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Analysis of the AnGR biodiversity status using pedigree data

Modul no. 2: Conservation and Sustainable Use of Animal Genetic Resources

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Czech University of Life Sciences Prague, Faculty of Agrobiology, Food and Natural Resources

Erasmus+ project 2021-1-SK01-KA220-HED-000032068

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Pedigree analysis

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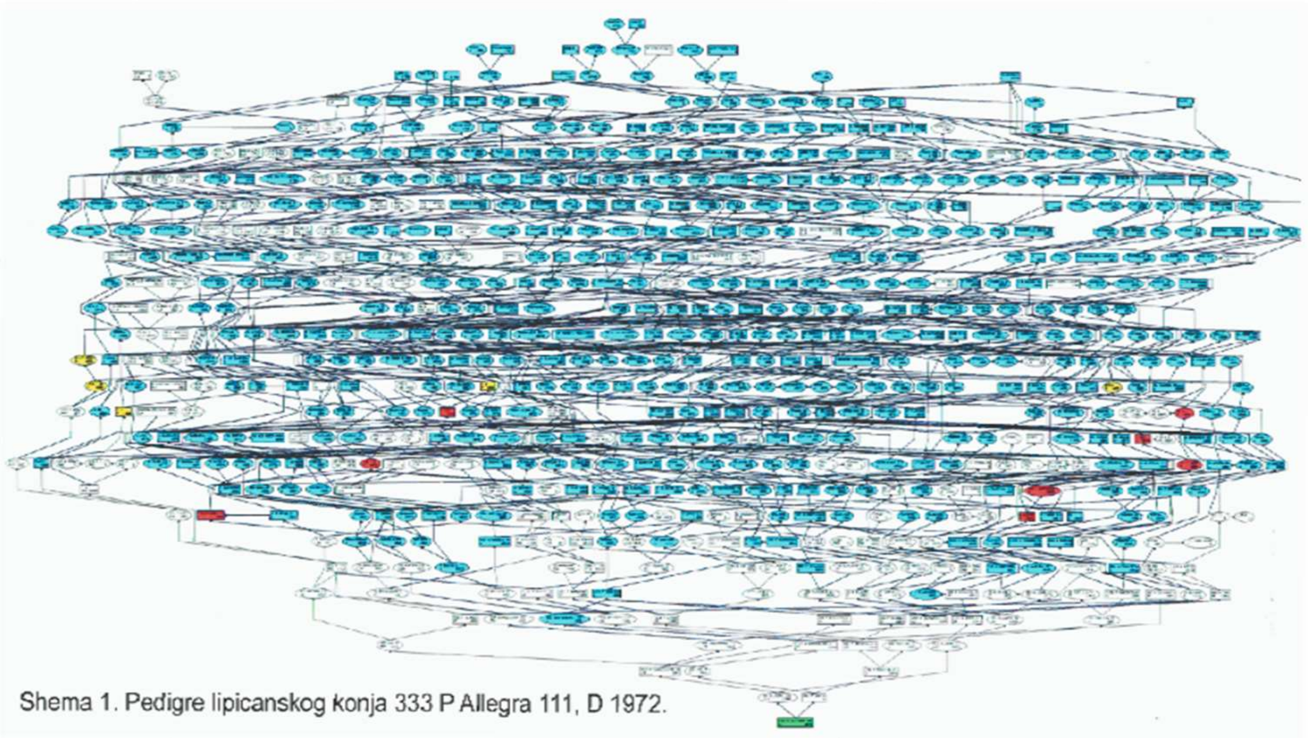
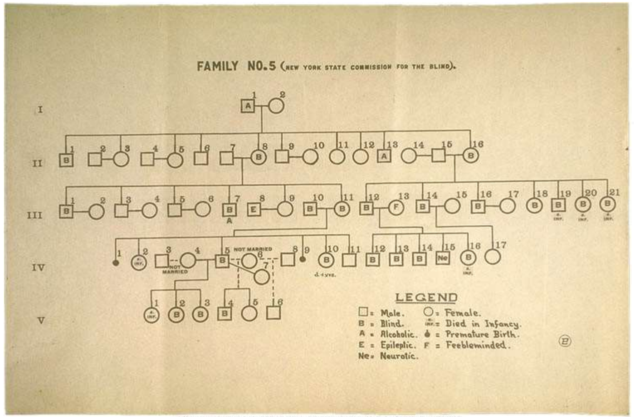
Type of pedigree records



Shema 1. Pedigre lipicanskog konja 333 P Allegra 111, D 1972.



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Example

ID	sire	dam	birth date	sex
1	0	0	0	male
2	0	0	0	female
3	1	0	12.03.1996	male
4	1	2	06.11.1999	female
5	1	2	06.11.1999	male
6	5	2	20.05.2001	meale
7	6	4	23.08.2005	female

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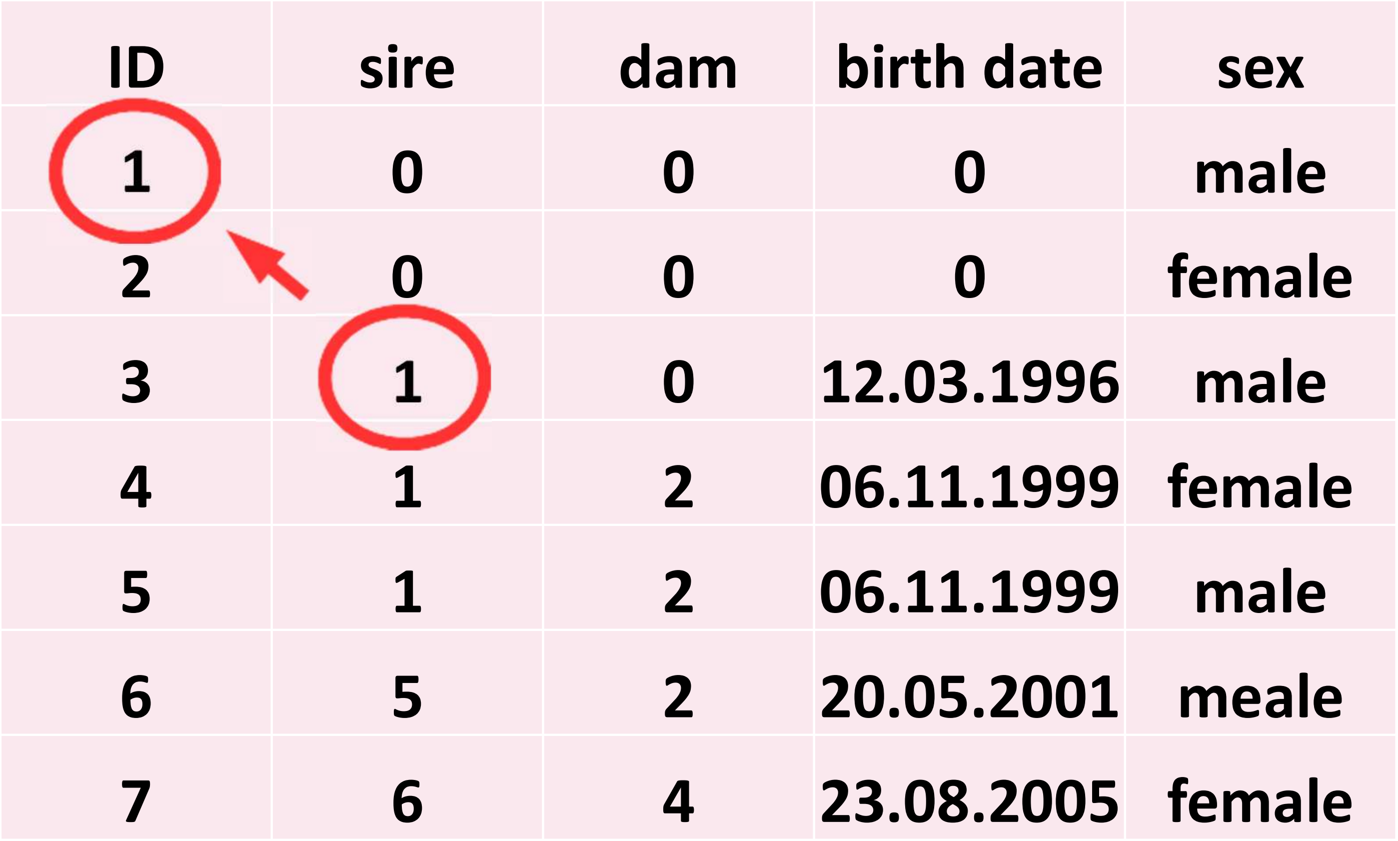
Example



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Inbreeding coefficient

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Classical pedigree coefficients

Identy by descent (IBD) describes status for copies of an allele that may be traced back through an arbitrary number of generations without mutation to a common ancestor of the organisms that carry the copies.

