

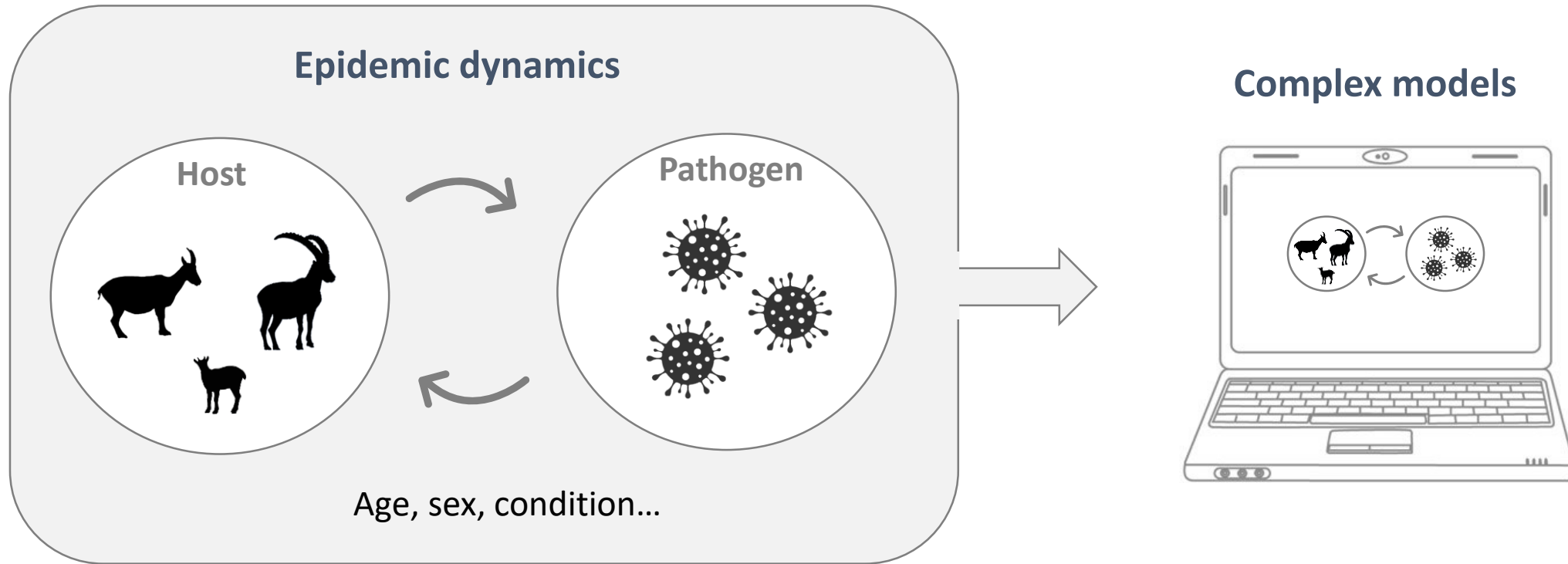
# Methodological challenges in estimating brucellosis transmission risk in an Alpine ibex population using Approximate Bayesian Computation

**Rémi Fay**, Sébastien Lambert, Anne Thébault, Pascal Marchand, Ariane Payne, Elodie Petit, Carole Toïgo, Emmanuelle Gilot-Fromont

