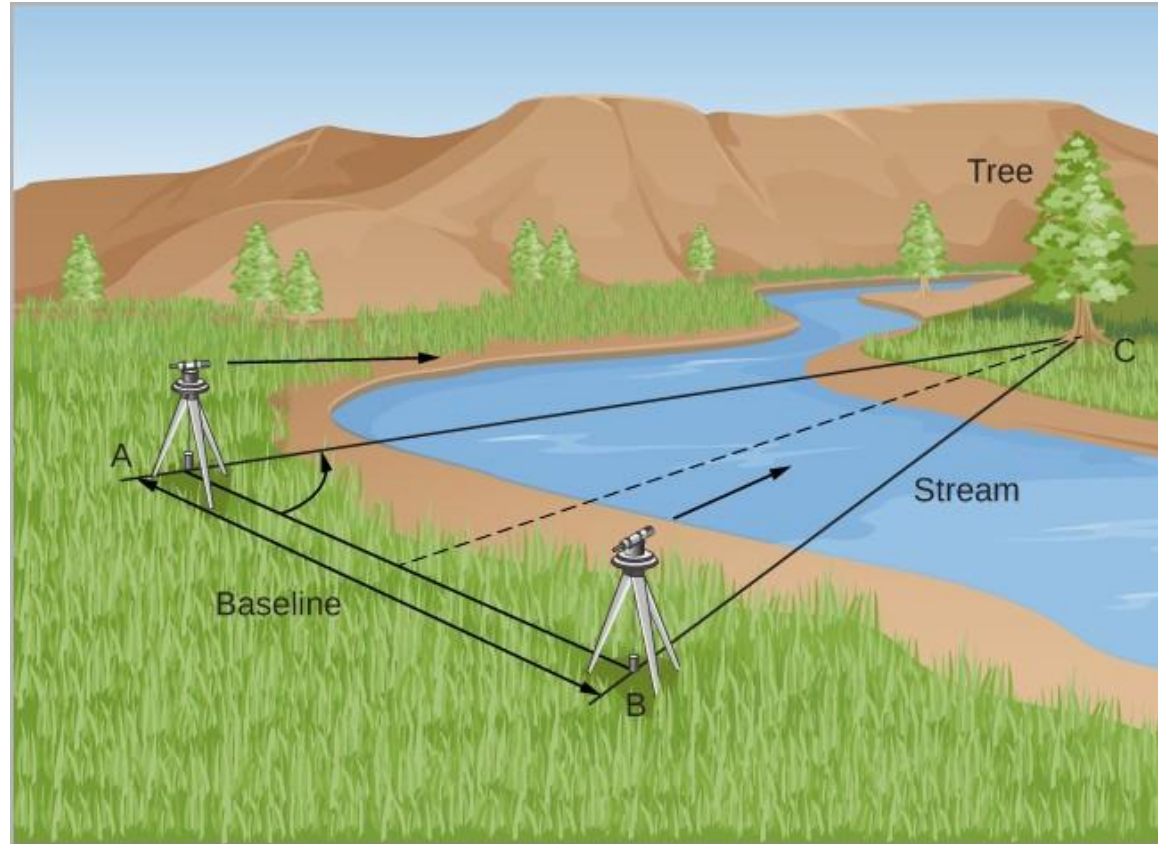


Triangulation in genetic genealogy

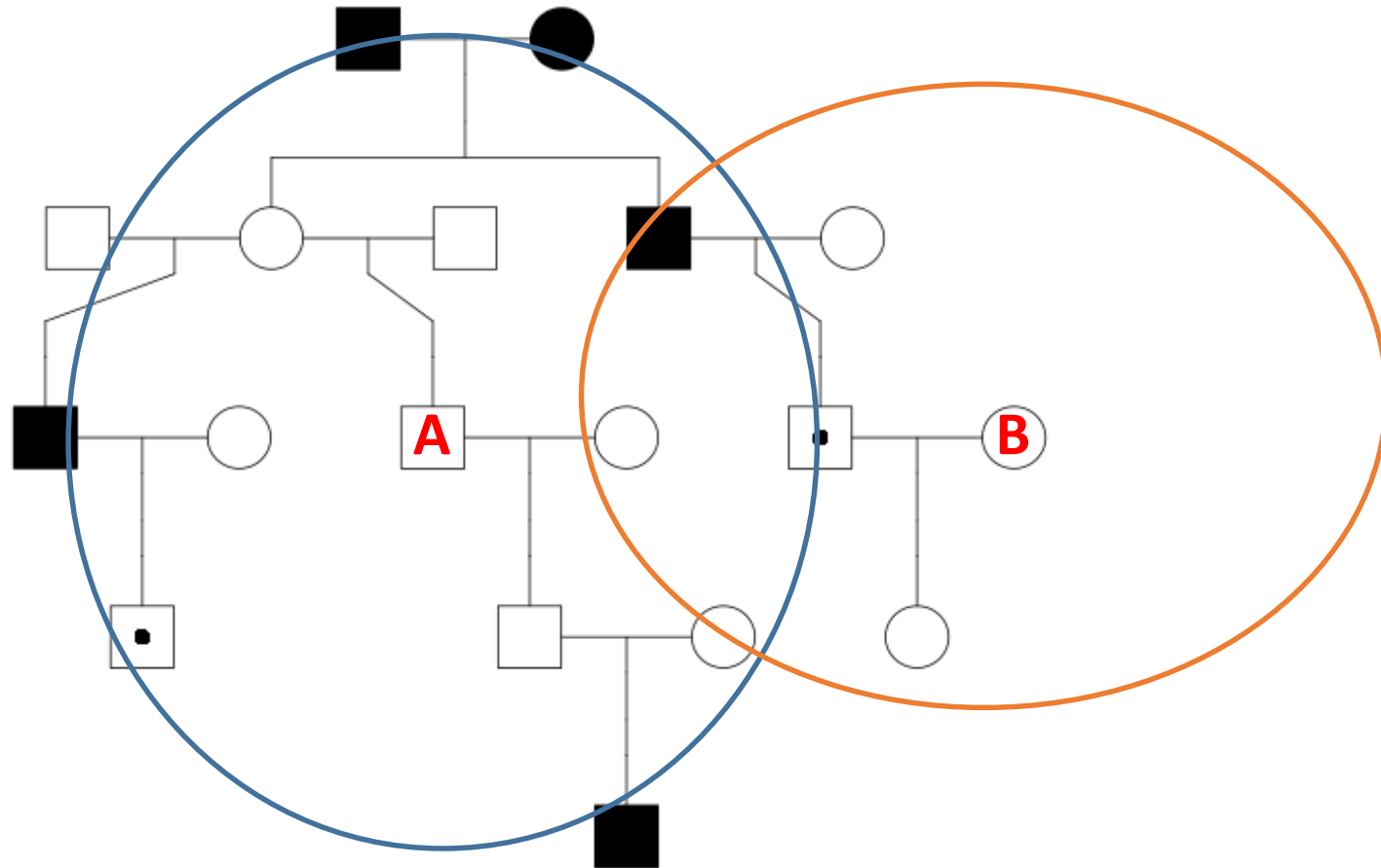


Statistical methods in genetic relatedness and pedigree analysis

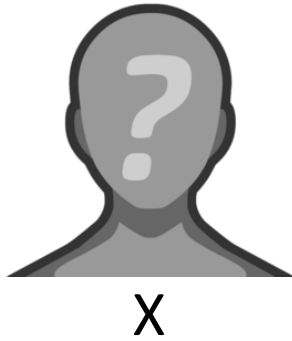
NORBIS course, 13th – 17th of June 2022, Oslo