Opposed to IBD is identity by state (IBS) which is coincidental possession of identical alleles (chemically identical).

Autozygosity is the state of the genotype where two alleles are identical by descent.

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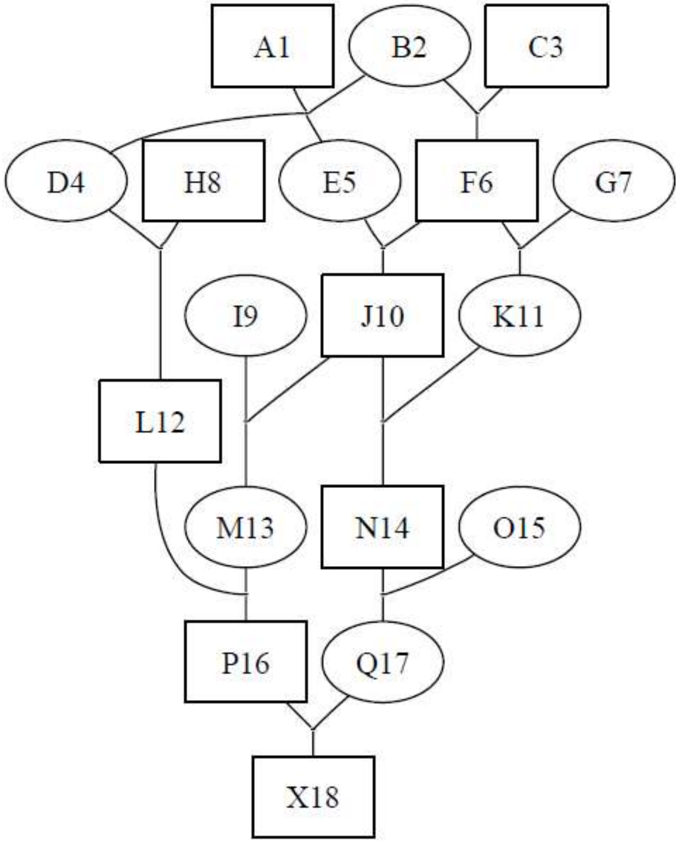
Inbreeding

Inbreeding coefficient (FX) is the quantitative measure of inbreeding defined by:

Malécot G (1948), as a probability that two homologue genes in an individual are identical by descent (autozygous).



Autozygosity is the state of the genotype where two alleles are (IBD).

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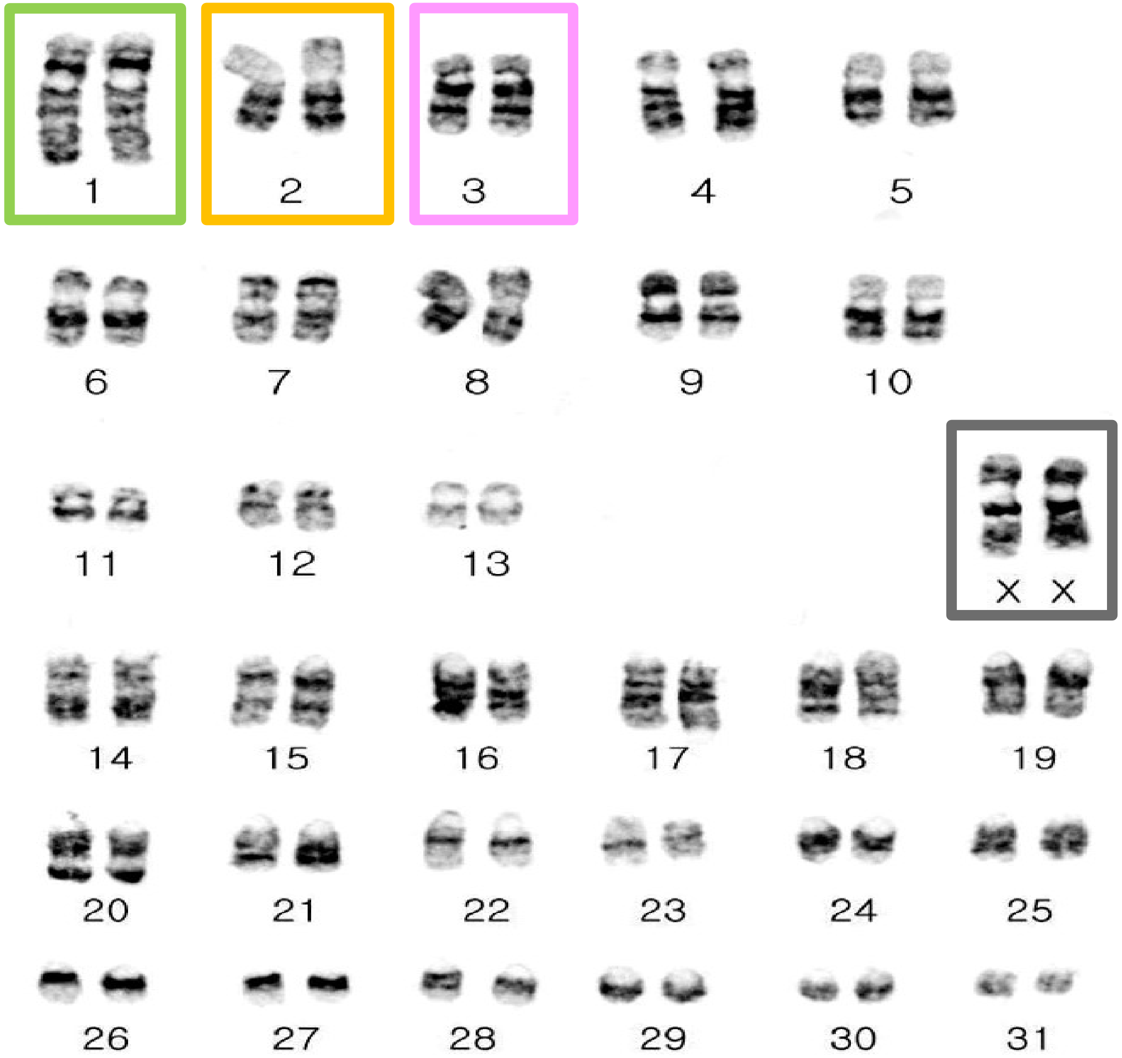
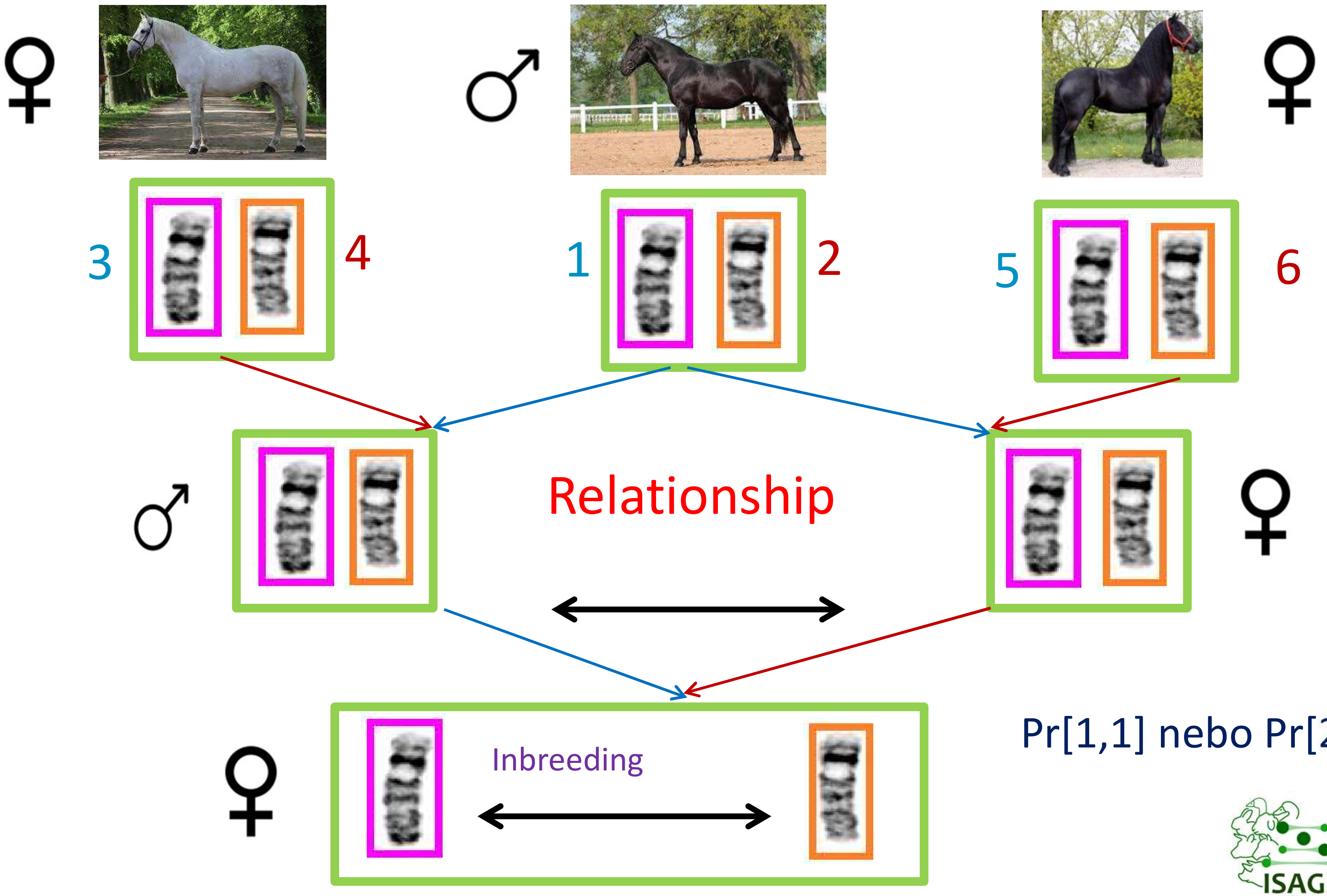
Female horse karyotype (2 x 32 chromosomes)



