

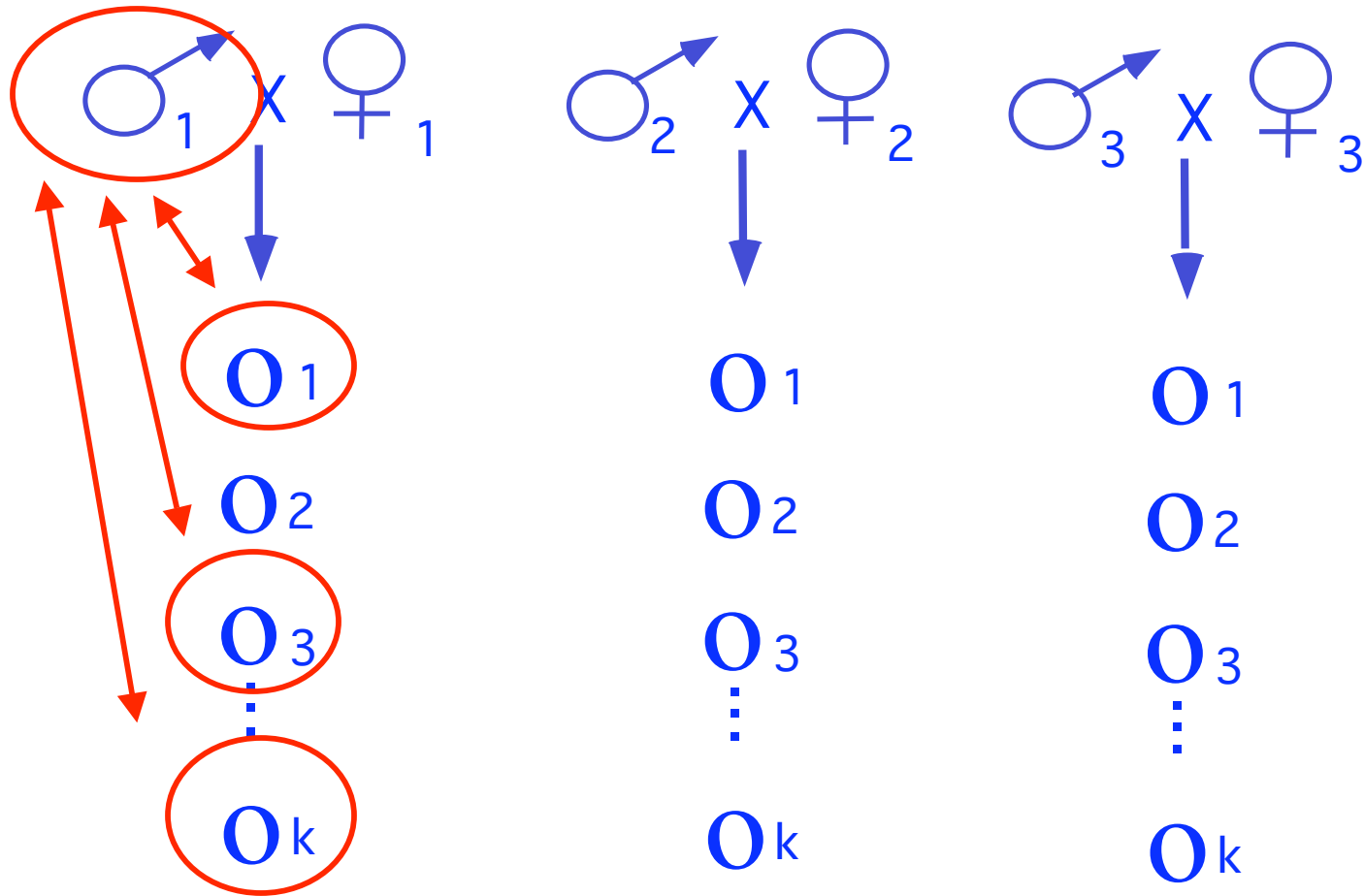
Lecture 6: Resemblance Between Relatives

Bruce Walsh lecture notes
Synbreed Course
3 July 2013

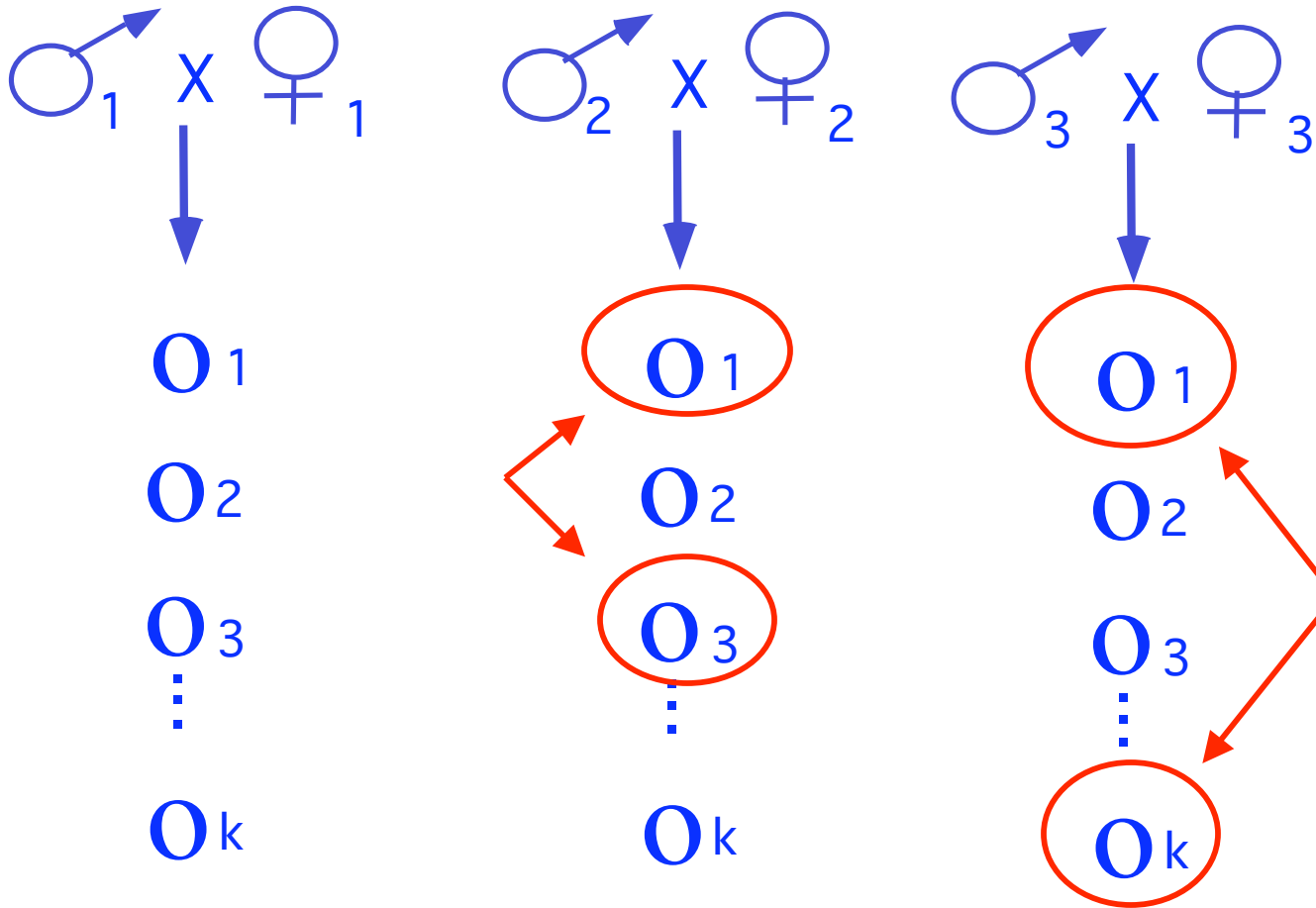
Heritability

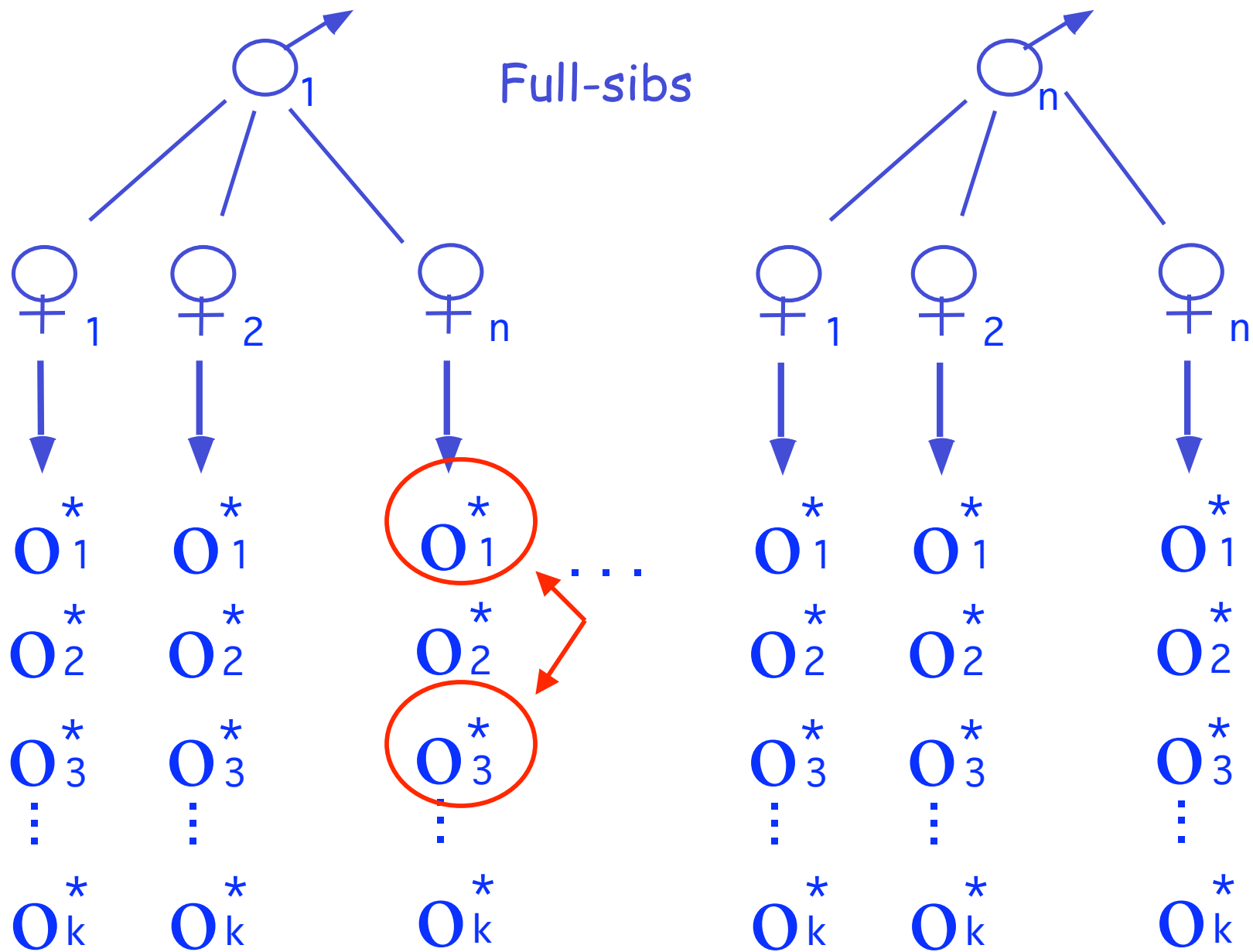
- Central concept in quantitative genetics
- Fraction of phenotypic variance due to additive genetic values (Breeding values)
 - $h^2 = V_A/V_P$
 - This is called the **narrow-sense heritability**
 - Phenotypes (and hence V_P) can be directly measured
 - Breeding values (and hence V_A) must be estimated
- Estimates of V_A require **known collections of relatives**

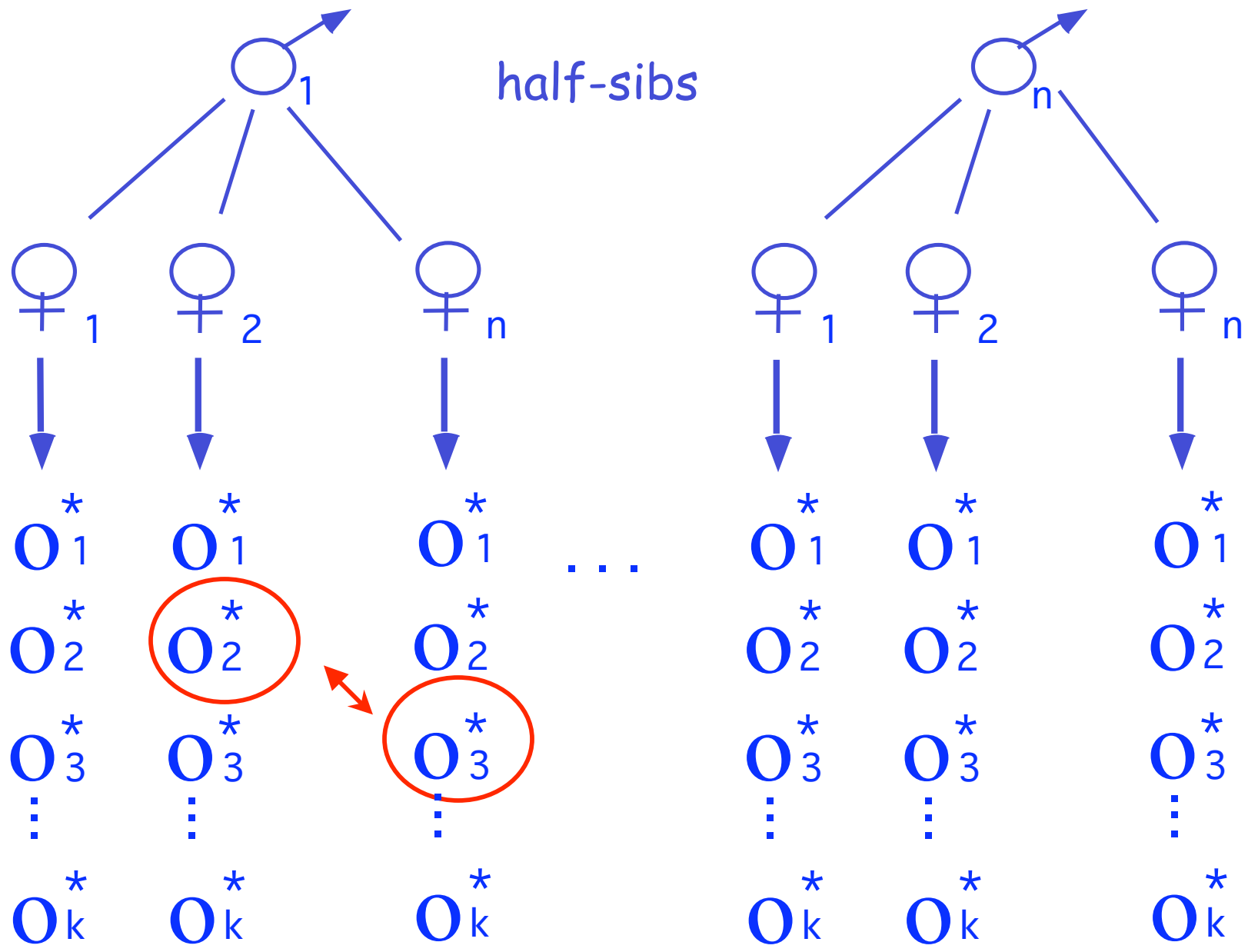
Ancestral relatives e.g., parent and offspring



Collateral relatives e.g. sibs







Broad-sense heritability

- Narrow-sense heritability h^2 applies when outcrossing,
 - $h^2 = \text{Var}(A)/\text{Var}(P)$
 - = the fraction of all trait variation due to variation in breeding (additive genetic) values
- **Broad-sense heritability H^2** applies when selecting among a series of pure lines
 - $H^2 = \text{Var}(G)/\text{Var}(P)$
 - = the fraction of all trait variation due to variation in **Genotypic values**

Defining H^2 for Plant Populations

Plant breeders often do not measure individual plants (especially with pure lines), but instead measure a **plot** or a **block** of individuals.

This replication can result in inconsistent measures of H^2 even for otherwise identical populations.

Let z_{ijkl} denote the value of the l -th replicate in plot k of genotype i in environment j . We can decompose this value as

$$z_{ijkl} = G_i + E_j + GE_{ij} + p_{ijk} + e_{ijkl}$$

Effect of the k -th plot

deviations of individual plants within this plot

Suppose we replicate the genotype over e environments, with r plots (replicates) per environment, and n individuals per plot.