ModAH conference - 28.08.2024

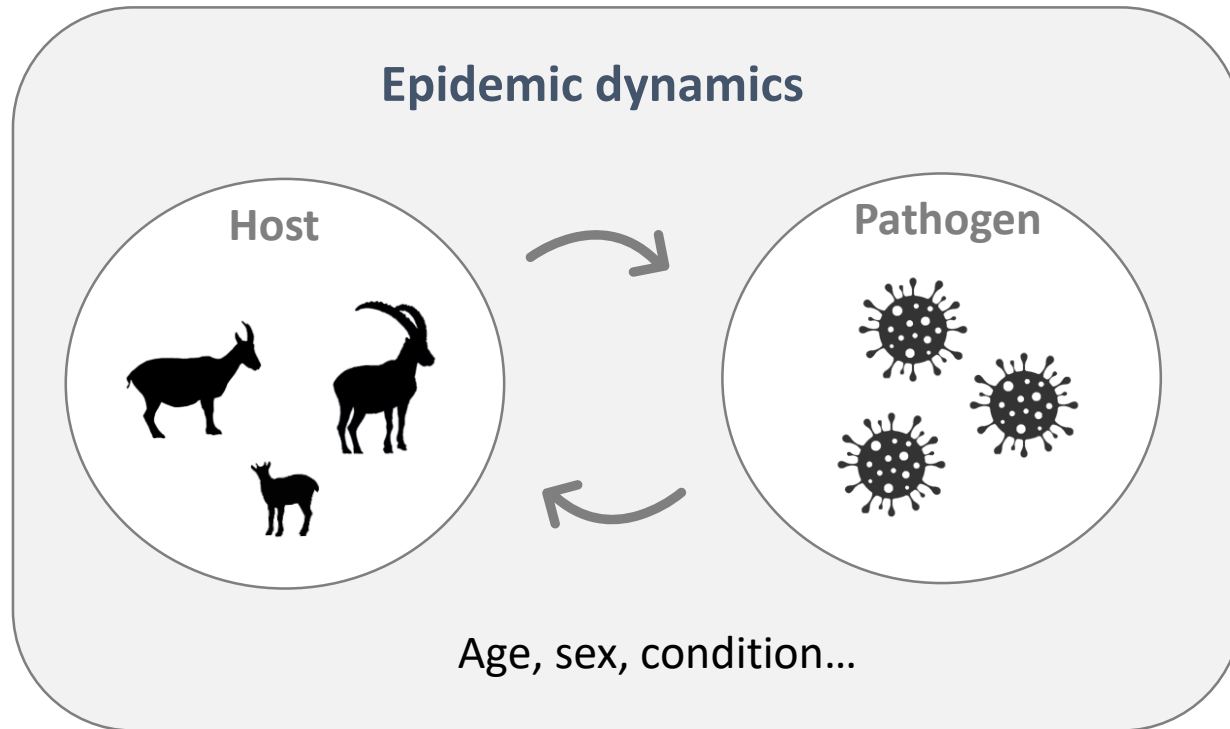


# Introduction

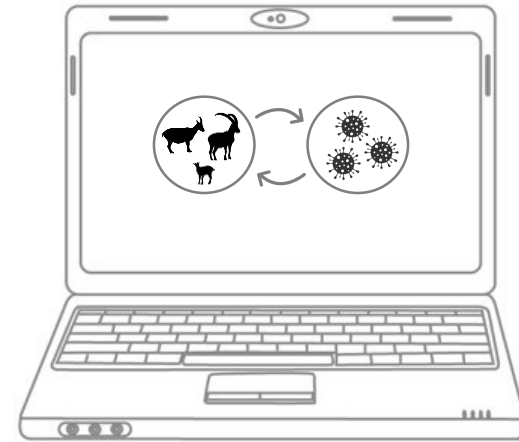




# Introduction



## Complex models



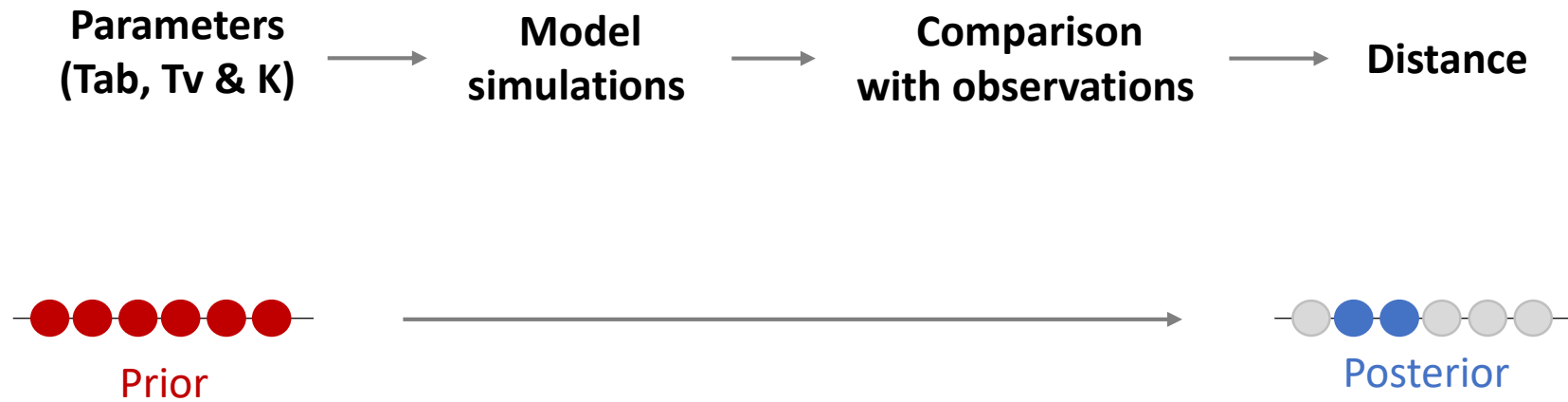
**Parameters**  
e.g. transmission rate





# Introduction

ABC method (Approximate Bayesian Computation)



Easy at first sight but could be complex in practice ...



# Study case

## Brucellosis epidemic (2012-2024)



Bacterial disease



Reservoir

Seroprevalence  
40%

### Two transmission pathways

Infectious Abortion & Birth  
→ horizontal + vertical transmissions

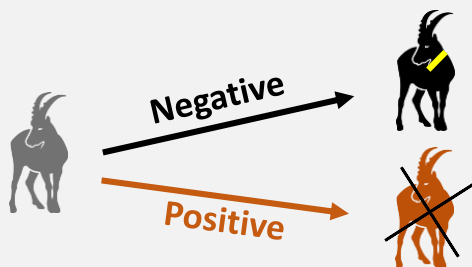
Venerian transmission



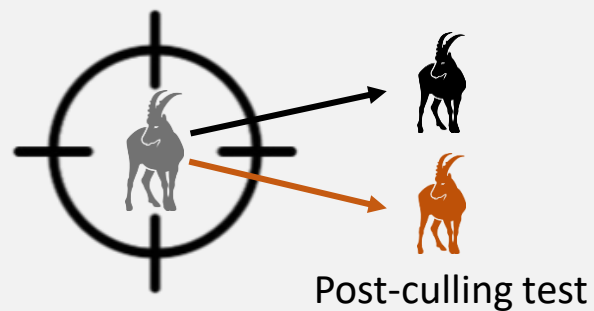
# Disease management & data collection

## Seroprevalence

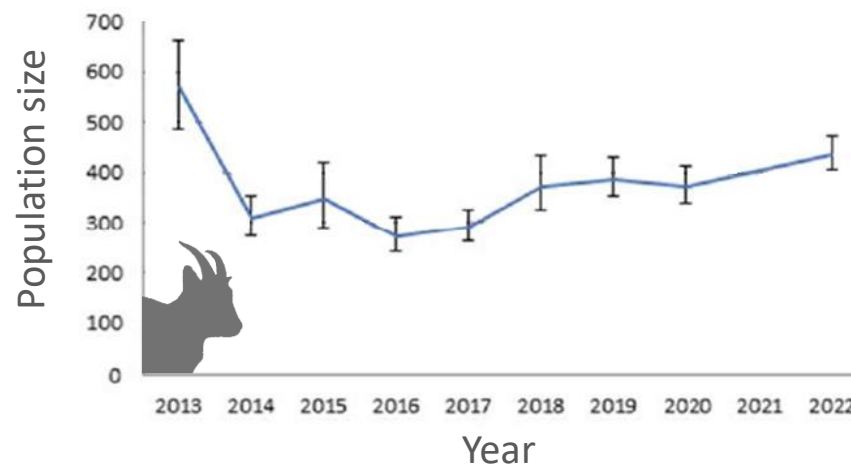
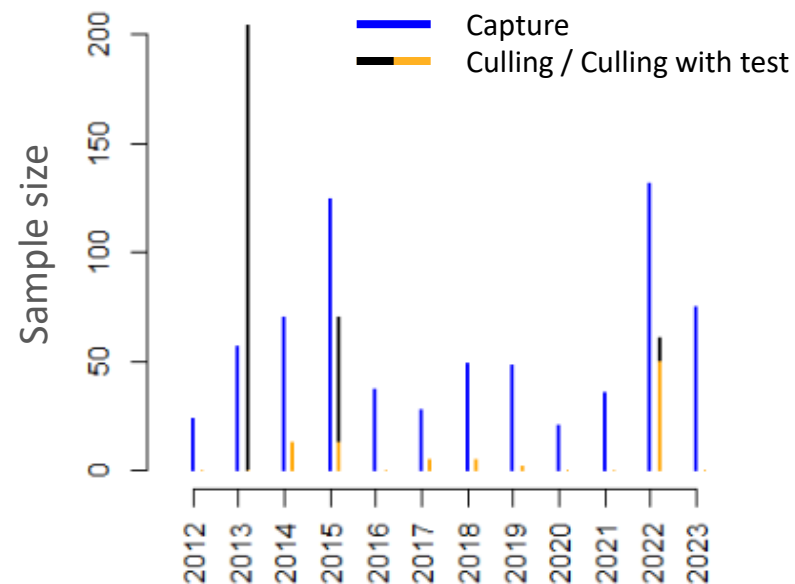
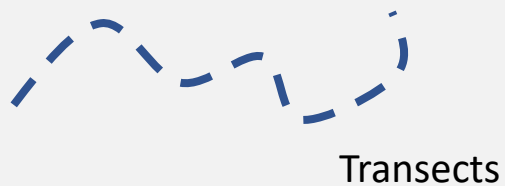
Captures