Chromosomaly identical by descent (IBD)?



♀ 3 4

♂ 1 2

♀ 5 6

♂ Relationship ♀

♀ Inbreeding

Pr[1,1] nebo Pr[2,2] =?

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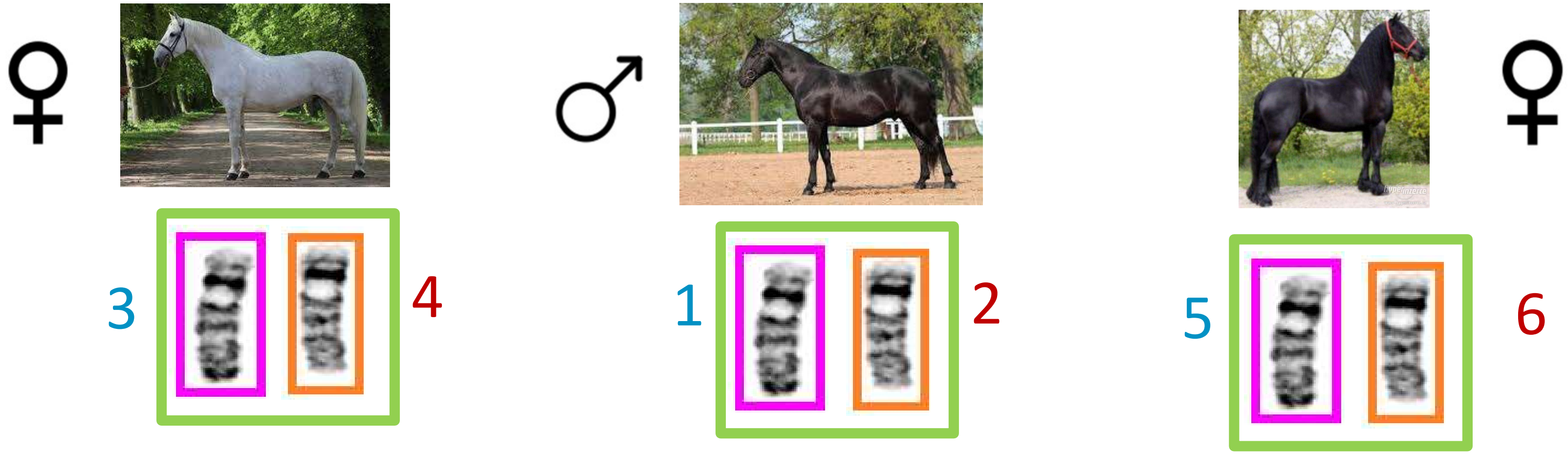
Chromosomaly identical by descent (IBD)?



Pr[1,1] nebo Pr[2,2] =?

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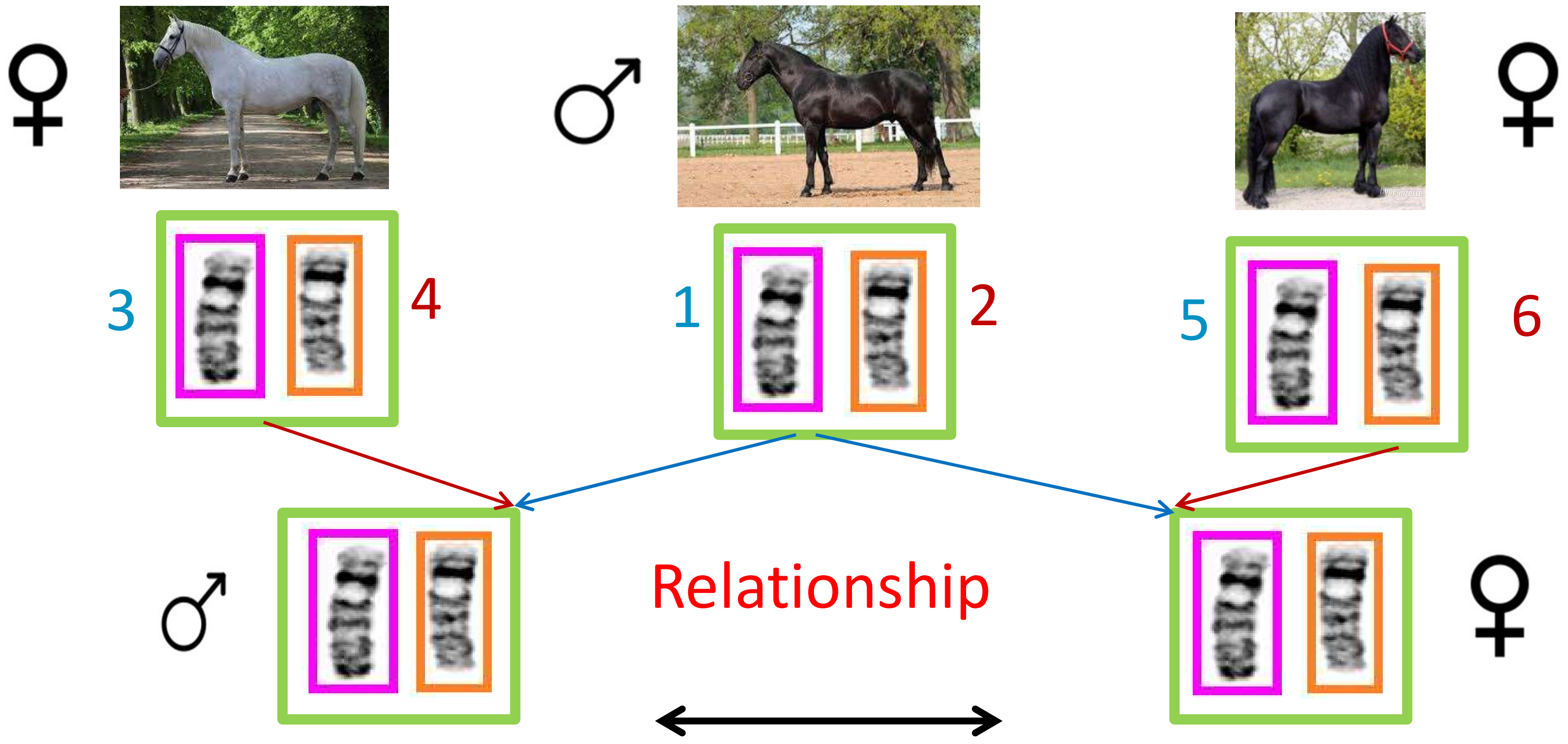