If we set our unit of measurement as the average over all plots, the phenotypic variance for the mean of line i becomes

$$\sigma^2(z_i) = \sigma_G^2 + \sigma_E^2 + \frac{\sigma_{GE}^2}{e} + \frac{\sigma_p^2}{er} + \frac{\sigma_e^2}{ern}$$

Thus, V_p , and $H^2 = V_G/V_p$, depend on our choice of e , r , and n

In order to compare broad-sense heritabilities we need to use a consistent design (same values of e , r , and n)

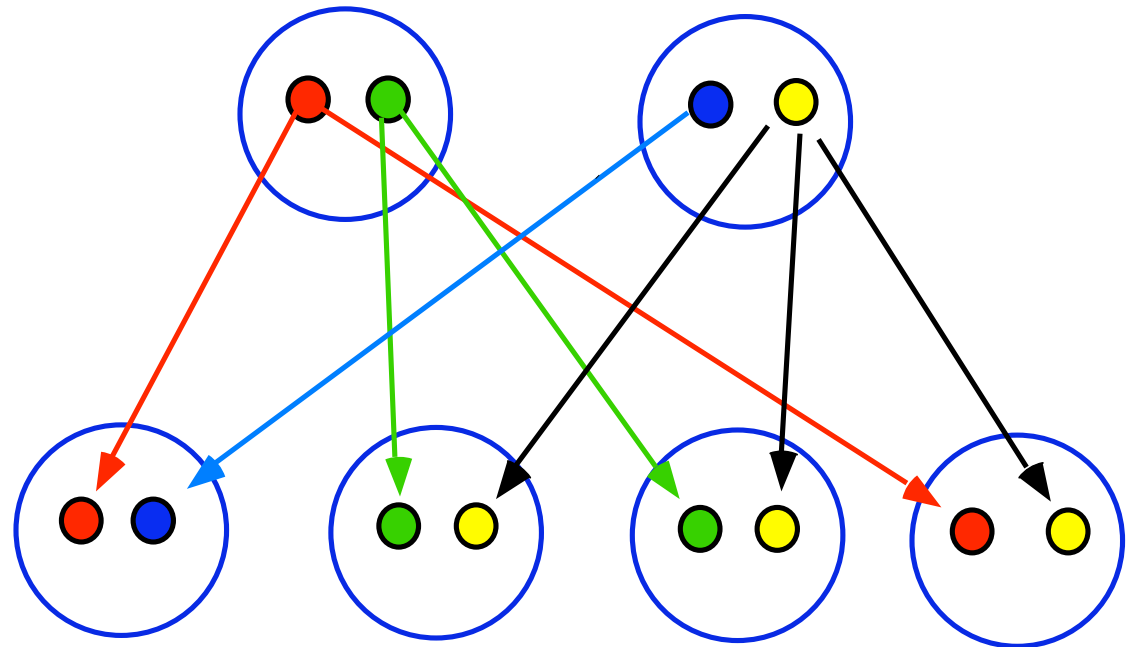
Key observations

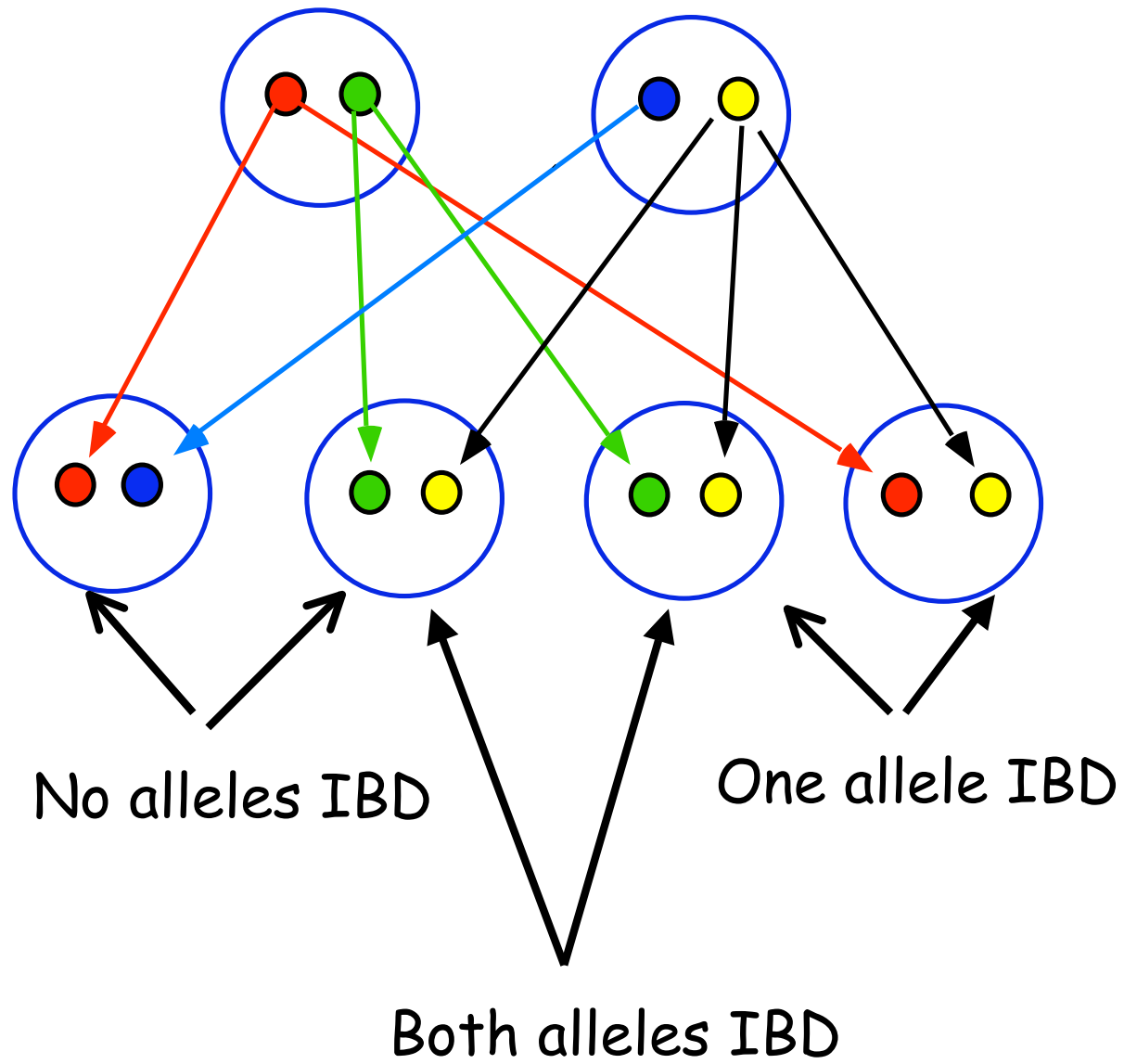
- The amount of **phenotypic resemblance** among relatives for the trait provides an indication of the amount of **genetic variation** for the trait.
- If trait variation has a significant genetic basis, the **closer the relatives**, the **more similar their appearance**
- The covariance between the phenotypic value of relatives measures the strength of this similarity, with larger Cov = more similarity

Genetic Covariance between relatives

Sharing alleles means having alleles that are **identical by descent (IBD)**: both copies can be traced back to a single copy in a recent common ancestor.

Genetic covariances arise because two **related individuals are more likely to share alleles** than are two unrelated individuals.

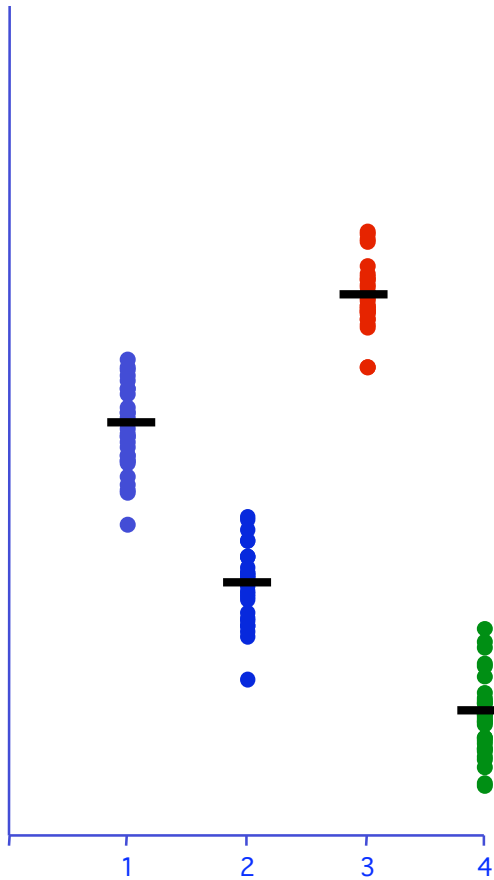




ANOVA: Analysis of variation

- Partitioning of trait variance into within- and among-group components
 - Between-group variance is the variance of the group means
- Two key ANOVA identities
 - Total variance = between-group variance + within-group variance
 - $\text{Var}(T) = \text{Var}(B) + \text{Var}(W)$
 - Variance(between groups) = covariance (within groups)
 - Intraclass correlation, $t = \text{Var}(B)/\text{Var}(T)$
- The more similar individuals are within a group (higher within-group covariance), the larger their between-group differences (variance in the group means)

Situation 1

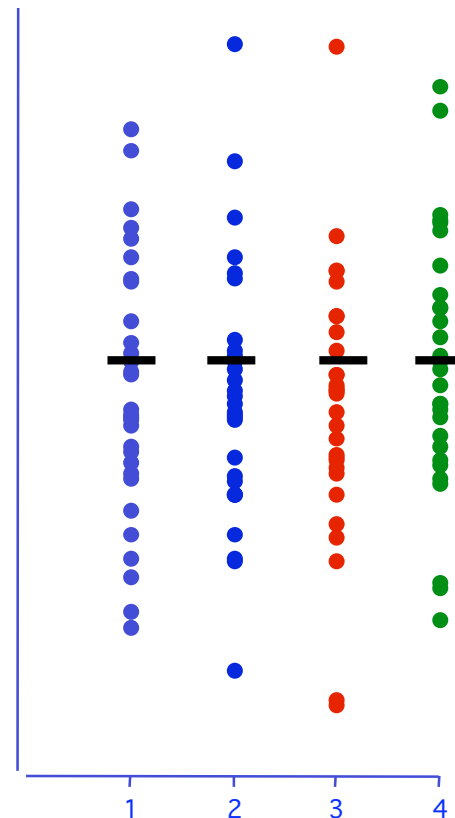


$$\text{Var}(B) = 2.5$$

$$\text{Var}(W) = 0.2 \quad \dagger = 2.5/2.7 = 0.93$$

$$\text{Var}(T) = 2.7$$

Situation 2



$$\text{Var}(B) = 0$$

$$\text{Var}(W) = 2.7$$

$$\text{Var}(T) = 2.7$$

$$\dagger = 0$$

Why $\text{cov}(\text{within}) = \text{variance}(\text{among})$?

- Let z_{ij} denote the j -th member of group i .
 - Here $z_{ij} = u + g_i + e_{ij}$
 - g_i is the group effect
 - e_{ij} the residual error
- Covariance within a group $\text{Cov}(z_{ij}, z_{ik})$
 - $= \text{Cov}(u + g_i + e_{ij}, u + g_i + e_{ik})$
 - $= \text{Cov}(g_i, g_i)$ as all other terms are uncorrelated
 - $\text{Cov}(g_i, g_i) = \text{Var}(g)$ is the among-group variance

Resemblance between relatives and variance components

- The phenotypic variance between relatives can be expressed in terms of genetic variance components
 - $\text{Cov}(z_x, z_y) = a_{xy} \text{Var}(A) + b_{xy} \text{Var}(D)$.
 - Under random-mating
 - The weights a and b depend on the nature of the relatives x and y , and are measures of how often they are expected to share alleles identical by descent
 - These are critical in predicting selection response

Parent-offspring genetic covariance

$\text{Cov}(G_p, G_o)$ --- Parents and offspring share
EXACTLY one allele IBD

Denote this common allele by A_1

$$\begin{array}{l} G_p = A_p + D_p = \alpha_1 + \alpha_x + D_{1x} \\ G_o = A_o + D_o = \alpha_1 + \alpha_y + D_{1y} \end{array}$$

IBD allele

Non-IBD alleles

$$\begin{aligned}
Cov(G_o, G_p) &= Cov(\alpha_1 + \alpha_x + D_{1x}, \alpha_1 + \alpha_y + D_{1y}) \\
&= Cov(\alpha_1, \alpha_1) + \cancel{Cov(\alpha_1, \alpha_y)} + \cancel{Cov(\alpha_1, D_{1y})} \\
&\quad + \cancel{Cov(\alpha_x, \alpha_1)} + \cancel{Cov(\alpha_x, \alpha_y)} + \cancel{Cov(\alpha_x, D_{1y})} \\
&\quad + \cancel{Cov(D_{1x}, \alpha_1)} + \cancel{Cov(D_{1x}, \alpha_y)} + \cancel{Cov(D_{1x}, D_{1y})}
\end{aligned}$$

All blue covariance terms are zero. By construction

- α and D are uncorrelated
- α from non-IBD alleles are uncorrelated
- D values are uncorrelated unless both alleles are IBD

$$Cov(\alpha_x, \alpha_y) = \begin{cases} 0 & \text{if } x \neq y, \text{ i.e., not IBD} \\ Var(A)/2 & \text{if } x = y, \text{ i.e., IBD} \end{cases}$$

$$Var(A) = Var(\alpha_1 + \alpha_2) = 2Var(\alpha_1)$$

so that

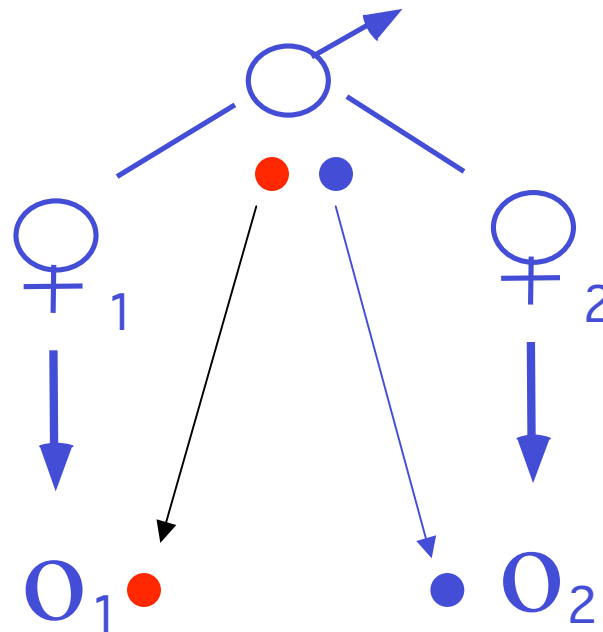
$$Var(\alpha_1) = Cov(\alpha_1, \alpha_1) = Var(A)/2$$

Hence, relatives sharing one allele IBD have a genetic covariance of $Var(A)/2$

The resulting parent-offspring genetic covariance becomes $Cov(G_p, G_o) = Var(A)/2$

Half-sibs

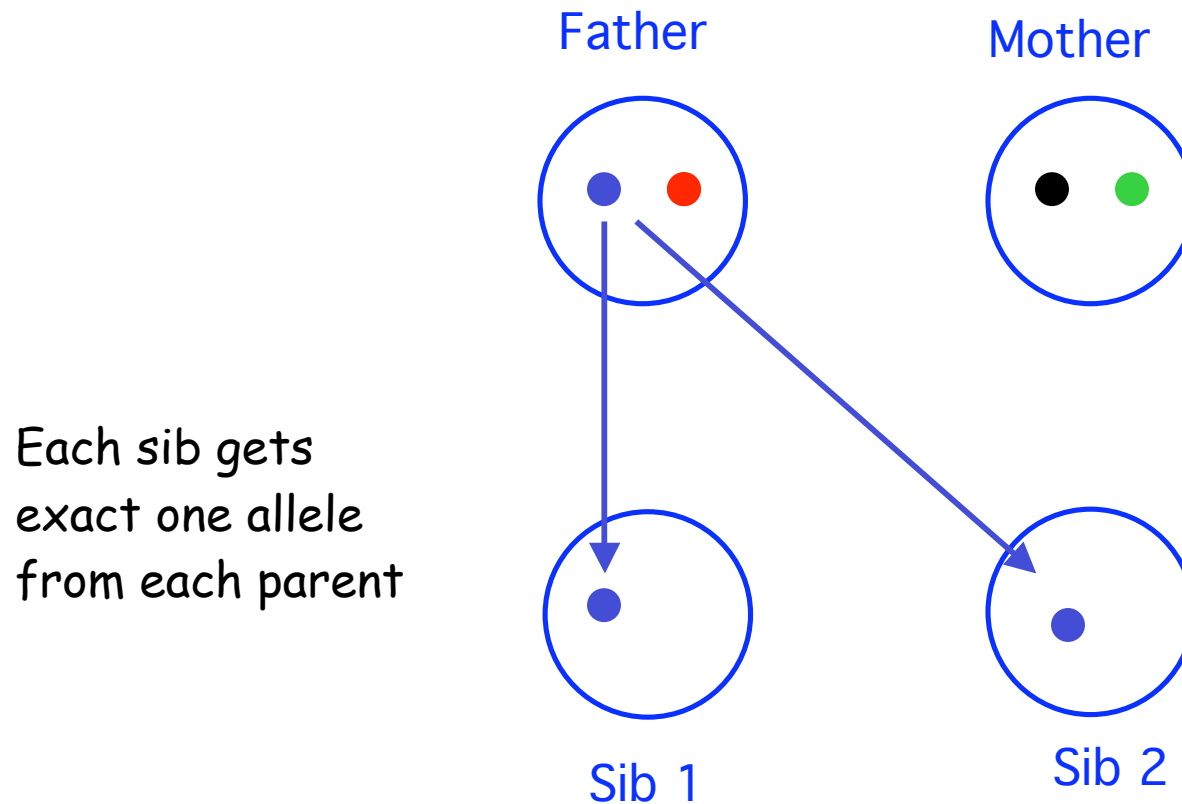
Each sib gets exactly one allele from common father, different alleles from the different mothers



