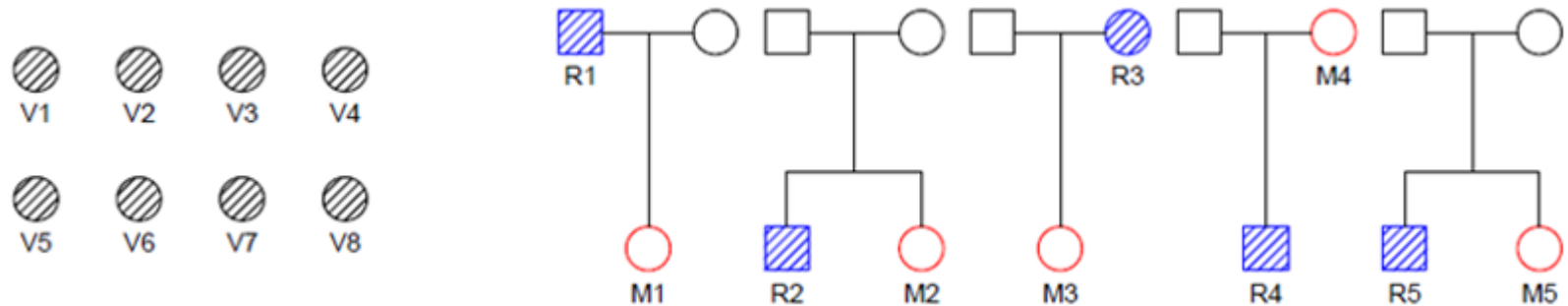+ **dvir**

# Lecture 4. Disaster victim identification

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Disaster Victim Identification (DVI)