Magnus Dehli Vigeland

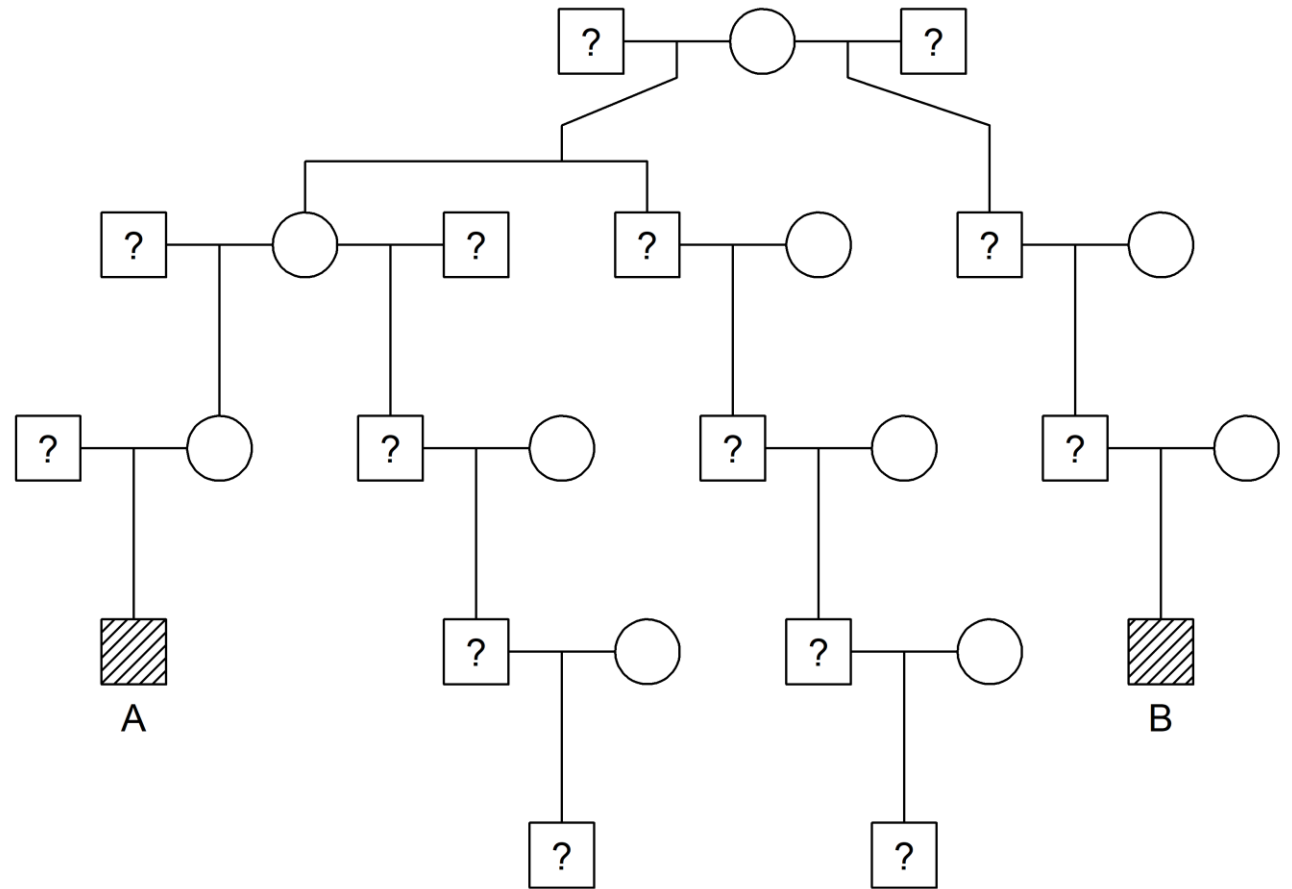
Triangulation in genealogy



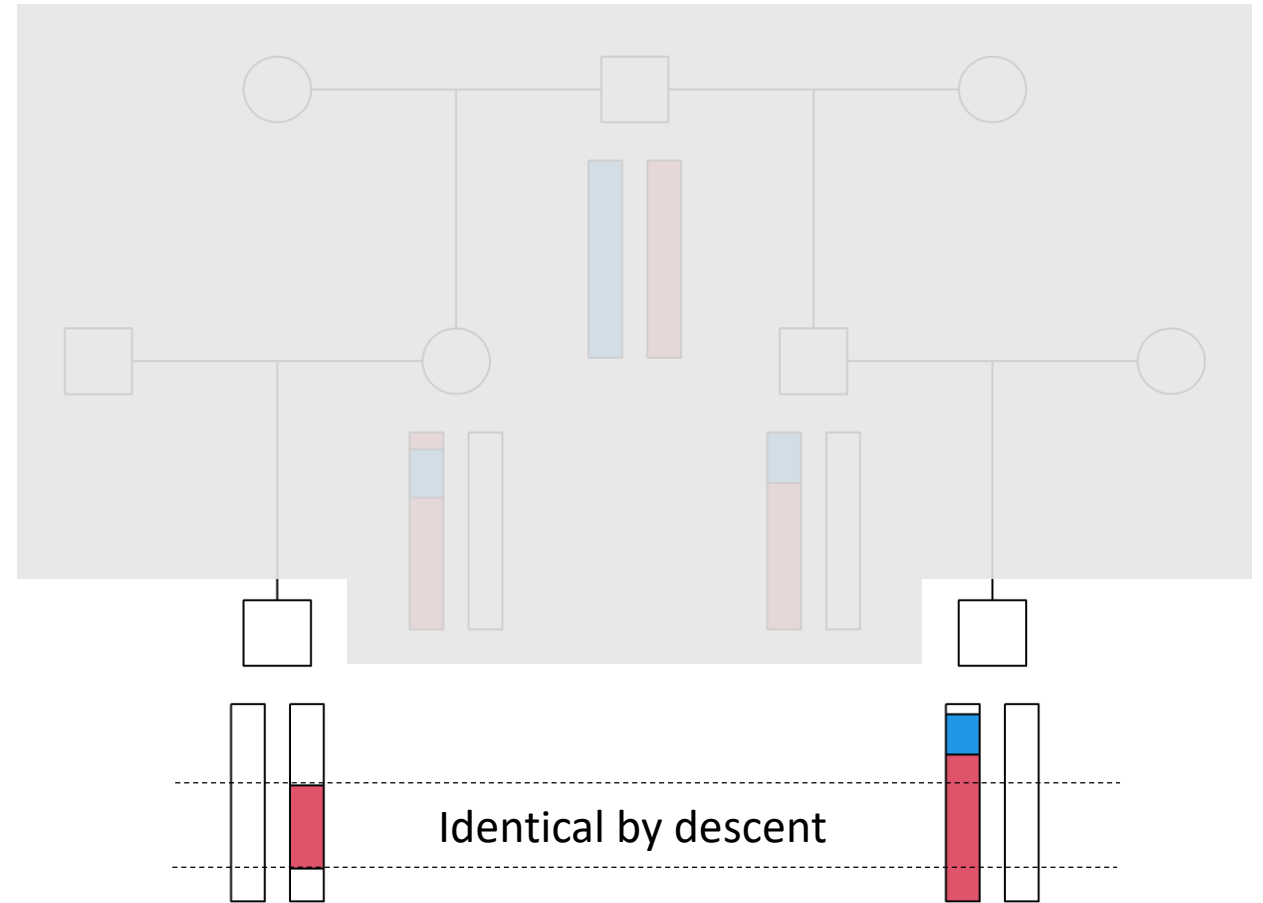
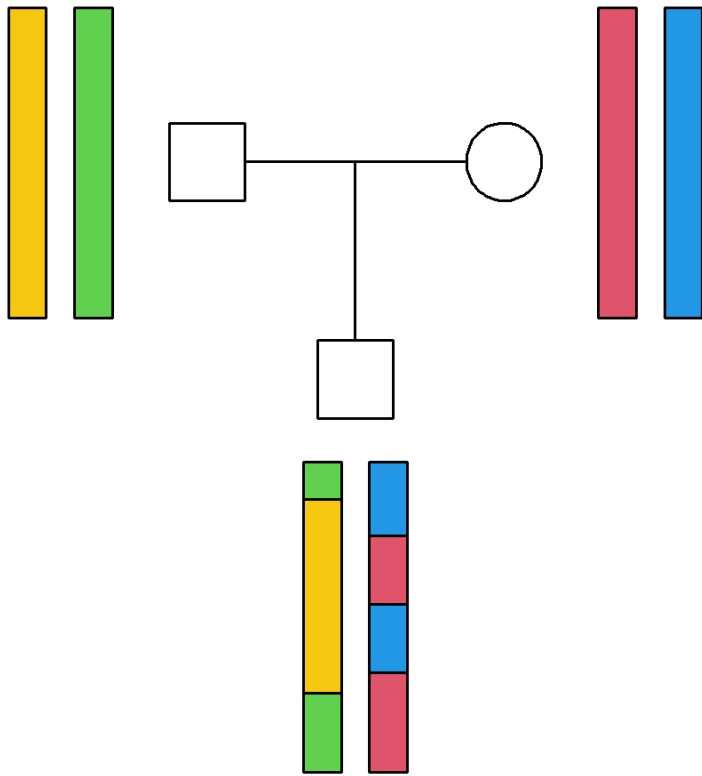
Who is Mr X?