The half-sibs share no alleles IBD
• occurs with probability 1/2

Hence, the genetic covariance of half-sibs is just
 $(1/2)\text{Var}(A)/2 = \text{Var}(A)/4$

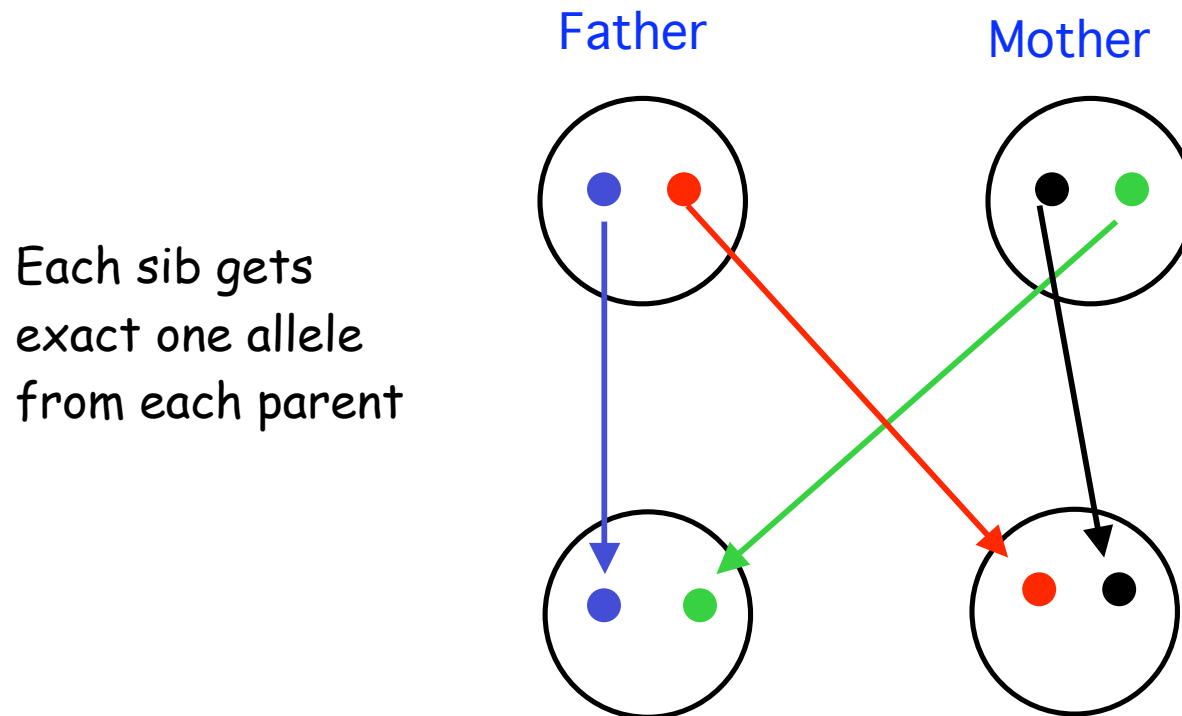
Full-sibs



$\text{Prob}(\text{Allele from father IBD}) = 1/2$. Given the allele in parent one, prob = $1/2$ that sib 2 gets same allele

$\text{Prob}(\text{Allele from father not IBD}) = 1/2$. Given the allele in parent one, prob = $1/2$ that sib 2 gets different allele

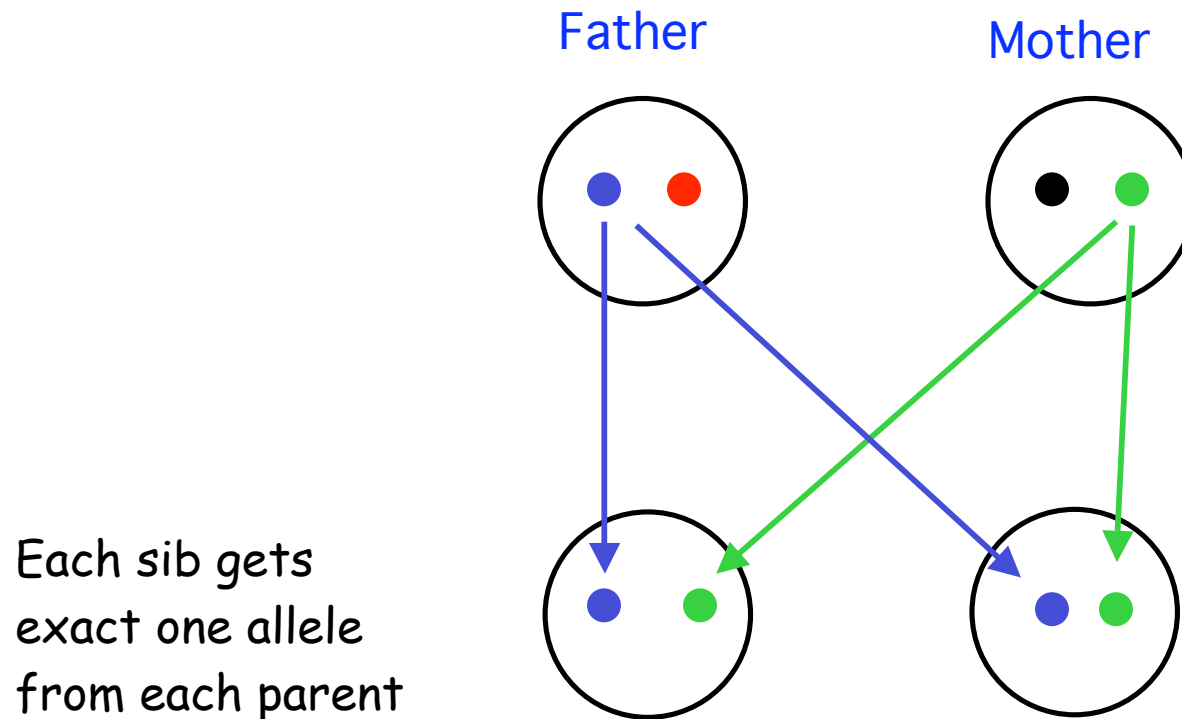
Full-sibs



Paternal allele not IBD [Prob = $1/2$]

Maternal allele not IBD [Prob = $1/2$]

Prob(sibs share 0 alleles IBD) = $1/2 * 1/2 = 1/4$



Paternal allele IBD [Prob = 1/2]

Maternal allele IBD [Prob = 1/2]

Prob(sibs share 2 alleles IBD) = $1/2 * 1/2 = 1/4$

Prob(share 1 allele IBD) = $1 - \text{Pr}(0) - \text{Pr}(2) = 1/2$

Resulting Genetic Covariance between full-sibs

IBD alleles	Probability	Contribution
0	1/4	0
1	1/2	$\text{Var}(A)/2$
2	1/4	$\text{Var}(A) + \text{Var}(D)$

$$\text{Cov}(\text{Full-sibs}) = \text{Var}(A)/2 + \text{Var}(D)/4$$

Genetic Covariances for General Relatives

Let $r = (1/2)\text{Prob}(1 \text{ allele IBD}) + \text{Prob}(2 \text{ alleles IBD})$

Let $u = \text{Prob}(\text{both alleles IBD})$

General genetic covariance between relatives

$$\text{Cov}(G) = r\text{Var}(A) + u\text{Var}(D)$$

When epistasis is present, additional terms appear

$$r^2\text{Var}(AA) + ru\text{Var}(AD) + u^2\text{Var}(DD) + r^3\text{Var}(AAA) +$$

Components of the Environmental Variance

Total environmental value

Specific environmental value,
any unique environmental effects
experienced by the individual


$$E = E_c + E_s$$

Common environmental value experienced
by all members of a family, e.g., shared
maternal effects

The Environmental variance can thus be written in terms of variance components as

$$V_E = V_{Ec} + V_{Es}$$

One can decompose the environmental further, if desired. For example, plant breeders have terms for the location variance, the year variance, and the location x year variance.

Shared environmental effects contribute to the phenotypic covariances of relatives

$$\begin{aligned}\text{Cov}(P_1, P_2) &= \text{Cov}(G_1 + E_1, G_2 + E_2) \\ &= \text{Cov}(G_1, G_2) + \text{Cov}(E_1, E_2)\end{aligned}$$

Shared environmental values are expected when sibs share the same mom due to common-family environment, so that $\text{Cov}(\text{Full sibs})$ and $\text{Cov}(\text{Maternal half-sibs})$ not only contain a genetic covariance, but an environmental covariance as well, V_{Ec}

$$\text{Cov}(\text{Full-sibs}) = \text{Var}(A)/2 + \text{Var}(D)/4 + V_{Ec}$$

More general relationships

- To obtain the expected covariance for any set of (random-mating) relatives, we normally need only compute r and u for that set of relatives
- With general inbreeding, becomes more complex (as three other terms, in addition to V_A and V_D arise)
- With crosses involving inbred and/or related parents, values for r and u are different from those presented above.

Coefficients of Coancestry

Suppose we pick a single allele each at random from two relatives. The probability that these are IBD is called Θ , the **coefficient of coancestry**

Θ_{xy} denotes the coefficient for relatives x and y

Consider an offspring z from a (hypothetical) cross of x and y . $\Theta_{xy} = f_z$, the inbreeding coefficient of z . Why? Because the offspring of x and y each get a randomly-chosen allele from each parent. The probability f_z that both alleles are IBD (the probability of inbreeding) is thus just Θ_{xy} .

θ and the coefficient on V_A

- The coefficient on the additive variance for the relatives x and y is just $2\theta_{xy}$.
- To see this,
 - let $A_i A_j$ denote the two alleles in x and $A_k A_l$ those in y .
 - $\text{Cov}(\text{breeding values}) = \text{Pr}(A_i \text{ ibd } A_k) \text{cov}(\alpha_i, \alpha_k) + \text{Pr}(A_i \text{ ibd } A_l) \text{cov}(\alpha_i, \alpha_l) + \text{Pr}(A_j \text{ ibd } A_k) \text{cov}(\alpha_j, \alpha_k) + \text{Pr}(A_j \text{ ibd } A_l) \text{cov}(\alpha_j, \alpha_l) = 4 \theta_{xy} \text{Var}(\alpha)$
 - Since $\text{Var}(A) = 2\text{Var}(\alpha)$, $\text{Cov} = 2 \theta_{xy} \text{Var}(A)$

Θ_{xx} : The coancestry of an individual with itself

Self x , what is the inbreeding coefficient of its offspring?

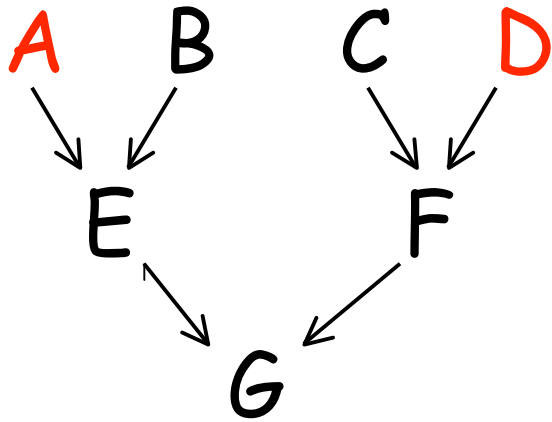
To compute Θ_{xx} , denote the two alleles in x by A_1 and A_2

	Draw A_1	Draw A_2
Draw A_1	IBD	f_x
Draw A_2	f_x	IBD

Hence, for a non-inbred individual, $\Theta_{xx} = 2/4 = 1/2$

If x is inbred, $f_x = \text{prob } A_1 \text{ and } A_2 \text{ IBD}$, $\Theta_{xx} = (1 + f_x)/2$

Example

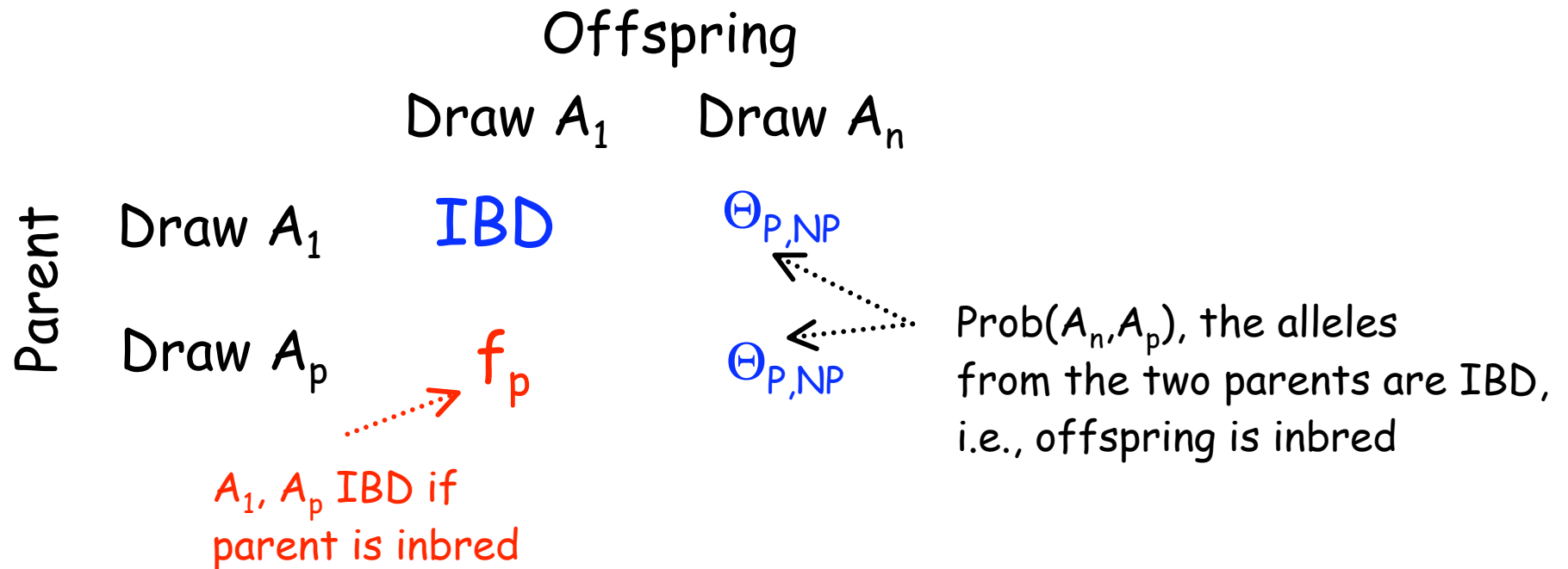


Consider the following pedigree
Suppose **A** and **D** are **fully-inbred**,
and related, lines with $\theta_{AD} = 0.5$.
Further, B and C are unrelated and
outcrossed individuals

Individual	A	B	C	D
f_x	1	0	0	1
$\theta_{xx} = (1 + f_x)/2$	1	1/2	1/2	1

The Parent-offspring Coancestry

Let A_1, A_n denote the two alleles in the offspring, where A_n is the allele from the nonfocal parent (NP), while A_1, A_p are the two alleles in the focal parent (P)



