A selection of ongoing work

Floral evolution

O'Meara*, Stacey Smith*, Armbruster, Harder, Hardy, Hileman, Hufford, Litt, Magallon, Stephen Smith, Stevens, Fenster, Diggle

Flexible trait evolution

O'Meara and Banbury^P

Phylogeographic models

O'Meara, Jackson^P, Morales-Garcia, Carstens

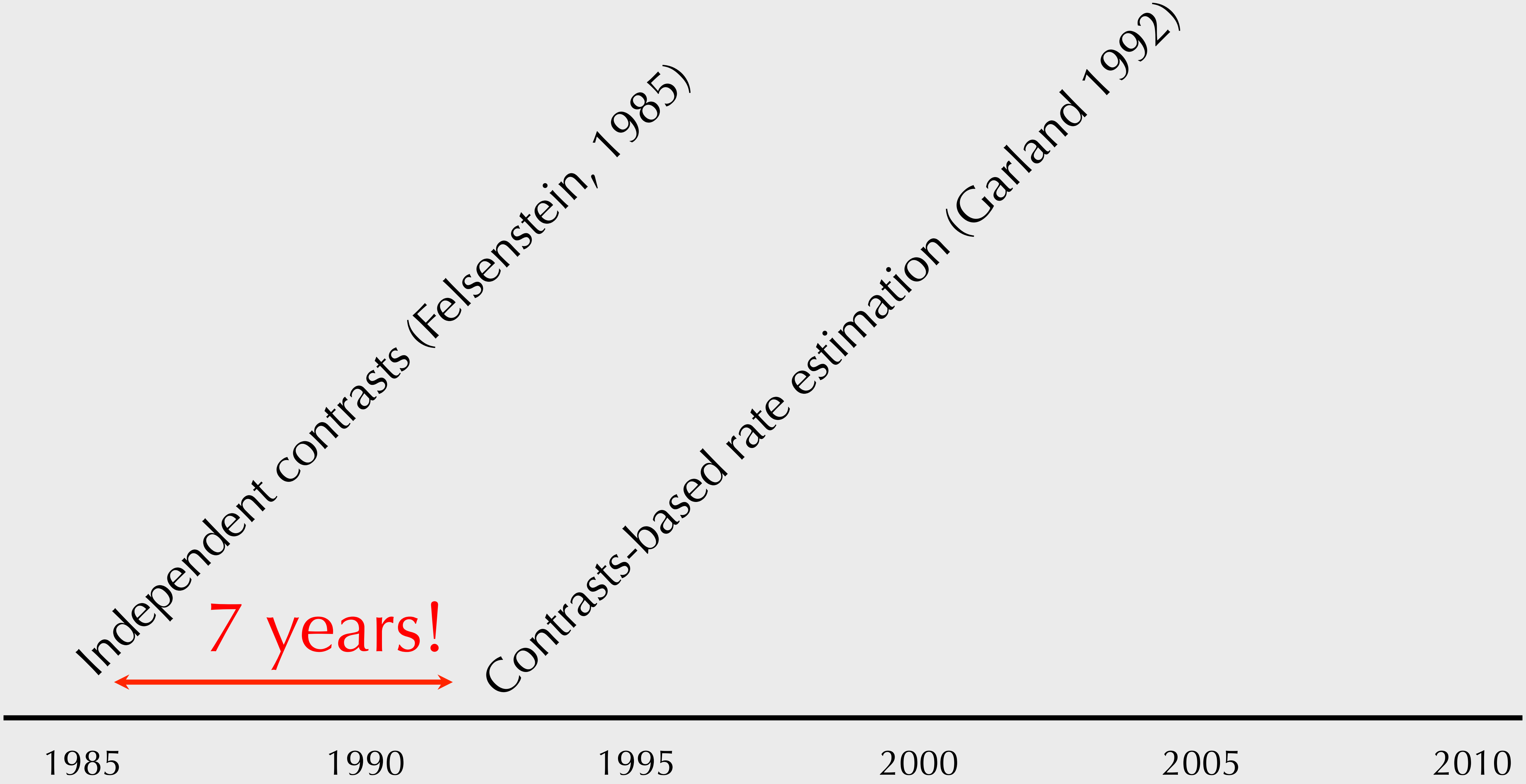
* = equal lead authors

^{P} = postdoc mentee

Independent contrasts (Felsenstein, 1985)

1985 1990 1995 2000 2005 2010

Progress in comparative methods



Independent contrasts (Felsenstein, 1985)

Contrasts-based rate estimation (Garland 1992)

7 years!

1985

1990

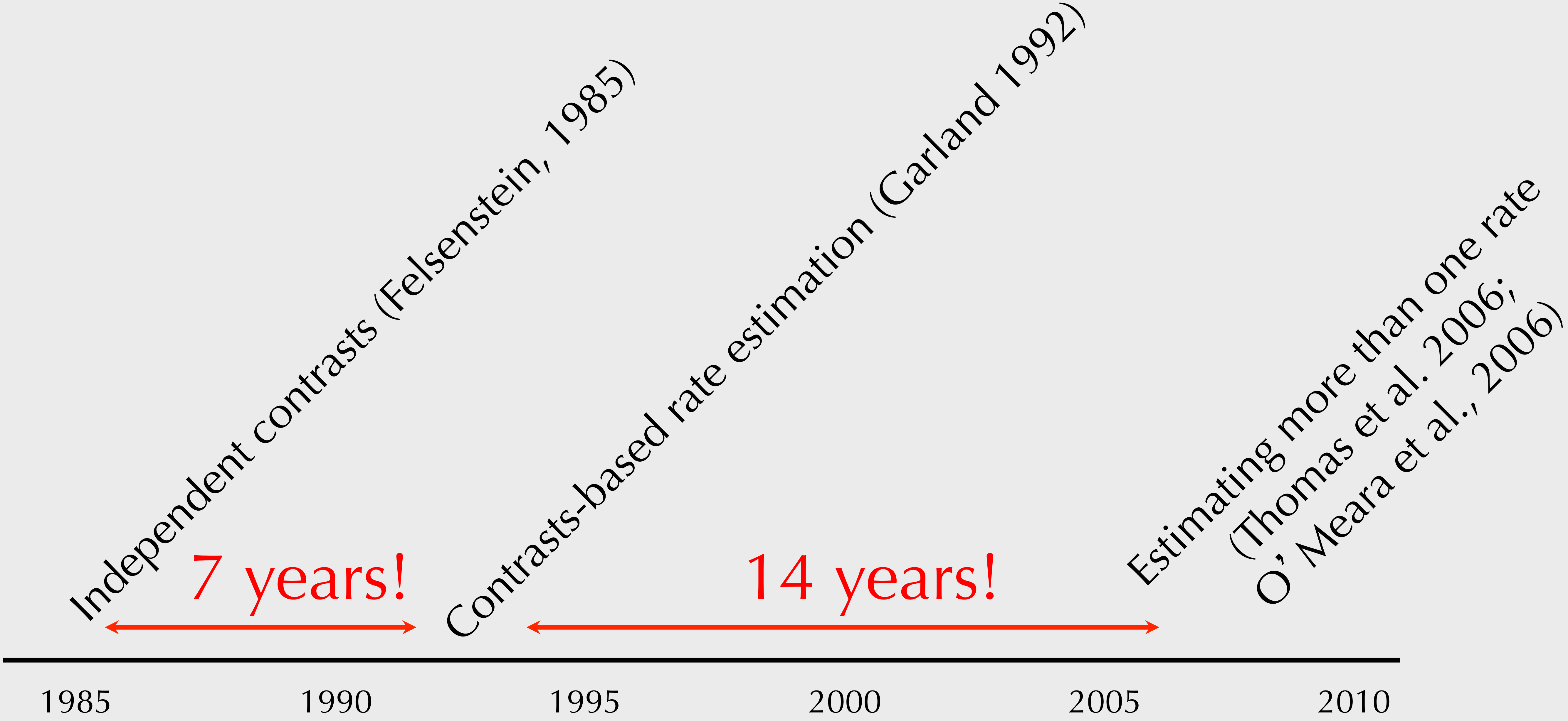
1995

2000

2005

2010

Progress in comparative methods



Independent contrasts (Felsenstein, 1985)

Contrasts-based rate estimation (Garland 1992)

Estimating more than one rate (Thomas et al. 2006; O' Meara et al., 2006)

7 years!

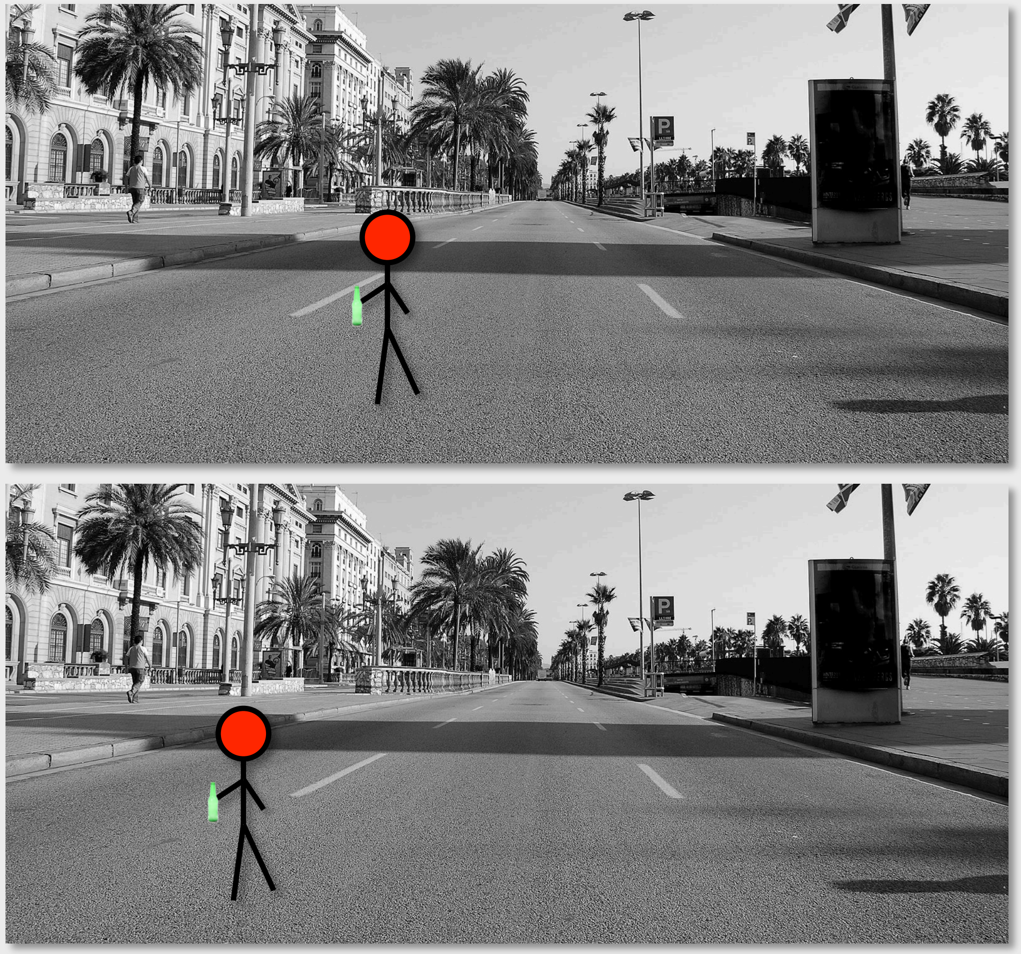
14 years!

