

My research

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Parameters estimated from phylogenies

- Effective population size (Kuhner et al. 1995)
- Rate of population growth or decline (Kuhner et al. 1998, Drummond et al. 2002)
- Migration rates and population structure (Beerli & Felsenstein 1999, Beerli & Felsenstein 2001, Ewing et al. 2004, Ewing & Rodrigo 2006)
- Recombination rates and reticulate ancestry (Kuhner et al. 2000, Bloomquist & Suchard 2010)

Workflow

Ecology

Molecular data

Alignment

Phylogeny

Parameter estimates

Lambda = ?

```
.GCTACCTTTATCCCTAGCCCCCTGCGCCC  
GTGAGGTCTGCTCTGGGTCCCTCGCCACC  
CCCTAGCTCCGTGCGCCACTCCGGCGGCC  
CCGGACTACGGTGGTTACCACGTGGCGG
```

-	V	H	L	T	A	D	E	K	A	A	V	T	A	L	W	G	K	V	N	
-	V	H	L	T	G	E	E	K	A	A	A	V	T	A	L	W	G	K	V	N
M	V	H	L	T	P	E	E	K	N	A	A	V	T	T	L	W	G	K	V	N
M	V	H	L	T	P	E	E	K	S	A	A	V	T	A	L	W	G	K	V	N

Lambda = 0.5

Multi-step

Ecology

Lambda = ?

Molecular data

```
GCTACCTTTATCCCTAGCCCCCTGCGCCC  
GTGAGGTCTGCTCTGGGTCCCTCGCCACC  
CCCTAGCTCCGTGCGCCACTCCGGCGGCC  
CCGGACTACGGTGGTTACCACGTGGCGG
```

Use best

Alignment

-	V	H	L	T	A	D	E	K	A	A	V	T	A	L	W	G	K	V	N	
-	V	H	L	T	G	E	E	K	A	A	A	V	T	A	L	W	G	K	V	N
M	V	H	L	T	P	E	E	K	N	A	A	V	T	T	L	W	G	K	V	N
M	V	H	L	T	P	E	E	K	S	A	A	V	T	A	L	W	G	K	V	N

Use best

Phylogeny

Use best

Parameter estimates

Lambda = 0.5 +/- 0.01

Joint inference

Ecology

Lambda = ?

Molecular data

```
.GCTACCTTTATCCCTAGCCCCCTGCGCCC  
GTGAGGTCTGCTCTGGGTCCCTCGCCACC  
CCCTAGCTCCGTGCGCCACTCCGGCGGCC  
CCGGACTACGGTGGTTACCACGTGGCGG
```

Alignments

T	A	D	E	K	A
T	G	E	E	K	A
T	P	E	E	K	N
T	P	E	E	K	S

Phylogenies

Parameter estimates

This alignment, this phylogeny
and $\lambda = 0.5$ have a 90% probability

Example

- Is he/she a researcher?
 - City: GRN
 - Address: NIEUWST
 - Last name: BER

Multi-step approach

- Step 1: find the best fitting city name: Groenlo
- Step 2: within Groenlo, find the best fitting street name: Nieuwstad
- Step 3: within Nieuwstad, find the best fitting last name: Bergsma
- Step 4: Bergsma cannot be found by Google
- Is he/she a researcher? 0%

Joint inference

- Look for combinations of GRN, NIEUWST, BER, probability
- Groenlo – Nieuwstad – Bergsma – 0%
- Groenlo – Nieuwstad – others – 0%
- Groenlo – other streets - 0%
- Groningen – Nieuwstraat – Bilderbeek – 100%
- Groningen – Nieuwstraat – others – 2%
- Groningen – other streets - 2%
- Chance he/she a researcher? 1%

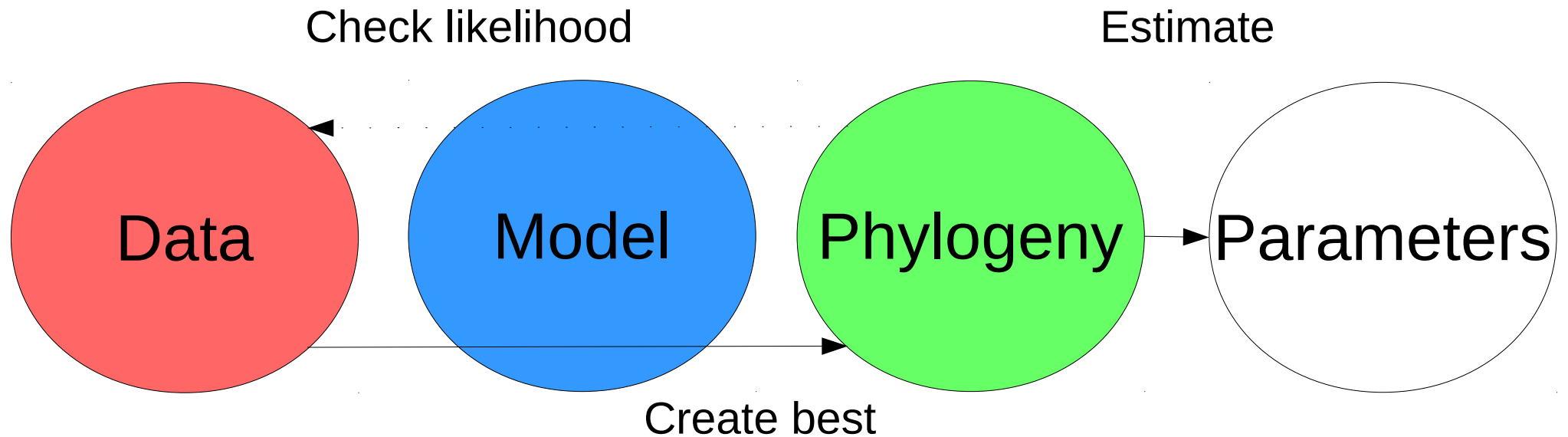
Current research

- From the same (unaligned) molecular data, different alignment programs result in different phylogenies (Wong et al, 2008)
- There is no difference between multi-step approach and joint inference, when starting from alignment data (but do use two tree models)(Hohna et al, 2015)

