

Lecture 1: Introductions

Statistical methods in genetic relatedness and pedigree analysis

NORBIS course, 13th – 17th of June 2022, Oslo

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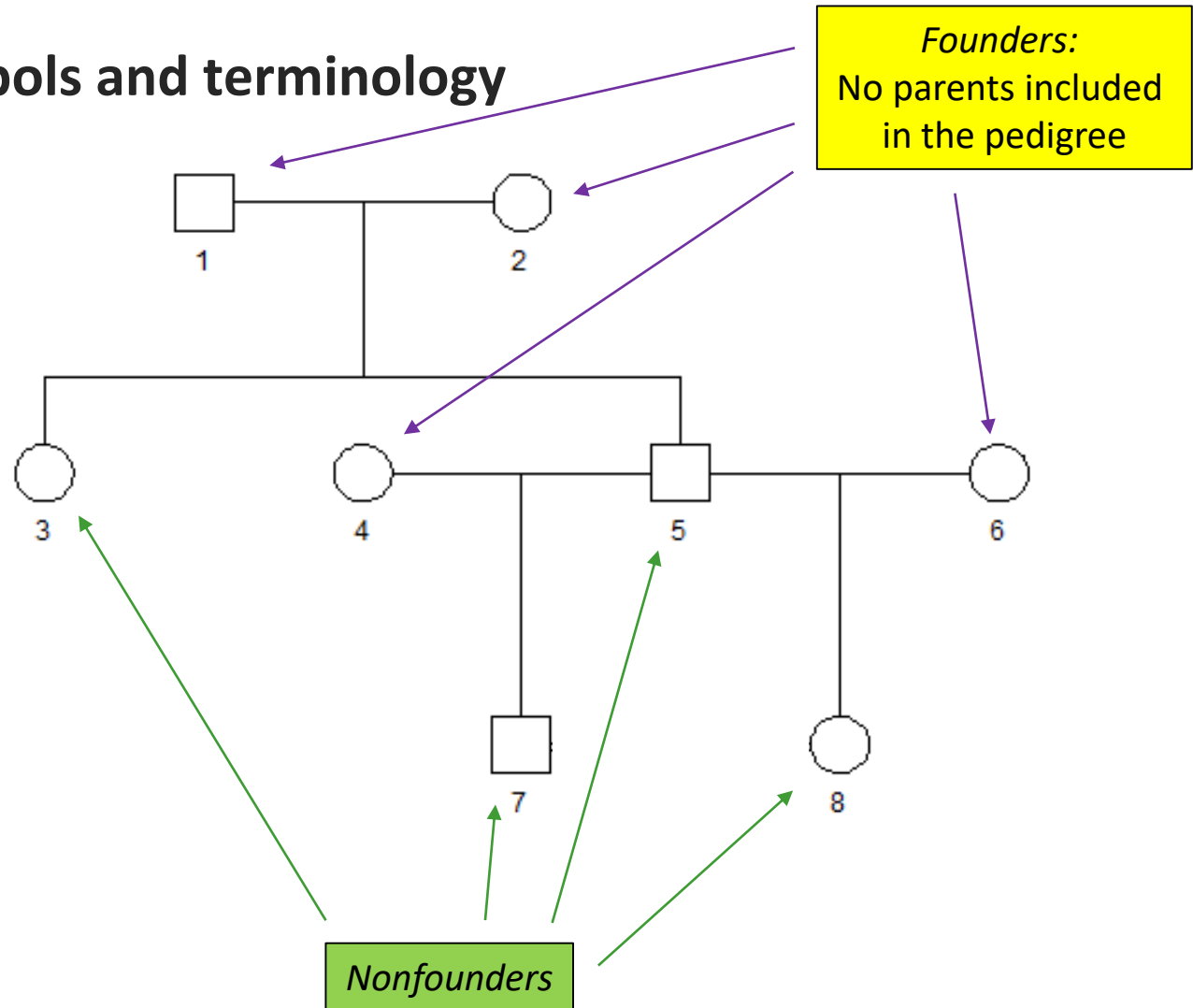
Outline

- Part I: *Pedigrees*
 - Pedigree symbols and terminology
 - Some common relationships
 - QuickPed
- Part II: *Genetics*
 - Terminology (Locus, allele, genotype, ...)
 - Mendelian inheritance
- Part III: *Probabilities (on pedigrees)*
 - Motivation: Real-life problems
 - Ingredients:
 - Hardy-Weinberg equilibrium
 - Mendelian transition probabilities
 - Computing pedigree likelihoods