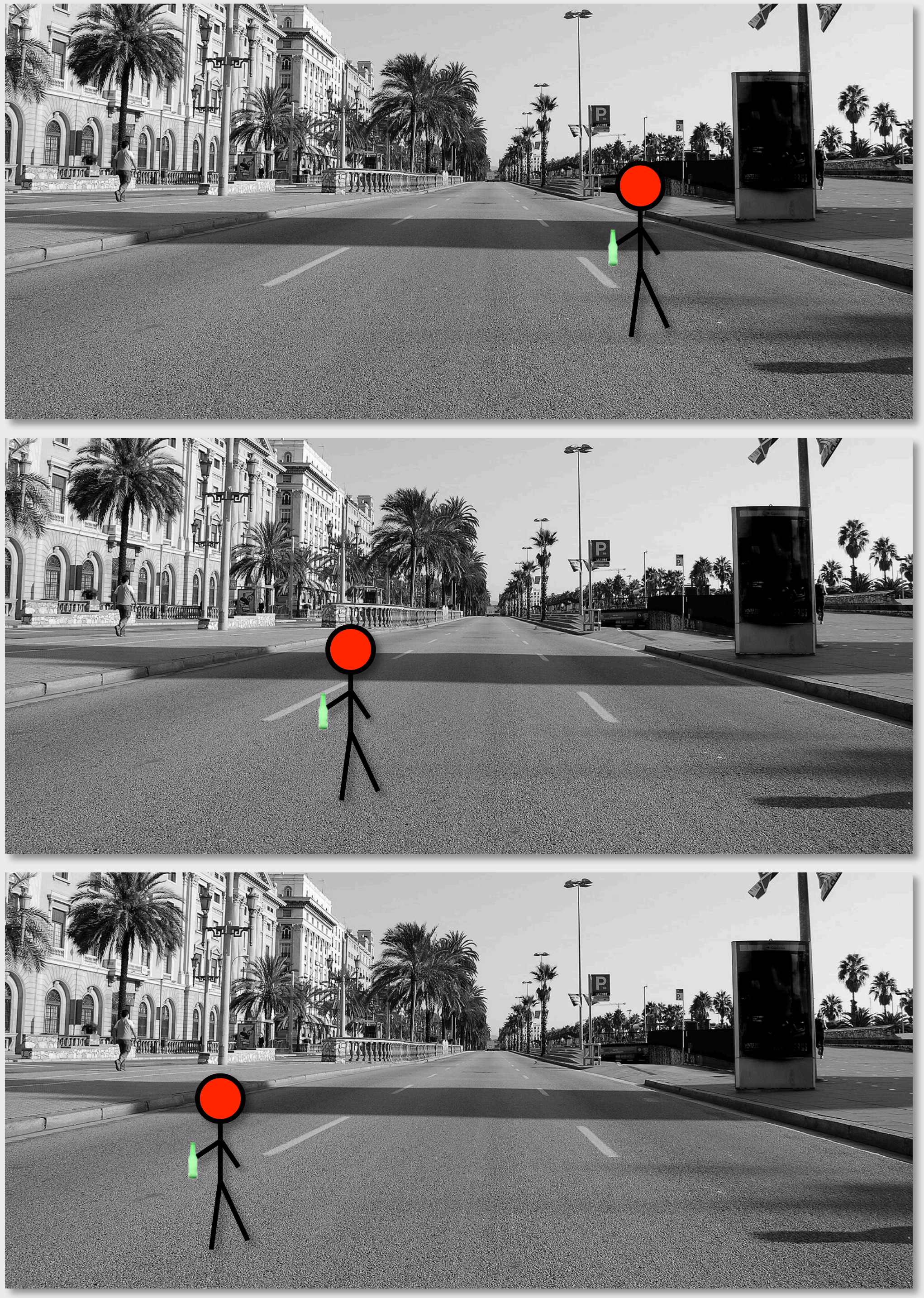
Progress in comparative methods

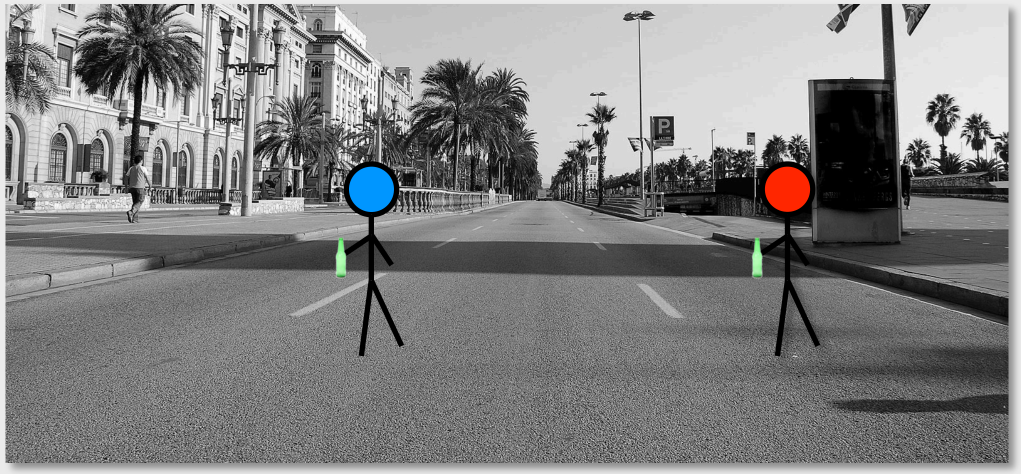
Multivariate normal

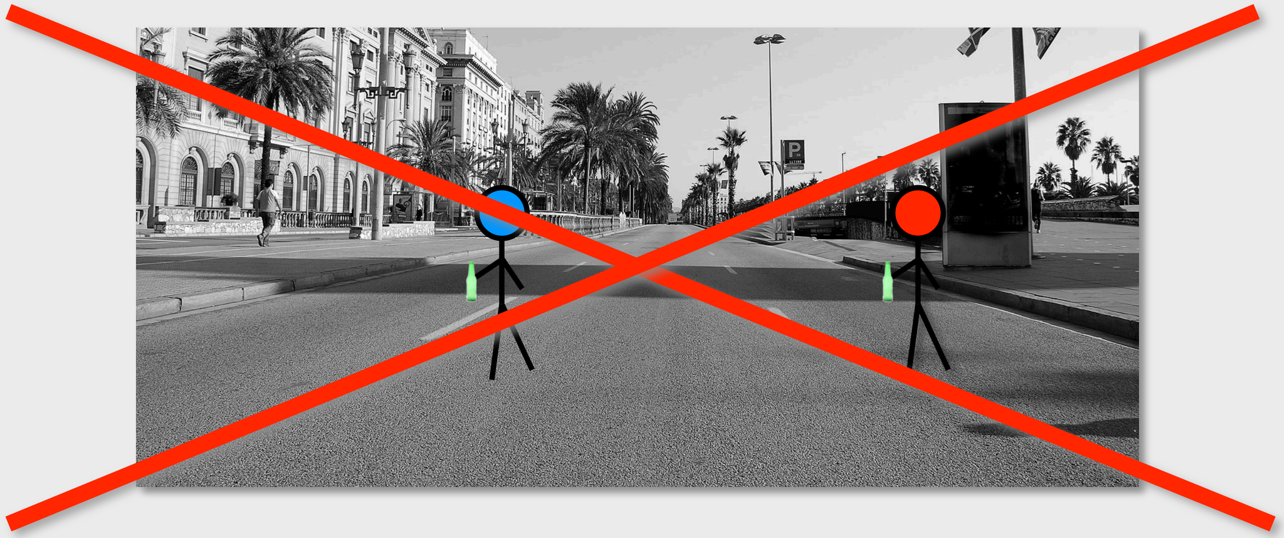
$$f(x) = \frac{1}{\sqrt{2\pi}\sqrt{|\Sigma|}} \exp\left(-\frac{1}{2}(x-\mu)'\Sigma^{-1}(x-\mu)\right)$$

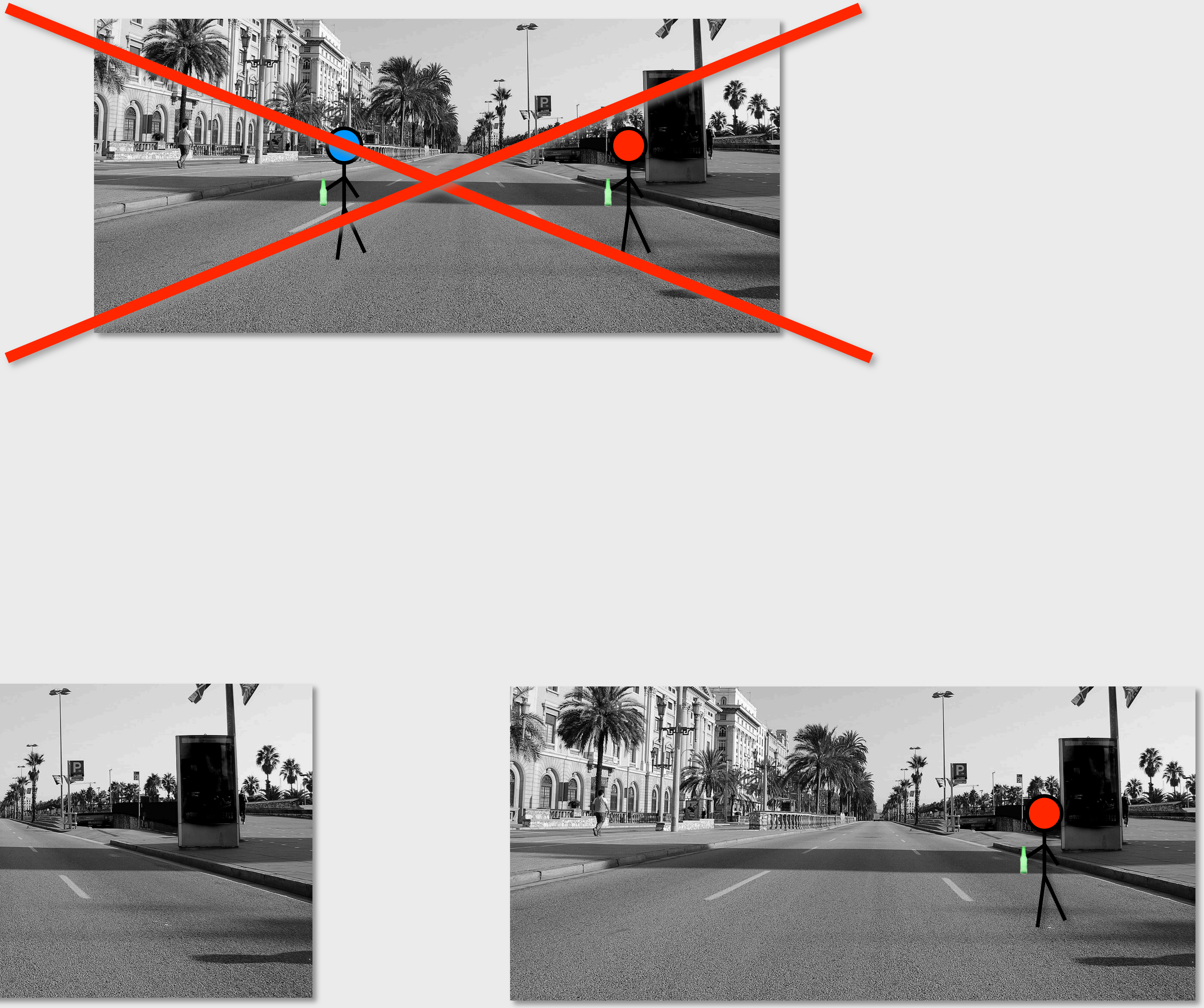
Model	Description	∑	μ
Classic Brownian motion	Single rate of change	Rate x shared time between every pair of species	State at root
Multiple rate Brownian motion	Multiple rates of change	Appropriate rate(s) x shared time between every pair of species	State at root
Multiple mean Ornstein-Uhlenbeck	Attraction to particular value(s), but constant attraction and wiggle	Transformation of rate x time matrix	Expected tip states given model
Multiple everything model	Multiple attractors, attraction, and wiggles	Transformation of rate x time matrix	Expected tip states given model











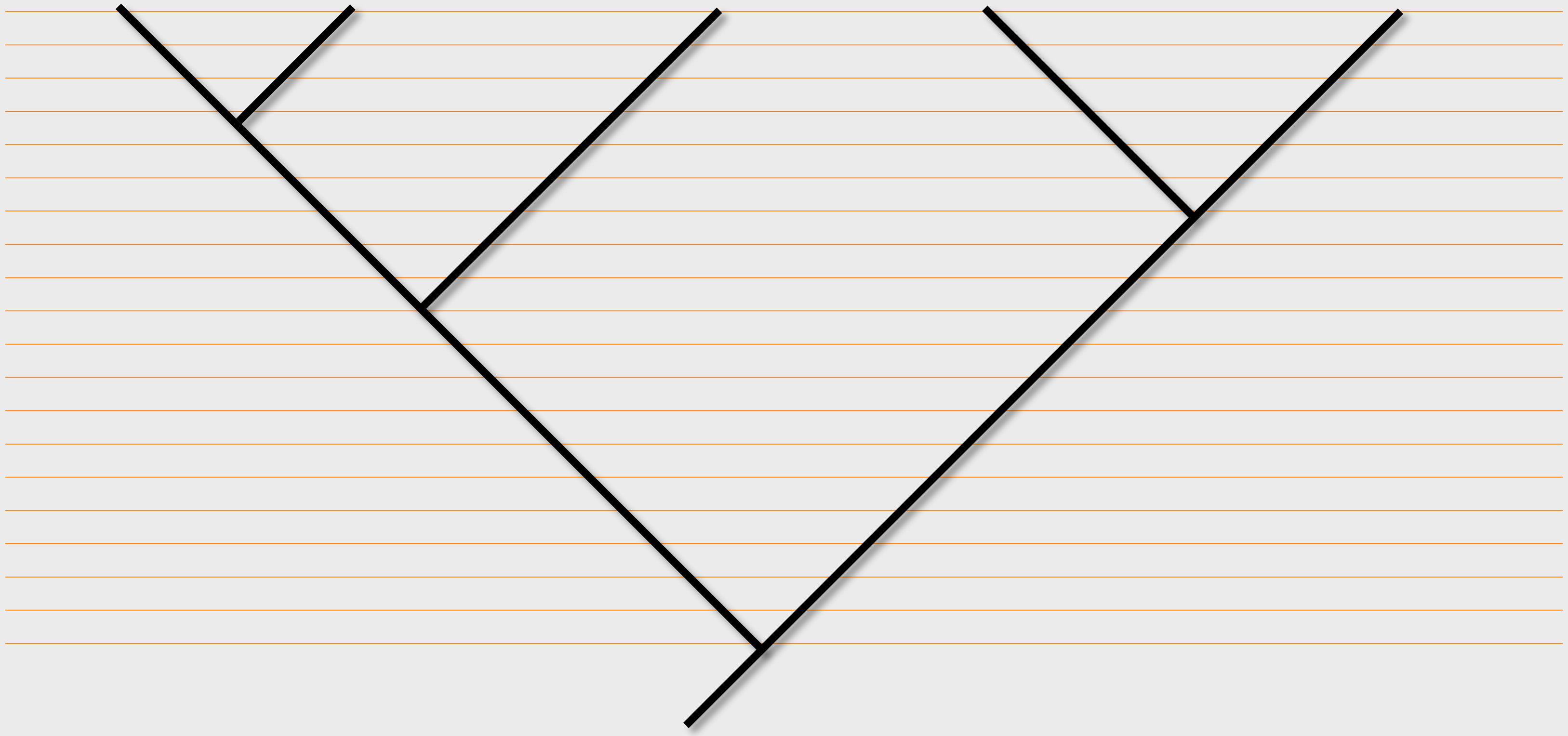
Hard or impossible to analyze currently:

- Bounded evolution
- Character displacement
- Mimicry
- Effect of varying external parameter
- Mixture of processes

Our goal: Allow empiricists to build and use their own models for comparative data

Our approach: Approximate Bayesian computation

Discrete time



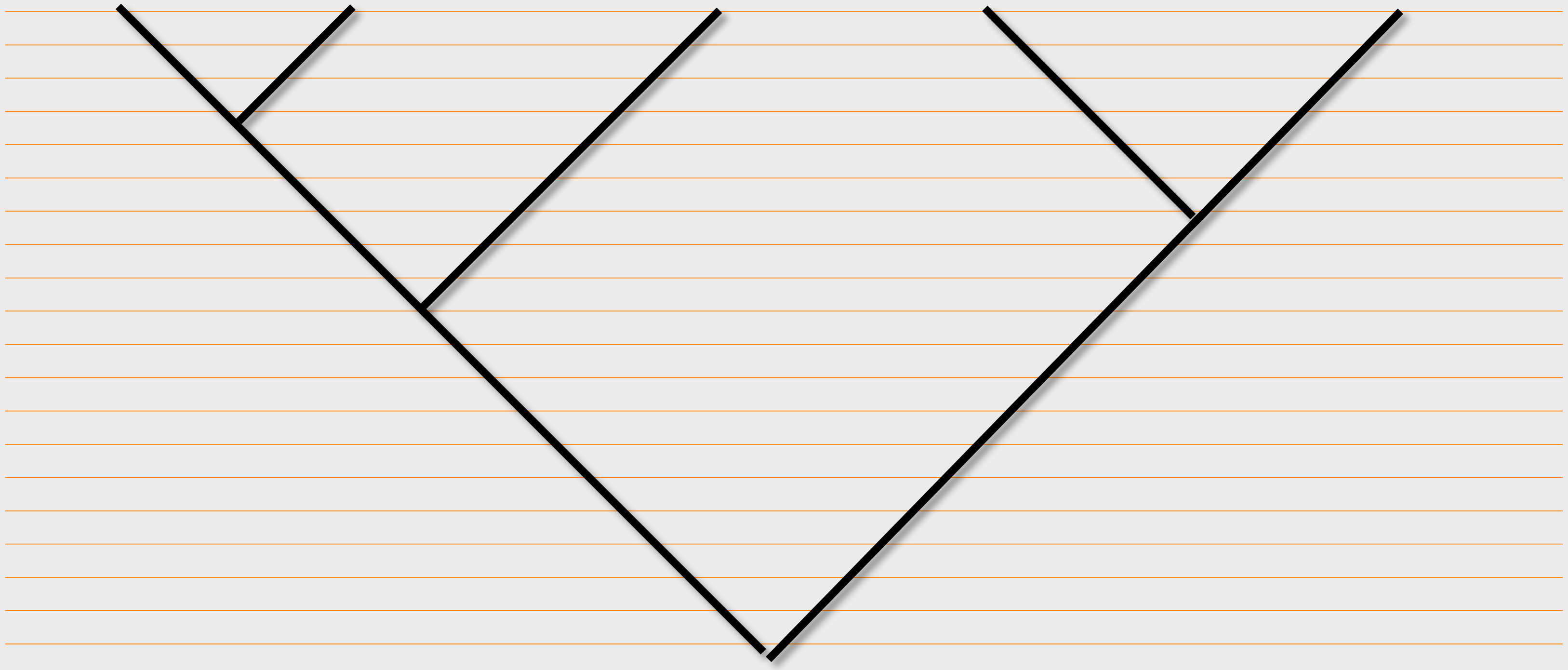
Continuous time is scary:

$$f(x) = \frac{1}{\sqrt{2\pi}\sqrt{|\Sigma|}} \exp\left(-\frac{1}{2}(x-\mu)'\Sigma^{-1}(x-\mu)\right)$$

Discrete time is not:

```
x(t+1) = x(t) + rnorm(n=1, mean=0, sd=0.4)
```

Discrete time



```
taxa[[i]]$nextstates= taxa[[i]]$states
                      + intrinsicFn(…)
                      + extrinsicFn(…)
```

Discrete time

`intrinsicFn()`	Model affecting evolution of a species independent of what the other species are doing
`extrinsicFn()`	Model affecting evolution of a species based on the traits of other species

Discrete time

```
intrinsicFn(model parameters, taxon state,
            time from present)
```

`model parameters`	Brownian motion rate, OU mean, trait minimum values, etc.
`taxon state`	Current state of focal taxon
`time from present`	Allows time-dependent models: was a max size constraint lifted from mammals 65 MYA?

Discrete time

```
extrinsicFn(model parameters, taxon state,
            states of other taxa,
            time from present)
```

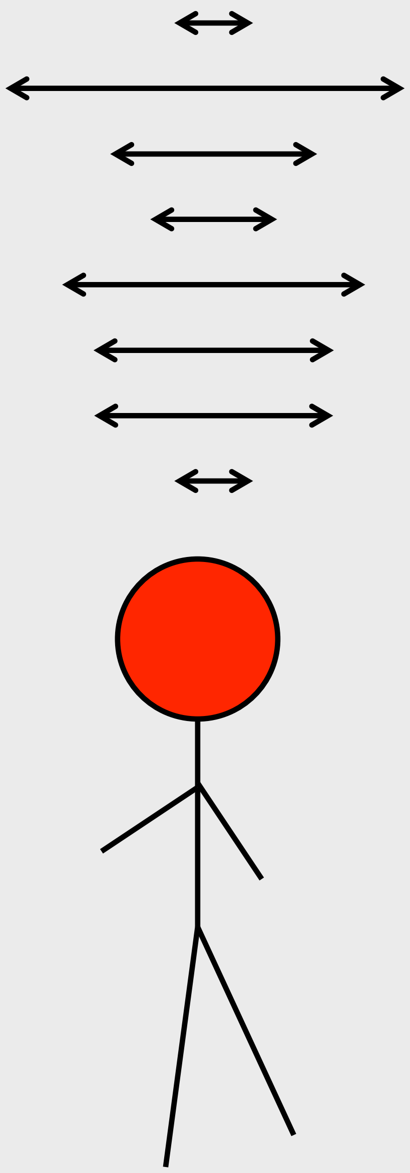
`states of other taxa`	Allows non-independence of species: character displacement, mimicry, etc.

Binomial: for probability heads:

Actual string: HTTHHHHT
Proportion heads: 5/8
Result of last flip: T

- Actual string:
  HTTHHHHT
- Prop. heads:
  5/8

If (observed – simulated) == 0
Count as match



If |observed – simulated| < ε
Count as match

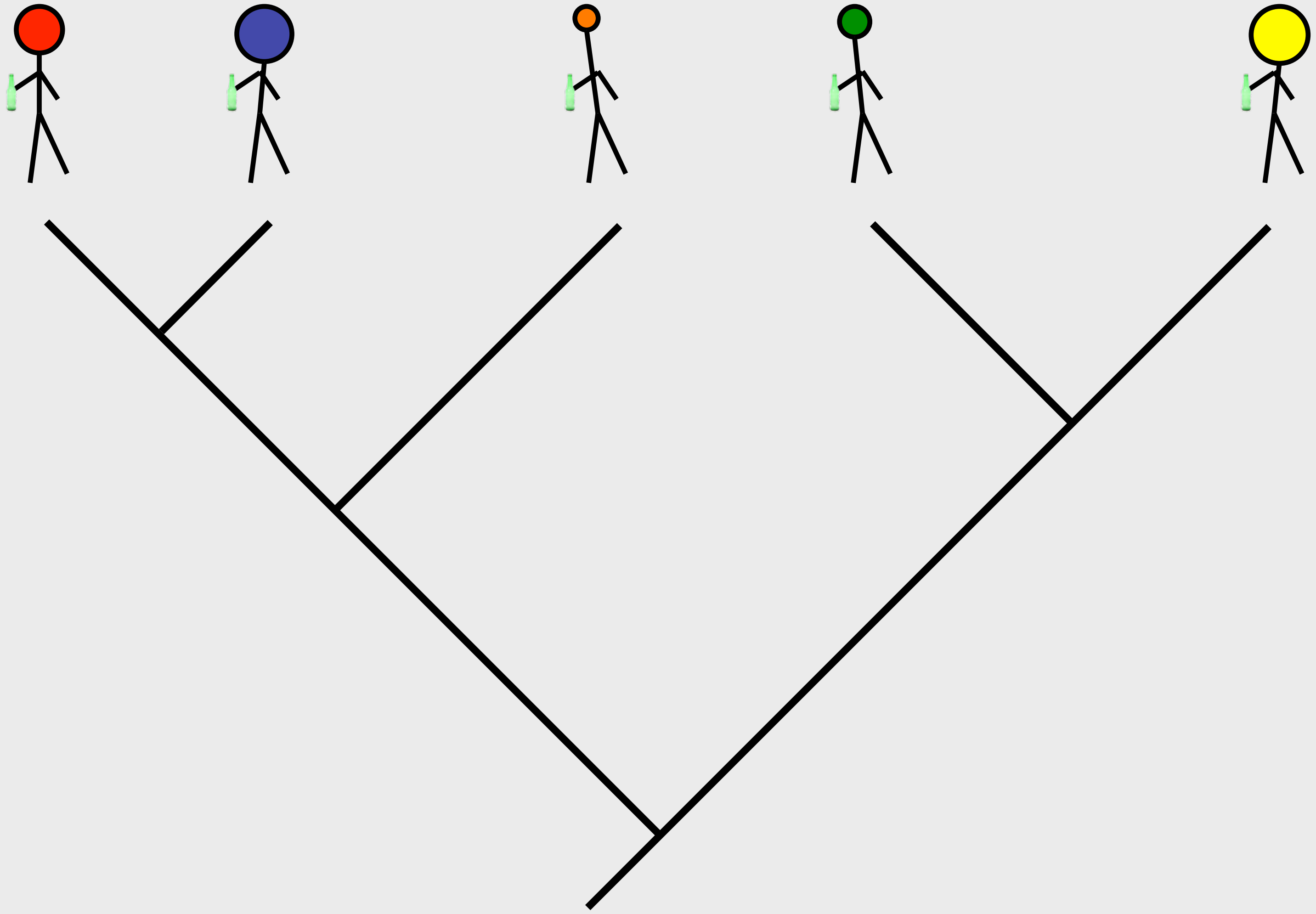
Sufficient summary statistics: contain all the info you need

