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## **Brucellosis dynamics in Alpine ibex: all caused by females?**

Sébastien Lambert, Emmanuelle Gilot-Fromont, Carole Toïgo, Pascal Marchand, Clément Calenge, Elodie Petit, Jean-Pierre Ganière, Bruno Garin-Bastuji, Dominique Gauthier, Jean-Michel Gaillard, et al.

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## Context

- *Brucella melitensis* infection in the Barge Massif
  - ✓ France officially free of brucellosis since 2003
  - ✓ Two human cases in 2012 related to dairy cattle
  - ✓ High seroprevalence in the ibex population, a protected species
  - ✓ Probable spill-back from Alpine ibex to cattle
- 1<sup>st</sup> case of maintenance in wild ruminants in Europe
- Concerns in **public health**, in **veterinary health**, and in **wildlife conservation**

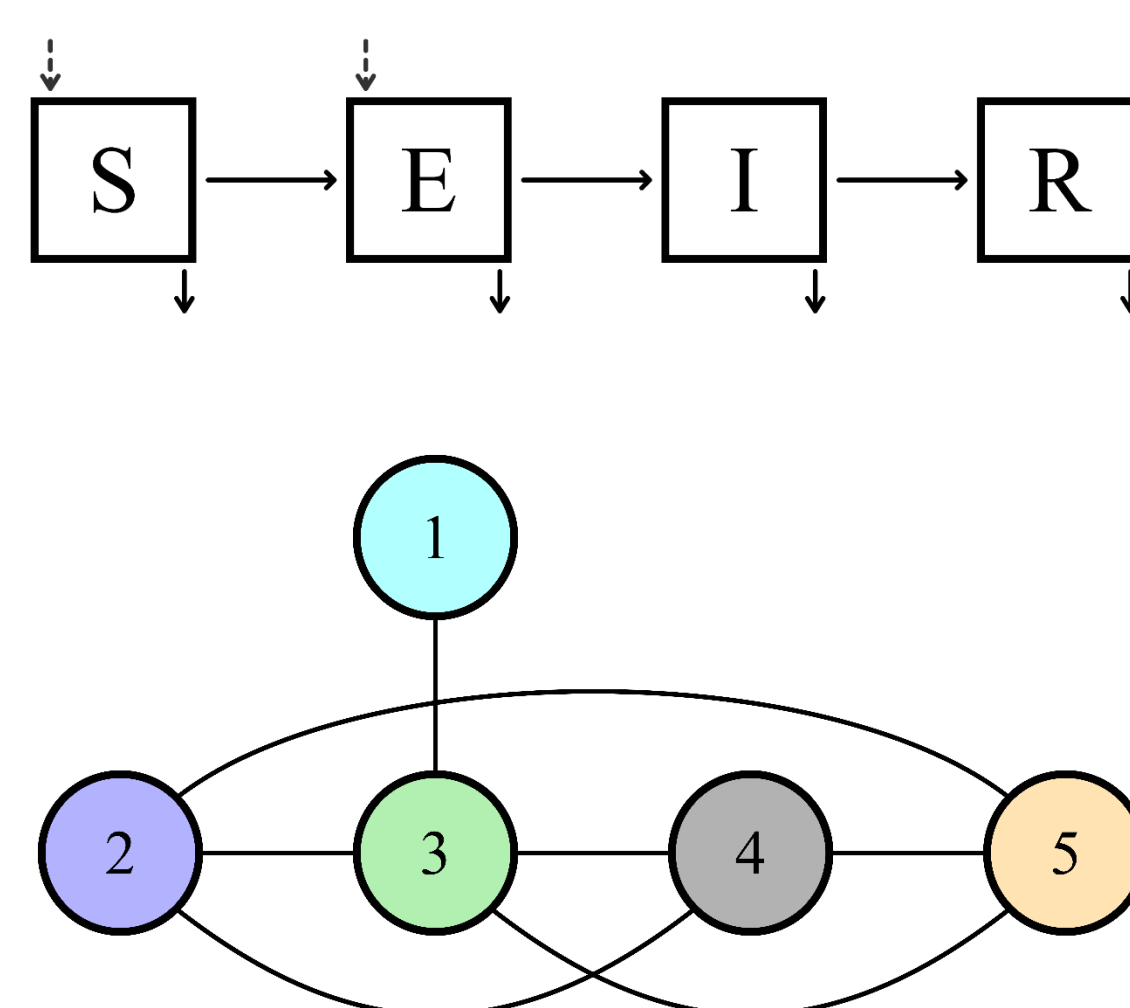


## Issues

- Several transmission routes <sup>1</sup>
  - **Issue #1**: quantification of transmission routes?
- Heterogeneity in pathogen transmission
  - ✓ Better target individuals most responsible for transmission <sup>2,3</sup>
  - ✓ Males play a critical role in other wildlife diseases of mammals (body size, home ranges) <sup>4</sup>
- **Issue #2**: quantification of transmission heterogeneity between genders

## Main features

- Two main transmission routes
  - ✓ ♂/♀ **Venereal** during mating (winter)
  - ✓ ♀ **Indirect** (abortions: spring / births: summer)
- Mating behaviour <sup>5</sup>
  - ✓ ♂ can access several ♀
  - ✓ ♀ accept only one ♂
- Social behaviour
  - ✓ Spring-summer: contacts ♀ – ♀  $\gg$  ♀ – ♂ <sup>6</sup>
  - ✓ 5 socio-spatial units: only ♂ move (mating ++) <sup>7</sup>



## Model formulation

- Individual-based model
  - ✓ Each individual followed from birth to death
  - ✓ Susceptible → Pre-infectious → Infectious → Non-infectious
  - ✓ Transmission parameter for each transmission routes (epidemiological data)
- Metapopulation model
  - ✓ Within-unit contacts only
  - ✓ Between-units explicit movements of ♂ (GPS data)

