

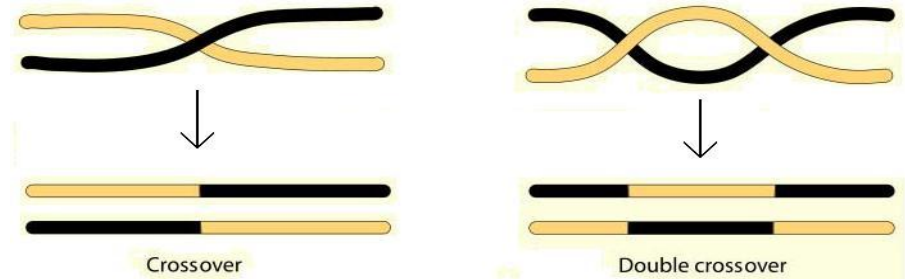
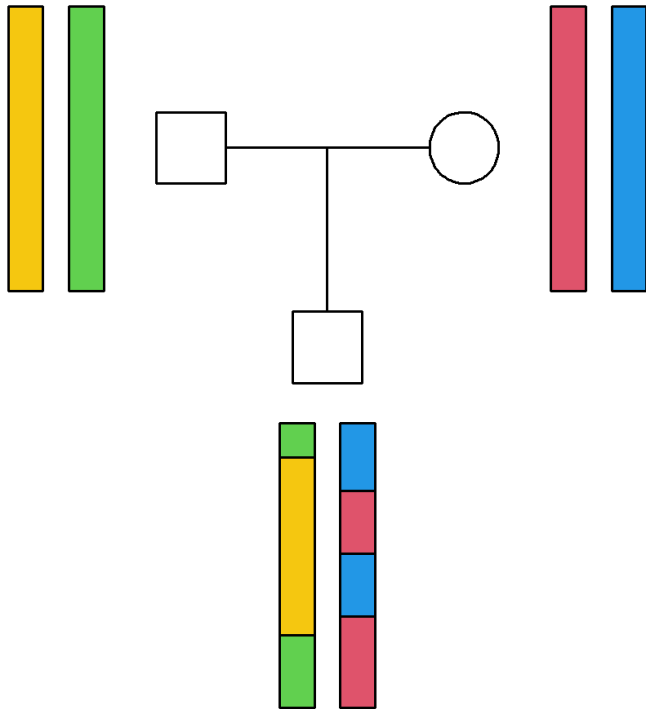
Lecture 5: IBD segments and realised relatedness or

Why are some siblings more alike than others?