Relationship

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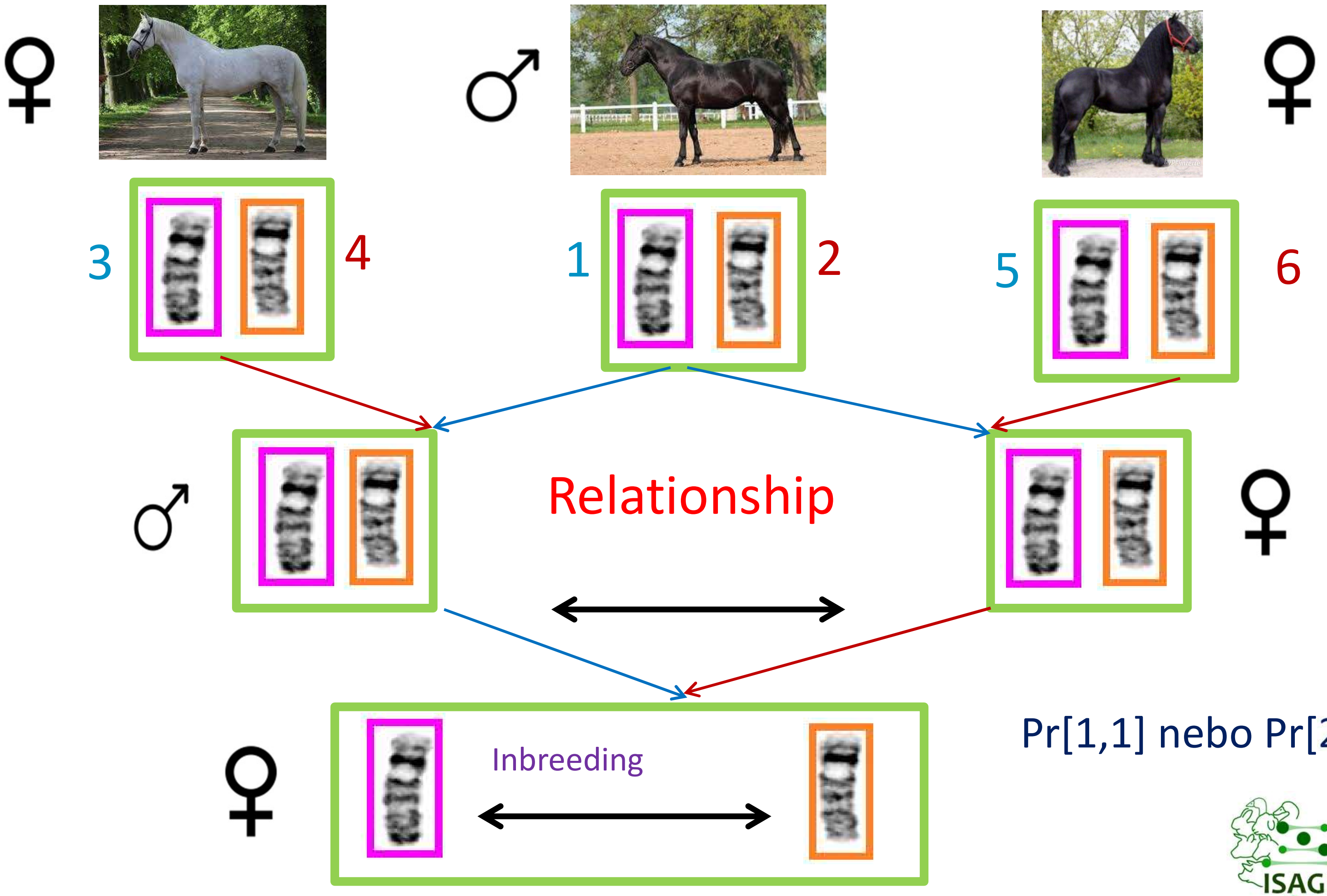

Relationship

Inbreeding

Pr[1,1] nebo Pr[2,2] =?

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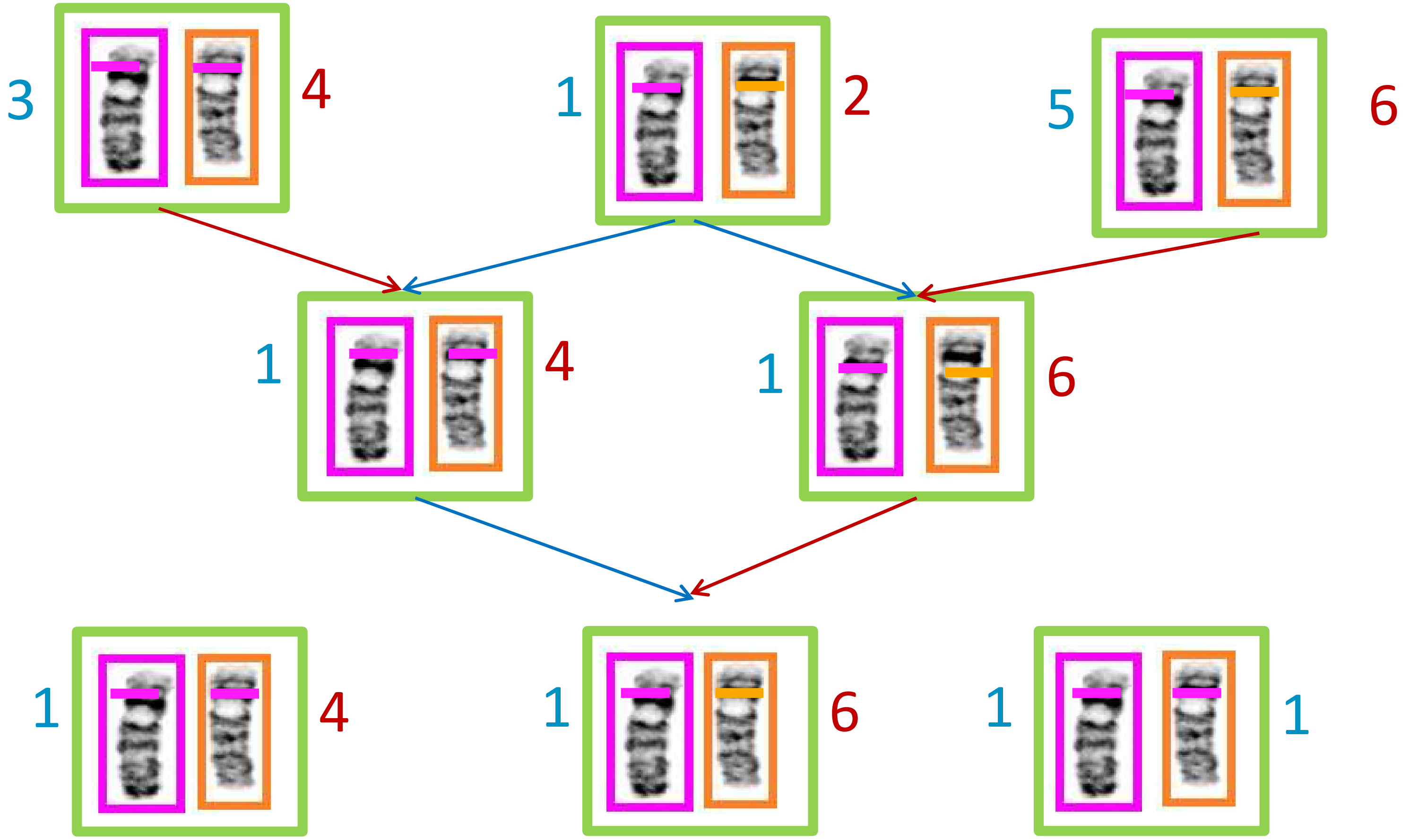
For two alleles segregating in a population



Homozygote
(IBS)

Heterozygote
(DBS & DBD)

Autozygote
(IBD)

