

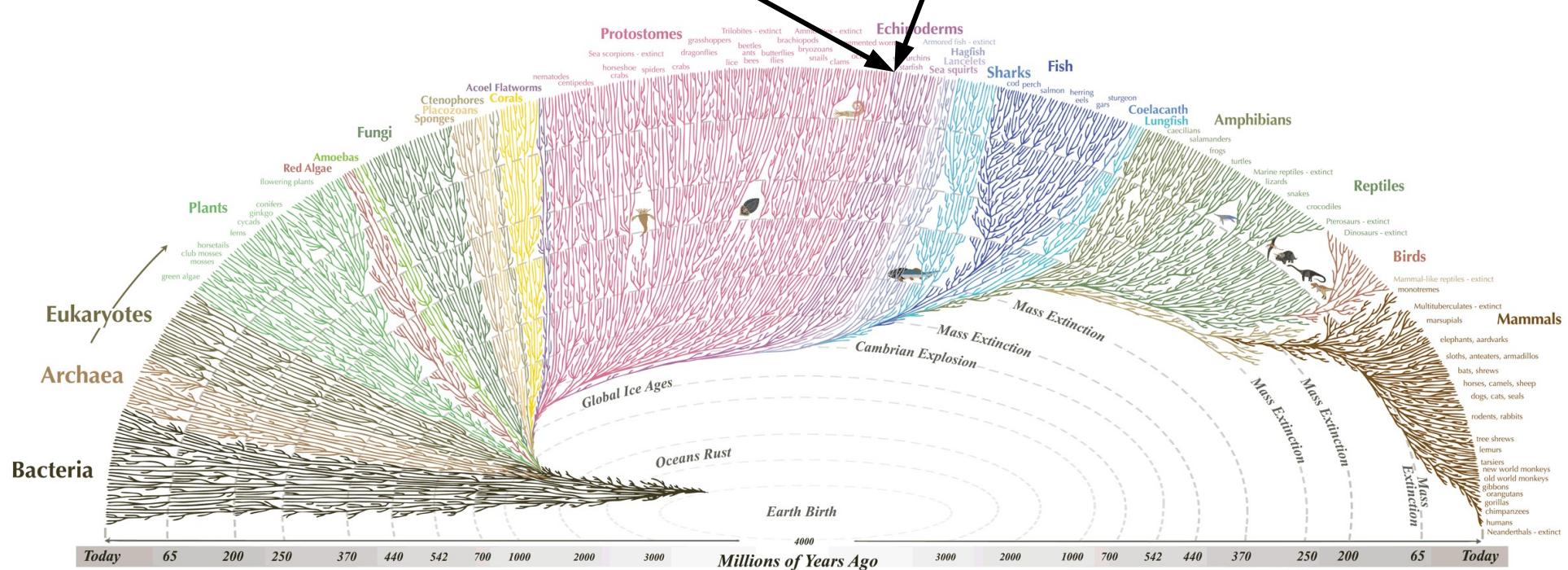
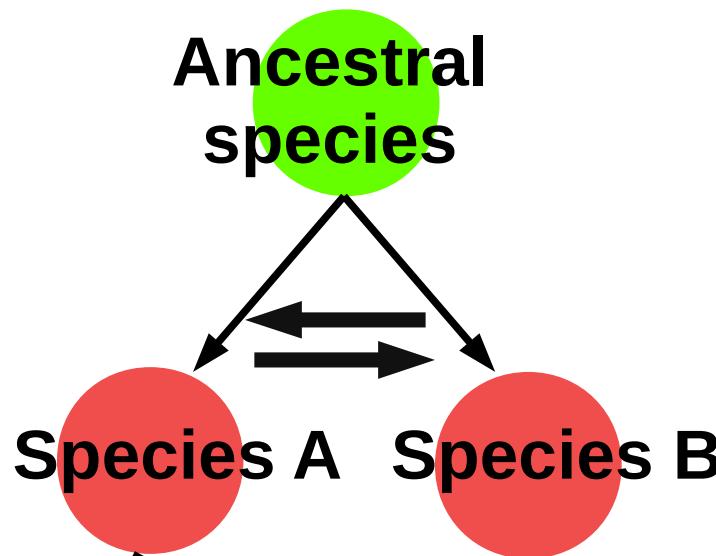
Before starting :

1) open your terminal

**2) go to your directory named ABC_WGD obtained from
git-hub**

3) tape git pull

Speciation

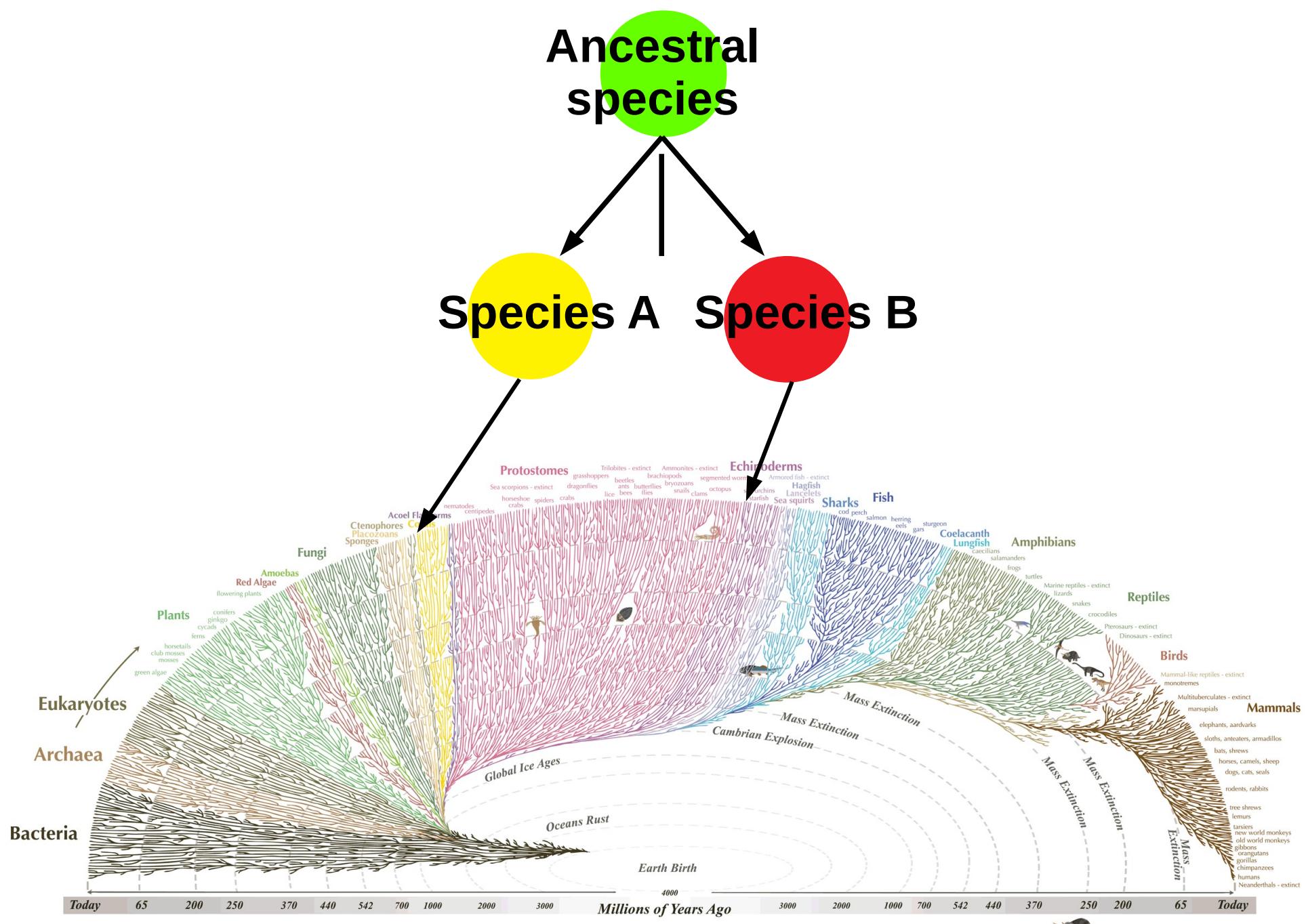


All the major and many of the minor living branches of life are shown on this diagram, but only a few of those that have gone extinct are shown. Example: Dinosaurs - extinct



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Speciation

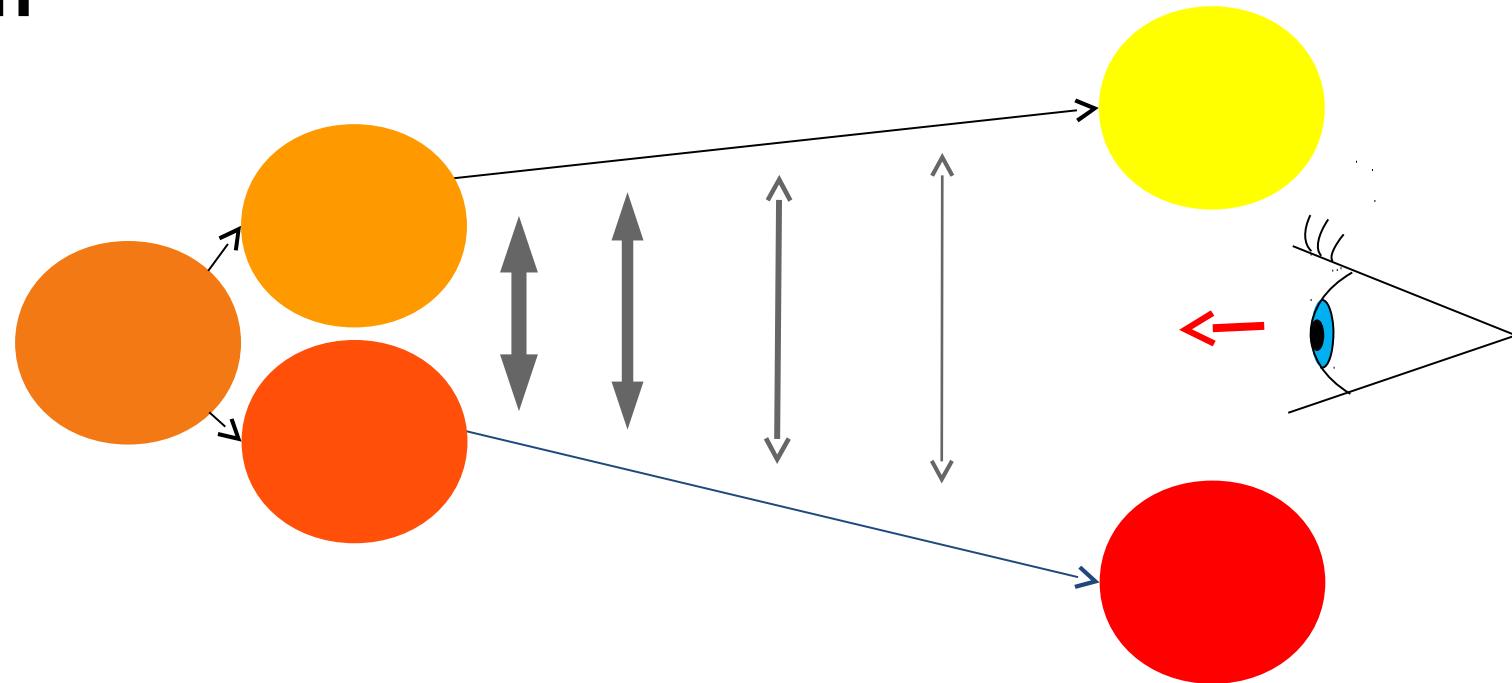


All the major and many of the minor living branches of life are shown on this diagram, but only a few of those that have gone extinct are shown. Example: Dinosaurs - extinct



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Speciation



Genome A

Genome A

Genome A

Genome B

Genome B

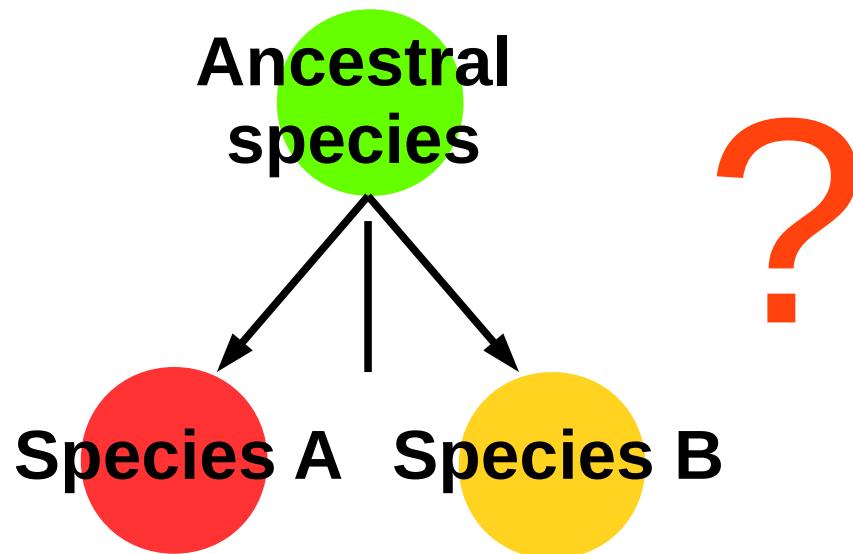
Genome B

2 populations from
the same species

2 semi-isolated
species

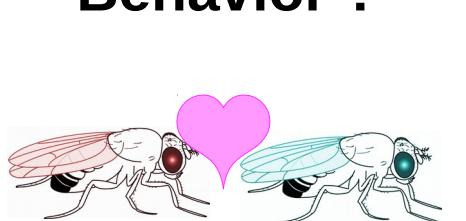
2 isolated species

Q1 : What is the nature of species barriers ?



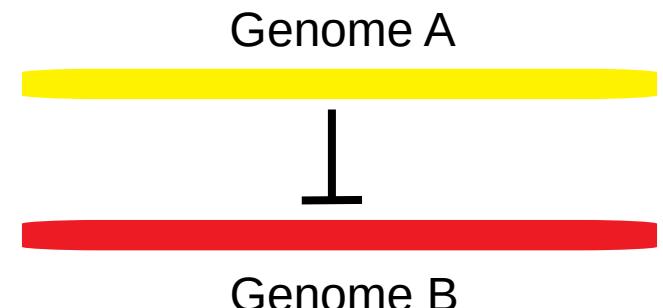
Ecological ?

Environnement



Behavior ?

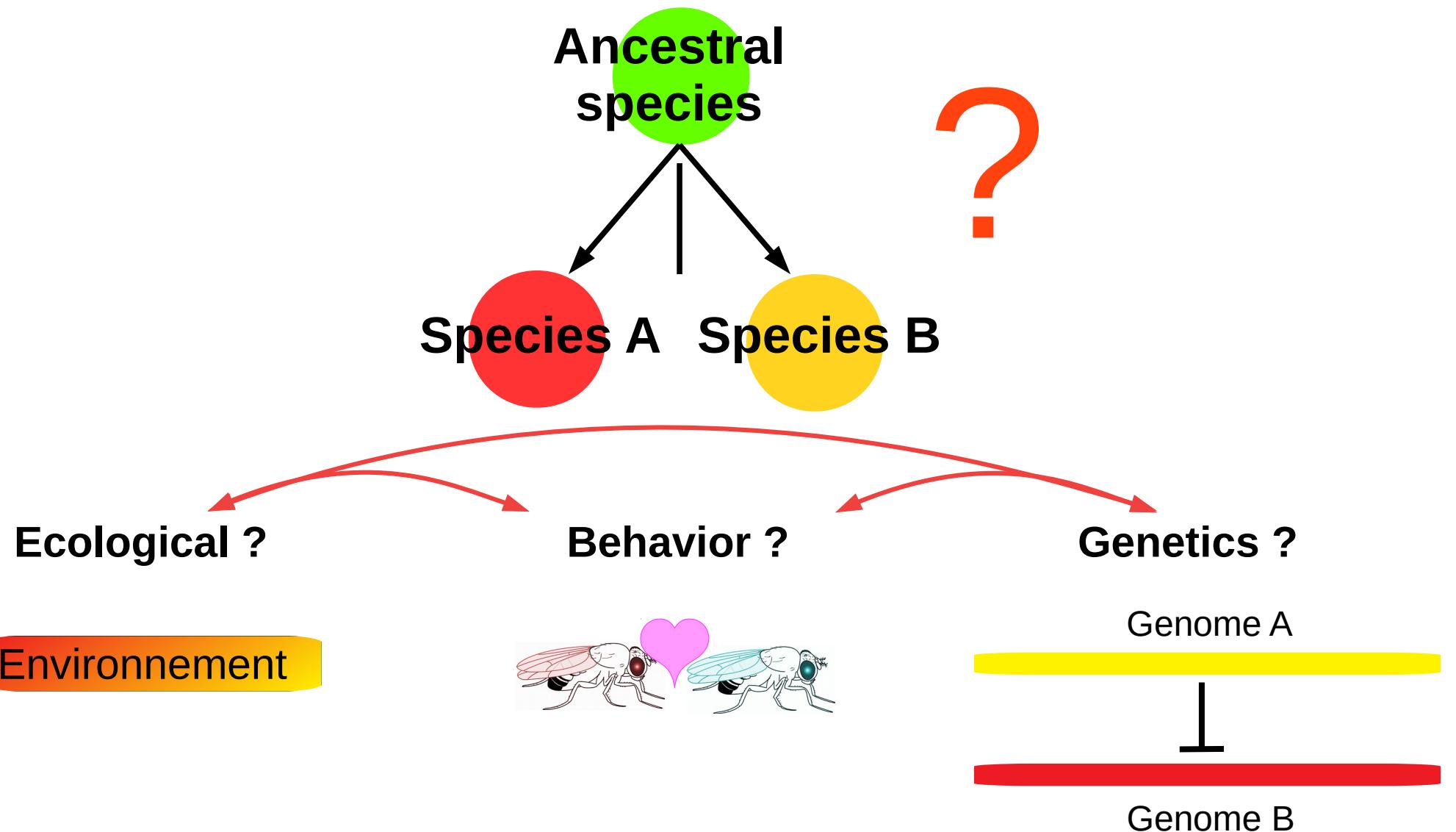
Genetics ?



Genome A

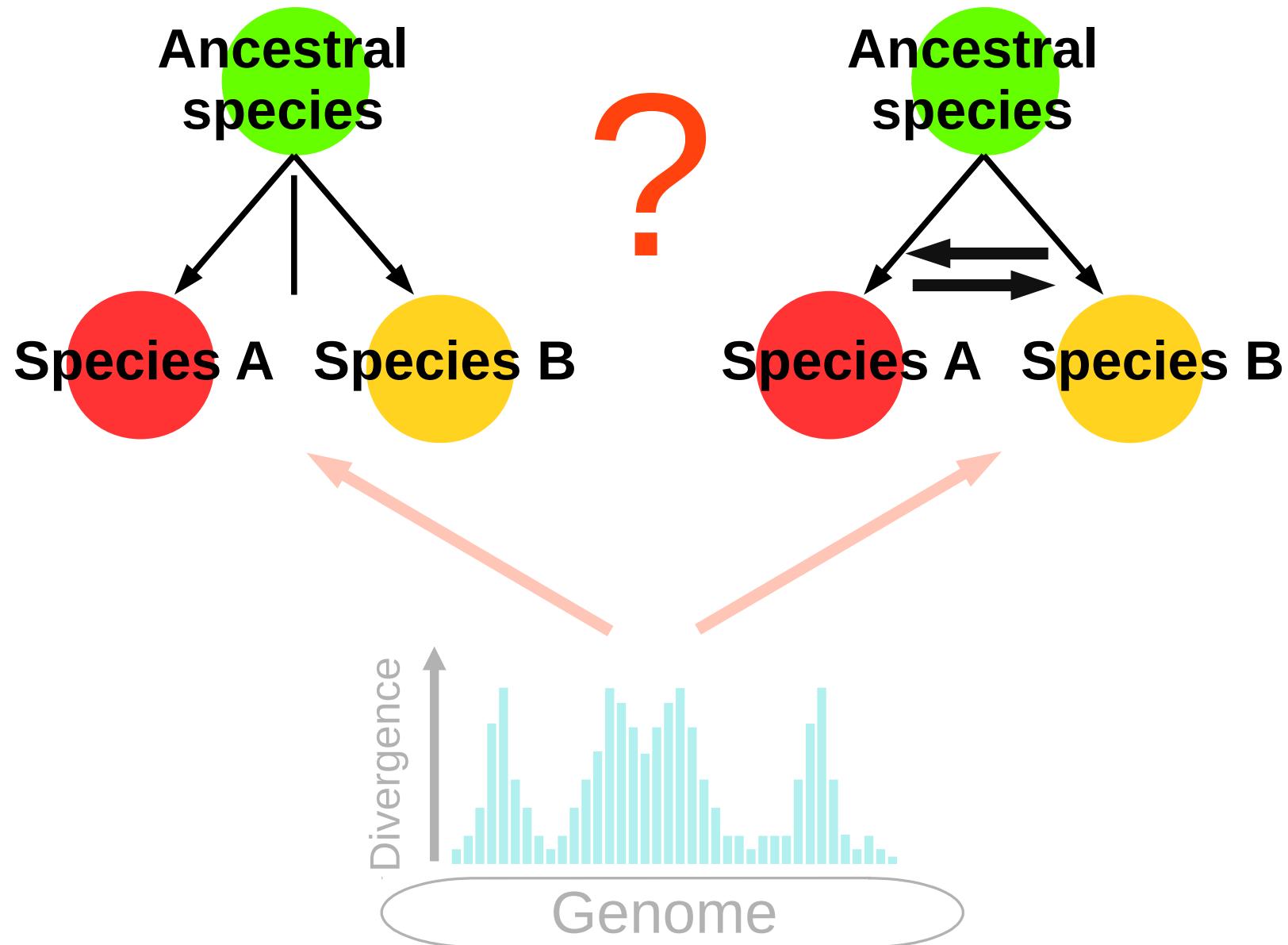
Genome B

Q1 : What is the nature of species barriers ?



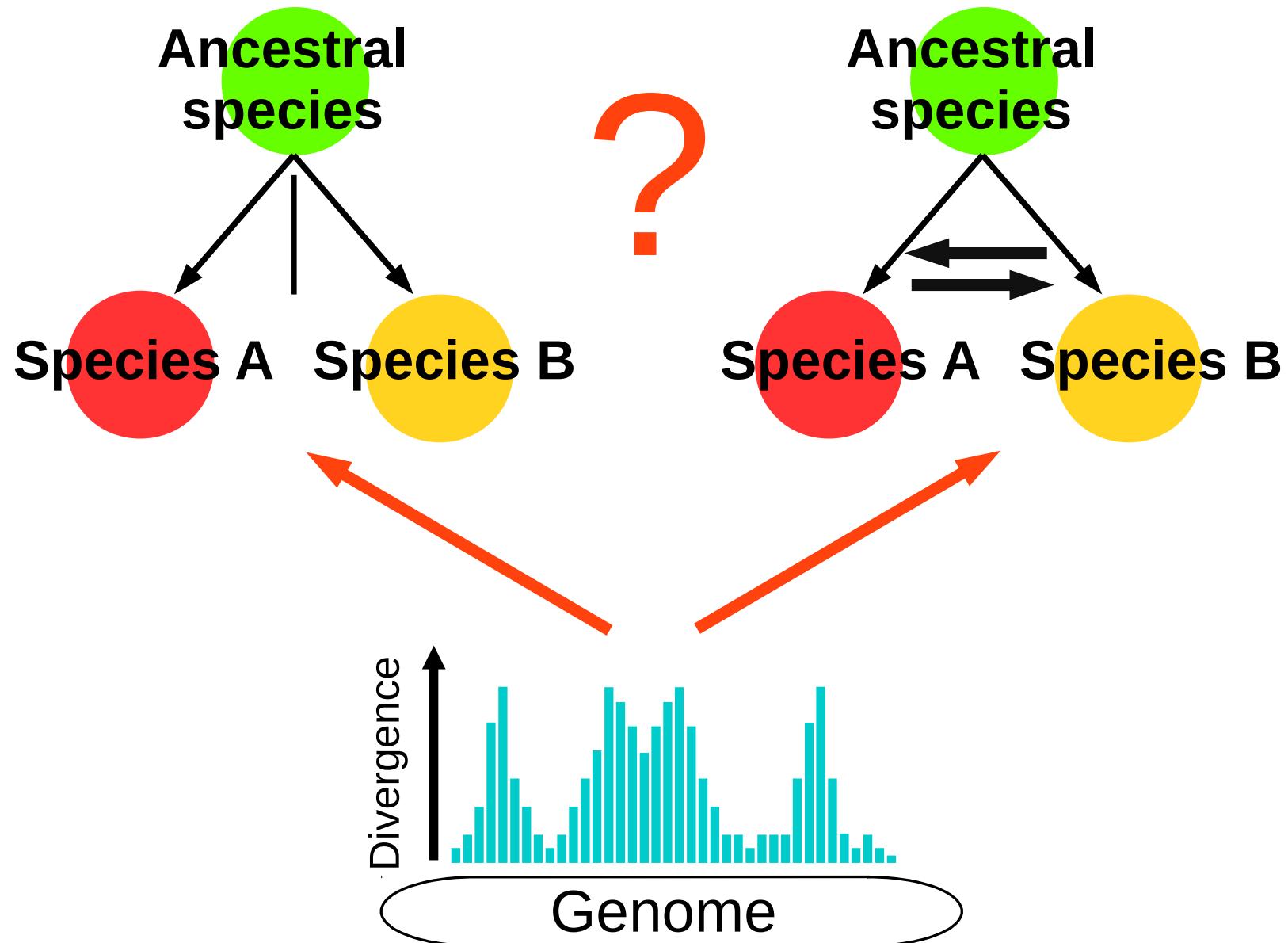
Q1 : What is the **nature** of species barriers ?

Q2 : What is the **historical context** in which barriers have been appeared ?

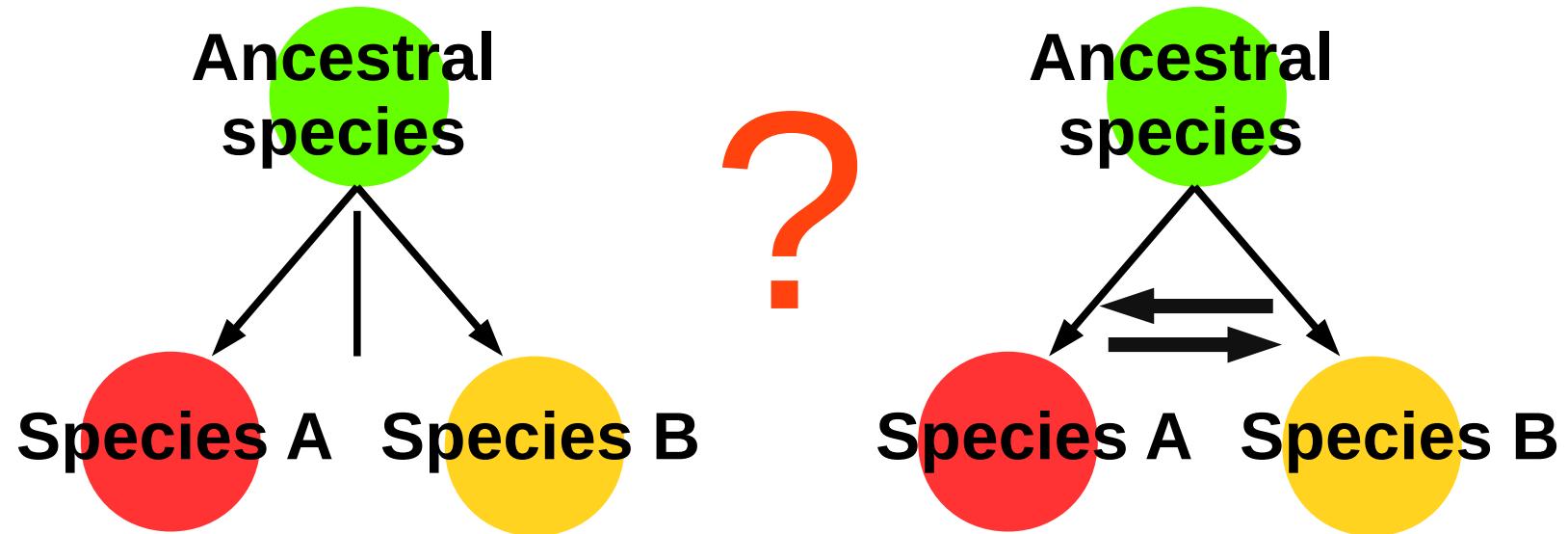


Q1 : What is the **nature** of species barriers ?

Q2 : What is the **historical context** in which barriers have been appeared ?