Magnus Dehli Vigeland

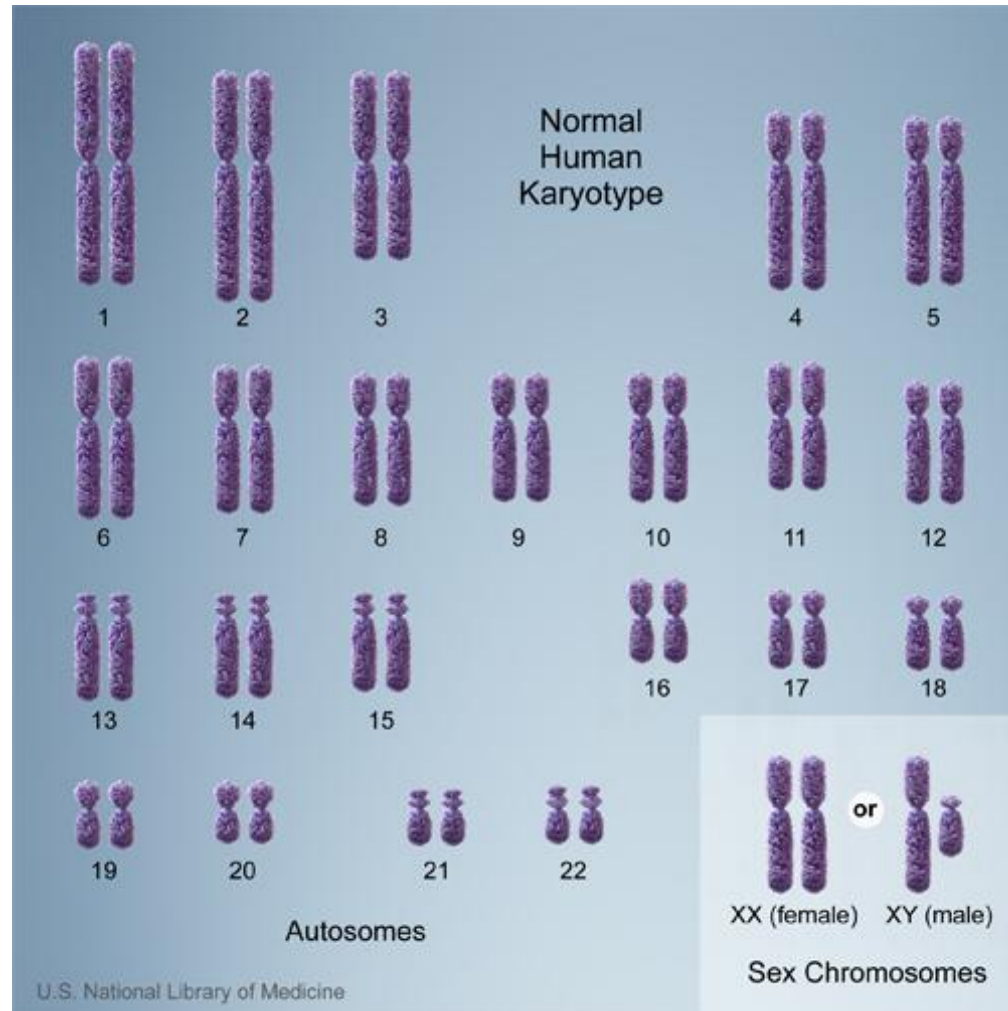
Workshop - Alcalá de Henares - 2026

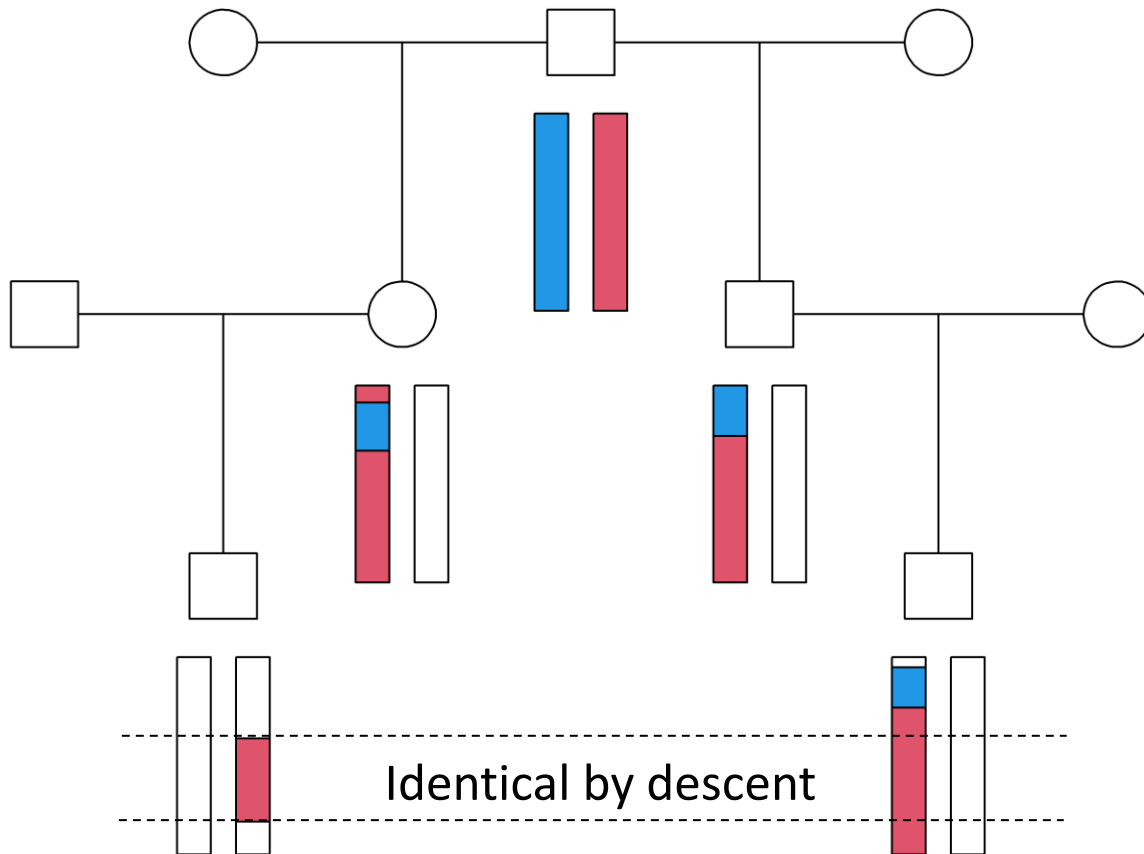
Meiotic recombination

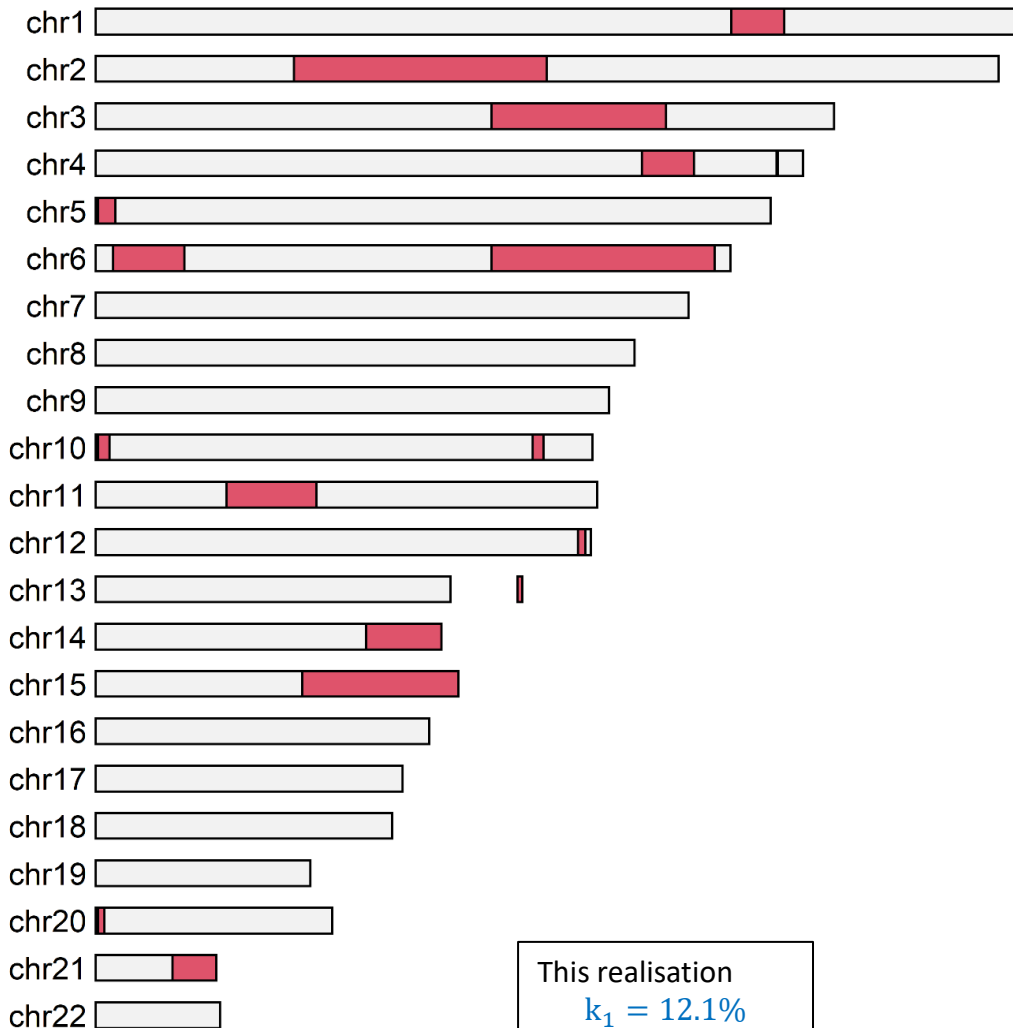


- **Genetic distance** between two loci:
= *average # crossovers per meiosis*
- Units:
 - 1 Morgan (M) = 1 crossover per meiosis
 - 1 centiMorgan (cM) = 0.01 M
- The human genome: Ca 30 Morgan

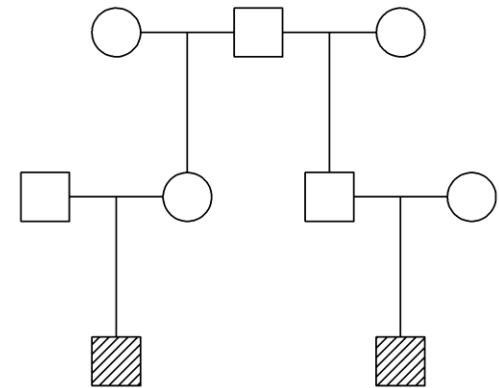
Rule of thumb: One crossover per chromosome arm





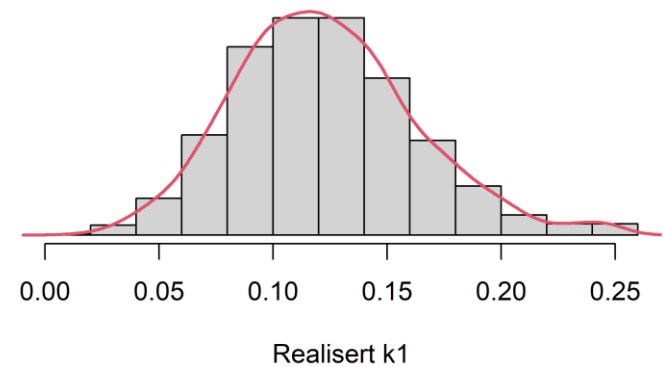


This realisation
 $k_1 = 12.1\%$

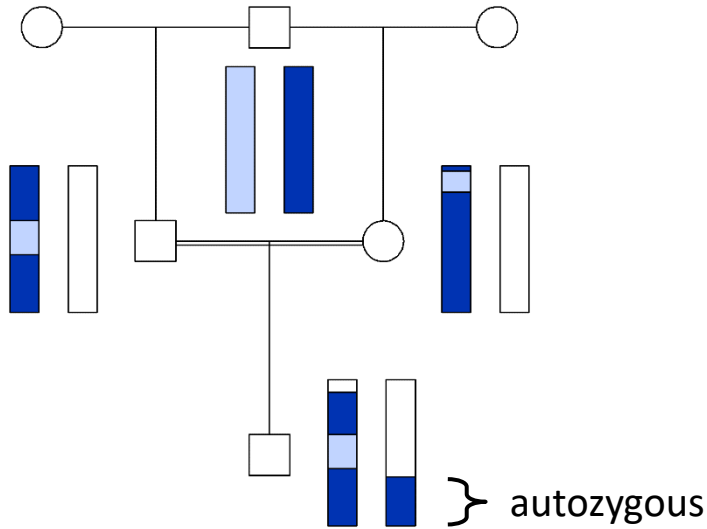


Half first cousins, expected sharing:

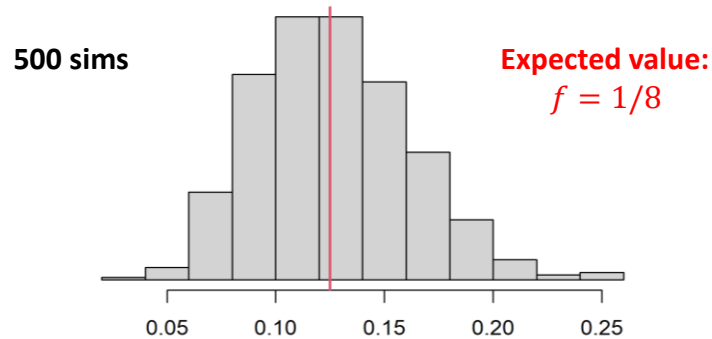
$$\kappa_1 = 2 \cdot \left(\frac{1}{2}\right)^4 = \frac{1}{8} = 12.5\%$$