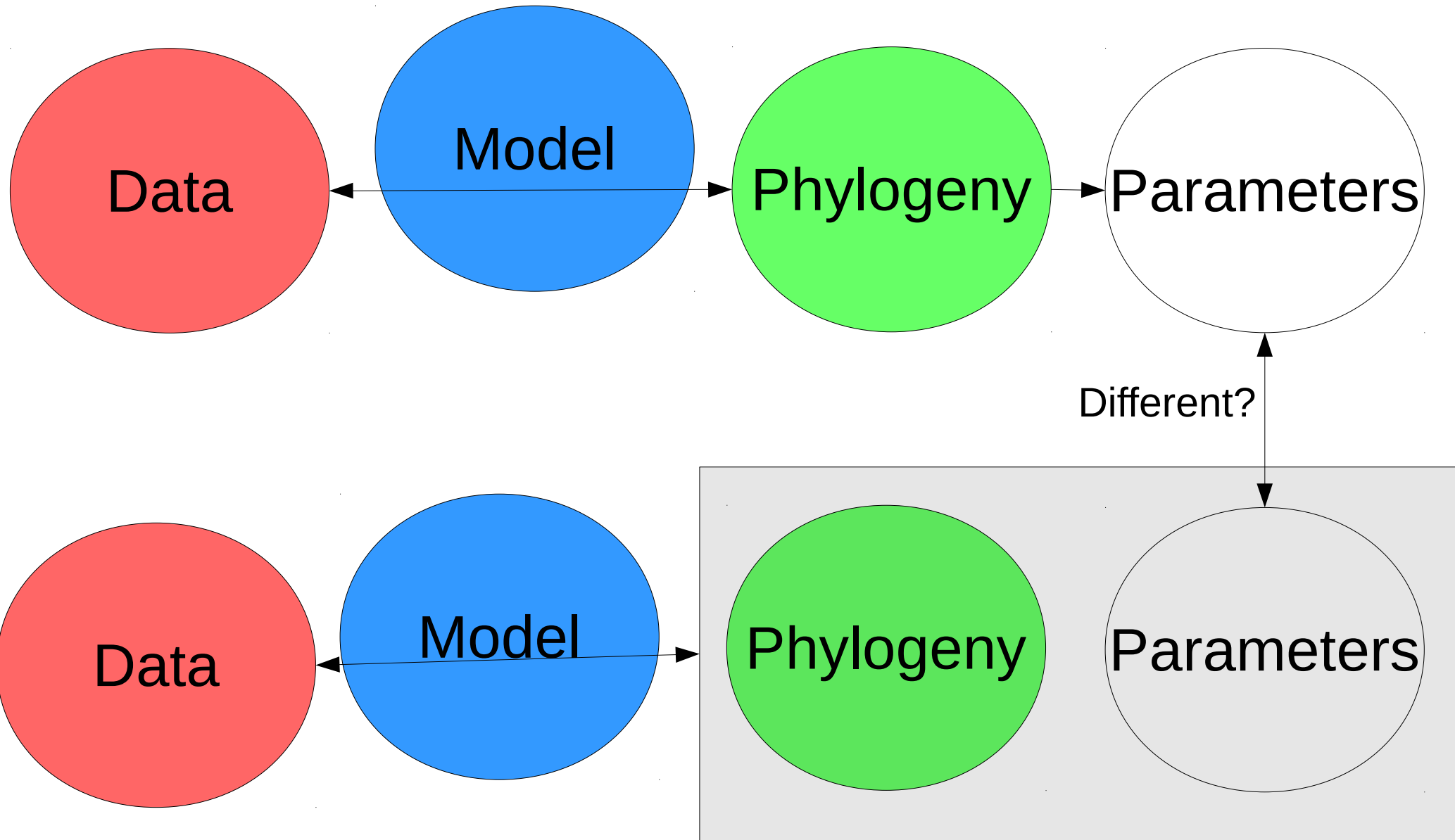
Experiments

- Can parameters be estimated from phylogeny, or must these be inferred jointly with the phylogeny itself?
- Which model fits the data best?
- Does it matter which model is used?