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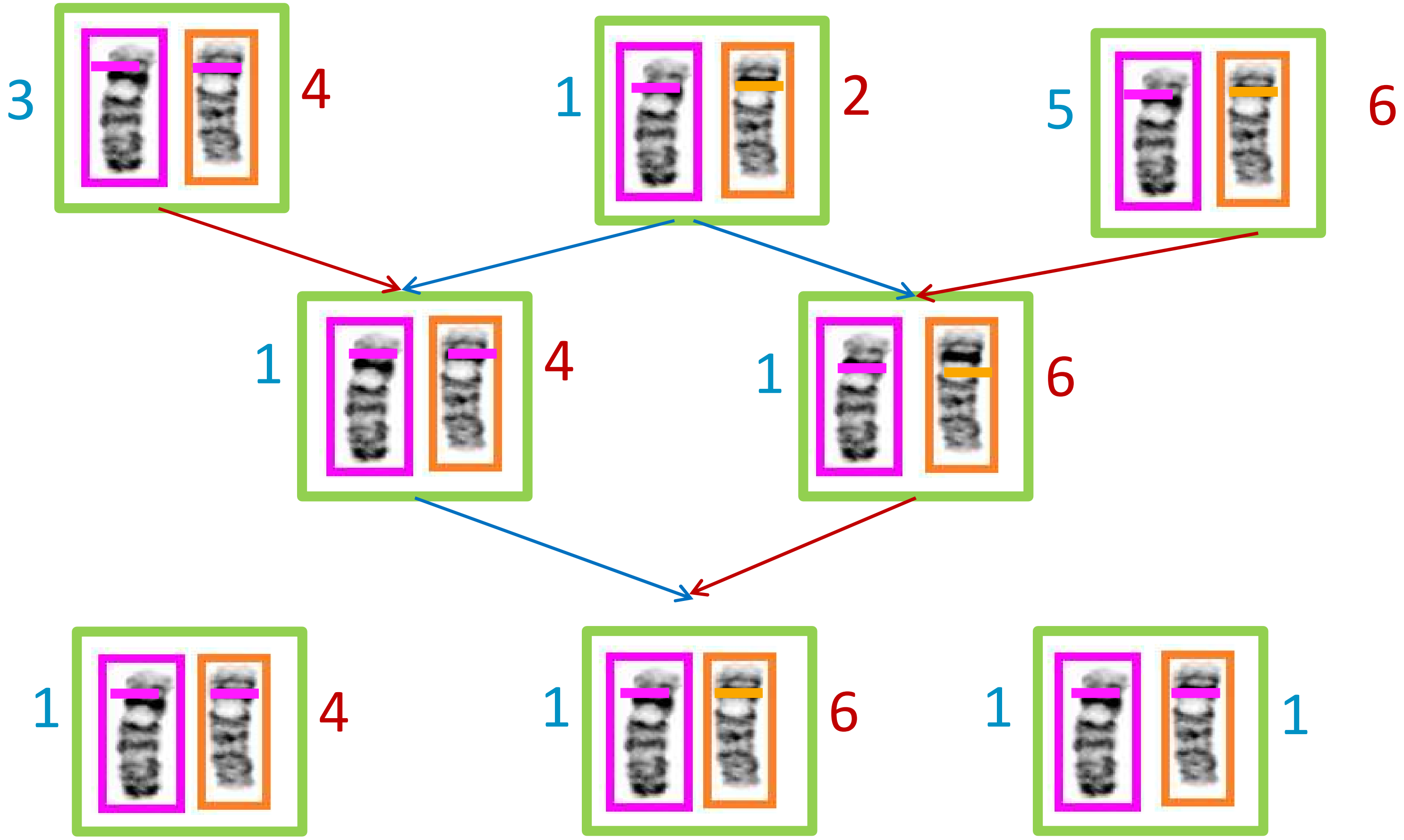
For two alleles segregating in a population



Homozygote (IBS)

Heterozygote (DBS & DBD)

Autozygote (IBD)

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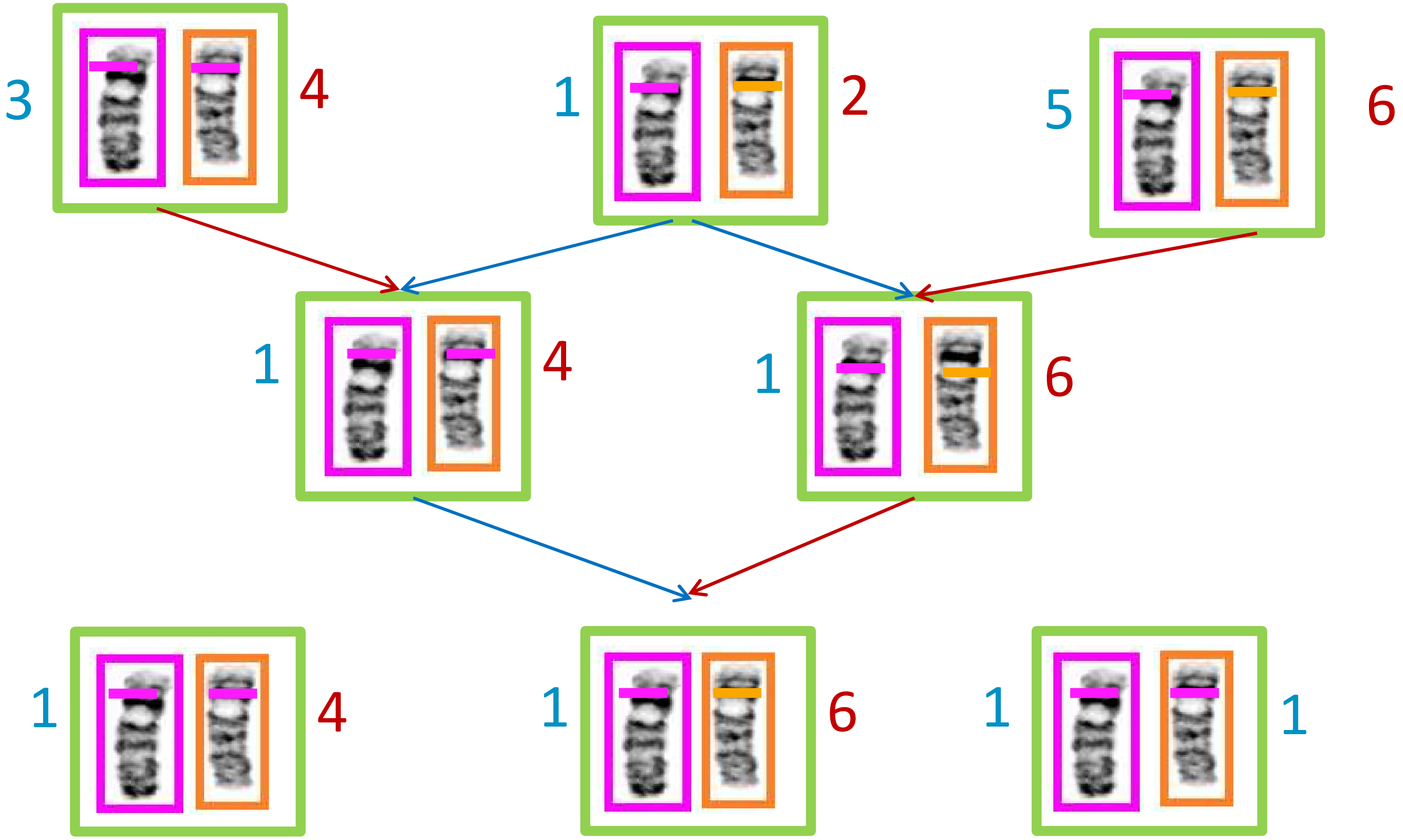
For two alleles segregating in a population



Homozygote
(IBS)

Heterozygote
(DBS & DBD)

Autozygote
(IBD)

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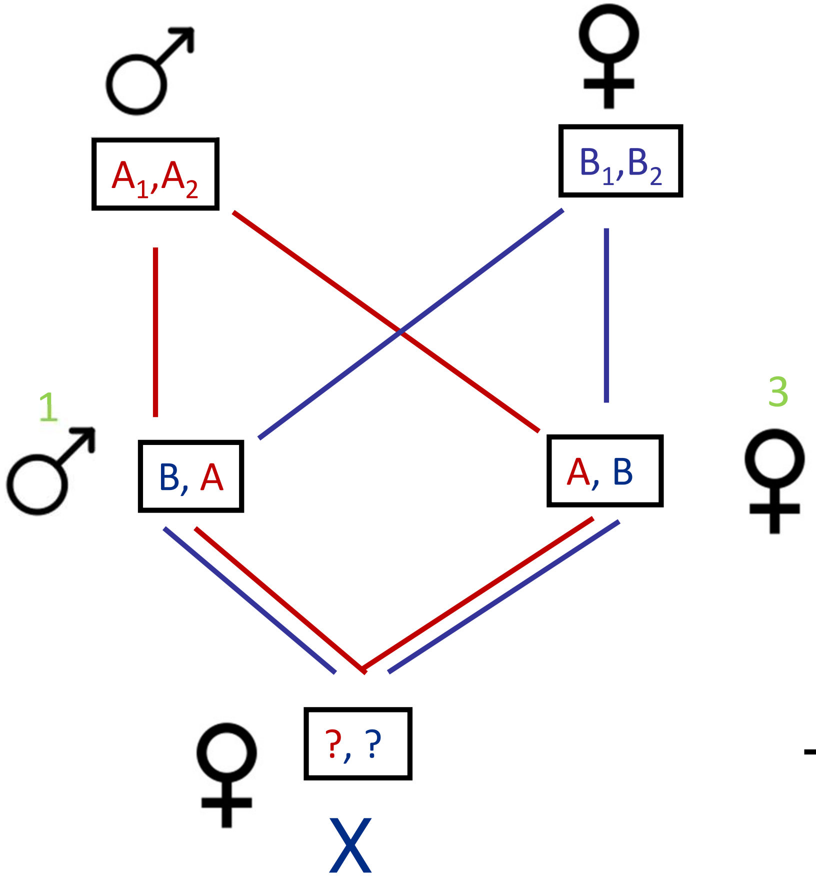
F_X = Pr(A1 ≡ A1) nebo Pr(A2 ≡ A2) a Pr(B1 ≡ B1) nebo Pr(B2 ≡ B2) = ?