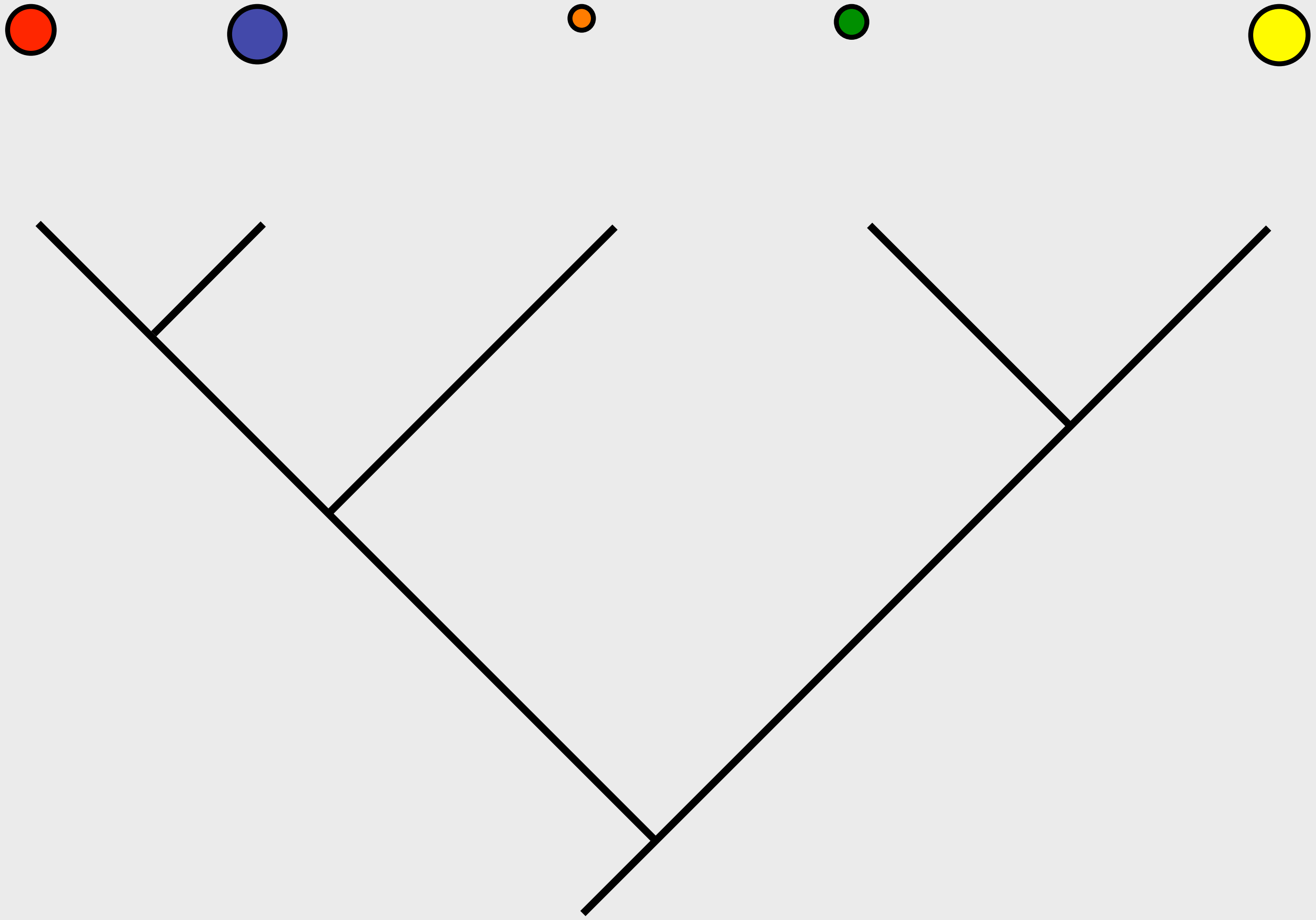
Binomial: for probability heads:

Actual string: HTTHHHHT
Proportion heads: 5/8
Result of last flip: T

Sufficient summary statistics: contain all the info you need

But perhaps there are no sufficient summary statistics, or sufficiency is unknown.

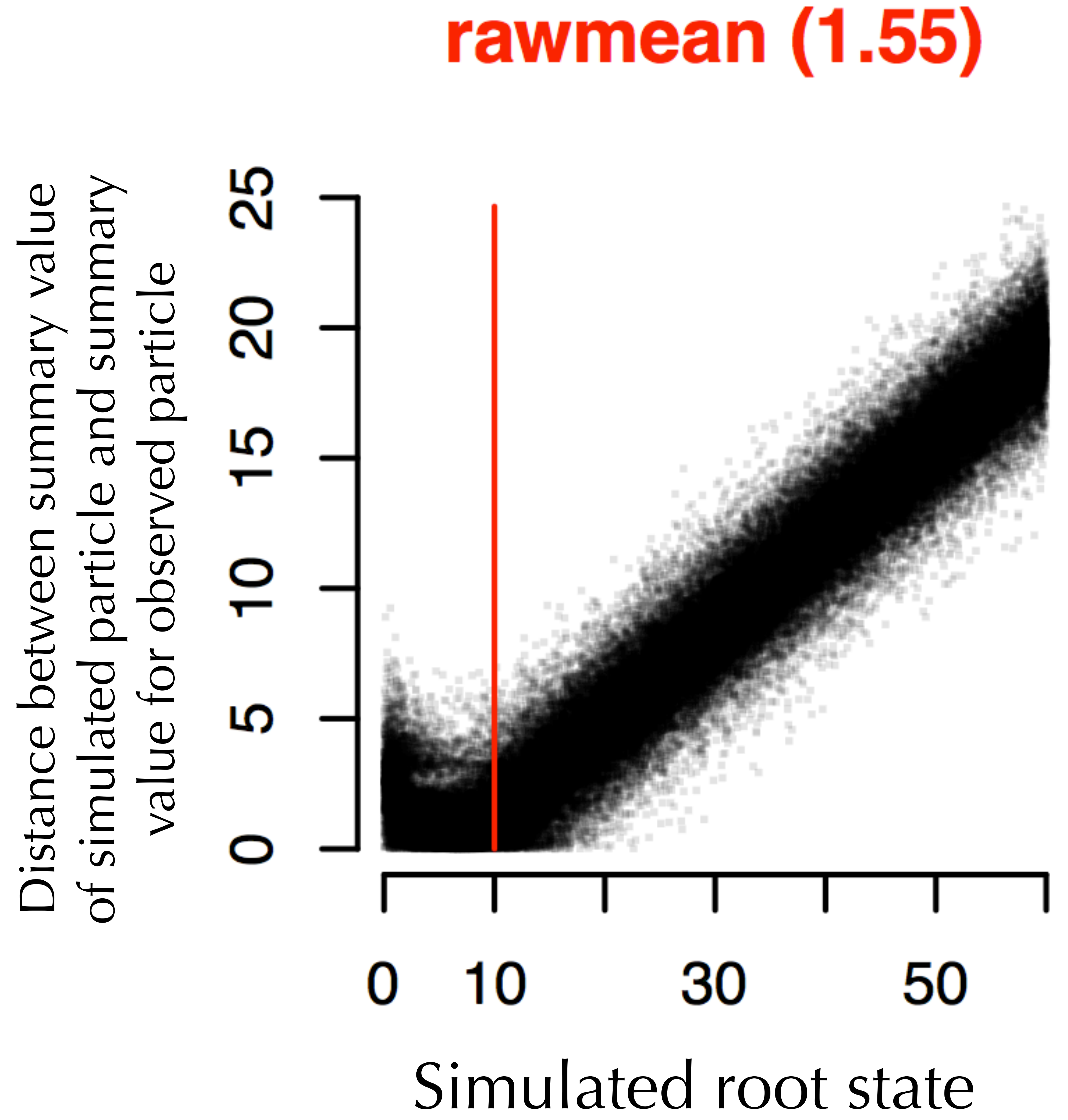




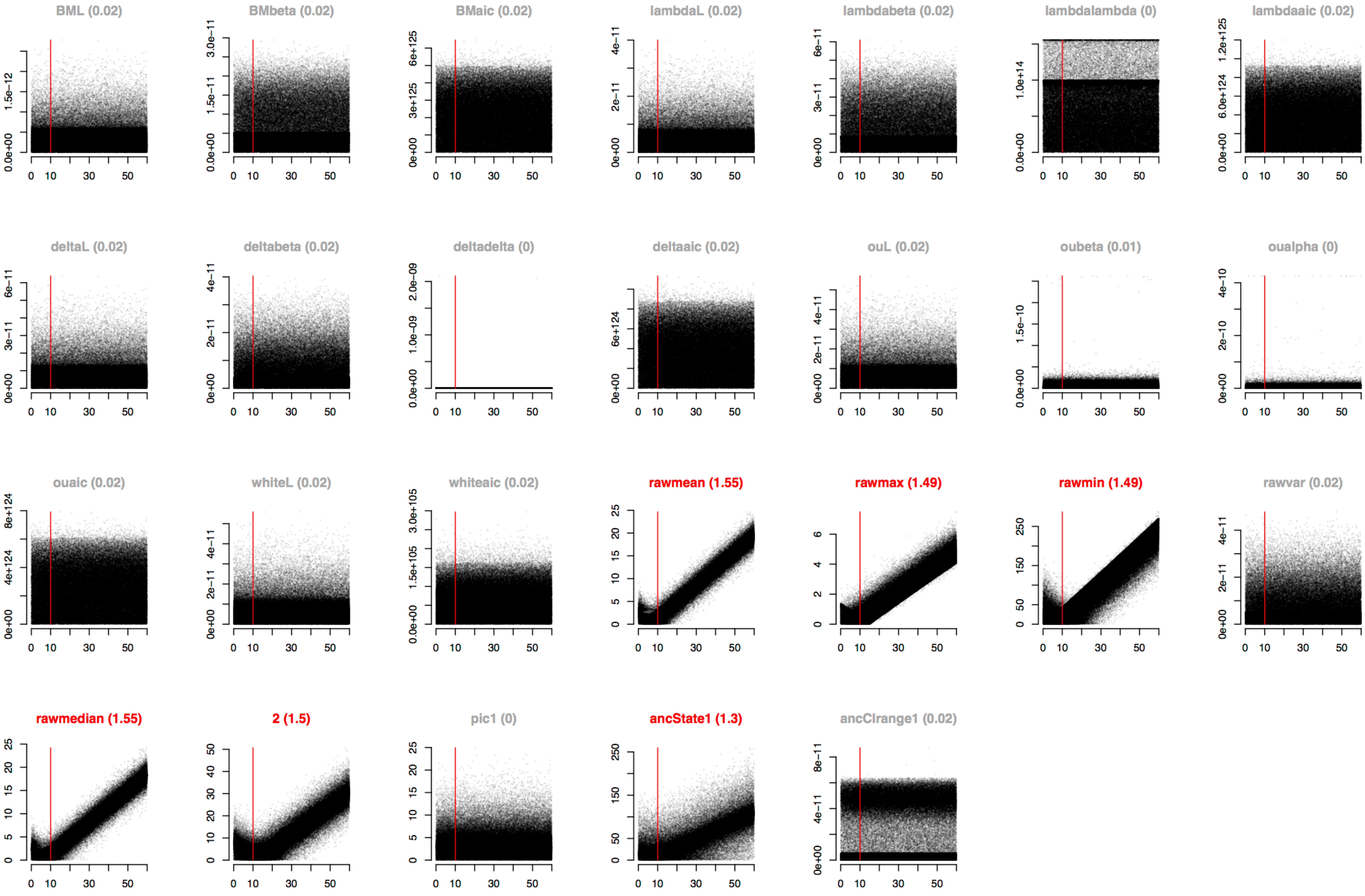
Our approach: multiple summary stats

Model	Values used	Software
Brownian motion model	Rate, lnL, AIC	Geiger (Harmon et al., 2009)
Lambda model	Lambda, beta, lnL, AIC	
Delta model	Delta, beta, lnL, AIC	
Ornstein-Uhlenbeck	Alpha, beta, lnL, AIC	
White noise	lnL, AIC	
Trait raw values	Trait mean, median, max, min, variance	R
Tip values	All	
Contrasts	All	Ape (Paradis et al. 2004)
Ancestral states	All	
Width of ancestral state confidence interval	All	

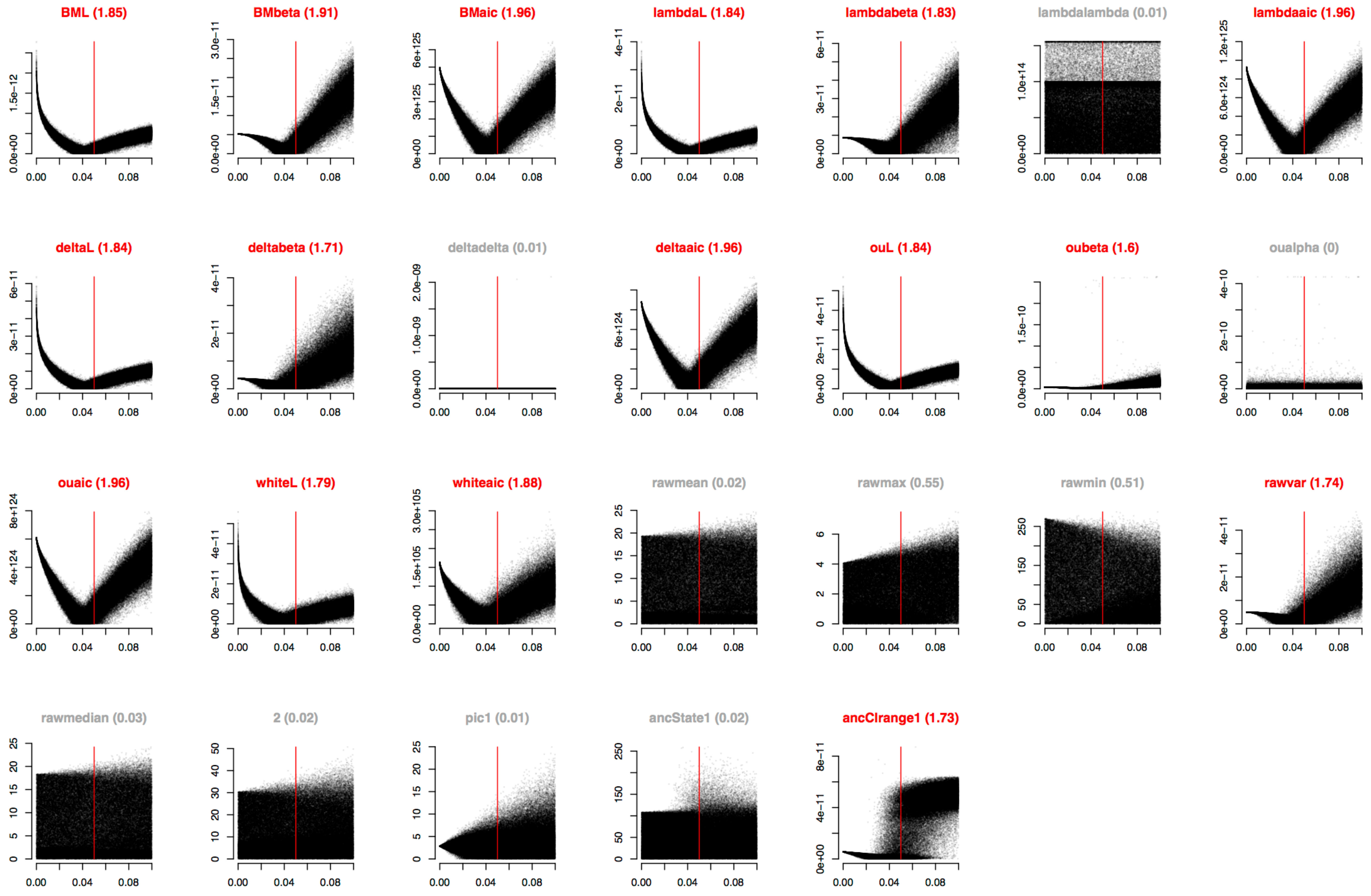
Root state


rawmean (1.55)
Distance between summary value of simulated particle and summary value for observed particle
0
5
10
15
20
25
0
10
30
50
Simulated root state