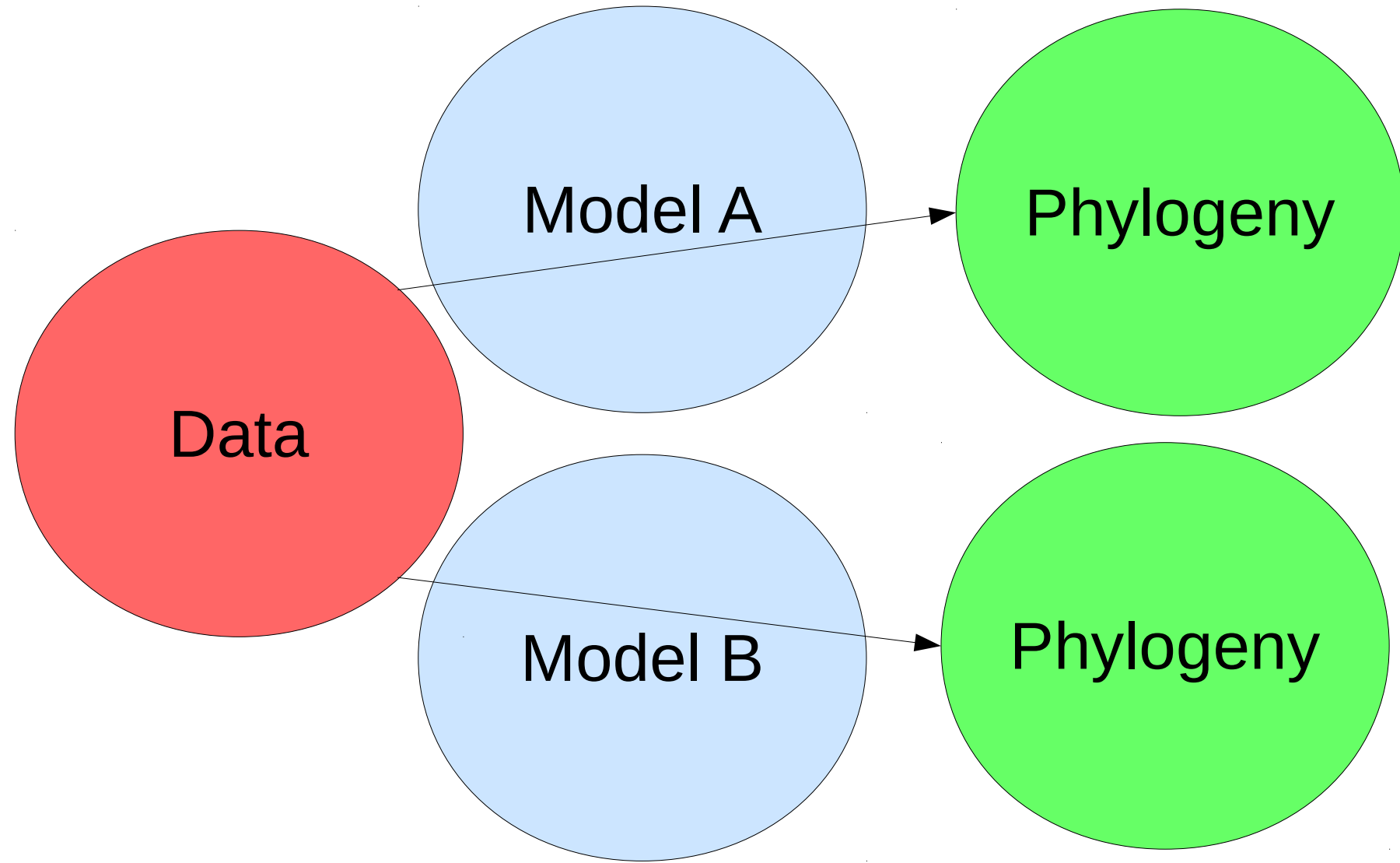
Experiments



Experiments

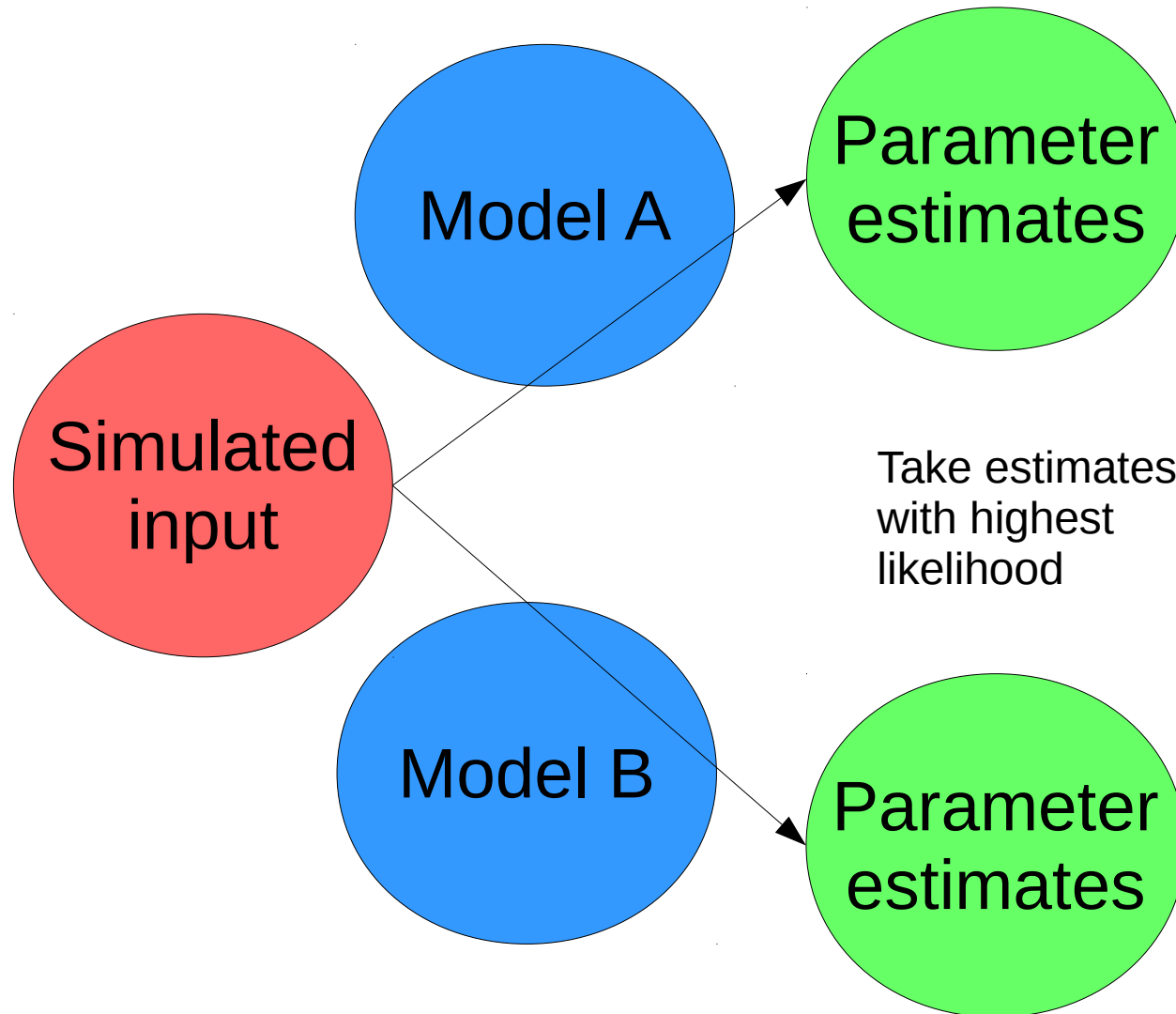


Model unknown?