Culling



## Population size estimates



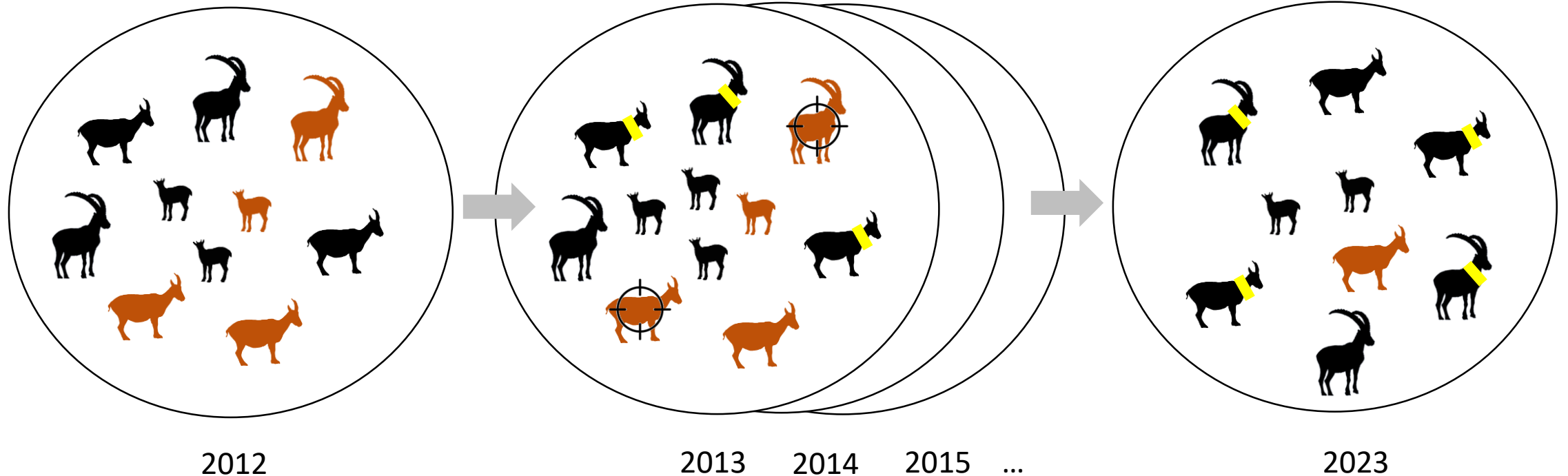


# The model

## Individual Based Model

Time step = week

Individual state = age, sex, sector & health condition (SEIR)





# The model

Unknown parameters to be estimated

**Tab** = Transmissions risk per infectious abortion and birth

**Tv** = Venerian transmission risk

**K** = Carring capacity

→ Maximum population size that can be sustained by the environment





# Parameter estimation

ABC method (Approximate Bayesian Computation)



Abc package

→ Algorithme « rejection »



# Summary statistics

## Seroprevalence

**Proportion** [0;1]

**220 estimates**

(11 years \* 5 sectors \* 2 sexes \* 2 age-classes)

**Robust estimates**

## Population size

**Abundance** [0;+inf]

**11 estimates**

(11 years)

**Quite uncertain ...**



# Summary statistics

## Seroprevalence

**Proportion** [0;1]

**220 estimates**

(11 years \* 5 sectors \* 2 sexes \* 2 age-classes)

**Robust estimates**



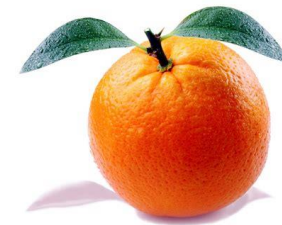
## Population size

**Abundance** [0;+inf]

**11 estimates**

(11 years)