Goal of the day: Comparing alternative scenarios of demographic history



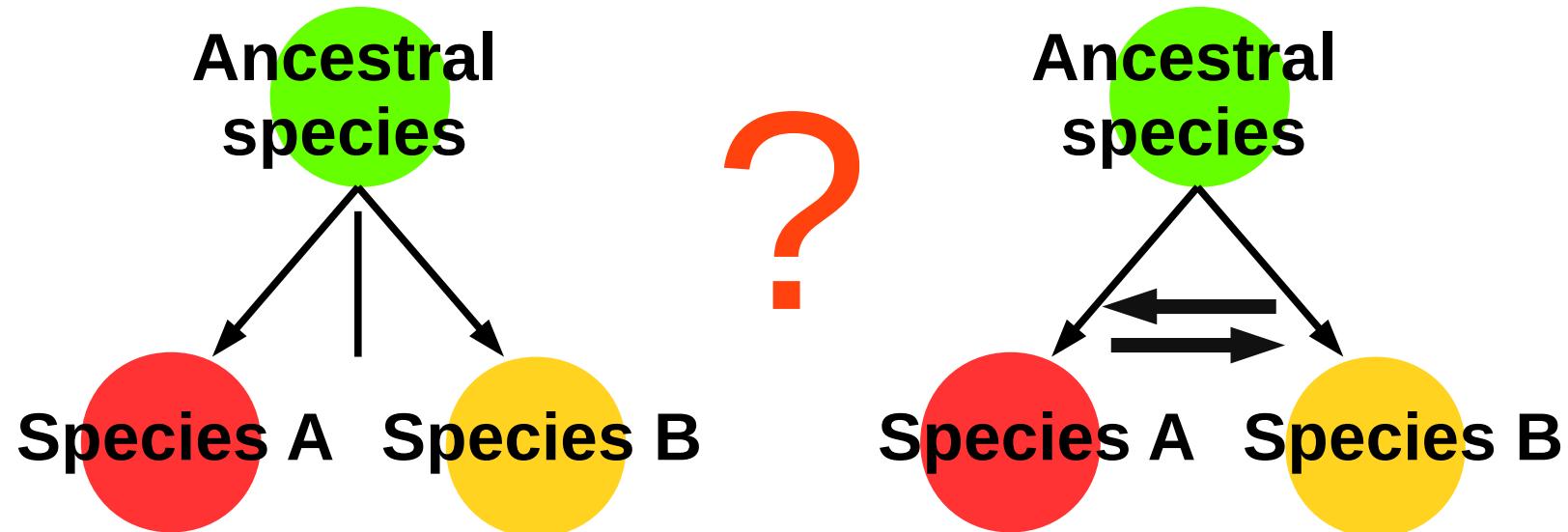
Migration versus isolation ?

*Disomic versus tetrasomic versus
heterosomic ?*

Autopolyploid versus allopolyploid ?

Bottleneck versus constant population size ?

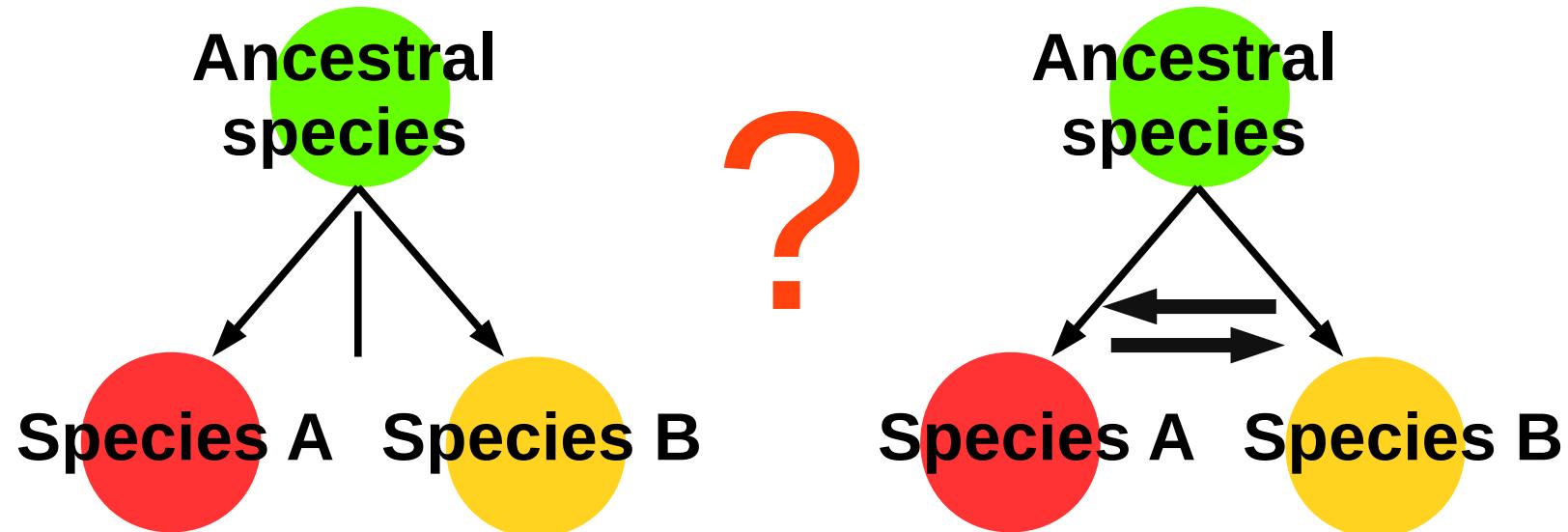
Goal of the day: Comparing alternative scenarios of demographic history



1) Basic Bayesian inferences

2) Approximate Bayesian Computation (ABC)

Goal of the day: Comparing alternative scenarios of demographic history



1) Basic Bayesian inferences

2) Approximate Bayesian Computation (ABC)

Main goal : understanding the method, not (only) the tool !

Basic Bayesian inferences

Set of 5 dice



4-sided



6-sided



8-sided



12-sided



20-sided

- 1) I randomly take a die among the 5
- 2) I throw it twice
- 3) observed 7 and 8

Q : what are the probabilities of each die based on these observations?

Basic Bayesian inferences

Set of 5 dice



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From the first observation : $X = 7$

$$P(\text{die}, i | 7) = [P(7 | \text{die}, i) \times P(\text{die}, i)] / P(7)$$



probability of the die i given
that the event '7' occurred

Q : what are the probabilities of each die based on these observations?

From the first observation : $X = 7$

$$P(\text{die}, i | 7) = [P(7 | \text{die}, i) \times P(\text{die}, i)] / P(7)$$

i in $[4, 6, 8, 12, 20]$

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probability to observe
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probability of the die i given
that the event '7' occurred

a priori probability
of the die i

probability to observe
the event '7' for the die i

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From the first observation : $X = 7$

$$P(\text{die},i | 7) = [P(7 | \text{die},i) \times P(\text{die},i)] / P(7)$$



?



?



?



?



?

Q : what are the probabilities of each die based on these observations?

From the first observation : $X = 7$

$$P(\text{die},i \mid 7) = [P(7 \mid \text{die},i) \times P(\text{die},i)] / P(7)$$



?

0



?

0



?



?



?

Q : what are the probabilities of each die based on these observations?

From the first observation : $X = 7$

$$P(\text{die},i \mid 7) = [P(7 \mid \text{die},i) \times P(\text{die},i)] / P(7)$$



?

0



?

0



?

1/8



?

1/12



?

1/20

Q : what are the probabilities of each die based on these observations?

From the first observation : $X = 7$

$$P(\text{die},i \mid 7) = [P(7 \mid \text{die},i) \times P(\text{die},i)] / P(7)$$



?

0

1/5



?

0

1/5



?

1/8

1/5



?

1/12

1/5



?

1/20

1/5

Q : what are the probabilities of each die based on these observations?

From the first observation : $X = 7$

$$P(\text{die}, i | 7) = [P(7 | \text{die}, i) \times P(\text{die}, i)] / P(7)$$

	?	0	1/5
	?	0	1/5
	?	1/8	1/5
	?	1/12	1/5
	?	1/20	1/5

$$P(7) = \sum_{i=1} P(i).P(7|i)$$

Q : what are the probabilities of each die based on these observations?

From the first observation : $X = 7$

$$P(\text{die},i | 7) = [P(7 | \text{die},i) \times P(\text{die},i)] / P(7)$$

	?	0	1/5	
	?	0	1/5	
	?	1/8	1/5	0.052
	?	1/12	1/5	
	?	1/20	1/5	

In R : `sum(rep(1/5, 5) * c(0,0, 1/8, 1/12, 1/20)) ~ 0.052`

Q : what are the probabilities of each die based on these observations?

From the first observation : $X = 7$

$$P(\text{die},i | 7) = [P(7 | \text{die},i) \times P(\text{die},i)] / P(7)$$



$$0 * 1/5 * P(7) = 0$$

$$0$$

$$1/5$$



$$0 * 1/5 * P(7) = 0$$

$$0$$

$$1/5$$



$$1/8 * 1/5 * P(7) = 48.39\%$$

$$1/8$$

$$1/5$$

$$0.052$$



$$1/12 * 1/5 * P(7) = 32.26\%$$

$$1/12$$

$$1/5$$



$$1/20 * 1/5 * P(7) = 19.35\%$$

$$1/20$$

$$1/5$$

Q : what are the probabilities of each die based on these observations?

From the second observation : $X = 8$

$$P(\text{die},i \mid 7) = [P(7 \mid \text{die},i) \times P(\text{die},i)] / P(7)$$



$$0 * 1/5 * P(7) = 0$$



$$0 * 1/5 * P(7) = 0$$



$$1/8 * 1/5 * P(7) = 48.39\%$$



$$1/12 * 1/5 * P(7) = 32.26\%$$



$$1/20 * 1/5 * P(7) = 19.35\%$$

How these probabilities evolve taking into account the second observation $X=8$?

Q : what are the probabilities of each die based on these observations?

From the second observation : $X = 8$

$$P(\text{die},i | 8) = [P(8 | \text{die},i) \times P(\text{die},i)] / P(8)$$



?

0



?

0



?

1/8



?

1/12



?

1/20

Q : what are the probabilities of each die based on these observations?

From the second observation : $X = 8$

$$P(\text{die},i | 8) = [P(8 | \text{die},i) \times P(\text{die},i)] / P(8)$$



?

0

1/5 → 0



?

0

1/5 → 0



?

1/8

1/5 → 0.4839



?

1/12

1/5 → 0.3226



?

1/20

1/5 → 0.1935

Q : what are the probabilities of each die based on these observations?

From the second observation : $X = 8$

$$P(\text{die},i | 8) = [P(8 | \text{die},i) \times P(\text{die},i)] / P(8)$$

	?	0	0
	?	0	0
	?	1/8	0.4839
	?	1/12	0.3226
	?	1/20	0.1935

In R : `sum(c(0,0,0.4839,0.3226,0.1935) * c(0,0,1/8,1/12,1/20))`

Q : what are the probabilities of each die based on these observations?

From the second observation : $X = 8$

$$P(\text{die},i | 8) = [P(8 | \text{die},i) \times P(\text{die},i)] / P(8)$$



0

0

0

0

48.39%



62.33 %

32.26%

27.7 %

19.35%

9.97 %

Q : what are the probabilities of each die based on these observations?

From the second observation : $X = 8$

$$P(\text{die},i | 8) = [P(8 | \text{die},i) \times P(\text{die},i)] / P(8)$$



	0	0
	0	0
	48.39%	→ 62.33 %
	32.26%	27.7 %
	19.35%	9.97 %

Here we have N=2 observations

How probabilities evolve with the number of observations ?

Exploring the effects of the number of observations on inferences using the R-function **bayes**

In R :`source('comparison_ABC_bayes.R')`
`bayes(observations=c(7, 8), dies=c(4, 6, 8, 12, 20))`

The bayes function returns the probability of each of the proposed die given a series of observations.

```
bayes(observations=c(7, 8), dices=c(4, 6, 8, 12, 20))
 4 6      8      12      20 best_model post_proba
0 0 0.62327 0.27701 0.09972           D8      0.62327
```

Exploring the effects of the number of observations on inferences using the R-function **bayes**

In R :`source('comparison_ABC_bayes.R')`
`bayes(observations=c(7, 8), dies=c(4, 6, 8, 12, 20))`

observations = vector containing a serie of N observations for a given die i .

dies = prior distribution of the model comparison. Vector containing a serie of d possible die.

Exploring the effects of the number of observations on inferences using the R-function **bayes**

In R :`source('comparison_ABC_bayes.R')`
`bayes(observations=c(7, 8), dies=c(4, 6, 8, 12, 20))`

observations = vector containing a serie of N observations for a given die i .

dies = prior distribution of the model comparison. Vector containing a serie of d possible die.

Bonus : simulating a die roll by using random sampling from a discrete uniform distribution (R function : sample)

$N = 10$

`observations = sample(1:8, N, replace=T)`

Exploring the effects of the number of observations on inferences using the R-function **bayes**

In R :`source('comparison_ABC_bayes.R')`
`bayes(observations=c(7, 8), dies=c(4, 6, 8, 12, 20))`

observations = vector containing a serie of N observations for a given die i .

dies = prior distribution of the model comparison. Vector containing a serie of d possible die.

```
> real_dice = 8
> N_observations = 3
> observations = sample(1:real_dice, N_observations, replace=T)
>
> bayes(observations = observations, dices = c(4, 6, 8, 12, 20))
  4 6       8       12       20 best_model post_proba
1 0 0 0.73513 0.21782 0.04705           D8      0.73513
```

Exploring the effects of the number of observations on inferences using the R-function **bayes**

In R :`source('comparison_ABC_bayes.R')`
`bayes(observations=c(7, 8), dies=c(4, 6, 8, 12, 20))`

observations = vector containing a serie of N observations for a given die i .

dies = prior distribution of the model comparison. Vector containing a serie of d possible die.

```
> real_dice = 8
> N_observations = 3
> observations = sample(1:real_dice, N_observations, replace=T)
>
> bayes(observations = observations, dices = c(4, 6, 8, 12, 20))
  4   6     8     12     20 best_model post_proba
1 0  0  0.73513  0.21782  0.04705           D8      0.73513
```

Correct inference !

Exploring the effects of the number of observations on inferences using the R-function **bayes**

In R :`source('comparison_ABC_bayes.R')`
`bayes(observations=c(7, 8), dies=c(4, 6, 8, 12, 20))`

observations = vector containing a serie of N observations for a given die i .

dies = prior distribution of the model comparison. Vector containing a serie of d possible die.

```
> real_dice = 8                                Bad inference
> N_observations = 3
> observations = sample(1:real_dice, N_observations, replace=T)
> bayes(observations = observations, dies = c(4, 6, 8, 12, 20))
      4          6          8         12         20 best_model post_proba
1 0.68197 0.20207 0.08525 0.02526 0.00546           D4    0.68197
> observations
[1] 3 1 1
```

Exploring the effects of the number of observations on inferences using the R-function **bayes**

In R :`source('comparison_ABC_bayes.R')`
`bayes(observations=c(7, 8), dies=c(4, 6, 8, 12, 20))`

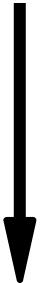
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> real_dice = 8                                Bad inference
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> bayes(observations = observations, dies = c(4, 6, 8, 12, 20))
   4          6          8         12         20 best_model post_proba
1 0.68197  0.20207  0.08525  0.02526  0.00546           D4      0.68197
> observations
[1] 3 1 1
```

Before applying ANY inference method

Before applying ANY inference method



know the limits of the
method!

Before applying ANY inference method



know the limits of the
method!

What is the error rate ?

When is the method wrong?

Exploring the effects of the number of observations on inferences using the R-function **bayes**

In R :`source('comparison_ABC_bayes.R')`
`bayes(observations=c(7, 8), dies=c(4, 6, 8, 12, 20))`

observations = vector containing a serie of N observations for a given die i . Can be obtained as follow :
`observations = sample(1:8, N, replace=T)`

dies = prior distribution of the model comparison. Vector containing a serie of d possible die.

Measure empirically (using loops in R) the inference errors for:

- . the die of your choice
- . different values of N

How much the sampling size affects inferences ?

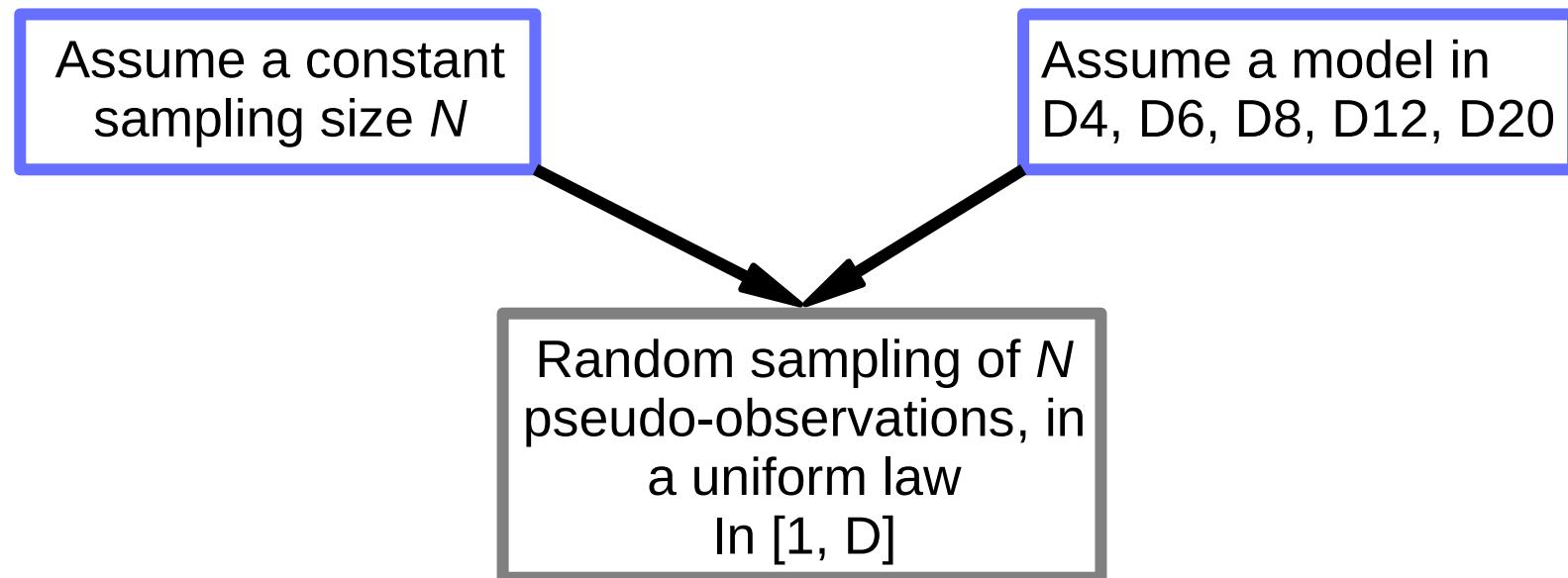
How alternative models compete each others ?

Assume a constant
sampling size N

Assume a model in
D4, D6, D8, D12, D20

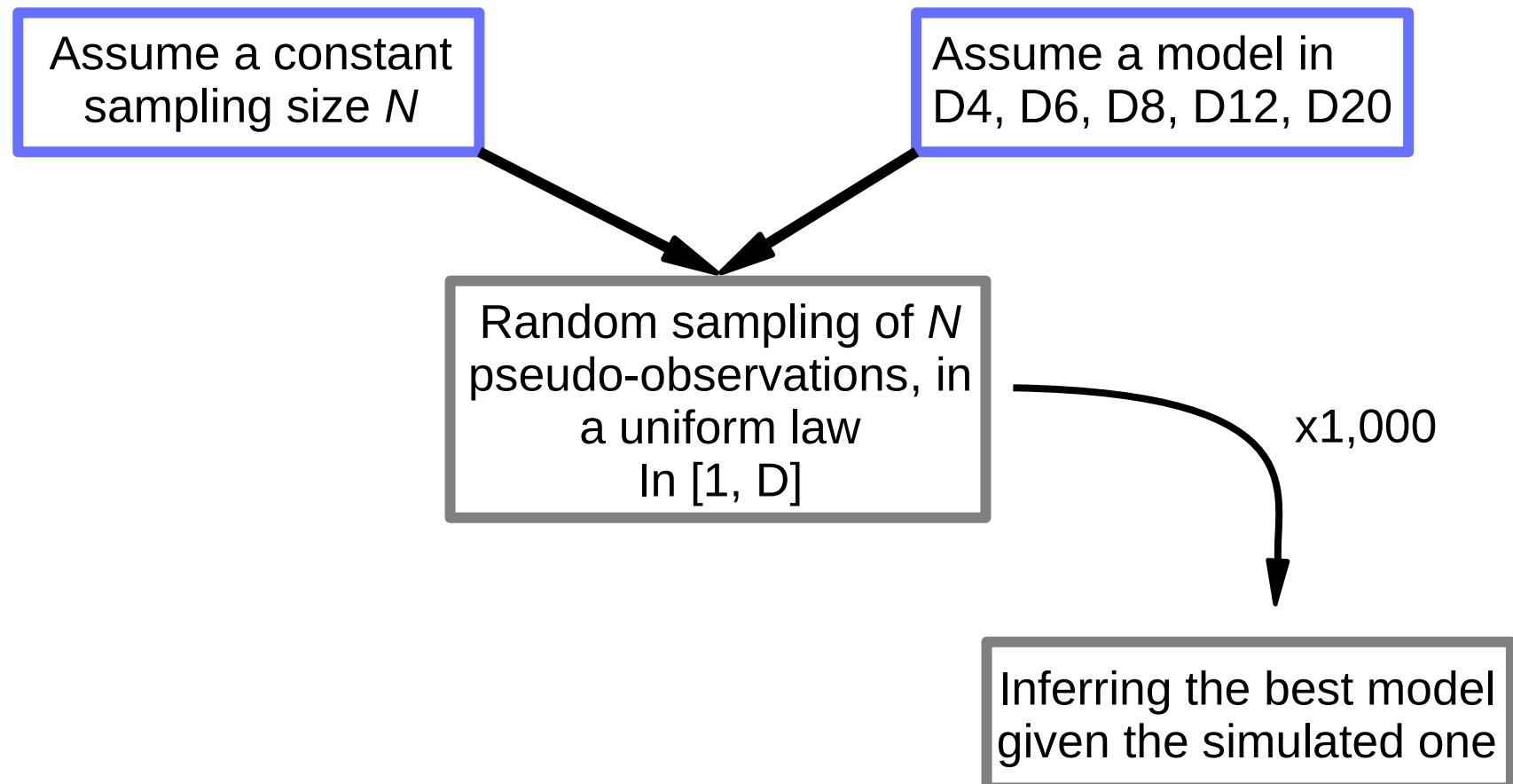
How much the sampling size affects inferences ?

How alternative models compete each others ?



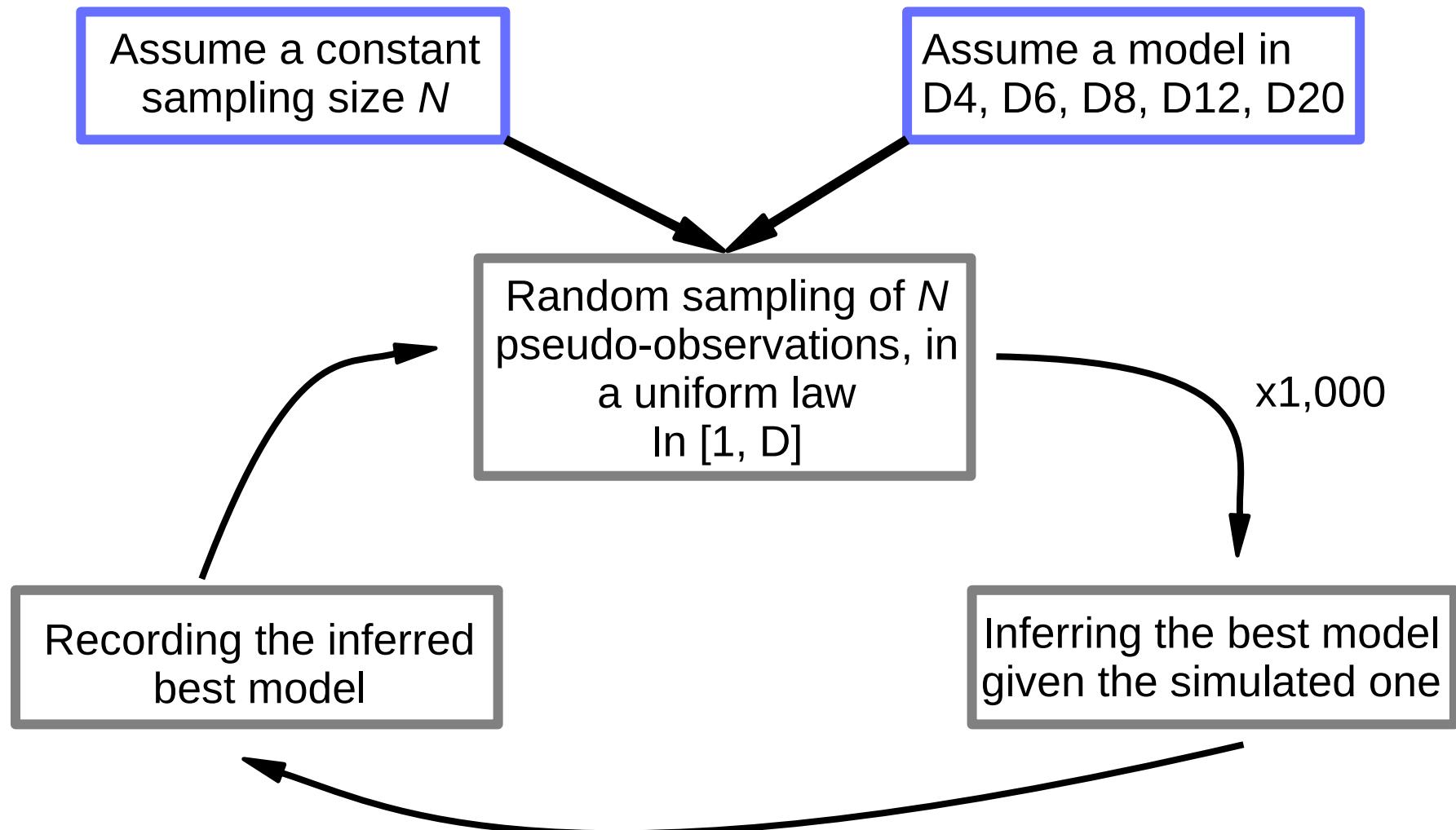
How much the sampling size affects inferences ?

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How much the sampling size affects inferences ?

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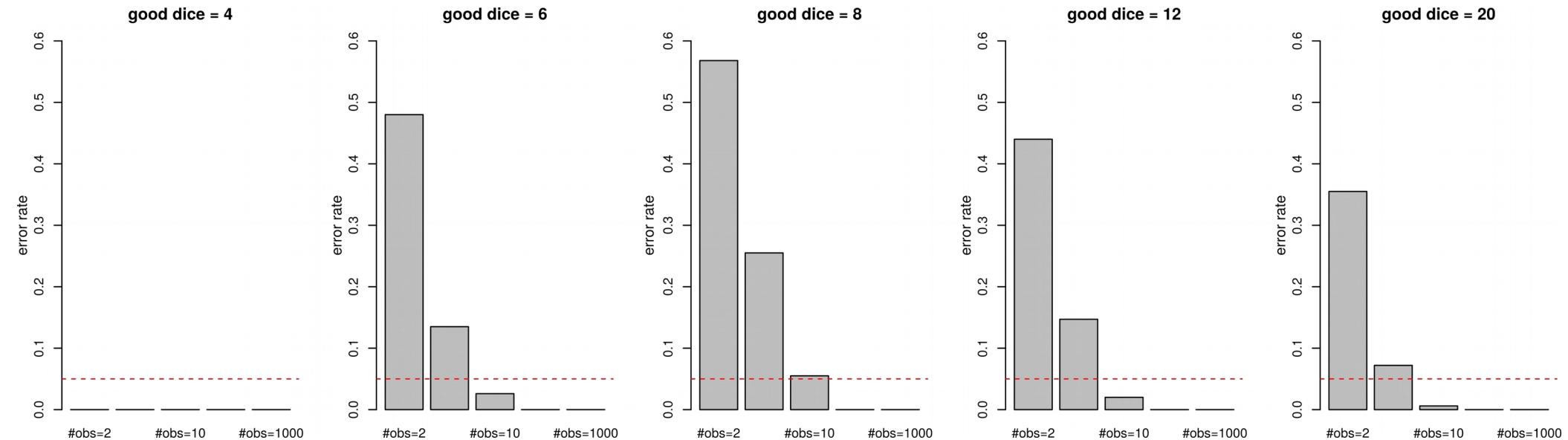
In R :`source('comparison_ABC_bayes.R')`
`plot_bayes_error(good_die=8, nReplicates=1000)`

Function made to show the error rate over Bayesian inferences

`good_die` = the correct die for which we know the identity that we will try to recapture using classic Bayesian inference

`nReplicates` = number of tests over which we will measure an error rate

How much the sampling size affects inferences ?





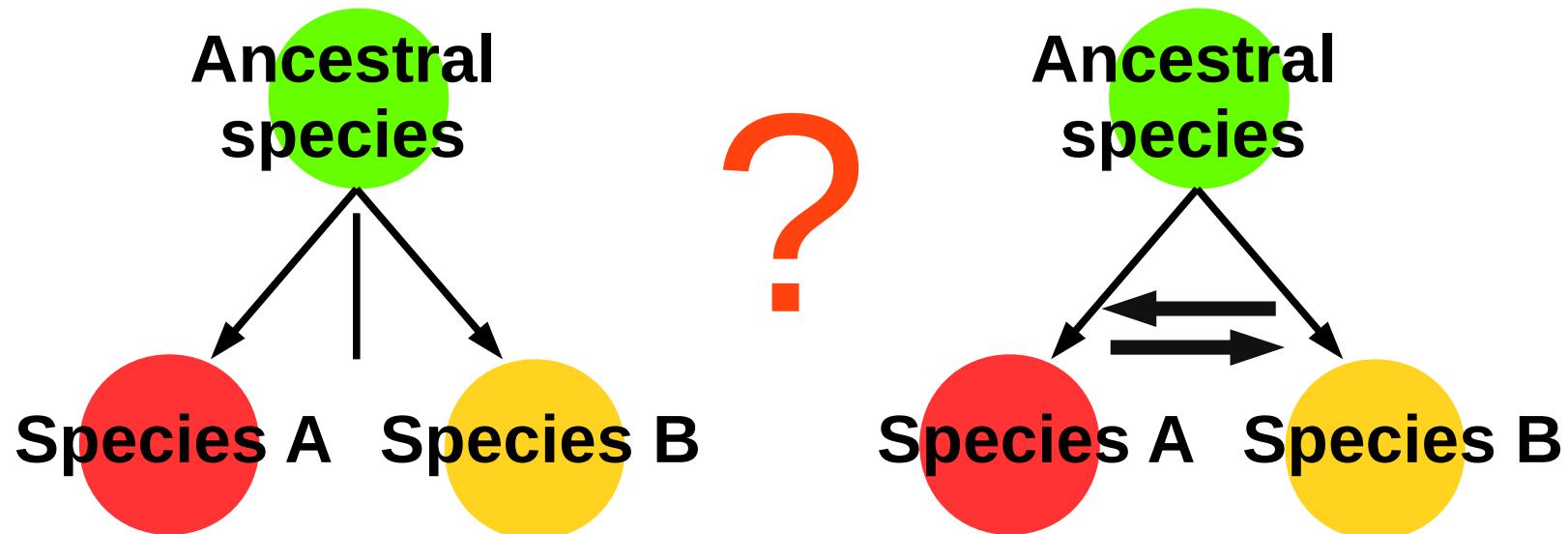
?



$$P(\text{Model},i \mid \text{Data}) = [P(\text{Data} \mid \text{Model},i) \times P(\text{Model},i)] / P(\text{Data})$$

Problem : the exact likelihood function is not available for all models

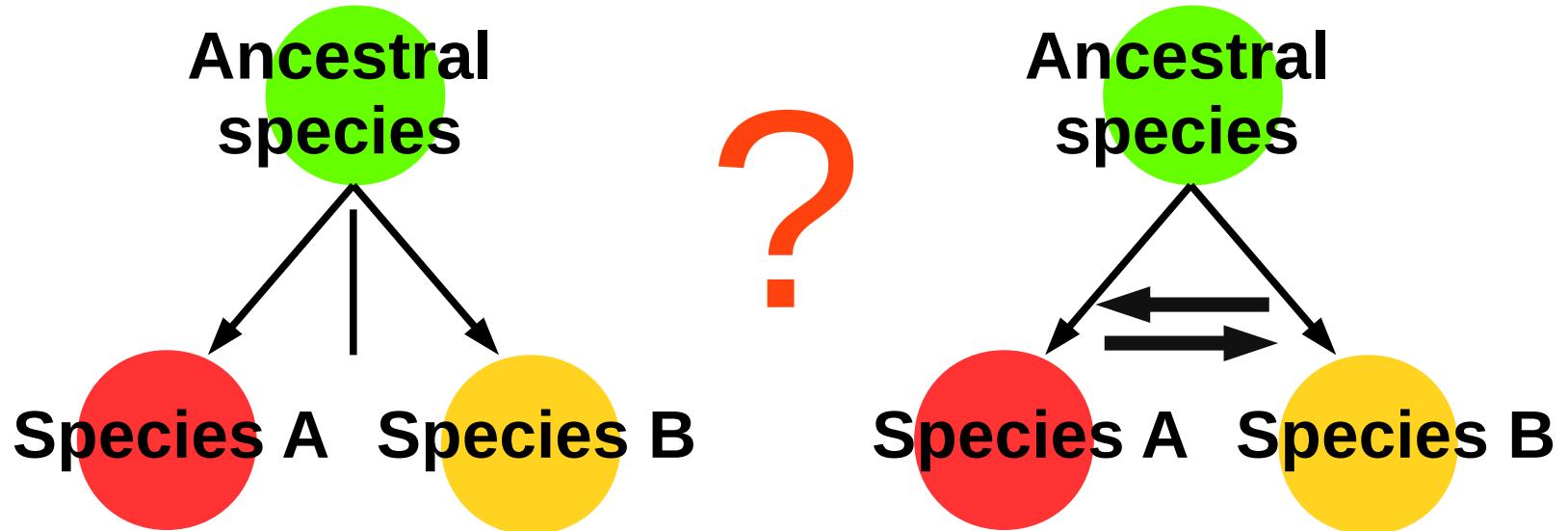
Approximated by ABC (approximate Bayesian computation)



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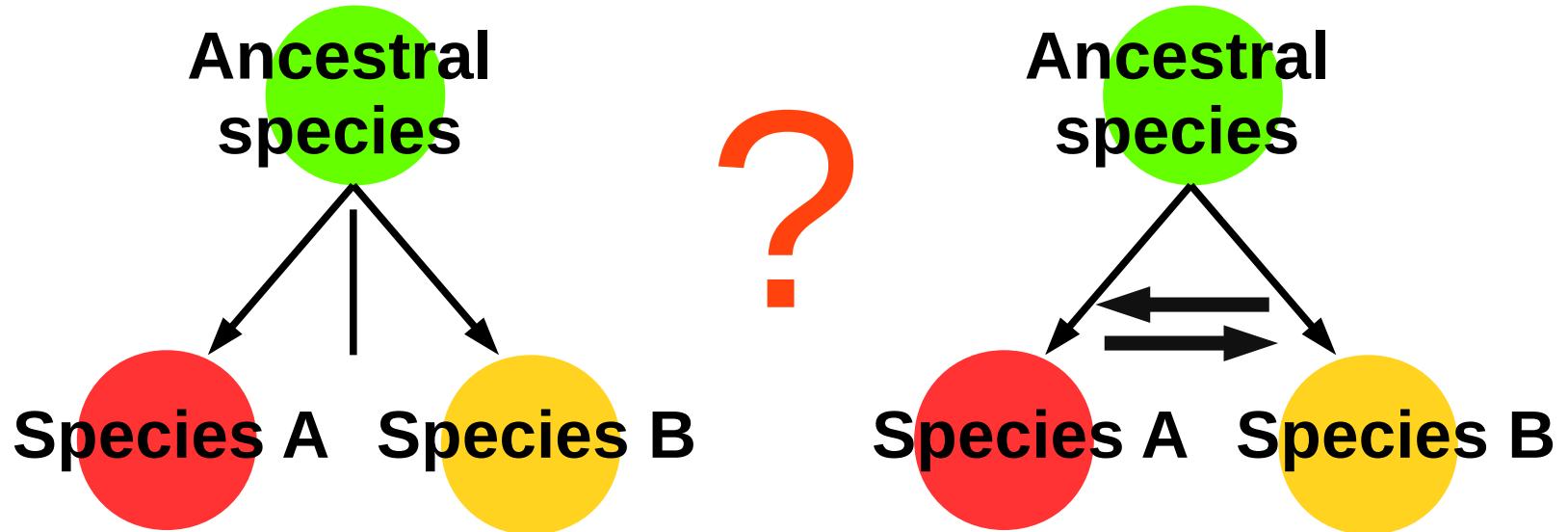
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$$P(\text{Model}, i \mid \text{Data}) = [P(\text{Data} \mid \text{Model}, i) \times P(\text{Model}, i)] / P(\text{Data})$$

Problem : the exact likelihood function is not available for all models

Approximated by ABC (approximate Bayesian computation)

ABC in 3 steps

1) summarizing the data with descriptive statistics