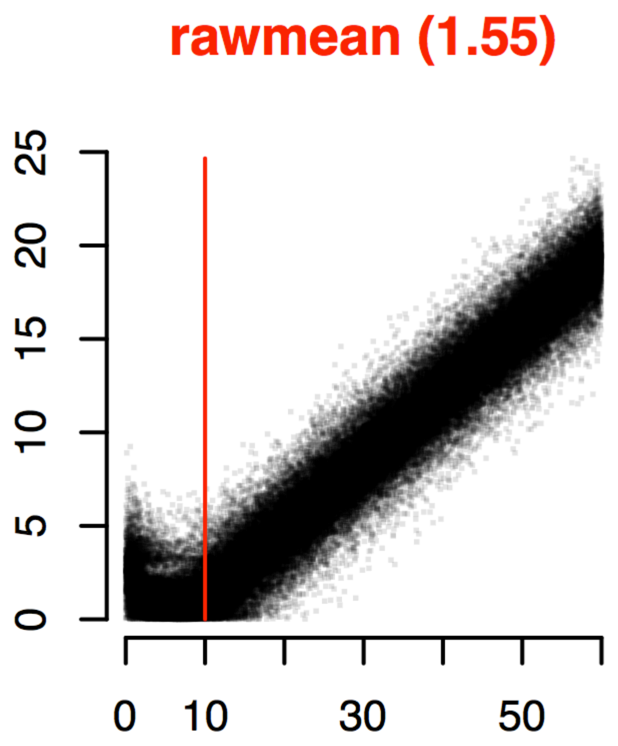
Root state

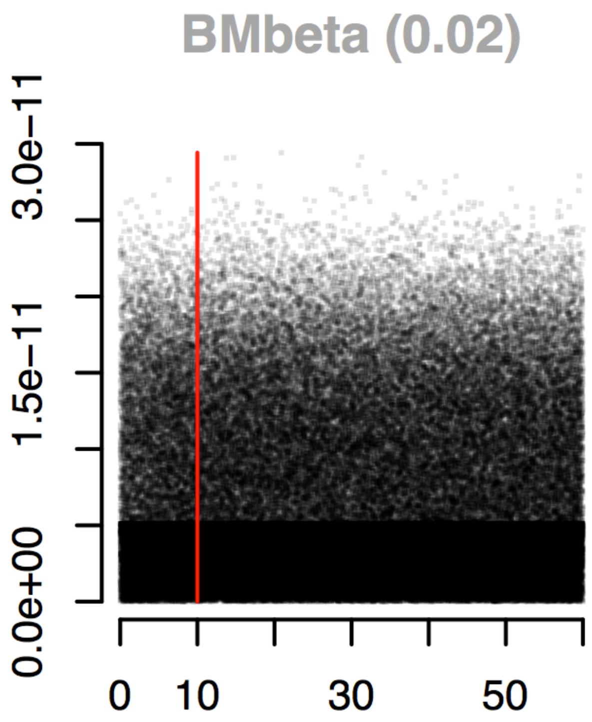

BML (0.02)
BMbeta (0.02)
BMaic (0.02)
lambdaL (0.02)
lambdabeta (0.02)
lambdalambda (0)
lambdaaic (0.02)
deltaL (0.02)
deltabeta (0.02)
deltadelta (0)
deltaaic (0.02)
ouL (0.02)
oubeta (0.01)
oualpha (0)
ouaic (0.02)
whiteL (0.02)
whiteaic (0.02)
rawmean (1.55)
rawmax (1.49)
rawmin (1.49)
rawvar (0.02)
rawmedian (1.55)
2 (1.5)
pic1 (0)
ancState1 (1.3)
ancCIrange1 (0.02)
0 10 30 50
0.0e+00 1.5e-12
0.0e+00 1.5e-11 3.0e-11
0e+00 3e+125 6e+125
0e+00 2e-11 4e-11
0e+00 3e-11 6e-11
0.0e+00 1.0e+14
0.0e+00 6.0e+124 1.2e+125
0e+00 3e-11 6e-11
0e+00 2e-11 4e-11
0.0e+00 1.0e-09 2.0e-09
0e+00 6e+124
0e+00 2e-11 4e-11
0.0e+00 1.5e-10
0e+00 2e-10 4e-10
0e+00 4e+124 8e+124
0e+00 2e-11 4e-11
0.0e+00 1.5e+105 3.0e+105
0 5 10 15 20 25
0 2 4 6
0 50 150 250
0e+00 2e-11 4e-11
0 5 10 15 20 25
0 10 20 30 40 50
0 5 10 15 20 25
0 50 150 250
0e+00 4e-11 8e-11

Brownian rate

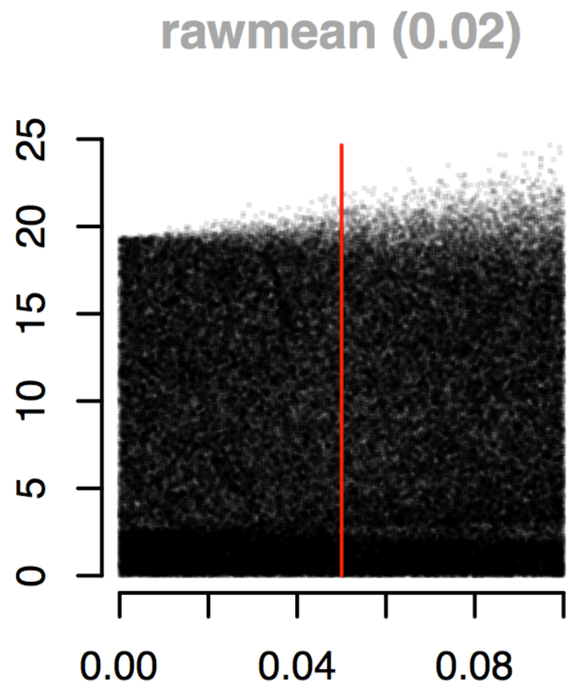


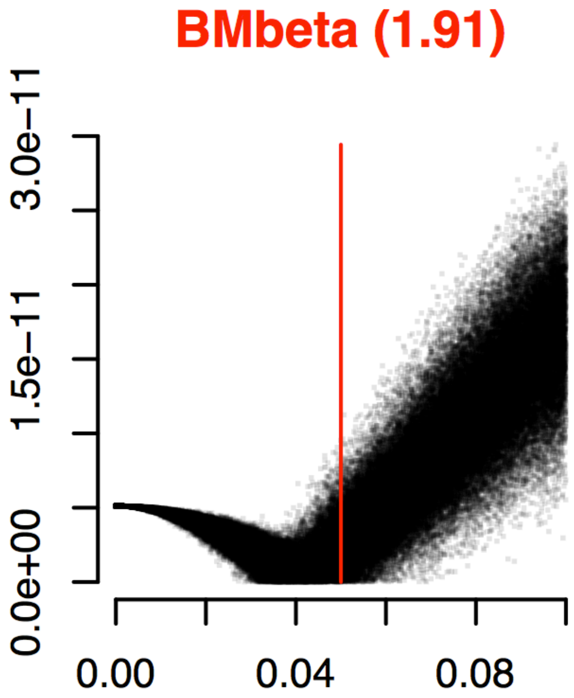
Root state


rawmean (1.55)


BMbeta (0.02)

Brownian
rate


rawmean (0.02)


BMbeta (1.91)

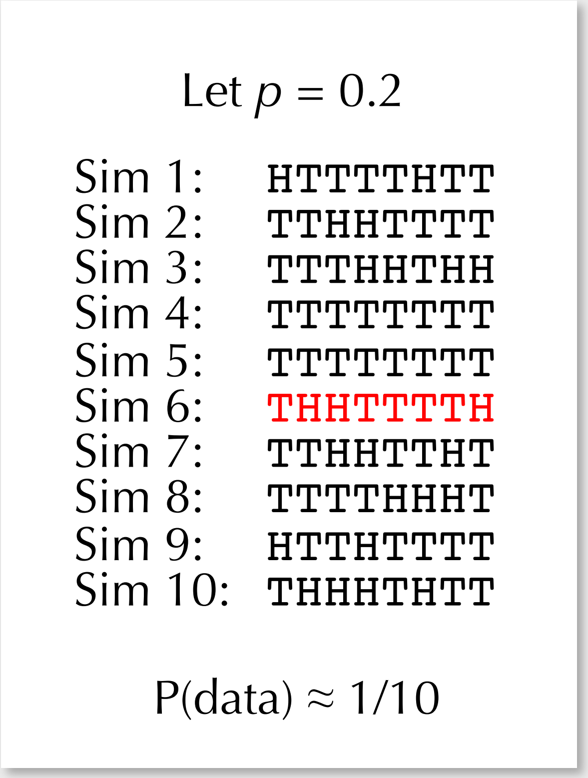
Bayes Rule

Prob(*parameter* | *data*) =

Prob(*data* | *parameter*) *x*
Prob(*parameter*) ÷
normalizing term

Bayes Rule

Prob(*parameter* | *data*) = Prob(*data* | *parameter*) *x*
Prob(*parameter*) ÷
normalizing term



Let $p = 0.2$

Sim 1: `HTTTTHTT`
Sim 2: `TTHHTTTT`
Sim 3: `TTTHHTHH`
Sim 4: `TTTTTTTT`
Sim 5: `TTTTTTTT`
Sim 6: `THHTTTTH`
Sim 7: `TTHHTTHT`
Sim 8: `TTTTHHHT`
Sim 9: `HTTHTTTT`
Sim 10: `THHHTHTT`