Pair	Segments (cM)
X-A	10, 30.3, 7.4, 21.8, 10.7, 23.8, 11.3, 15.7, 45.7, 9.4
X-B	7.4, 15.7, 17.7, 20.5, 18.3, 11.1



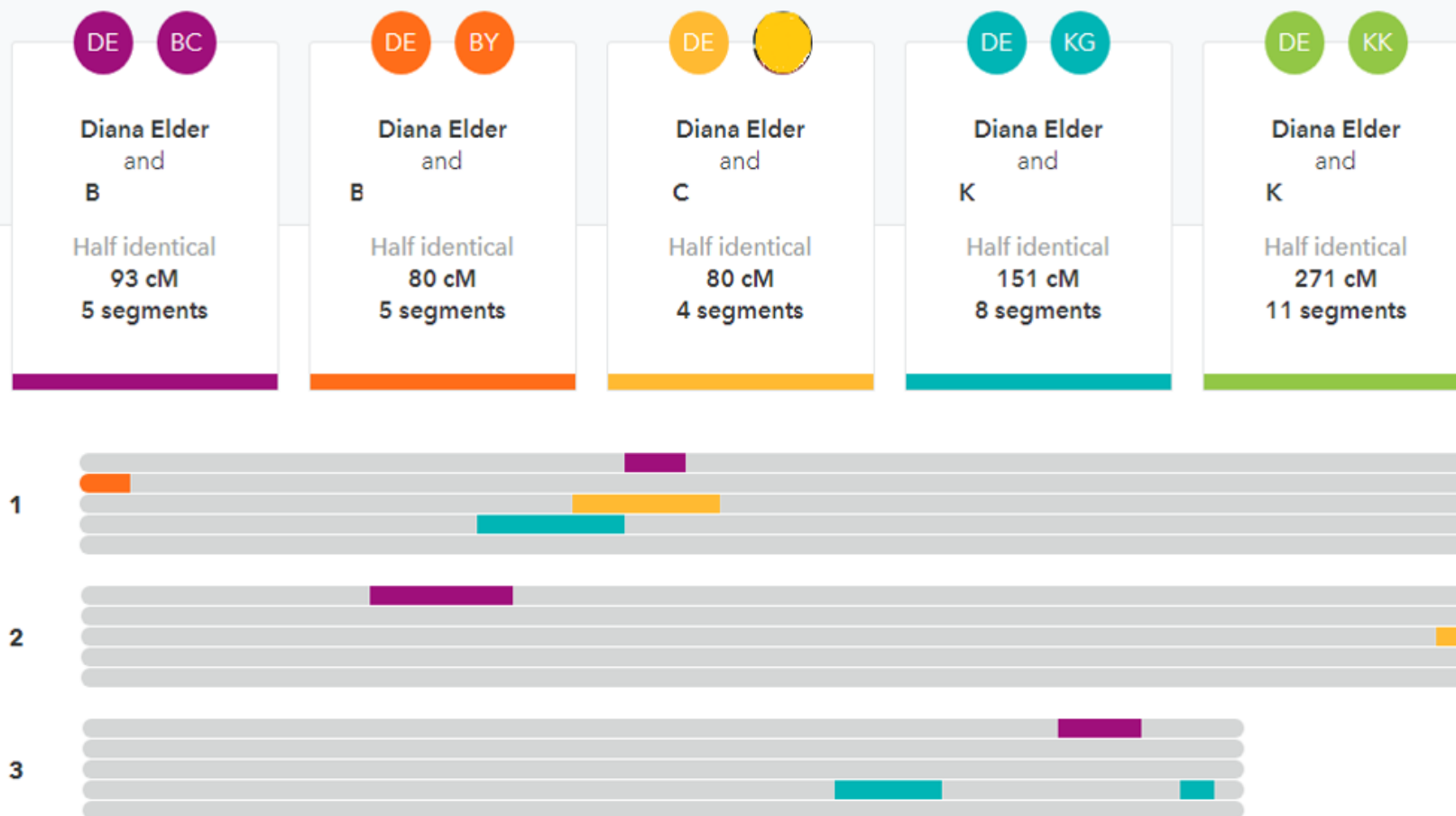
Recap: Recombination and IBD



[List](#)
[Map](#)
[Frequently Asked Questions](#)

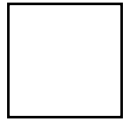
Now comparing DNA segments.

Select different relatives or friends to compare.

[View all DNA Relatives](#)


Estimation of pairwise relatedness

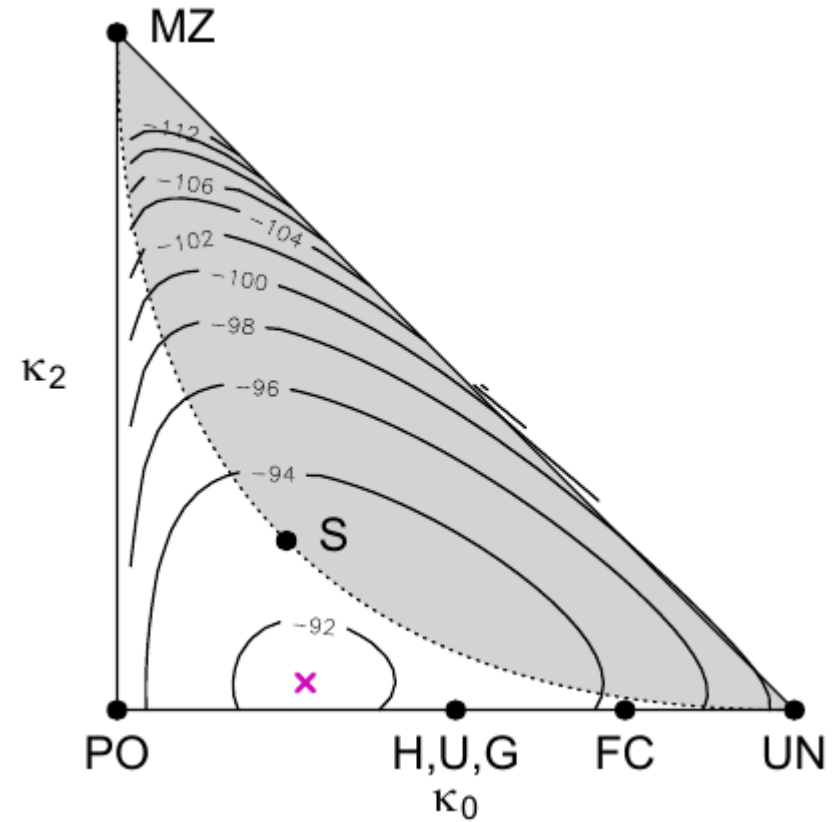
1) Marker-based MLE (Thompson 1975)