## Within-unit transmission

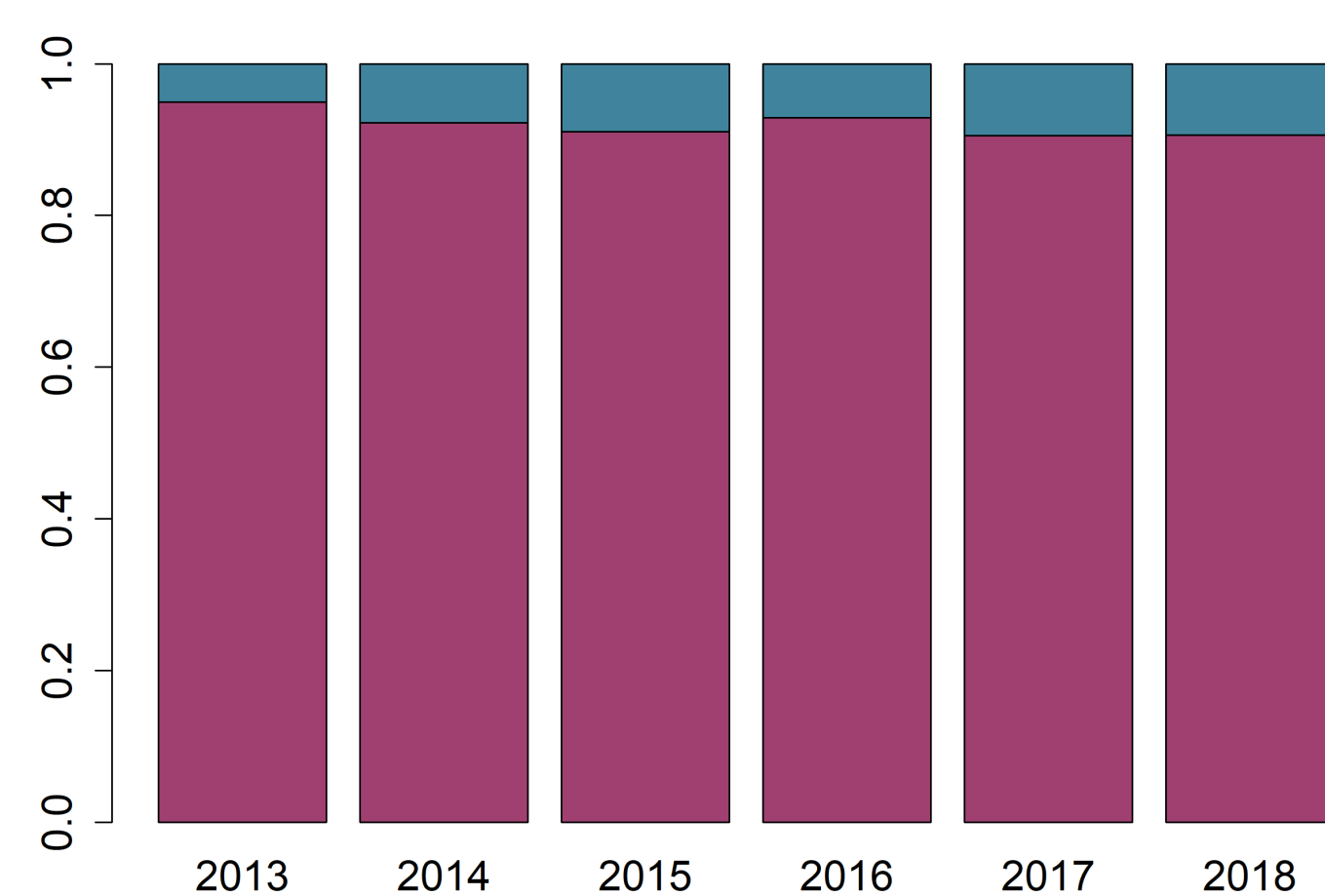
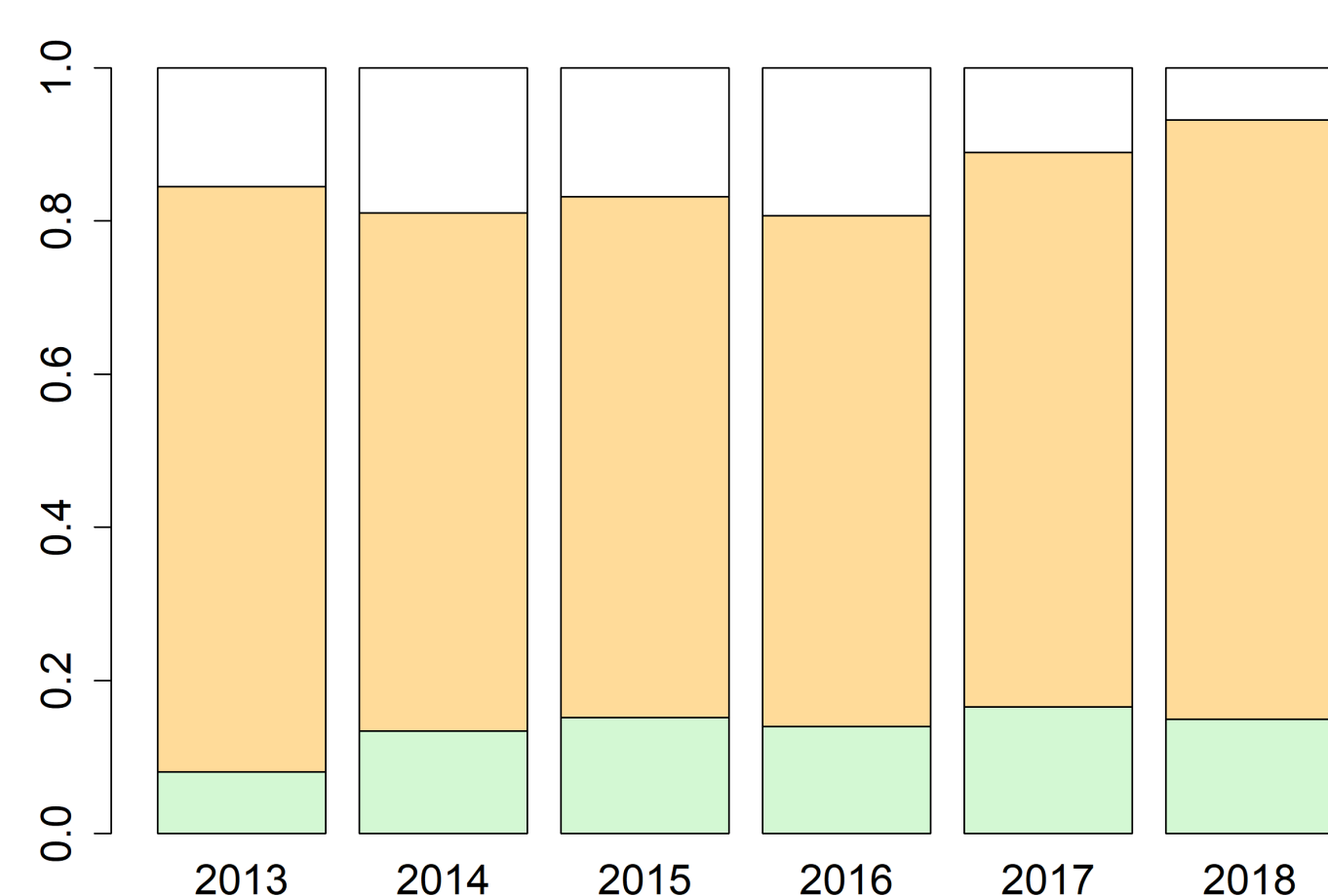
- **Hypotheses**: maintenance of the infection by ♀
  - ✓ Prediction issue #1: **indirect**  $\gg$  **venereal**
  - ✓ Prediction issue #2: transmission from ♀  $\gg$  ♂