```
data = sample( 1:8, 10, replace = T )  
print(data)  
[1] 5 4 6 6 1 7 3 4 2 2
```

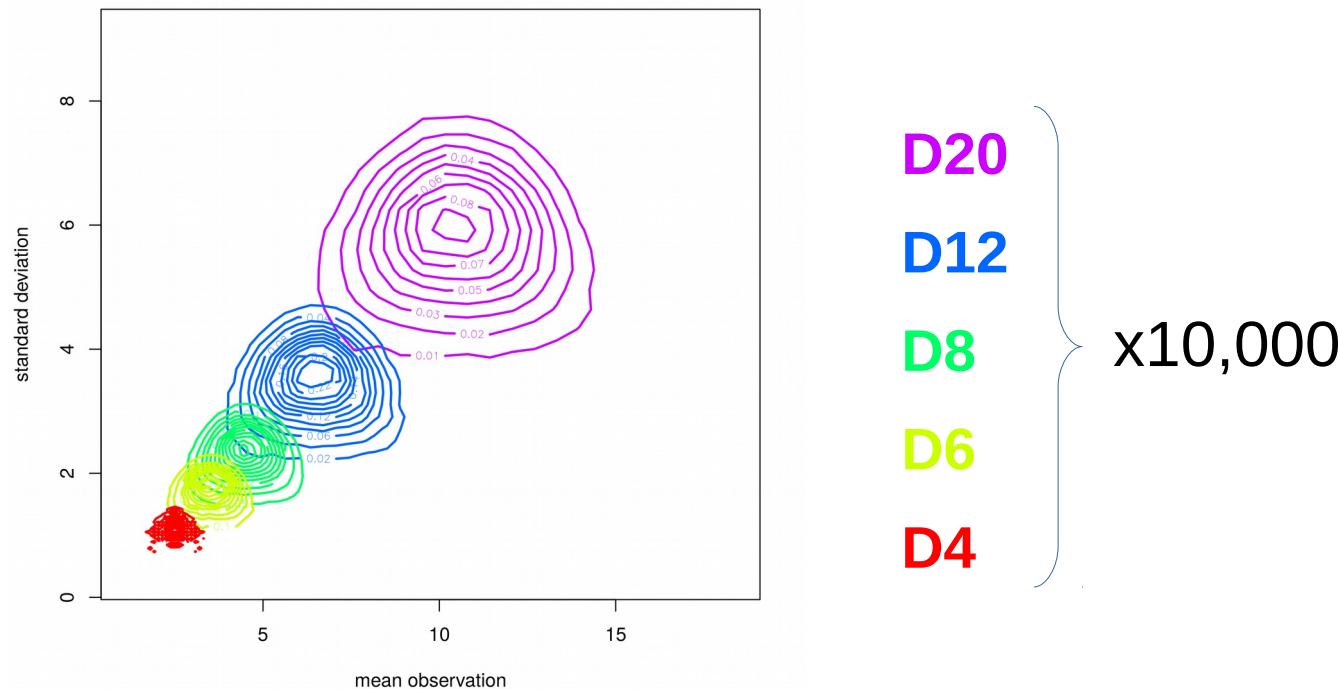
ABC in 3 steps

1) summarizing the data with descriptive statistics