16/17
7/9.3



15/17
9.3/9.3



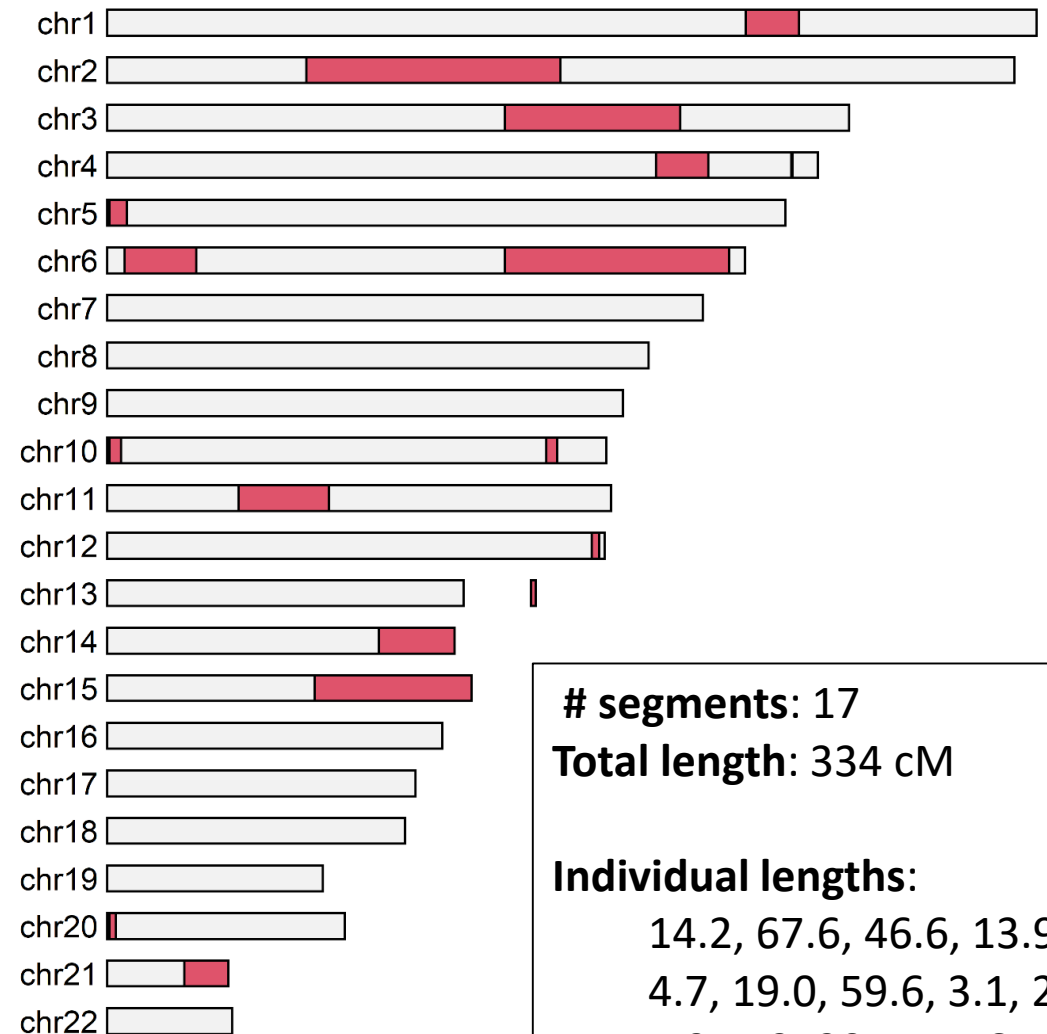
Estimation of pairwise relatedness

2) IBD segments

- Compare observed data with simulated distributions from a range of relationships.
- *Naive Bayes* classification

Shiny app:

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



segments: 17

Total length: 334 cM

Individual lengths:

14.2, 67.6, 46.6, 13.9, 0.3,
4.7, 19.0, 59.6, 3.1, 2.9, 24.0,
1.9, 1.3, 20.1, 41.6, 1.7, 11.7

Relationship classifier based on IBD segments

Observed data

Segment type

- ☒ Pairwise sharing
☐ Autozygous

Cutoff

Segment lengths

14.2, 67.6, 46.6, 13.9, 0.3, 4.7, 19.0, 59.6, 3.1, 2.9,
24.0, 1.9, 1.3, 20.1, 41.6, 1.7, 11.7

Classify

Simulate example

Relationship

Grandparent (pat)

Simulate

Relationship classifier based on IBD segments

Observed data

Segment type

- ☒ Pairwise sharing
- ☐ Autozygous

Cutoff

0

Segment lengths

14.2, 67.6, 46.6, 13.9, 0.3, 4.7, 19.0, 59.6, 3.1, 2.9, 24.0, 1.9, 1.3, 20.1, 41.6, 1.7, 11.7

Classify

Simulate example

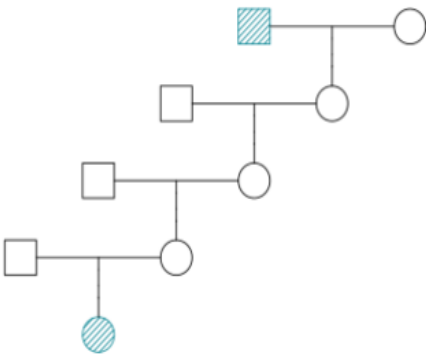
Relationship

Grandparent (pat)

Simulate

1. Great-great-grandp (mmm)

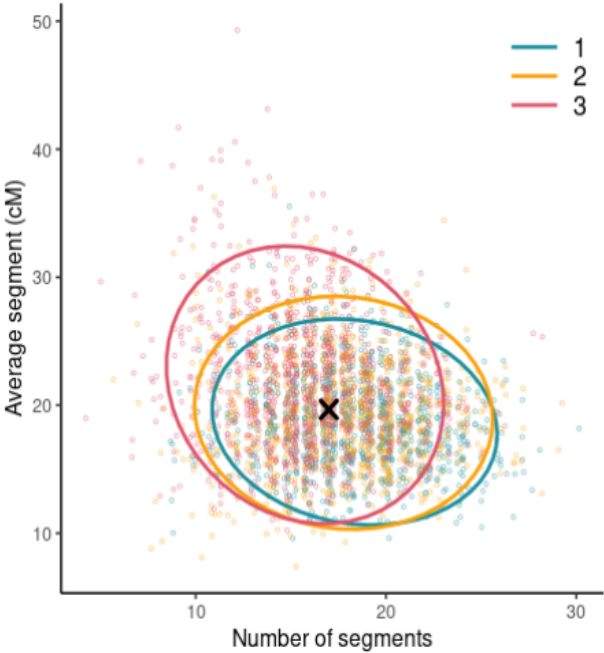
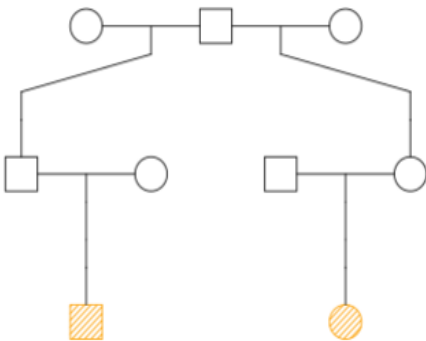
P = 13.7%



Relationship	Posterior
Great-great-grandp (mmm)	0.14
Half first cousins (ppm)	0.14
Half first cousins (ppp)	0.12
Half first cousins (mpm)	0.10
1st cousins 1r (ppp)	0.09
Great-great-grandp (pmm)	0.09

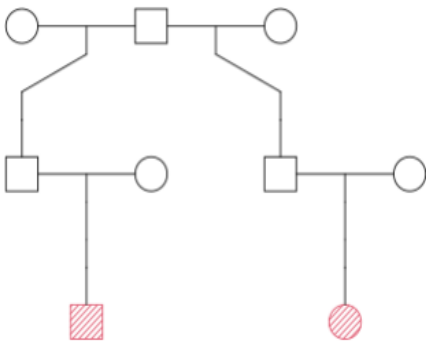
2. Half first cousins (ppm)

P = 13.6%



3. Half first cousins (ppp)

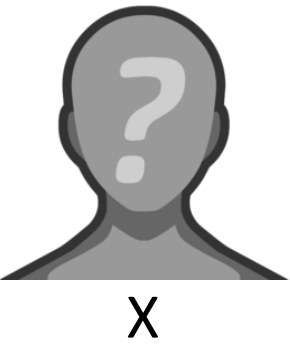
P = 11.9%



Type	Posterior
Half first cousins	0.49
Great-great-grandp	0.28
1st cousins 1r	0.22
2nd cousins	0.01