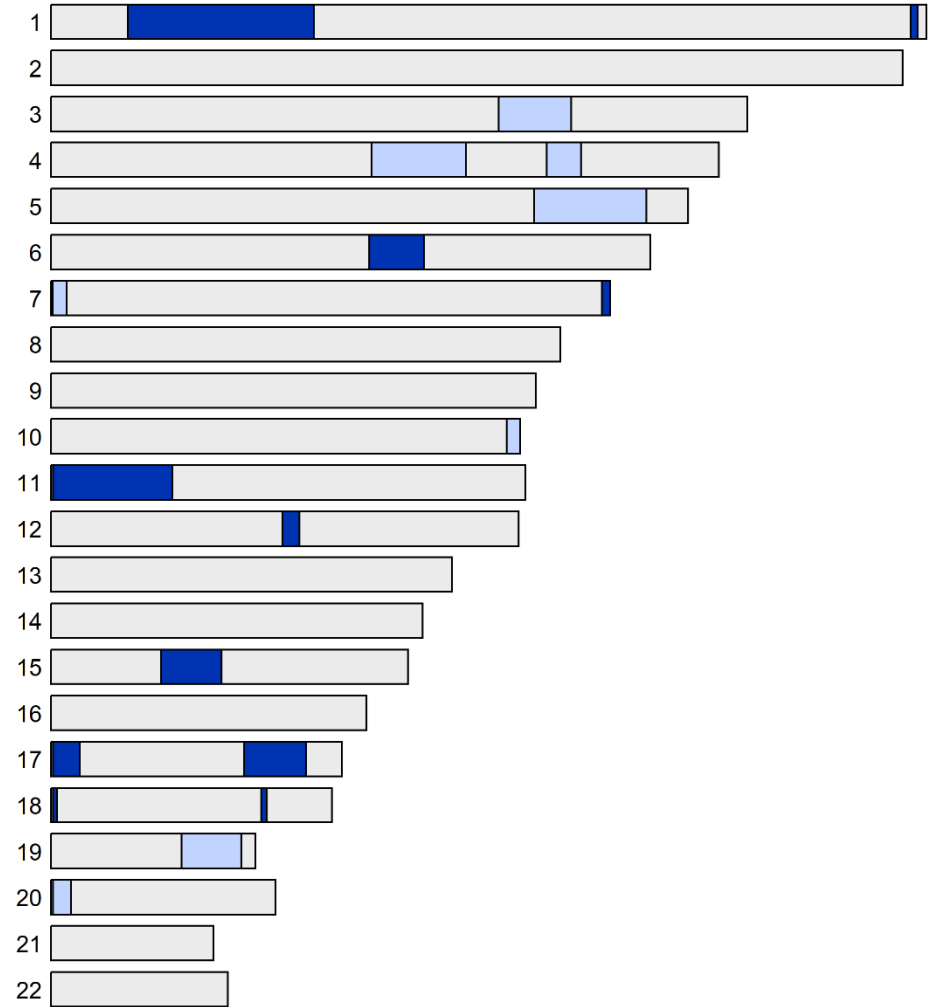
Realised inbreeding



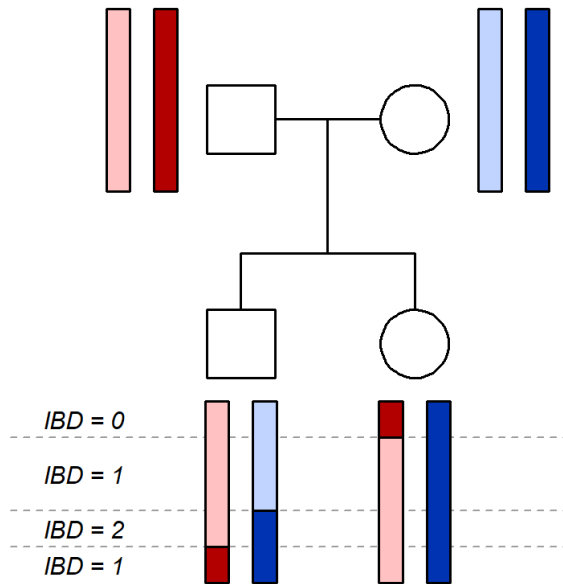
f_R = autozygous fraction of genome



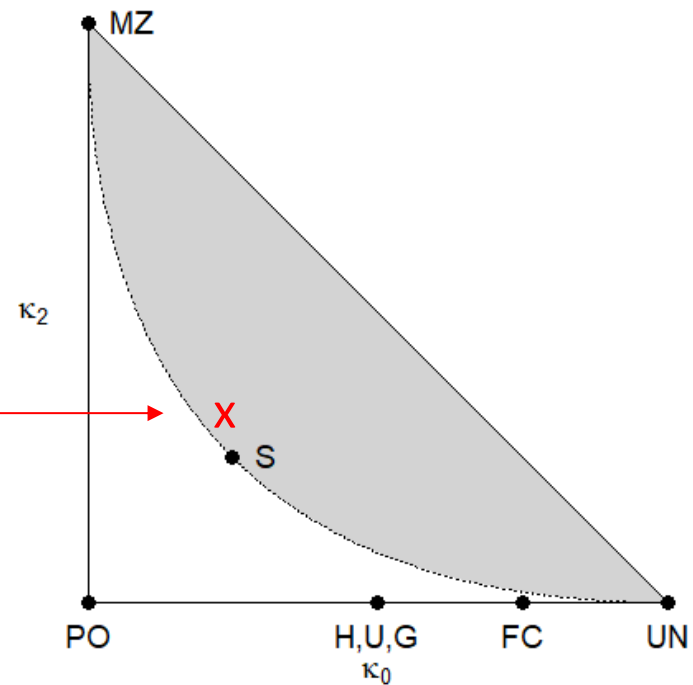
Autozygous segments



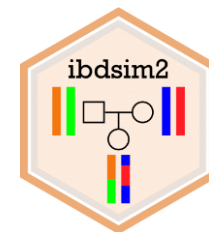
Realised IBD coefficients



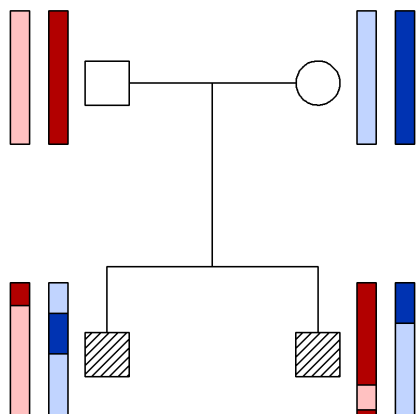
Realised IBD coefficients:
Proportions of genome with $IBD = 0, 1, 2$



Variation in realised IBD coefficients



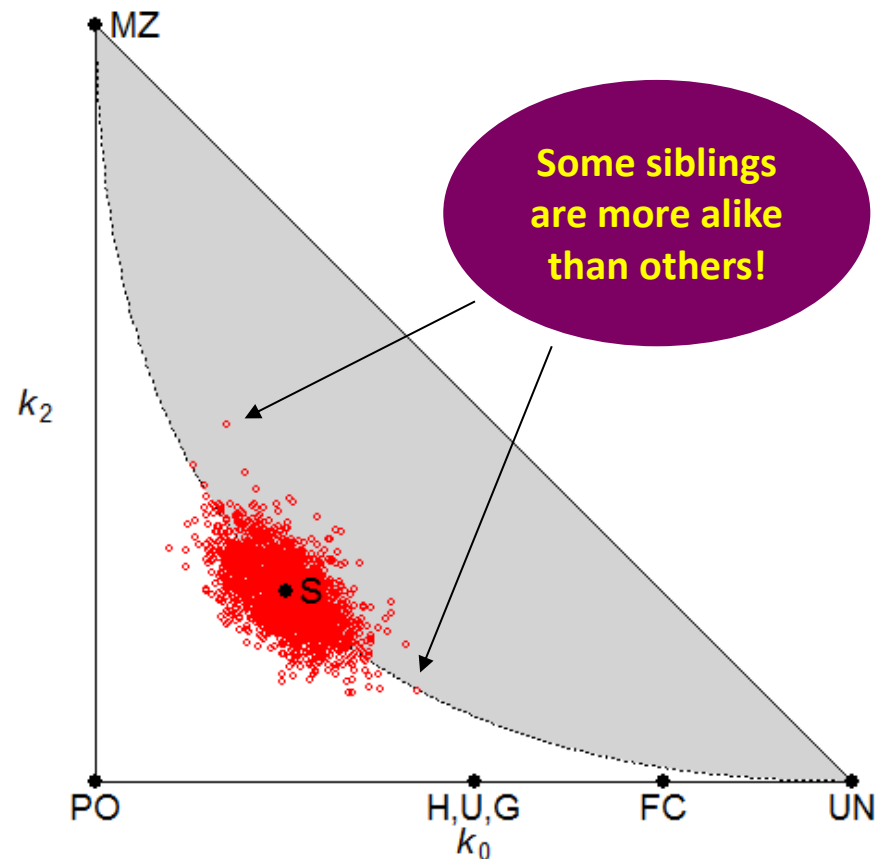
1000 simulations



```
> library(pedsuite)
> library(ibdsim2)

> x = nuclearPed(2)
> s = ibdsim(x, N = 1000)
> k = realisedKappa(s, ids = 3:4)

> showInTriangle(k)
```



Variation depends on the genome



Human:

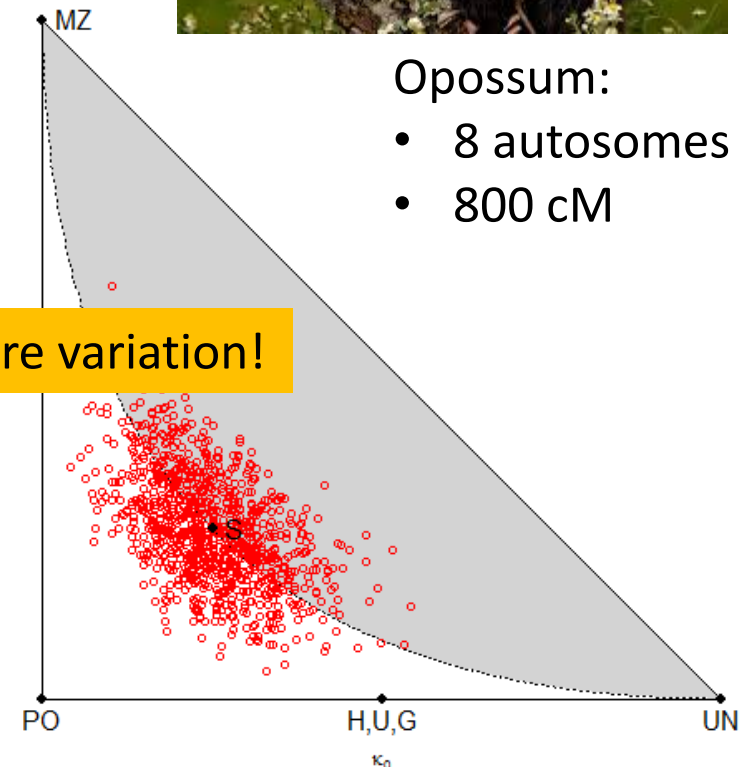
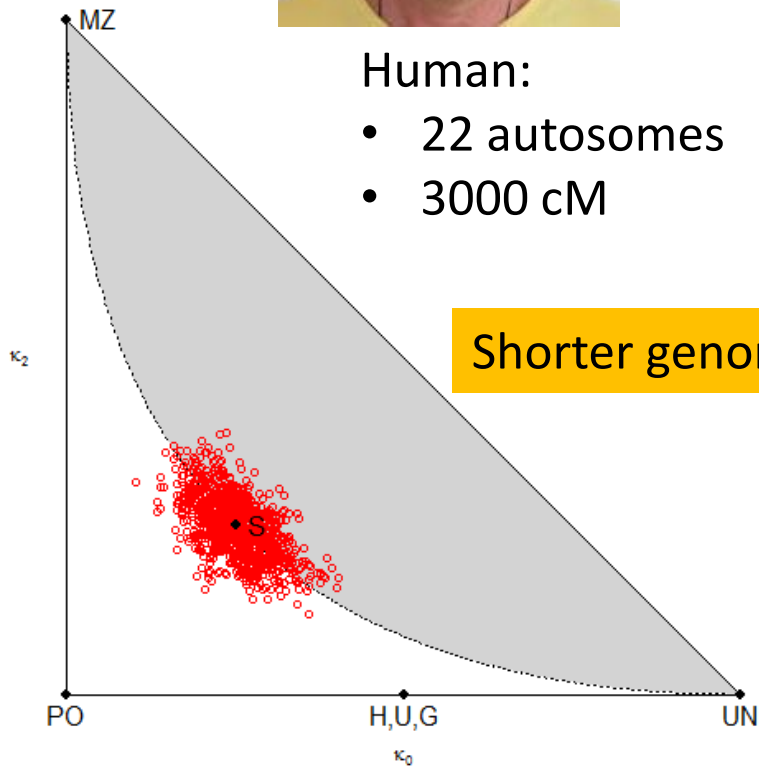
- 22 autosomes
- 3000 cM



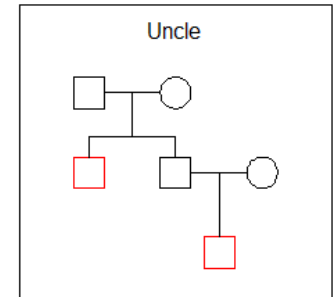
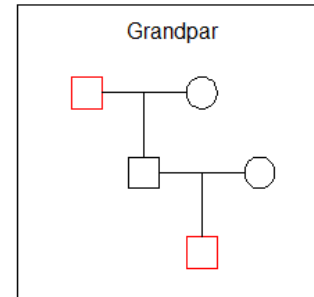
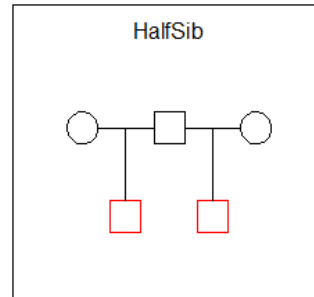
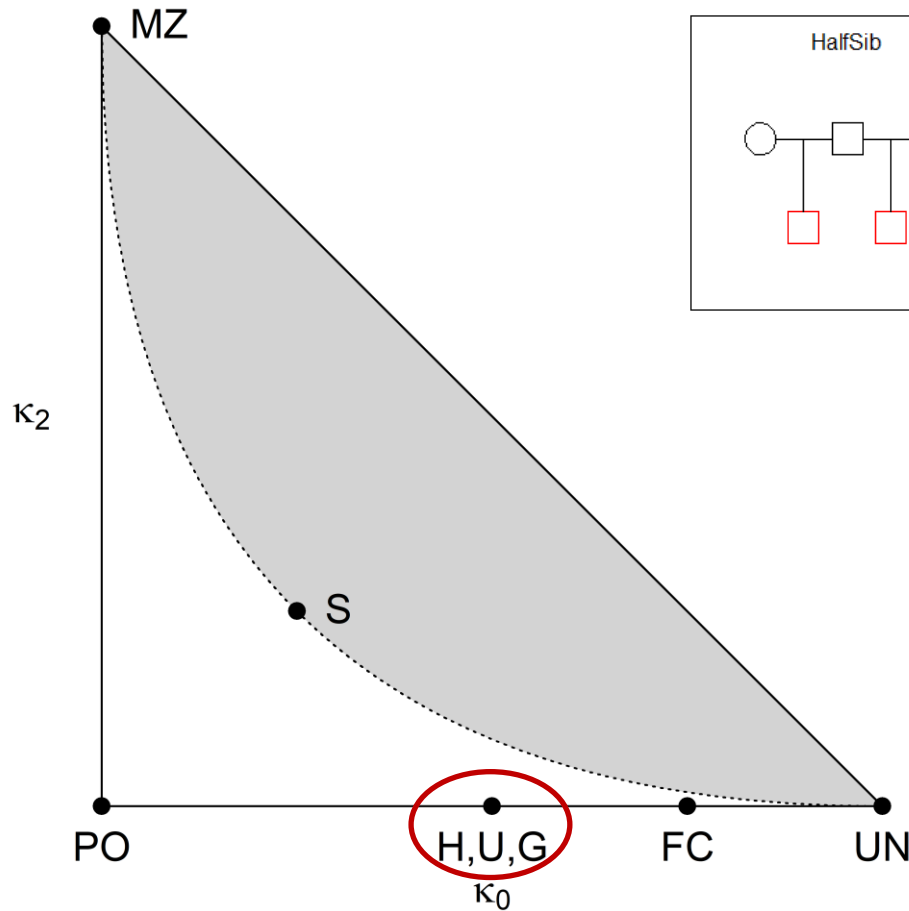
Opossum:

- 8 autosomes
- 800 cM

Shorter genome = more variation!



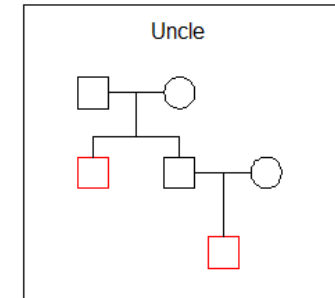
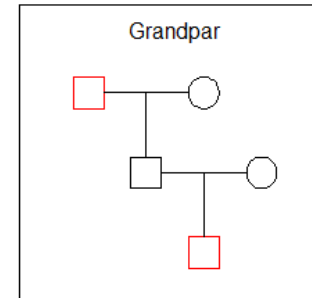
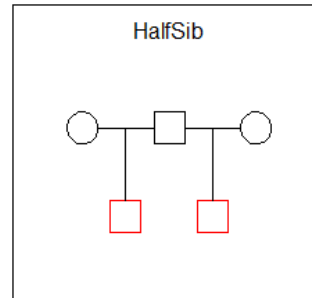
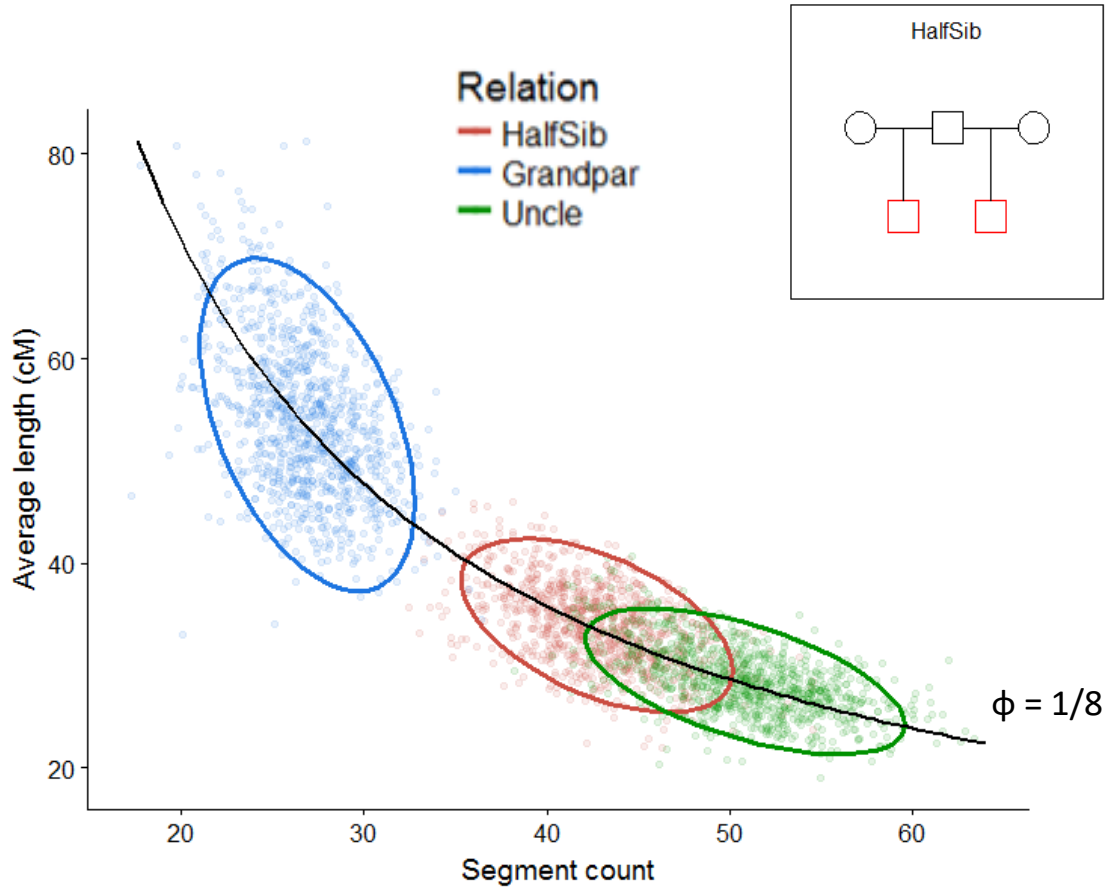
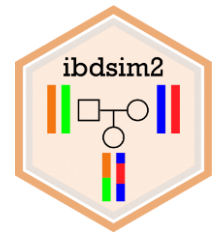
Indistinguishable relationships?



$$\begin{aligned}\kappa_0 &= 0.5 \\ \kappa_1 &= 0.5 \\ \kappa_2 &= 0\end{aligned}$$



Simulated IBD distributions



In theory distinguishable with linked markers!