As IBD is „unobservable“ quantity we use pedigree to derive *probability* that two homologue genes in an individual are IBD.

a. $Pr(A_1:A_1)$ or $Pr(A_2:A_2)$
$= (1/2)^3 (1 + 0)$

b. $Pr(B_1:B_1)$ or $Pr(B_2:B_2)$
$= (1/2)^3 (1 + 0)$

$F_X = (1/2)^3 + (1/2)^3$
= 0,250

3 $\boxed{F_X = \Sigma(1/2)^n}$

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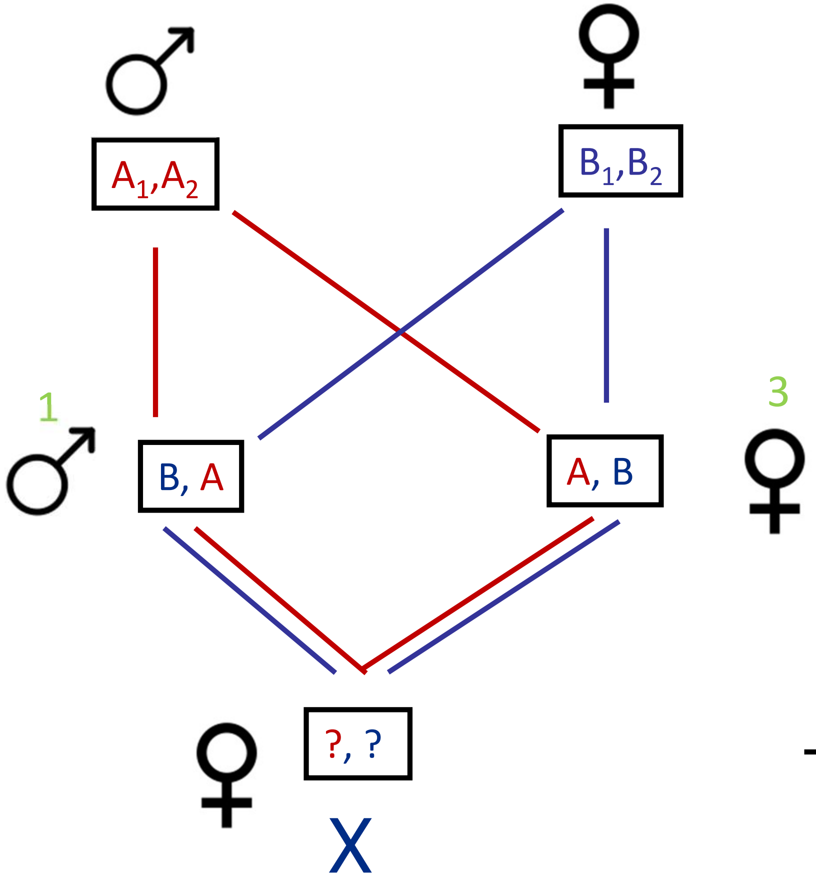
F_X = Pr(A1 ≡ A1) nebo Pr(A2 ≡ A2) a Pr(B1 ≡ B1) nebo Pr(B2 ≡ B2) = ?



As IBD is „unobservable“ quantity we use pedigree to derive *probability* that two homologue genes in an individual are IBD.

---

a. $\Pr(A_1{:}A_1)$ or $\Pr(A_2{:}A_2)$
$= (1/2)^3\,(1 + 0)$

b. $\Pr(B_1{:}B_1)$ or $\Pr(B_2{:}B_2)$
$= (1/2)^3\,(1 + 0)$

$F_X = (1/2)^3 + (1/2)^3$
= 0,250

③ $\boxed{F_X = \Sigma(1/2)^n}$

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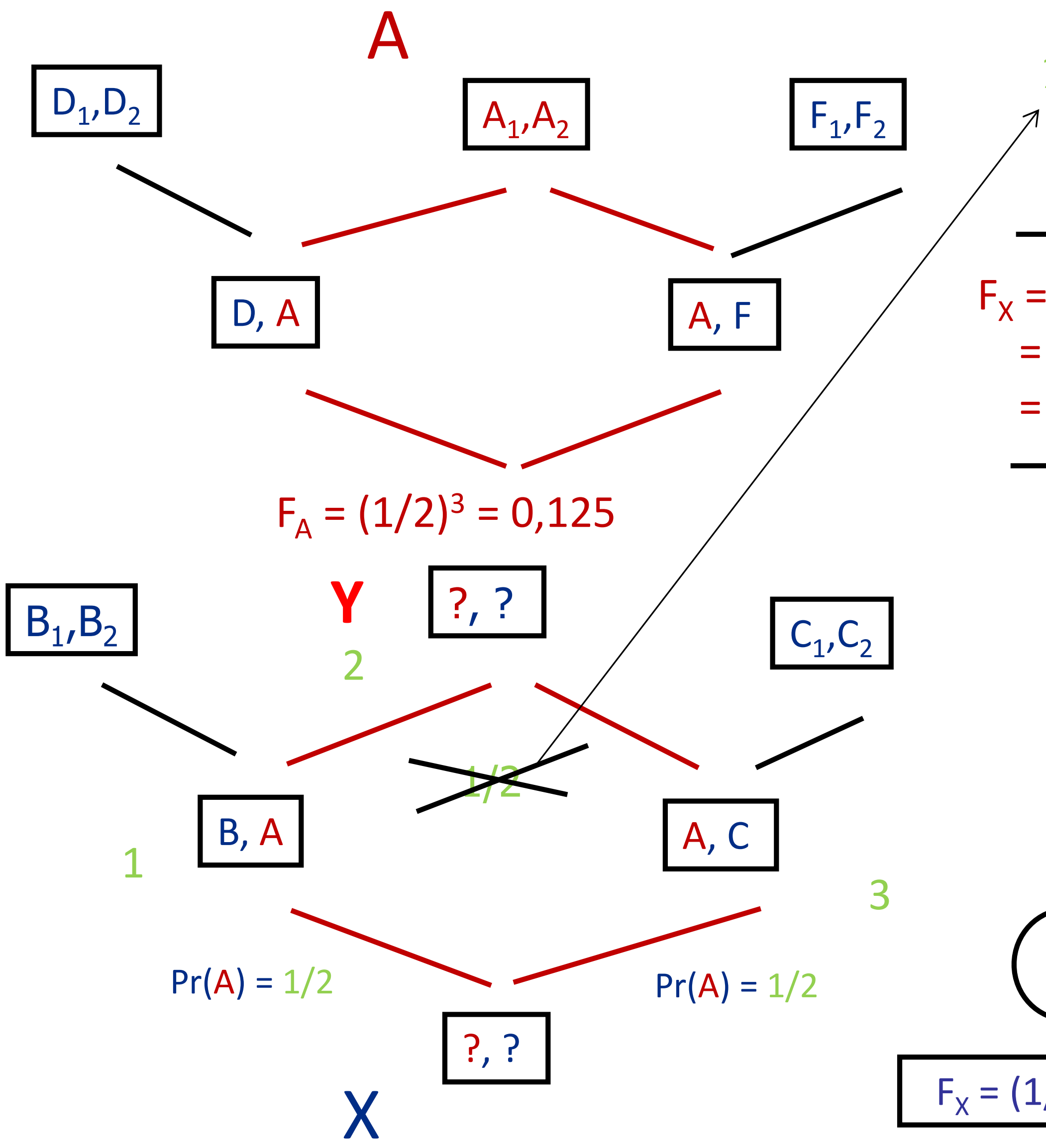

A

D_1,D_2 A_1,A_2 F_1,F_2

D, A   A, F

$F_A = (1/2)^3 = 0{,}125$

Y   ?, ?

2

B_1,B_2 C_1,C_2

$\cancel{1/2}$

B, A   A, C

1   3

Pr(A) = 1/2   Pr(A) = 1/2

?, ?