- DVI
  - Match list of unidentified persons against a list of missing persons
  - Special case:
    - Missing Person Identification
- Cases
  - Missing grandchildren of Argentina
  - World Trade Center attack
  - Spitsbergen civil aircraft disaster
  - Balkan conflicts
  - Drowned immigrants
  - Thailand tsunami
- Methods and software
  - Exclusion and inclusion power
  - Treat *each* victim (PM approach) or *each* family (AM approach) at a time
  - Joint approach. GLR
    - library(dvir)
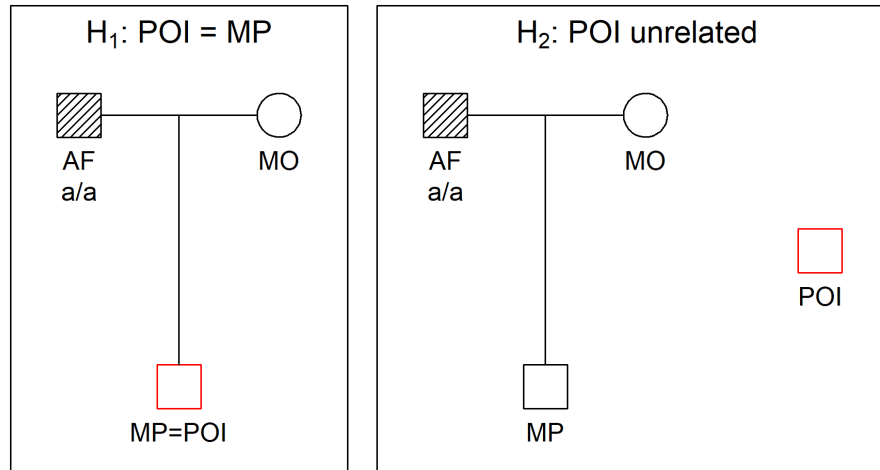 - DIVIANA (Magnus)
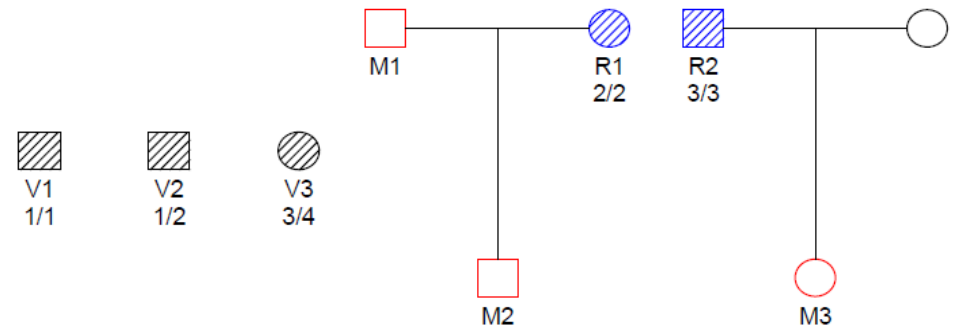
First: Missing Person Identification
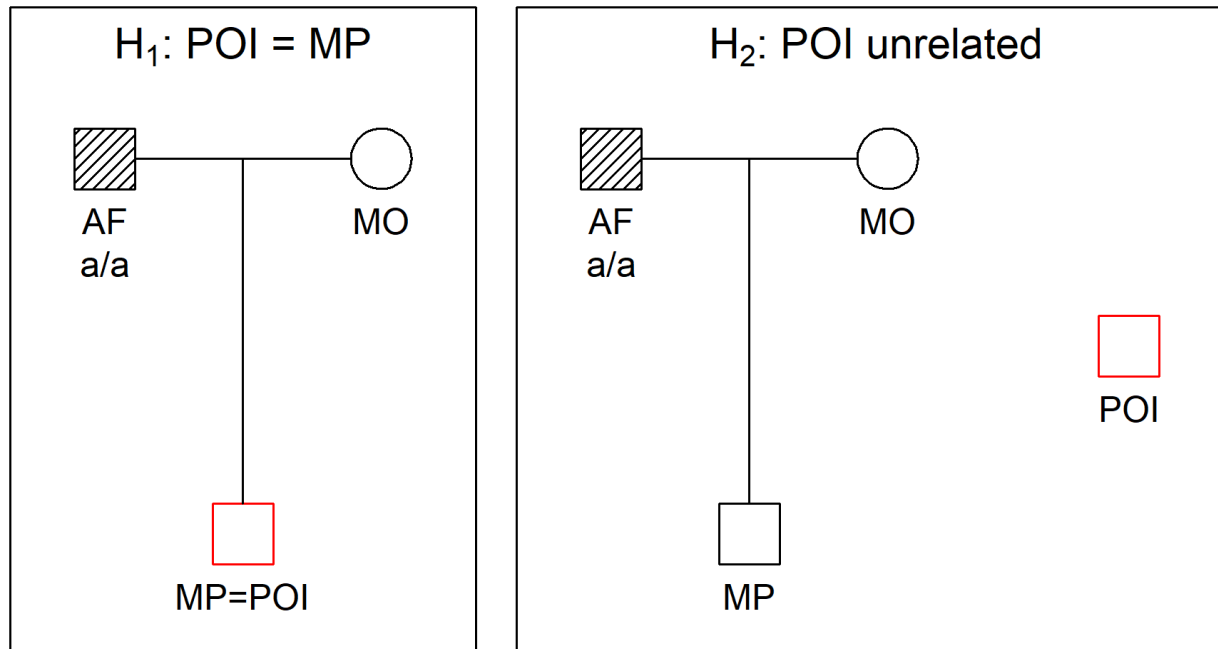
- Special case of DVI:
    - ✓ Only one *missing person* (MP) in each reference family
    - ✓ Possibly many reference families and many *persons of interest* (POIs)
    - ✓ Each case treated independently

Exclusion power

- Sufficient data to *exclude* an unrelated POI?
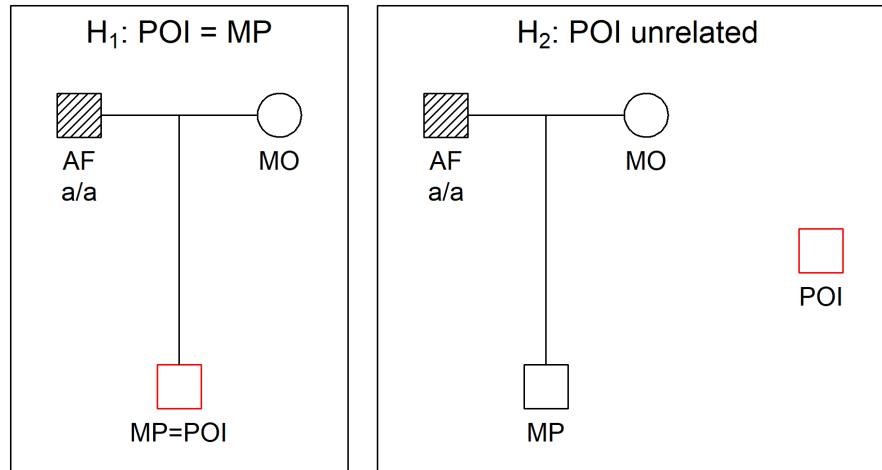
- **Exclusion power**