METRO

HOME NEWS SPORT ENTERTAINMENT LIFESTYLE
UK WORLD WEIRD TECH



FASHION CULTURE

Ou, Awkward... Meghan Markle and Prince Harry are Apparently Related

By Meghan McKenna Date November 2, 2017

FASHION BEAUTY GIFT GUIDE

Let's not forget – Prince Harry and Meghan Markle are actually (very distant) cousins

Richard Hartley-Parkinson for Metro.co.uk Monday 27 Nov 2017 11:35 am 18.8k

Brigitte

SPIELE NEWSLETTER VIDEO GEWINNSPIELE FORUM F-MAG ACADEMY SHOPPING ABC
Aktuell Mode Beauty Rezepte Gesund Liebe Familie Leben Horor

Stammbaum erforscht: Prinz Harry und Meghan Markle sind Cousins!

universitetssykehus



STJERNER: Meghan Markle og prins Harry viser endelig kjærligheten sin offentlig, etter å ha holdt forholdet svært privat i lang tid. Nå kommer det frem at paret, som er fra to forskjellige kontinenter, faktisk er i slekt. Foto: NTB scanpix

Prins Harry er i slekt med kjæresten

SE OG HØR

View c

1.1K shares

(Picture: Mail Online)

Ralph BOWES
(1480–1516)
of Streatlam, Co Durham
High Sheriff

GRANDCHILDREN

Sir George BOWES
Loyal to Queen Elizabeth I
during the rising of the North, 1596

Bridget BOWES
Married John Hussey
of Dorking

GREAT-GRANDSON

Sir William BOWES MP
(1657–1707)
During reign of Charles II
Royalist

GRANDSON

Captain Christopher HUSSEY
(1598/9–1686)
A founder of Nantucket, Massachusetts

Sir George BOWES MP
(1707–1770)

Huldah HUSSEY
(1643–1740)
Married Lieutenant John SMITH

Married John ... art

FOUR

Claude George
(1854–1948)
14th Earl of Strathmore

Lee MERRILL

Lady Elizabeth BOWES LYON
(1900–2001)
HM Queen Elizabeth
The Queen Mother

George David MERRILL
(1861–1924)

Gertrude May MERRILL
(1887–1938)
Married Frederick George SANDERS

HM The Queen
(1926–)

Doris SANDERS
(1921–)
Married Gordon Arnold Markle

Lady Diana Spencer
(1961–1997)

HRH Prince of Wales
(1948–)

Thomas Wayne Markle
(1944–)

Doria L. Ragland
(1956–)

PRINCE HARRY

(RACHEL) MEGHAN MARKLE

~~15th Cousins~~

- 14
- 13
- 10
- 9
- 8
- 4
- 3
- 2
- 1

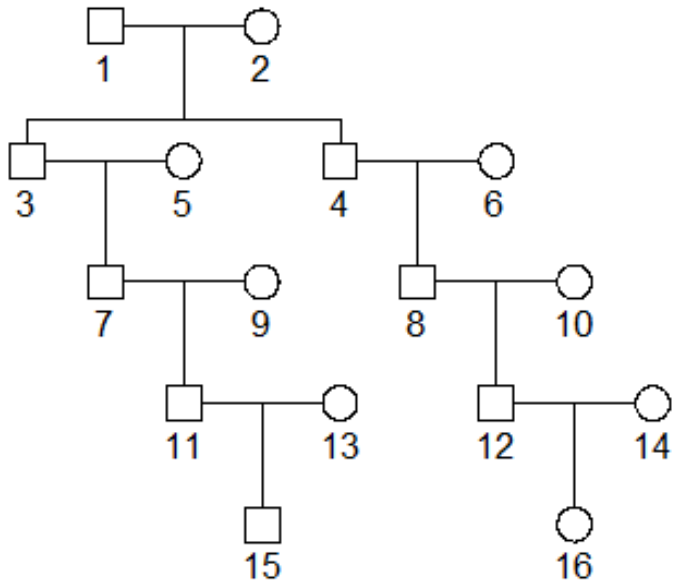
- 15
- 13
- 11
- 10
- 9
- 5
- 4
- 3
- 2
- 1

P(any IBD) ≈ 0



13th cousins once removed

The probability of zero IBD



N'th cousins	$P(\text{zero IBD})$
first	0.0 %
second	0.0 %
third	1.5 %
fourth	28 %
fifth	67 %

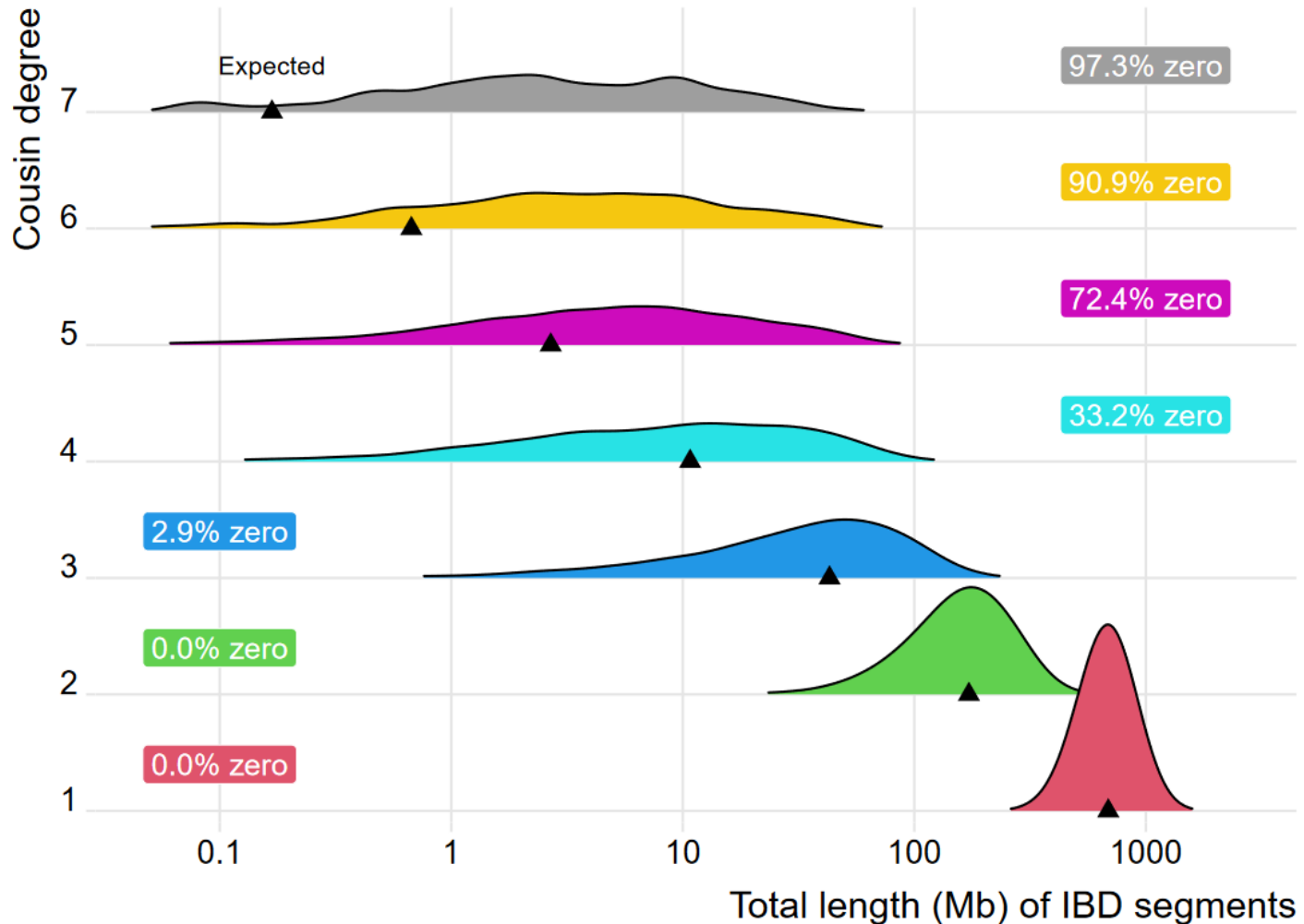
Third cousins

Expected fraction with IBD = 1:

$$k_1 = \frac{1}{64}$$

Two individuals can have a common ancestor without being genetically related

Distant cousins share either **nothing** or **quite a bit**

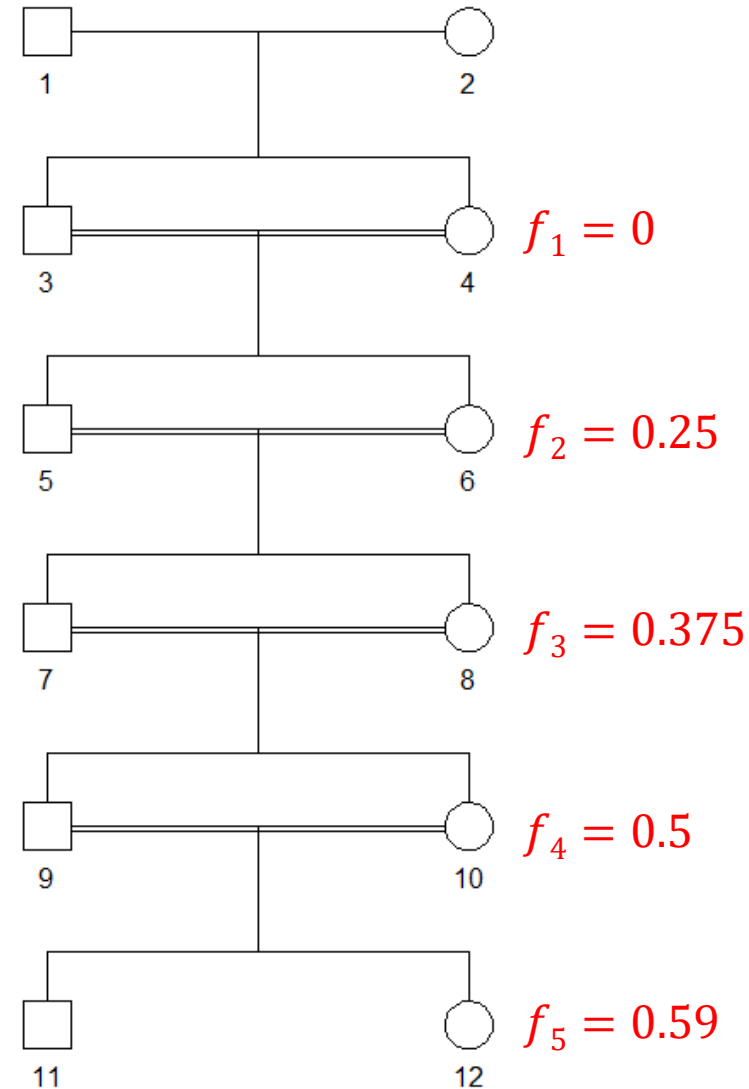


Reversely:

Is 100 % inbreeding possible?

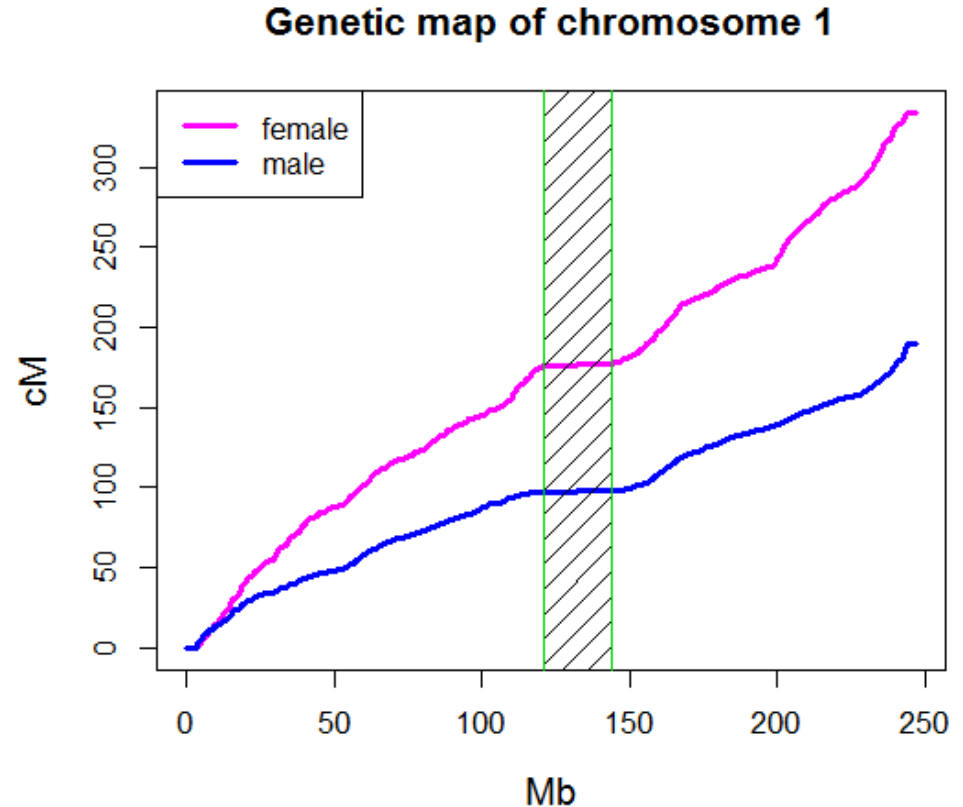
- Continuous full-sib mating
- Easy to show:
 - inbreeding coefficient $f \rightarrow 1$
- In finite pedigree:
 - pedigree-based f will *never* reach 1

After ~30 generations,
But: the **realised inbreeding**
typically reaches 1



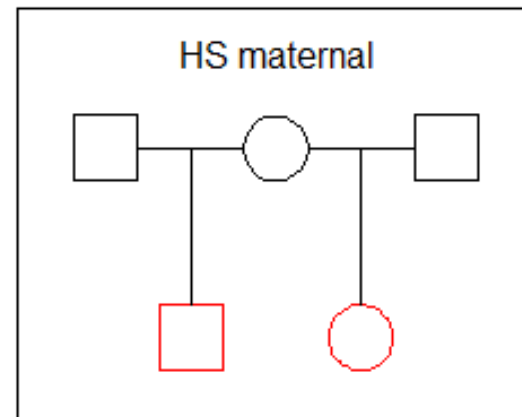
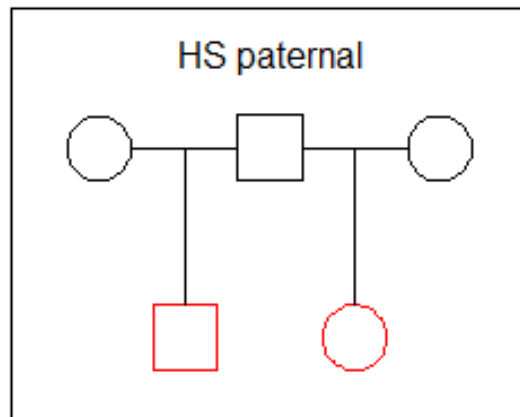
The importance of sex

- Rule of thumb:
 $1 \text{ cM} \approx 1 \text{ Mb}$
- But: crossover rates vary
 - across the genome
 - males vs. females

