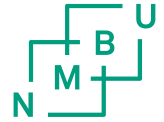


# Repetition: Relationship estimation

Thore Egeland

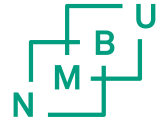
Copenhagen May 20-23 2014



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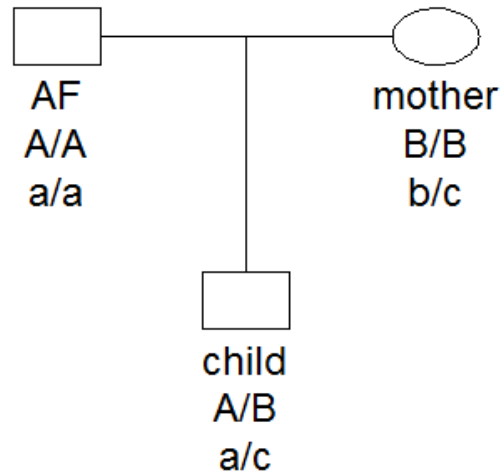
- Standard paternity case
- Complications
- Exercises. Familias 3

# Exercise S1. Standard paternity case

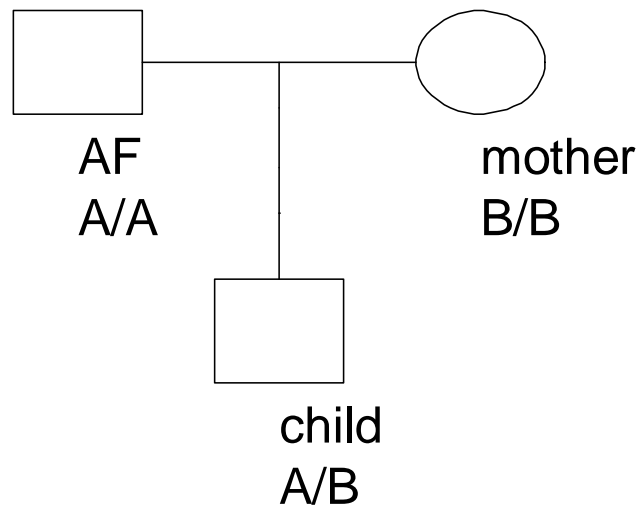


- $H_1$ : The alleged father (AF) is the real father
- $H_2$ : AF and the child are unrelated.

**Figure1. Standard paternity case.**



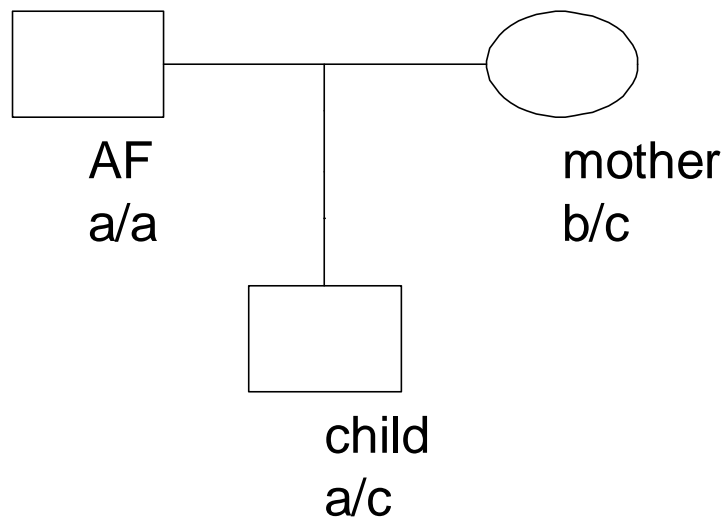
## Standard paternity



$$\begin{aligned}
 LR &= \frac{\text{probability of data given } AF \text{ father}}{\text{probability of data given } AF \text{ unrelated}} \\
 &= \frac{P(\text{child} \mid \text{mother}, AF)}{P(\text{child} \mid \text{mother})} = \frac{1}{p_A} = \frac{1}{0.05} = 20.
 \end{aligned}$$

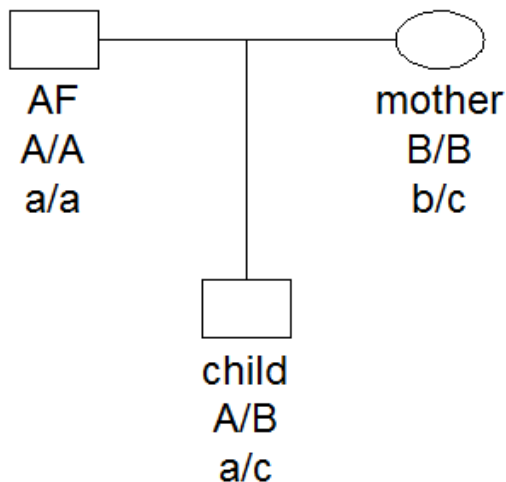
- Interpretation: The data is 20 times more likely assuming AF to be the father compared to the alternative that some unknown man is the father.