$$EP = P(\text{data incompat. with ped} \mid POI \text{ unrelated})$$

- Can be computed exactly
  (Egeland, Pinto, Vigeland, 2014).

In forrel:
> exclusionPower()
> missingPersonEP()

Inclusion power
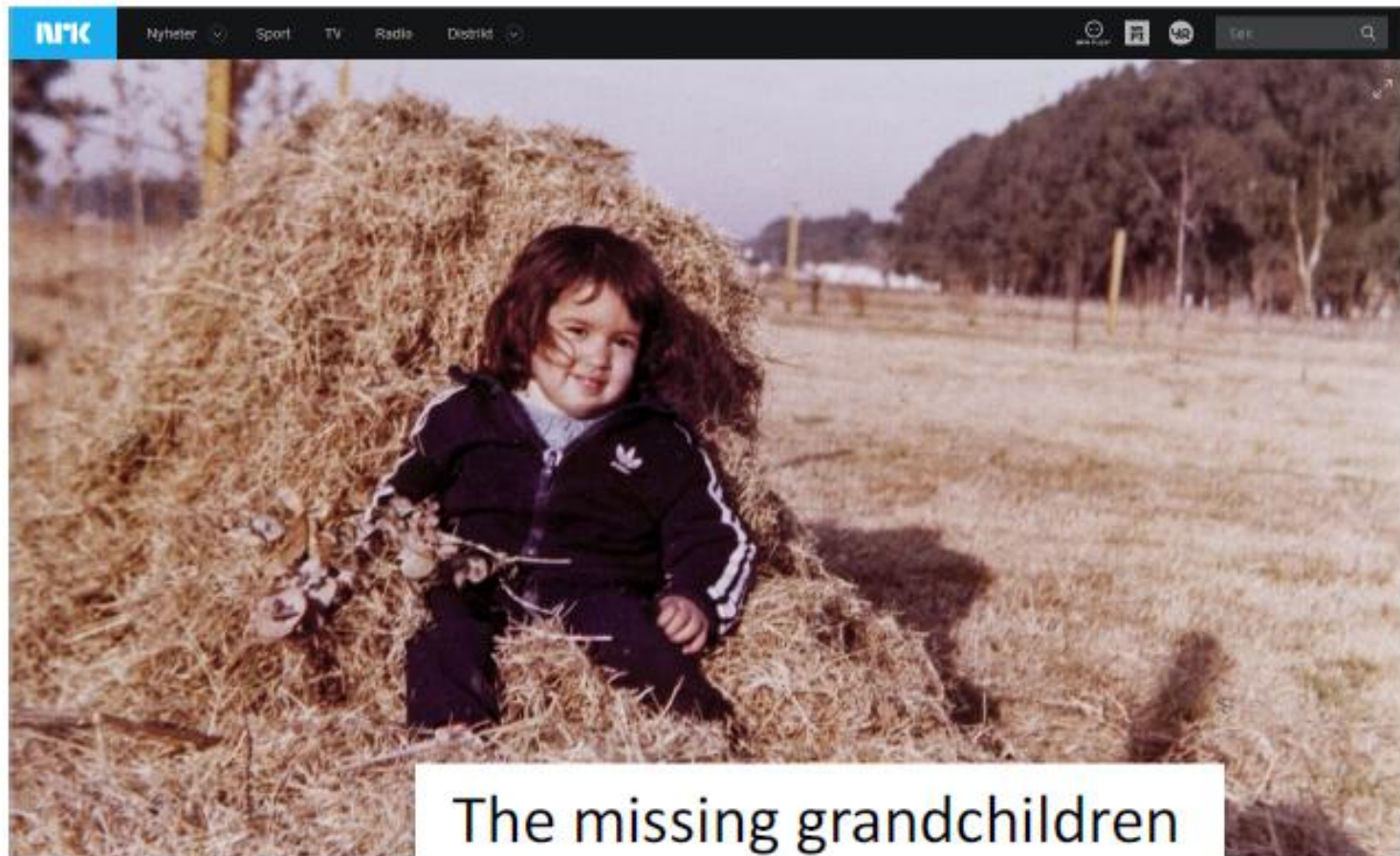

- Sufficient data to give a positive match if POI = MP?
- **Inclusion power** (or *exceedance probability*):

