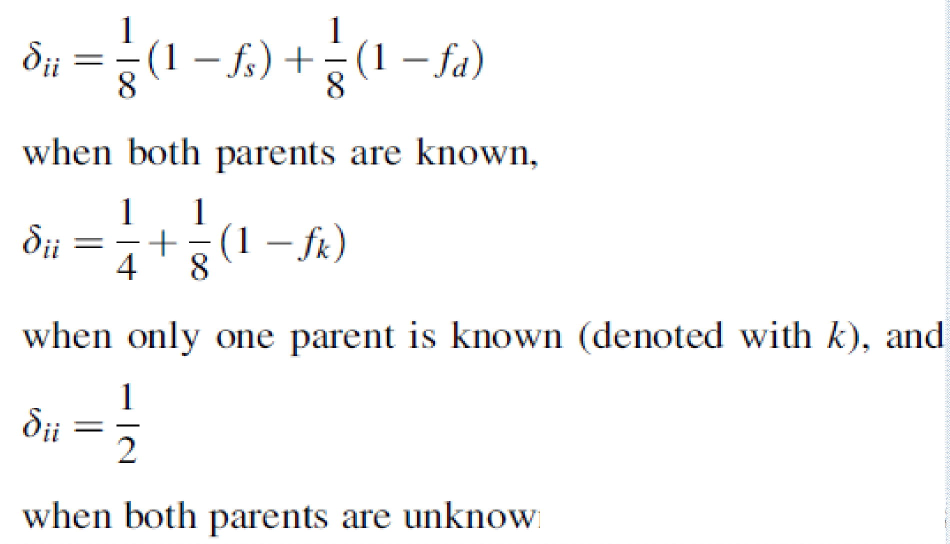
when only one parent is known (denoted with k), and

$$\delta_{ii} = \frac{1}{2}$$

when both parents are unknown.



$$\Phi_{ij} = \frac{1}{2}(\Phi_{is'} + \Phi_{id'}) + \delta_{ij}$$



$$\delta_{ii} = \frac{1}{8}(1 - f_s) + \frac{1}{8}(1 - f_d)$$

when both parents are known,

$$\delta_{ii} = \frac{1}{4} + \frac{1}{8}(1 - f_k)$$

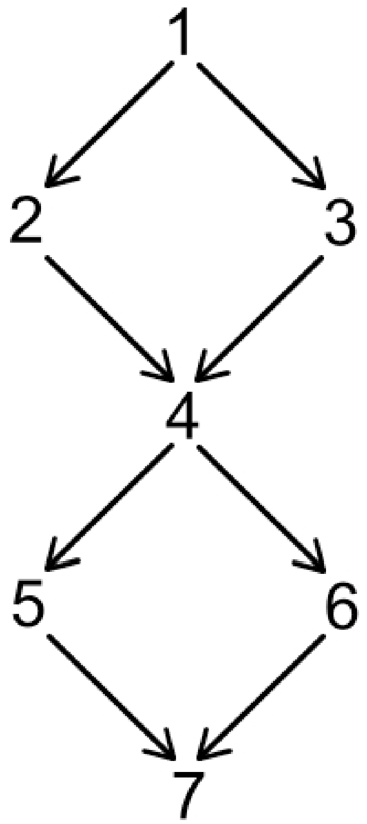
when only one parent is known (denoted with k), and

$$\delta_{ii} = \frac{1}{2}$$

when both parents are unknow

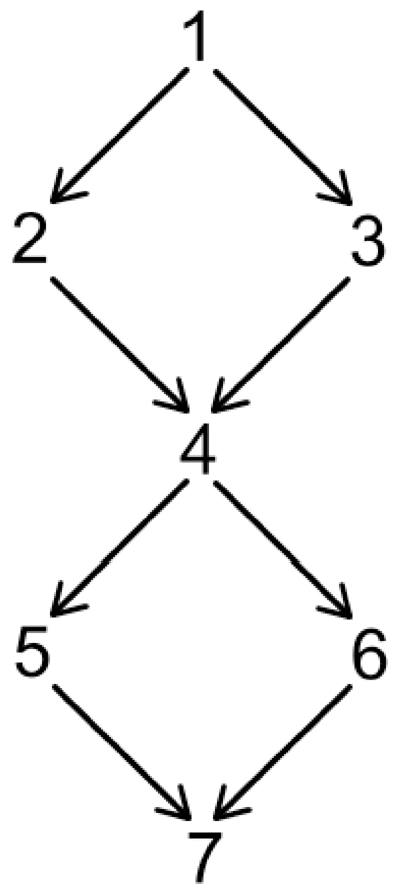
- **Under this assumption, each animal of the population can be considered as a "partial founder", contributing to the variability of the population with an amount proportional to its corresponding δ diagonal element.**