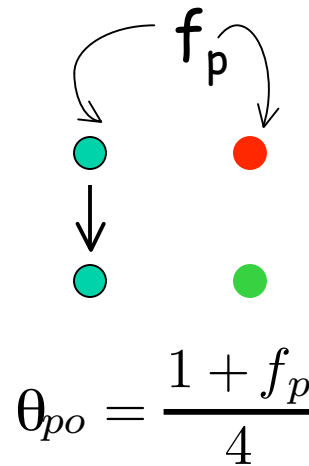
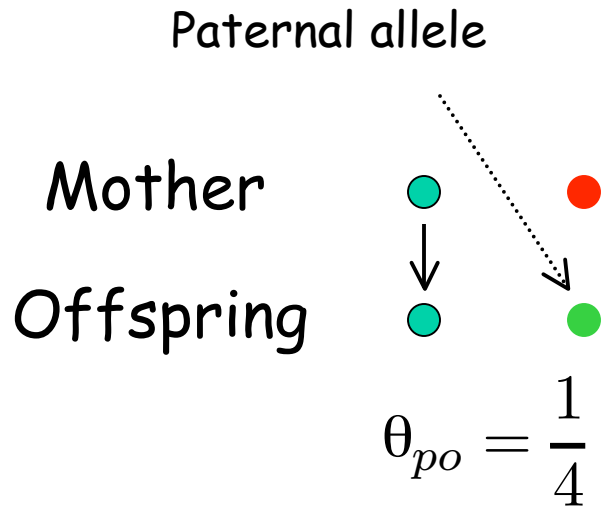
For a non-inbred individual, $\Theta_{PO} = 1/4$

General:

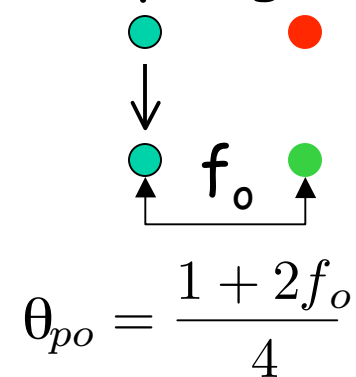
$$\Theta_{PO} = (1 + f_p + 2\Theta_{P,NP})/4 = (1 + f_p + 2f_o)/4$$

Θ_{op} = Parent & Offspring

Parent inbred



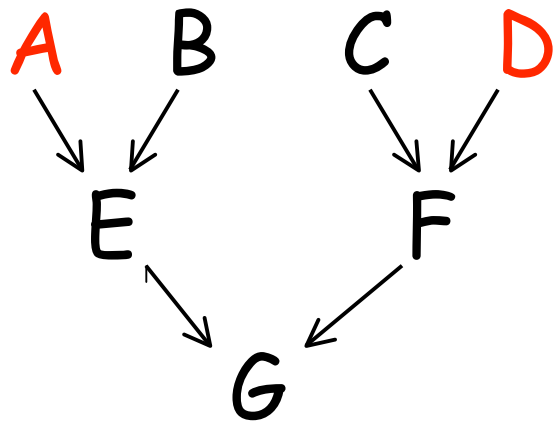
Offspring inbred



$1/2$ = Prob random offspring allele from father. Prob = $\theta_{mf} = f_o$ that this allele is IBD to mother giving a contribution of $f_o/2$

$$\theta_{po} = \frac{1}{4}(1 + f_p + 2\theta_{mf})$$

This is just $2f_o$



From before

$$\theta_{AA} = \theta_{DD} = 1; \theta_{BB} = \theta_{CC} = 1/2;$$

$$\theta_{AD} = 1/2,$$

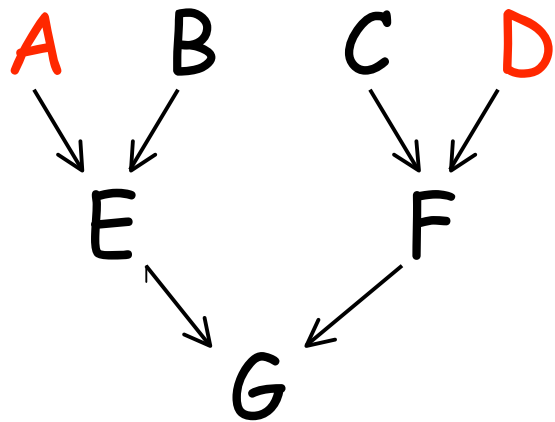
$$\theta_{AB} = \theta_{AC} = \theta_{BC} = \theta_{BD} = \theta_{CD} = 0$$

Consider A - E (inbred parent - offspring)

$$\theta_{AE} = (1+f_A)/4 = (1+1)/4 = 1/2. \text{ Same value for } \theta_{DF}$$

Consider B - E (outbred parent - offspring)

$$\theta_{BE} = (1+f_B)/4 = (1+0)/4 = 1/4. \text{ Same value for } \theta_{CF}$$



From before

$$\theta_{AA} = \theta_{DD} = 1; \theta_{BB} = \theta_{CC} = 1/2;$$

$$\theta_{AD} = 1/2,$$

$$\theta_{AB} = \theta_{AC} = \theta_{BC} = \theta_{BD} = \theta_{CD} = 0$$

What about θ_{EF} ?

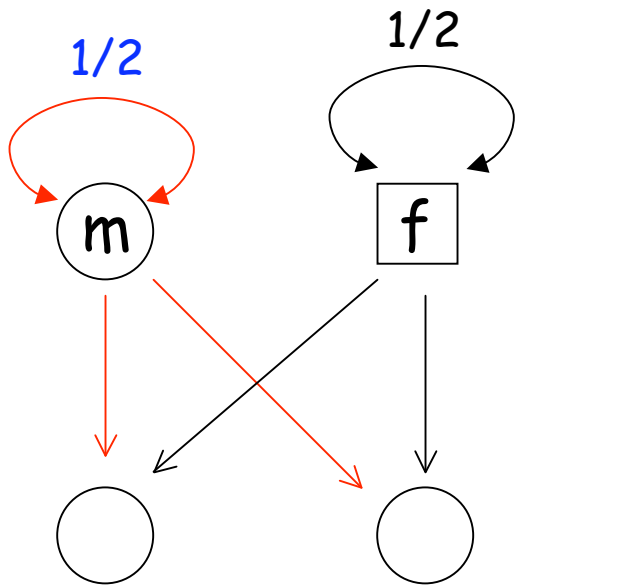
The randomly-chosen allele from E has equal chance of being from A or B. Likewise for F (from C or D)

Of these four possible combinations (A&C, A&D, B&C, B&D), only an allele from A and an allele from D have a chance of being IBD, which is $\theta_{AD} = 1/2$.

$$\text{Hence, } \theta_{EF} = \theta_{AD} / 4 = 1/8$$

Full sibs (x and y) from parents m and f

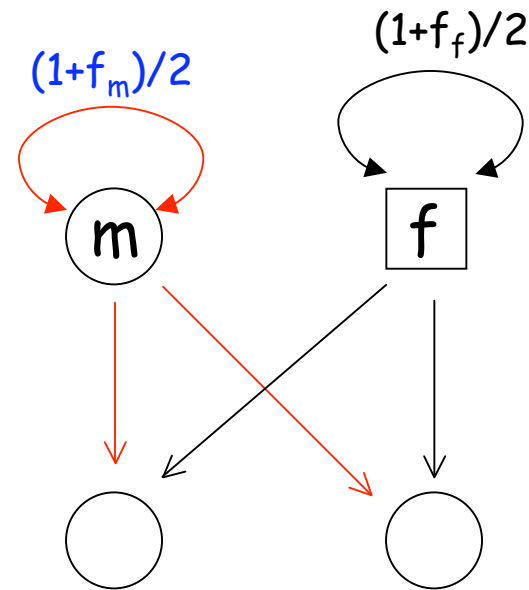
$$\Theta = 1/8 + 1/8 = 1/4$$



$$(1/2)(1/2)(1/2) \quad (1/2)(1/2)(1/2)$$

Unrelated, non-inbred
parents

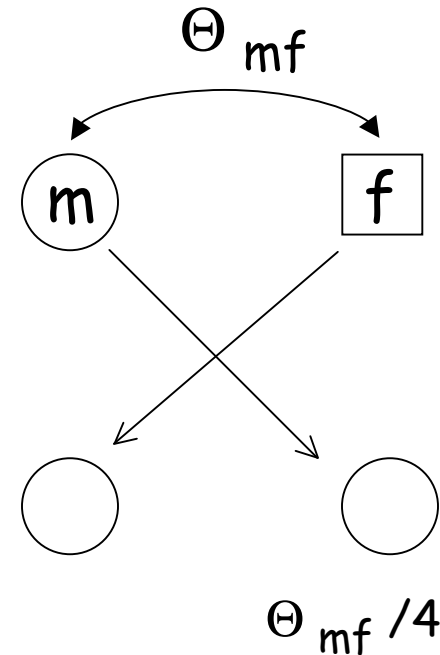
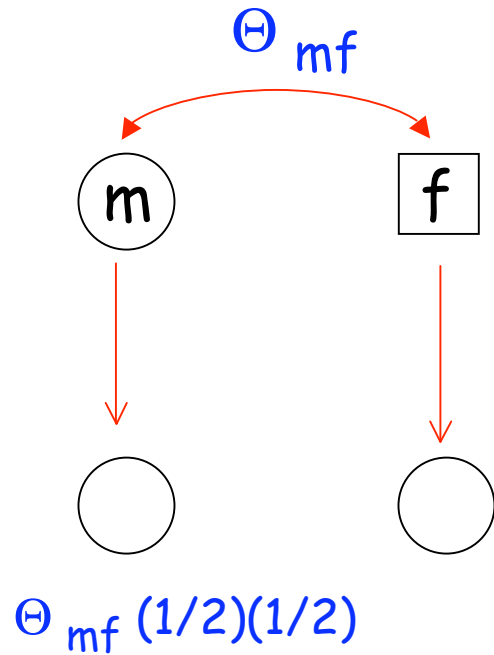
$$\Theta = (2 + f_m + f_f)/8$$



$$[(1 + f_m)/2] (1/2)(1/2) \quad [(1 + f_f)/2] (1/2)(1/2)$$

Unrelated, inbred
parents

Full sibs (x and y) from parents m and f



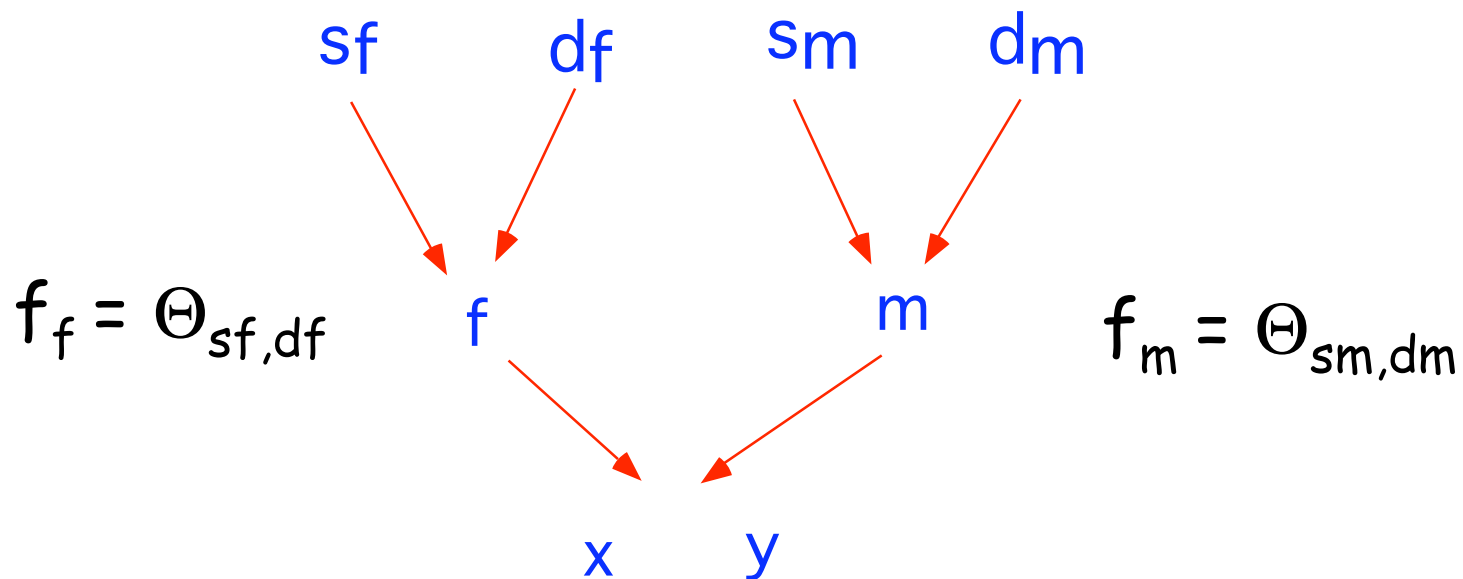
Parents inbred & related.

Two additional paths to add
to $\Theta = (2 + f_m + f_f) / 8$

This gives $\Theta = (2 + f_m + f_f + 4 \Theta_{mf}) / 8$

Full sibs (x and y) from parents m and f

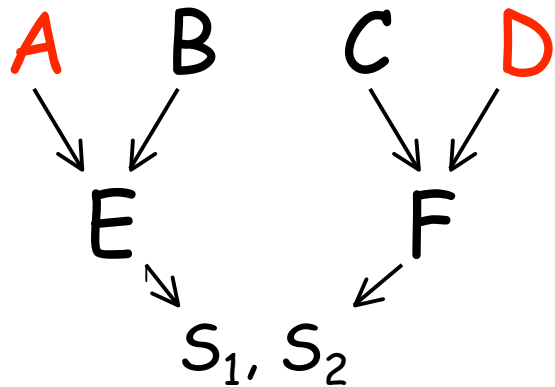
$$\Theta_{xy} = (2 + f_m + f_f + 4\Theta_{mf})/8$$



Putting all this together gives

$$\Theta_{xy} = (2 + \Theta_{sm,dm} + \Theta_{sf,df} + 4\Theta_{mf})/8$$

Example



From before

$$\theta_{AA} = \theta_{DD} = 1; \theta_{BB} = \theta_{CC} = 1/2;$$

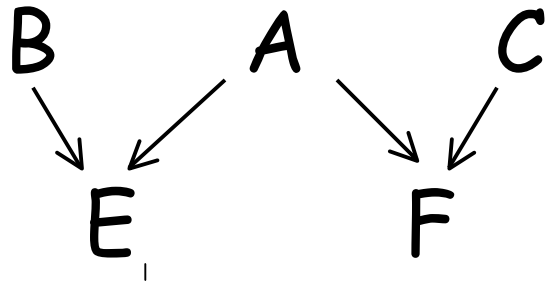
$$\theta_{AD} = 1/2, \theta_{EF} = 1/8,$$

$$\theta_{AB} = \theta_{AC} = \theta_{BC} = \theta_{BD} = \theta_{CD} = 0$$

$$\Theta_{xy} = (2 + \Theta_{AB} + \Theta_{CD} + 4\Theta_{EF})/8$$

$$\theta_{S_1 S_2} = (2 + 0 + 0 + 4[1/8])/8 = (4 + 1)/16 = 5/16$$

Half-sibs



A is the common parent

- Using the same arguments as above,

$$\begin{aligned}\theta_{EF} &= (\theta_{AA} + \theta_{AB} + \theta_{AC} + \theta_{BC})/4 \\ &= ([1 + f_A]/2 + \theta_{AB} + \theta_{AC} + \theta_{BC})/4\end{aligned}$$

Hence, if B and C unrelated,

$$\theta_{EF} = (1 + f_A)/8$$

Computing Θ_{xy} -- chain counting

Θ can be obtained for any structure of pedigree

Two components: First are paths through a single common ancestor (i) of both x and y

$$\Theta_{xy} = \sum_i \Theta_{ii} \binom{1}{2}^{n_i-1} + \sum_j \sum_{j=k} \Theta_{jk} \binom{1}{2}^{n_{jk}-2}$$

Coefficient of coancestry of i

n_i = Number of individuals (including x and y) in path connecting x and y through i