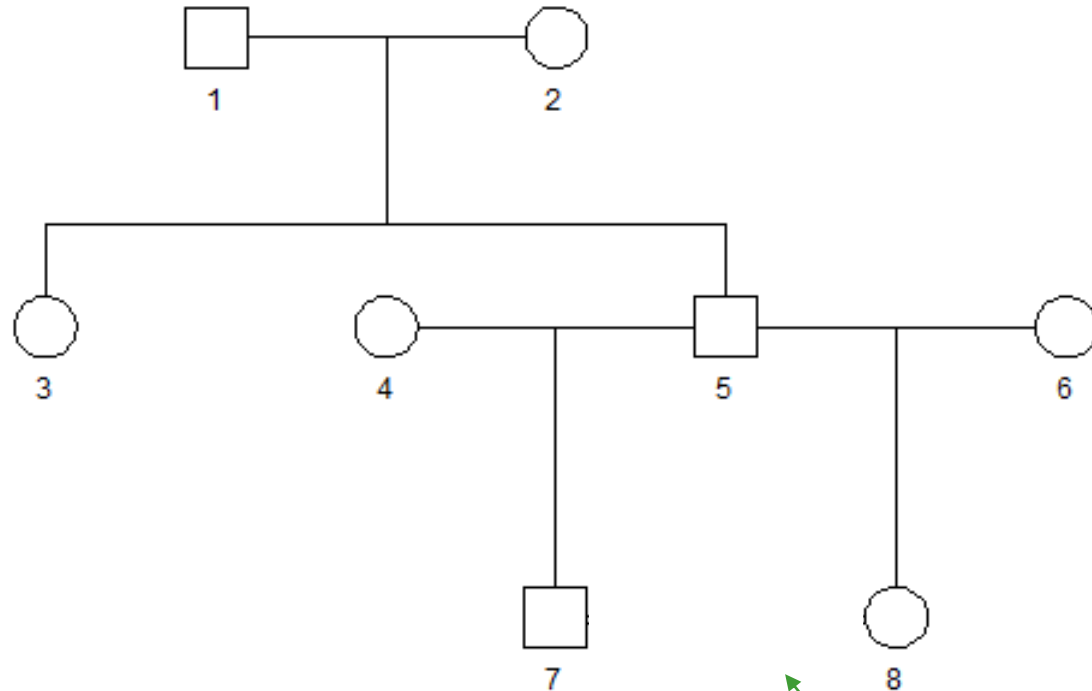
Part I: Pedigrees

Pedigrees: Symbols and terminology

□ = male
○ = female



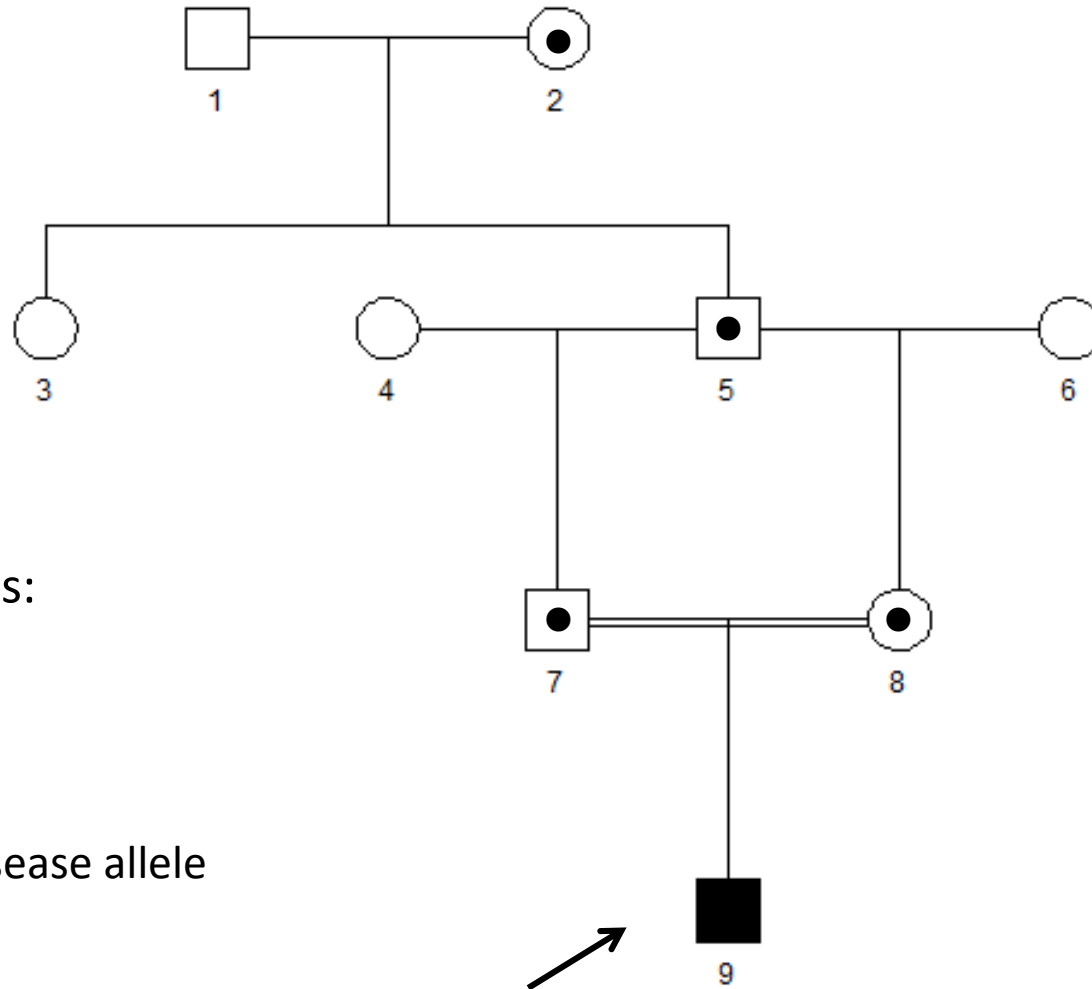
Pedigrees: Symbols and terminology



□ = male
○ = female

*Consanguineous
marriage*

Pedigrees: Symbols and terminology



Medical pedigrees:



= affected

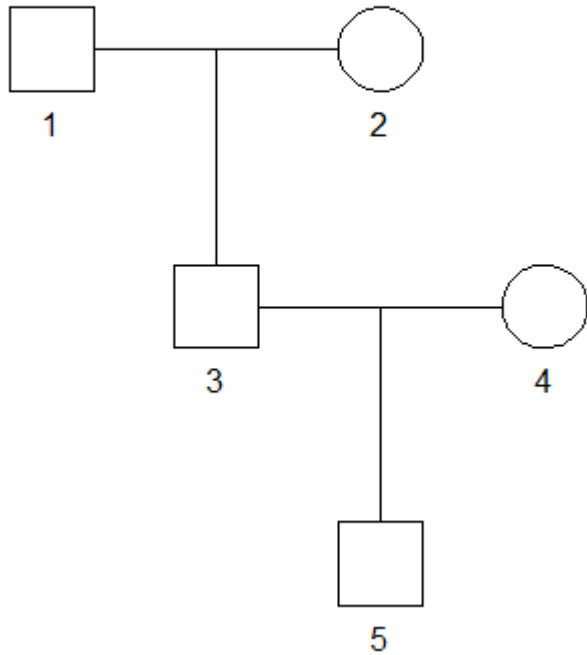


= unaffected

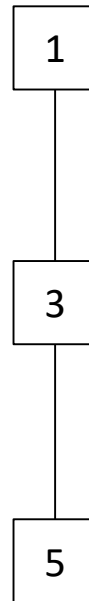


= carrier of disease allele

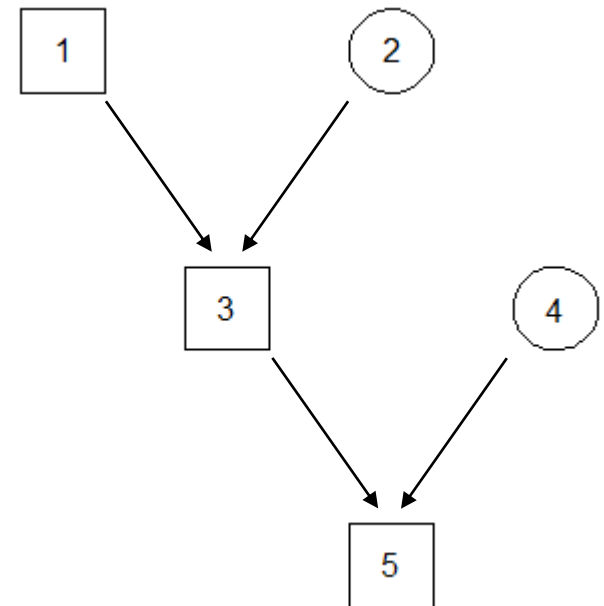
Alternative ways of drawing pedigrees



Standard



Simplified

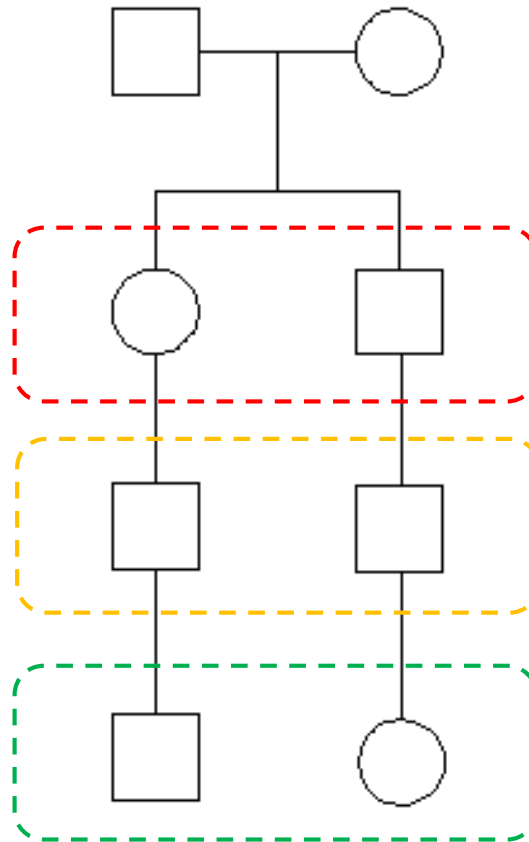


Directed acyclic graph

Some common relationships

(and some less common...)