$$IP_{10000} = P(LR > 10000 \mid POI = MP)$$

- Can be computed by simulation!
  - Unconditional → <u>average</u> for all pedigrees of this type
  - Conditional → probability for <u>this particular case</u>

In forrel:
> missingPersonIP()

The missing grandchildren of Argentina

Argentina 1976 – 1983: Dirty War

- Military dictatorship
- *War* against guerrillas

- Opponents killed or disappeared

- *About 500 children abducted*
  - kidnapped with their parents or born in captivity
  - parents killed
  - raised by police or military families

History

- 1977: *Grandmothers of Plaza de Mayo*
  - weekly marches ever since
  - https://www.abuelas.org.ar

- 1983: Mary-Claire King, US geneticist
  - Collaboration with the Grandmothers
  - HLA typing + blood groups
  - First grandchild recovered using genetics

- 1987: National Genetic Data Bank (BNDG)

- 2007: Argentine Forensic Anthropology Team

- 2023: In total 132 reunifications by BNDG

Exclusion and inclusion

- POI1 = 12/12 is excluded if mutations are ignored since the alleles of his father are among 9/10/13
- POI2 is
  - ✓ not excluded
  - ✓ included if LR > 10000

Power analysis
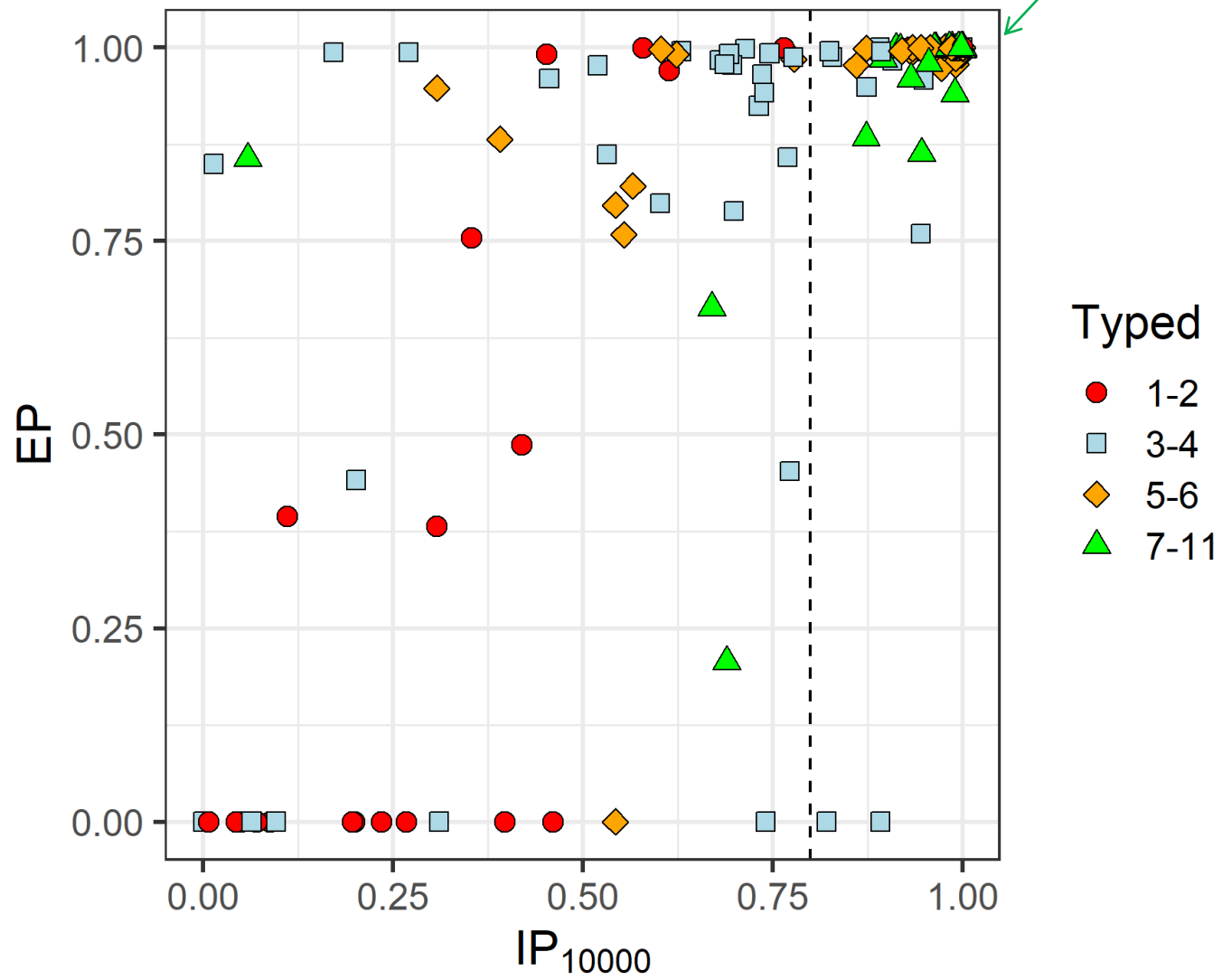
- Power evaluation of ~200 families in the BNDG database
  - most of them unsolved