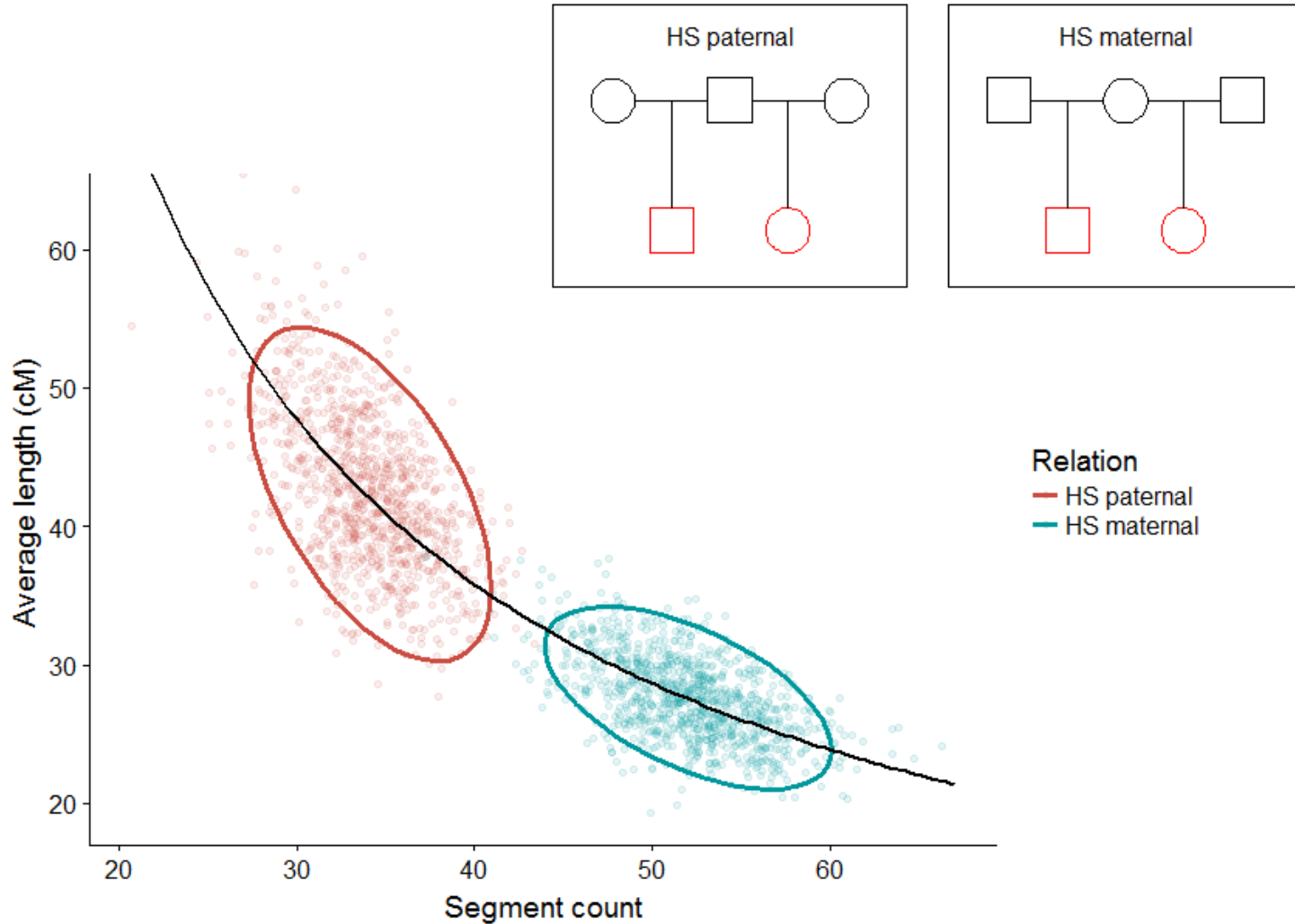


Females have a much longer genome!

Can we separate these??



Yes!



IBD sharing by family members

Purpose: Estimate and visualise distributions of genomic segments shared identical-by-descent (IBD) between related individuals, or within inbred individuals (autozygosity). Recombination is simulated down through the pedigree, using detailed, sex-specific crossover rates for the human genome (Halldorsson et al., 2019).

More information: This program is a frontend for the R package `ibdsim2`, which is part of the `pedsuite` ecosystem for pedigree analysis. Details about the simulations can be found in the package documentation, and in the book *Pedigree analysis in R*. Please cite this book if you use the app in your work.

Pedigree 1

Built-in pedigree

Half-sibs, maternal

Load ped file

Individuals

4, 5

Label

Ped 1

PARAMETERS

Chromosome

1 - 22 X

Crossover model

χ^2 Haldane

Sex-specific map

On Off

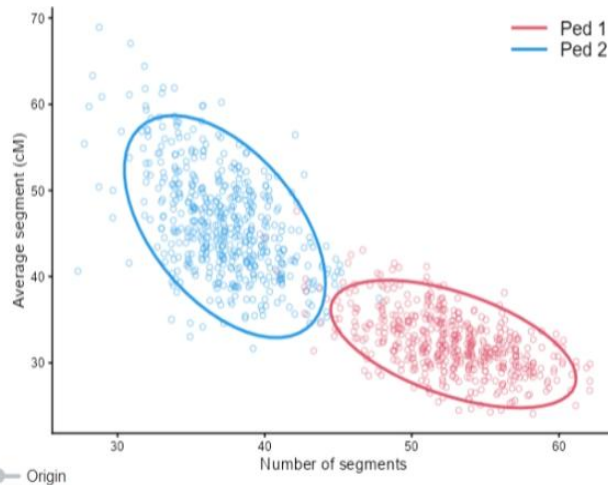
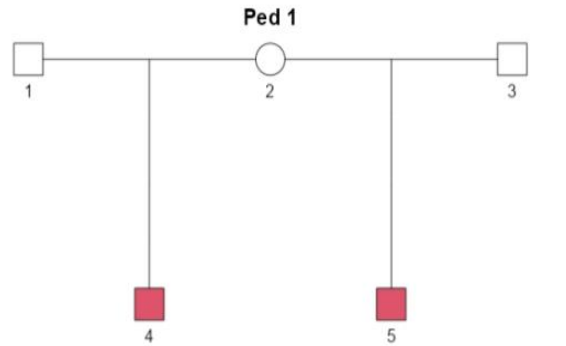
Cutoff

0

Seed

123

Simulate!



Pedigree 2

Pedigree 2

Built-in pedigree

Half-sibs, paternal

Load ped file

Individuals

4, 5

Label

Ped 2

PARAMETERS

Chromosome

1 - 22 X

Crossover model

χ^2 Haldane

Sex-specific map

On Off

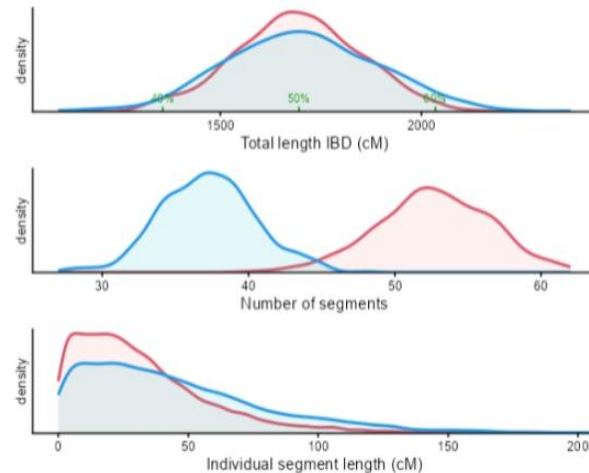
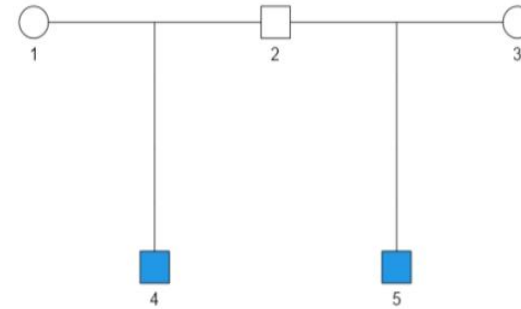
Cutoff

0

Seed

123

Simulate!



Settings

Number of sims

500

Length unit

cM Mb

Download data

Analysis

Sharing Autozygosity

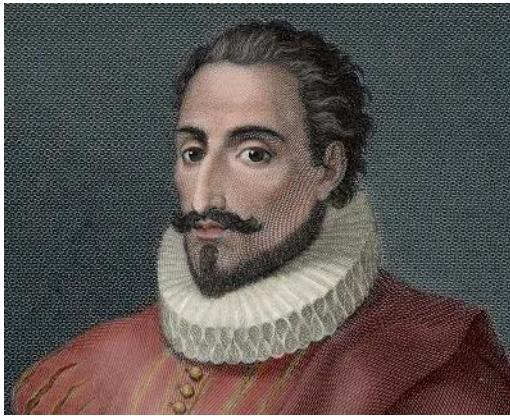
Observed data

Total length

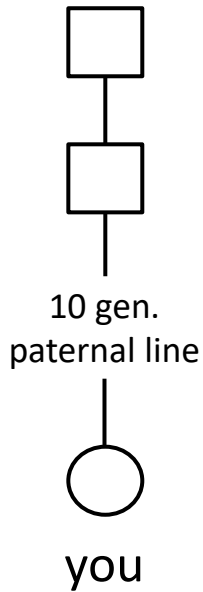
Count

Segments

This is version 2.3.2.9000 of `ibdsim2` (changelog). For bug reports, feature requests, or other comments, please file an issue at <https://github.com/magnusdv/ibdsim2/issues>.