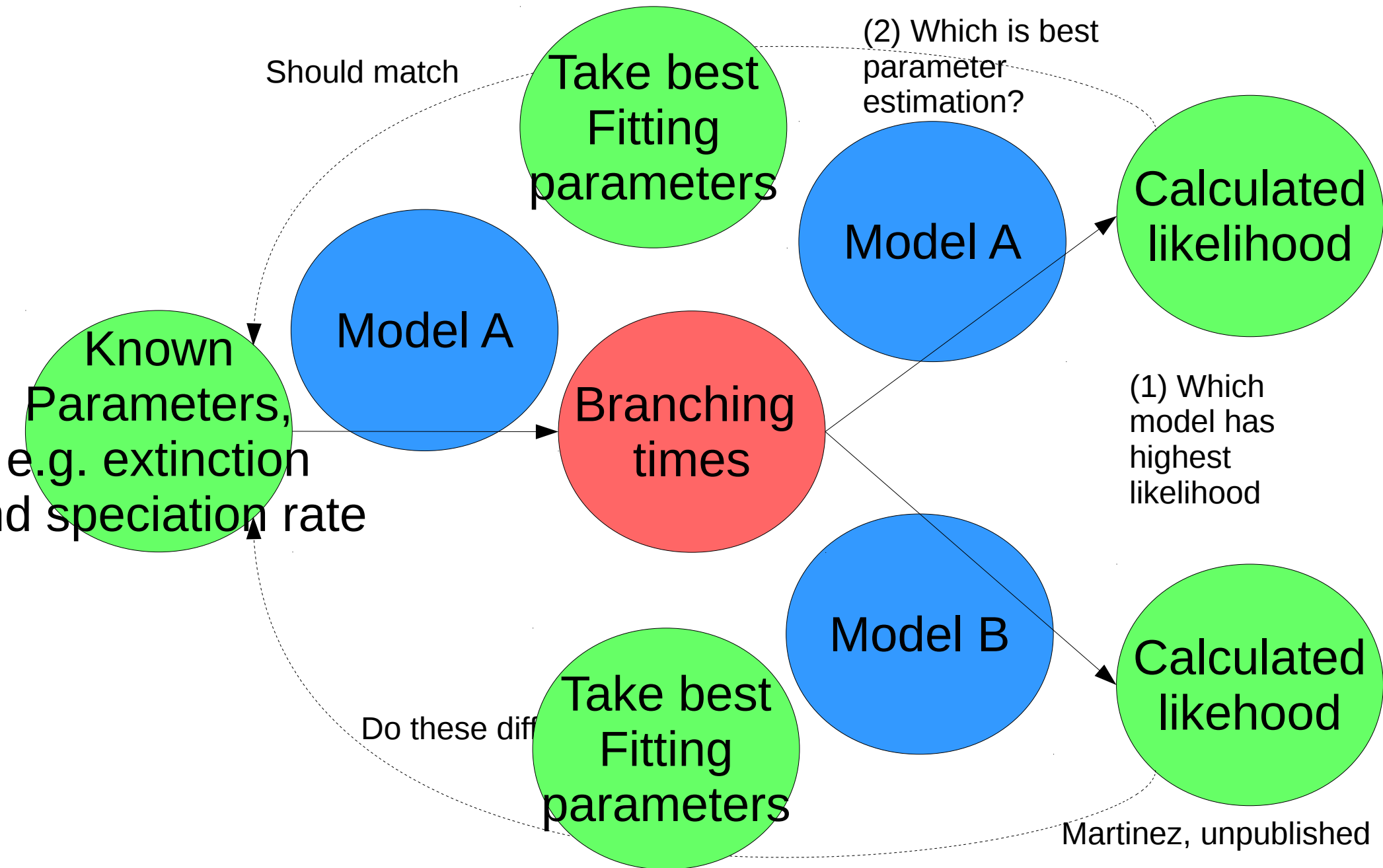


Take phylogeny with the highest likelihood

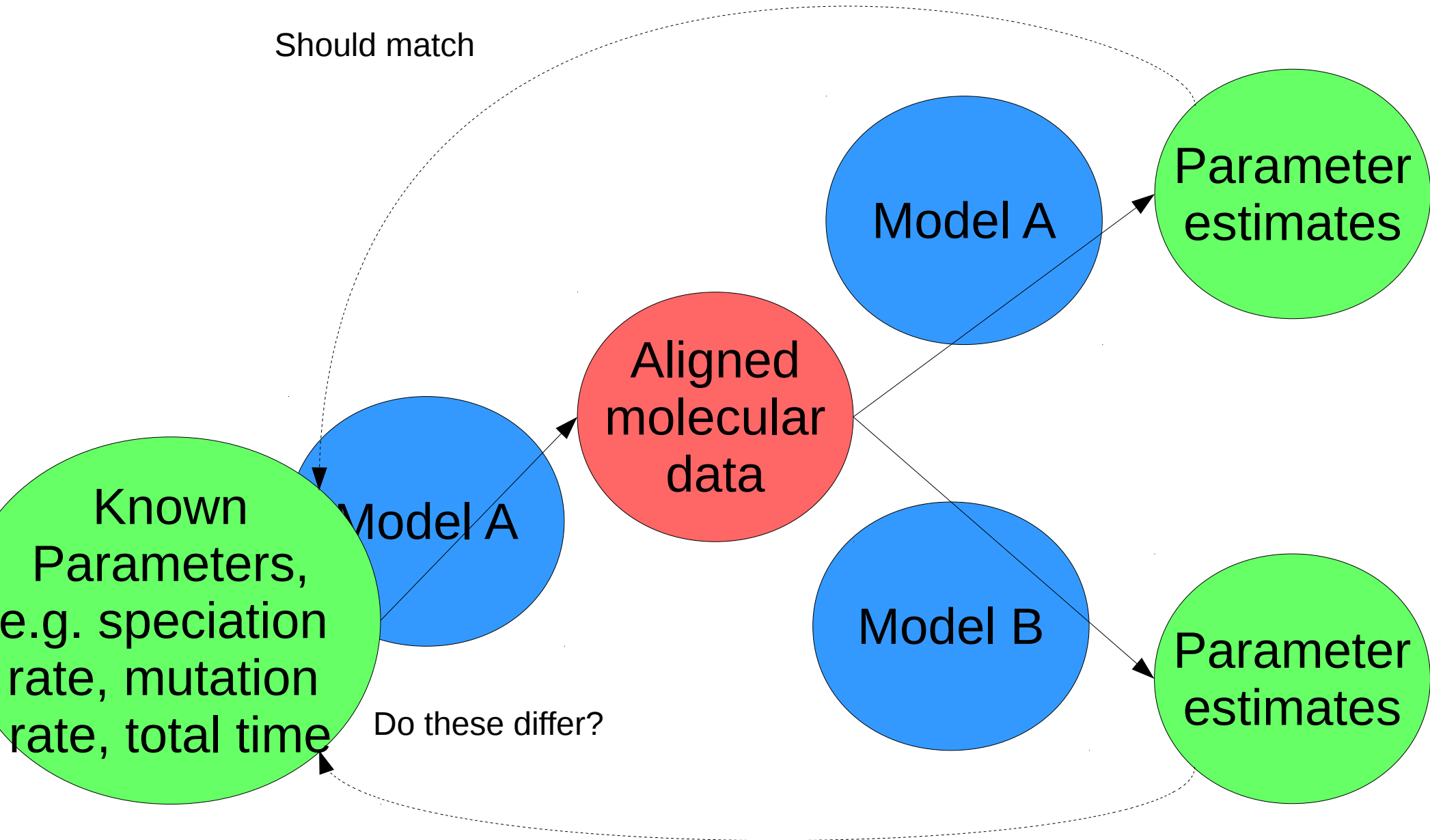
Model unknown



Does model matter?