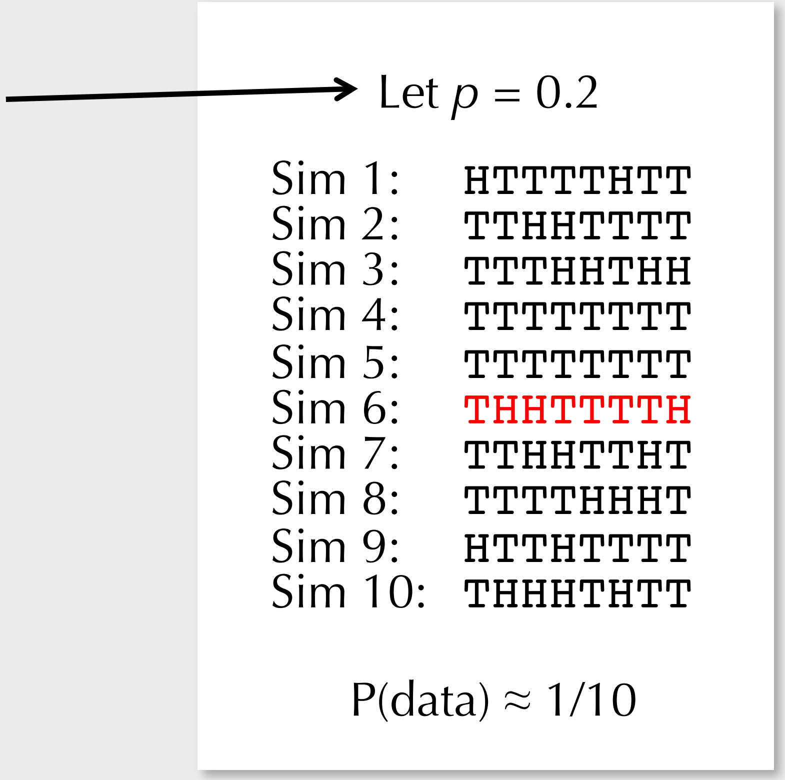
P(data) ≈ 1/10

Bayes Rule

Prob(*parameter* | *data*) =

Prob(*data* | *parameter*) x
Prob(*parameter*) ÷
normalizing term

Sample p
from prior



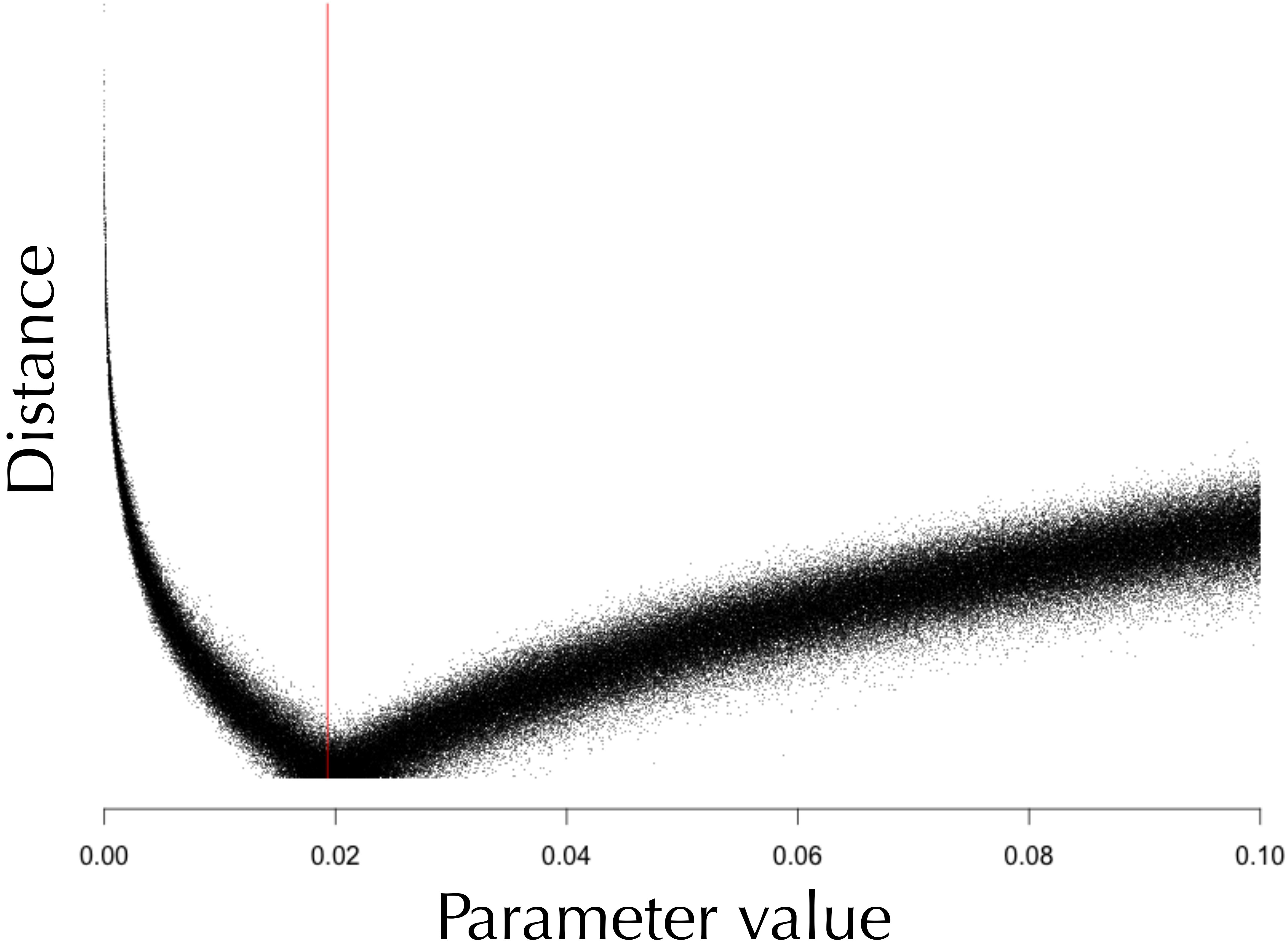
Let $p = 0.2$

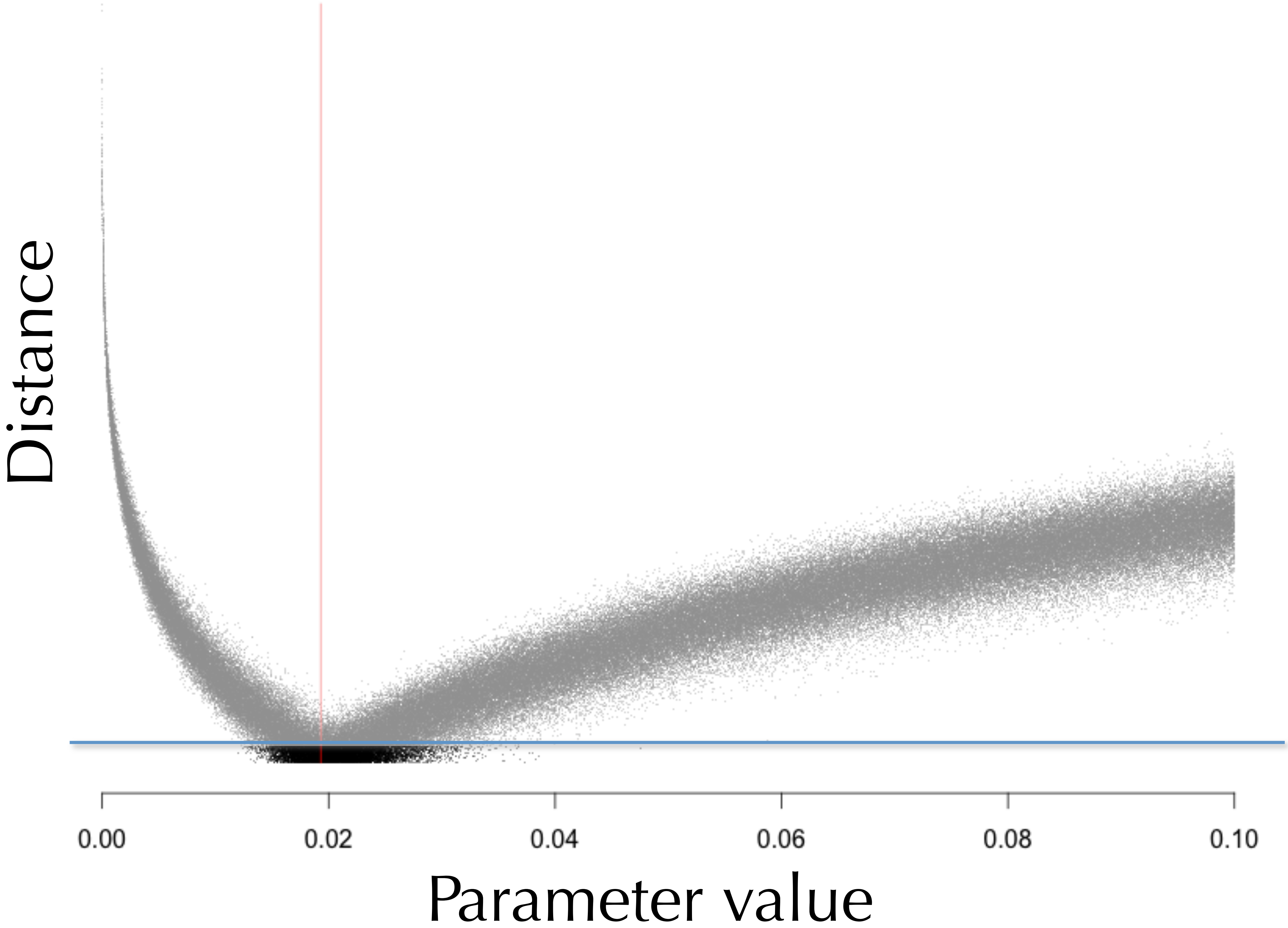
Sim 1: HTTTTHTT
Sim 2: TTHHTTTT
Sim 3: TTTHHTHH
Sim 4: TTTTTTTT
Sim 5: TTTTTTTT
Sim 6: THHTTTTH
Sim 7: TTHHTTHT
Sim 8: TTTTHHHT
Sim 9: HTTHTTTT
Sim 10: THHHTHTT