**Quite uncertain ...**



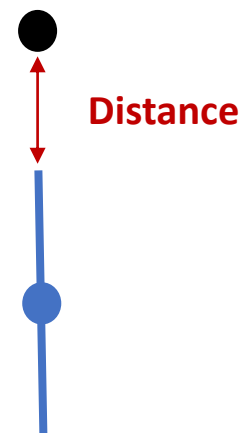


# Summary statistics

Seroprevalence = point estimate



Population size = range





# Summary statistics

## Weight attribution

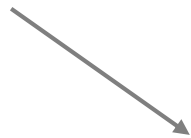
Seroprevalence



distance 1



Normalization



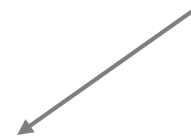
Population size



distance 2



Normalization



**Final distance =  
distance 1 + distance 2**

**50%**

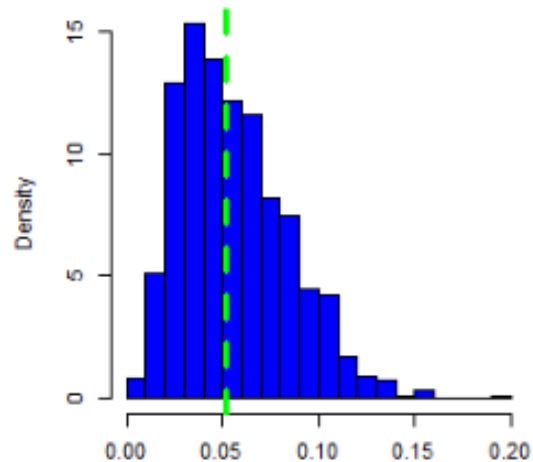
**50%**



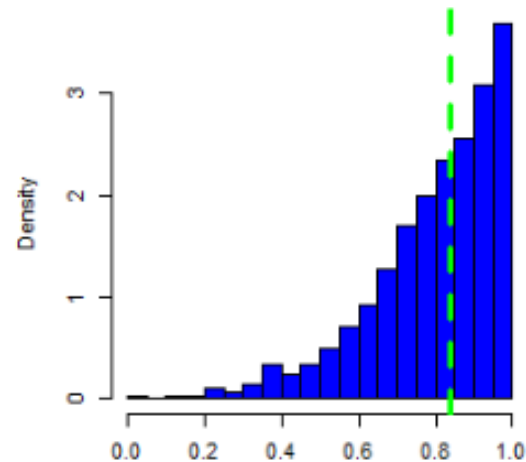
# Summary statistics



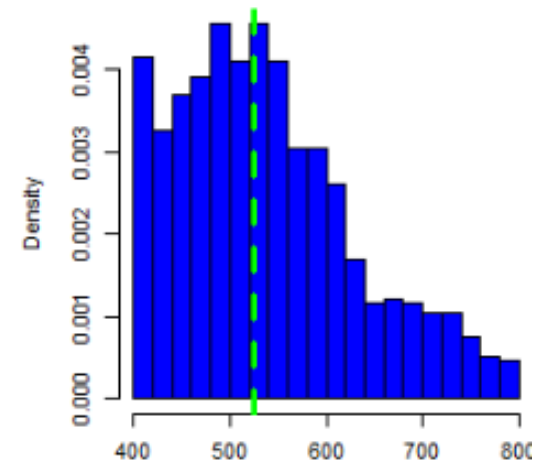
### Tab



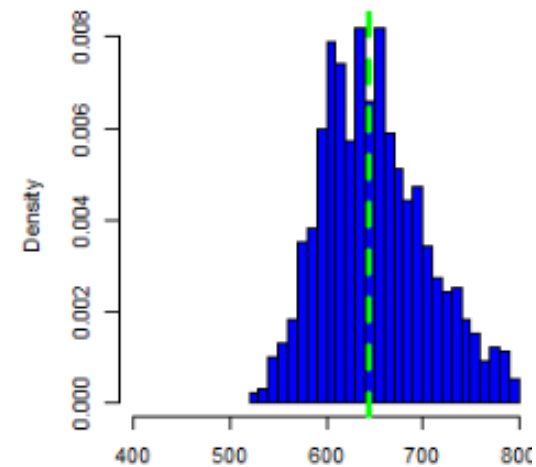
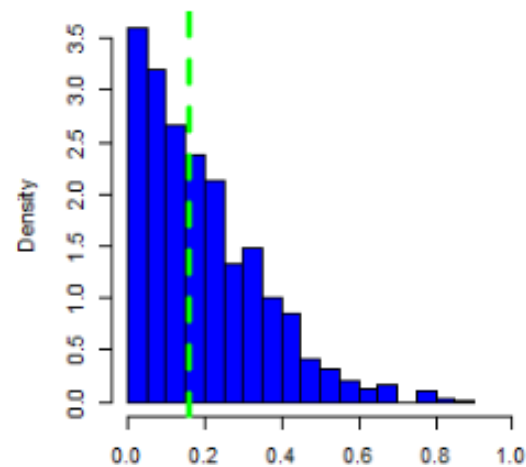
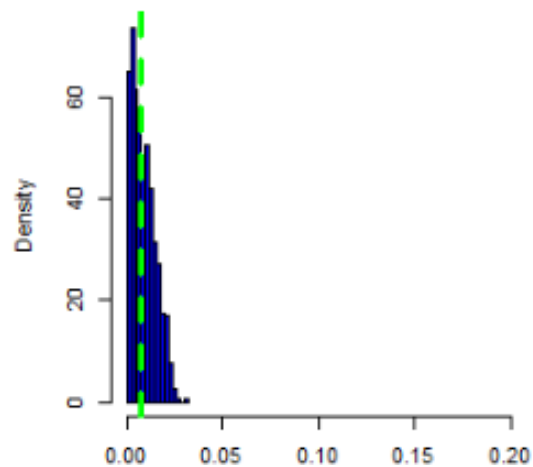
### Tv