Typed	Families	Parent(s) typed	2nd degree only
1	11	5	5
2	20	5	15
3	29	7	20
4	41	6	33
5	29	7	14
6	26	5	14
7	14	0	8
8	14	0	9
9	5	0	3
10+	7	0	5
Total	**196**	**35**	**126**

Missing	Total	mtDNA	Y
Male	27	27	25
Female	17	17	-
Unknown	152	142	108
Total	**196**	**186**	**133**

- For each family: Compute IP_{10000} and EP
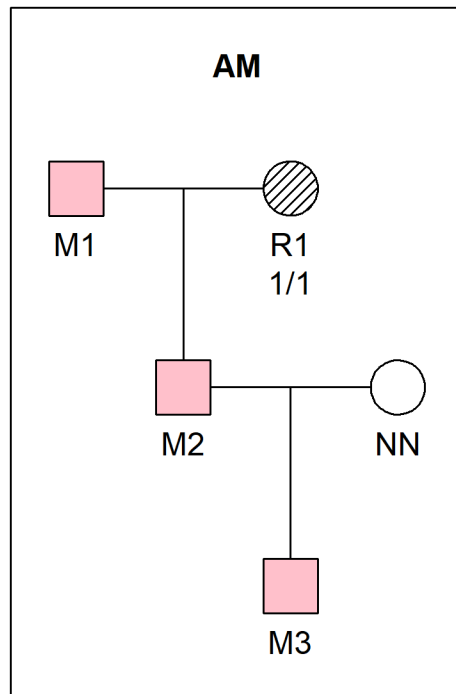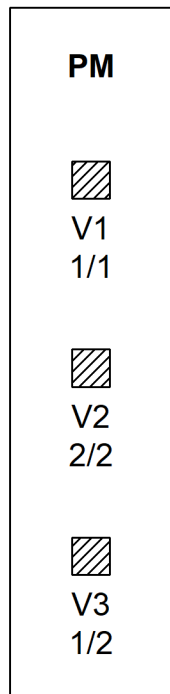
Disaster victim identification (DVI)
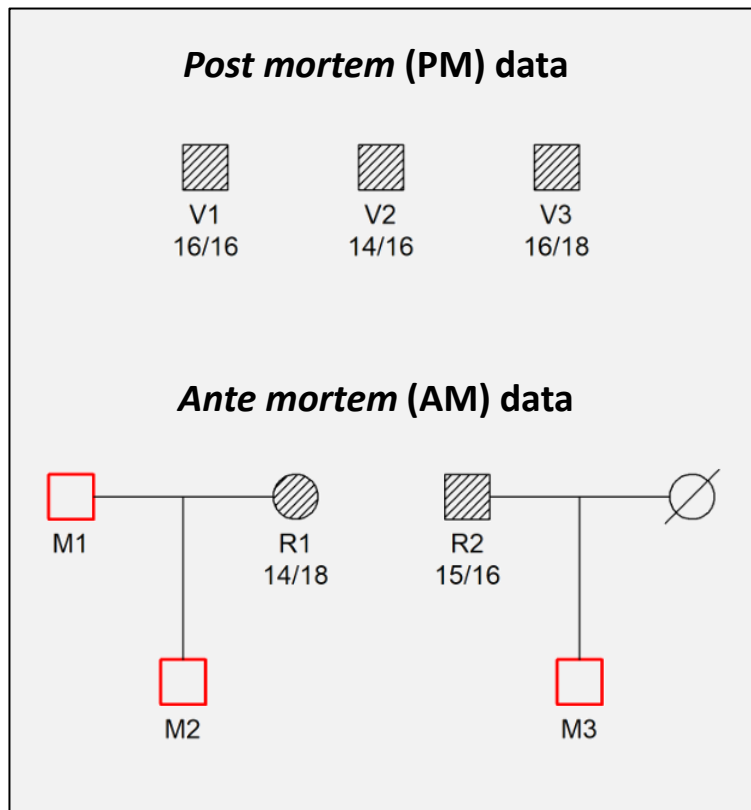
Initial steps