- **Results**:
  - ✓ Within-unit:  $\geq 95\%$  of transmission

✓ Issue #1

✓ Issue #2

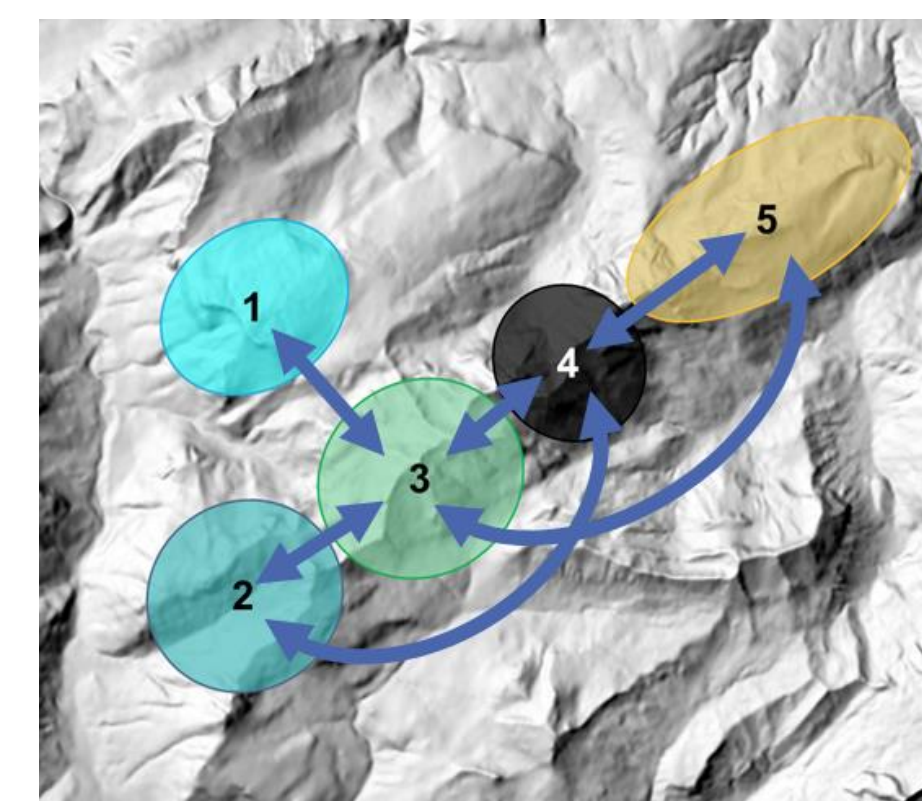


✓ OK with prediction