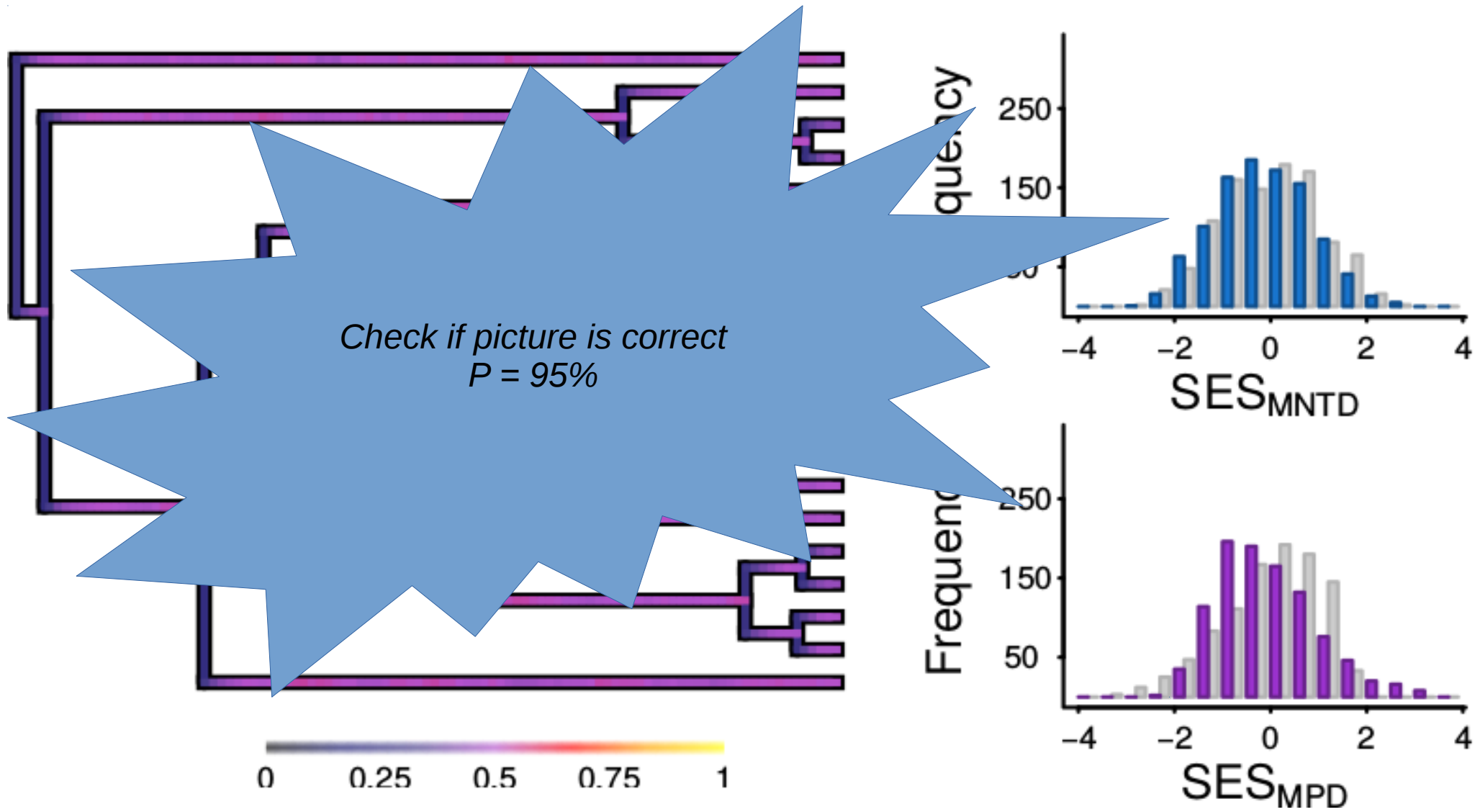
Does model matter?



Does model matter?

Random-draw