Cousin relationships

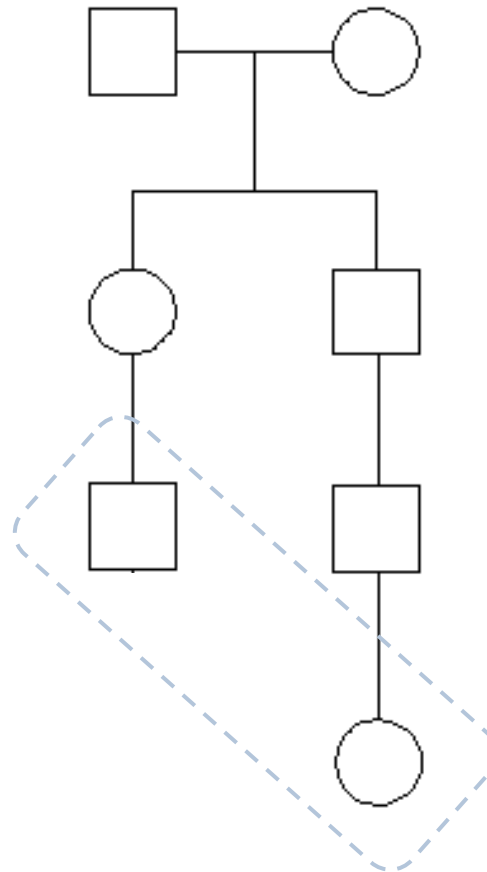


Full siblings

First cousins

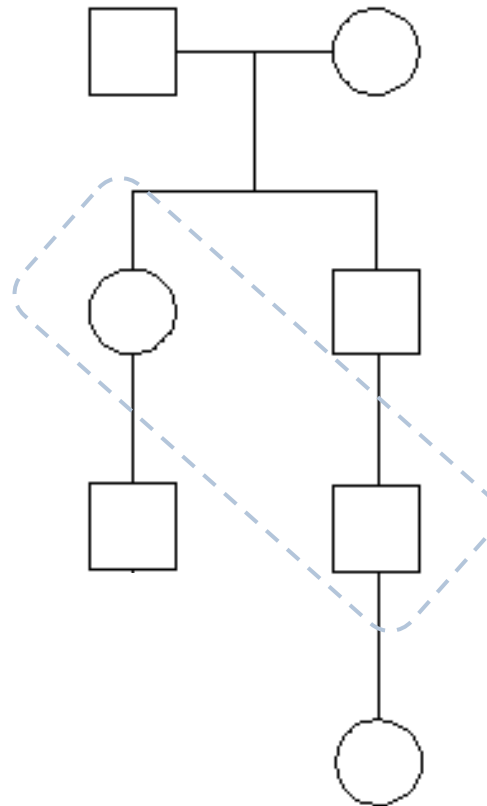
Second cousins

Cousin relationships



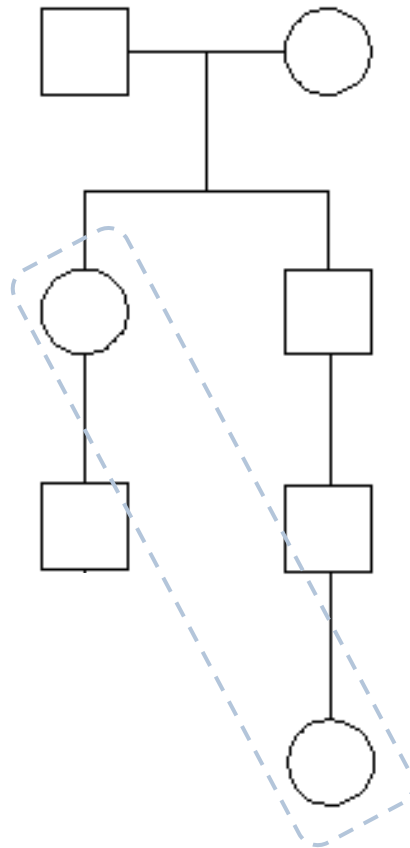
First cousins
once removed

Cousin relationships



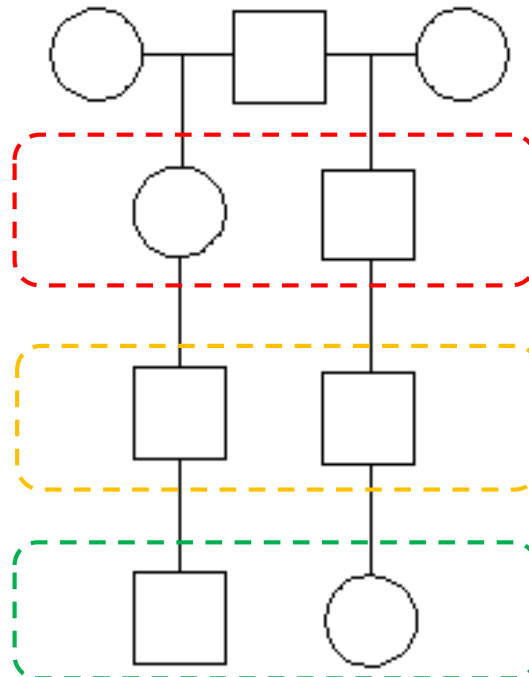
Aunt - nephew

Cousin relationships



Grandaunt

Half cousin relationships

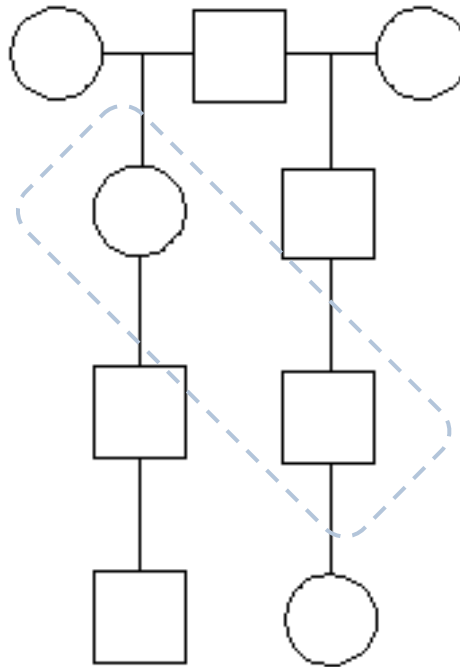


Half siblings (paternal)