### K



Correction

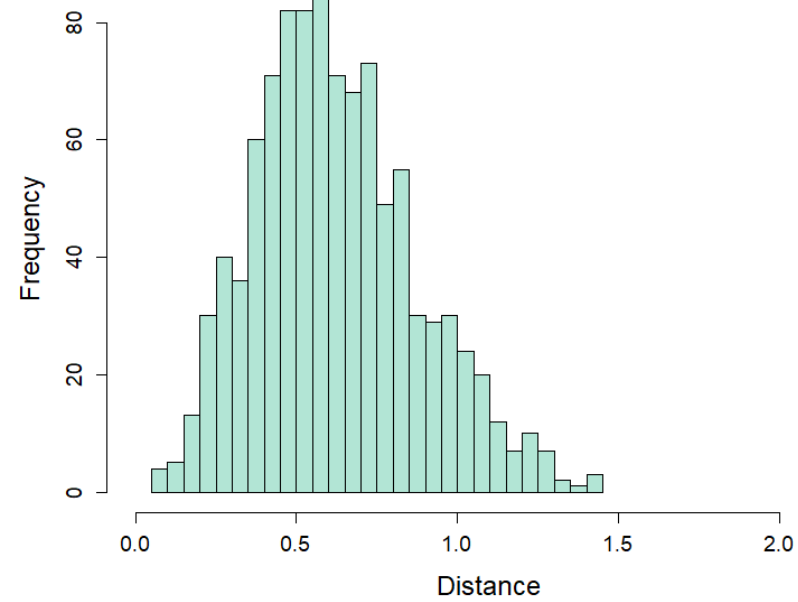


Parameter value



# Distance computation

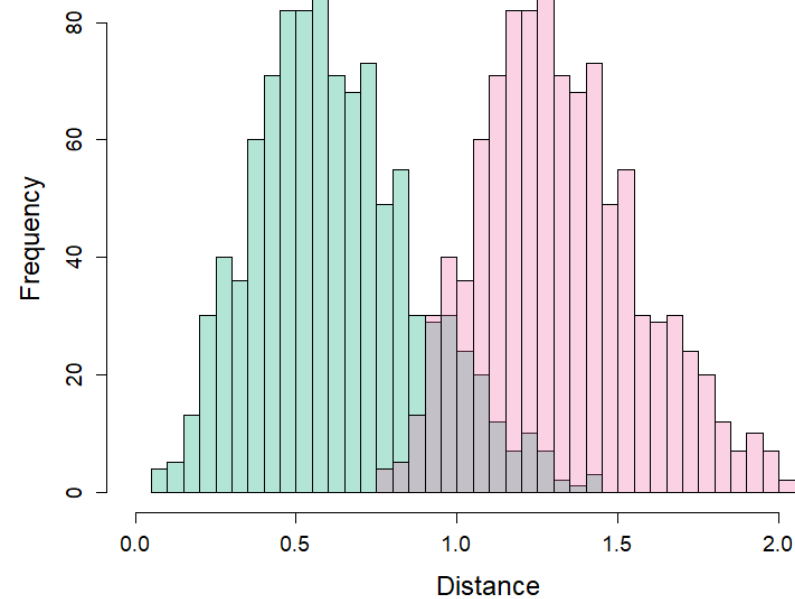
## Uncertainty in distance estimation





# Distance computation

## Uncertainty in distance estimation



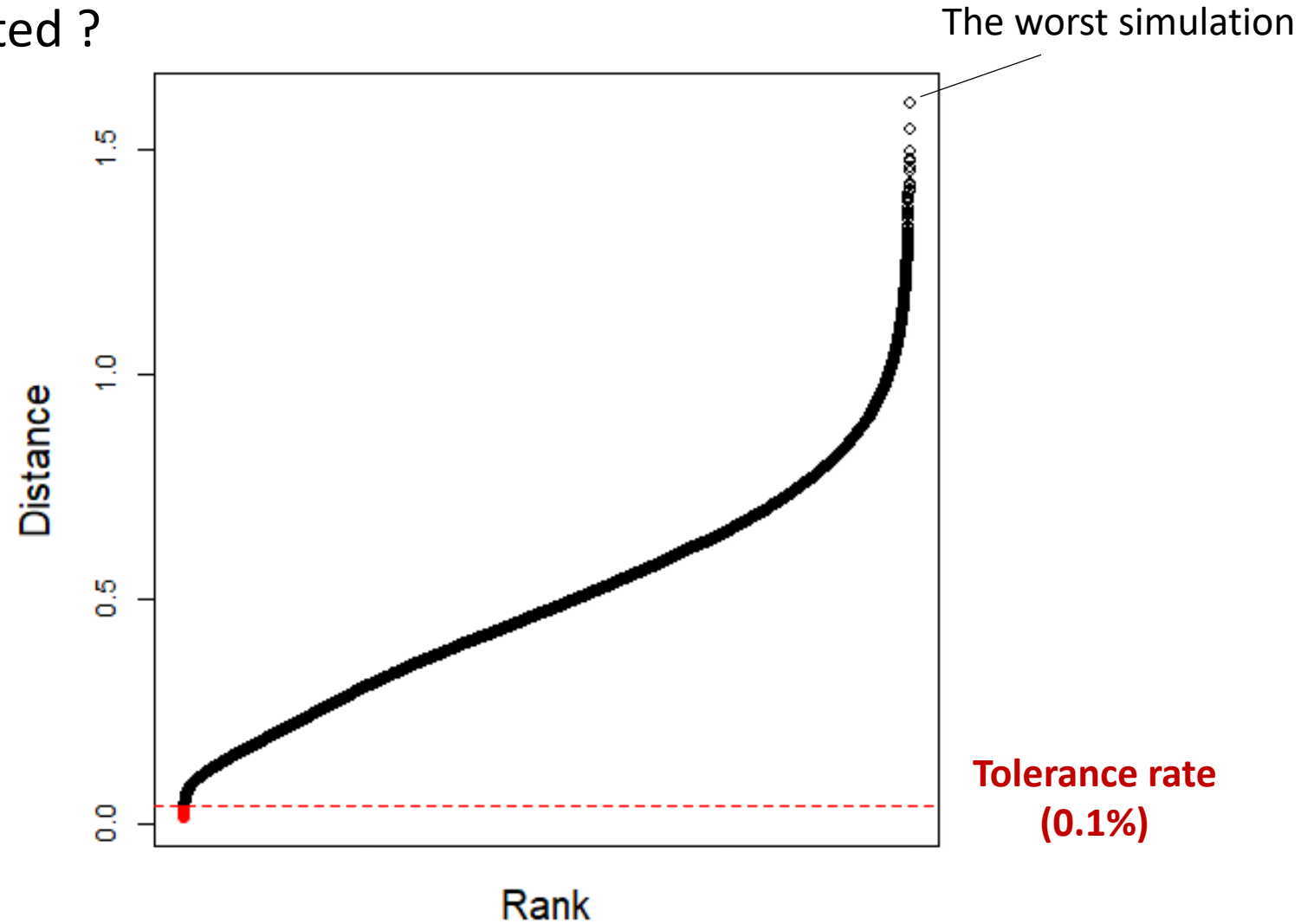
→ Simulation repetitions can improve discrimination between candidate parameters





# Distance computation

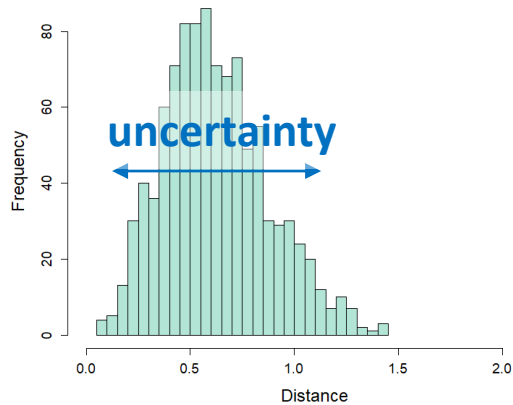
Which simulations have to be repeated ?



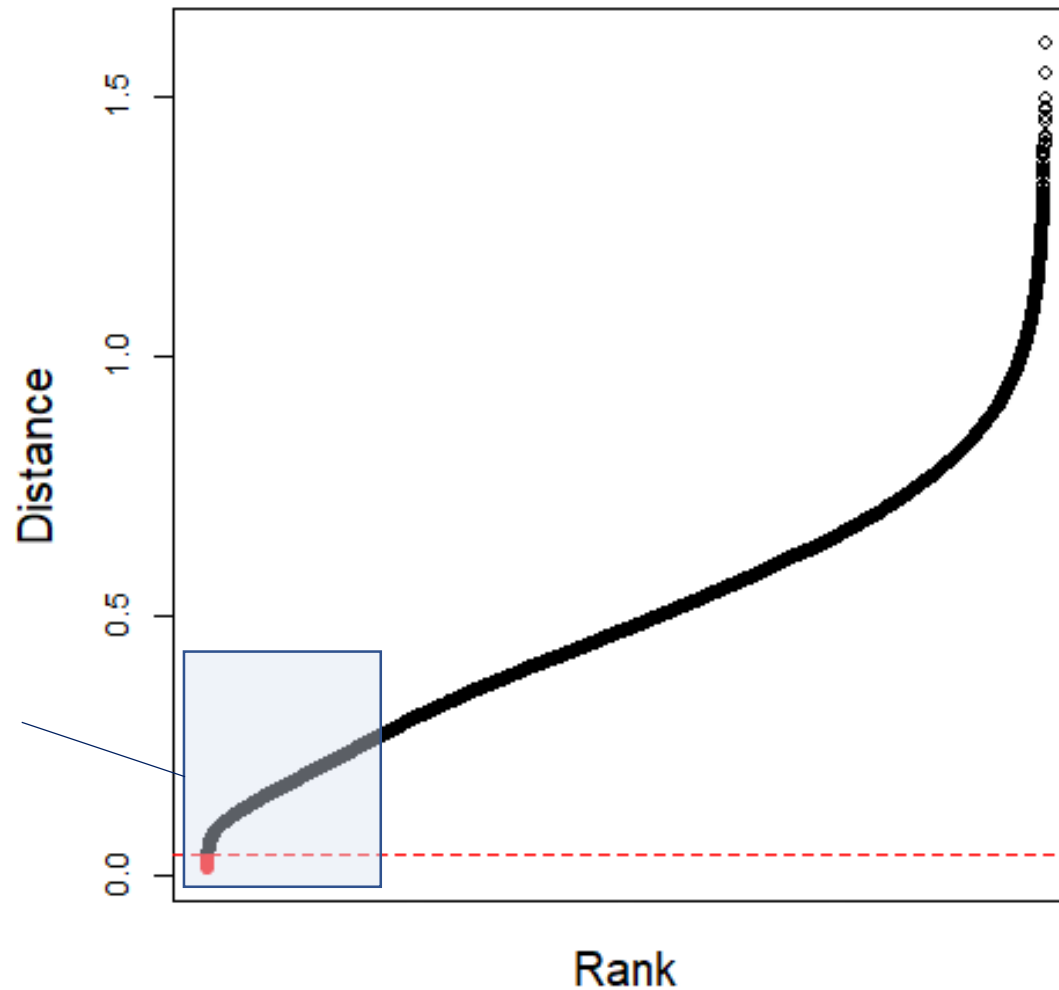


# Distance computation

Which simulations have to be repeated ?