```
data = sample( 1:8, 10, replace = T )  
print(data)  
[1] 5 4 6 6 1 7 3 4 2 2
```

2) random simulations of the statistics under the compared models



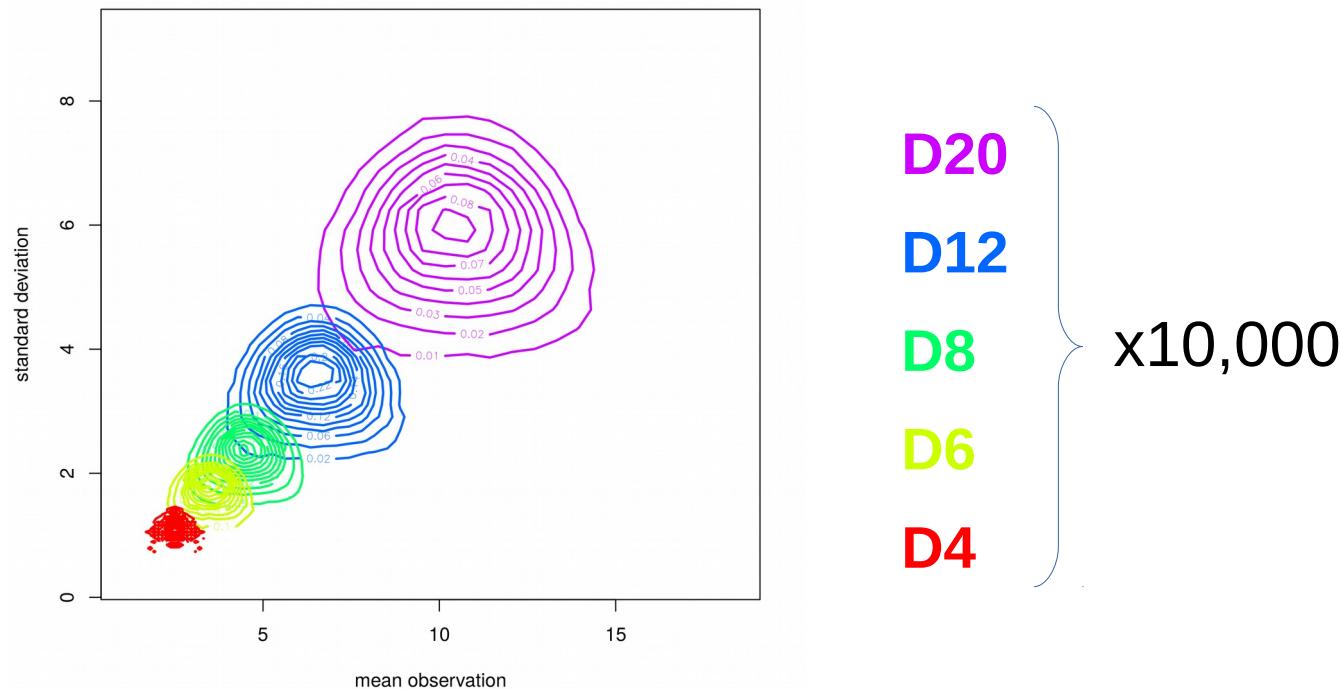
ABC in 3 steps

1) summarizing the data with descriptive statistics



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data = sample( 1:8, 10, replace = T )  
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```

2) random simulations of the statistics under the compared models



3) statistical comparison between the observation and the simulations

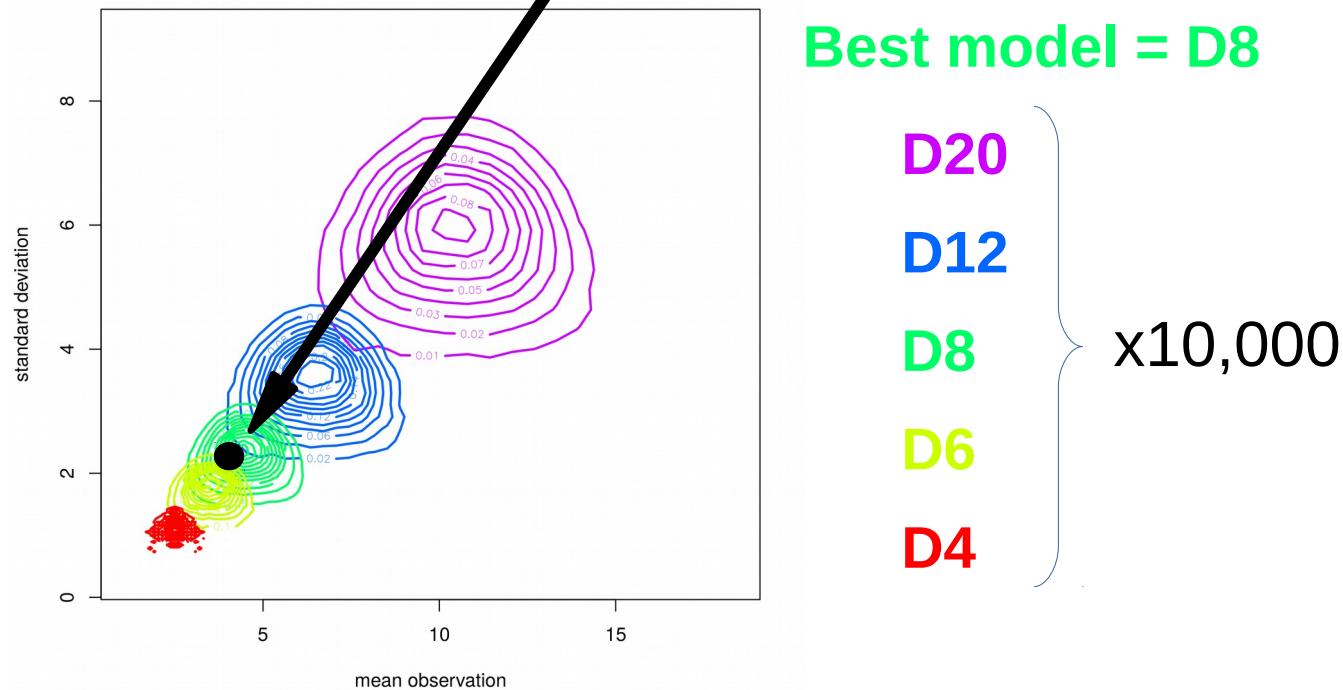
ABC in 3 steps

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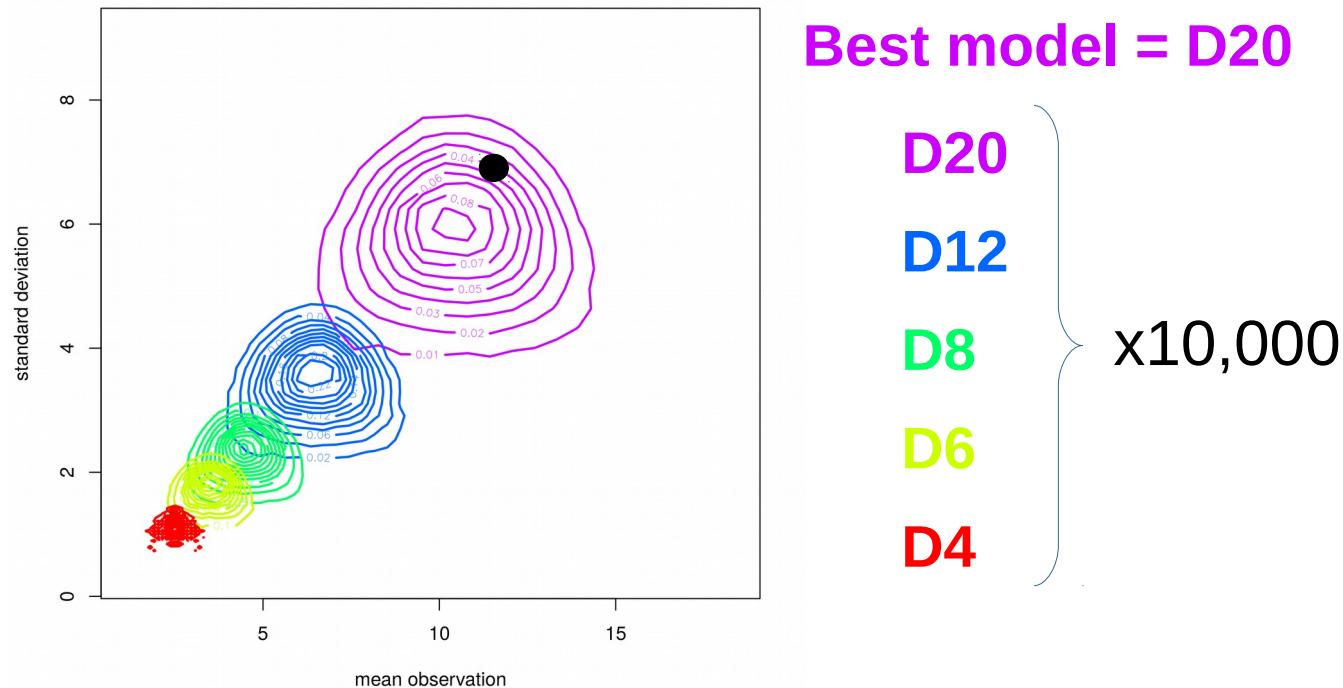
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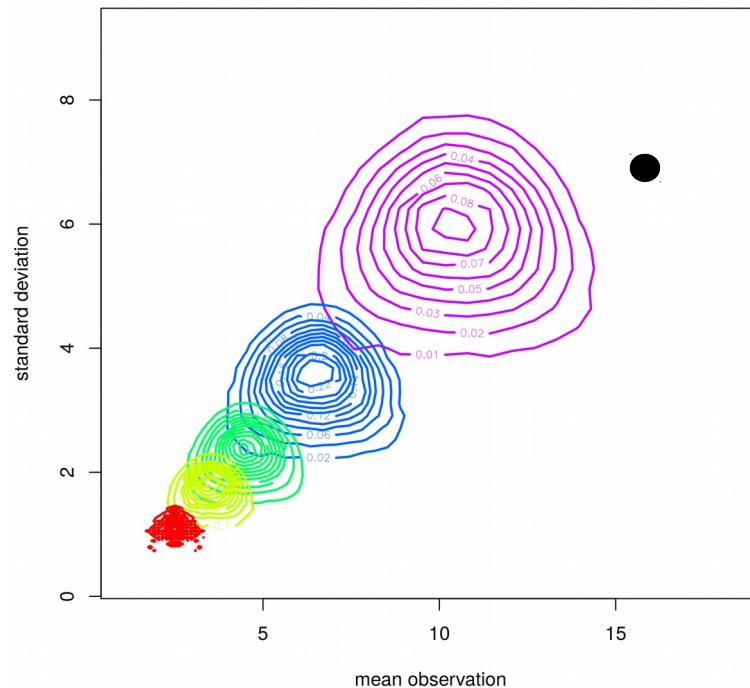
ABC in 3 steps

1) summarizing the data with descriptive statistics



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```

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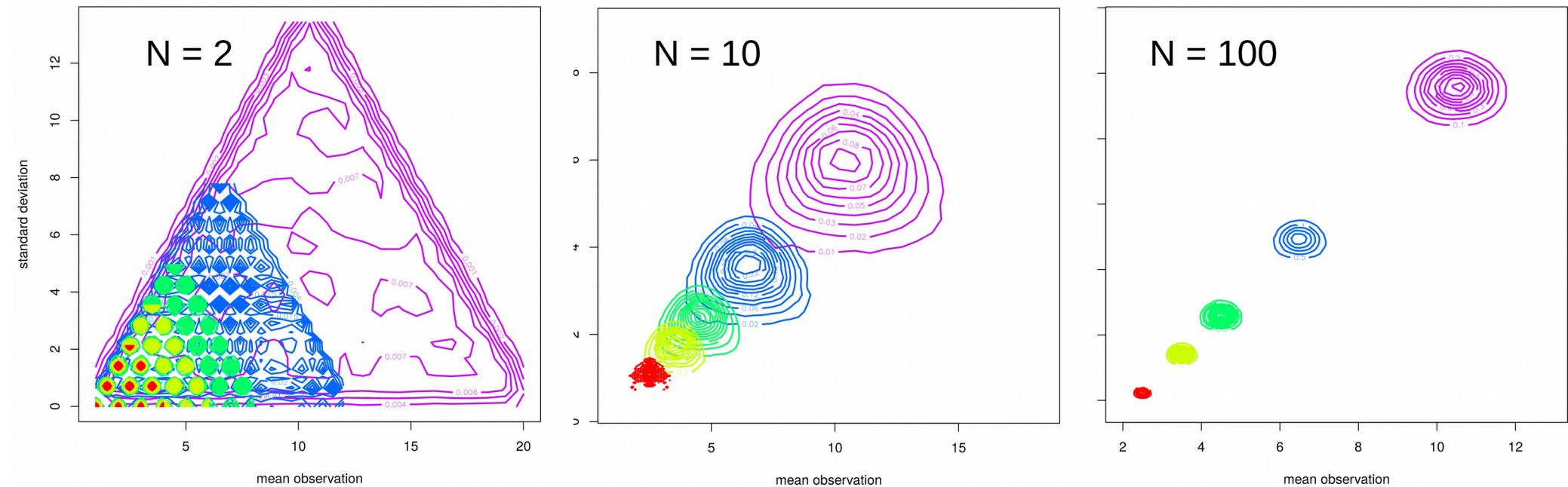
Best model = D20 (still the case)

D20
D12
D8
D6
D4

x10,000

3) statistical comparison between the observation and the simulations

Simulating the same sample size than for the observed dataset



Statistical comparison using Random Forests

One Random Forest = thousands of Decision Trees

Statistical comparison using Random Forests

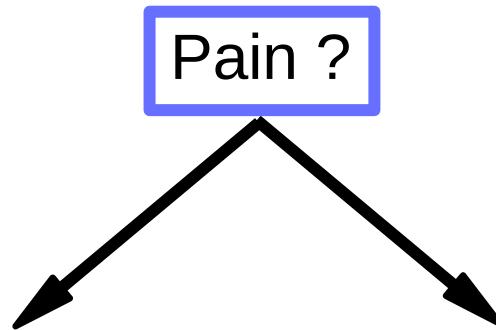
One Random Forest = thousands of Decision Trees

One Decision Tree = a succession of dichotomous criteria leading to
a decision

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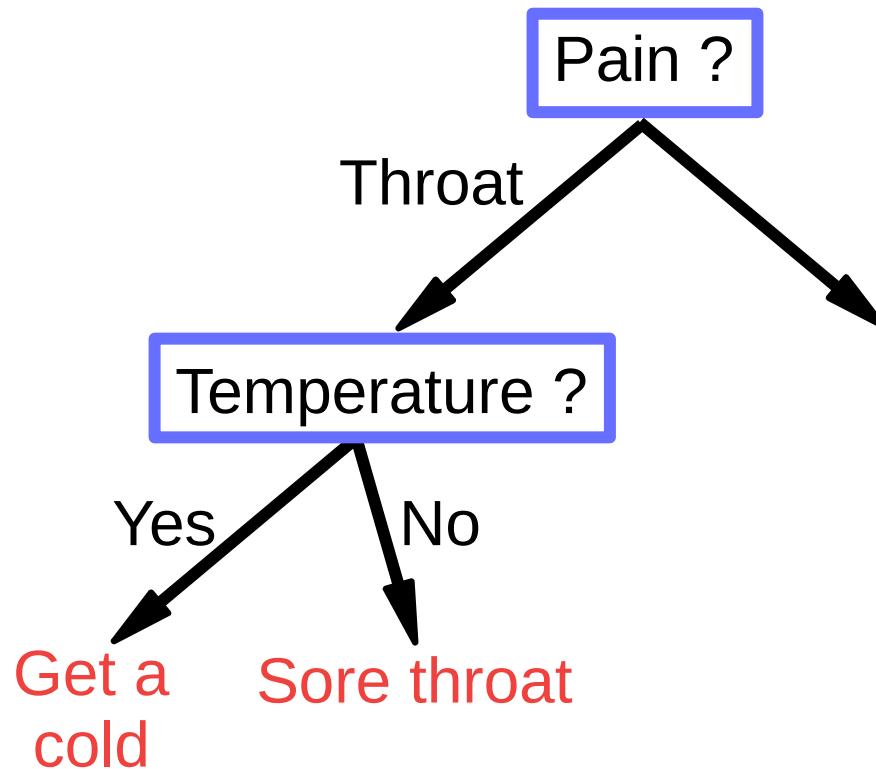
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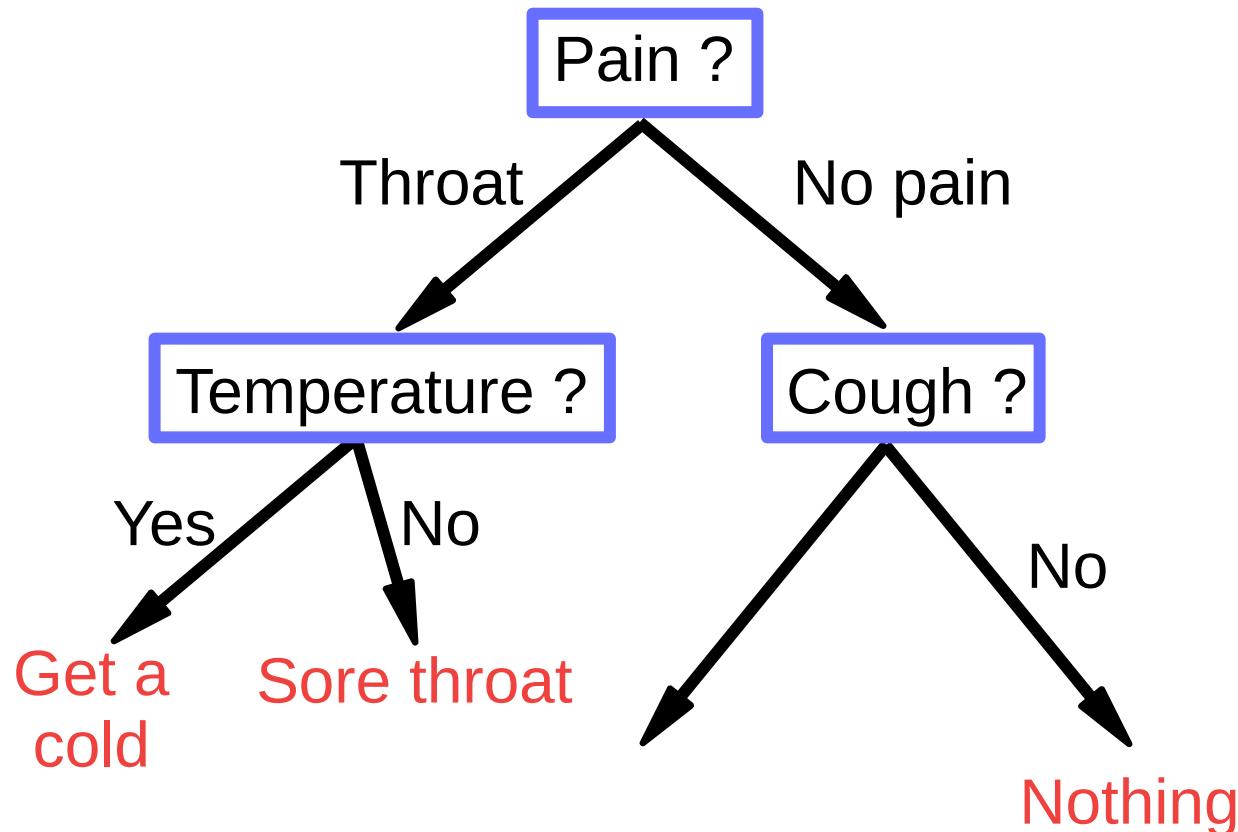
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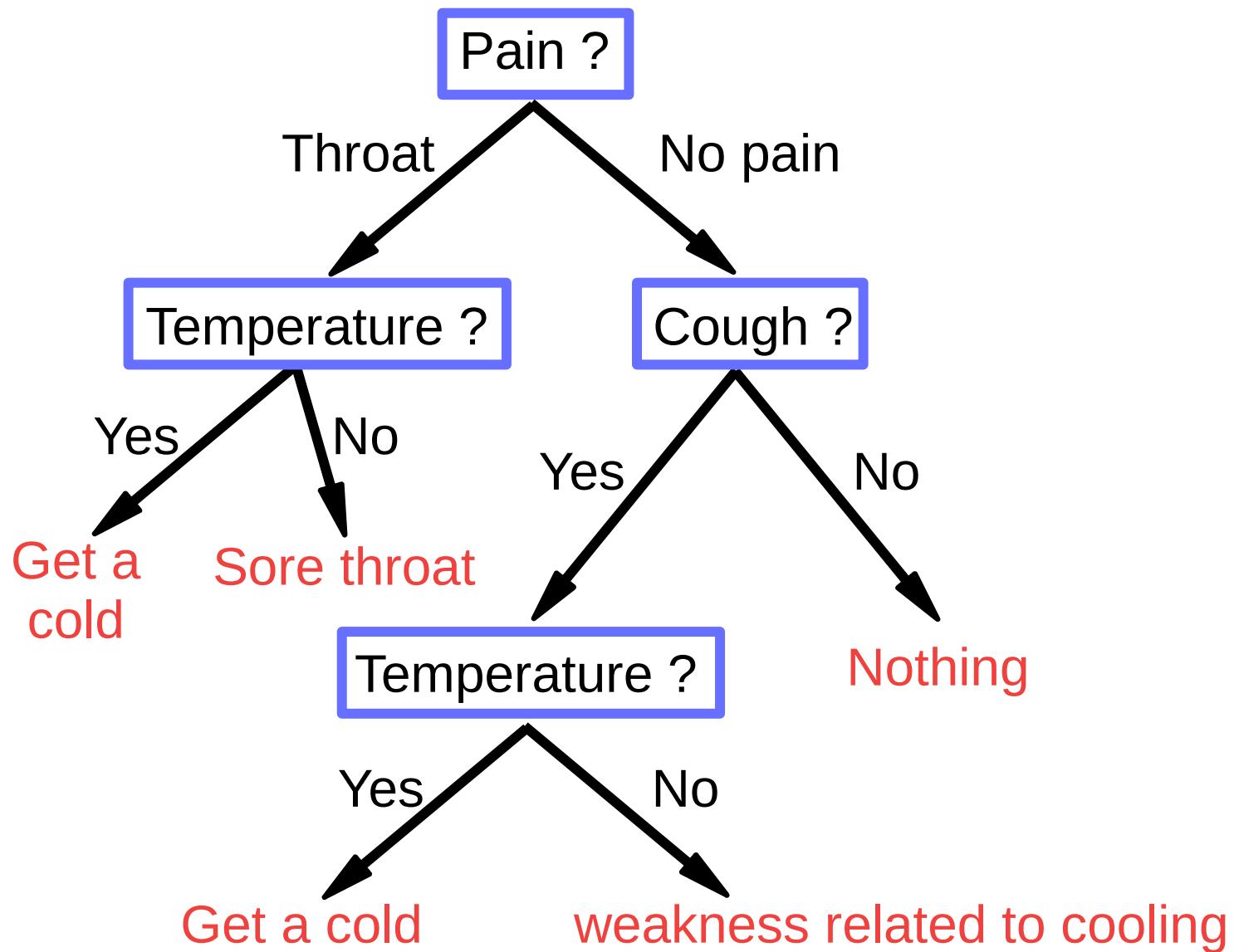
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Statistical comparison using Random Forests

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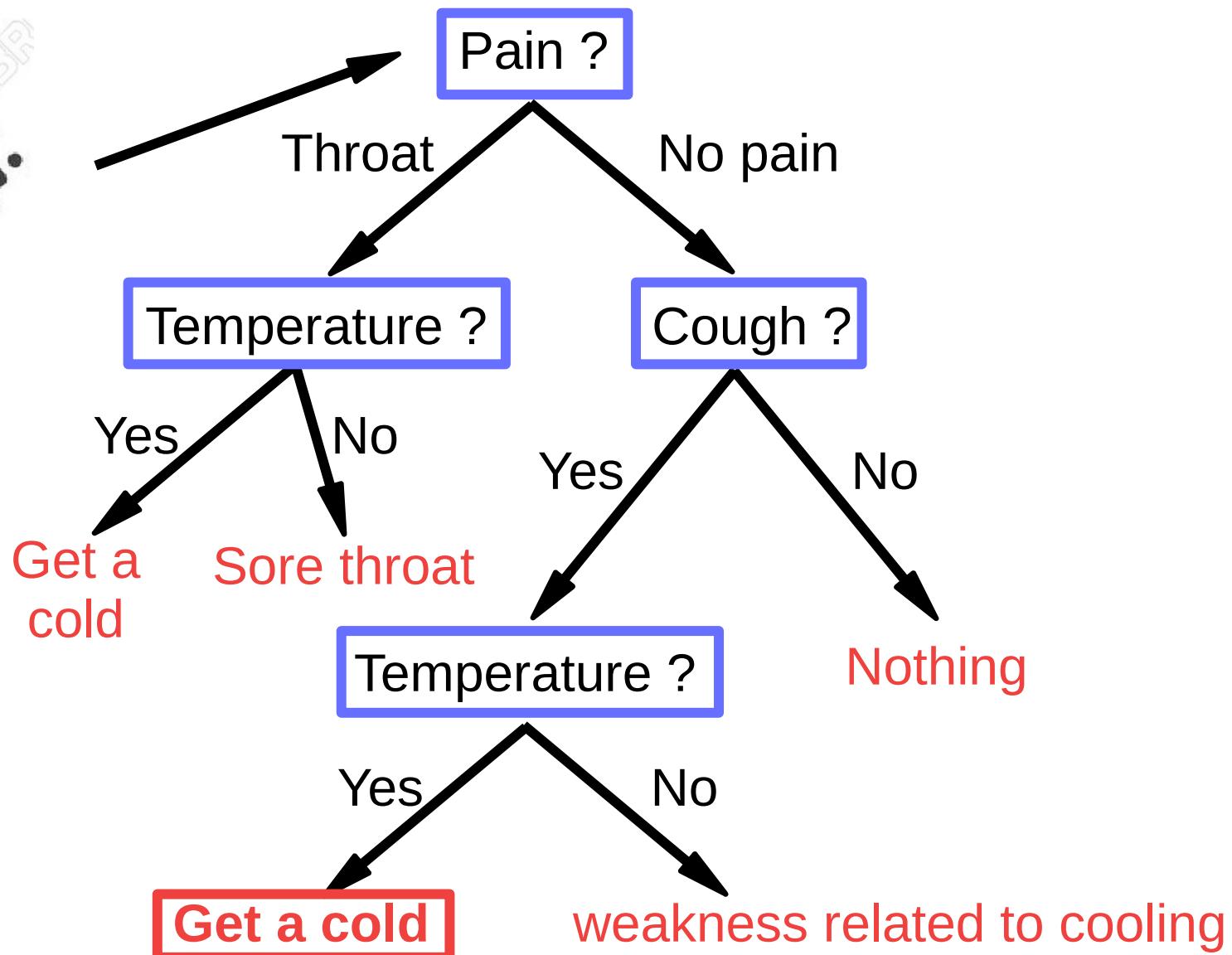
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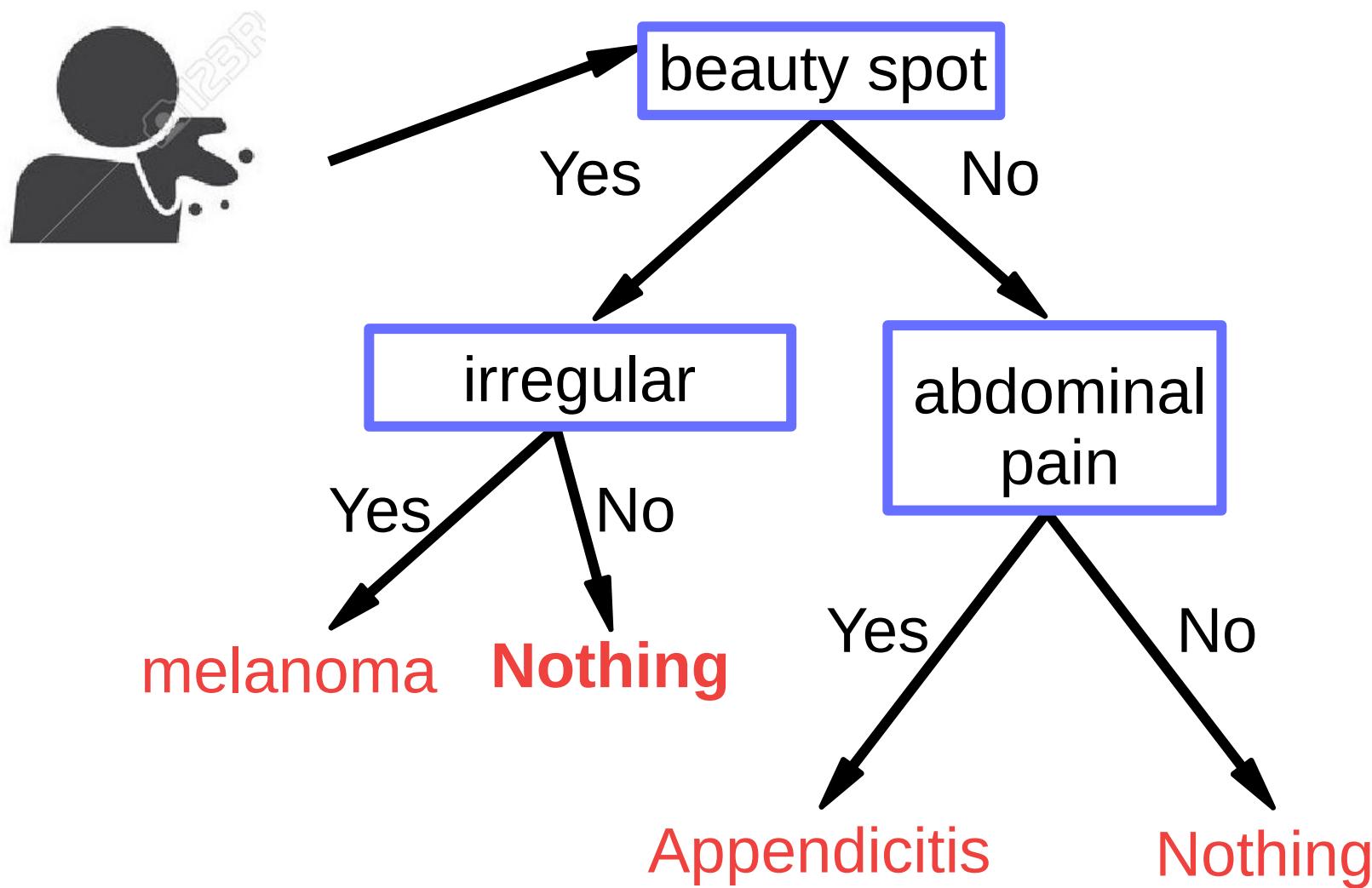
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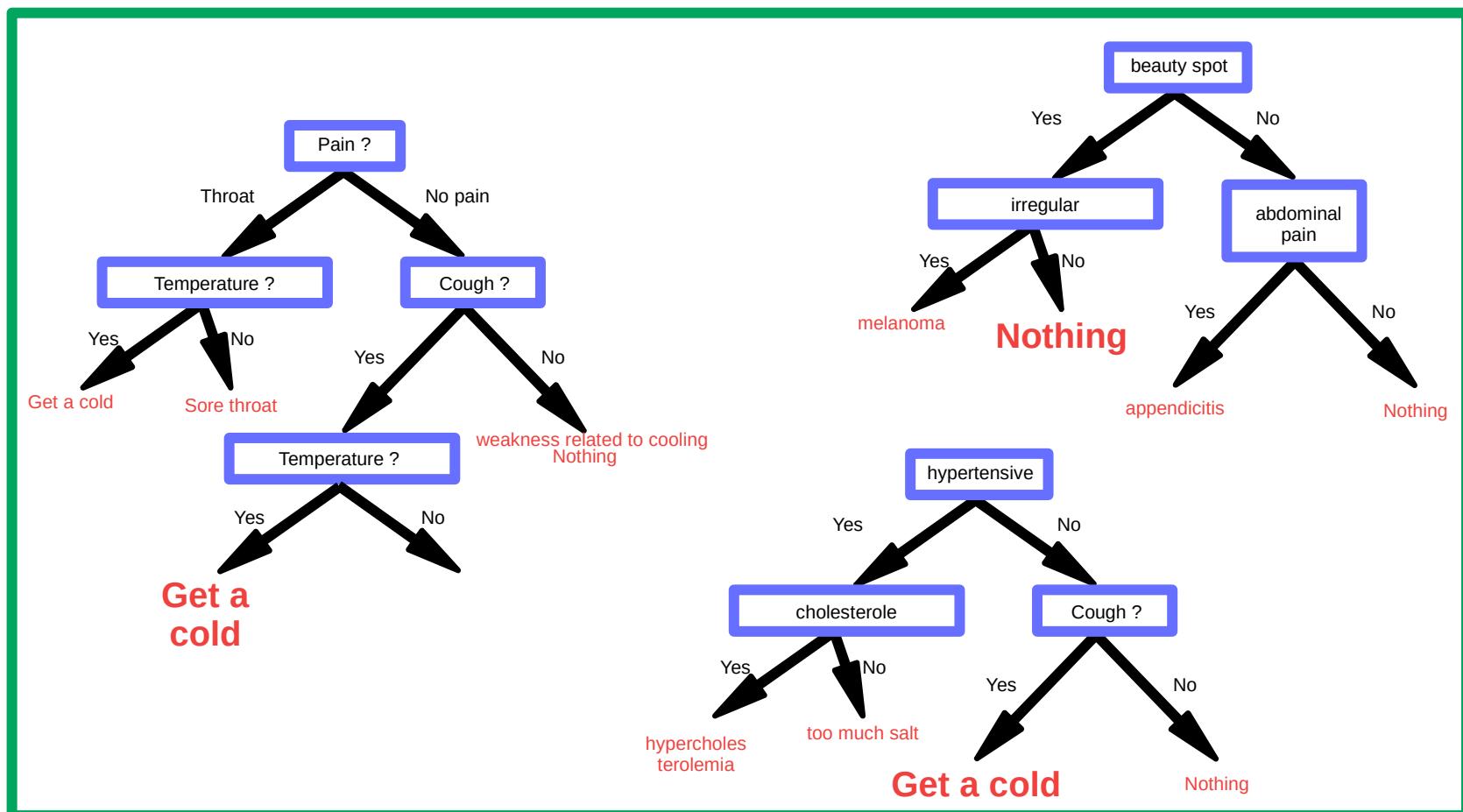
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One Random Forest = thousands of Decision Trees

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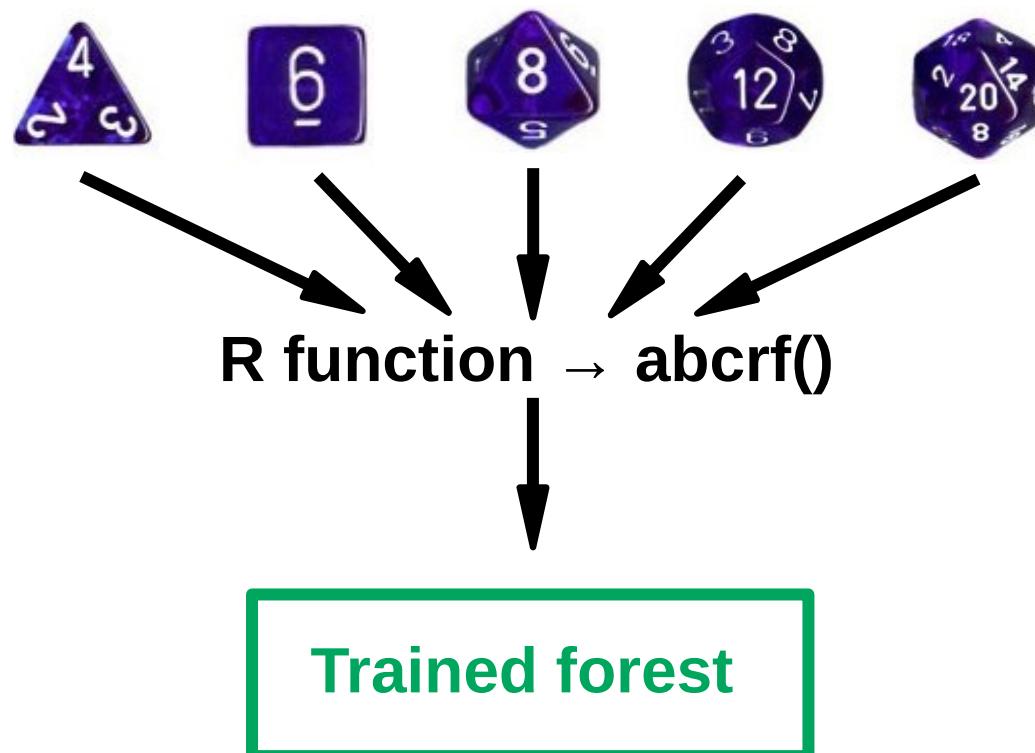
Statistical comparison using Random Forests



Get a cold (by majority)

Statistical comparison using Random Forests

Two steps : 1) growing **the forest** (= learning or training step) using the R function **abcrf()**
2) making the inference for the observed dataset using the R function **predict()**



Statistical comparison using Random Forests

Two steps : 1) growing **the forest** (= learning or training step) using the R function **abcrf()**



For each model, we will produce 10,000 series of N observations
(i.e. of N die rolls)

Statistical comparison using Random Forests

Two steps : 1) growing **the forest** (= learning or training step) using the R function **abcrf()**



For each model, we will produce 10,000 series of N die rolls

```
nSimulations = 10000

simulations_die_8 = as.data.frame(matrix(NA, ncol=N, nrow=nSimulations))

for(i in 1:nSimulations){
  simulations_die_8[i,] = sample(1:8, N, replace=T)
}

colnames(simulations_die_8) = paste( rep('obs', N), 1:N, sep=' ')
```

Statistical comparison using Random Forests

Two steps : 1) growing **the forest** (= learning or training step) using the R function **abcrf()**

```
N = 10

nSimulations = 10000

simulations_die_4 = as.data.frame(matrix(NA, ncol=N, nrow=nSimulations))
simulations_die_6 = as.data.frame(matrix(NA, ncol=N, nrow=nSimulations))
simulations_die_8 = as.data.frame(matrix(NA, ncol=N, nrow=nSimulations))
simulations_die_12 = as.data.frame(matrix(NA, ncol=N, nrow=nSimulations))
simulations_die_20 = as.data.frame(matrix(NA, ncol=N, nrow=nSimulations))

for(i in 1:nSimulations){
    simulations_die_4[i,] = sample(1:4, N, replace=T)
    simulations_die_6[i,] = sample(1:6, N, replace=T)
    simulations_die_8[i,] = sample(1:8, N, replace=T)
    simulations_die_12[i,] = sample(1:12, N, replace=T)
    simulations_die_20[i,] = sample(1:20, N, replace=T)
}

colnames(simulations_die_4) = paste(rep('obs', N), 1:N, sep=' ')
colnames(simulations_die_6) = paste(rep('obs', N), 1:N, sep=' ')
colnames(simulations_die_8) = paste(rep('obs', N), 1:N, sep=' ')
colnames(simulations_die_12) = paste(rep('obs', N), 1:N, sep=' ')
colnames(simulations_die_20) = paste(rep('obs', N), 1:N, sep=' ')
```

Statistical comparison using Random Forests

Two steps : 1) growing **the forest** (= learning or training step) using the R function **abcrf()**

Gathering all simulations in the same data.frame

```
all_simulations = rbind(simulations_die_4, simulations_die_6, simulations_die_8, simulations_die_12, simulations_die_20)
```

Statistical comparison using Random Forests

Two steps : 1) growing **the forest** (= learning or training step) using the R function **abcrf()**

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Getting a correspondance between each row of « all_simulations » and the associated models

```
modIndexes = rep(c('D4', 'D6', 'D8', 'D12', 'D20'), each = nSimulations)
```

Statistical comparison using Random Forests

Two steps : 1) growing **the forest** (= learning or training step) using the R function **abcrf()**

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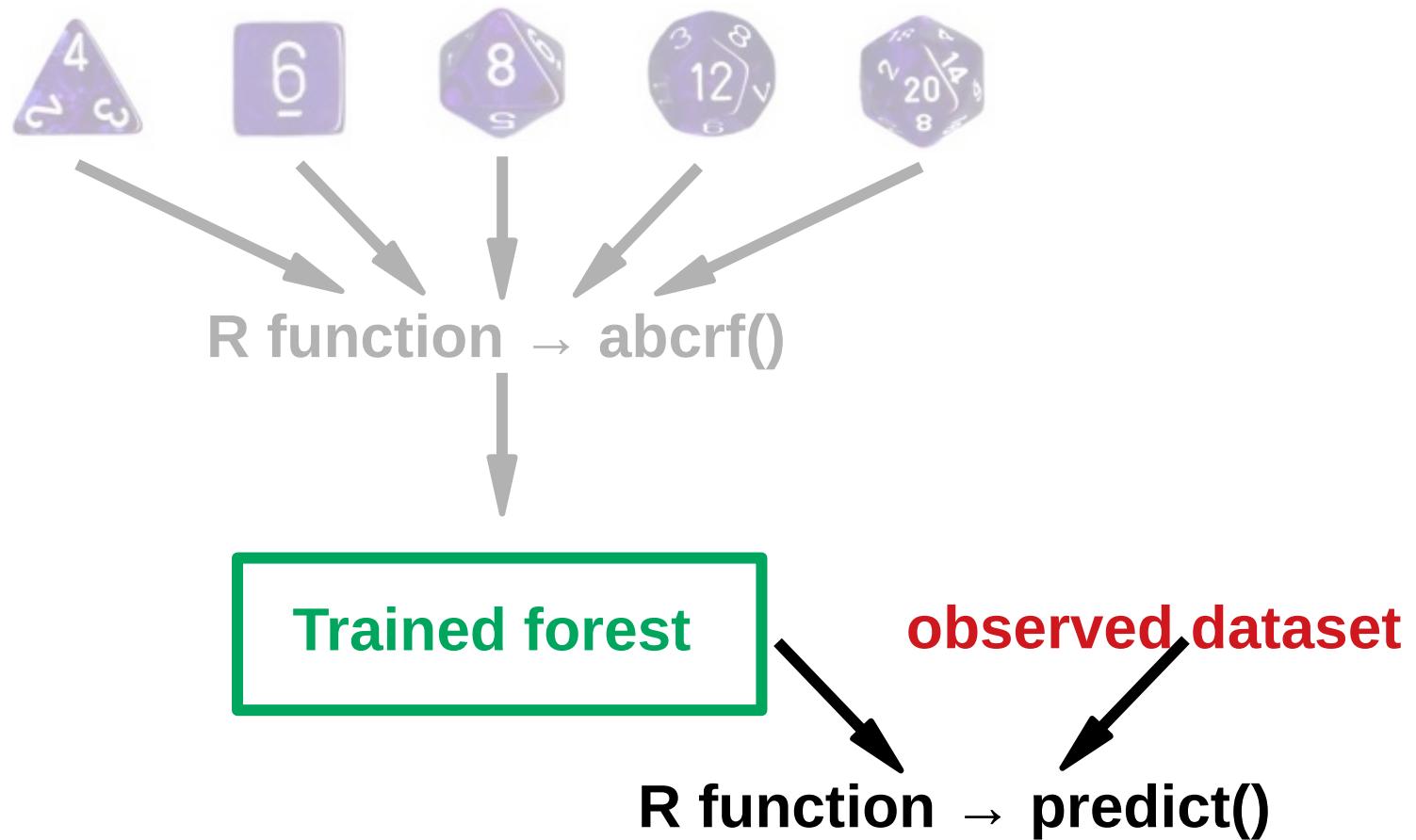
```
modIndexes = rep(c('D4', 'D6', 'D8', 'D12', 'D20'), each = nSimulations)
```

Training the forest

```
mod = abcrf(modIndexes~, data = data.frame(modIndexes, all_simulations), ntree = 1000, paral = T, ncores = 3)
```

Statistical comparison using Random Forests

Two steps : 1) growing **the forest** (= learning or training step) using the R function **abcrf()**
2) making the inference for the **observed dataset** using the R function **predict()**



Statistical comparison using Random Forests

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```
mod = abcrf(modIndexes~, data = data.frame(modIndexes, all_simulations), ntree = 1000, paral = T, ncores = 3)
```

Trained forest = mod

2) making the inference for the **observed dataset** using the R function **predict()**

Producing some « pseudo observations »

```
observations = matrix(sample(1:8, N, replace=T), nrow=1, ncol=N)
observations = as.data.frame(observations)
names(observations) = paste(rep('obs', N), 1:N, sep='')
```