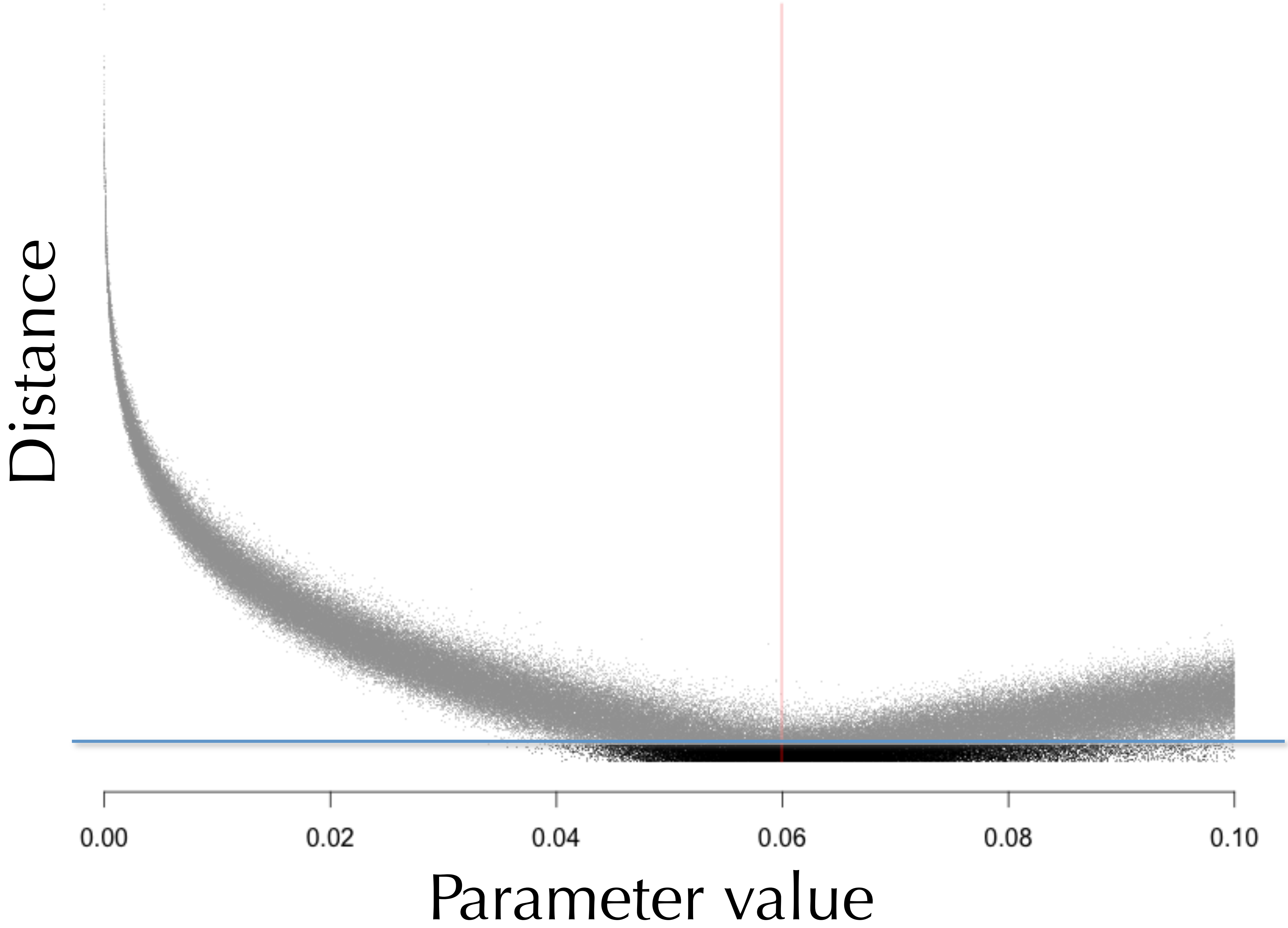
P(data) ≈ 1/10

Rejection

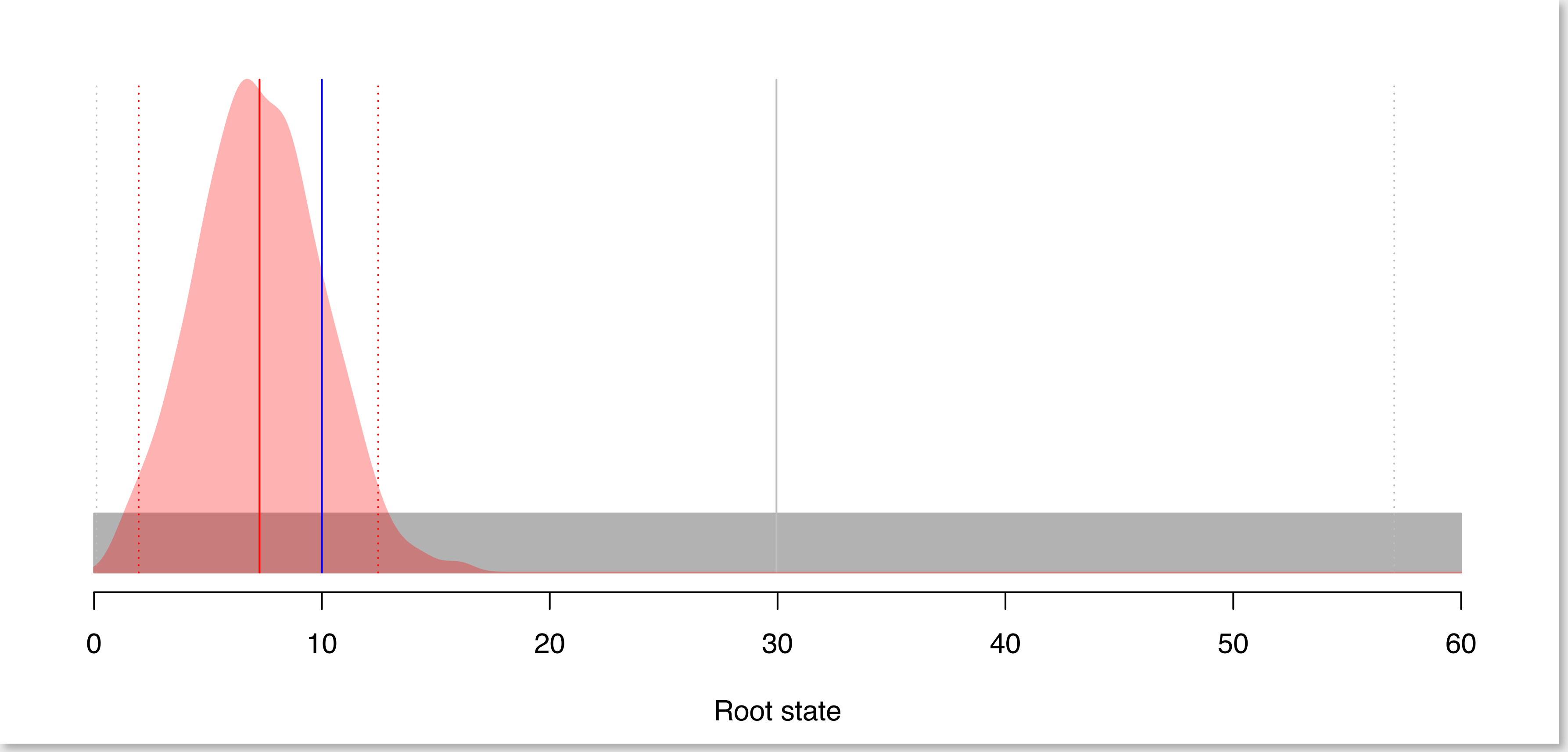
1. Sample parameters from prior distributions
2. Simulate data using those parameters
3. Summary(simulated data)
4. If |Summary(observed data) – Summary(simulated data)| < ε , save that simulation
5. The distribution of parameters of saved simulations = posterior distribution of those parameters


Distance
0.00
0.02
0.04
0.06
0.08
0.10
Parameter value

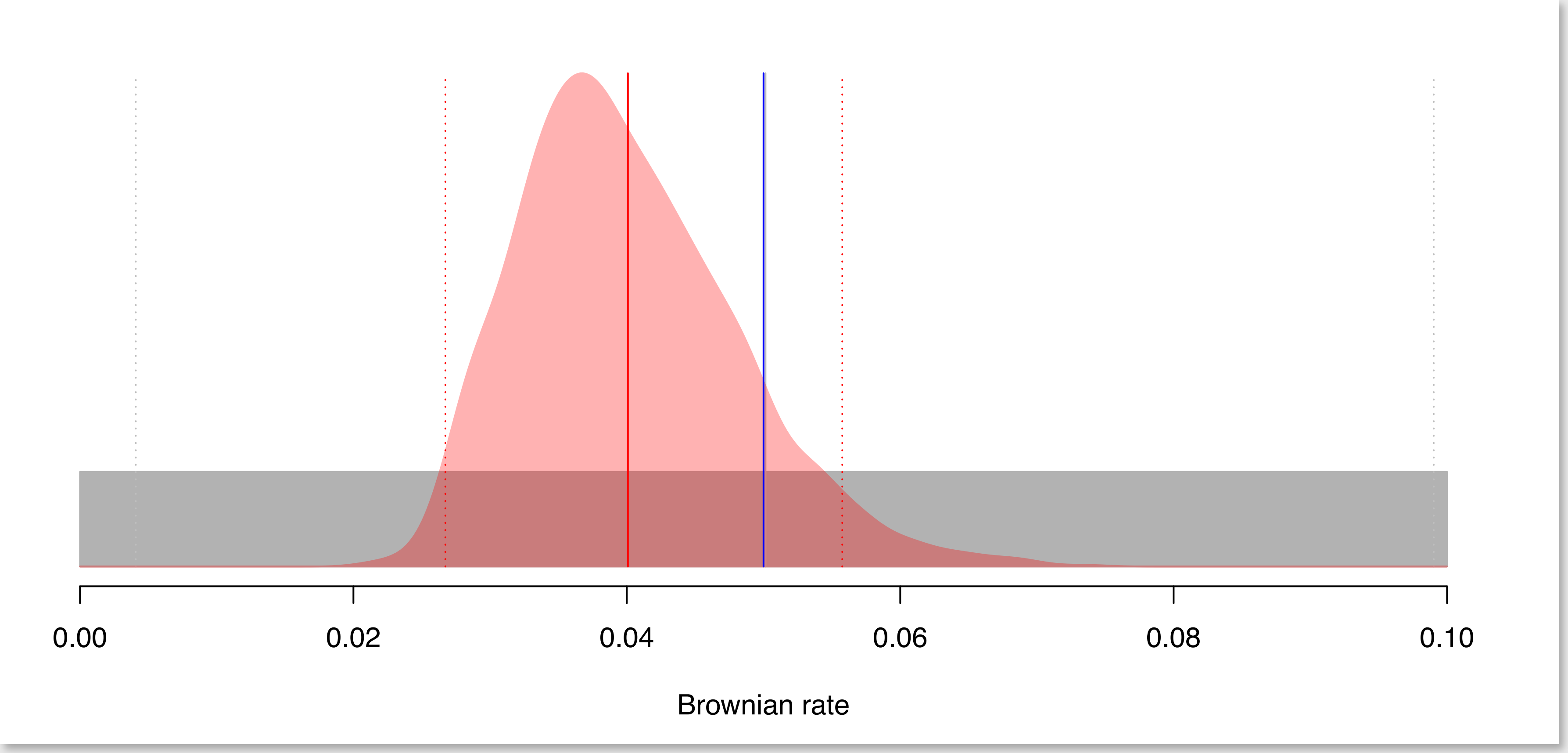

Distance
0.00
0.02
0.04
0.06
0.08
0.10
Parameter value


Distance
0.00
0.02
0.04
0.06
0.08
0.10
Parameter value

Root state

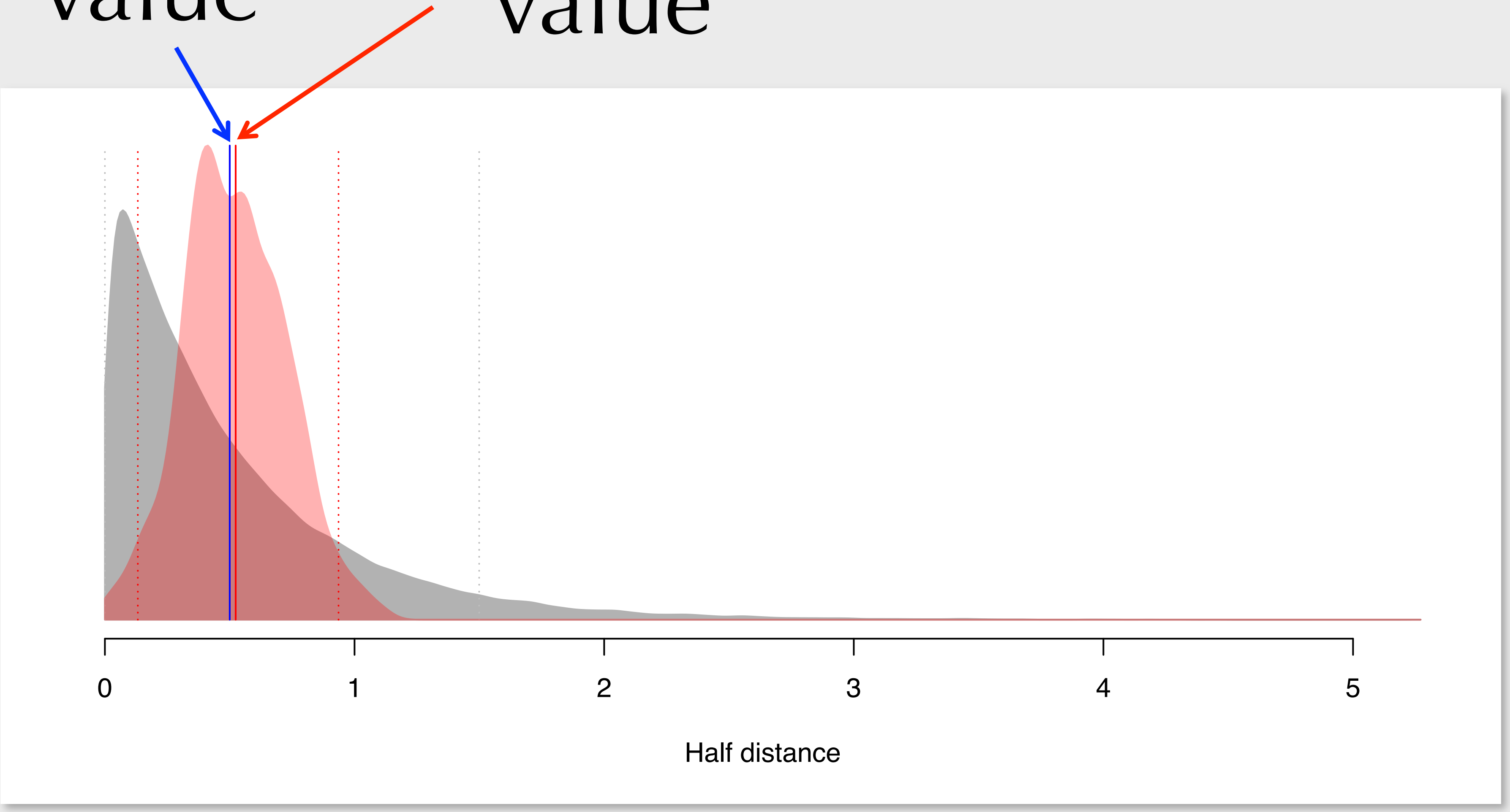


Brownian rate



Character displacement

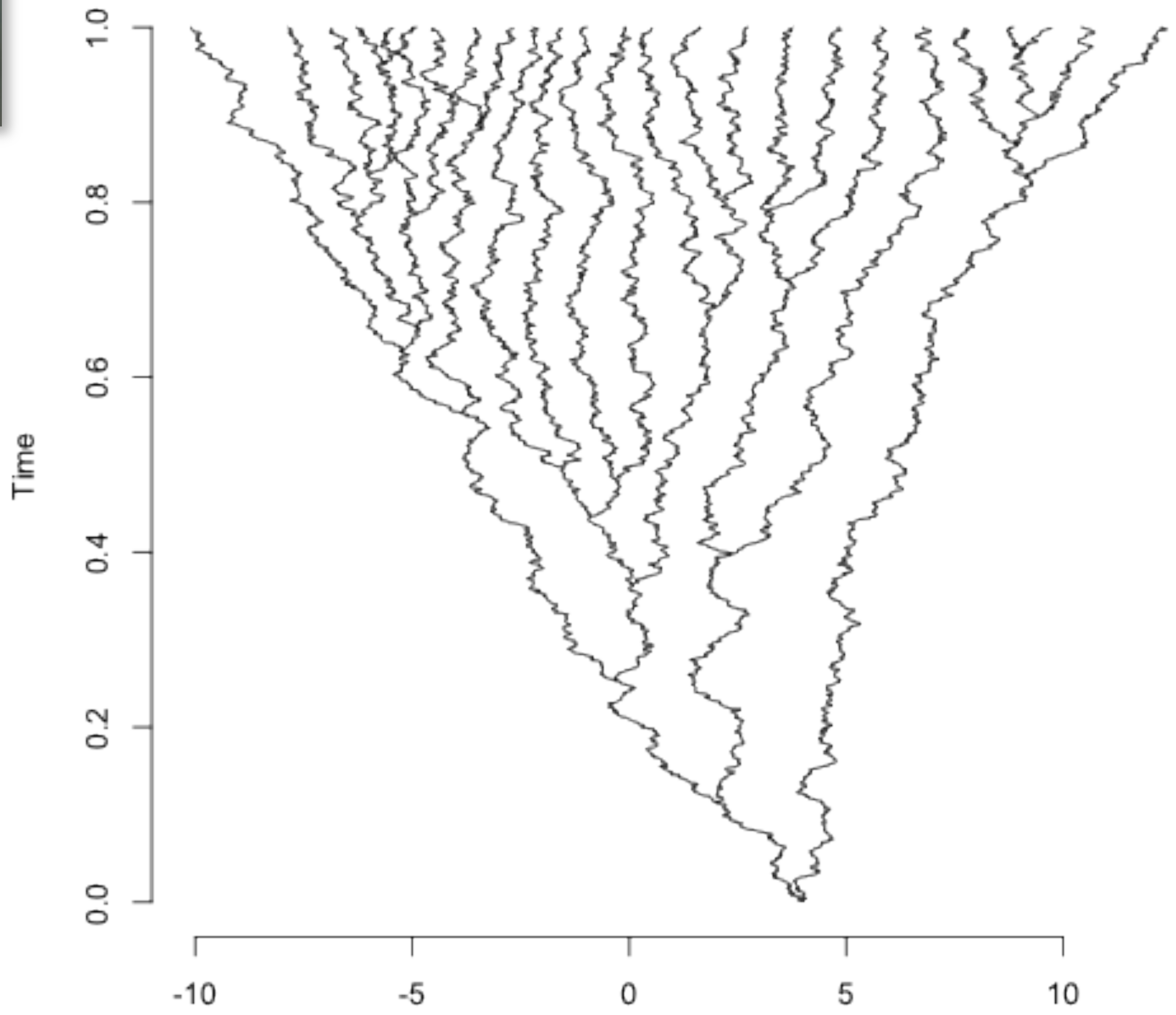
(phenotypic distance at which repulsion is half the maximum repulsion)