Best simulations area  
(20%)

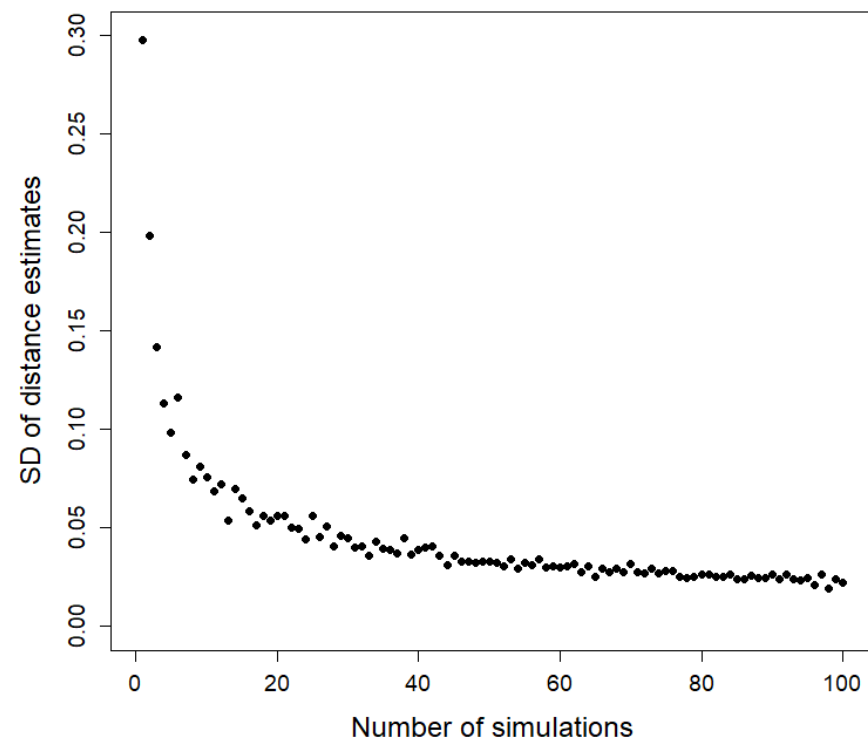


Tolerance rate  
(0.1%)



# Distance computation

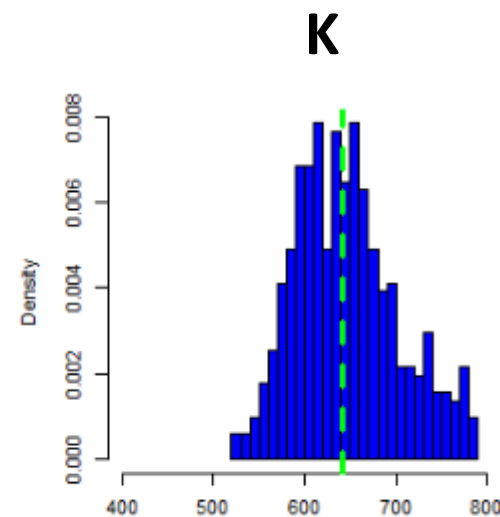
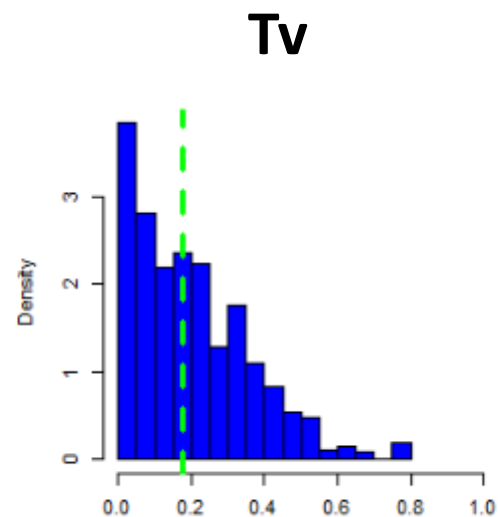
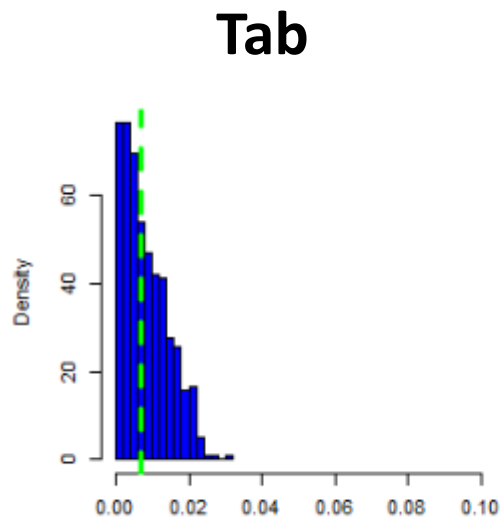
How many repetitions are needed ?



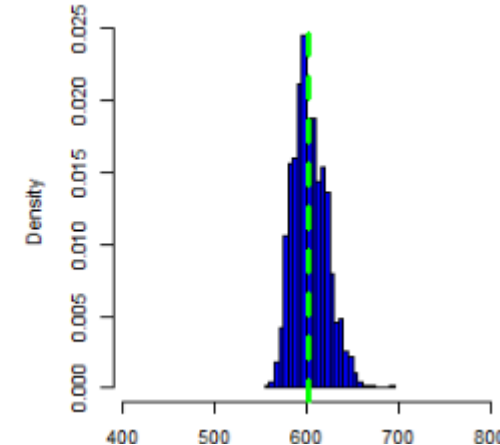
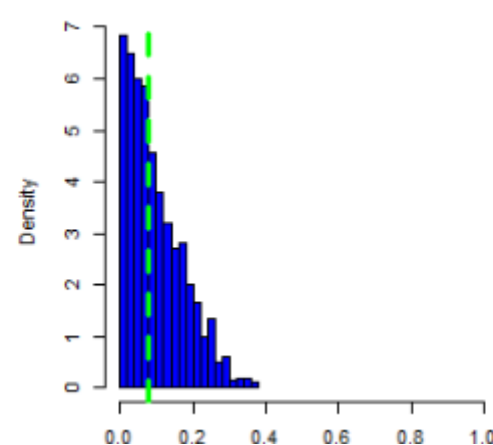
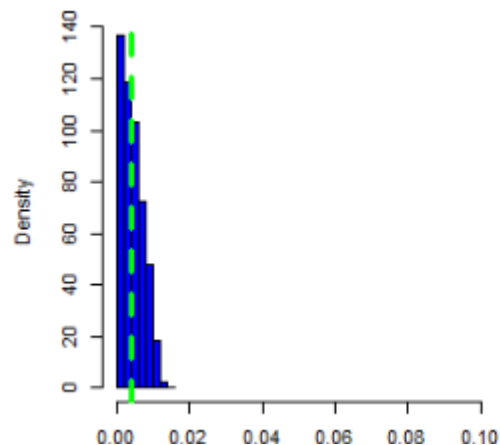