✓ OK with prediction

## Between-units transmission

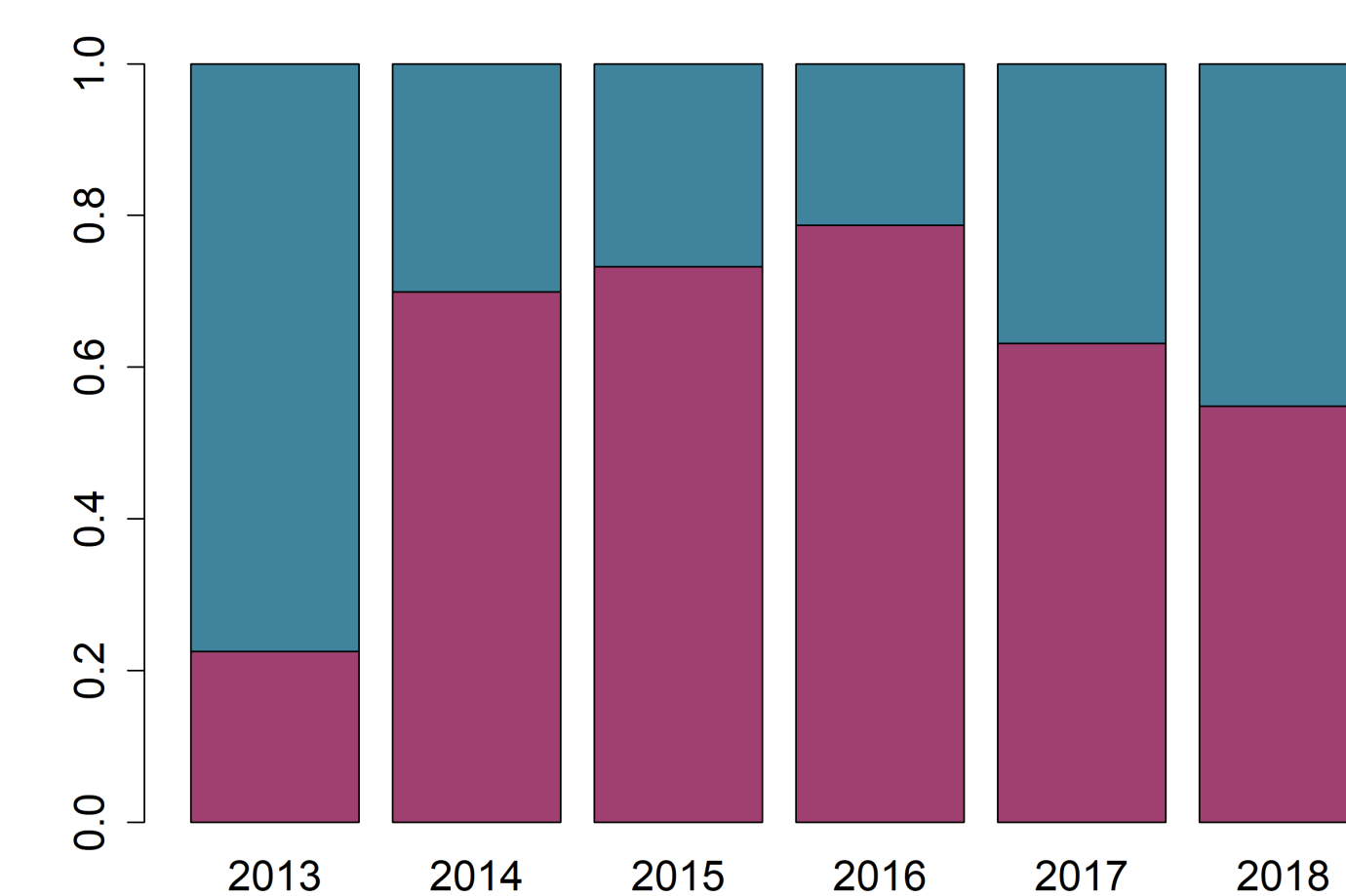
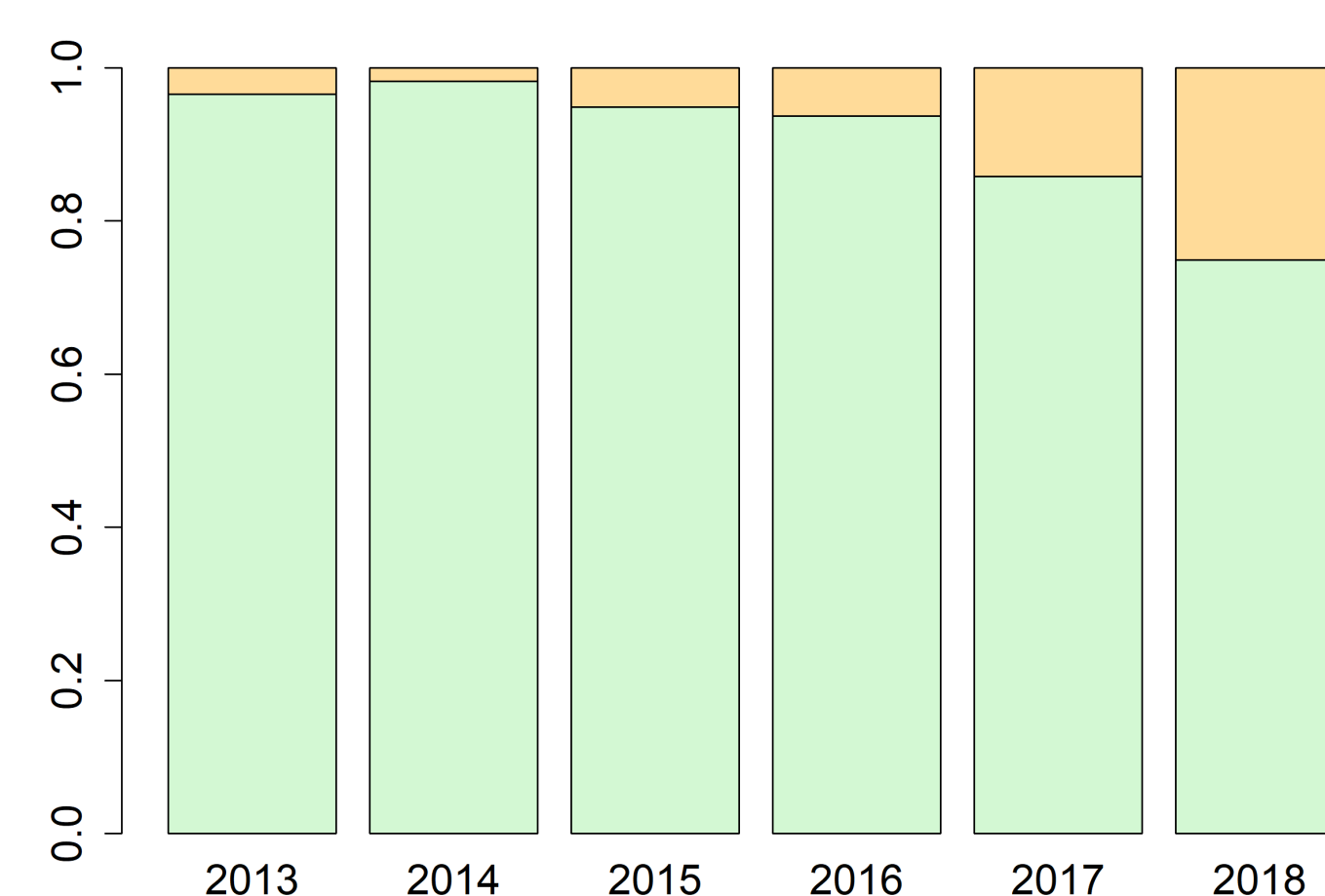
- **Hypotheses**: spread of the infection by ♂
  - ✓ Prediction issue #1: **venereal**  $\gg$  **indirect**
  - ✓ Prediction issue #2: transmission from ♂  $\gg$  ♀