Statistical comparison using Random Forests

Two steps : 1) growing **the forest** (= learning or training step) using the R function **abcrf()**

```
mod = abcrf(modIndexes~, data = data.frame(modIndexes, all_simulations), ntree = 1000, paral = T, ncores = 3)
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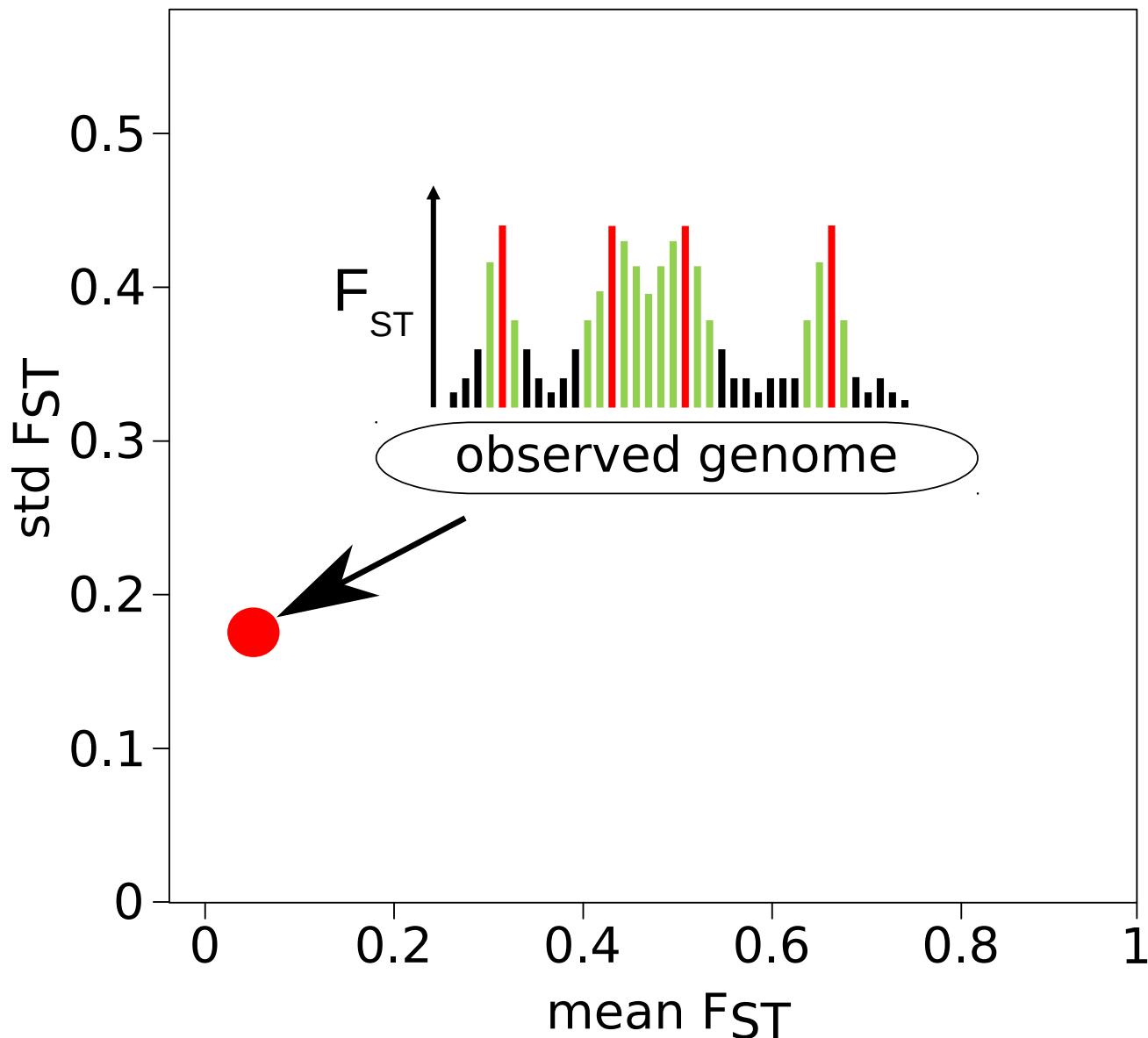
Using the trained machine learning 