- Merge identical samples
- Direct matching
- Remove non-identifiable
- Exclude

- Pairwise LR. H_1: Vi = Mj vs. H_2: unrelated

$$\begin{array}{c} & M1 & M2 & M3 \\ V1 \\ V2 \\ V3 \end{array} \begin{bmatrix} 1 & 0 & 0.39 \\ 1 & 16142 & 0 \\ 1 & 0 & 6266 \end{bmatrix}$$

Challenge: Sometimes pairwise fails

PM

V1
1/1

V2
2/2

V3
1/2

AM

M1   R1
      1/1

M2   NN

M3

	M1	M2	M3
V1	1	20	10.5
V2	1	0	0.5
V3	1	10	5.5

Pairwise LRs indicate V1 = M2, but

- **V1 = M2 is impossible
  if V2 is among the missing**
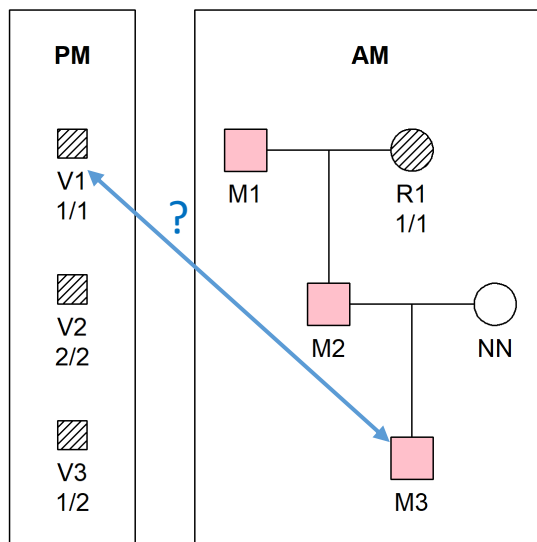
Joint solution

Joint likelihoods, sorted
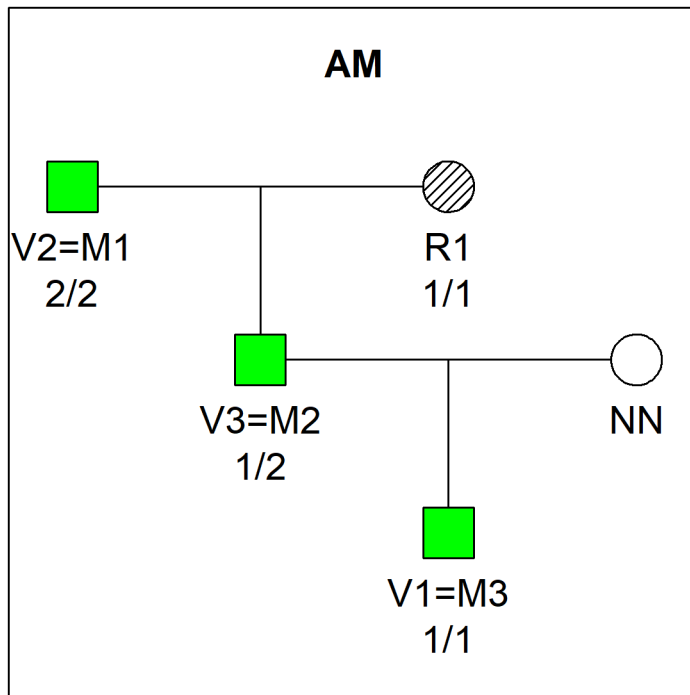
	V1	V2	V3	loglik	LR
1	M3	M1	M2	-15.67181	2000.0
2	M2	*	M1	-17.97439	200.0
3	M2	*	M3	-17.97439	200.0
4	*	M1	M2	-17.97439	200.0
5	M3	*	M2	-18.66754	100.0
	...	...	...	...	...
6	*	M3	M2	-18.66754	100.0
	...	...	...	...	...
19	*	*	*	-23.27271	1.0
	...	...	...	...	...
34	*	M3	*	-Inf	0.0