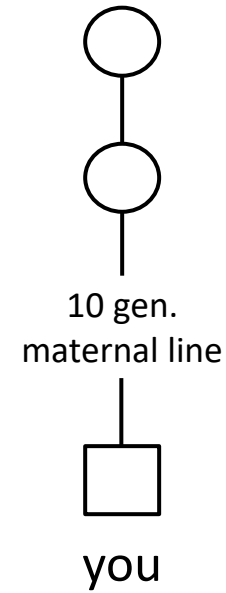
Miguel de Cervantes



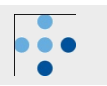
P(some IBD) = 38%



Isabella I of Castile



P(some IBD) = 51%



Summary of genetic relatedness

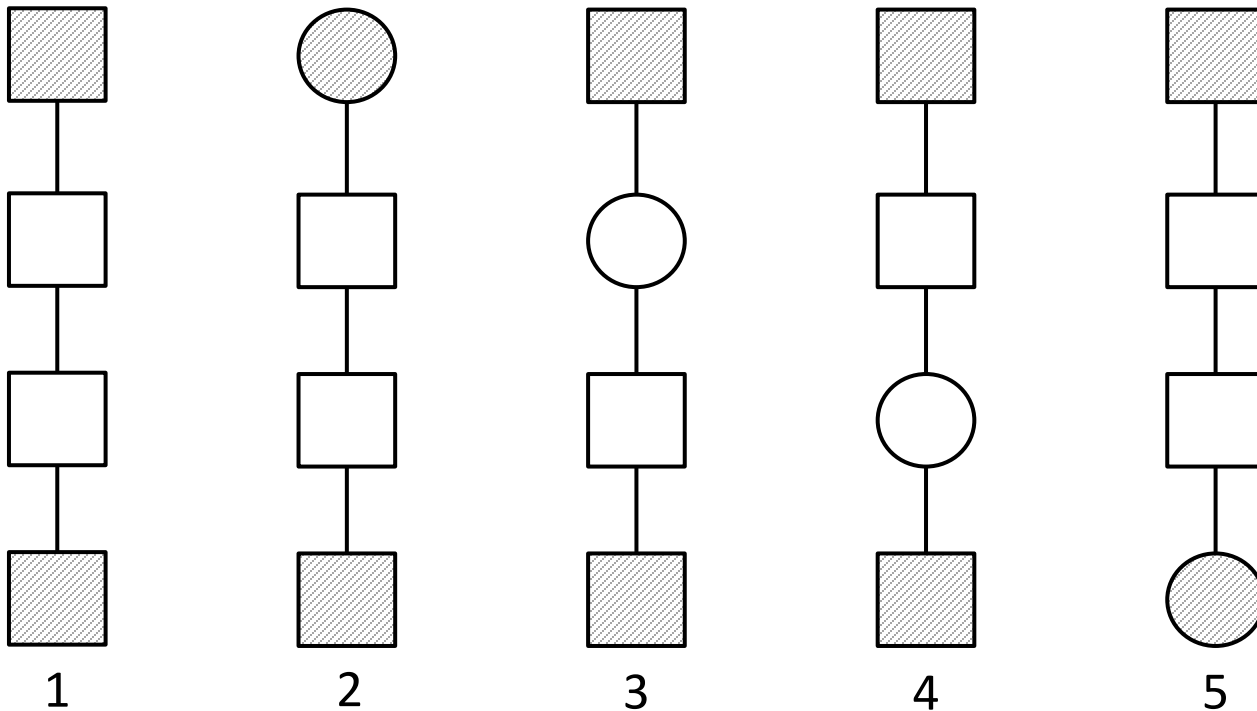
- Pedigree-based measures:
 - the kinship/inbreeding coefficient φ
 - the kappa coefficients $\kappa = (\kappa_0, \kappa_1, \kappa_2)$
- Each coefficient is
 - the **probability** of observing a certain IBD pattern **in a random locus**
 - the **expected proportion of the genome** in this state
- Realised relatedness:
 - IBD **segments** determined by meiotic recombination
 - females recombine more than males
 - may separate relationships with equal kappa's
 - 0% and 100% realised identity is possible!

So...what does it mean to be related?

- Pedigree based definition: $\varphi > 0$
potentially having alleles IBD
- Genomic definition (**realised** relatedness):
actually having alleles IBD

Epilogue

- Which of these relationships are genetically different?



- Answer: $1 = 2 = 5$ and $3 = 4$



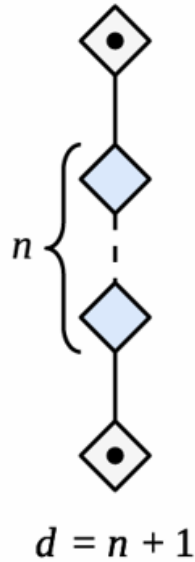
Henrik Nordtorp

Theorem

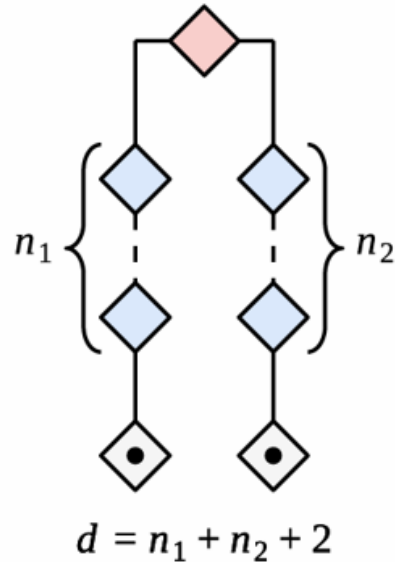
Two unilineal relationships have identical IBD distributions if and only if they have the same ...

- ❖ Type (A-D)
- ❖ Degree
- ❖ Anchor females/males
- ❖ Free females/males

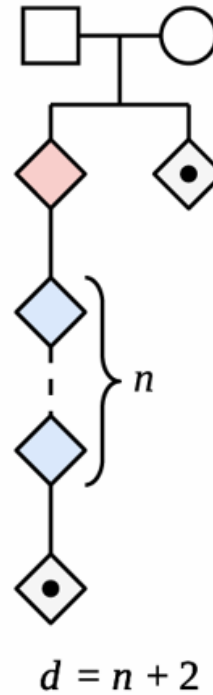
A



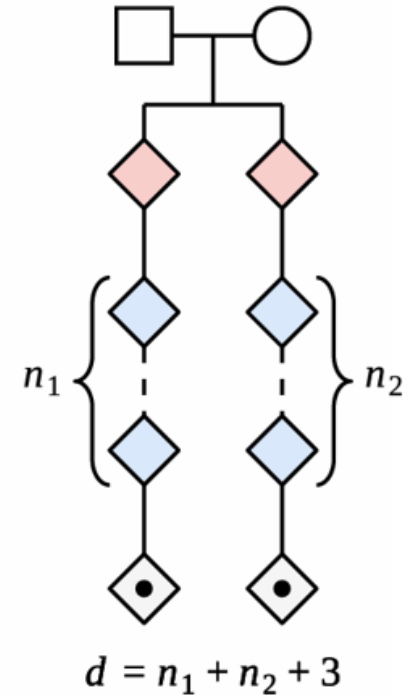
B

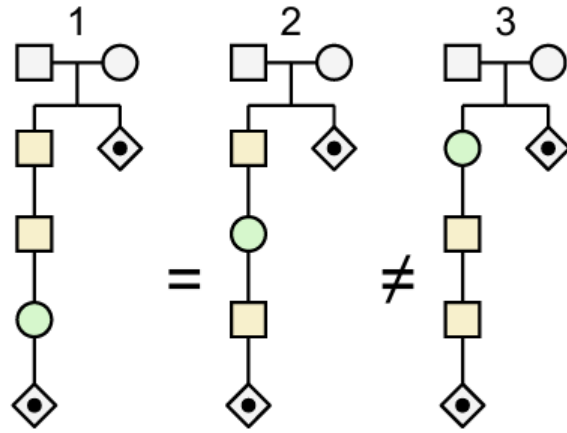
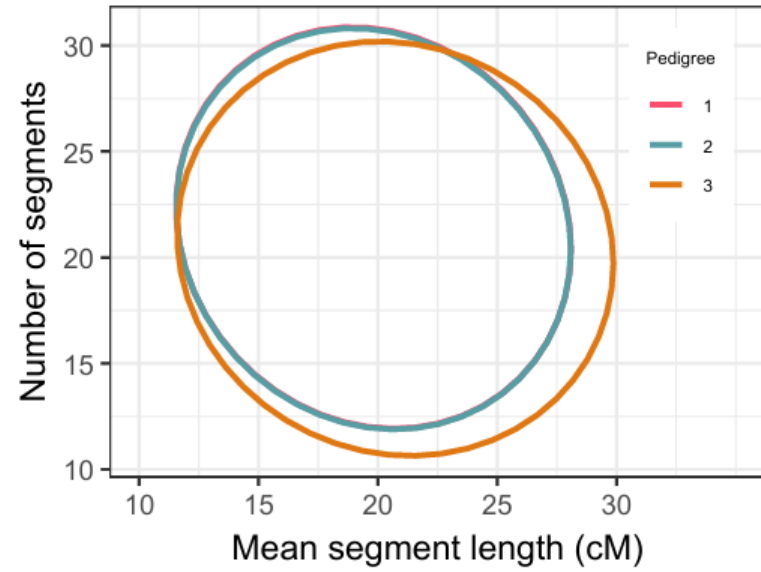
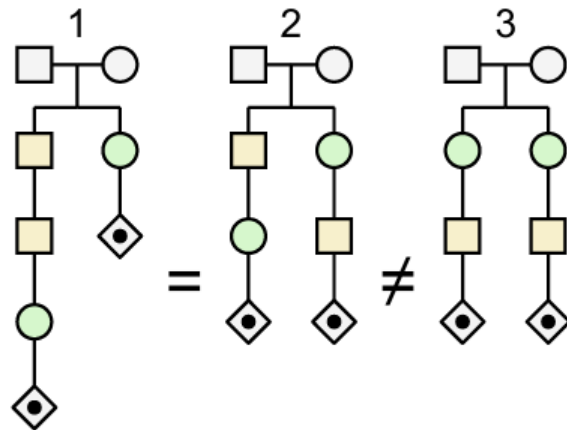


C



D



A**B****C****D**