For instance, the contribution of animal 1 to the coacestry matrix is:



$$\Phi^{(1)} = \begin{bmatrix} {}^1/_2 & {}^1/_4 & {}^1/_4 & {}^1/_4 & {}^1/_8 & {}^1/_8 & {}^1/_8 \\ {}^1/_4 & {}^1/_8 & {}^1/_8 & {}^1/_8 & {}^1/_{16} & {}^1/_{16} & {}^1/_{16} \\ {}^1/_4 & {}^1/_8 & {}^1/_8 & {}^1/_8 & {}^1/_{16} & {}^1/_{16} & {}^1/_{16} \\ {}^1/_4 & {}^1/_8 & {}^1/_8 & {}^1/_8 & {}^1/_{16} & {}^1/_{16} & {}^1/_{16} \\ {}^1/_8 & {}^1/_{16} & {}^1/_{16} & {}^1/_{16} & {}^1/_{32} & {}^1/_{32} & {}^1/_{32} \\ {}^1/_8 & {}^1/_{16} & {}^1/_{16} & {}^1/_{16} & {}^1/_{32} & {}^1/_{32} & {}^1/_{32} \\ {}^1/_8 & {}^1/_{16} & {}^1/_{16} & {}^1/_{16} & {}^1/_{32} & {}^1/_{32} & {}^1/_{32} \end{bmatrix}$$

And the contribution of animal 4 to the coacestry matrix is:

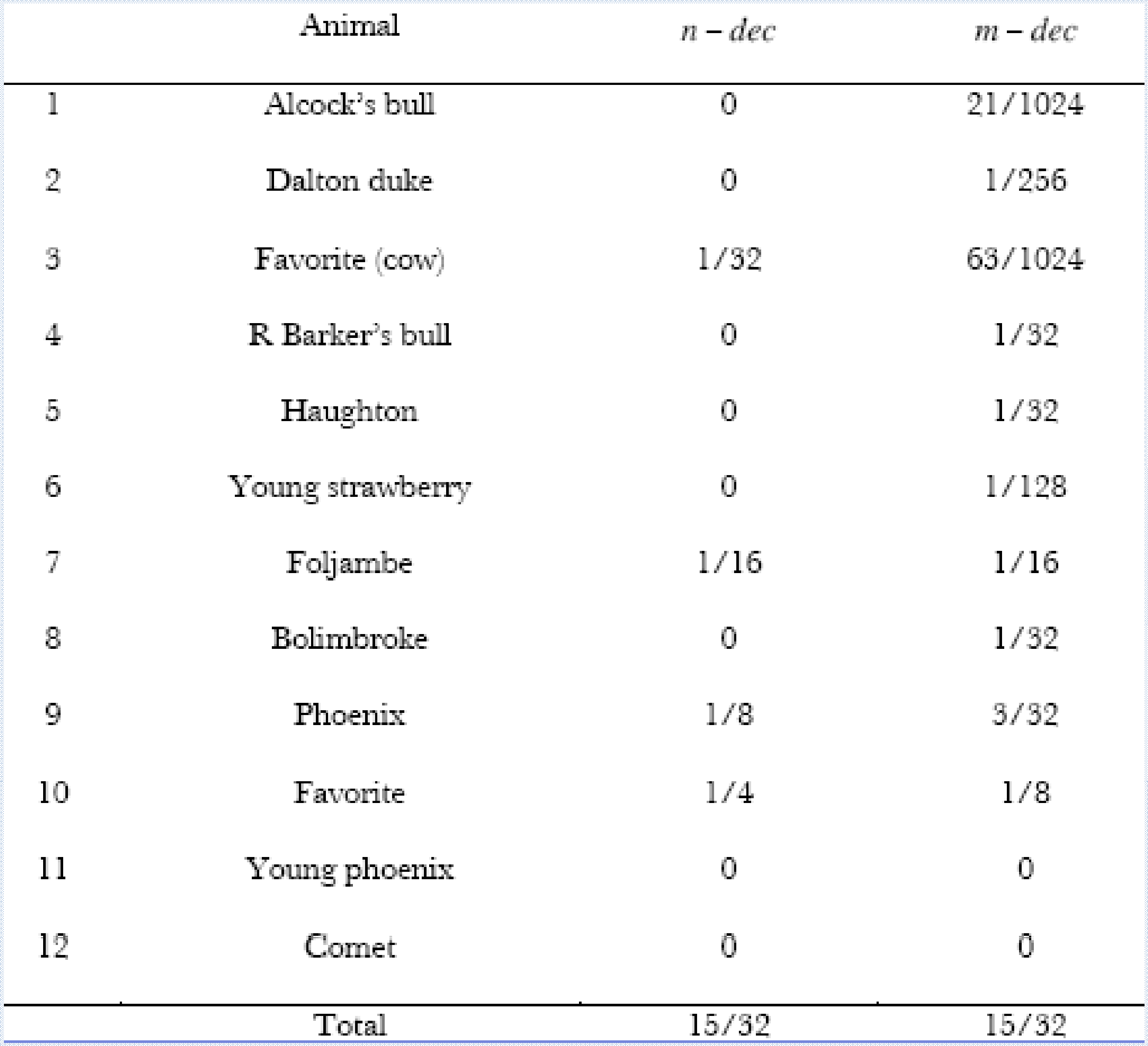


$$\Phi^{(4)} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & {}^1\!/_4 & {}^1\!/_8 & {}^1\!/_8 & {}^1\!/_8 \\ 0 & 0 & 0 & {}^1\!/_8 & {}^1\!/_{16} & {}^1\!/_{16} & {}^1\!/_{16} \\ 0 & 0 & 0 & {}^1\!/_8 & {}^1\!/_{16} & {}^1\!/_{16} & {}^1\!/_{16} \\ 0 & 0 & 0 & {}^1\!/_8 & {}^1\!/_{16} & {}^1\!/_{16} & {}^1\!/_{16} \end{bmatrix}$$

Example: Analyzing the pedigree of Comet

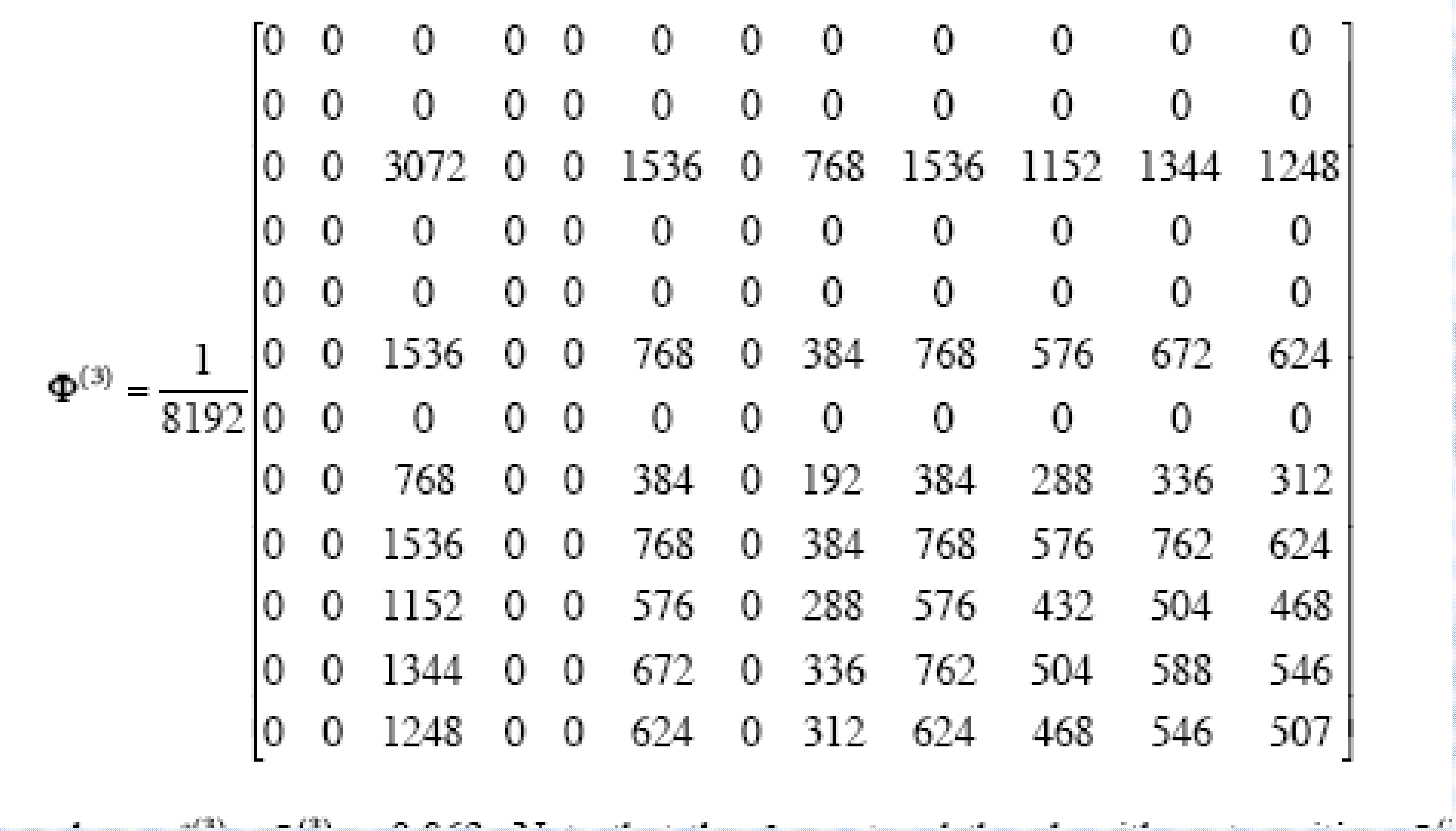
A Shorthorn bull born in 1804 that became an icon in cattle breeding. Its inbreeding coefficient was calculated by WRIGHT (1922) from a small pedigree