X

$\Pr(A_1{:}A_1)$ nebo $\Pr(A_2{:}A_2)$

$½\,(1 + F_A)$

$$F_X = (1/2)^2\ 1/2\ (1 + F_A)$$
$$= (1/2)^2\ 1/2\ (1 + 0.125)$$
$$= 0.1406$$

$$\boxed{F_X = (1/2)^n\,(1 + F_A)}$$

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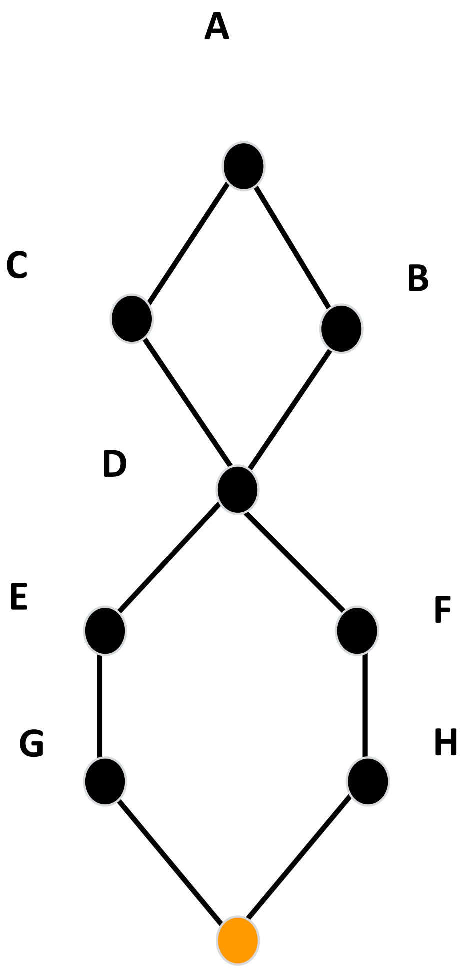

$F_X = ?$

$GE\underline{D}FH = (1/2)^5$

$F_X = \quad (1+F_D)$

$F_F = C\underline{A}B = (1/2)^3$

$F_X = 0.03125\ (1+125) = 0.03515625$

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Basic formula - Inbreeding coefficient

③ ① ②

$$F_X = \sum (1/2)^n \, (1+F_A)$$

F_X = inbreeding coefficient

n = number of individuals in the path through one parent and back through the other parent to the common ancestor.

F_A = inbreeding coefficient of the common ancestor

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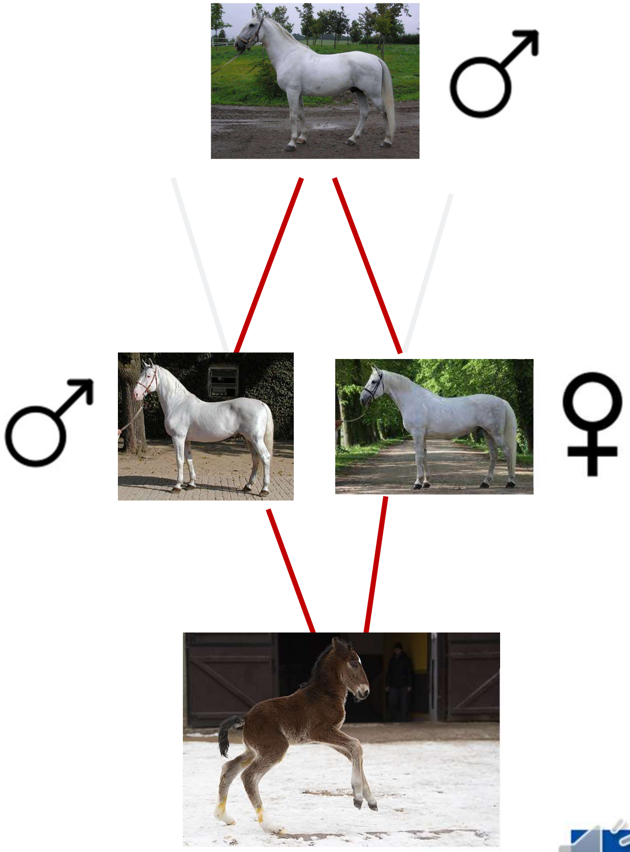
Interpretating the meaning of inbreeding coefficient

The individual inbreeding coefficient (F_X) is defined as:

a. the proportion of an individual´s genome that is autozygous (homozygous & IBD),

or equivalently,

b. the probability of a randomly sampled locus in the genome to be autozygous.



$F_X = 0.125 = (1/8)$

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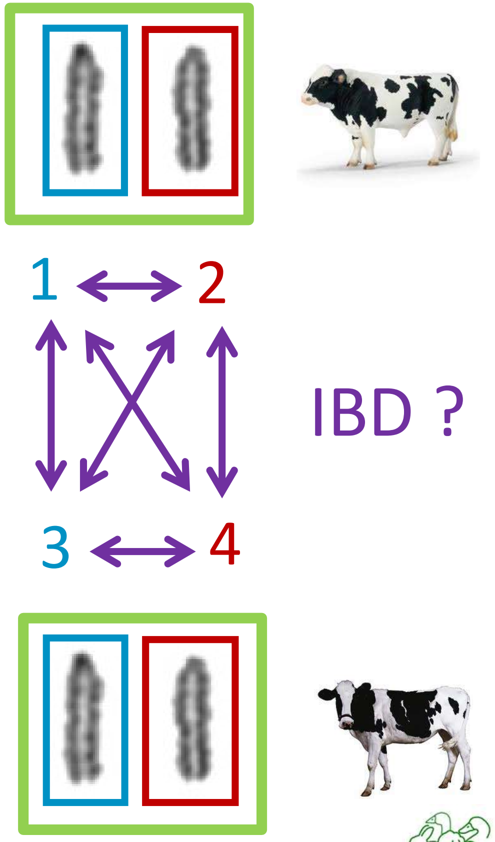
Classical concept based on the pedigree

Relatedness

All measures of relatedness are based on the IBD concept as two individuals (animals) are related only if they share (at least one) chromosomes, chromosomal segments, alleles, SNPs ..., that are identical by descent (IBD).

Note: Common ancestor required !



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Kinship coefficient (Coancestry coefficient)

f_{XY} (Θ)

Defined as the probability that an allele drawn at random from one individual (X) is identical by descent to a random allele from the other individual (Y).

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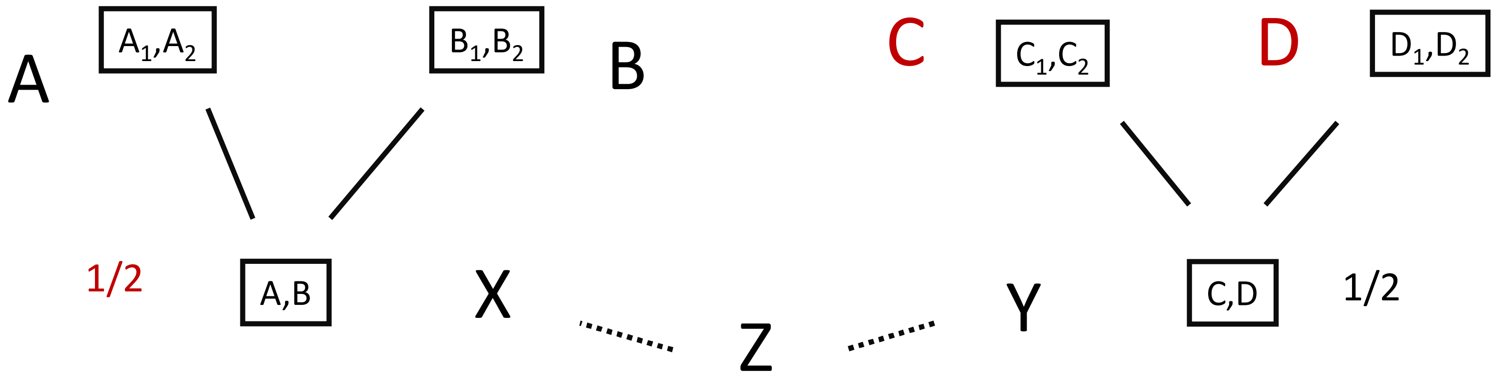

$$- f_{XY} = ¼f_{AC} * ¼f_{AD} * ¼f_{BC} * ¼f_{BD}$$
$$= ¼(f_{AC} + f_{AD} + f_{BC} + f_{BD})$$

$$- f_{XY} = F_Z$$

$$- f_{ZZ} = ½ (1+F_Z)$$

Note that f_{XY} of two individuals is the same as the inbreeding coefficient of their hypothetical offsprings.