DAMOCLES

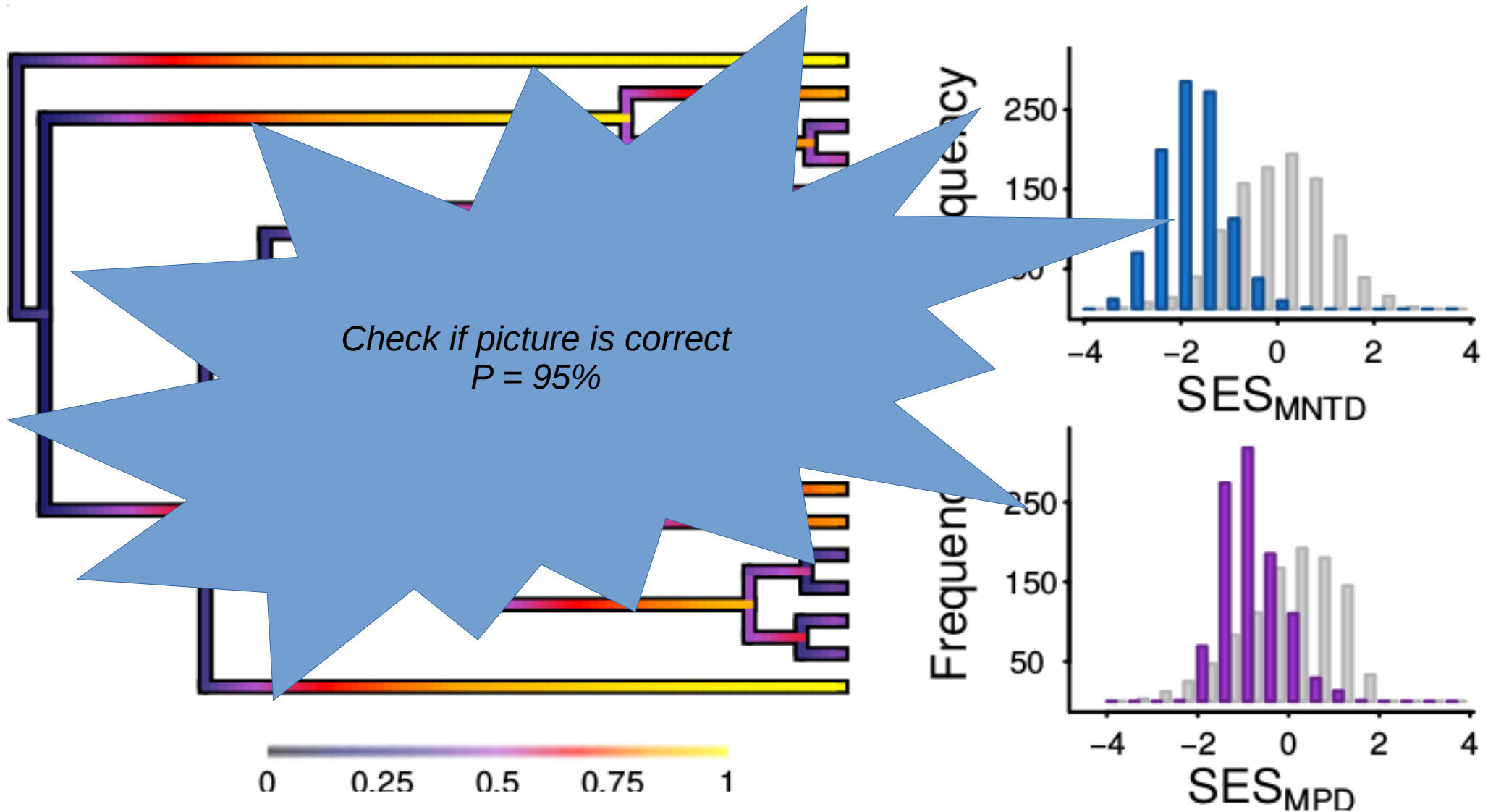


High extinction rate

Does model matter?