Kinship	Posterior
1/32	0.99
1/64	0.01

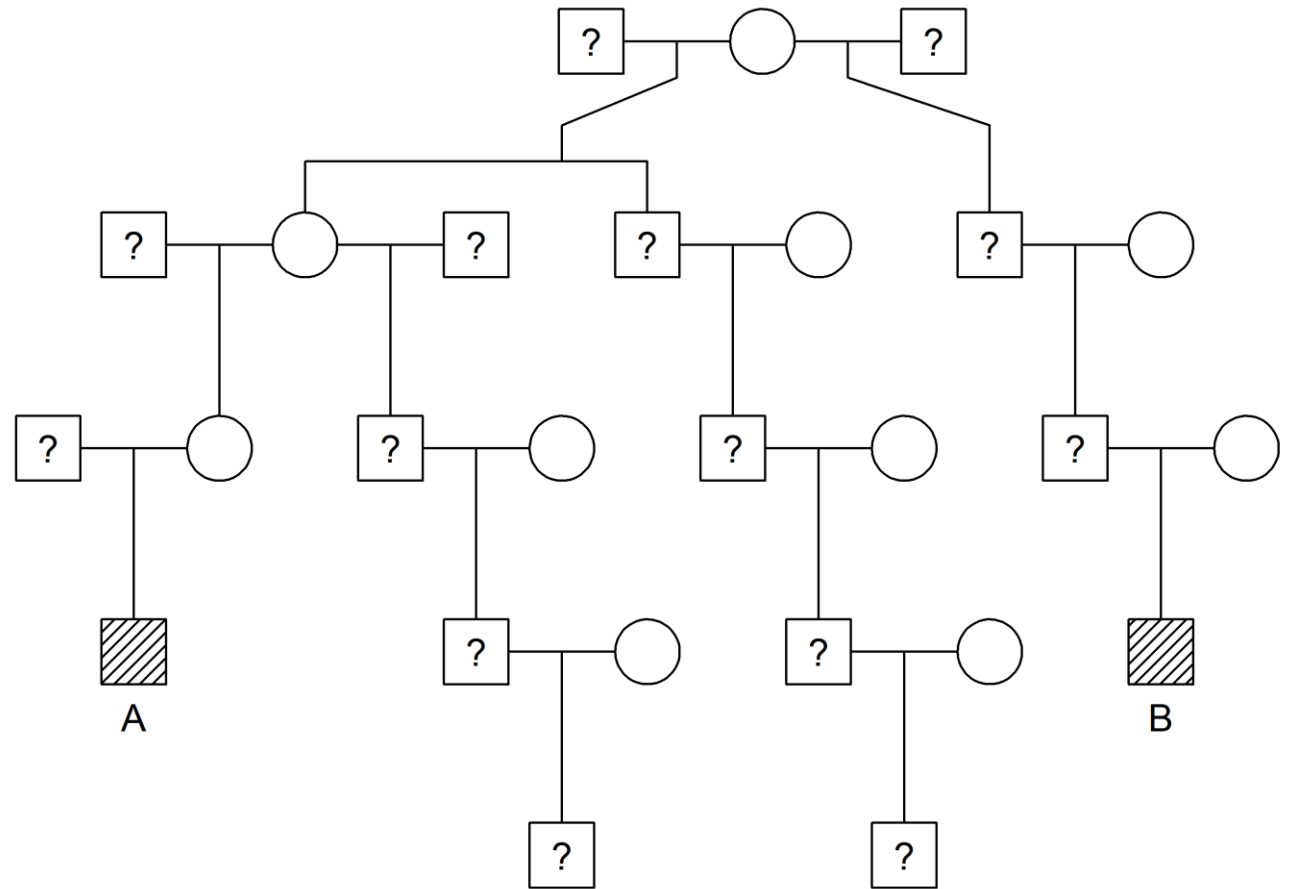
For triangulation: Joint estimation



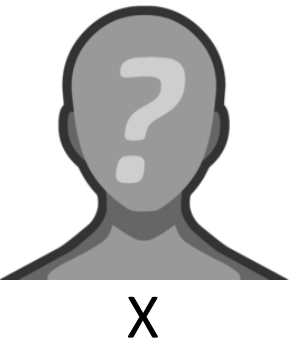
Pair	Segments (cM)
X-A	10, 30.3, 7.4, 21.8, 10.7, 23.8, 11.3, 15.7, 45.7, 9.4
X-B	7.4, 15.7, 17.7, 20.5, 18.3, 11.1

Procedure

- Simulate IBD patterns for the entire pedigree (**ibdsim2**)
- For each individual Y:
 - Shared segments A-Y and B-Y
 - Empirical distributions
 - Compare with observed data
 - **Posterior triangulation probability**



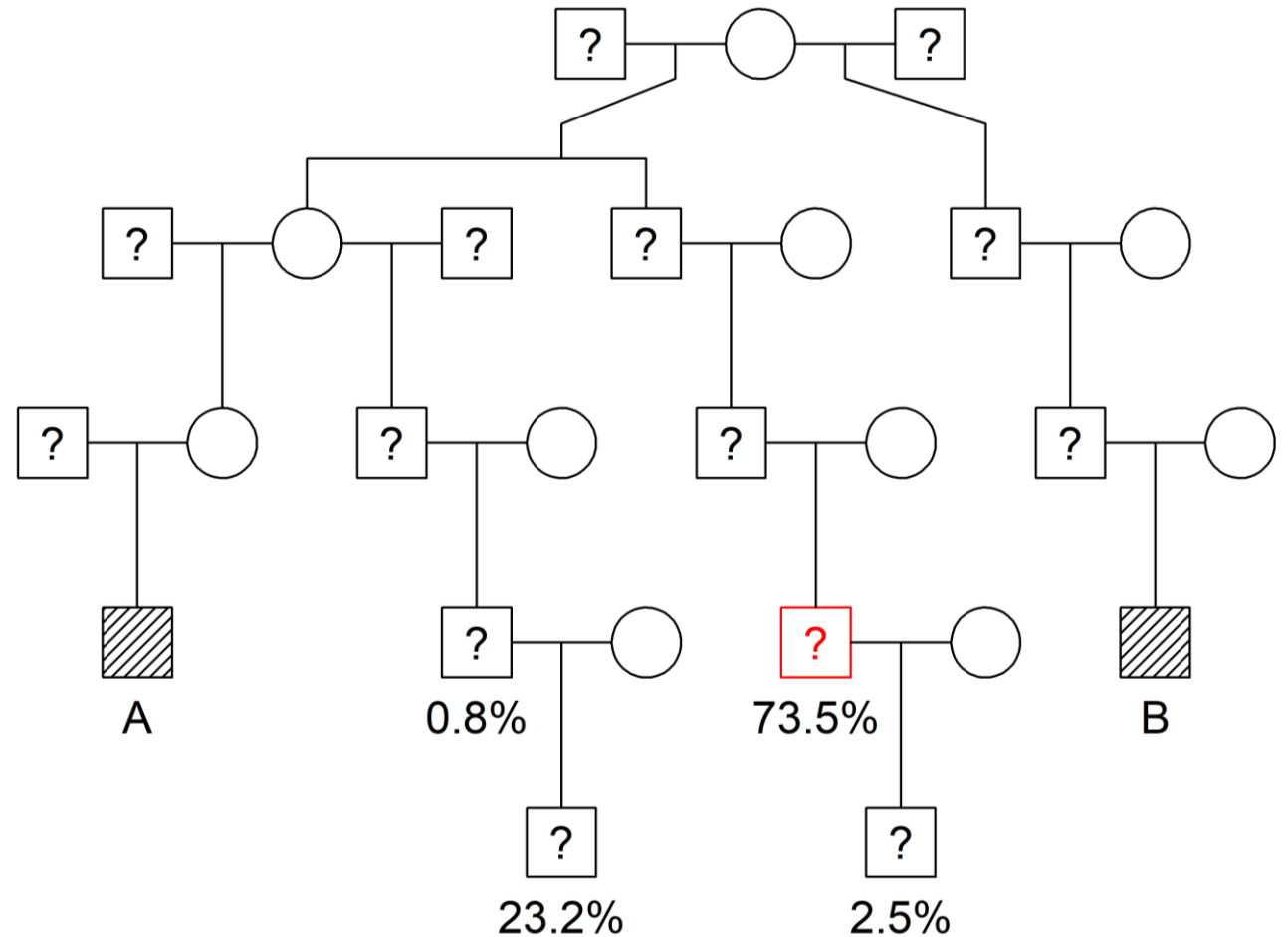
For triangulation: Joint estimation



Pair	Segments (cM)
X-A	10, 30.3, 7.4, 21.8, 10.7, 23.8, 11.3, 15.7, 45.7, 9.4
X-B	7.4, 15.7, 17.7, 20.5, 18.3, 11.1