The contributions to the inbreeding of Comet: The most relevant Mendelian contributions are those of Favorite (0.125), Phoenix (0.094) and Favorite (cow) (0.062), meaning the 25 60% of the total inbreeding



	Animal	$n-dec$	$m-dec$
1	Alcock's bull	0	21/1024
2	Dalton duke	0	1/256
3	Favorite (cow)	1/32	63/1024
4	R Barker's bull	0	1/32
5	Haughton	0	1/32
6	Young strawberry	0	1/128
7	Foljambe	1/16	1/16
8	Bolimbroke	0	1/32
9	Phoenix	1/8	3/32
10	Favorite	1/4	1/8
11	Young phoenix	0	0
12	Comet	0	0
	Total	15/32	15/32

And the contribution of the cow *Favourite* to the coacestry matrix is:



$$\Phi^{(3)} = \frac{1}{8192}\begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 3072 & 0 & 0 & 1536 & 0 & 768 & 1536 & 1152 & 1344 & 1248 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1536 & 0 & 0 & 768 & 0 & 384 & 768 & 576 & 672 & 624 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 768 & 0 & 0 & 384 & 0 & 192 & 384 & 288 & 336 & 312 \\ 0 & 0 & 1536 & 0 & 0 & 768 & 0 & 384 & 768 & 576 & 762 & 624 \\ 0 & 0 & 1152 & 0 & 0 & 576 & 0 & 288 & 576 & 432 & 504 & 468 \\ 0 & 0 & 1344 & 0 & 0 & 672 & 0 & 336 & 762 & 504 & 588 & 546 \\ 0 & 0 & 1248 & 0 & 0 & 624 & 0 & 312 & 624 & 468 & 546 & 507 \end{bmatrix}$$

CONCLUSION

In the last years there has been an important development of the genealogical analysis that it has been overlooked

Despite that,

-It allows a nice description of the evolution of genetic variability in conservation programmes

-It allows a nice description of

- ***the efficiency of selection programmes***
- ***the relative impact of selection decisions***

García-Cortes, L.A., Martínez-Avila and M. A. Toro, 2008 Partition of the genetic trend to validate multiple selection decisions. **Animal** ,2:6, pp 821–824

García-Cortes, L.A., Martínez-Avila and M. A. Toro, 2010. Fine decomposition of the inbreeding and the coancestry coefficients by using the tabular method. **Conservation Genetics**. DOI 10.1007/s10592-010-0084-x