AM

V2=M1
2/2

R1
1/1

V3=M2
1/2

NN

V1=M3
1/1

- Two problems:
  - ✓ LR uses V1 = '*', V2 = '*', V3 = '*' as comparison
  - ✓ How do we test e.g. H_1: V1 = M3 vs. H_2: V1 = '*'?

A tool for interpreting joint results:
Generalised likelihood ratio (GLR)

$$\text{GLR} = \frac{\max_{i \in H_1} L_i}{\max_{j \in H_2} L_j}$$

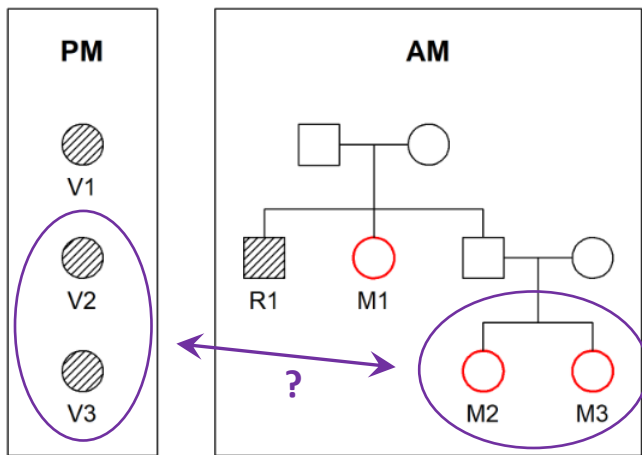|	V1	V2	V3	loglik	LR
1	M3	M1	M2	-15.67181	2000.0
2	M2	*	M1	-17.97439	200.0
3	M2	*	M3	-17.97439	200.0
4	*	M1	M2	-17.97439	200.0
5	M3	*	M2	-18.66754	100.0
	...	...	...	...	...
6	*	M3	M2	-18.66754	100.0
	...	...	...	...	...
19	*	*	*	-23.27271	1.0
	...	...	...	...	...
34	*	M3	*	-Inf	0.0

$$\text{GLR} = \frac{LR_1}{LR_2} = \frac{2000}{200} = 10$$

Interpretation of $GLR = x$

$$\text{GLR} = \frac{\max_{i \in H_1} L_i}{\max_{j \in H_2} L_j}$$

The best explanation of the data given H1

is x times more likely

than the best explanation given H2

Symmetric matches

Question 2:

{V1, V2} = {M2, M3} ?

Joint likelihoods

	V1	V2	V3	loglik	
1	M1	M2	M3	-257.7	✓
2	M1	M3	M2	-257.7	✓
3	*	M2	M3	-268.9	✓
4	*	M3	M2	-268.9	✓
5	M2	M1	M3	-272.6	✗
6	M3	M1	M2	-272.6	✗
7	M1	*	M2	-276.5	✗
8	M1	*	M3	-276.5	✗
9	M2	M3	M1	-276.6	✗
⋮					
32	*	*	*	-286.0	✗
33	*	M1	*	-286.5	✗
34	*	*	M1	-292.2	✗

Strong evidence

$$\text{GLR} = \frac{L_1}{L_5} = 2.9 \times 10^6$$

Potential problem: Related victims

- Assume V1 and V2 are related, e.g. father son, but not related to R1

- Then {V1, V2} may be wrongly identified as {M1, M2} if family F2 is not included