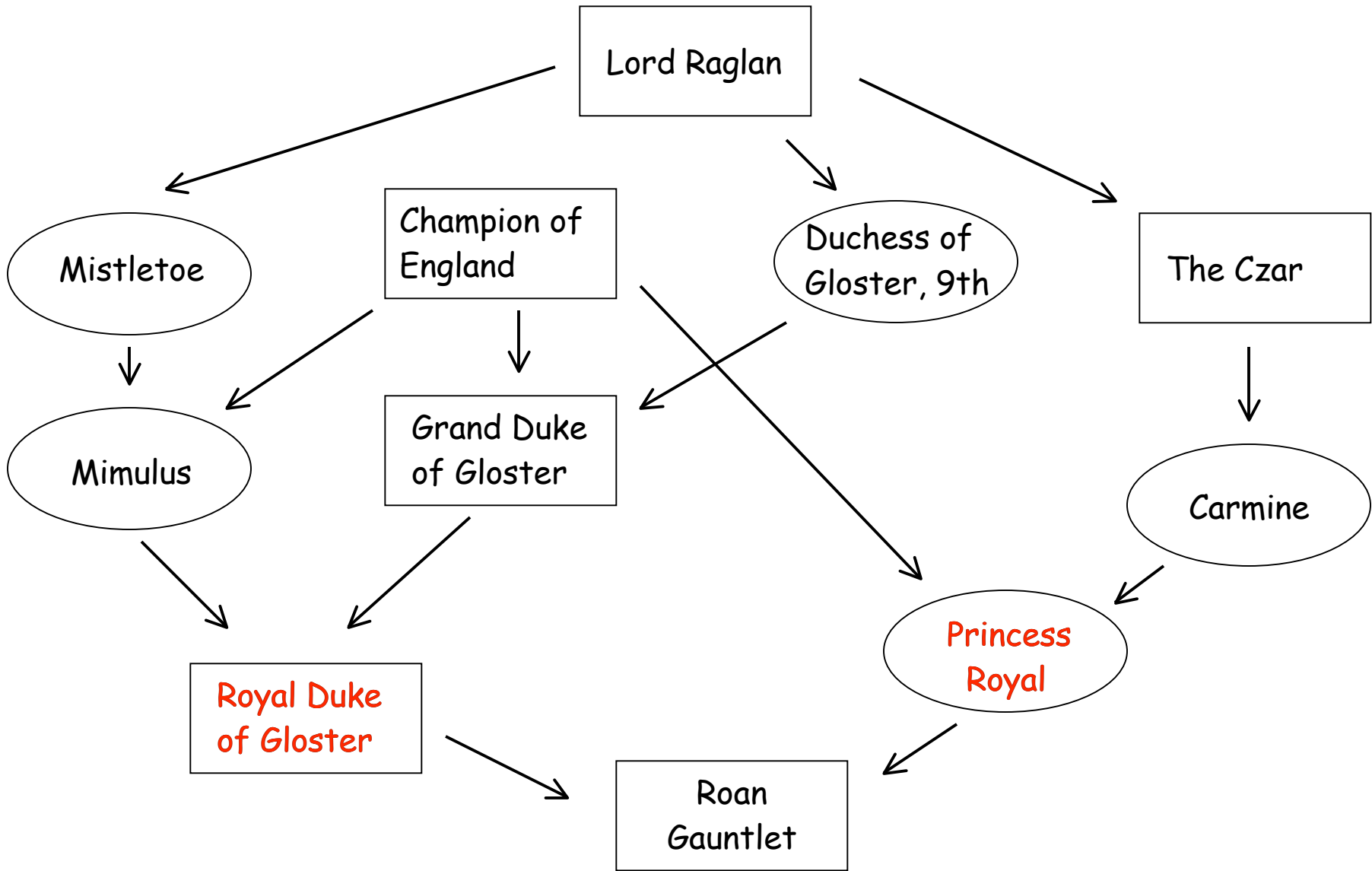
Computing Θ_{xy} -- chain counting

Second component: Paths from x through j and paths from y through k, j & k related

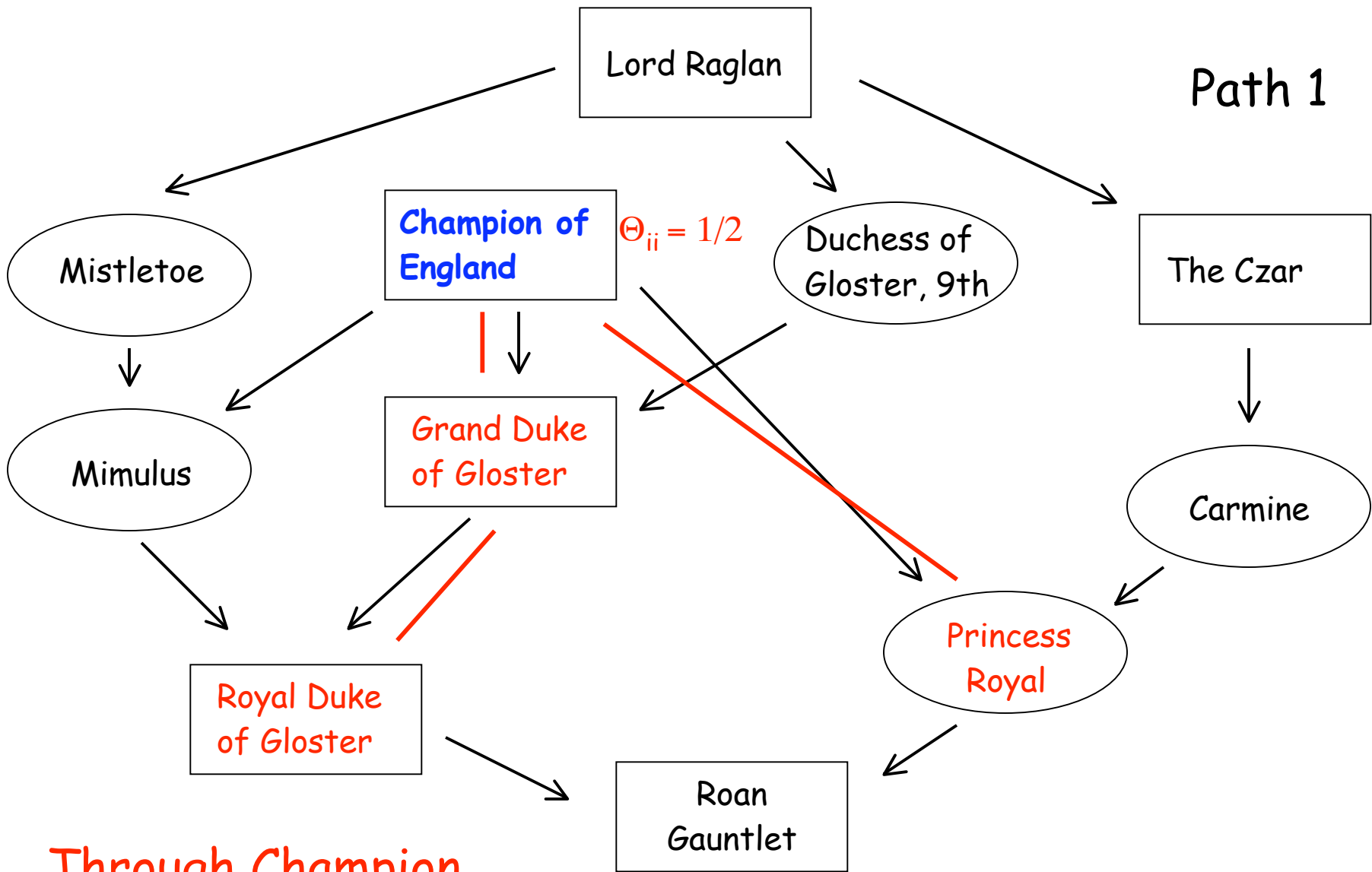
$$\Theta_{xy} = \sum_i \Theta_{ii} \binom{1}{2}^{n_i-1} + \sum_j \sum_{j=k} \Theta_{jk} \binom{1}{2}^{n_{jk}-2}$$

Coefficient of coancestry
of j and k

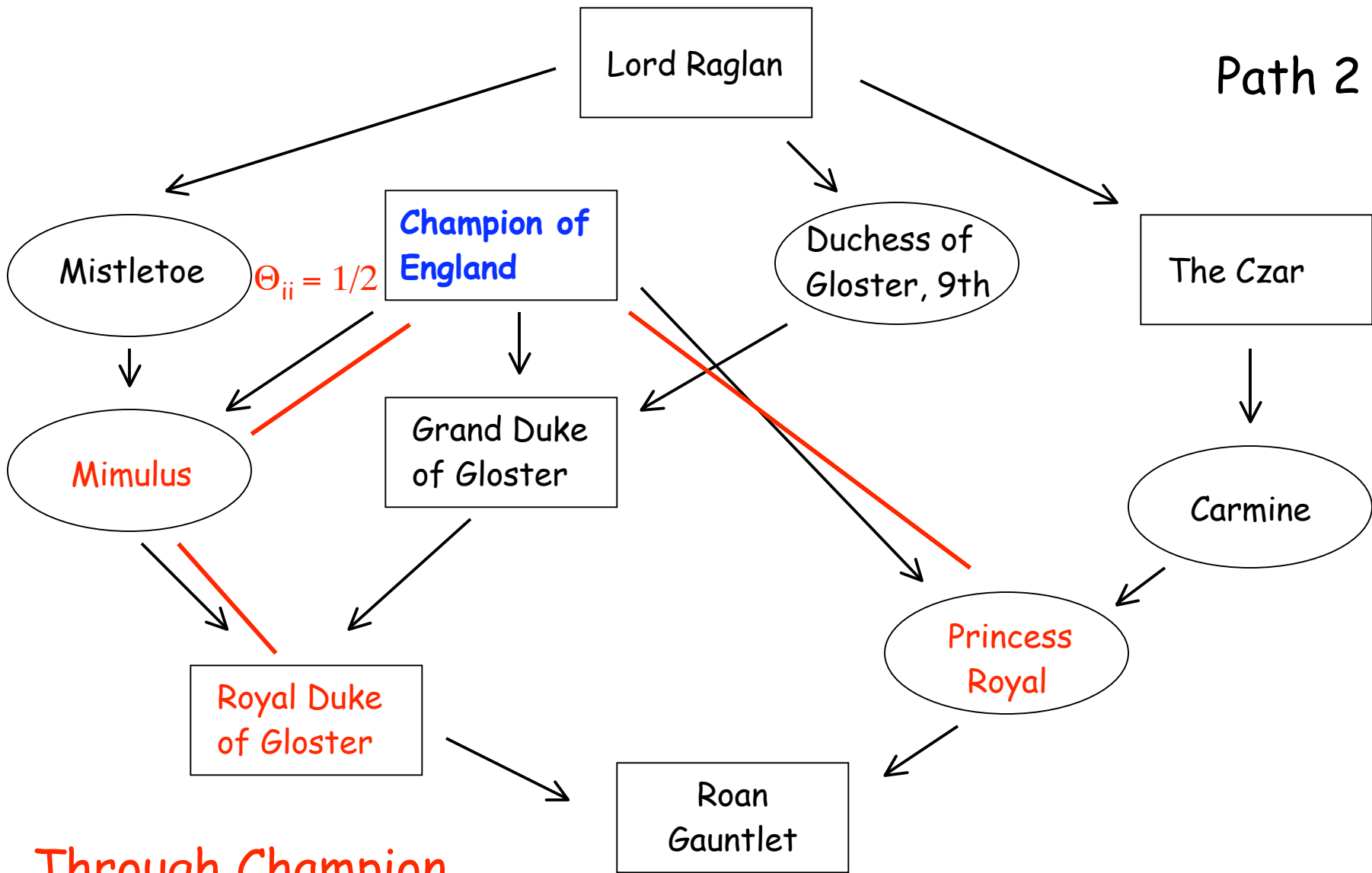
Number of individuals,
including x and y
on the path leading
from two different
(but related) ancestors
j and k



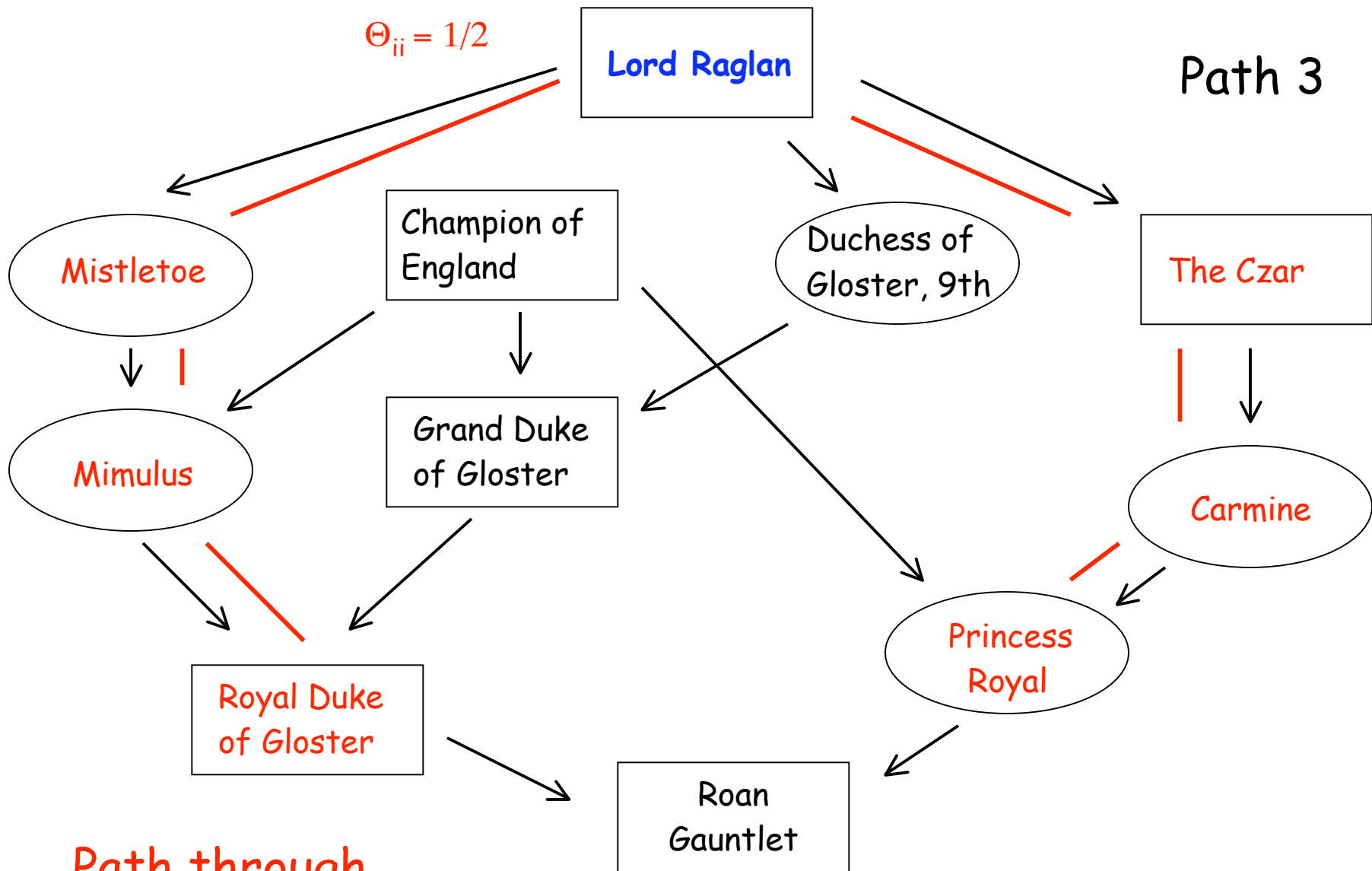
Compute θ for Royal Duke of Gloster and Princess Royal



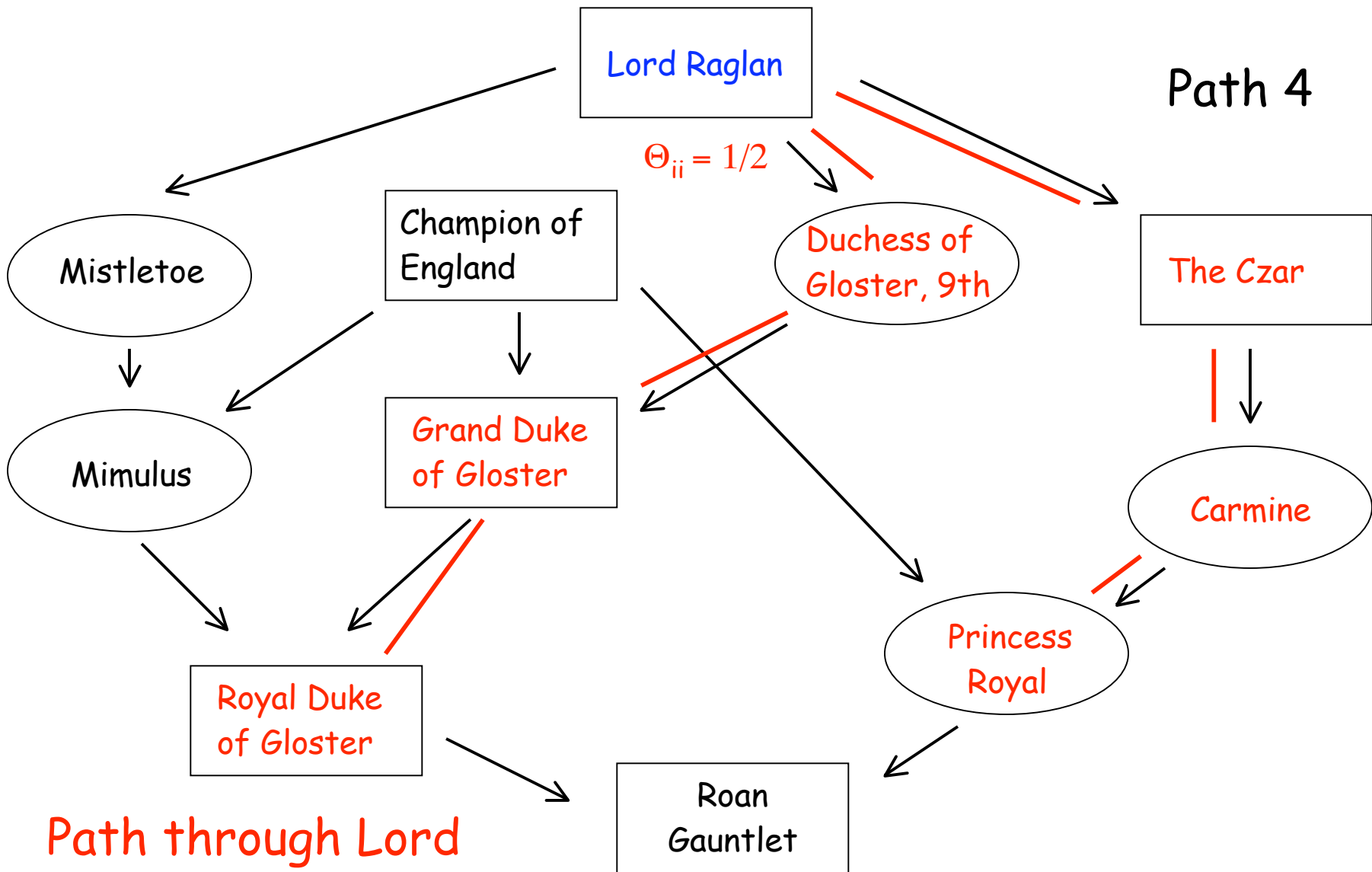
Through Champion
of England, $n = 4$
contribution = $(1/2)(1/2)^3$