Half first cousins

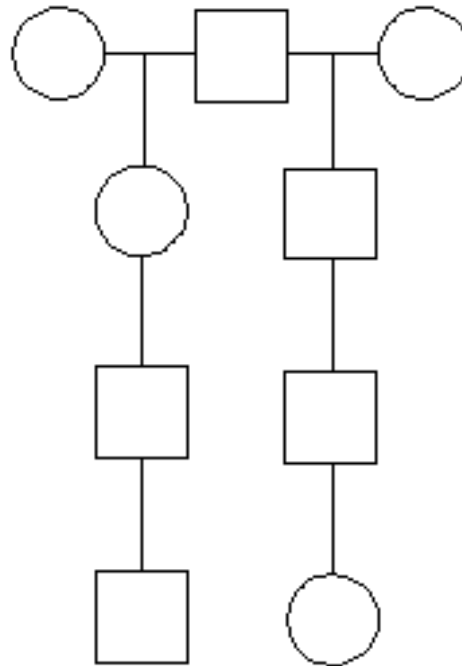
Half second cousins

Half cousin relationships

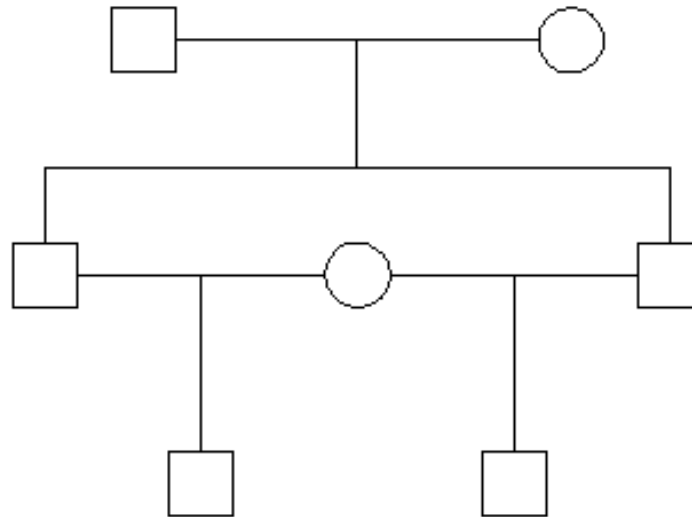


Half aunt /
half nephew

Half cousin relationships

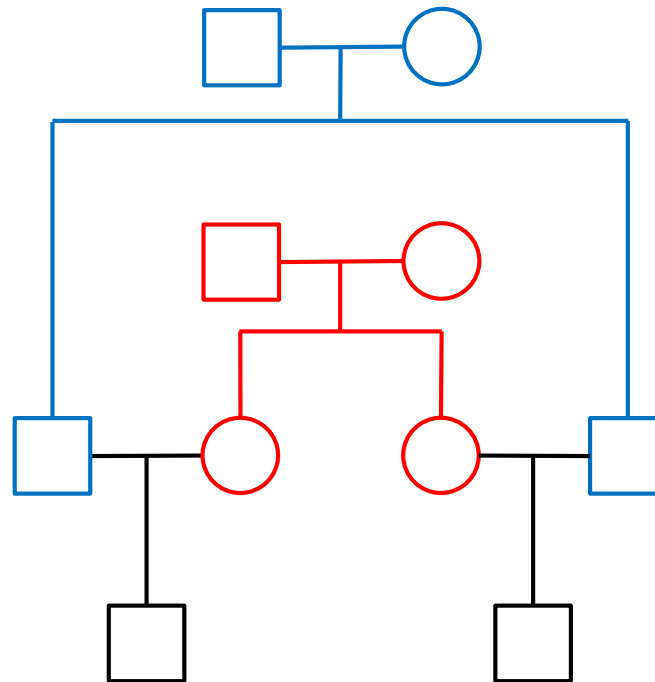


More complicated relationships



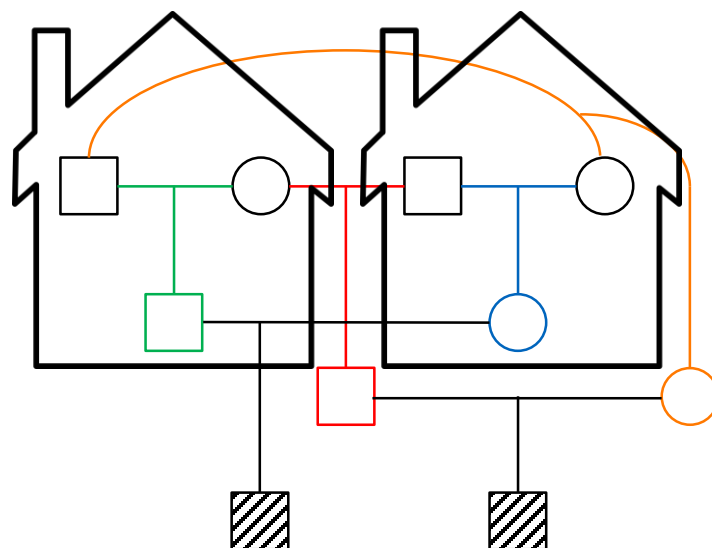
3/4 siblings

What about this?



Double first cousins

The connoisseur's favourite



Quadruple half first cousins!

What software
exists to create
pedigrees?



It depends!

- medical genetics
- forensic genetics
- animal pedigrees
- amateur genealogy

In this course:

- R
- QuickPed



QuickPed: An Interactive Pedigree Creator

<https://magnusdv.shinyapps.io/quickped/>

Purpose: This tool provides a quick way to create pedigree plots and files, and for analysing the relatedness between pedigree members.

Instructions: Choose a suitable start pedigree and modify it by selecting members (by clicking on them in the plot) and using appropriate buttons. For example, to create a new child, select the parents and press *Son* or *Daughter*. (If just one parent is selected, a new spouse is also created.)

More information: Check out the [user manual](#) for various tips and tricks, including an introduction to relatedness coefficients. There is also a [paper](#) about QuickPed published in BMC Bioinformatics.

Quick start

Built-in pedigree

Trio ▼

or

Load a ped file



Reset all

Modify

Add

Son

Daughter

Sibling

Parents

Remove

Individuals

Selection

Switch

Sex

Affected

Carrier

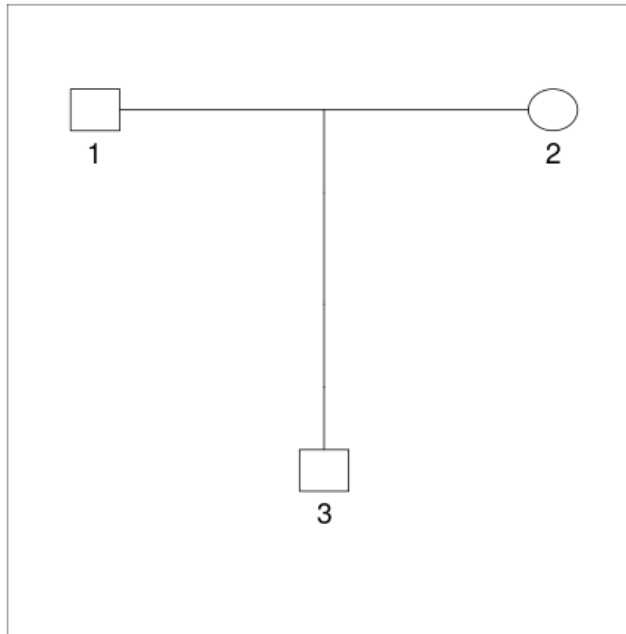
Deceased

Twins

MZ

DZ

Undo



Labels

1, 2, 3, ..

I-1, I-2, ..