```
predicted_dice = predict(mod, observations, training=data.frame(modIndexes, all_simulations),
ntree = 1000, paral = T, ncores=2)
```

Before Lunch :

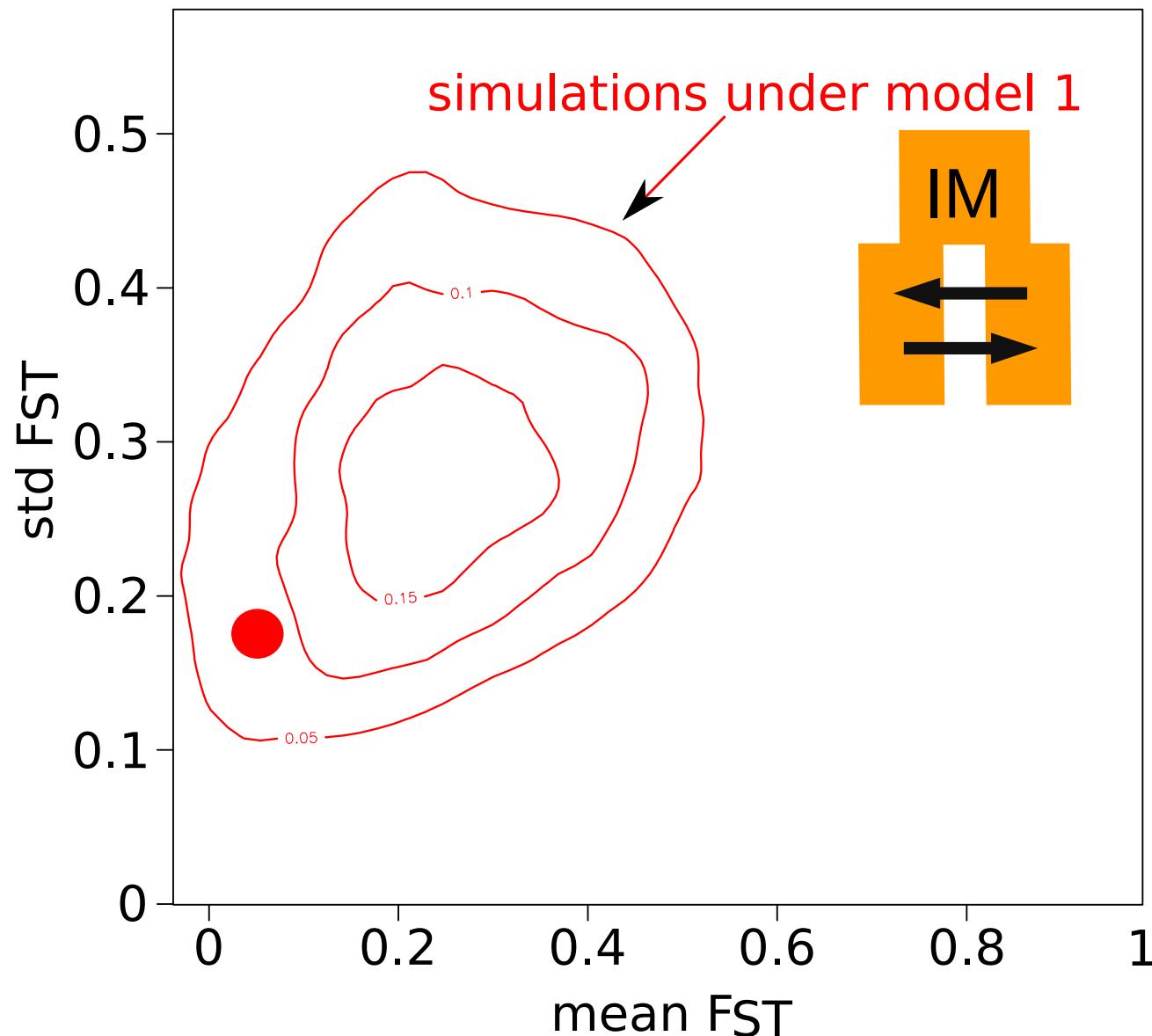
Comparing the Bayesian posterior probability with the approximated posterior probability for different conditions !

approximate Bayesian computation



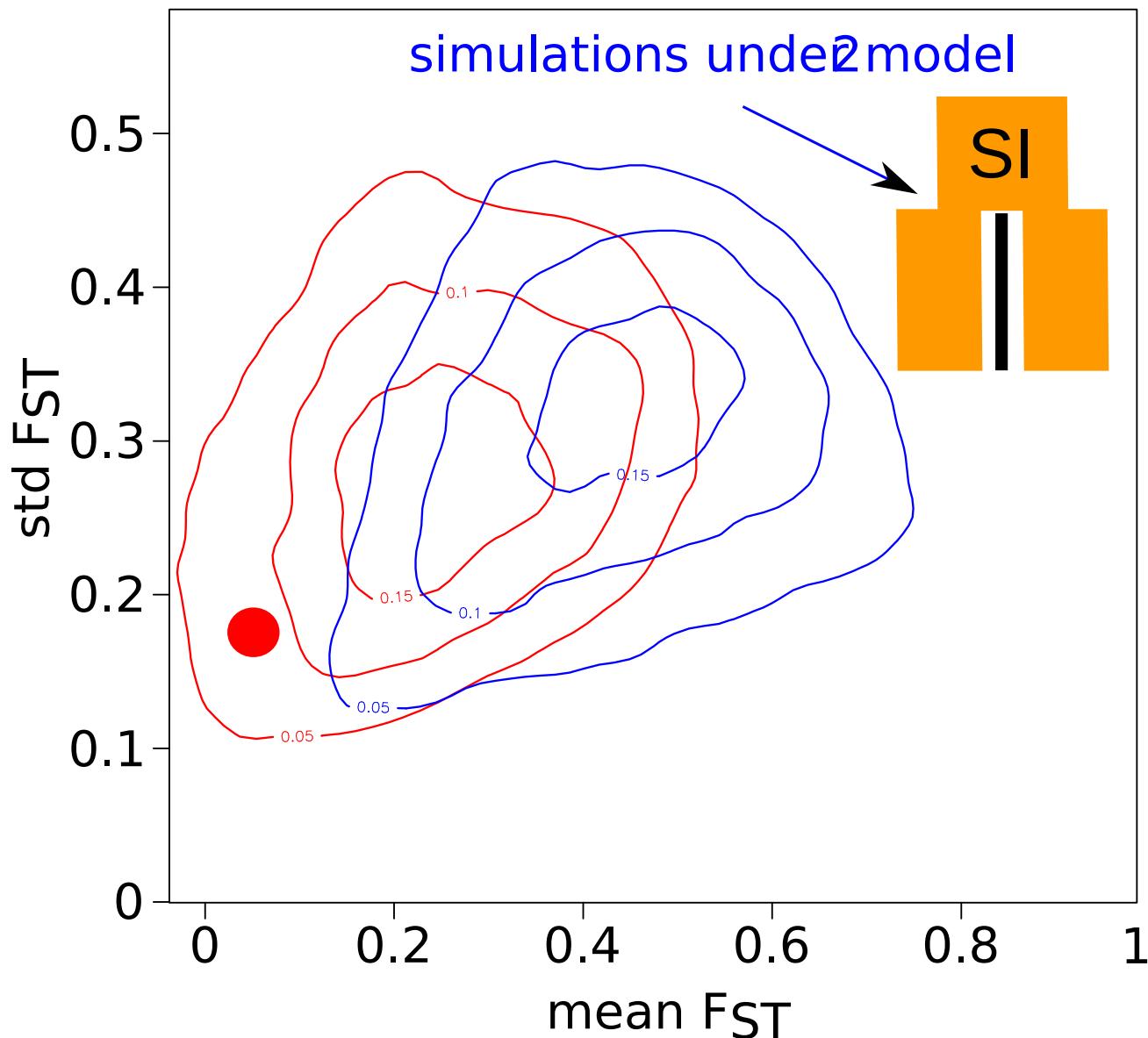
- 1) summarizing the data with descriptive statistics
- 2) random simulations under the compared models
- 3) statistical comparison between the observation and the simulations

approximate Bayesian computation



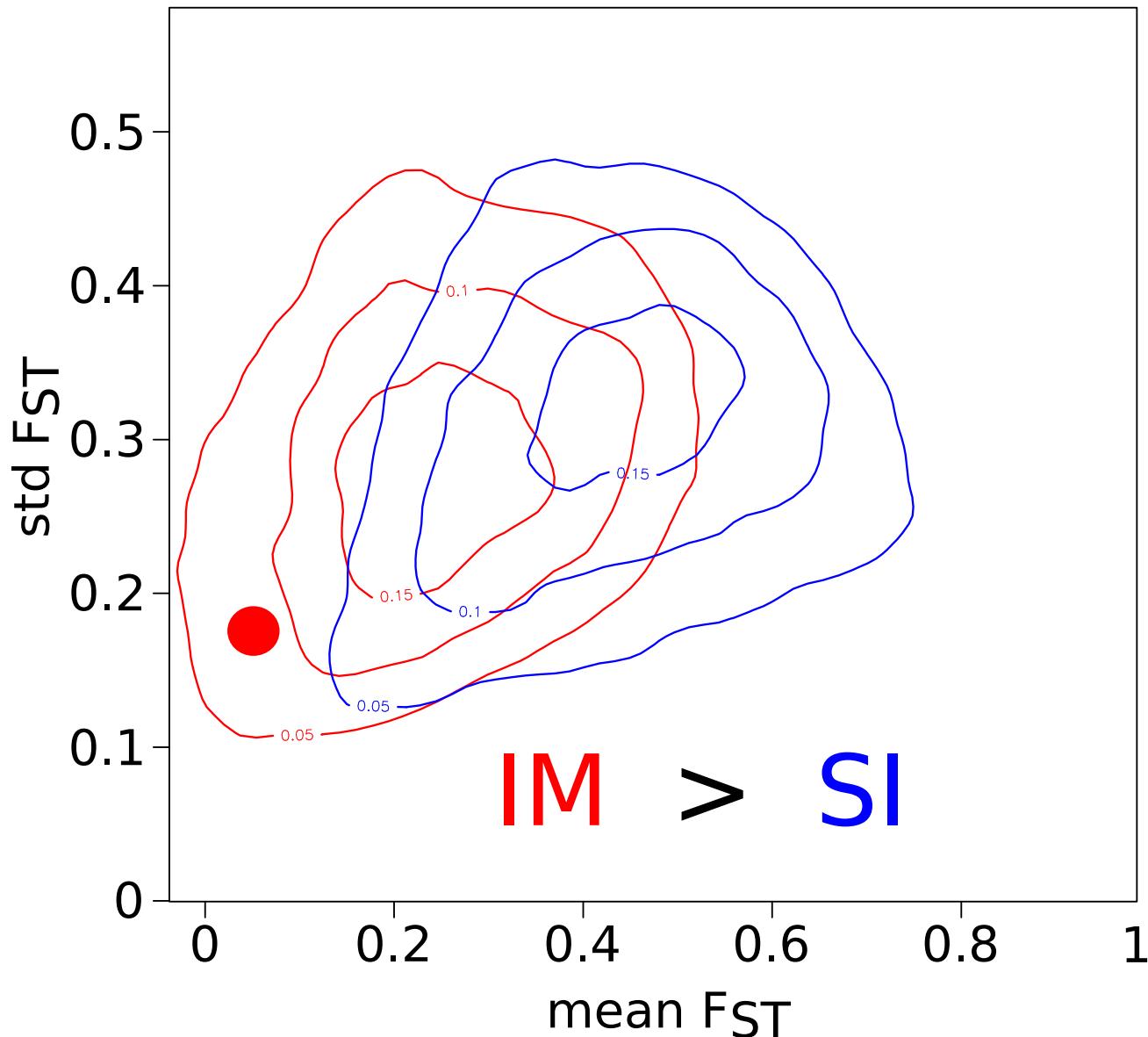
- 1) summarizing the data with descriptive statistics
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approximate Bayesian computation



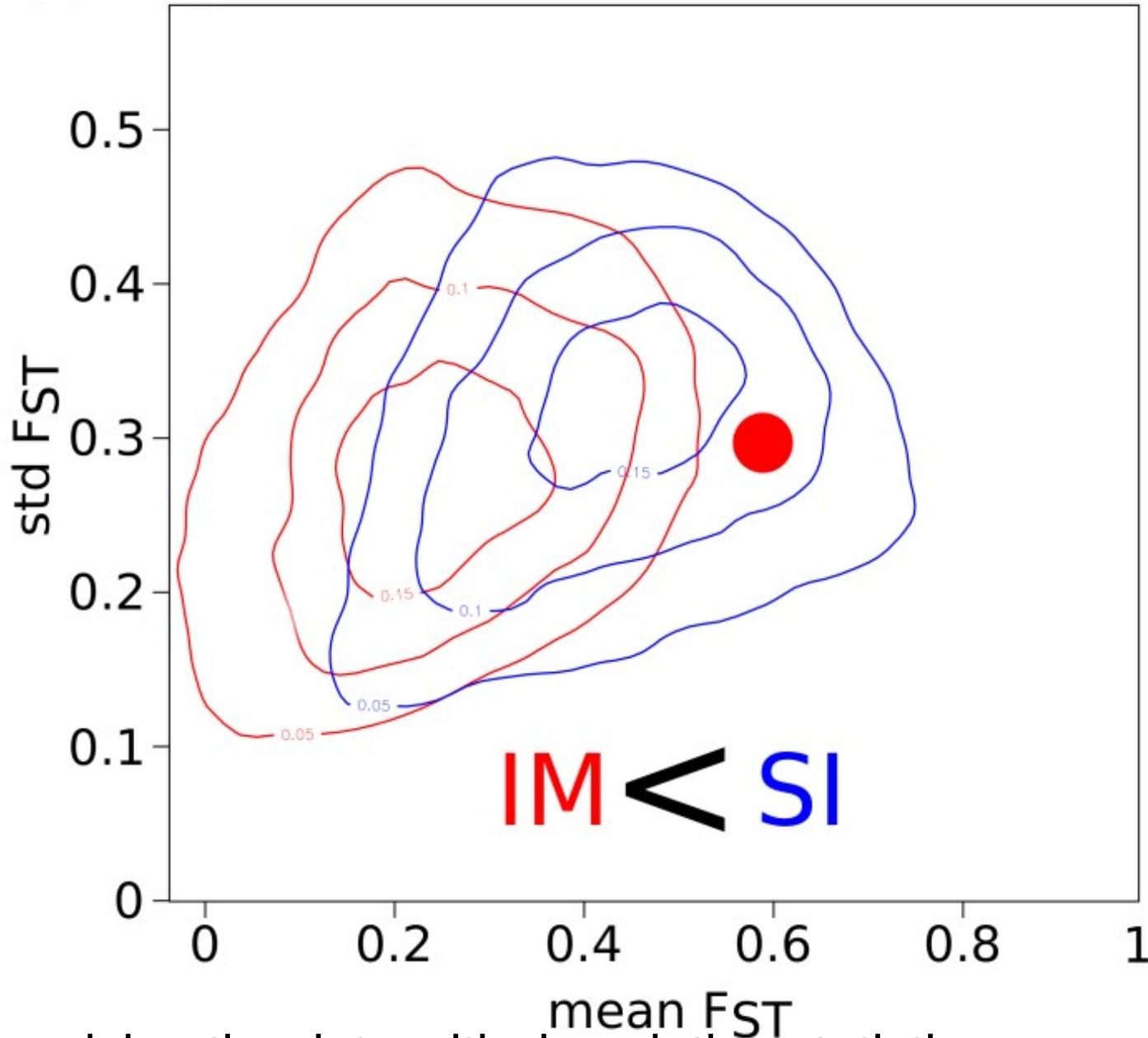
- 1) summarizing the data with descriptive statistics
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- 3) statistical comparison between the observation and the simulations

approximate Bayesian computation



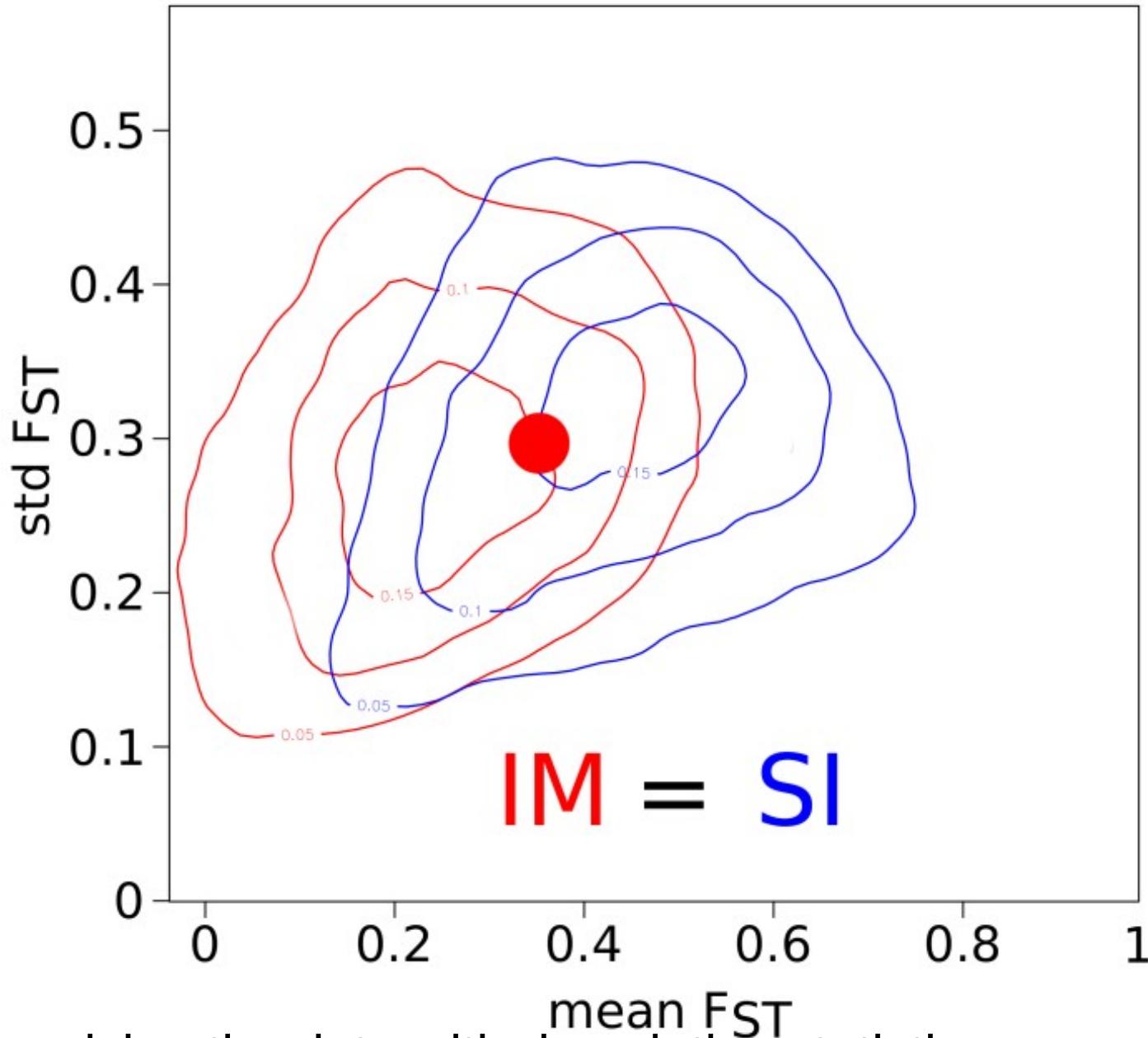
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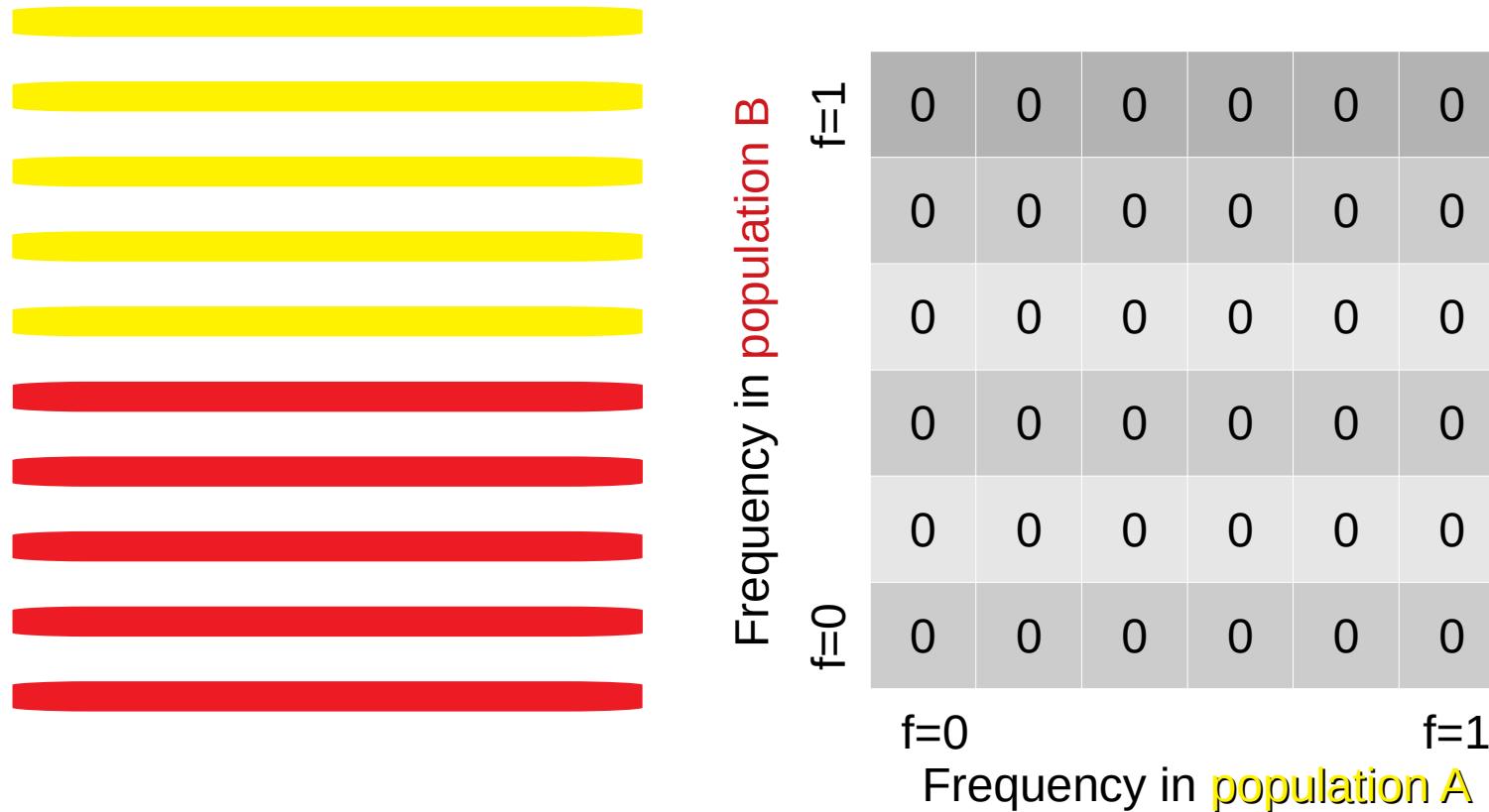
approximate Bayesian computation



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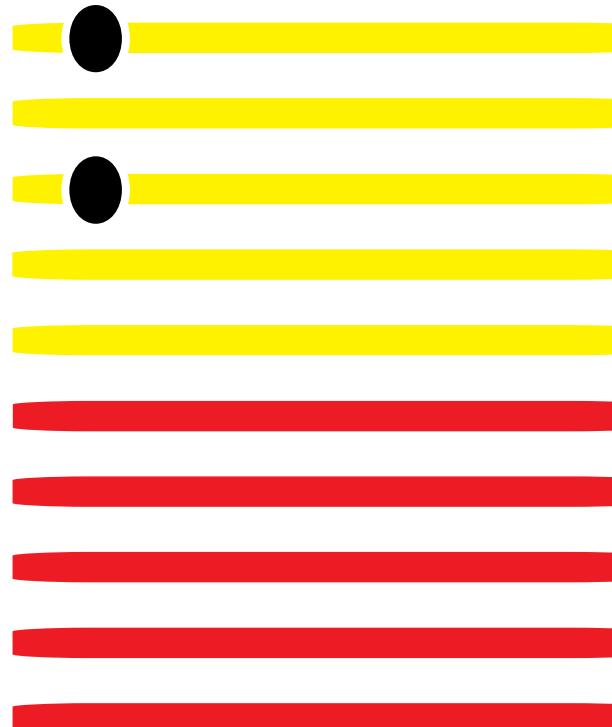
Summarizing the information about history from sequenced genomes

Describing the joint site frequency spectrum (**jSFS**) :



Summarizing the information about history from sequenced genomes

Describing the joint site frequency spectrum (**jSFS**) :



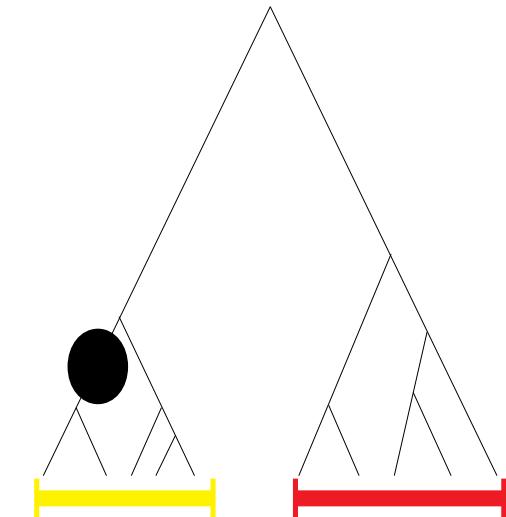
Frequency in population B

f=1

f=0

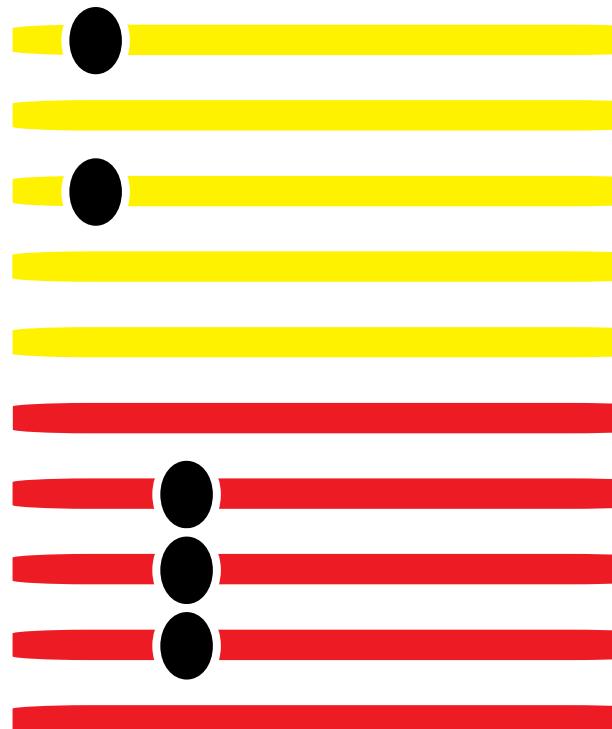
	f=1	f=0	f=1	f=0	f=1
f=1	0	0	0	0	0
f=0	0	0	0	0	0
f=1	0	0	0	0	0
f=0	0	0	0	0	0
f=1	0	0	0	0	0
f=0	0	0	+1	0	0
f=1	0	0	0	0	0

Frequency in population A



Summarizing the information about history from sequenced genomes

Describing the joint site frequency spectrum (**jSFS**) :



Frequency in population B

f=1

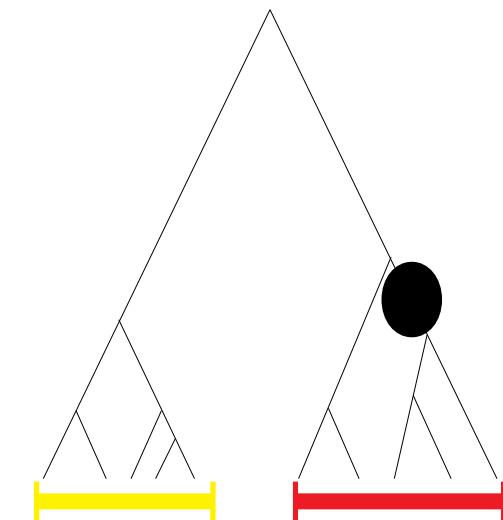
f=0

0	0	0	0	0	0
0	0	0	0	0	0
+1	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
0	0	1	0	0	0

f=0

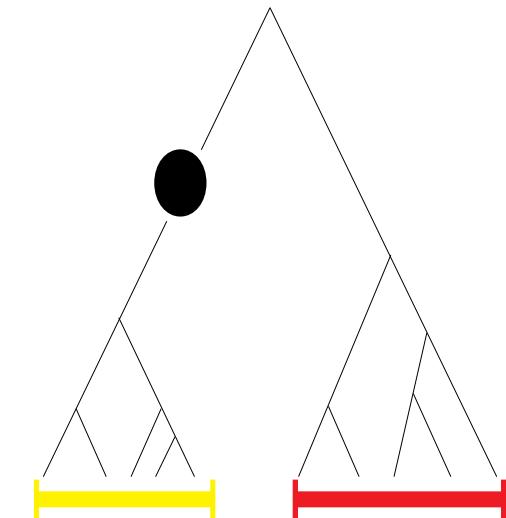
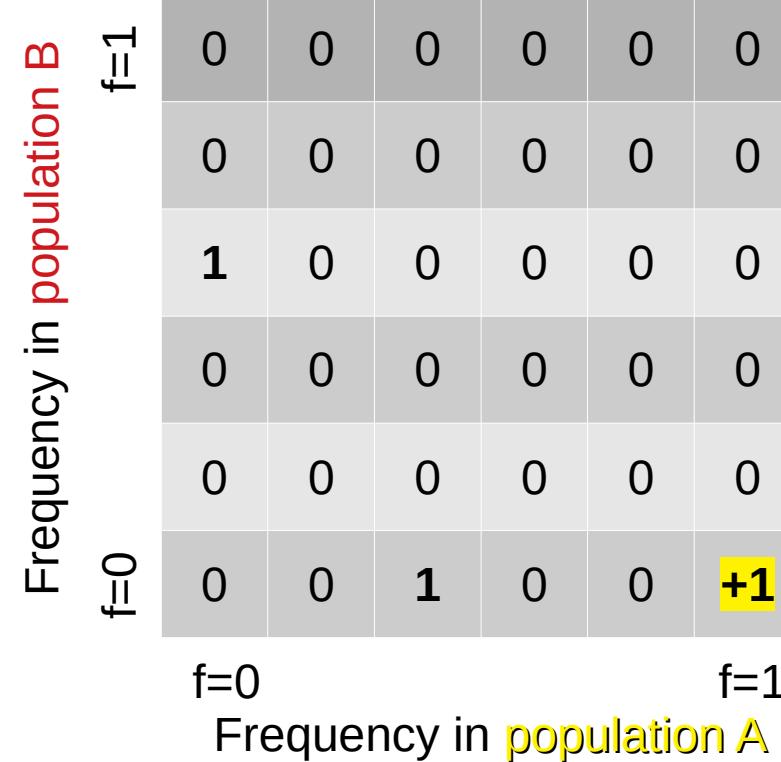
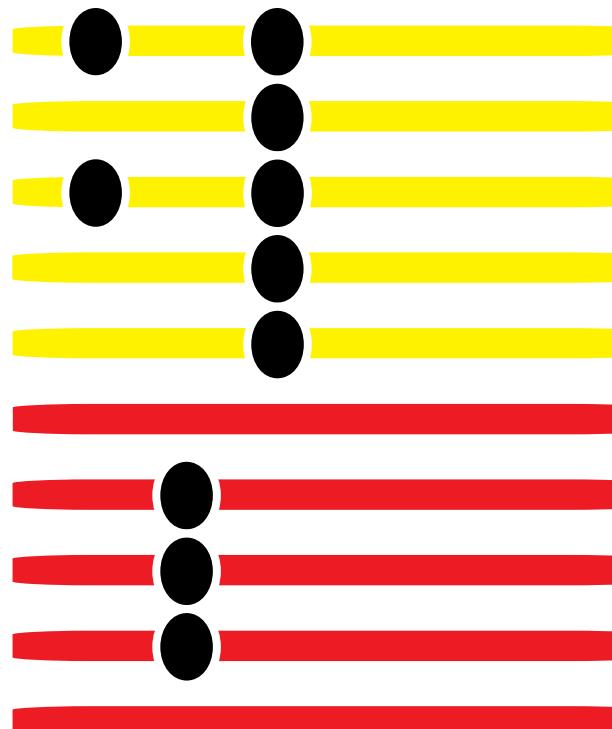
f=1

Frequency in population A



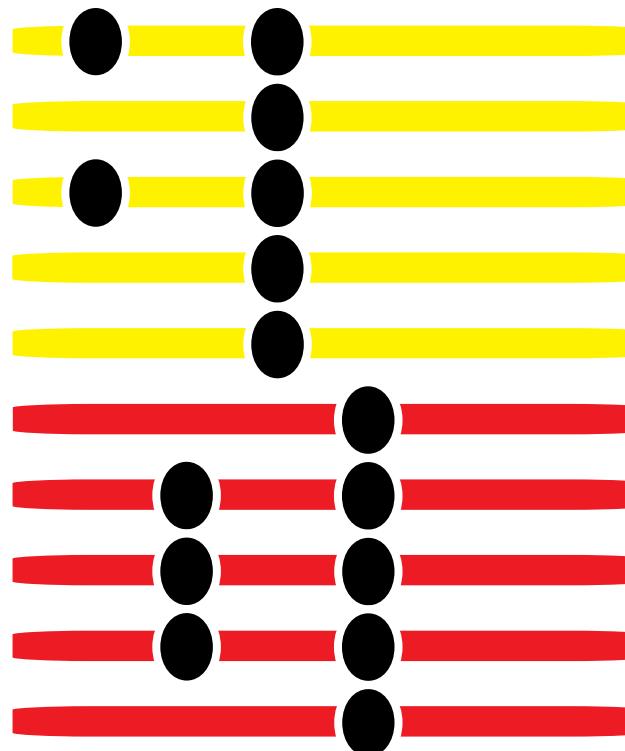
Summarizing the information about history from sequenced genomes

Describing the joint site frequency spectrum (**jSFS**) :



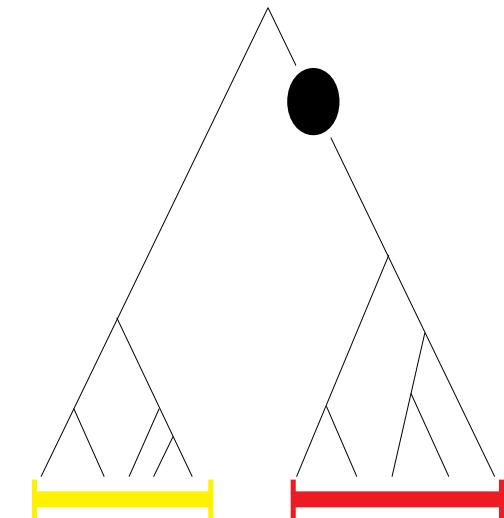
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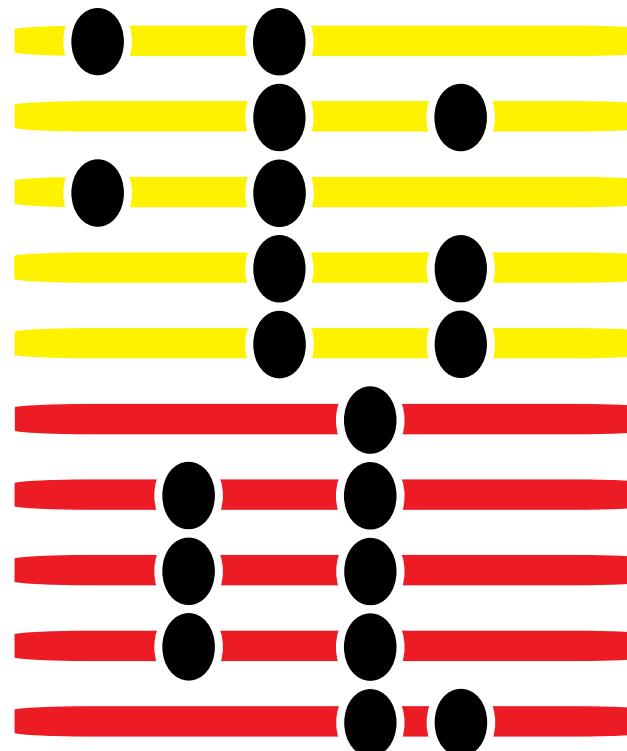
		Frequency in population B					