Random-draw

DAMOCLES



Low extinction rate

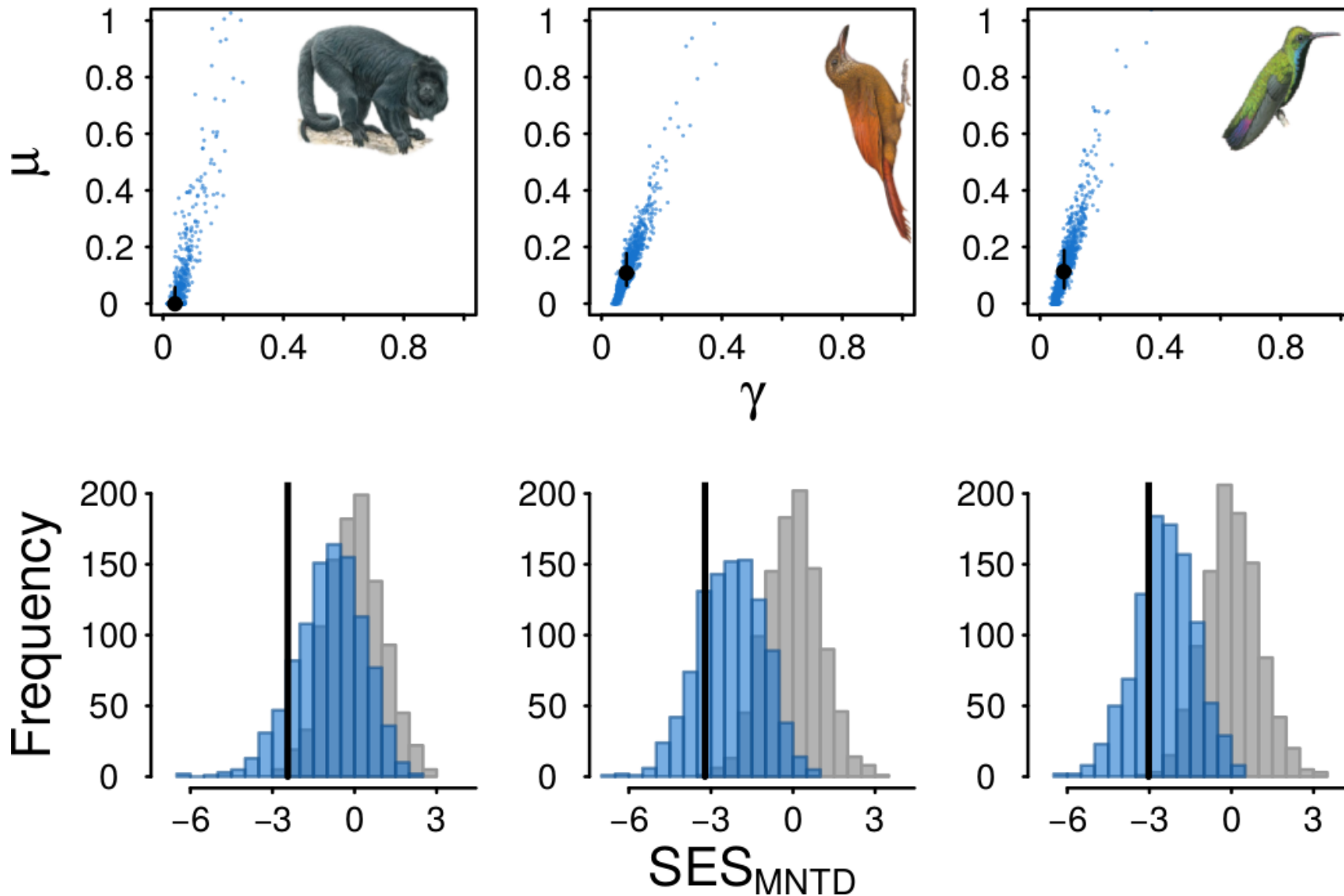
A Pigot & RS Etienne, 2015

Does model matter?

Random-draw

DAMOCLES

Observed



Does model matter?