☒ Show all ☐ Hide all

1

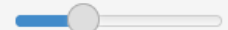
2

3

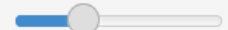
Update

Plot settings

Width



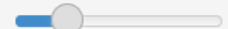
Height



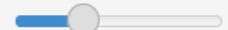
Expansion



Symbol size



Margins



↓ PNG

↓ PDF

Relationships



Ped file

Include

☒ Headers

☐ Family ID

☐ Affection status

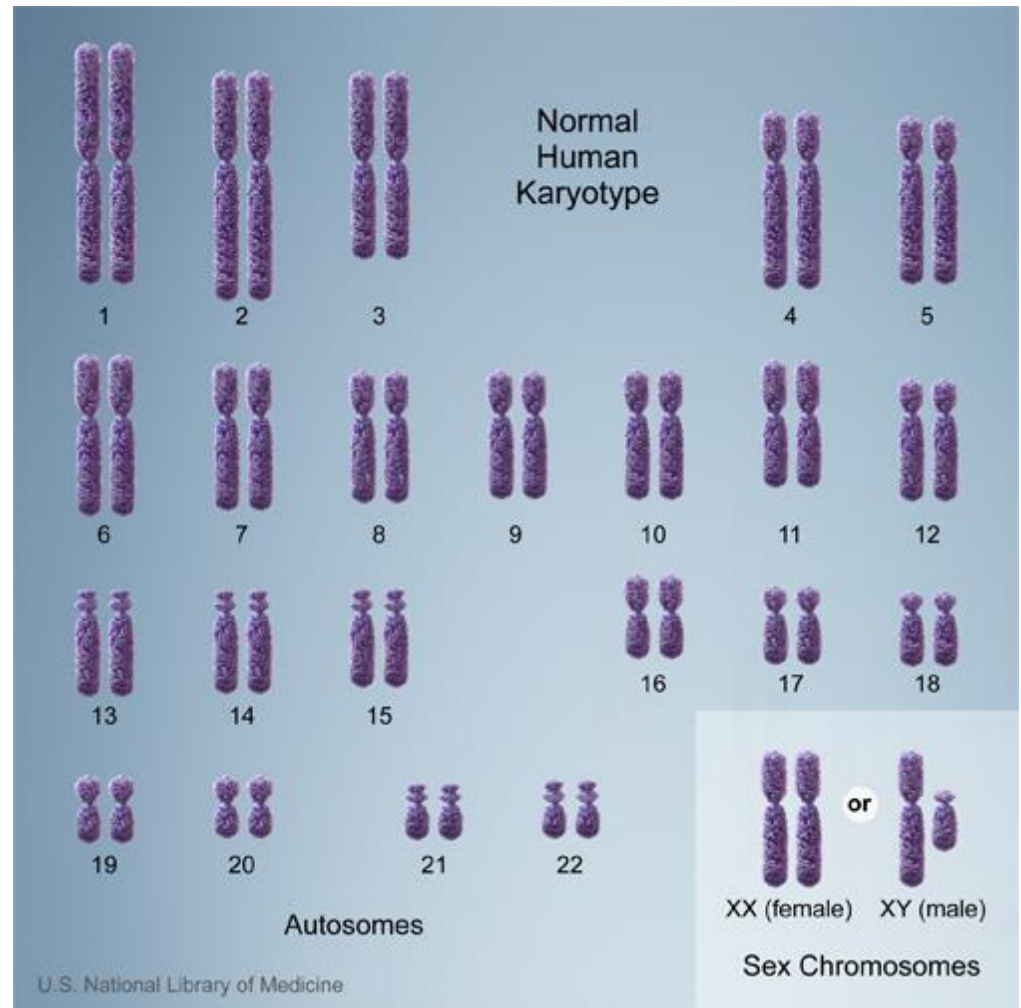
↓ Save ped file

Part II: Genetics

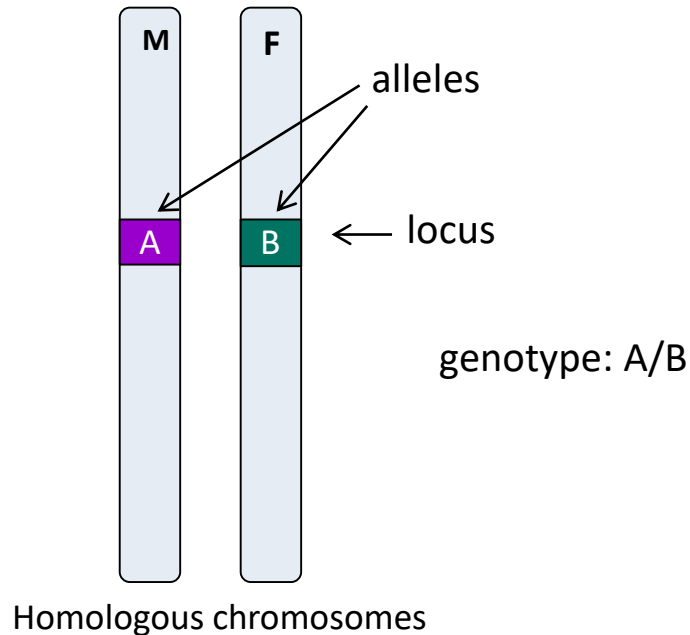
Human Genetics

Some important terms

- Locus
- Allele
- Genotype
- Genetic markers
 - SNPs
 - microsatellites



Locus, allele, genotype



- **LOCUS** = a specific place in the genome
- **ALLELE** = any of the alternative forms of a locus
- **GENOTYPE** = the set (usually: pair) of alleles carried at a given locus

Genetic markers

- Small parts of the genome which ...
 - have known position
 - vary in the population
 - are easy to genotype
- SNPs (single nucleotide polymorphisms)
 - two alleles
 - usual requirement: MAF > 1%
= minor allele frequency
 - very common in the genome (millions!)
 - used in medical genetics +++
- STRs (short tandem repeats) = microsatellites
 - consecutive repeats of 2-5 bases
 - multiallelic: 5 - 70 alleles
 - allele names: # repeats
 - used in forensics

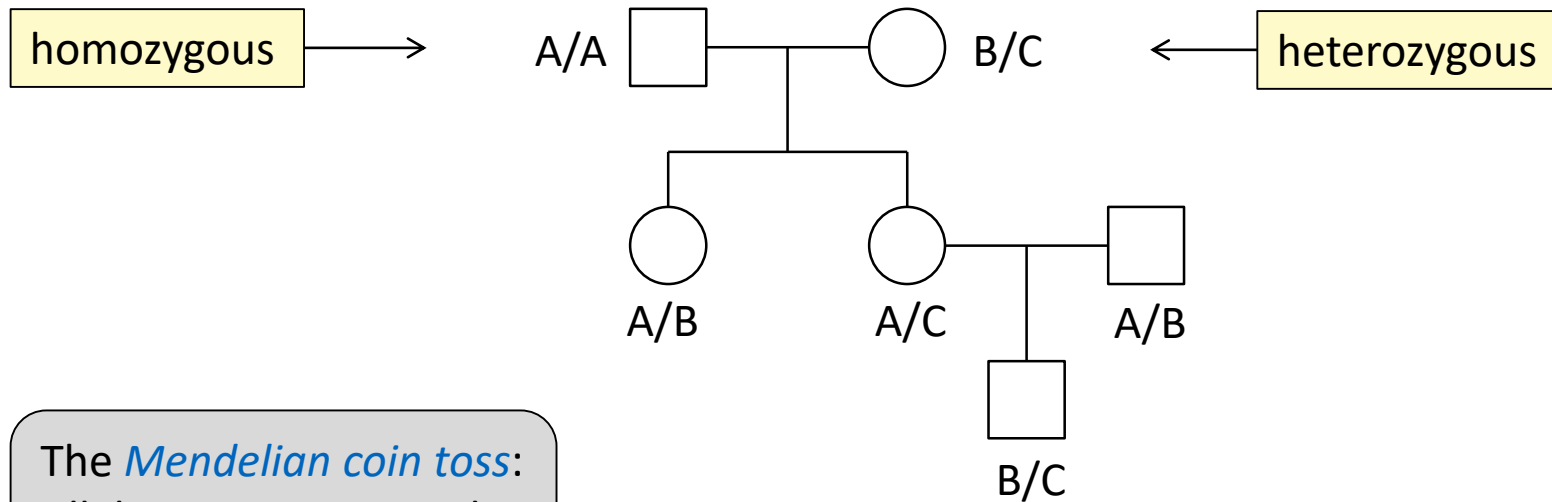


```
...CCGTTATATGGGC...  
...CCGTTAGATGGGC...  
...CCGTTATATGGGC...  
...CCGTTATATGGGC...  
...CCGTTAGATGGGC...
```

```
...ACG TTAG TTAG TTAG TTAG AAC..  
...ACG TTAG TTAG AAC..  
...ACG TTAG TTAG TTAG TTAG TTAG AAC..
```


Mendelian inheritance: Autosomal (chromosomes 1-22)

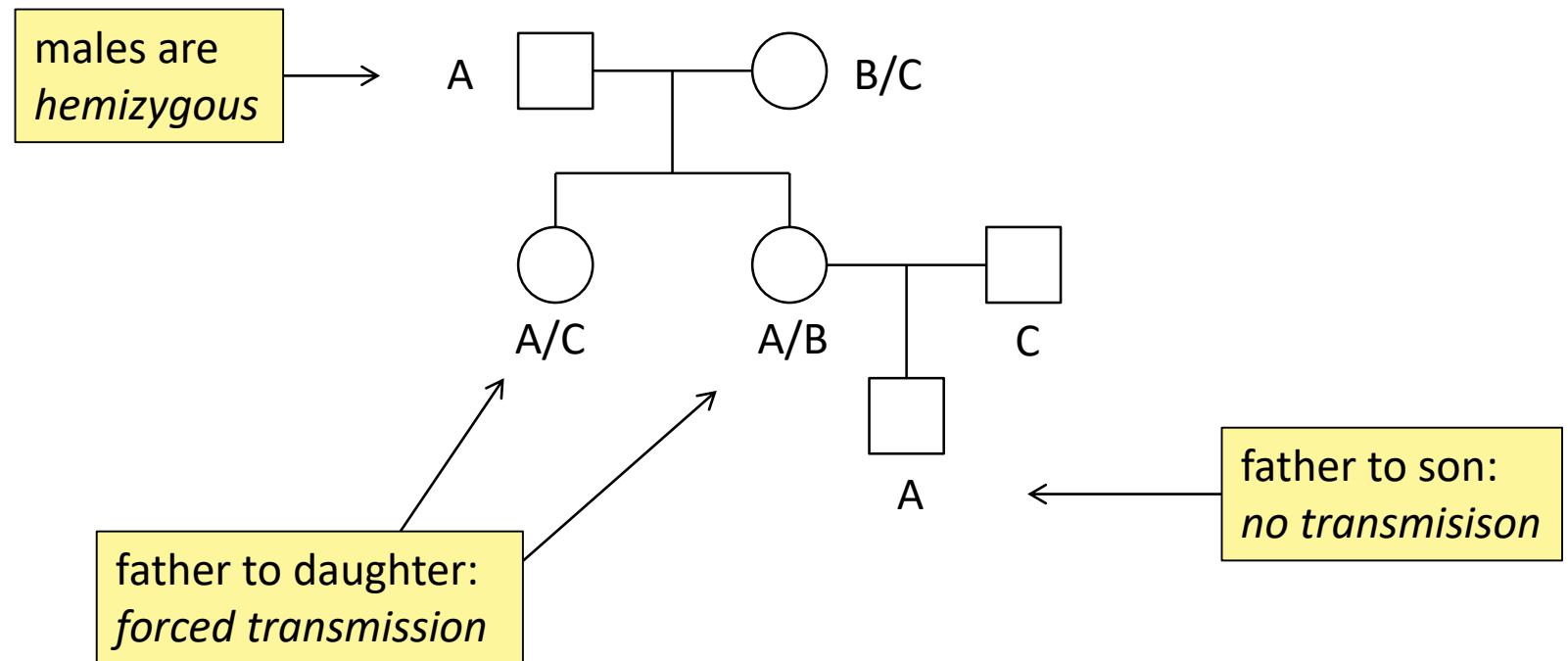
Example: autosomal marker with 3 alleles: A, B, C