## Standard paternity c



$$LR = \frac{P(\text{child} \mid \text{mother}, \text{AF})}{P(\text{child} \mid \text{mother})} = \frac{0.5}{0.5 p_a} = \frac{0.5}{0.5 * 0.1} = 10.$$

**Figure1. Standard paternity case.**



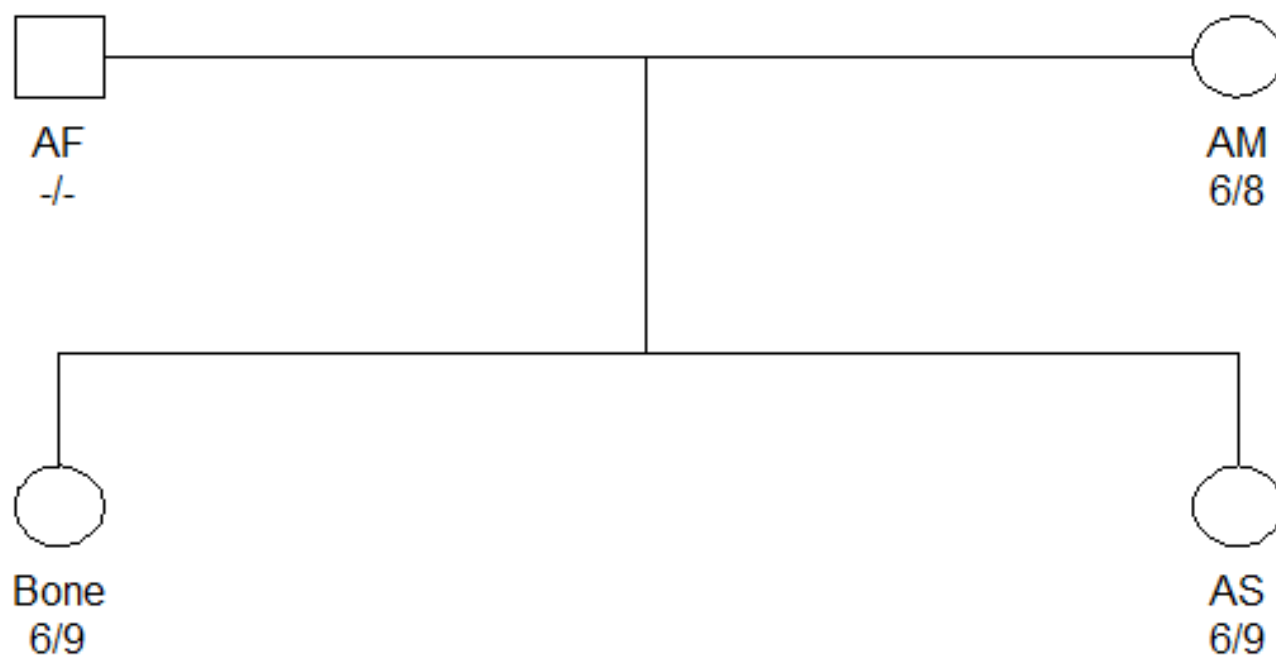
$$LR = 20 * 10 = 200.$$

- Interpretation: The data is 200 times more likely assuming AF to be the father compared to the alternative that some unknown man is the father”.

### Exercise S3 Cap paper challenge (“bone”)

- $H_1$ : The individual providing the bone is the daughter of AM and sister of AS.
- $H_2$ : The individual providing the bone is not related to the tested individuals (AM,AS) of Figure 3

**Figure 3. CAP paper challenge. Marker F13B.  
Frequencies: 6:0.086, 8:0.152, 9:0.328, rest:0.434**



# Full sibs

# Half sibs

Pedigree Name: AS and Bone Full sibs

Parent	Child
AF	Bone
AF	AS
AM	Bone
AM	AS

Buttons: OK, Persons, Remove

Add Parent:  Child:  Add

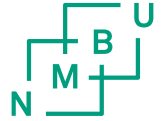
Pedigree Name: AS and Bone Half sibs

Parent	Child
AM	Bone
AM	AS

Buttons: OK, Persons, Remove

Add Parent:  Child:  Add

The father AF is not typed but included in the full sibs alternative to the left to define Bone and AS to be full sisters.



# Complications

- Non-standard cases.
  - Complications:
    1. Complex pedigrees
    2. Theta-correction
    3. Mutations
    4. Silent alleles
    5. Drop-out