Through Champion
of England, $n = 4$
Contribution = $(1/2)(1/2)^3$

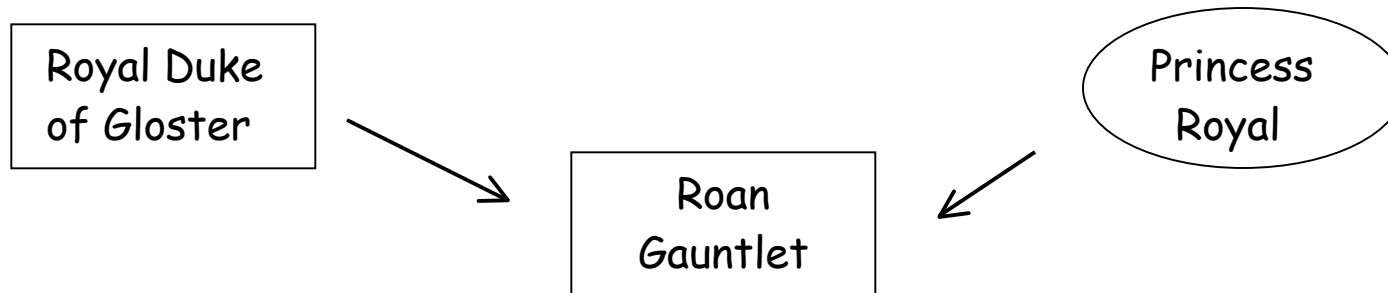


Path through
 Lord Raglan, $n = 7$
 Contribution = $(1/2)(1/2)^6$



Path through Lord Raglan, $n = 7$

Contribution = $(1/2)(1/2)^6$



Four distinct paths:

Path 1: $(1/2)^4$

Path 2: $(1/2)^4$

Path 3: $(1/2)^7$

Path 4: $(1/2)^7$

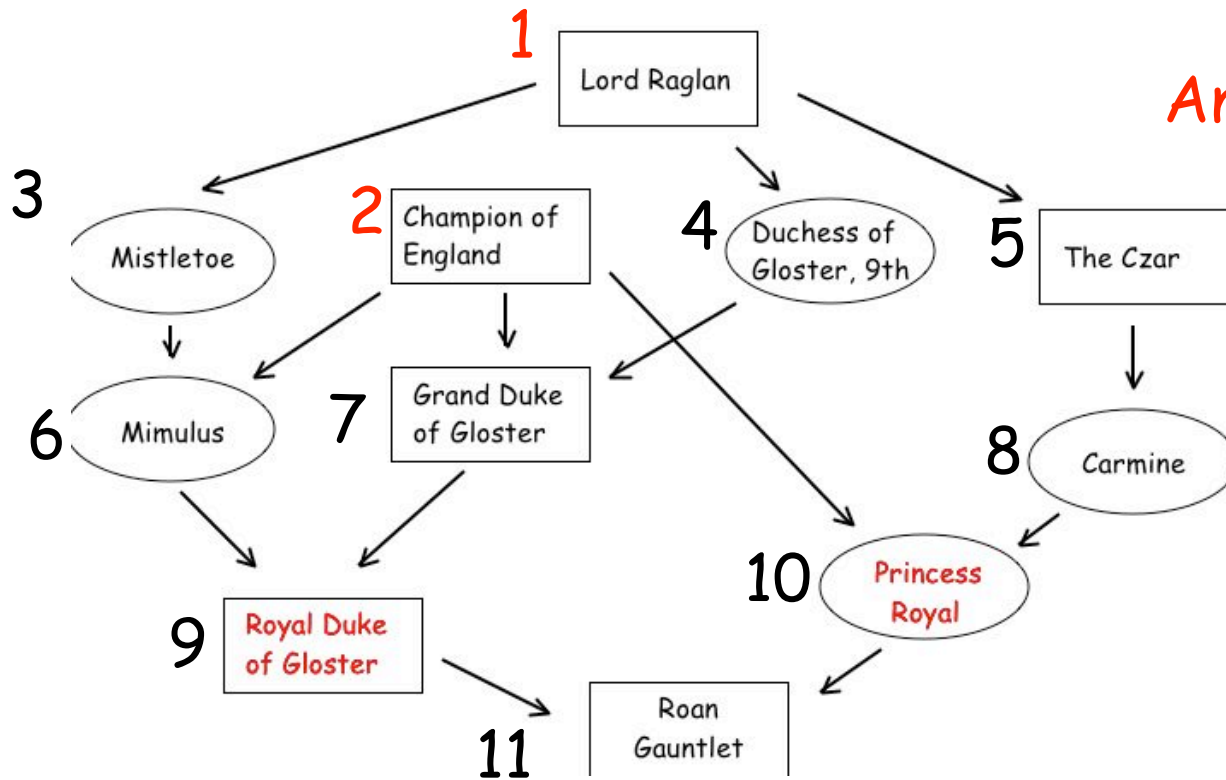
total: 0.141

**f for Roan Gauntlet
= 0.141**

Computing θ_{xy} -- The Recursive Method

- There is a simple recursive method for generating the elements $A_{ij} = 2 \theta_{ij}$ of a relationship matrix (used for BLUP selection). For ease of reading, we use the notation $A(i,j) = A_{ij}$
 - Basic idea is that the founding individuals of the pedigree are assumed to be unrelated and not inbred (although this can also be accommodated). These founders are assigned values of $A(i,i) = 1$.
 - Likewise, any unknown parent of any future individual is assumed to be unrelated to all others in the pedigree and not inbred, and they are also assigned a value of $A(i,i) = 1$.
 - Let S_i and D_i denote the sire and dam (father and mother) of individual i . For this offspring $A(i,i) = 1 + A(S_i, D_i)/2$
 - $A(i,j) = A(j,i) = [A(j,S_i) + A(j,D_i)]/2 = [A(i,S_j) + A(i,D_j)]/2$
 - The recursive (or tabular) method starts with the founding parents and then proceeds down the pedigree in a recursive fashion to fill out A for the desired pedigree.

Example



Ancestors are 1 & 2

$$A(1,1) = A(2,2) = 1$$

$$A(1,2) = 0$$

3, 4, 5, 8 all have unknown parents (only a single arrow to them)

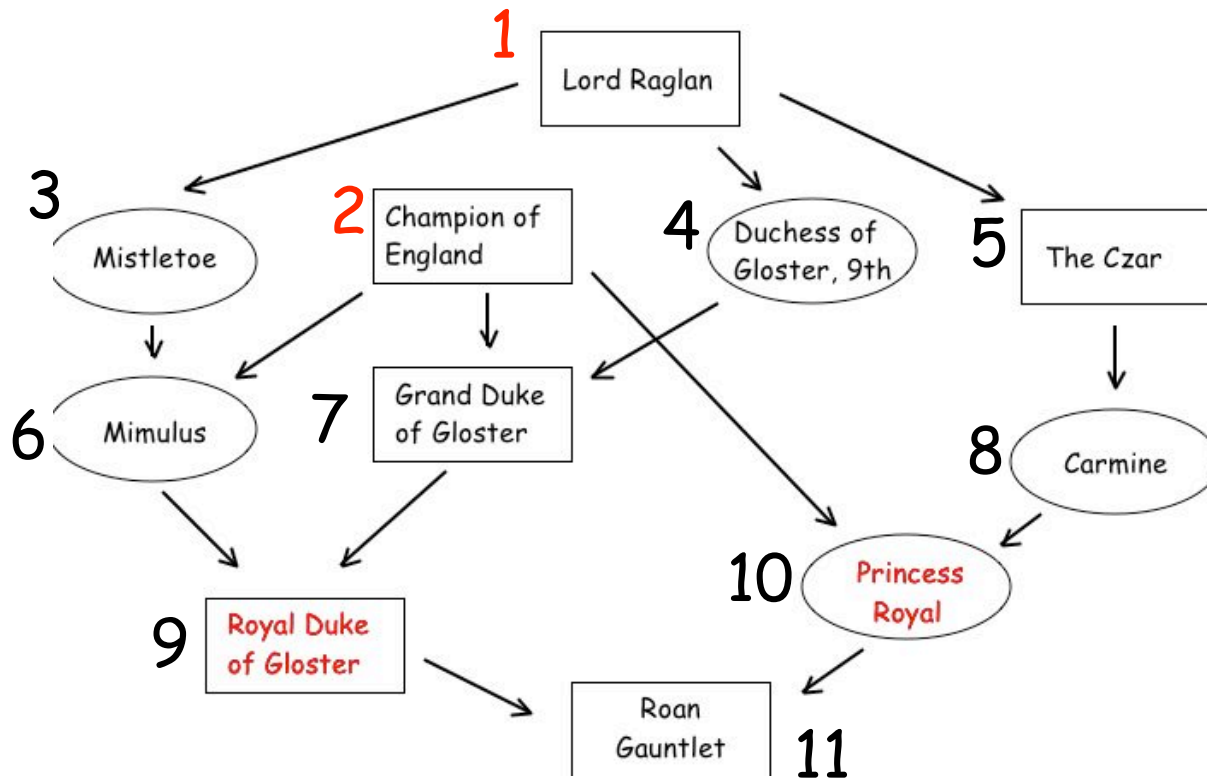
$$3: S_3 = 1, D_3 = \text{Unknown}, A(3,3) = 1 + A(S_3, D_3)/2 = 1 + A(1, \text{unk})/2 = 1$$

$$A(1,3) = [A(1, S_3) + A(1, D_3)]/2 = [A(1,1) + A(1, \text{unk})]/2 = 1/2.$$

Note also that $A(1,4) = A(1,5) = 1/2$, $A(4,4) = A(5,5) = 1$.

$$A(3,4) = [A(3, S_4) + A(3, D_4)]/2 = [A(3,1) + A(3, \text{unk})]/2 = (1/2 + 0)/2 = 1/4.$$

Same for $A(3,5) = 1/4$. 2 is unrelated to 3, 4, 5, giving $A(2,3) = A(2,4) = A(2,5) = 0$.



So far

	1	2	3	4	5
1	1	0	1/2	1/2	1/2
2	0	1	0	0	0
3	1/2	0	1	1/4	1/4
4	1/2	0	1/4	1	1/4
5	1/2	0	1/4	1/4	1

$$6: S_6 = 2, D_6 = 3. A(6,6) = 1 + A(S_6, D_6)/2 = 1 + A(2,3)/2 = 1$$

$$A(6,1) = [A(1, S_6) + A(1, D_6)]/2 = [A(1,2) + A(1,3)]/2 = [0 + 1/2]/2 = 1/4$$

$$A(6,2) = [A(2, S_6) + A(2, D_6)]/2 = [A(2,2) + A(2,3)]/2 = [1 + 0]/2 = 1/2$$

$$A(6,3) = [A(3, S_6) + A(3, D_6)]/2 = [A(3,2) + A(3,3)]/2 = [0 + 1]/2 = 1/2$$

$$A(6,4) = [A(4, S_6) + A(4, D_6)]/2 = [A(4,2) + A(4,3)]/2 = [0 + 1/4]/2 = 1/8$$

$$A(6,5) = [A(5, S_6) + A(5, D_6)]/2 = [A(5,2) + A(5,3)]/2 = (0 + 1/4)/2 = 1/8$$

$$7: S_7 = 2, D_7 = 4. A(7,7) = 1 + A(S_7, D_7)/2 = 1 + A(2,4)/2 = 1 + 0/2 = 1$$

$$A(6,7) = [A(6, S_7) + A(6, D_7)]/2 = [A(6,2) + A(6,4)]/2 = (1/2 + 1/8)/2 = 5/16$$

$$8: S_8 = 5, D_8 = \text{unk}. A(8,8) = 1 + A(S_8, D_8)/2 = 1 + A(5, \text{unk})/2 = 1.$$

$$A(6,8) = [A(6, S_8) + A(6, D_8)]/2 = [A(6,5) + A(6, \text{unk})]/2 = (1/8)/2 = 1/16$$

$$9: S_9 = 7, D_9 = 6. A(9,9) = 1 + A(S_9, D_9)/2 = 1 + A(6,7)/2 = 1 + 5/32 = 1.156 \leftarrow \text{inbred!}$$

The coefficient of fraternity

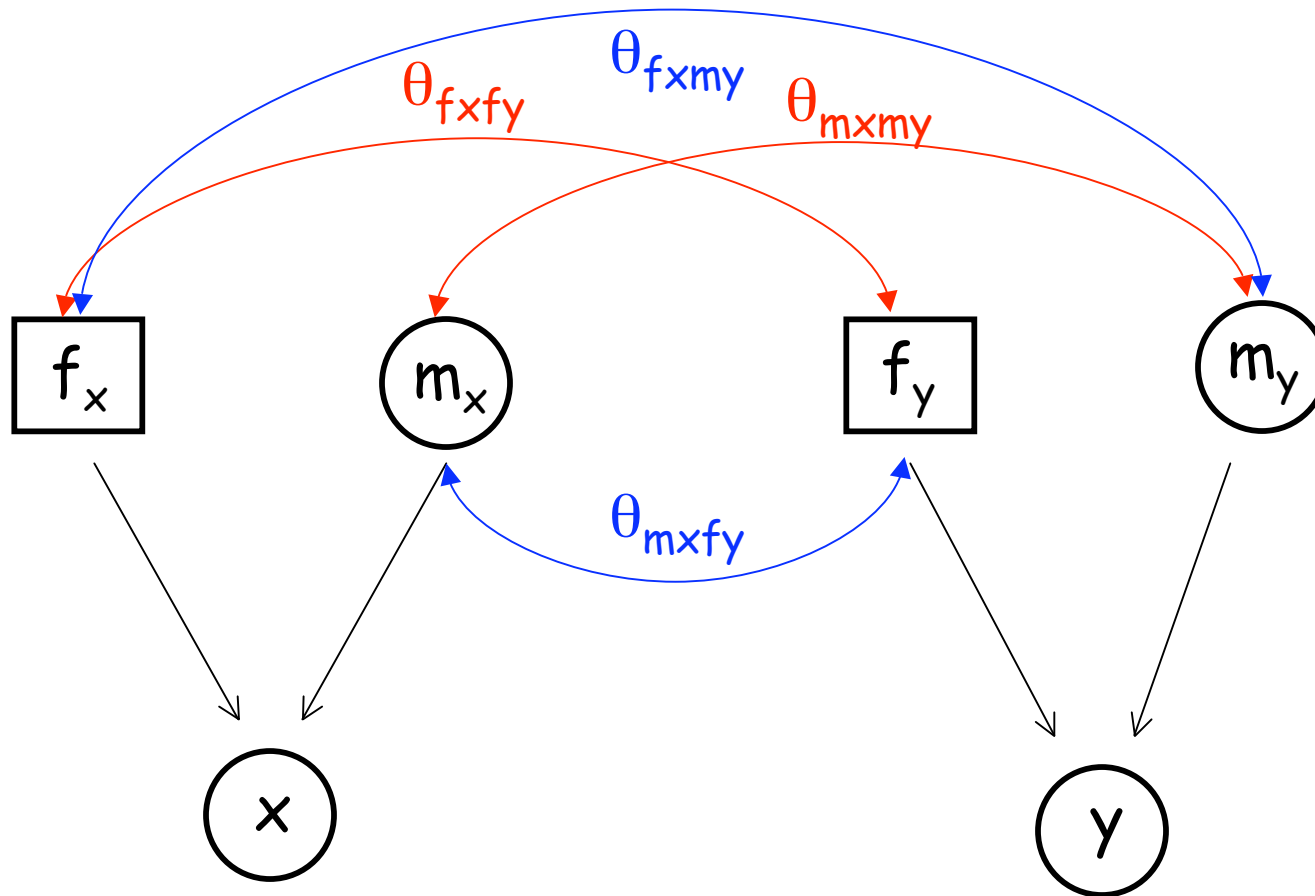
- While (twice) the coefficient of coancestry gives the weight on the additive variance for two relatives, a related measure of IBD status among relatives gives the weight on the dominance variance
- The probability that the two alleles in individual x are IBD to two alleles in individual y is denoted Δ_{xy} , and is called the **coefficient of fraternity**.
- This can be expressed as a function of the coefficients of coancestry for the parents of (m_x and f_x) of x and the parents (m_y and f_y) of y .
 - $\Delta_{xy} = \theta_{m_x m_y} \theta_{f_x f_y} + \theta_{m_x f_y} \theta_{f_x m_y}$