The *Mendelian coin toss*:
Alleles are transmitted
with **50% chance**.

Mendelian inheritance: X-linked

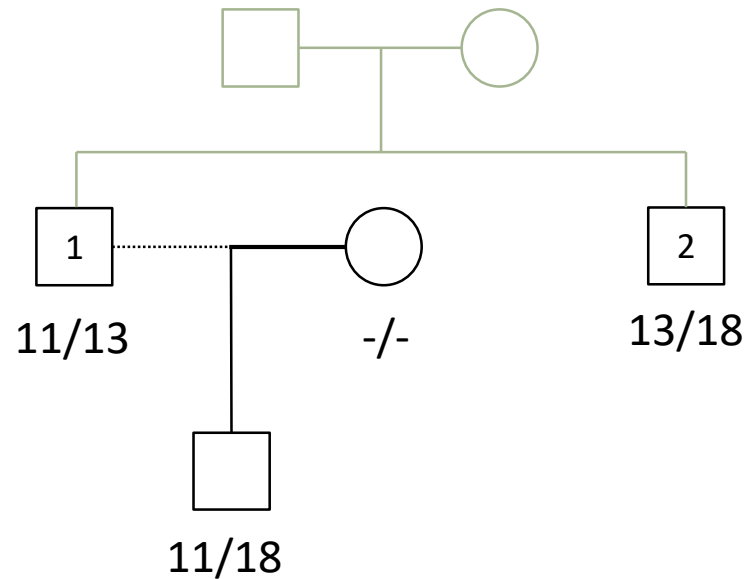
Example: X-linked marker with 3 alleles: A, B, C



Part III: Probabilities on pedigrees

Questions related to pedigrees with genotypes

Questions related to pedigrees with genotypes

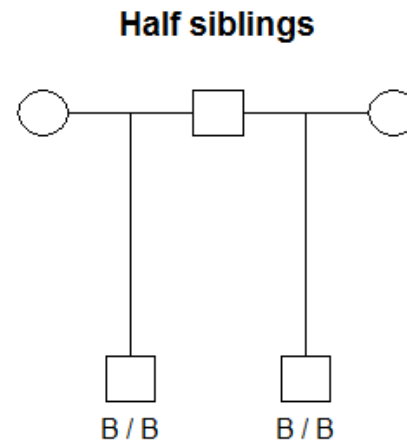
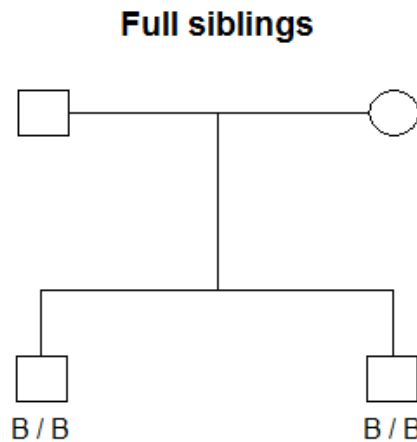


Suppose:

- 11 is common
- 18 is rare

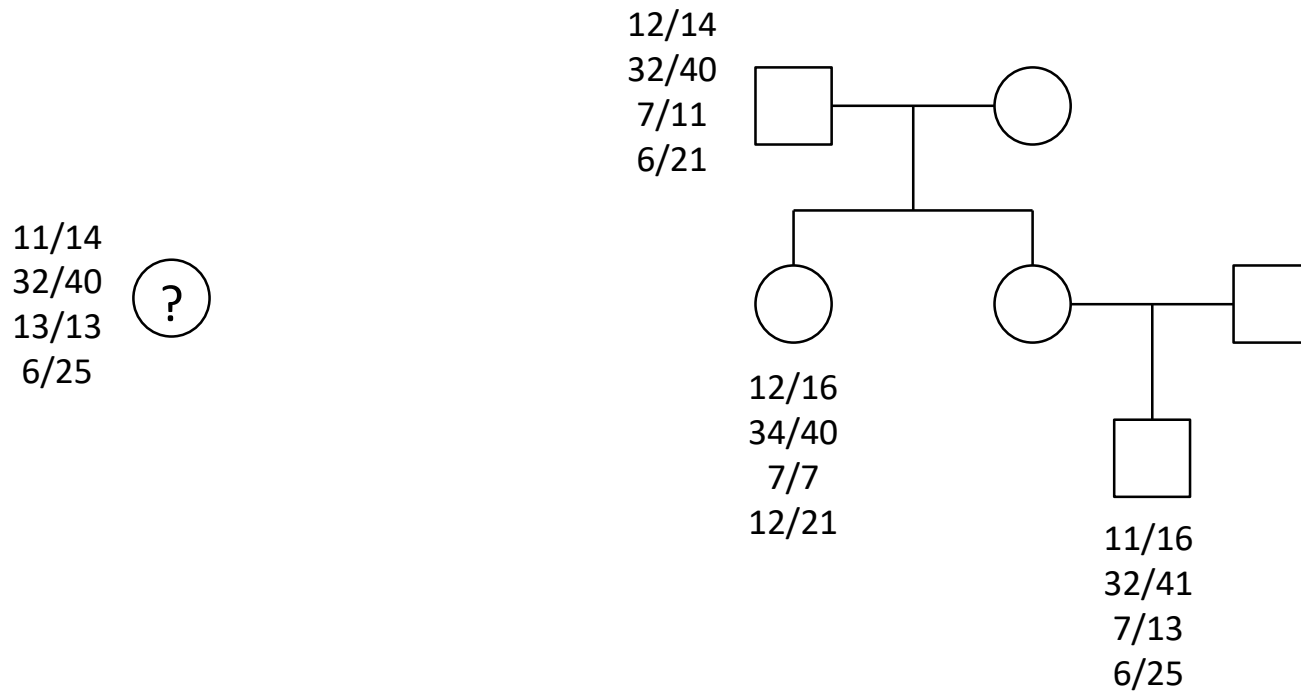
Who is the true father?

Questions related to pedigrees with genotypes



Brothers or half brothers?

Questions related to pedigrees with genotypes



Is this woman related to the family?