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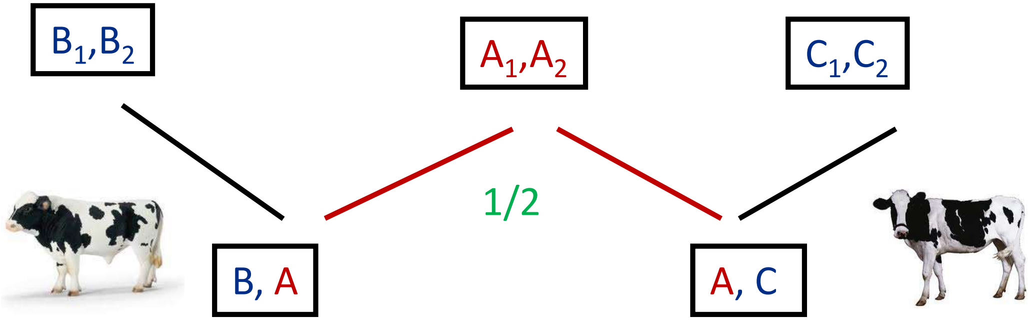

$$f_{XY} = ¼(f_{BA} + f_{BC} + f_{AA} + f_{AC})$$

$$= ¼(0 + 0 + ½\,1 + 0) = 0.125$$

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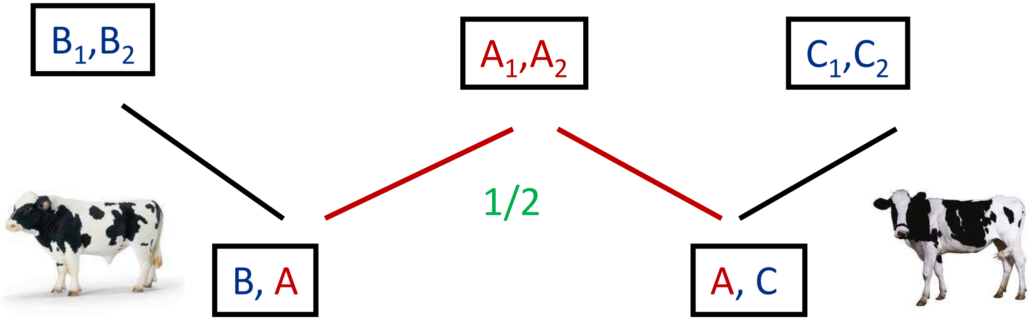

B_1,B_2

A_1,A_2

C_1,C_2

1/2

B, A

A, C

$$f_{XY} = \tfrac{1}{4}(f_{BA} + f_{BC} + f_{AA} + f_{AC})$$

$$= \tfrac{1}{4}(0 + 0 + \tfrac{1}{2}\,1 + 0) = 0.125$$

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Relationship coefficient (RXY; Wright, 1922)

R_{XY} , after Wright, is the correlation between genic (additive) values of two individuals (correlation between breeding values of two individual).

$$R_{XY} = \frac{\sum[(1/2^{n})(1+F_{A})]}{\sqrt{(1+F_{X})(1+F_{Y})}}$$

$$R_{XY} = 2\ f_{XY} \ / \ \boxed{[(1+F_X)(1+F_Y)]^{0.5}}$$

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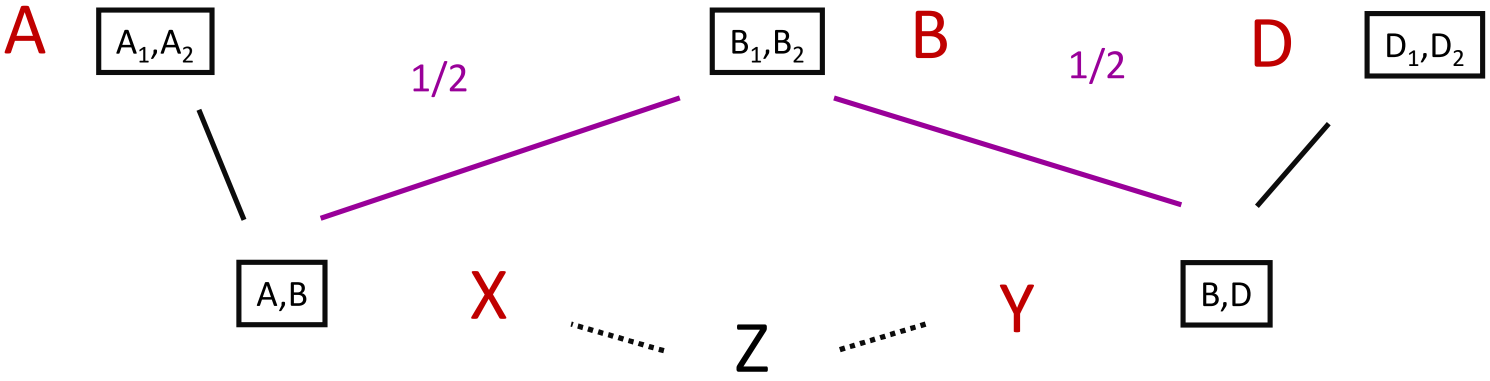

$$R_{XY} = [\sum(1/2)^n (1+F_A)] / [(1+F_X)*(1+F_Y)]^{1/2}$$

$$= [(1/2)^2 * 1]/1 = 0.25$$

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Additive (Numerator) relationship coefficient

Additive genetic relationship (aXY), is a quantitative measure of similarity that is related to the number of alleles in common between two individuals.

The minimum value of a_{XY} is 0, the maximum value is 2.

The last value is obtained for the relationship of fully inbred individual with itself, as we can expect that for an arbitrary allele at a particular locus there will be 2 alleles IBD at this locus in the same individual.

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Tabular method

⇩ POPULATION

ADDITIVE RELATIONSHIP MATRIX

- additive (genetic) relationship (a_{XY}) between all individuals in the population (pedigree),

→ off diagonal values..

- inbreeding coefficients (FZ) for all individuals in the population (pedigree),

→ derived from the diagonal ($F_Z = a_{ZZ} – 1$, as $a_{ZZ}=2f_{XY}= 2*0,5 (1+F_Z)$.

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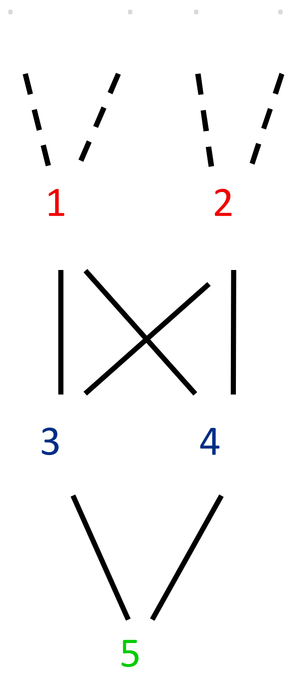
ADDITIVE (NUMERATOR) RELATIONSHIP MATRIX



Pedigree

j/i	1 (.,.)	2 (.,.)	3 (1,2)	4 (1,2)	5 (3,4)
1 (.,.)	1	0	1/2	1/2	1/2
2 (.,.)	0	1	1/2	1/2	1/2
3 (1,2)	1/2	1/2	1	1/2	3/4
4 (1,2)	1/2	1/2	1/2	1	3/4
5 (3,4)	1/2	1/2	3/4	3/4	5/4

$$f_{ZZ} = \frac{1}{2}(1+F_Z) \Leftrightarrow 2f_{ZZ} = (1+F_Z) \Leftrightarrow F_Z = 2f_{ZZ} - 1$$

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Relationships between coefficients

The additive affinity coefficient corresponds to twice the coancestry coefficient.

$$a_{XY} = 2\ f_{XY}\ (2\Theta)$$

Additive relationship coefficient equals to the Wrights ‘s (1922) relationship coefficient (RXY) for two non-inbreed individuals.

$$a_{XY} = 2\ f_{XY} / \cancel{[(1+F_X)(1+F_Y)]^{0.5}}$$

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Relationships between coefficients

- If individuals X & Y are not inbred, relationship coefficient is then equal to the numerator i.e. additive genetic relationship and, also, twice kinship coefficient of those two individuals as well as twice inbreeding coefficient of their potential offspring.

$$R_{XY} = a_{XY} / [(1+F_X)(1+F_Y)]^{1/2}$$

$$= a_{xy} / (a_{xx}\, a_{yy})^{1/2}$$

$$F_Z = f_{XY} = \frac{1}{2} a_{XY}$$

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Thank you for your attations

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Picture sources

- https://www.nhkladruby.cz/fotogalerie
- https://www.researchgate.net/figure/GBG-banded-female-horse-karyotype-drawn-from-a-single-early-metaphase-cell-350-bands_fig1_261592417
- Pedigre lipicanskog konja 333 P Alegra 111, D 1972

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