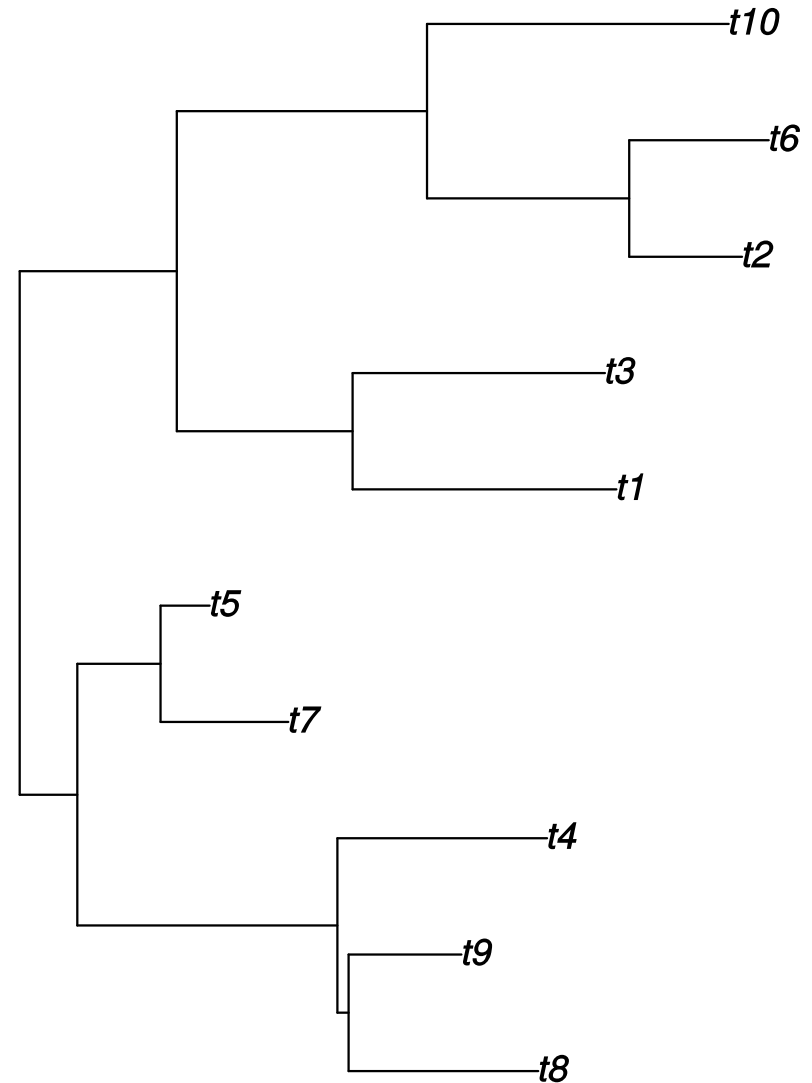
- Comparing a time and density-dependent model
 - Time-dependent: fast to calculate, no mechanism
 - Density dependent: more difficult to calculate, has biological mechanism
- If both yield identical results, using a time-dependent model is proven to be acceptable

Generating null phylogenies

- Can be done in R:

```
library(ape);  
p = rtree(10)  
plot(p)
```

- Random tree
- Algorithm from Paradis, 2012

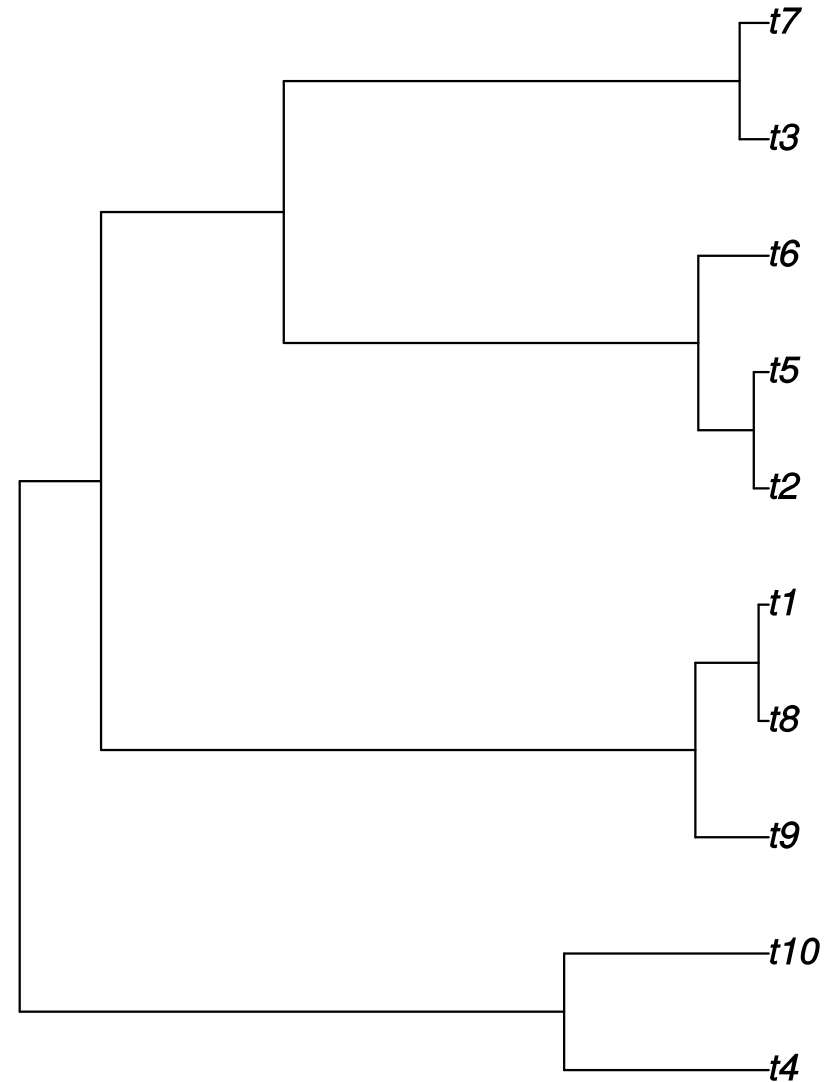


Generating null phylogenies

- Can be done in R:

```
library(ape);  
p = rcoal(10)  
plot(p)
```

- Random coalescent tree: only those individuals sampled at the current time
- Algorithm from Paradis, 2012



Markov Chain

- Memoryless states
- Probabilistic state transitions