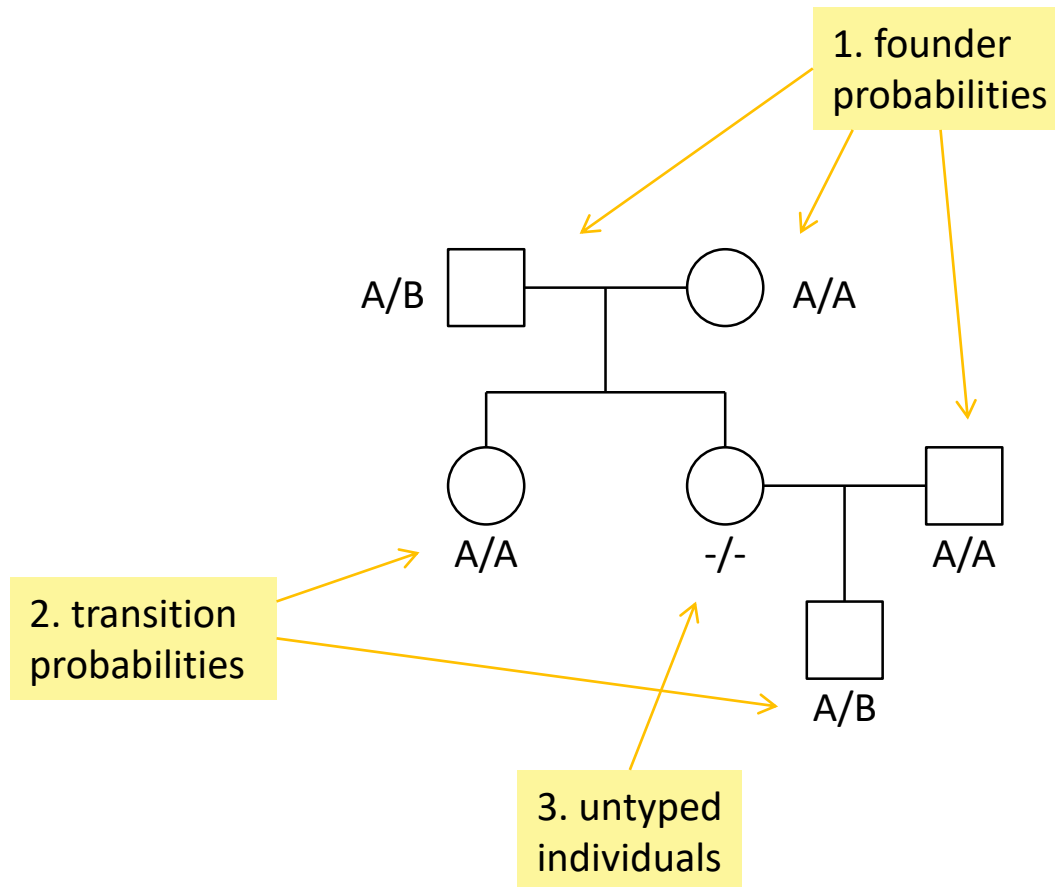
- Many applications involve probabilities of the following form

$$P(\text{genotypes} \mid \text{pedigree}, \underbrace{\text{inheritance model, allele freqs, ...}}_{\Theta})$$

- Often referred to as a *pedigree likelihood*:

$$L(\text{pedigree} \mid \text{data}) = P(\text{data} \mid \text{pedigree}, \Theta)$$

Ingredients for likelihood computations



Ingredient 1: Founder probabilities

- Suppose the allele frequencies are:

$$P(A) = p$$

$$P(B) = q$$



- What are the frequencies of the genotypes AA , AB , BB ?
- Under certain assumptions, the alleles can be treated as **independent**:

$$P(AA) = P(A) * P(A) = p^2$$

$$P(BB) = P(B) * P(B) = q^2$$

$$P(AB) = P(AB \text{ or } BA) = pq + qp = 2pq$$



two possible orderings!

The Hardy-Weinberg principle

Assumptions:

- infinite population
- random mating
- no selection
- no mutations
- no migration

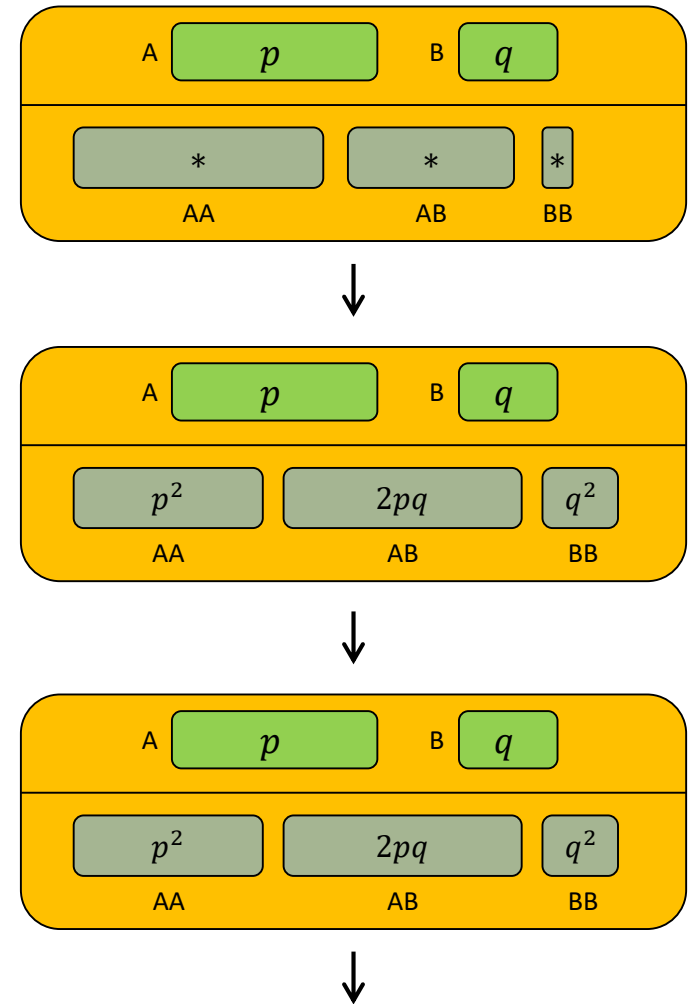
Hardy (1908): Shows

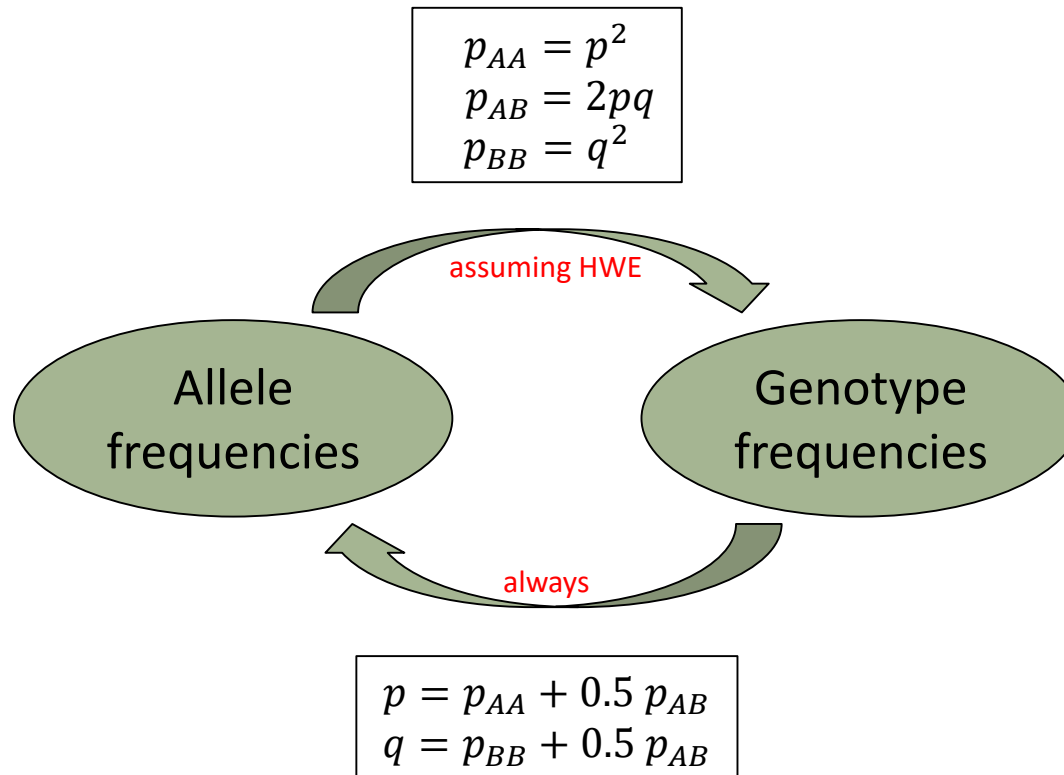
«... using a little mathematics of the multiplication table kind»:

- allele freqs are unchanged from generation to generation
- after 1 generation the genotype freqs stay unchanged

$$\begin{aligned}P(AA) &= p^2 \\P(AB) &= 2pq \\P(BB) &= q^2\end{aligned}$$

HW equilibrium

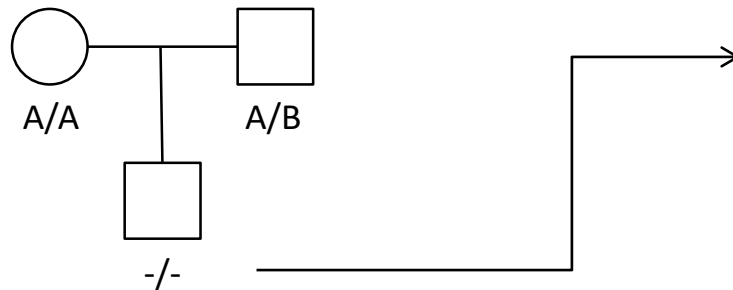




Ingredient 2: Transition probabilities

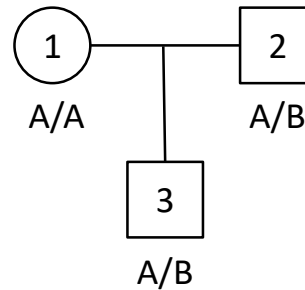
$$P(g_{child} | g_{parents})$$

- Easy - directly from Mendel's laws!



child parents	A/A	AB	BB
AA × AA	1	0	0
AA × AB	0.5	0.5	0
AA × BB	0	1	0
AB × AA	0.5	0.5	0
AB × AB	0.25	0.5	0.25
AB × BB	0	0.5	0.5
BB × AA	0	1	0
BB × AB	0	0.5	0.5
BB × BB	0	0	1

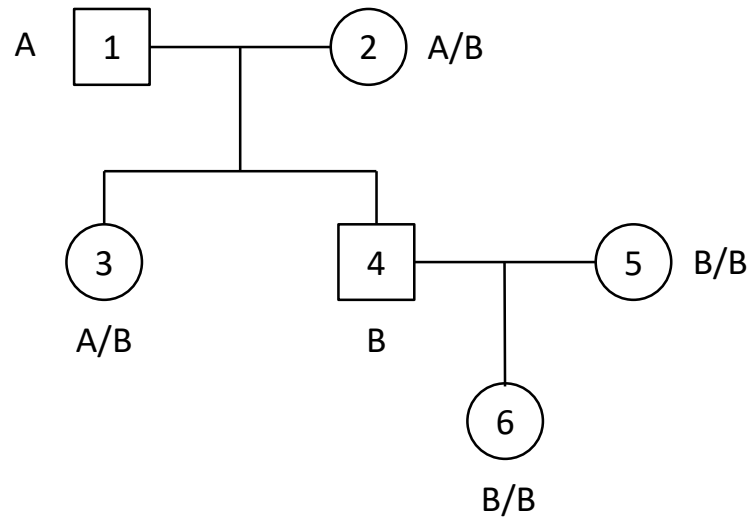
Example



$$\begin{aligned} L &= P(g_1, g_2, g_3) \\ &= P(g_1) \cdot P(g_2) \cdot P(g_3 \mid g_1, g_2) \\ &= P(AA) \cdot P(AB) \cdot P(AB \mid \text{parents} = AA \times AB) \\ &= p^2 \cdot 2pq \cdot 0.5 \\ &= p^3q \end{aligned}$$

assuming HWE!

Example on X



$$L = P(\text{genotypes} \mid \text{pedigree}, p, q)$$

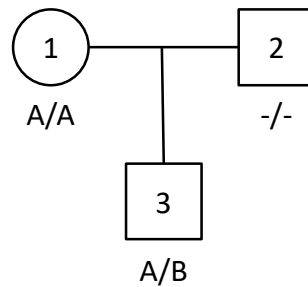
$$= \overset{1}{p} \cdot \overset{2}{2pq} \cdot \overset{3}{0.5} \cdot \overset{4}{0.5} \cdot \overset{5}{q^2} \cdot \overset{6}{1}$$

$$= 0.5 p^2 q^3$$

← contribution from each individual

Ingredient 3: How to deal with untyped individuals

Solution: Sum of all possible genotypes for the untyped



$$\begin{aligned} P(g_1, g_3) &= \sum_{g_2} P(g_1, g_2, g_3) = \sum_{g_2} P(g_1) \cdot P(g_2) \cdot P(g_3|g_1, g_2) \\ &= P(AA) \cdot P(\textcolor{red}{AA}) \cdot P(AB|AA \times \textcolor{red}{AA}) + P(AA) \cdot P(\textcolor{purple}{AB}) \cdot P(AB|AA \times \textcolor{purple}{AB}) + P(AA) \cdot P(\textcolor{green}{BB}) \cdot P(AB|AA \times \textcolor{green}{BB}) \\ &= p^2 \cdot p^2 \cdot 0 + p^2 \cdot 2pq \cdot 0.5 + p^2 \cdot q^2 \cdot 1 \\ &= p^3q + p^2q^2 = p^2q(p + q) = \underline{p^2q} \end{aligned}$$

Pedigree likelihood: General formula

- Given:
 - pedigree with n individuals
 - k members are genotyped: g_1, g_2, \dots, g_k

- Then:

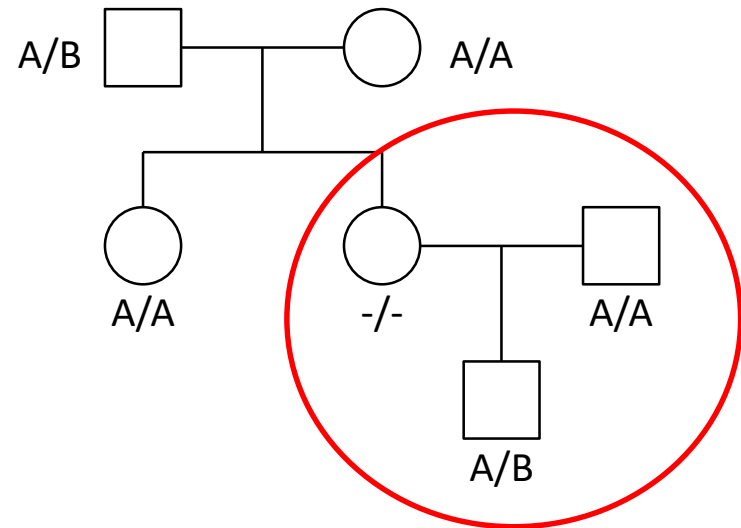
$$P(g_1, \dots, g_k) = \sum_{G_1} \sum_{G_2} \dots \sum_{G_n} \overbrace{P(g_1) \dots P(g_j)}^{\text{founders}} \cdot \overbrace{P(g_{j+1}|par) \dots P(g_n|par)}^{\text{non-founders}}$$

- If everyone is typed: Only one term \rightarrow easy
- Number of terms grows exponentially in $\#(\text{untyped})$
 - but clever algorithms exist!

G_i = set of possible
genotypes for individual i

Computer algorithms for pedigree likelihoods

- Elston-Stewart algorithm
 - a *peeling* algorithm
 - linear in pedigree size!
- Lander-Green
 - based on inheritance vectors
 - hidden Markov model
 - best choice with many *linked* markers
 - small/medium pedigrees only



Software for pedigree likelihoods

- R/ped suite
 - Elston-Stewart
 - mutations, theta correction, ++
- Familias
 - GUI for forensic applications
 - Elston-Stewart
 - handles mutations, theta correction, ++
- MERLIN
 - command line program
 - Lander-Green
 - gold standard for cases with dense SNP markers (but not too large pedigrees)
 - not mutations, not theta correction
- Other (old) software still in use
 - FastLink
 - Allegro
 - +++

Your turn: Exercises!