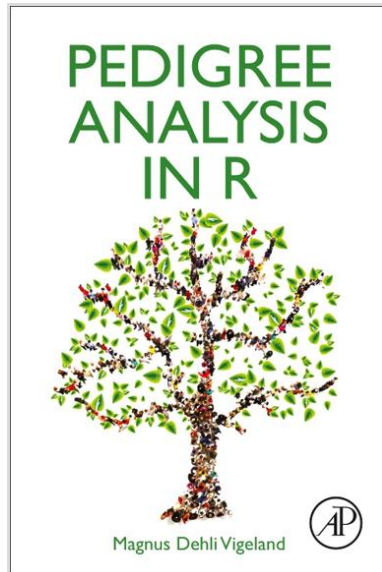| V1	V2	LR	posterior	LR0
M1*	M2*	4.77E+16	5.00E-01	4.77E+16
M2*	M1*	4.77E+16	5.00E-01	4.77E+16
M1	M2	4.14E+09	4.33E-08	4.77E+16
M2	M1	2.12E+04	2.23E-13	4.77E+16
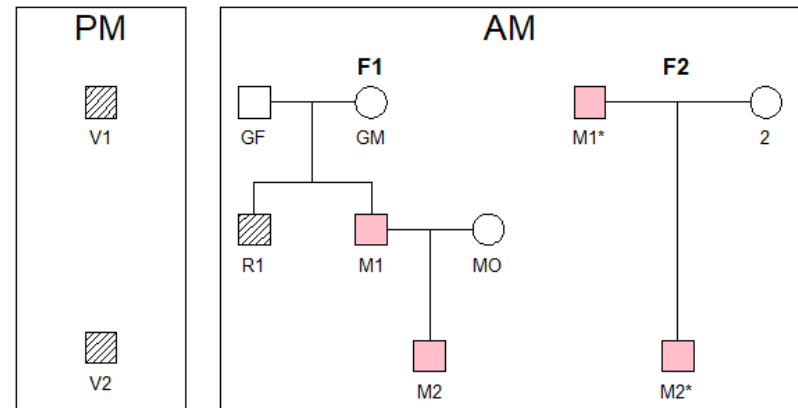
- Column LR0: Genotypes of references removed before calculation: need not include F2

Discussion

- ## What should be reported?
  - LR, GLR, and, or posterior?
  - Thresholds?
  - Verbal scales?

Biased selection of references
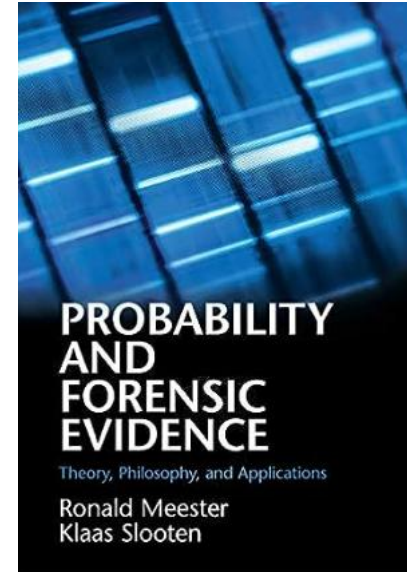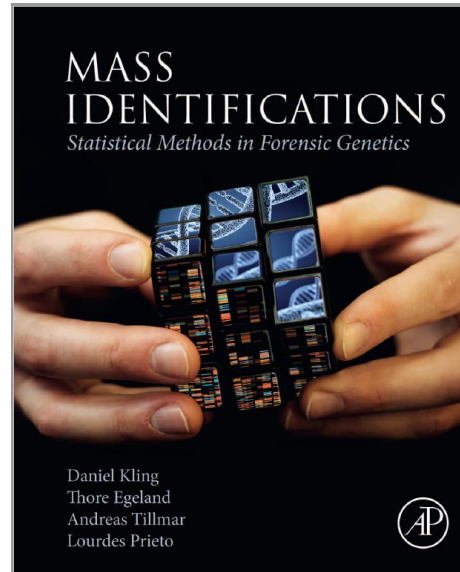
Kinship cases with partially specified hypotheses

Thore Egeland [a,b], Magnus Dehli Vigeland [a]

Forensic Science International: Genetics

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