		$f=1$	0	0	0	0	0
		$+1$	0	0	0	0	0
		1	0	0	0	0	0
		0	0	0	0	0	0
		0	0	0	0	0	0
		0	0	0	0	0	0
		0	0	1	0	0	1

Frequency in population A



Summarizing the information about history from sequenced genomes

Describing the joint site frequency spectrum (**jSFS**) :



Frequency in population B

f=1

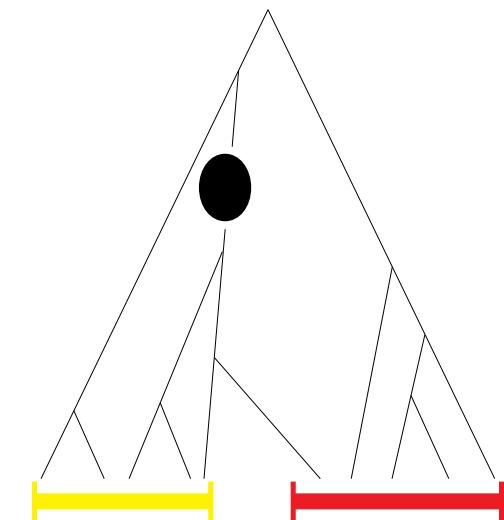
f=0

1	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
1	0	0	0	0	0
0	0	0	+1	0	0
0	0	0	1	0	1

f=0

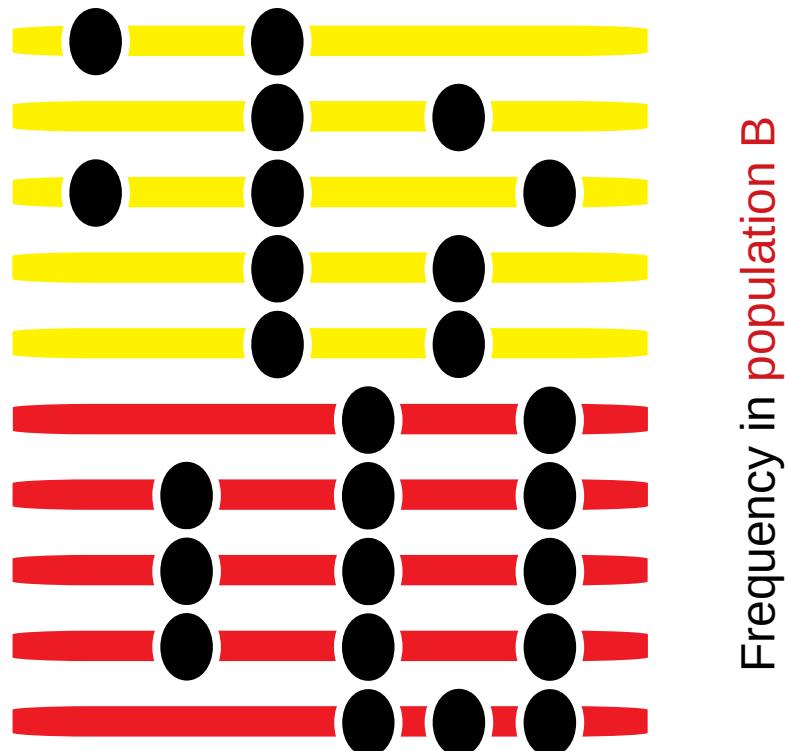
f=1

Frequency in population A

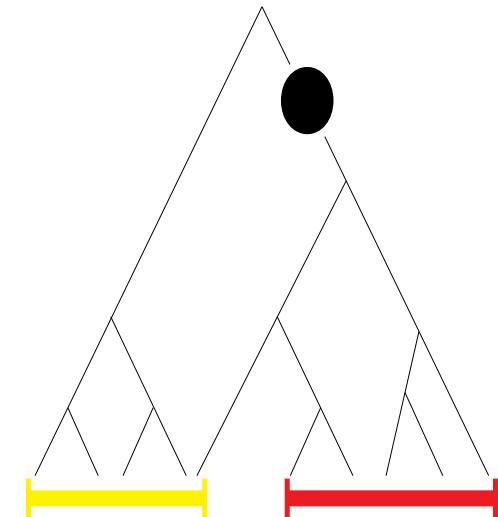


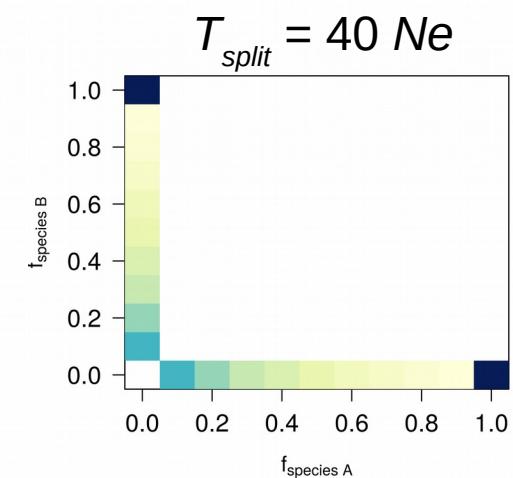
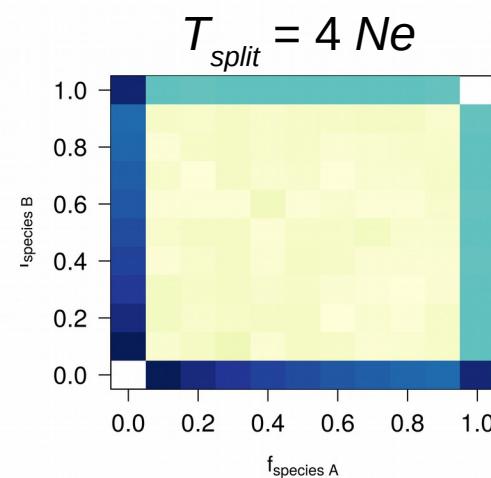
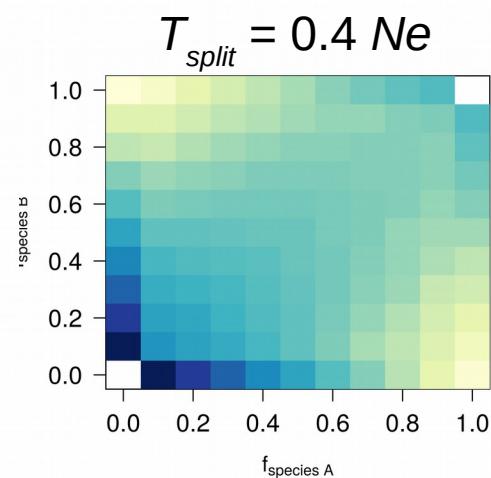
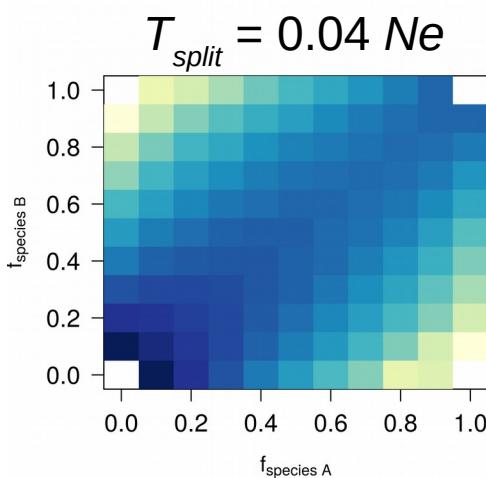
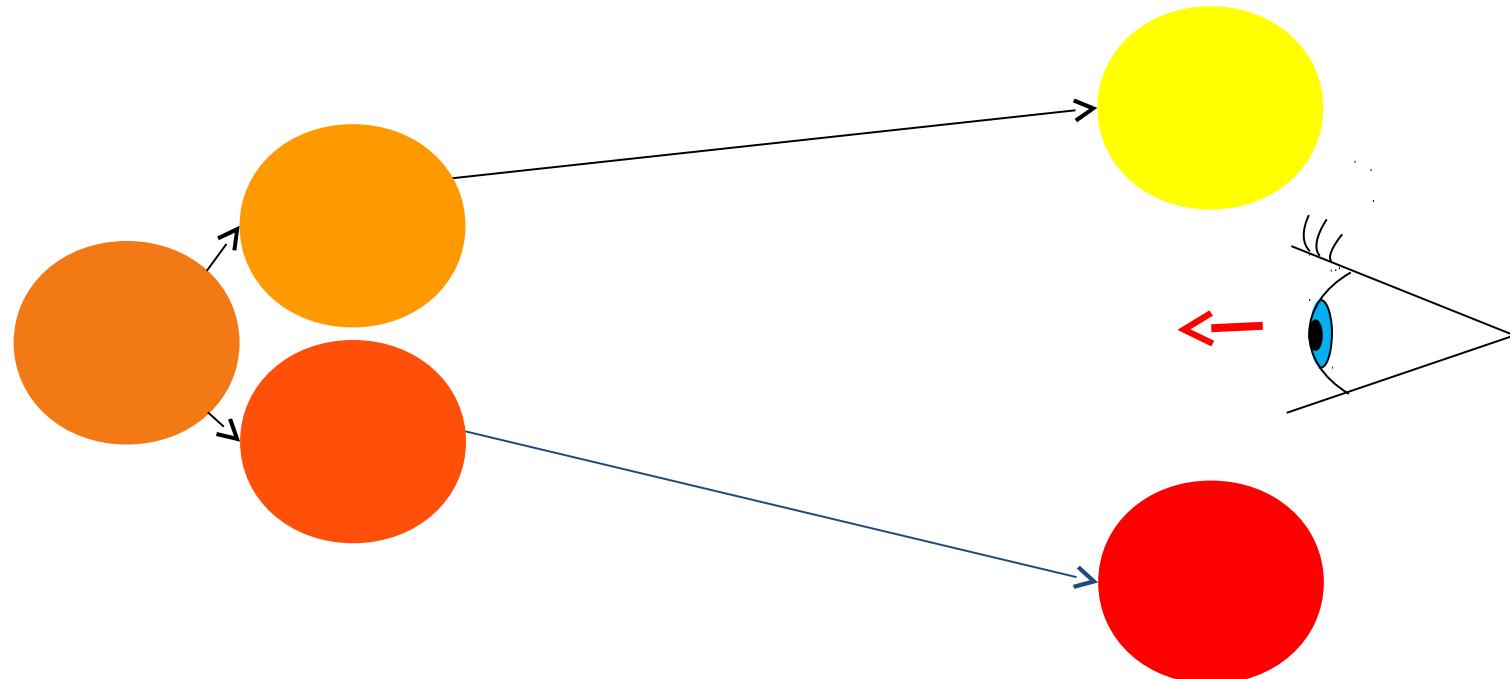
Summarizing the information about history from sequenced genomes

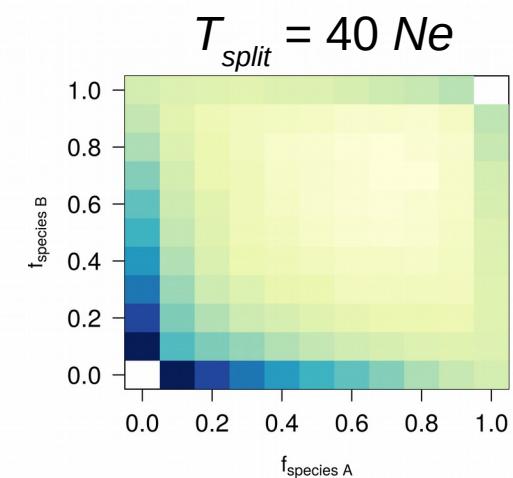
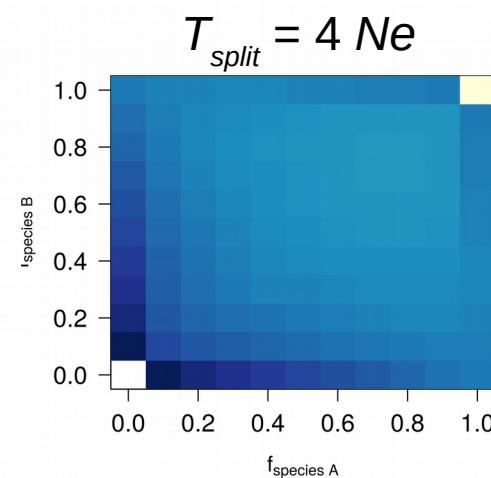
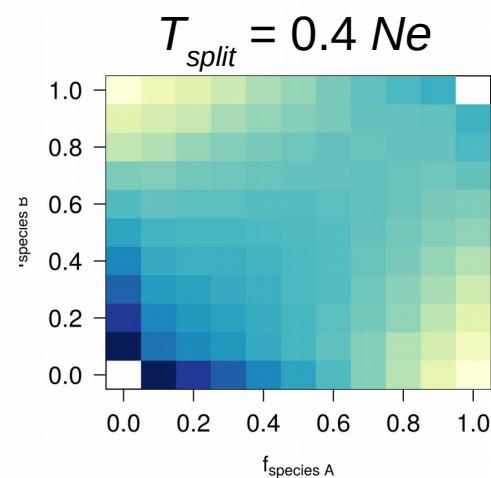
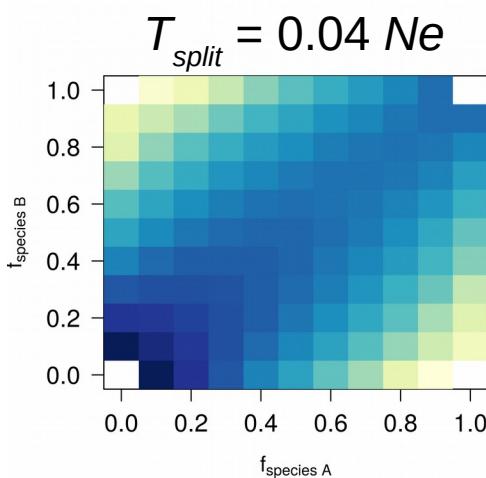
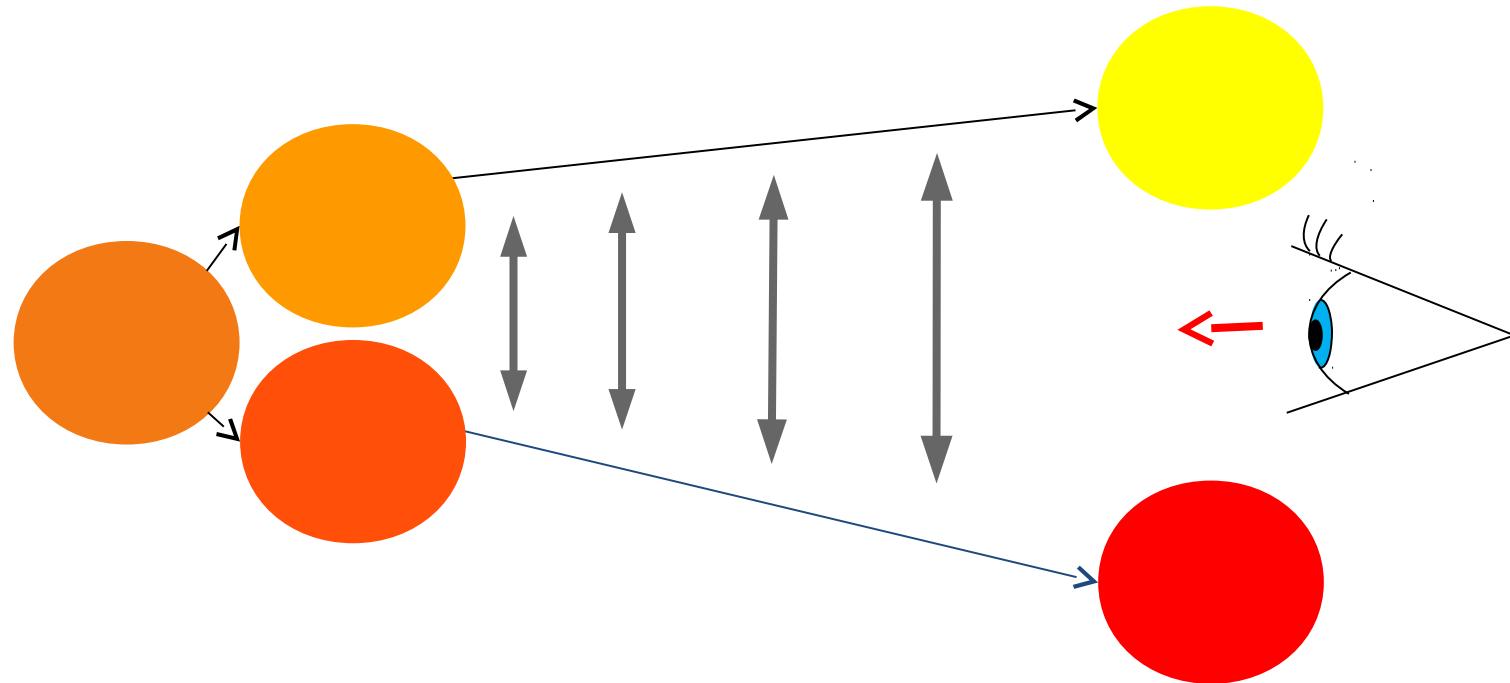
Describing the joint site frequency spectrum (**jSFS**) :



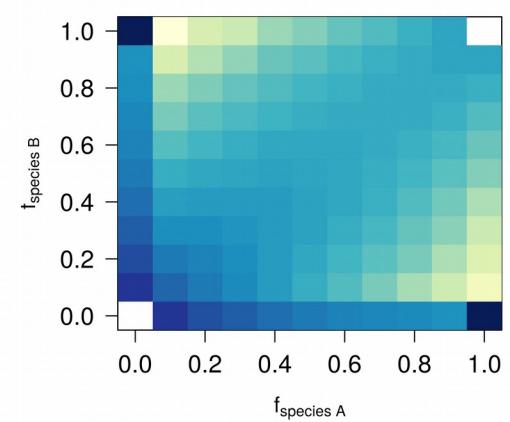
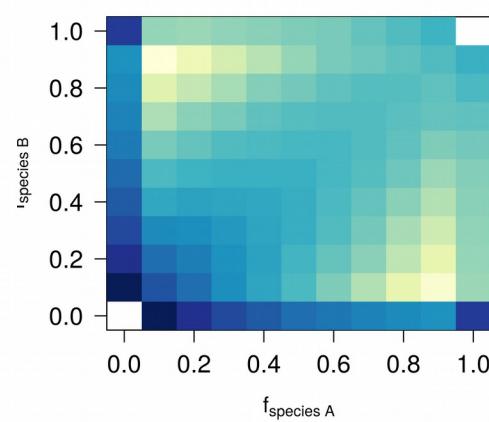
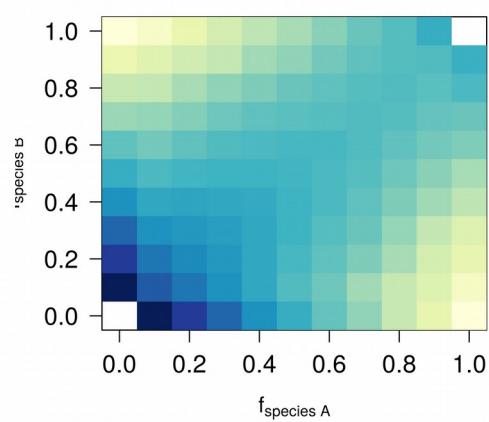
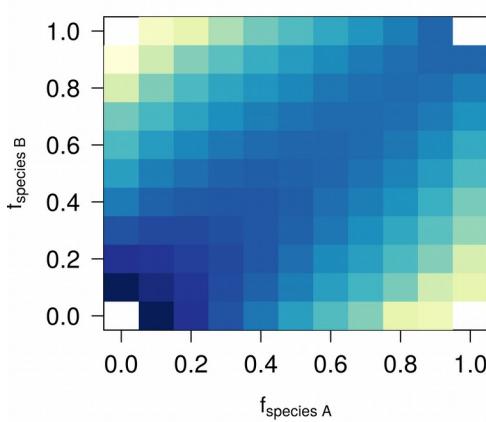
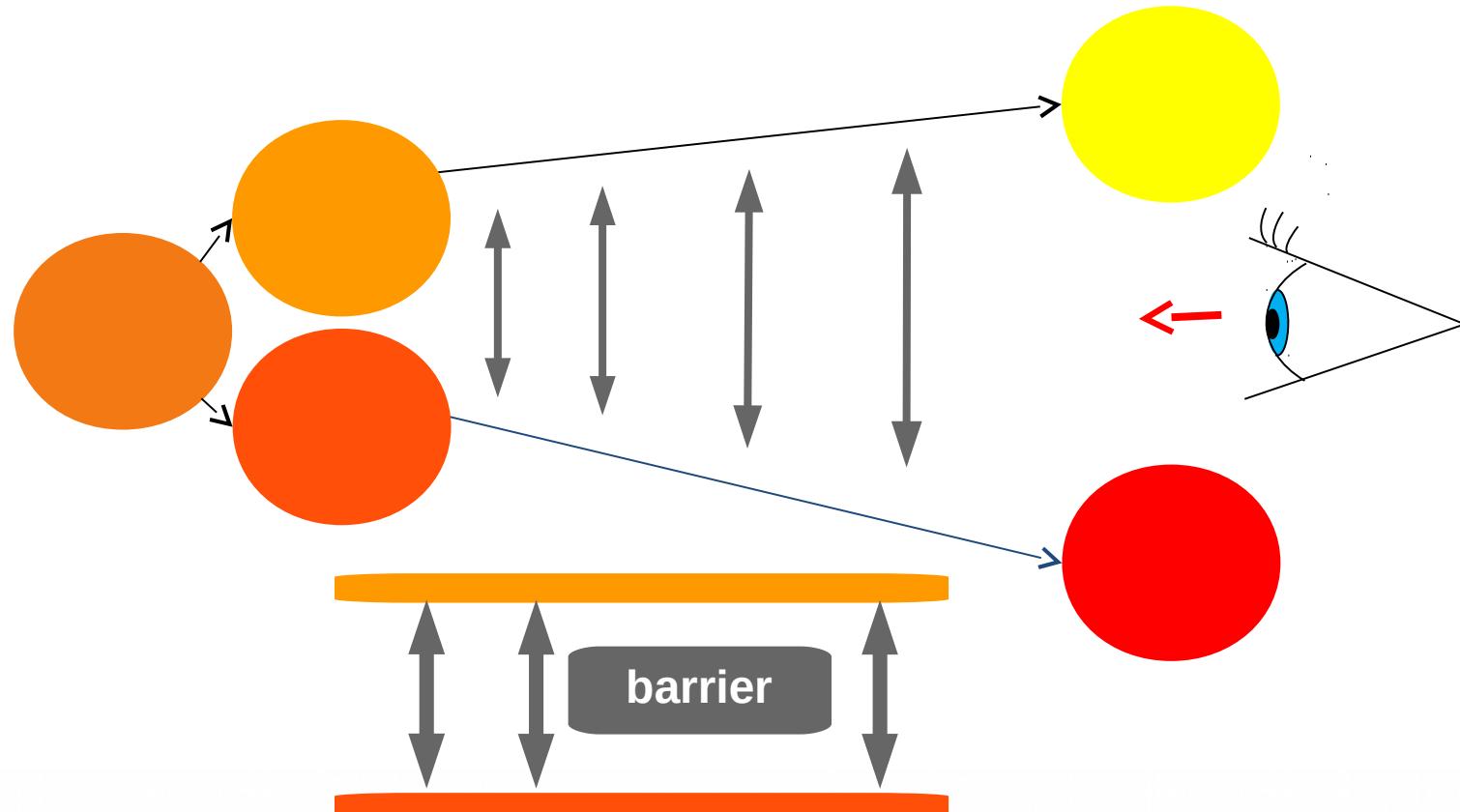
f=1	1	+1	0	0	0	0
	0	0	0	0	0	0
	0	0	0	0	0	0
	1	0	0	0	0	0
	0	0	0	1	0	0
f=0	0	0	0	1	0	1





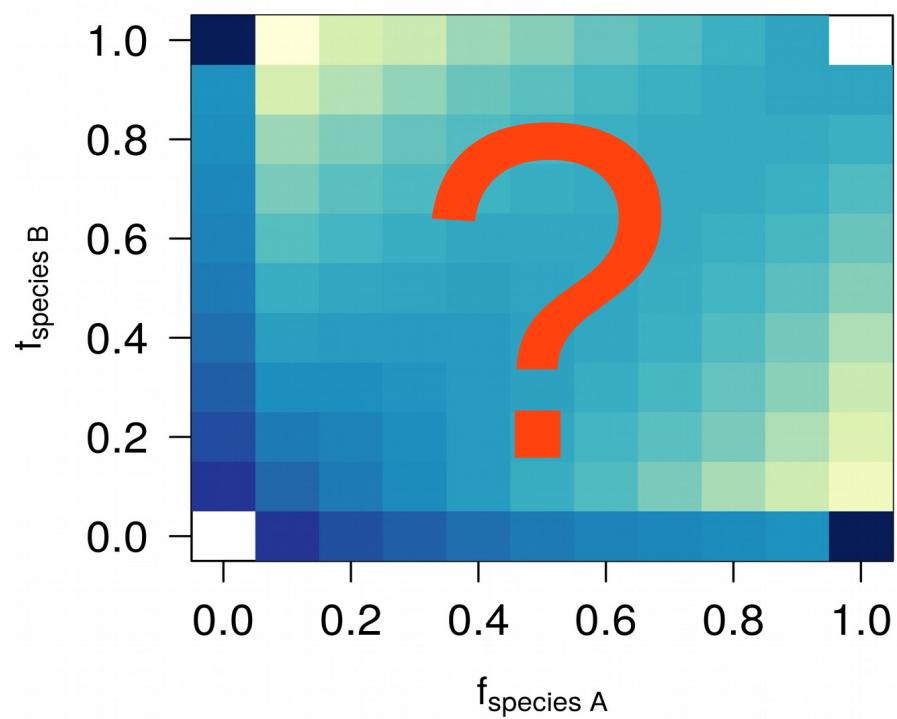
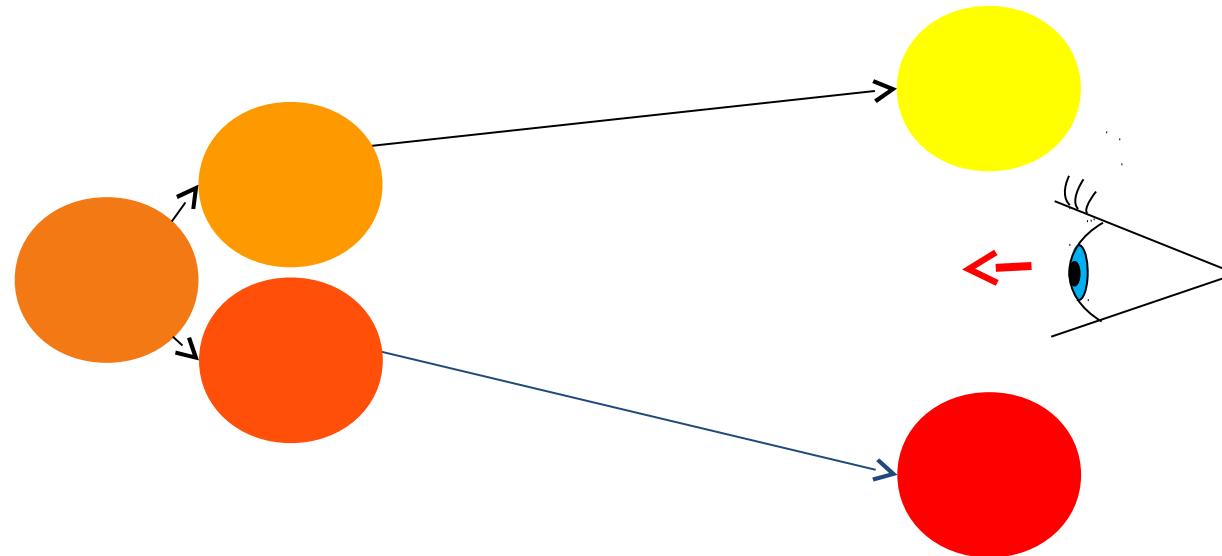


$N.m = 0.25$ (individual every four generations)

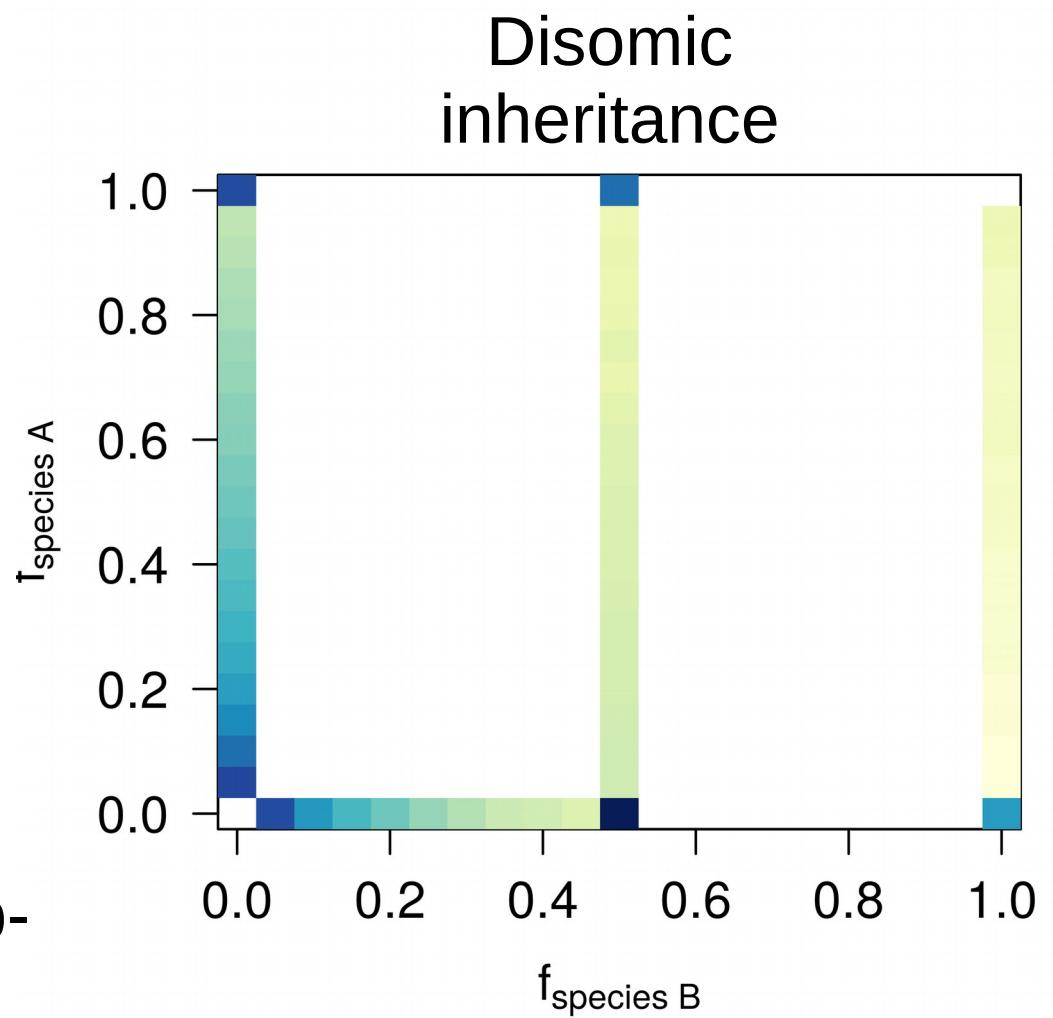
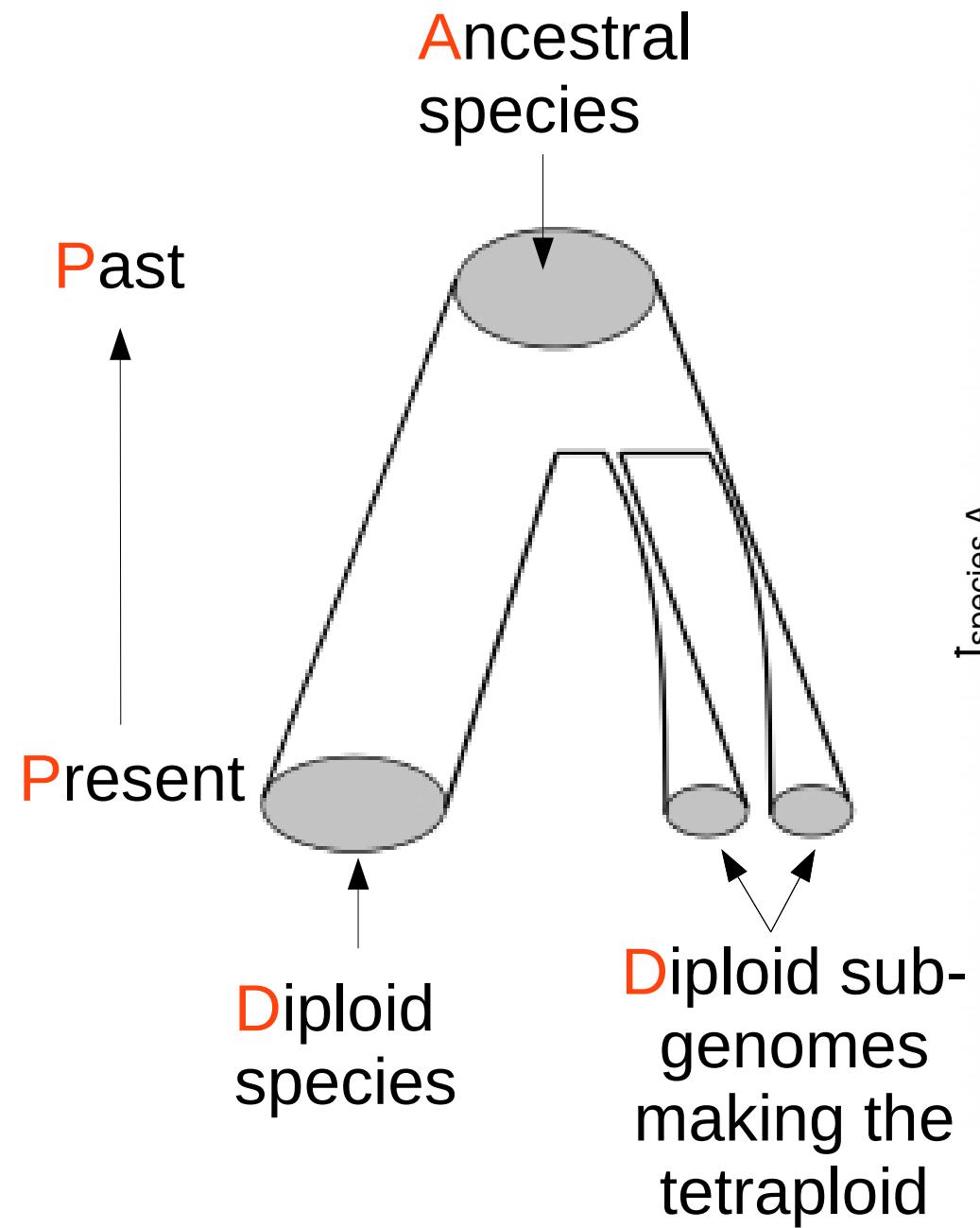


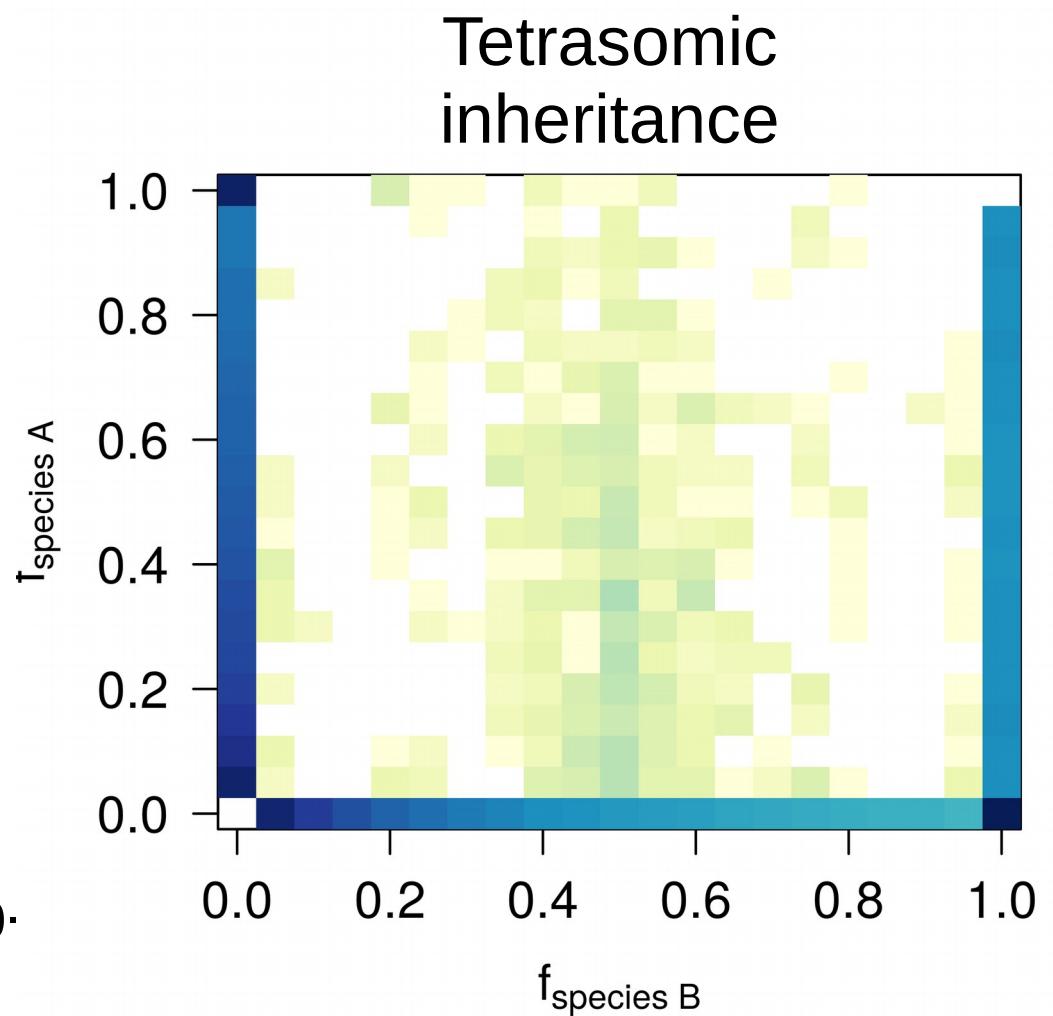
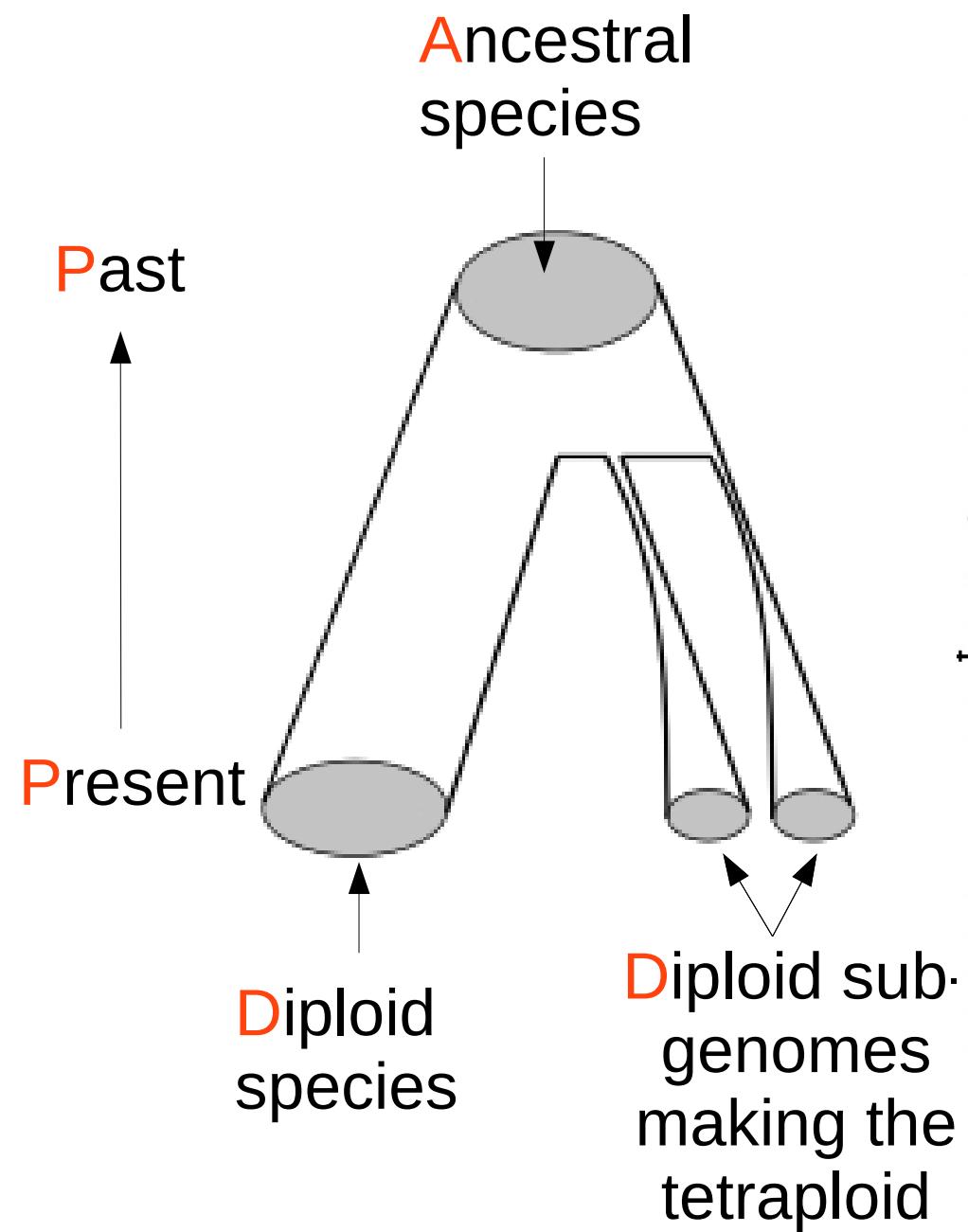
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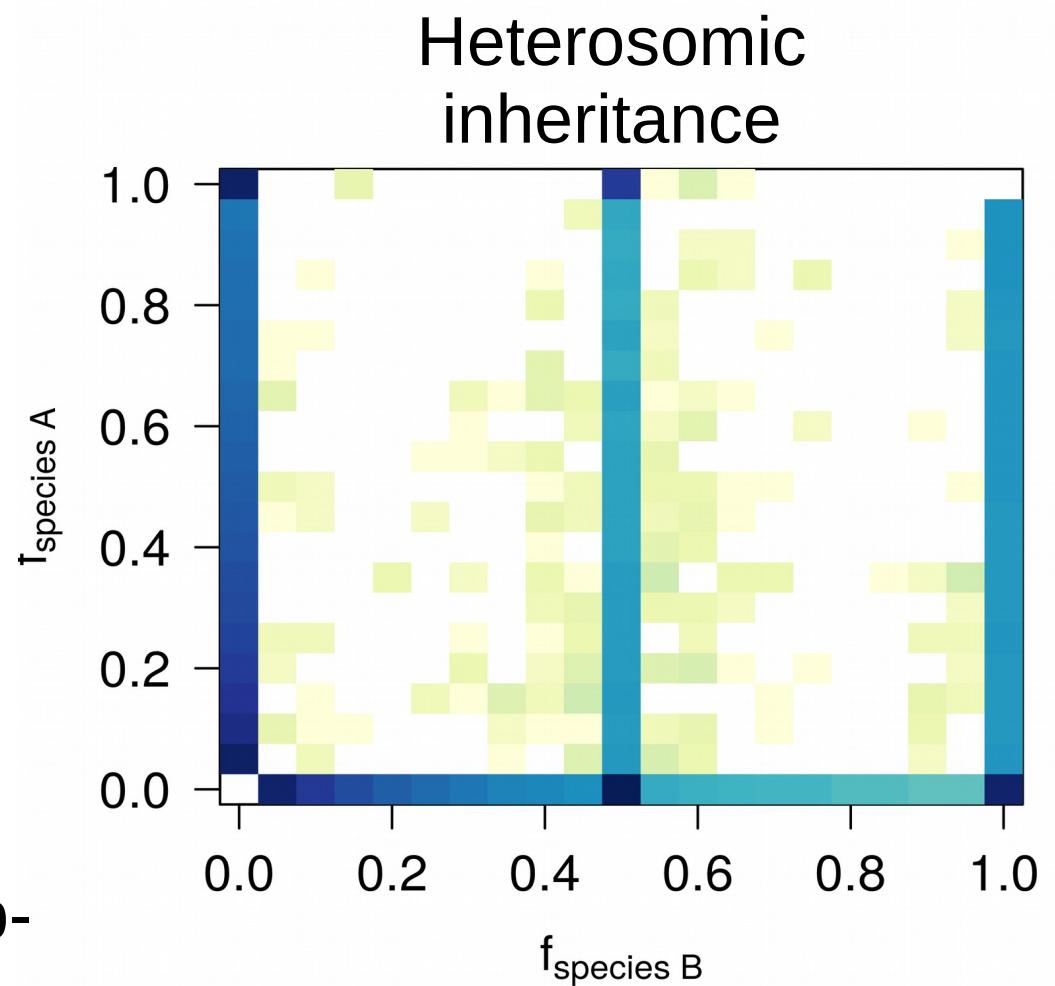
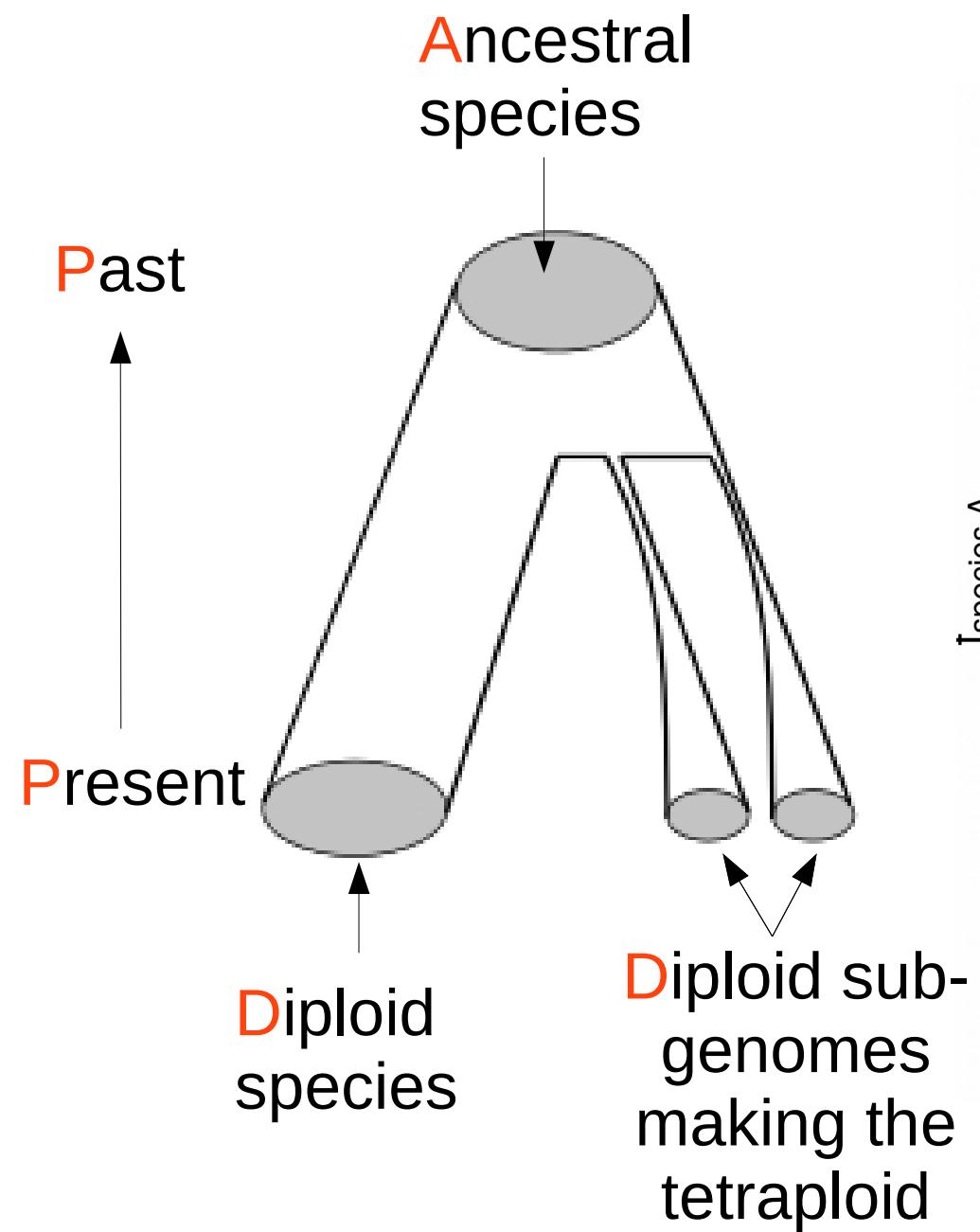
50 % of the genome linked to a barrier

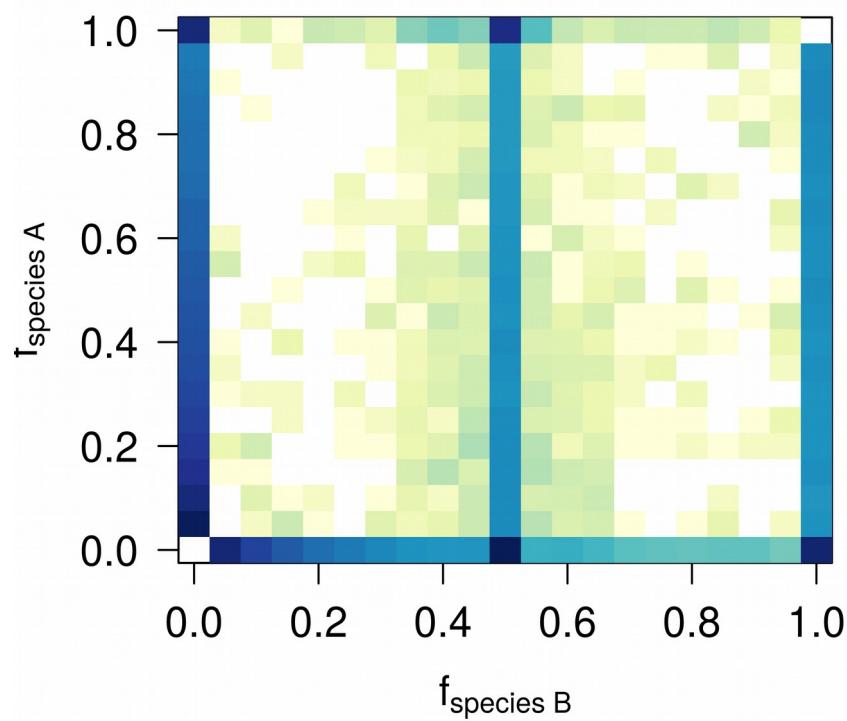
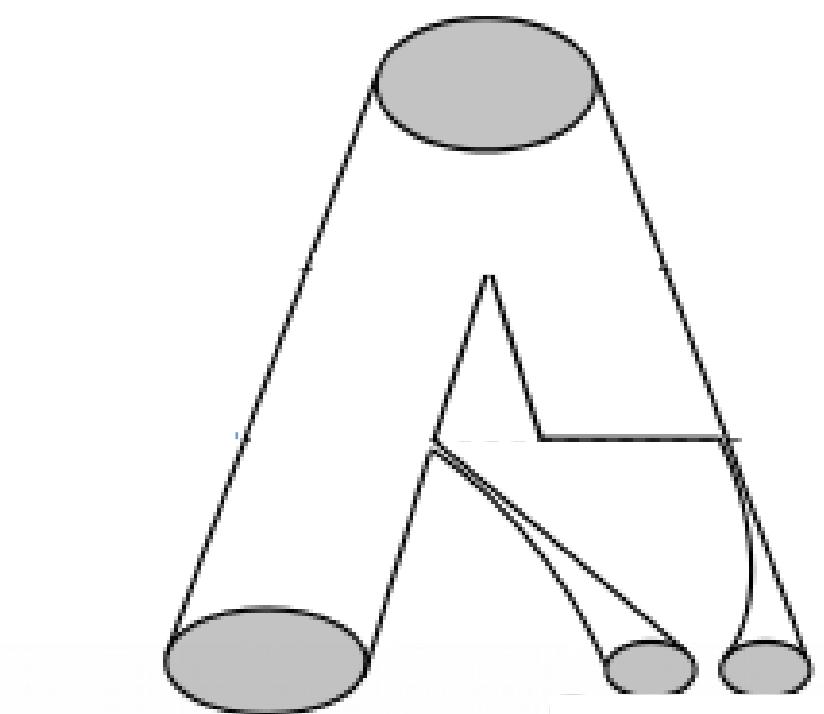
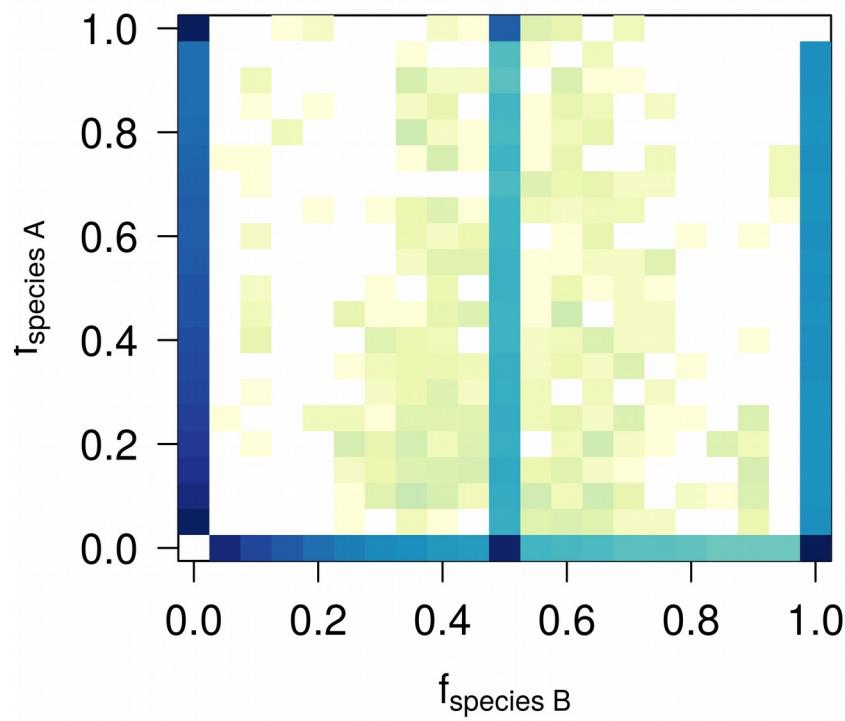
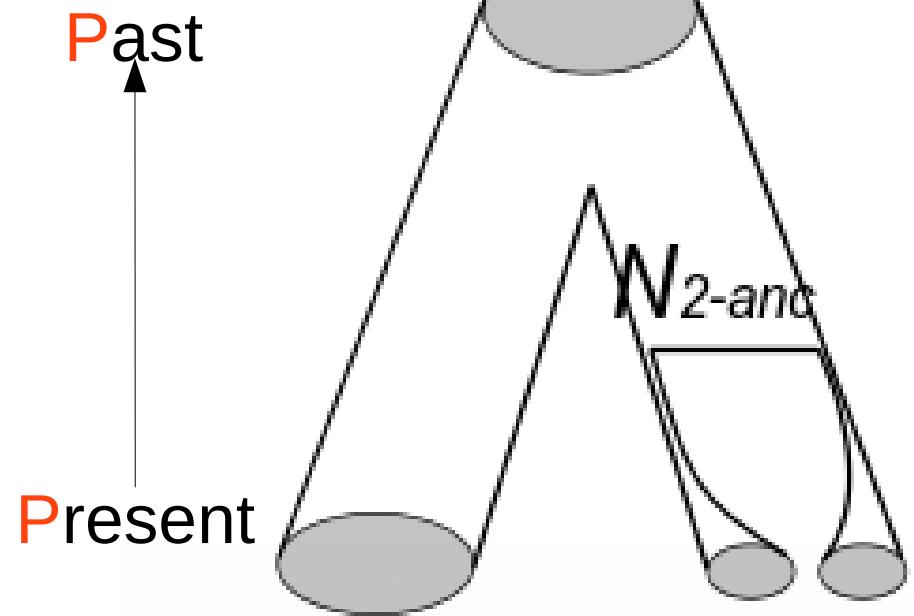


Your job → thinking about
jSFS in tetraploids :
1) auto versus allo ?
2) disomic versus tetrasomic ?
3) intermediate modes of inheritance ?









If the **current genetic data** are impacted by the **demographic history**



We can make inferences about the **demographic history** from the **current genetic data**

The first step : simulating genetic dataset under various demographic models

The first step : simulating genetic dataset under various demographic models

we need a **fast simulator**

Here → a coalescent one (named ms or msnsam)

The basic command line for ms