# Distance computation

No repetition



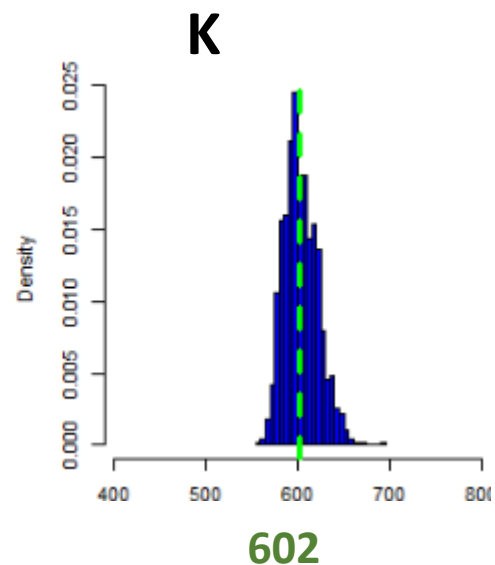
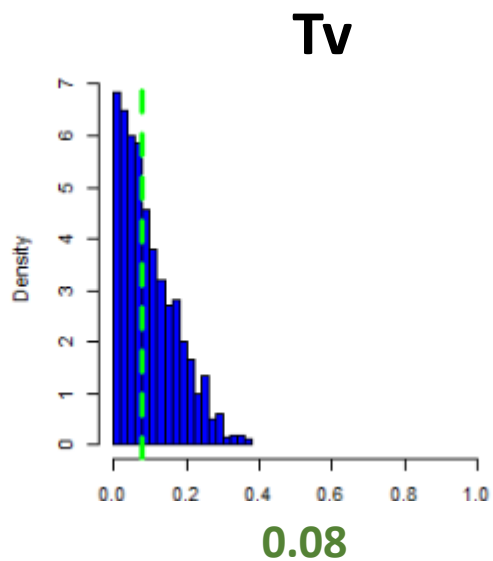
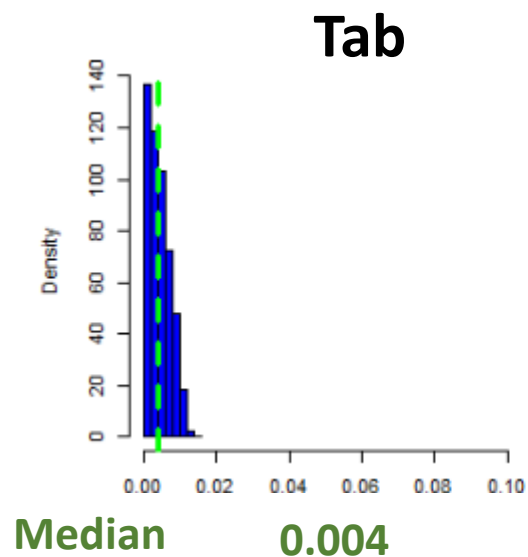
20 repetitions





# Parameter estimation

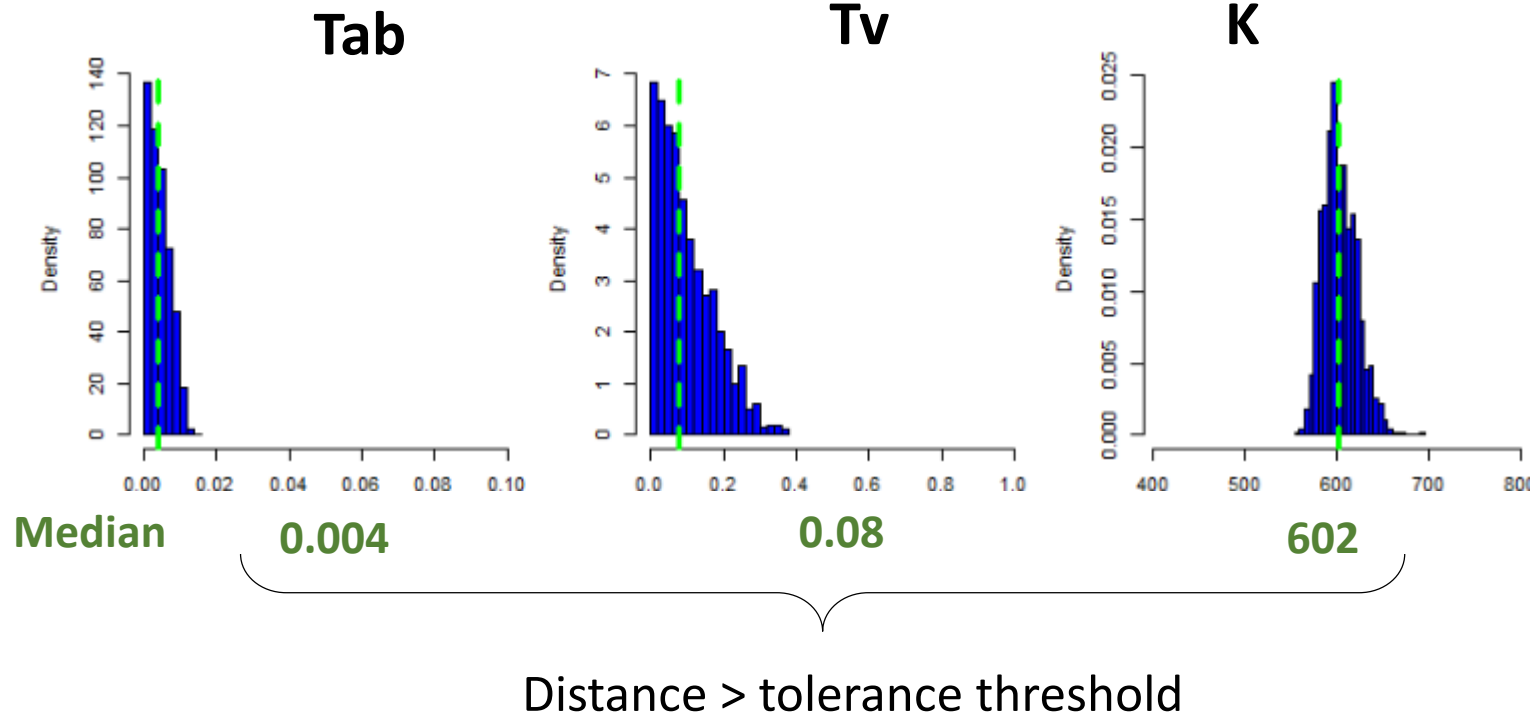
What are the best estimates ?