The coefficient of fraternity (cont)

- x and y can have both alleles IBD if
 - The allele from the father (fx) of x and the father (fy) of y are IBD (probability θ_{fxfy}) AND the allele from the mother (mx) of x and the mother (my) of y are IBD (probability θ_{mxmy}) , or $\theta_{fxfy} \theta_{mxmy}$
 - OR the allele from the mother (mx) of x and the father (fy) of y are IBD (probability θ_{mxfy}) AND the allele from the father (fx) of x and the mother (my) of y are IBD (probability θ_{fxmy}) , or $\theta_{mxfy} \theta_{fxmy}$
 - Putting these together gives
 - $\Delta_{xy} = \theta_{mxmy} \theta_{fxfy} + \theta_{mxfy} \theta_{fxmy}$

Δ_{xy} , The Coefficient of Fraternity

$\Delta_{xy} = \text{Prob}(\text{both alleles in } x \text{ \& } y \text{ IBD})$



$$\Delta_{xy} = \theta_{mxmy}\theta_{fxfy} + \theta_{mxfy}\theta_{fxmy}$$

Examples of Δ_{xy} : Full sibs

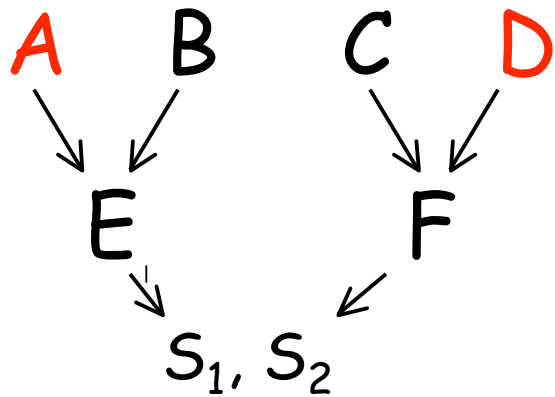
- Full sibs share same mom, dad
 - $m_x = m_y = m, f_x = f_y = f$
 - $\Delta_{xy} = \theta_{m \times m} \theta_{f \times f} + \theta_{m \times f} \theta_{f \times m} = \theta_{mm} \theta_{ff} + \theta_{mf}^2$
 - $\Delta_{xy} = (1+f_m)(1+f_f)/4 + \theta_{mf}^2$
- If parents unrelated, $\theta_{fm} = 0$, giving
 - $\Delta_{xy} = (1+f_m)(1+f_f)/4$
- If parents are unrelated and not inbred,
 - $\Delta_{xy} = 1/4$

Examples of Δ_{xy} : Half sibs

- Paternal half sibs share same dad, different moms
 - $f_x = f_y = f$; m_x and m_y
 - $\Delta_{xy} = \theta_{m_x m_y} \theta_{f_x f_y} + \theta_{m_x f_y} \theta_{f_x m_y} = \theta_{m_x m_y} \theta_{ff} + \theta_{m_x f} \theta_{m_y f}$
 - $\Delta_{xy} = \theta_{m_x m_y} (1+f_m)/2 + \theta_{m_x f} \theta_{m_y f}$
- If mothers are unrelated to each other and to the common father, $\theta_{m_x m_y} = \theta_{m_x f} = \theta_{m_y f} = 0$, giving
 - $\Delta_{xy} = 0$

When is Δ non-zero?

- Since $\Delta_{xy} = \theta_{mxmy}\theta_{fxfy} + \theta_{mxfy}\theta_{fxmy}$
- A nonzero value for Δ requires either
 - That the fathers of both x and y are related AND the mothers of both x and y are related
 - OR that the father of x is related to the mother of y AND the mother of x is related to the father of y



From before

$$\theta_{AA} = \theta_{DD} = 1; \theta_{BB} = \theta_{CC} = 1/2;$$

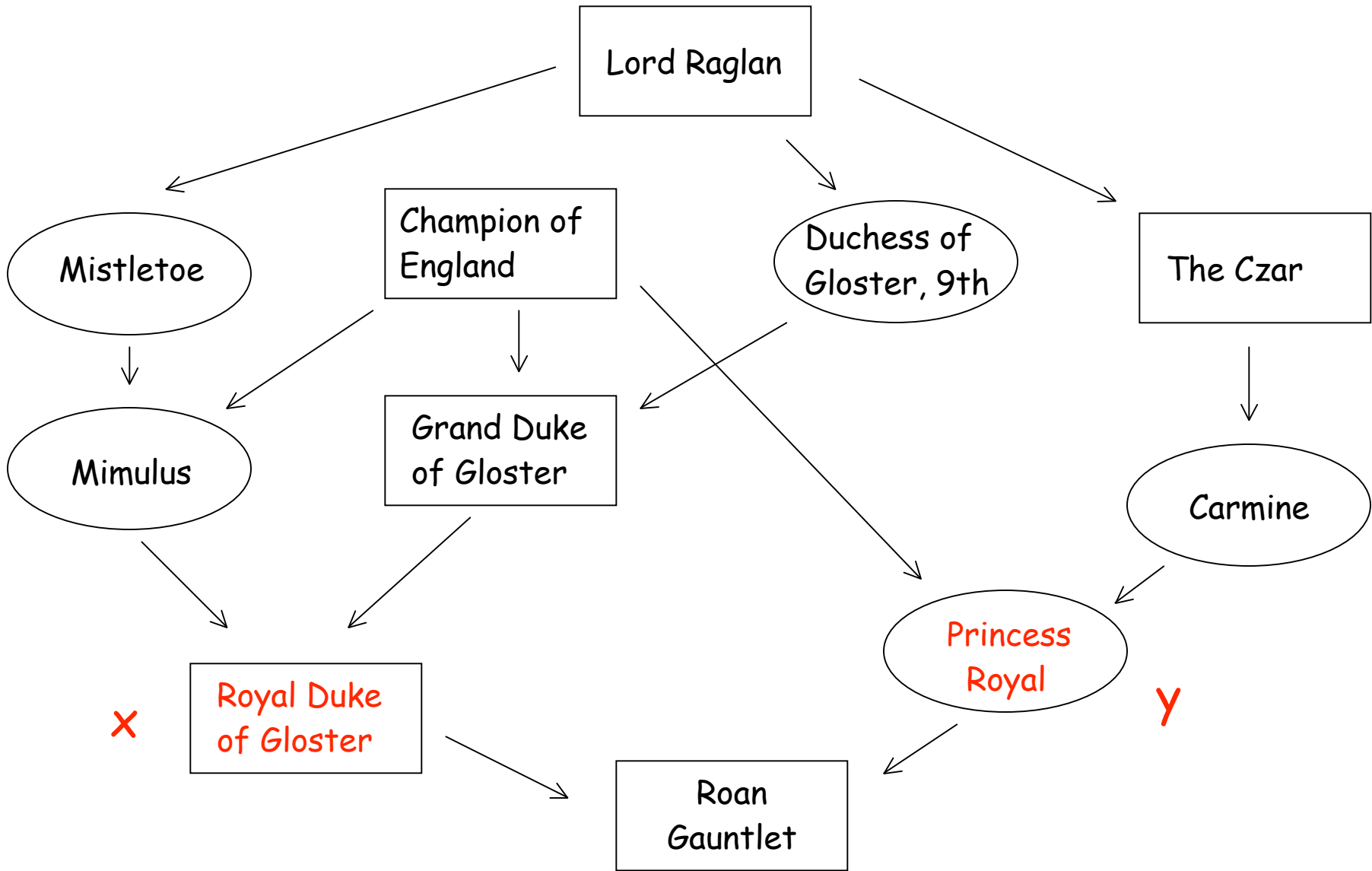
$$\theta_{AD} = 1/2, \theta_{EF} = 1/8,$$

$$\theta_{AB} = \theta_{AC} = \theta_{BC} = \theta_{BD} = \theta_{CD} = 0$$

What is Δ for the full sibs (S_1 and S_2)?

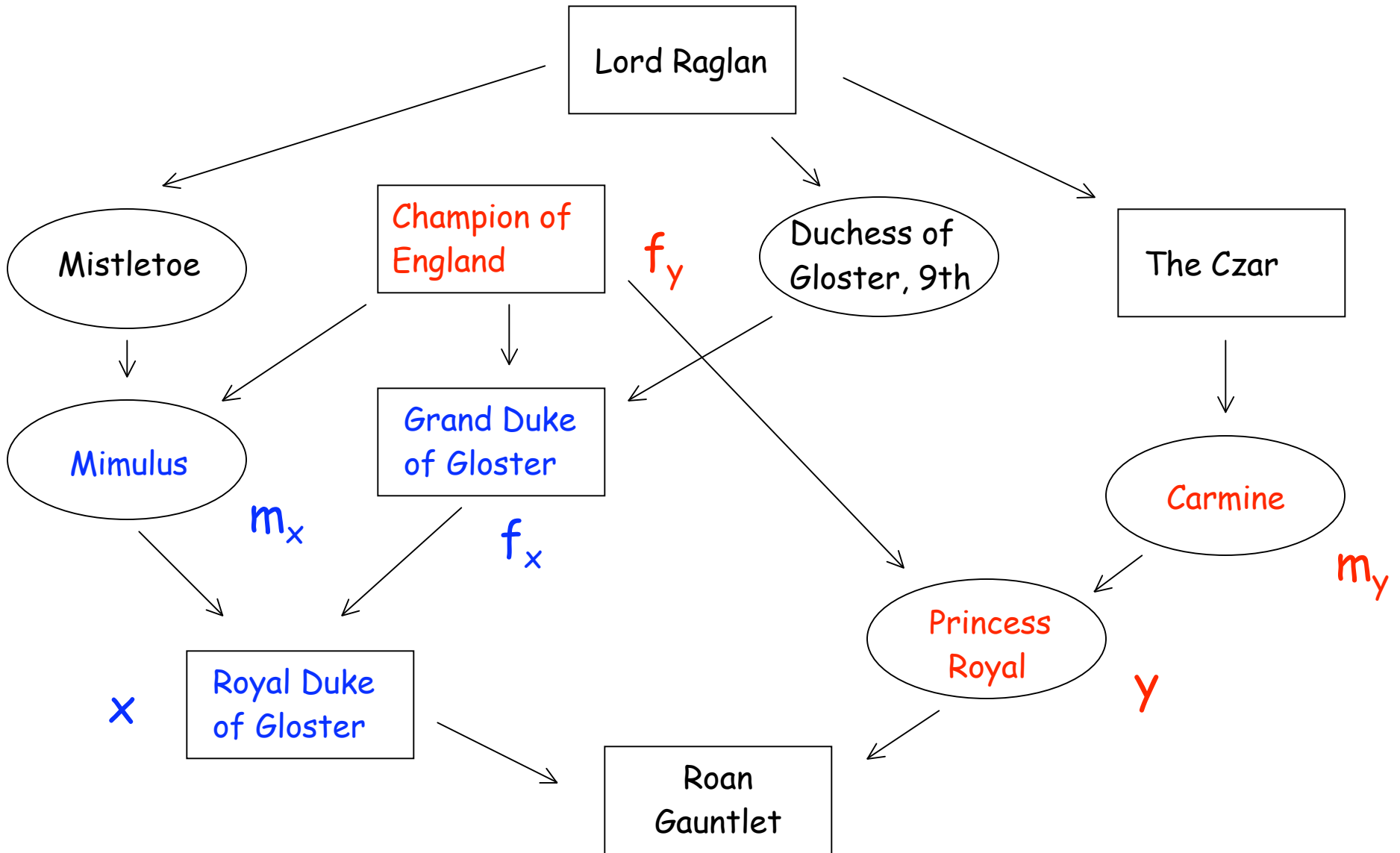
$$\Delta_{xy} = \theta_{m \times m y} \theta_{f \times f y} + \theta_{m \times f y} \theta_{f \times m y} = \theta_{EE} \theta_{FF} + \theta_{EF}^2$$

$$\begin{aligned} \text{Giving } \Delta_{xy} &= \theta_{EE} \theta_{FF} + \theta_{EF}^2 \\ &= (1/2)(1/2) + (1/8)^2 \\ &= 1/4 + 1/64 = 17/64 = 0.266 \end{aligned}$$



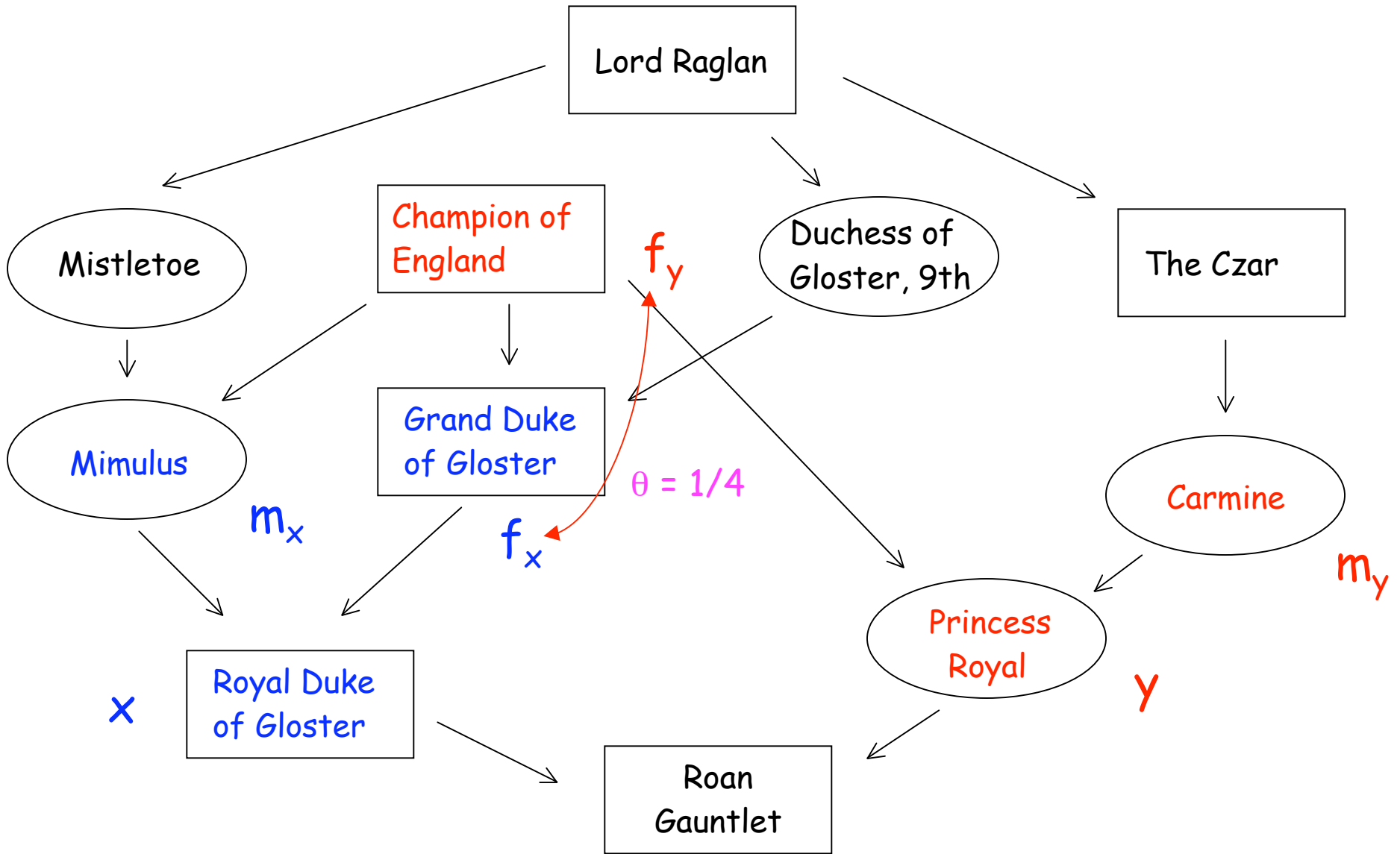
What is Δ for Royal Duke of Gloster and Princess Royal?