```
→ example msnsam 10 1 -t 5
```



Call the executable

The basic command line for ms

```
→ example msnsam 10 1 -t 5
```

Call the executable

The number of
sampled haploid
individuals

The basic command line for ms

```
→ example msnsam 10 1 -t 5
```

Call the executable

The number of
sampled haploid
individuals

The number of
replicates

The basic command line for ms

```
→ example msnsam 10 1 -t 5
```

Call the executable

The number of
sampled haploid
individuals

Theta : $4.N.\mu.L$

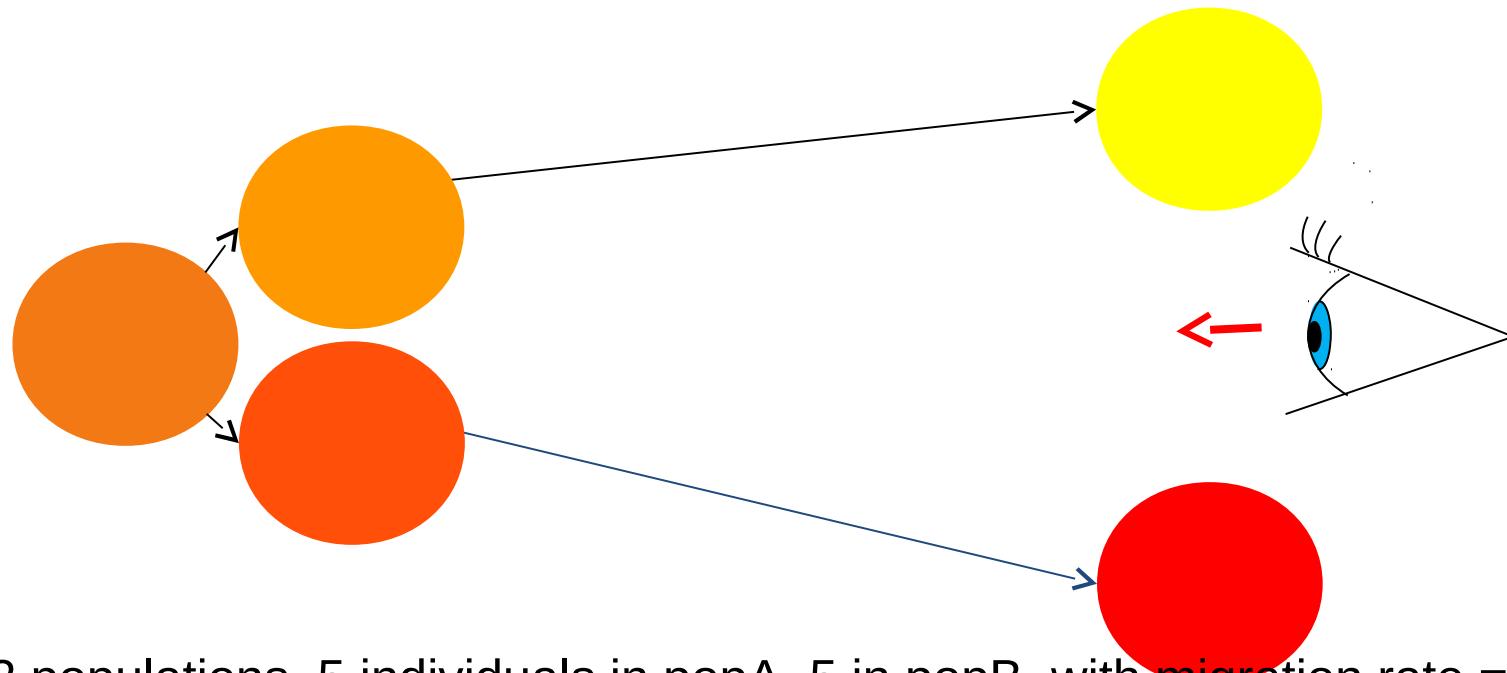
The number of
replicates

The basic command line for ms

```
→ example msnsm 10 1 -t 5
msnsm 10 1 -t 5
3579 27011 59243

//
segsites: 29
positions: 0.0095 0.0282 0.0496 0.0863 0.0906 0.1207 0.1535 0.1580 0.1861 0.2220 0.3254 0.3648 0.3797 0.3868 0.4242 0.5360 0.6244 0.632
9 0.6762 0.6978 0.6980 0.7396 0.7769 0.7870 0.7977 0.8215 0.8217 0.9178 0.9410
00000101000110011000000000000
10000000010001000101010000100
01101110001000101010000111010
00000101000110011000000000001
10000000010001000101010000100
00000101000110011000000000000
00000101100110011000000000000
00010101000110011000000000000
00000101000110011000101000000
00000101000110011000000000001
```

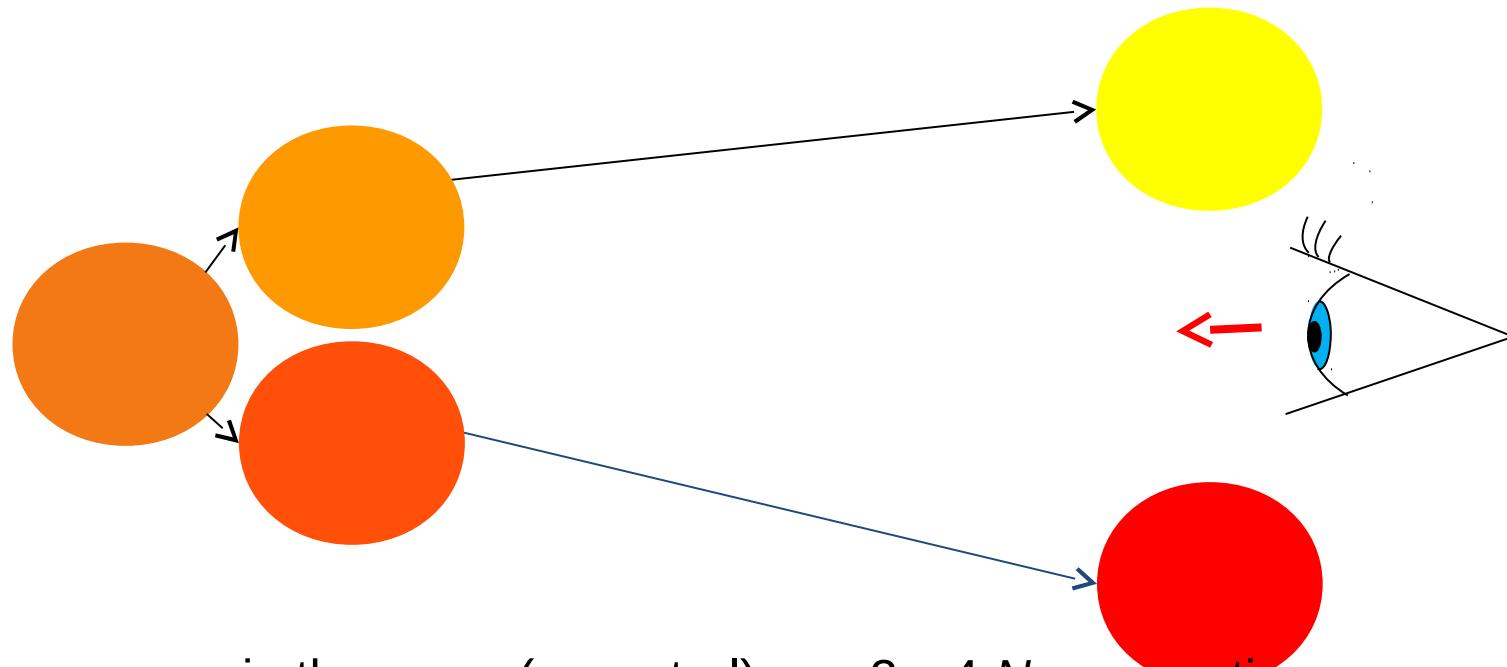
Adding population structure



An island of 2 populations, 5 individuals in popA, 5 in popB, with migration rate = 0

```
→ example msnsam 10 1 -t 5 -I 2 5 5 0 -ej 2 1 2  
msnsam 10 1 -t 5 -I 2 5 5 0 -ej 2 1 2  
20019 47964 40917
```

Adding population structure

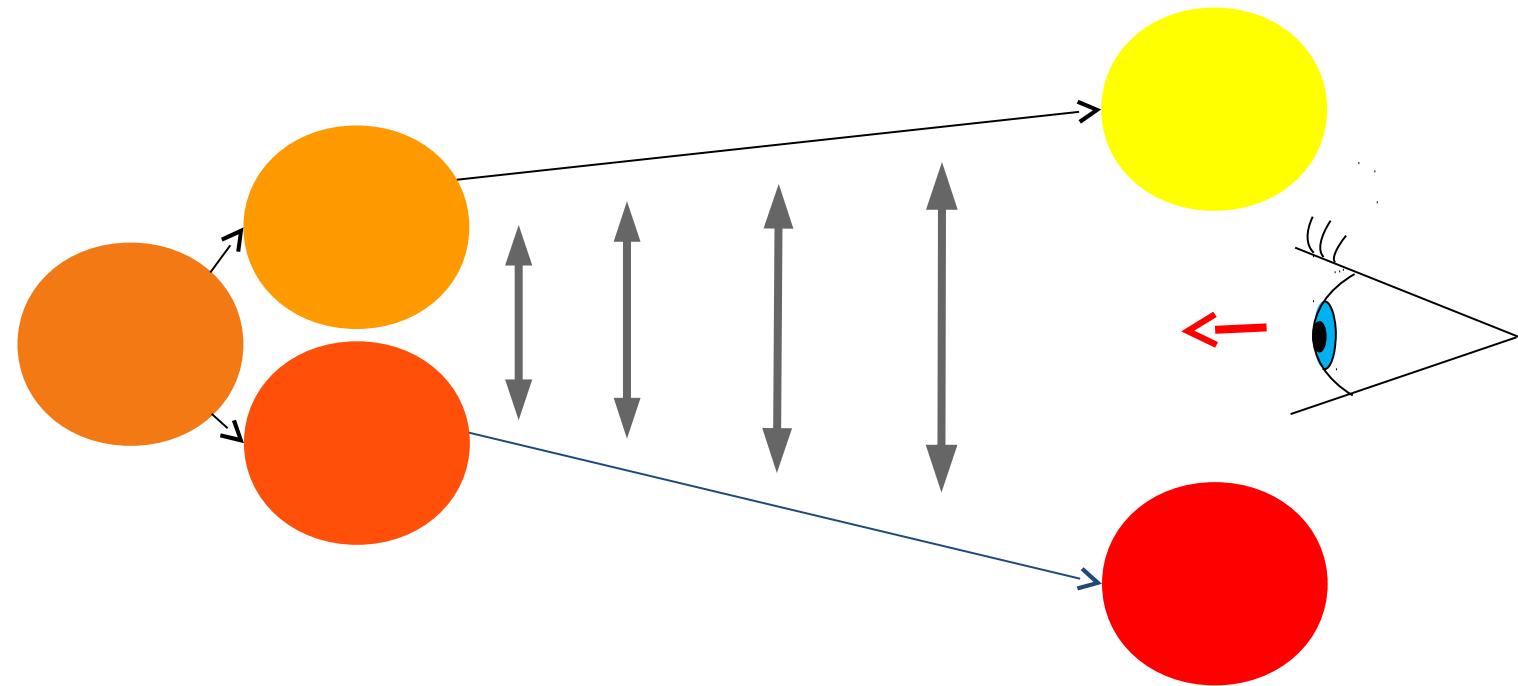


The populations merge in the same (ancestral) one $2 \times 4.Ne$ generations ago,

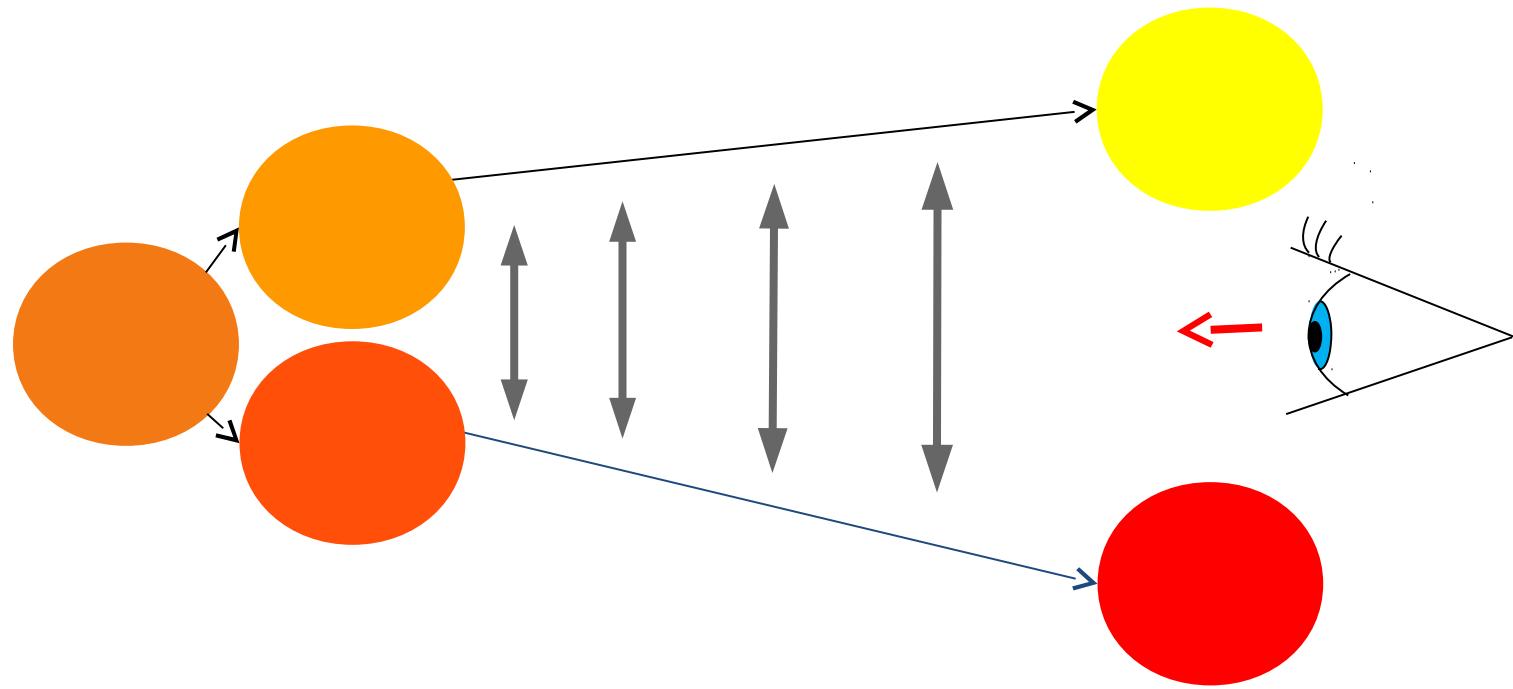
```
→ example msnsam 10 1 -t 5 -I 2 5 5 0 -ej 2 1 2
msnsam 10 1 -t 5 -I 2 5 5 0 -ej 2 1 2
20019 47964 40917
```

```
//  
segsites: 31  
positions: 0.0322 0.0763 0.1269 0.1434 0.1535 0.1582 0.1744 0.2082 0.2146 0.3203 0.3704 0.3707 0.3824 0.4339 0.4914 0.4958 0.5401 0.570  
3 0.6041 0.6540 0.6564 0.7023 0.7477 0.7960 0.8152 0.8171 0.8423 0.8722 0.8852 0.8980 0.9675  
100110000000000010001100000000  
10011000000000001000000010  
100110010000000010001100001001  
1001100001000000000100000010  
11011000000000000000100000010  
001000001000100000100000010100  
0010000001000000001000011100100  
00100100001011100100000000100  
0010001001000000001100010100100  
0010000001000000001000011100100
```

Adding population structure



Adding population structure



```
→ example msnsam 10 1 -t 5 -I 2 5 5 10 -ej 2 1 2  
msnsam 10 1 -t 5 -I 2 5 5 10 -ej 2 1 2  
3754 64515 32205
```

```
//  
segsites: 27  
positions: 0.0747 0.1319 0.1320 0.1668 0.1935 0.2148 0.2855 0.3563 0.3733 0.3841 0.4010 0.4368 0.4557 0.4892 0.5066 0.5160 0.5404 0.5406 0.5681 0.5910 0.6501 0.6986 0.7217 0.7515 0.7575 0.8053 0.9036  
0100100100000010000000000000  
0101100100000000001000010100  
01001001000100000100100000  
010010010010000010000010111  
0100100100000010000000000000  
010010010001000000100100000  
01001001000100000010000010110  
01001001000000000000000010100  
101001101100110100011001000  
010010010010000010000010110
```

For Ubuntu us<3rs

```
github git:(master) ✘ ./run_ABC_polyplloid.py
```

run_ABC_polyplloid.py is a python script usefull to run some random simulations of 9 models of speciation between a diploid and a tetraploid

It takes 3 arguments: 1) a demographic model; 2) the name of a file containing the arguments; 3) the name of the bpfile
The accepted models are:

```
diso1
diso2_auto
diso2_ally
tetra1
tetra2_auto
tetra2_ally
hetero1
hetero2_auto
hetero2_ally
```

command line: ./run_ABC_polyplloid.py [model] [name of the argfile] [bpfile]

The expected number of arguments is 3

For Mac u\$ers

```
ib git:(master) ✘ ./run_ABC_polyplloid_v2.py
```

run_ABC_polyplloid.py is a python script usefull to run some random simulations of models of speciation between a diploid and a tetraploid

It takes 4 arguments:

- 1) a demographic model (auto, allo);
- 2) a model of inheritance (disomic, heterosomic, tetrasomic);
- 3) the name of the bpfile;
- 4) the number of replicates (an integer)

The accepted models are:

```
auto
allo
```

command line: ./run_ABC_polyplloid.py [model] [inheritance] [bpfile] [nreps]

The expected number of arguments is 4

Example : simulating « allopolyploidization » + « tetrasomique »

```
./run_ABC_polyplloid.py hetero2_allo argfile_tetra2_allo.txt bpfile  
./run_ABC_polyplloid_v2.py allo tetrasomic bpfile 10000
```

Ubuntu

Mac

Example : simulating « allopolyploidization » + « tetrasomic »

```
./run_ABC_polyplloid.py hetero2_allo argfile_tetra2_allo.txt bpfile
```

```
./run_ABC_polyplloid_v2.py allo tetrasomic bpfile 10000
```

Ubuntu

Mac

Let's simulate those 4 models !

{ allo ; auto } x { disomic ; tetrasomic }