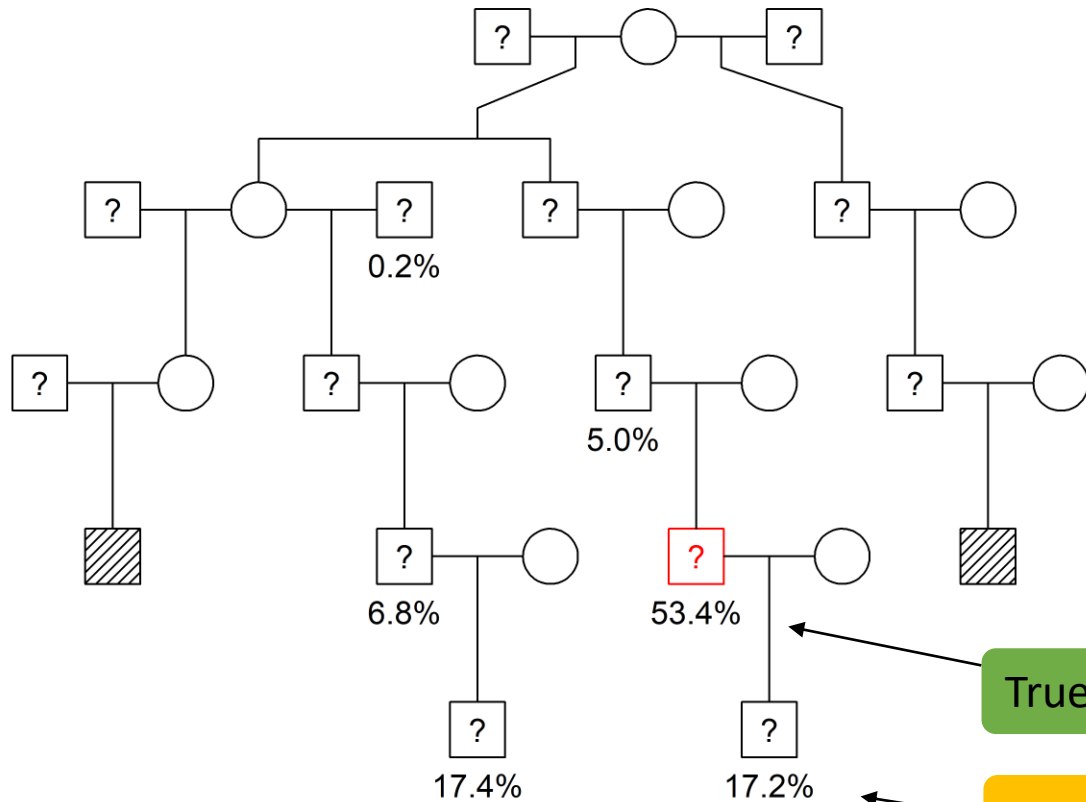
Procedure

- Simulate IBD patterns for the entire pedigree
- For each individual Y:
 - Shared segments A-Y and B-Y
 - Empirical distributions
 - Compare with observed data
 - **Posterior triangulation probability**

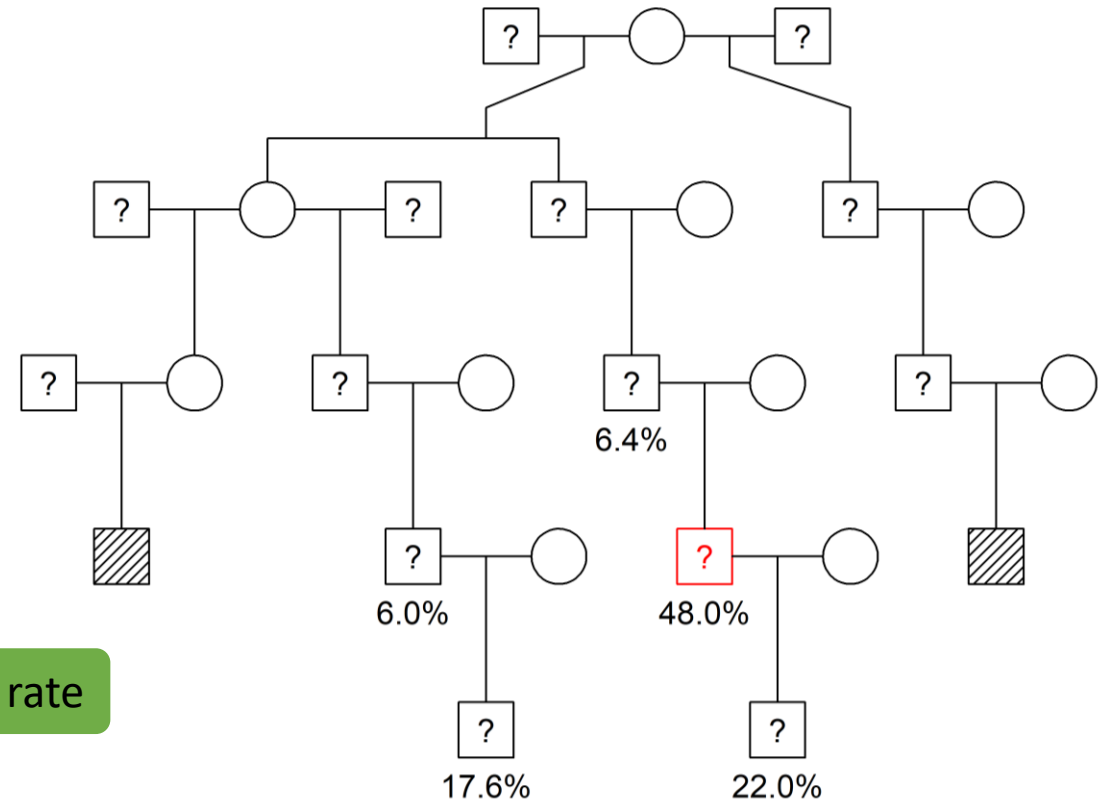


Triangulation power

(Cutoff: 0 cM. Training sims: 1000)



(Cutoff: 7 cM. Training sims: 1000)