$$\Delta_{xy} = \theta_{mxmy} \theta_{fxfy} + \theta_{mxfy} \theta_{fxmy}$$



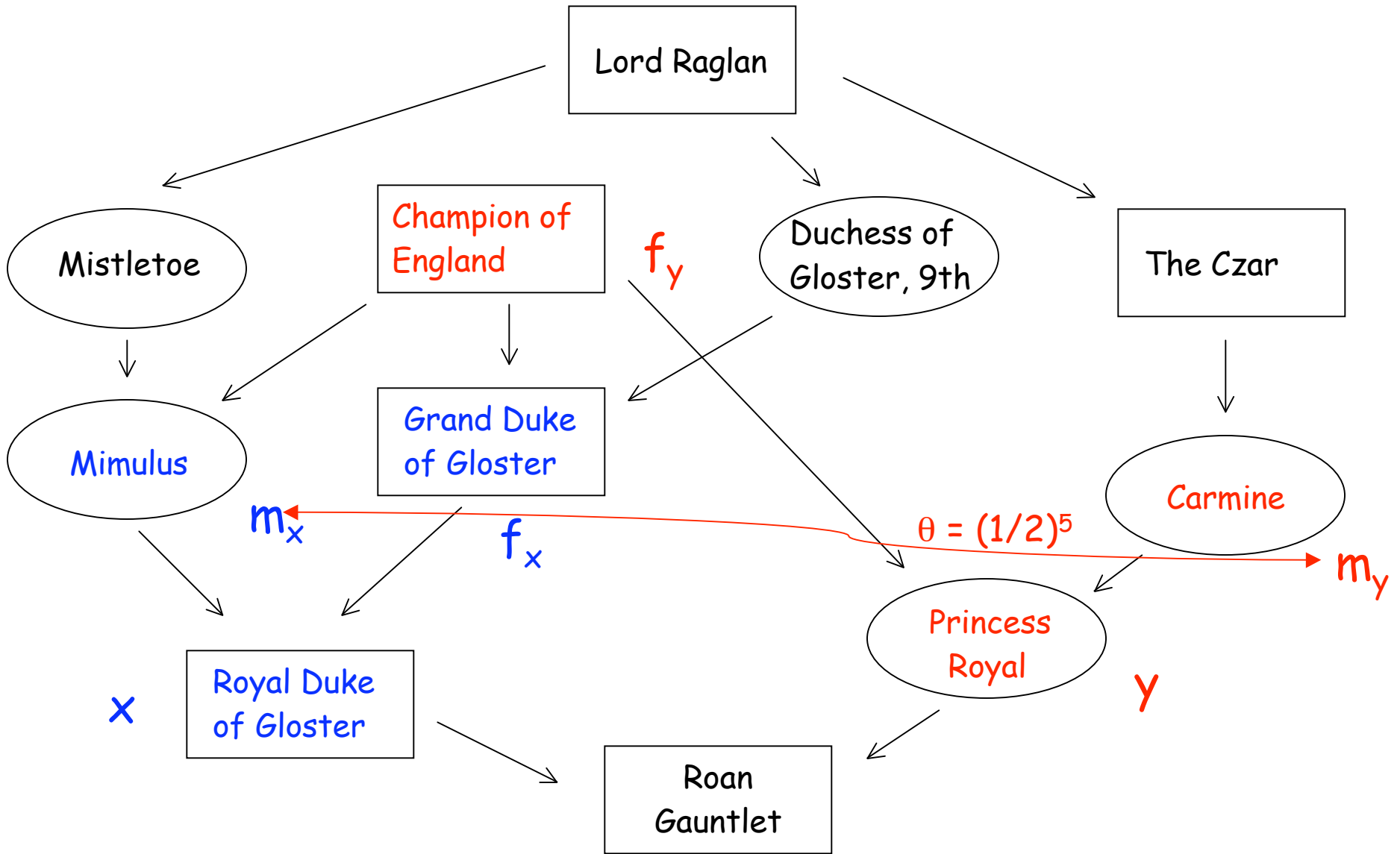
What is Δ for Royal Duke of Gloster and Princess Royal

$$\Delta_{xy} = \theta_{m_x m_y} \theta_{f_x f_y} + \theta_{m_x f_y} \theta_{f_x m_y}$$



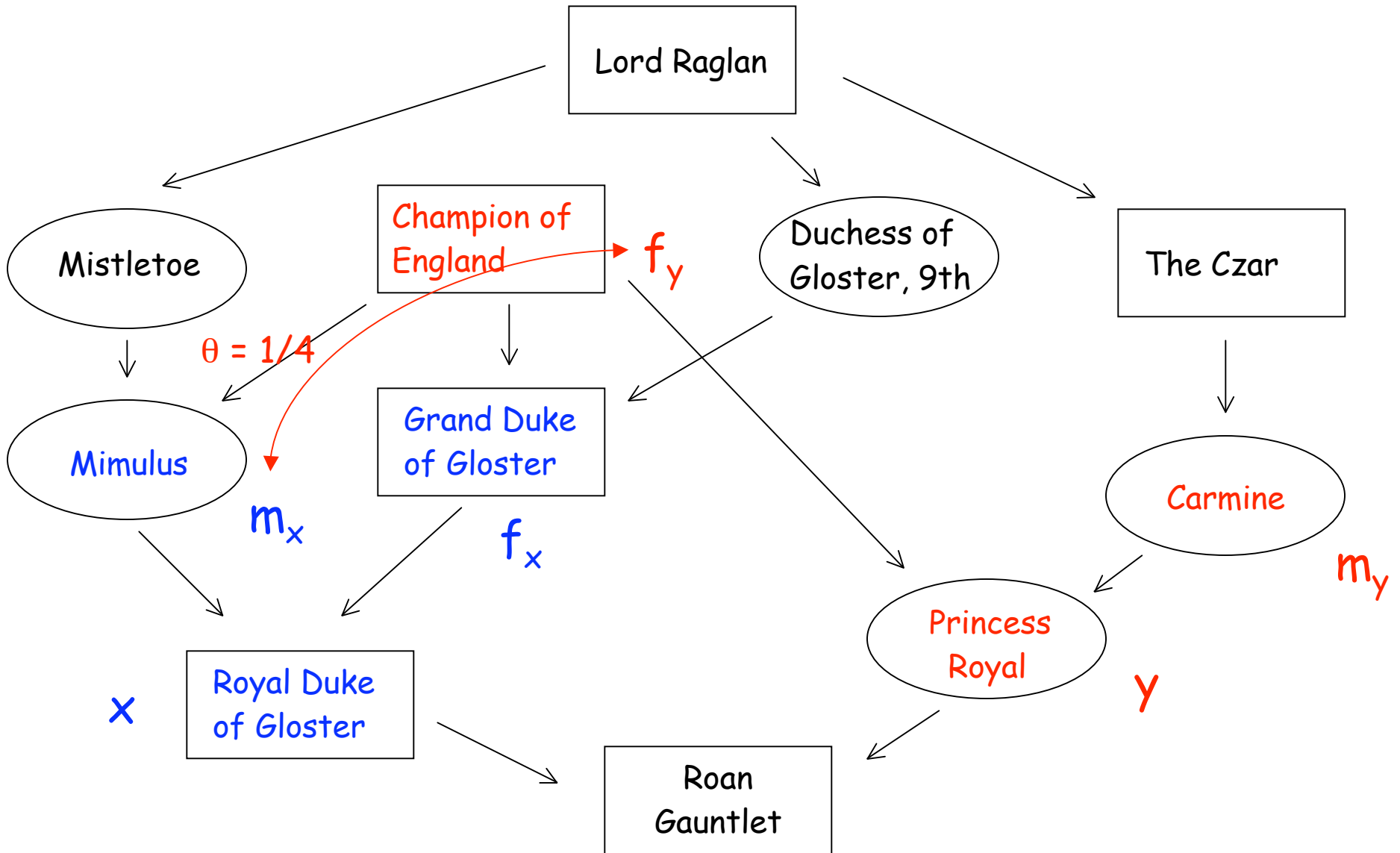
What is Δ for Royal Duke of Gloster and Princess Royal

$$\Delta_{xy} = \theta_{m_x m_y} (1/4) + \theta_{m_x f_y} \theta_{f_x m_y}$$



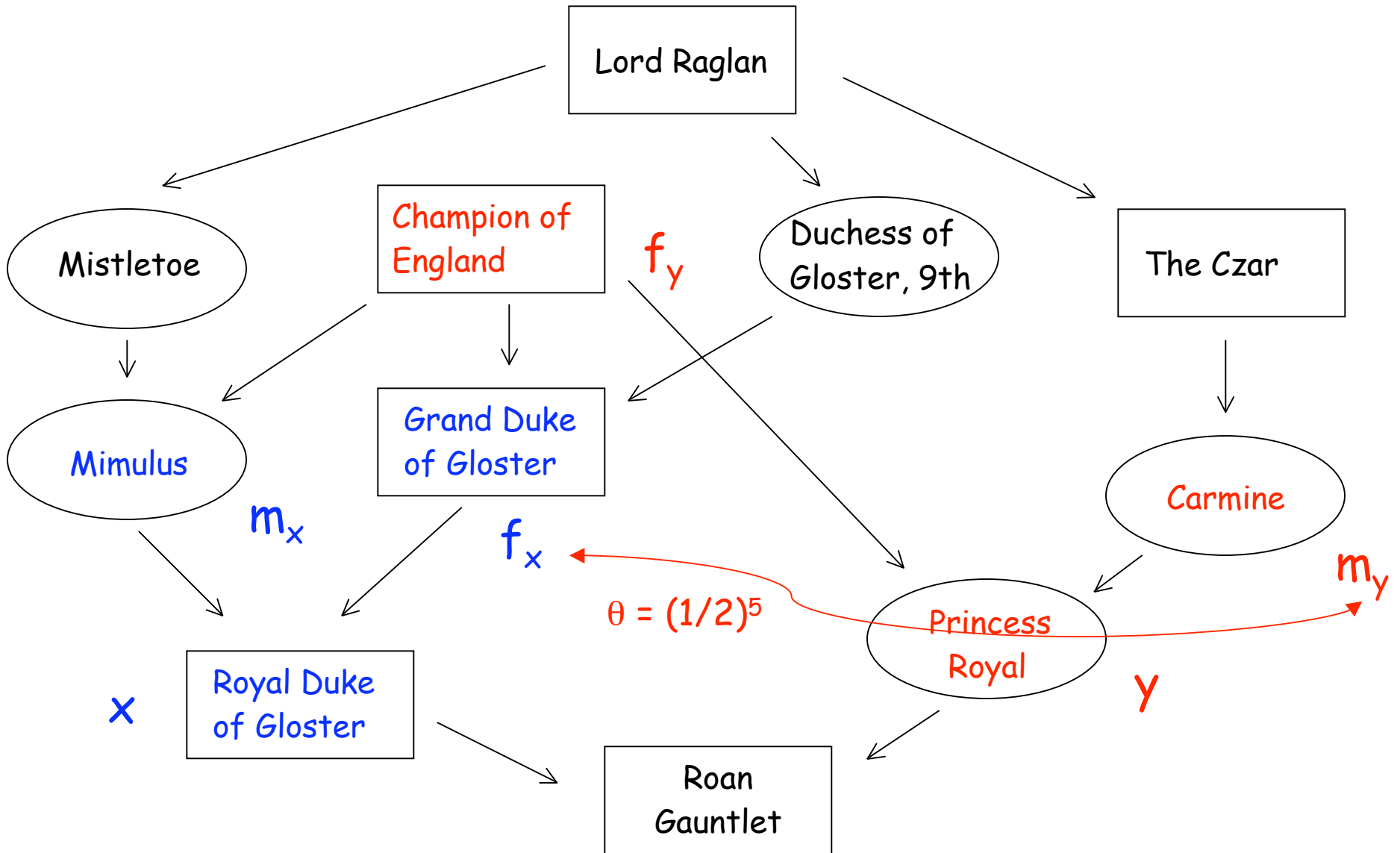
What is Δ for Royal Duke of Gloster and Princess Royal

$$\Delta_{xy} = (1/2)^5(1/4) + \theta_{m_x f_y} \theta_{f_x m_y}$$



What is Δ for Royal Duke of Gloster and Princess Royal

$$\Delta_{xy} = (1/2)^5(1/4) + (1/4)\theta_{f_x m_y}$$



What is Δ for Royal Duke of Gloster and Princess Royal

$$\Delta_{xy} = (1/2)^5(1/4) + (1/4) (1/2)^5 = (1/2)^6$$

Δ_{xy} and the coefficient on V_D

- The coefficient on the dominance variance for the relatives x and y is just Δ_{xy} .
- To see this,
 - let $A_i A_j$ denote the two alleles in x and $A_k A_l$ those in y .
 - Suppose that alleles i and k come from the mothers of these two relatives and alleles j and l from their fathers.
 - $\text{Cov}(\text{dominance values}) = \Pr(A_i \text{ ibd } A_k, A_j \text{ ibd } A_l) \text{cov}(\delta_{ij}, \delta_{kl}) + \Pr(A_i \text{ ibd } A_l, A_j \text{ ibd } A_k) \text{cov}(\delta_{ij}, \delta_{kl})$
 - $= (\theta_{fxfy} \theta_{mxmy} + \theta_{mxfy} \theta_{jxmy}) \text{Var}(D) = \Delta_{xy} \text{Var}(D)$

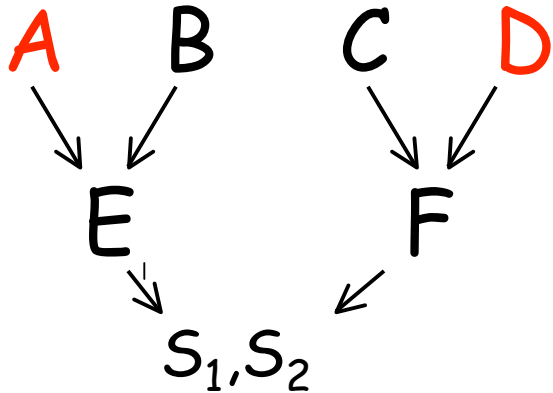
General Resemblance between relatives

$$2\theta_{xy} = r_{xy}, \quad u_{xy} = \Delta_{xy}$$

$$\text{Cov}(G_x, G_y) = 2\theta_{xy}V_A + \Delta_{xy}V_D$$

$$\begin{aligned} \text{Cov}(G_x, G_y) = & 2\theta_{xy}V_A + \Delta_{xy}V_D \\ & + (2\theta_{xy})^2V_{AA} + 2\theta_{xy}\Delta_{xy}V_{AD} + \Delta_{xy}^2V_{DD} + \dots \end{aligned}$$

Example



We found for full sibs S_1, S_2 that $\theta = 5/16$, hence $2\theta = 5/8$; $\Delta = 17/64$

Expected genetic covariance between this sibs is

$$(5/8)\text{Var}(A) + (17/64)\text{Var}(D) + (5/8)^2\text{Var}(AA) + (5/8)(17/64)\text{Var}(AD) + (17/64)^2\text{Var}(DD) + \dots$$

Covariance among selfed lines

- A common situation in plant breeding is that two inbred lines are crossed
 - the frequency of any segregating allele in the F_1/F_2 is $1/2$
 - Starting with the F_1 , a series of lines is formed by selfing, $S_k = F_{2+k}$.
 - The covariance among the various S_k lines is important in the response to selection in selfed lines
 - In particular, we want to covariance between an S_j and an S_k line whose last common ancestor was the S_i , with $i \leq j < k$

$$\text{Cov}(S_j, S_k | S_i) = (1 + f_{S_i}) \left(V_A + \frac{(1 - f_{S_j})(1 - f_{S_k})}{1 - f_{S_i}} V_D \right)$$

Autotetraploids

- Peanut, Potato, alfalfa, soybeans all examples of crops with at least some autotetraploid lines
- With autotetraploid, four alleles per locus, with a parent passing along two alleles to an offspring
- As a result, a parent can pass along the dominance contribution in G to an offspring
- Further, now there are four variance components associated with each locus

Genetic variances for autotetraploids

- $G = A + D + T + Q$
 - A (additive) and D (dominance, or **digenic effects**) as with diploids
 - T (**trigenic effects**) are the three-way interactions among alleles at a locus
 - Q (**quadrigenic effects**) are the four-way interactions at a locus
- Total genetic variance becomes
 - $V_G = V_A + V_D + V_T + V_Q$

Resemblance between autotetraploid relatives

Relatives	V_A	V_D	V_T	V_Q
Half-sibs	1/4	1/36		
Full-sibs	1/2	2/9	1/12	1/36
Parent-offspring	1/2	1/6		

Assumes unrelated, non-inbred parents