# Parameter estimation

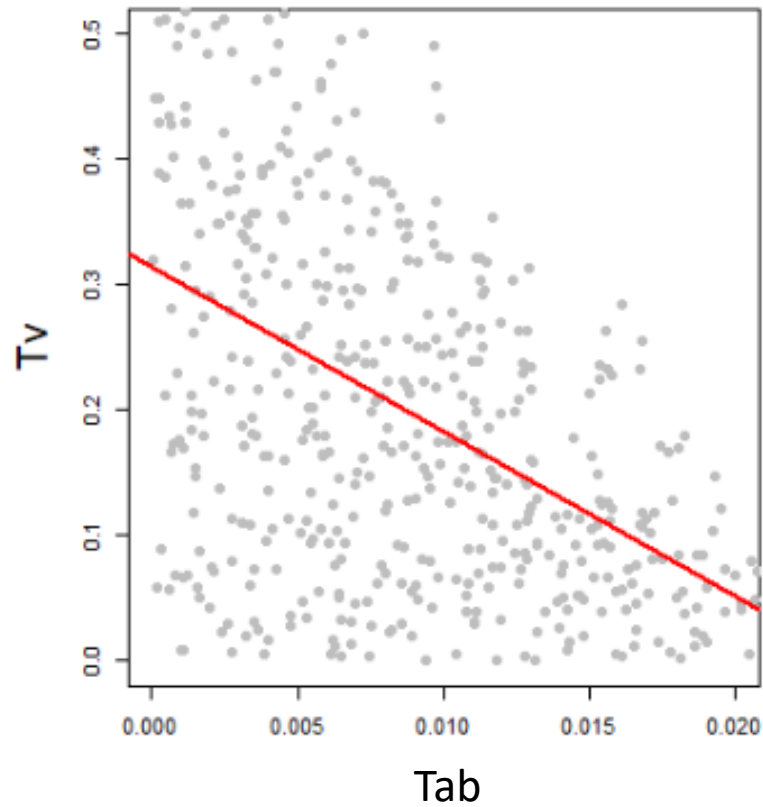
What are the best estimates ?





# Parameter estimation

What are the best estimates ?



→ Set of candidate parameters in the posterior distribution



# Conclusion

## **ABC: The devil is in the details**

- Pay attention to summary statistics definition
- Assess uncertainty in distance estimate
- Point estimate vs. distribution





# Conclusion

## ABC: The devil is in the details

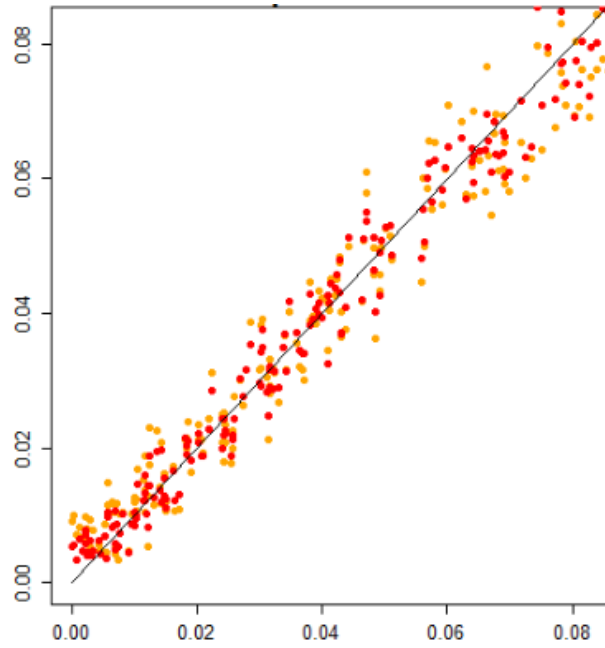
- Pay attention to summary statistics definition
- Assess uncertainty in distance estimate
- Point estimate vs. distribution

Thank you for your attention !

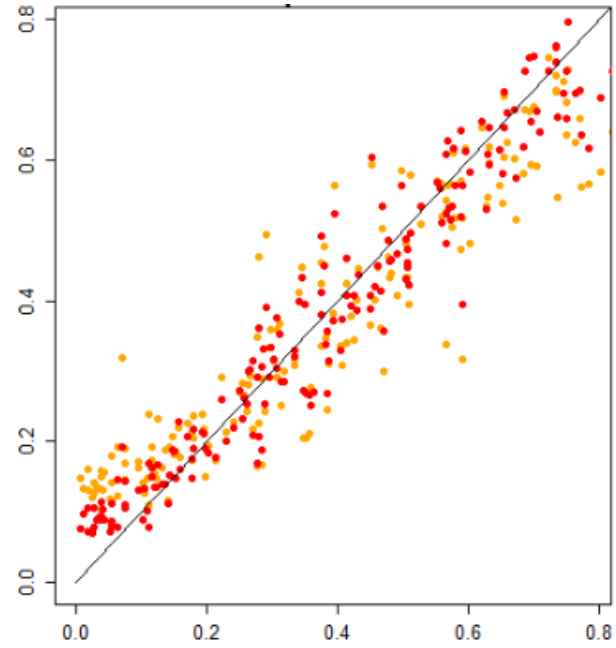


# Cross-validation test

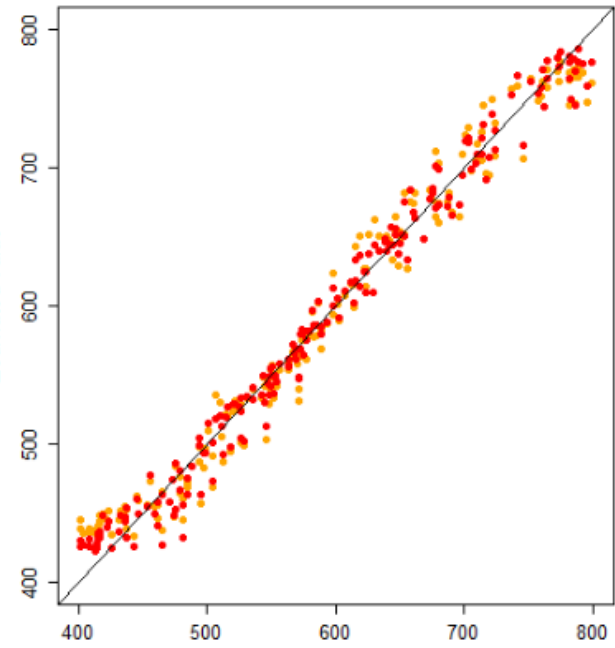
**Tab**



**Tv**



**K**





# Fit assessment