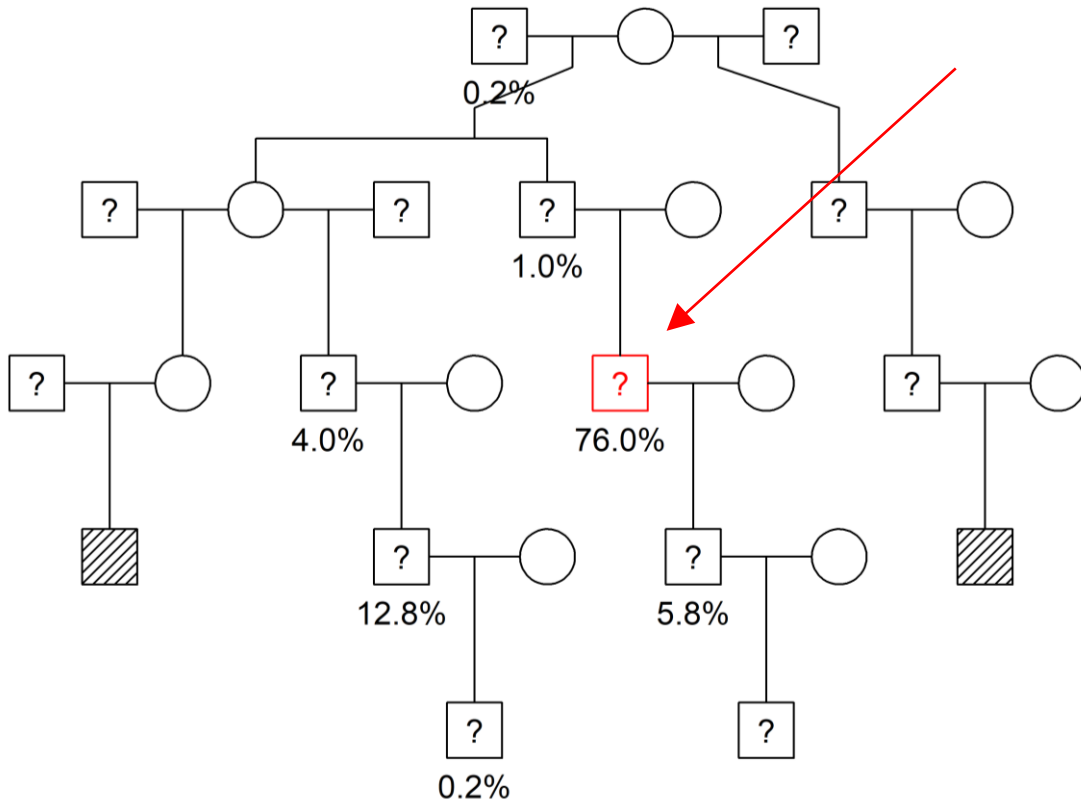


True positive rate

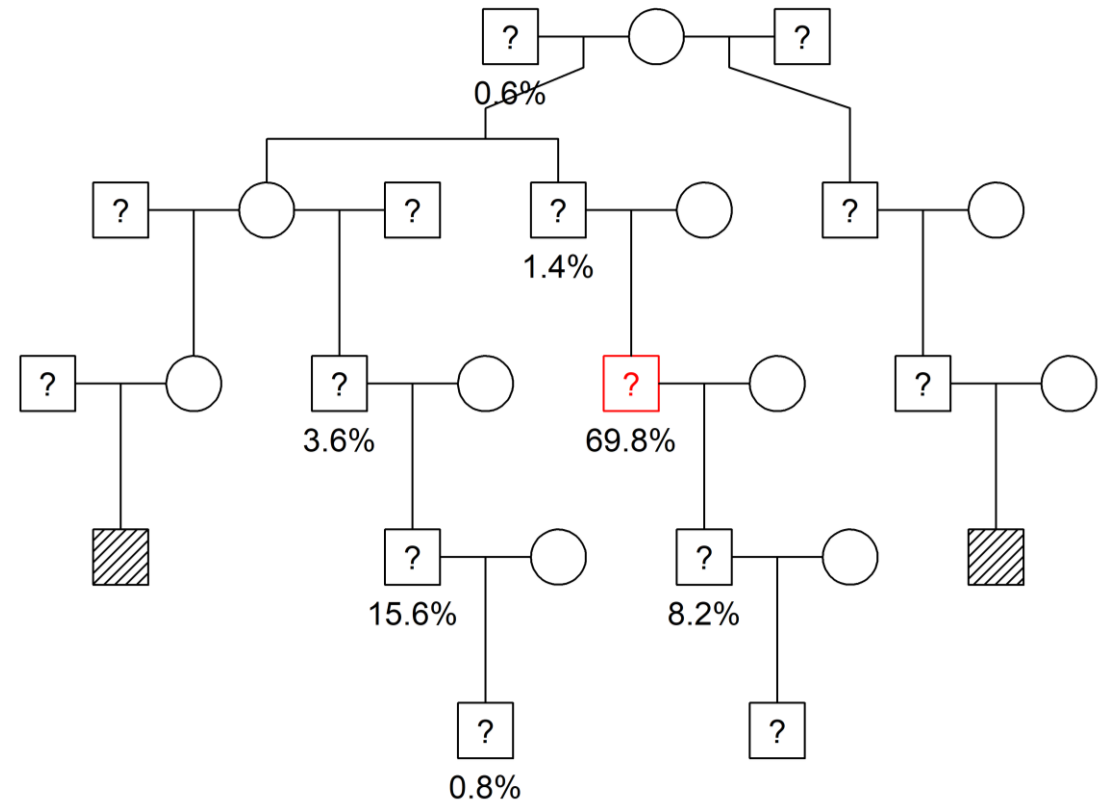
Error rate

Triangulation power - different Mr. X

(Cutoff: 0 cM. Training sims: 1000)

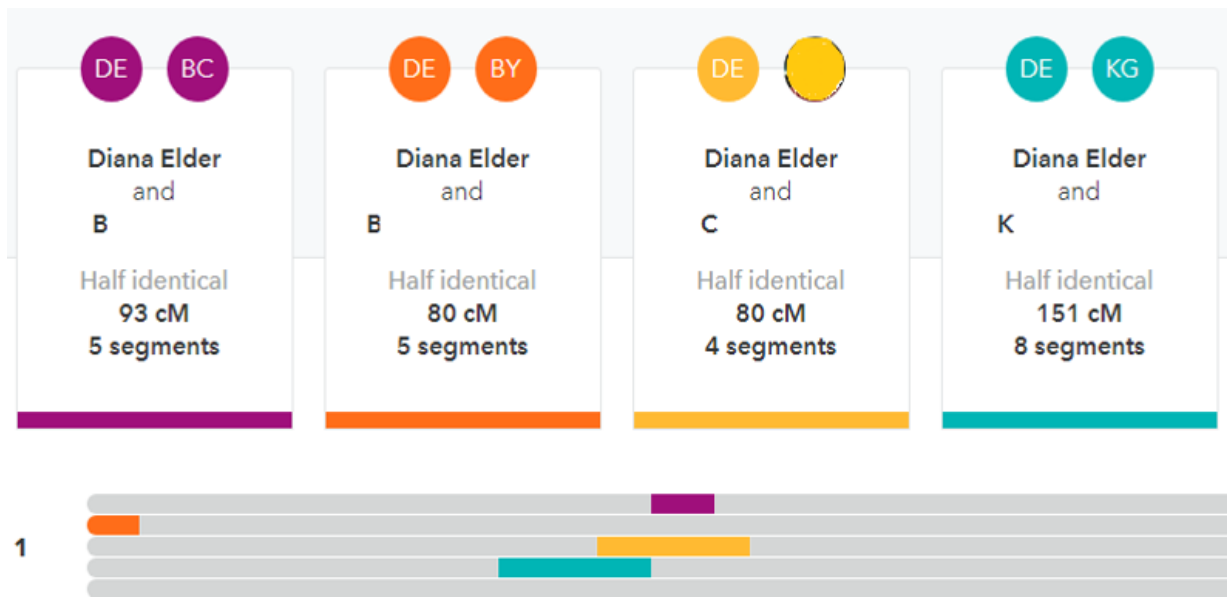


(Cutoff: 7 cM. Training sims: 1000)