- **Results**:
  - ✓ Between-units:  $\leq 5\%$  of transmission

✓ Issue #1

✓ Issue #2

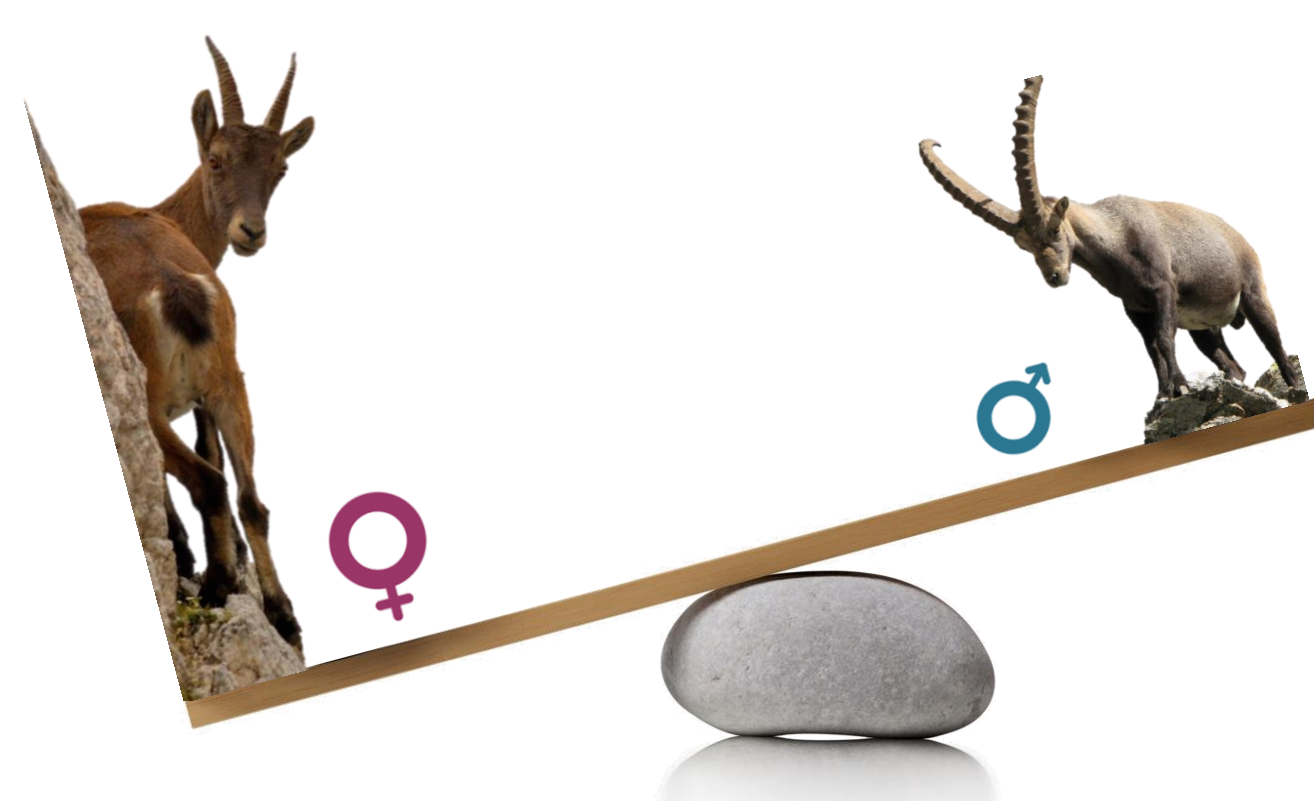


✓ OK with prediction

✗ Not OK with prediction

## Conclusion

- **Issue #1**: critical role of **indirect** transmission
- **Issue #2**:
  - ✓ Main source of transmission: ♀
  - ✓ ♂ get infected from ♀ of other units more than transmit infection to them
- Target disease management towards ♀



## Perspectives

- Quantification of heterogeneity ...
  - ✓ ... between age classes
  - ✓ ... between units
- Design and modelling of disease management strategies

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