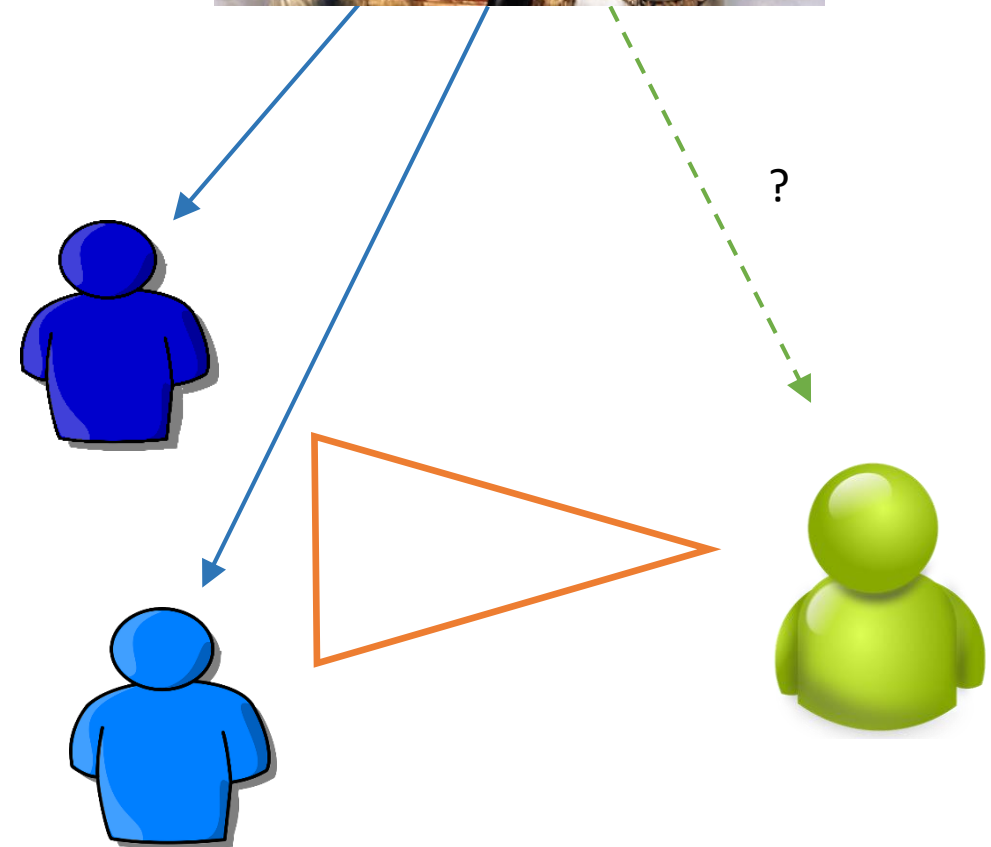


- Other meanings of triangulation in genealogy

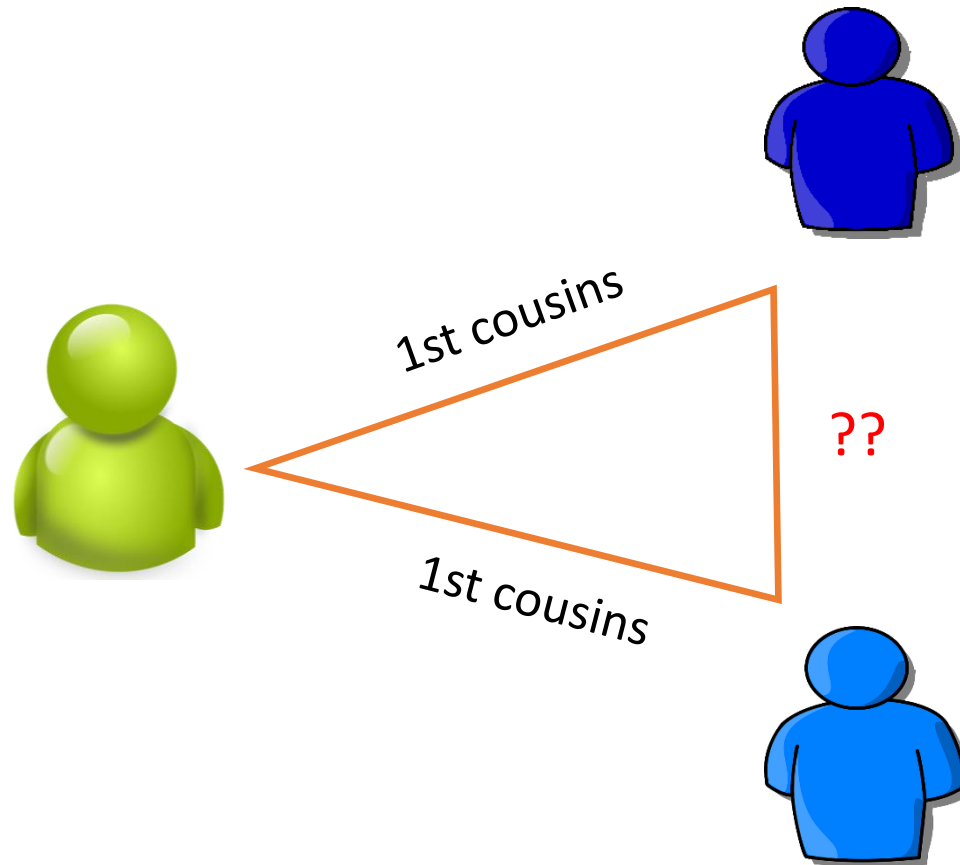
Triangulation 2: Support specific ancestor

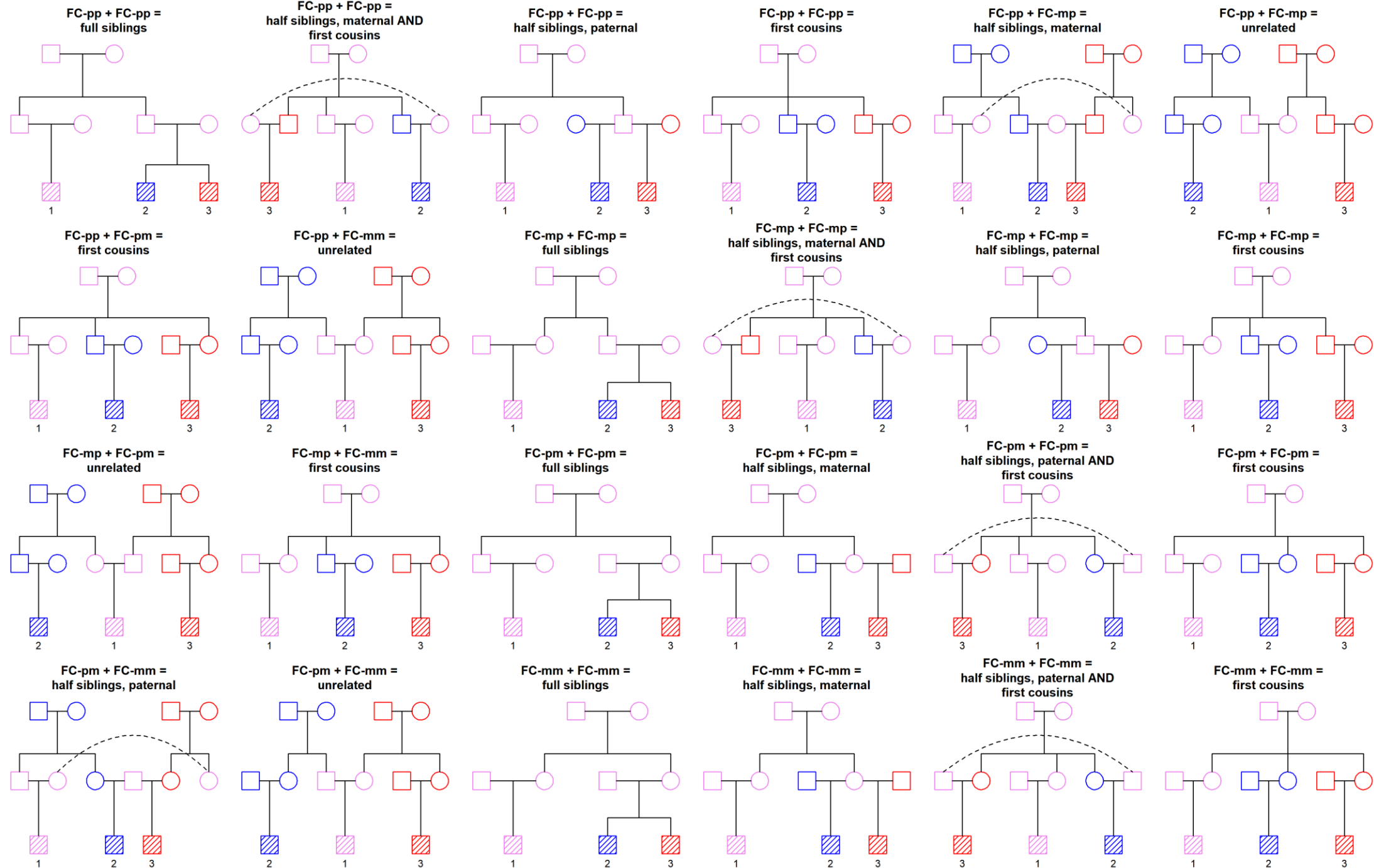


Requires overlapping segments between 3 or more individuals



Triangulation 3: What is the third relationship?





Now you should try
the exercises!