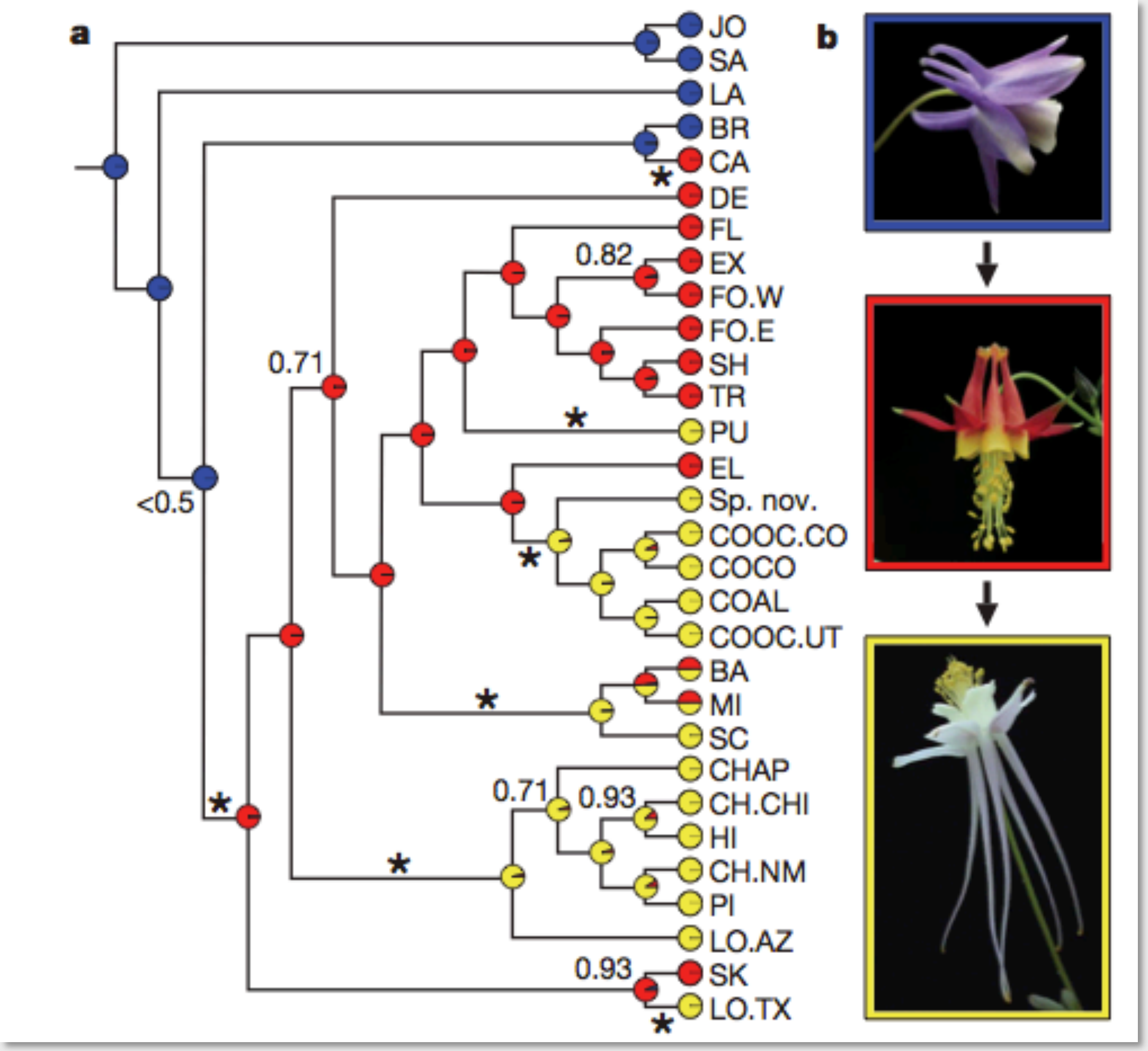


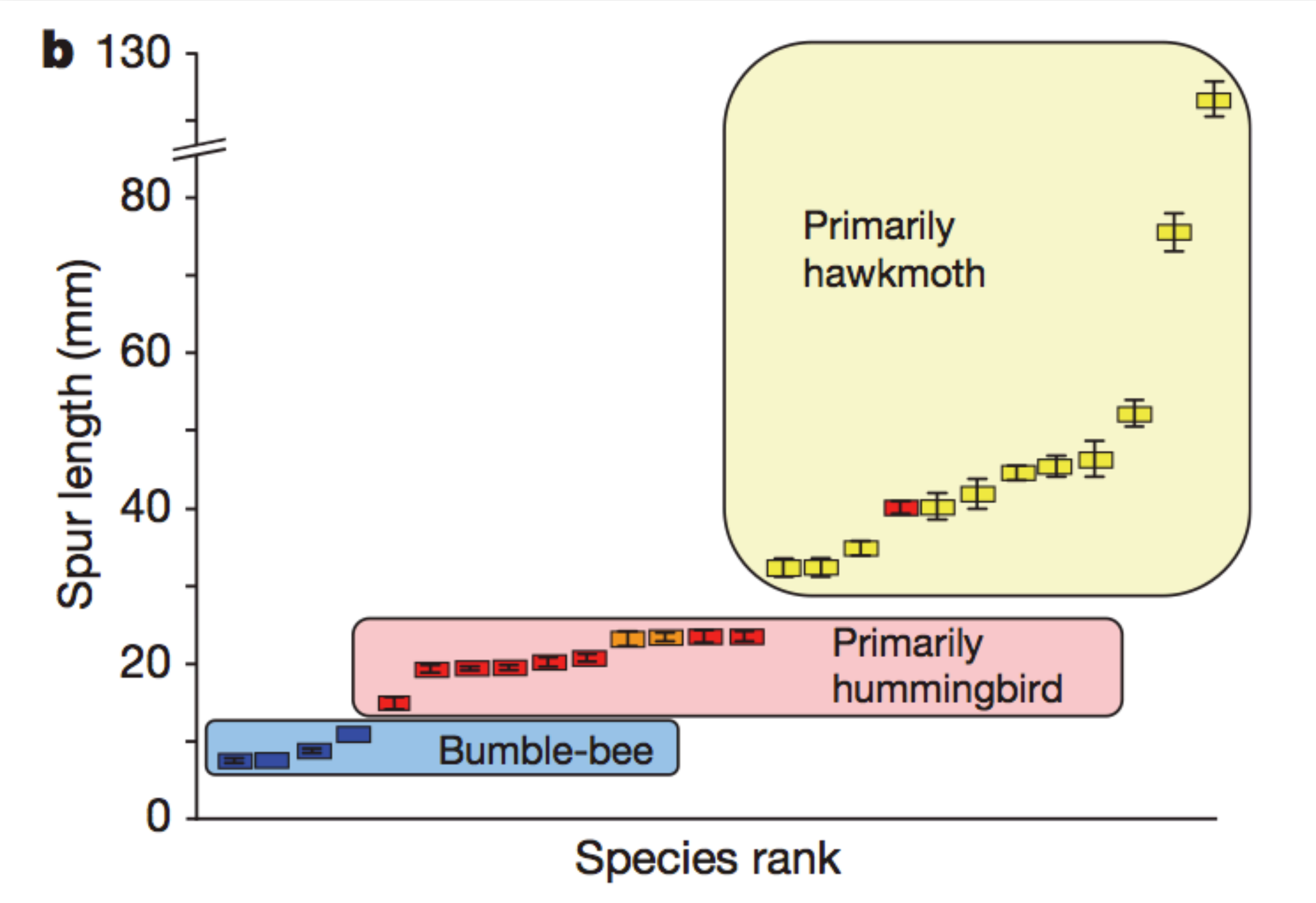
True value

Estimated value

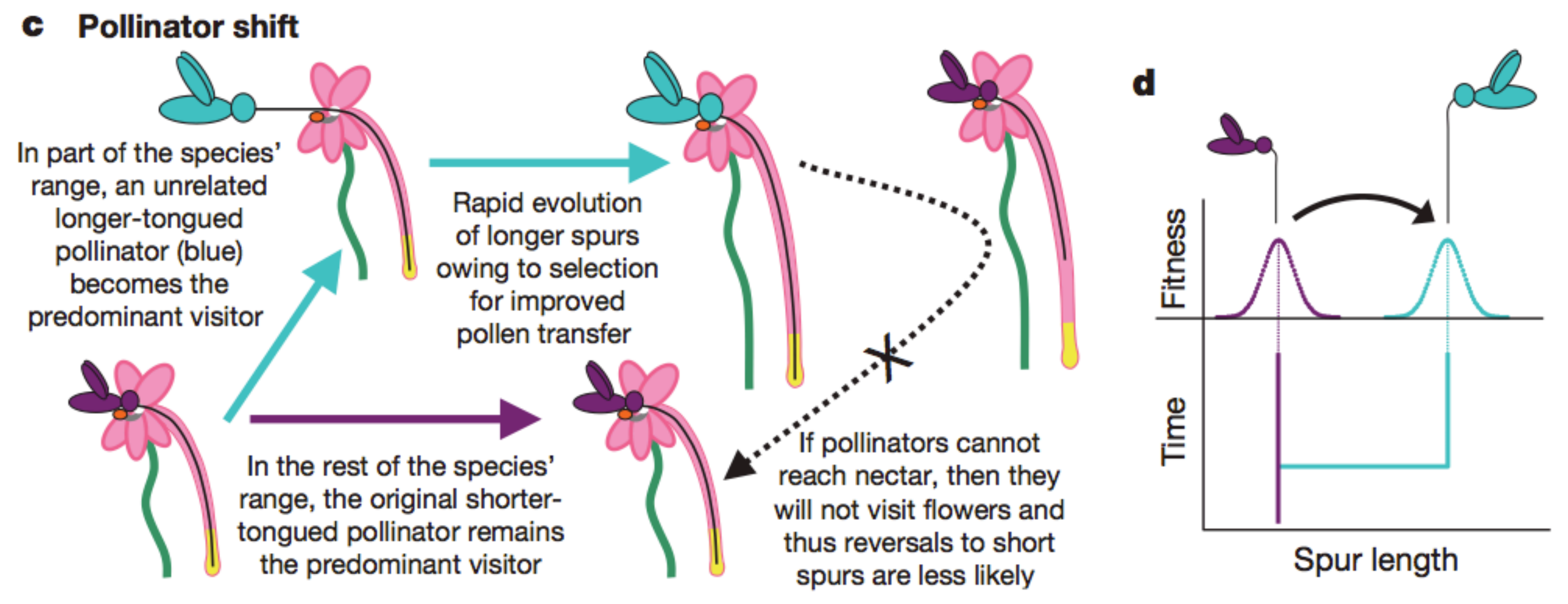
lanaré Sévi







Whittall & Hodges, 2007



Are there distinct peaks?

Yes, best-fitting model had three OU peaks.

Is evolution punctuated?

Yes, a model with change only at speciation events fits better than a gradual one.

Whittall & Hodges, 2007

```r
pollinatorShiftIntrinsic <-function(params, states, timefrompresent){
  #params[1] is sd for normal process,
  #params[2] is sd for jump size of shift,
  #params[3] is mean of shift (mean of normal process is zero),
  #params[4] is per generation probability of shift
  background.process <- TRUE
  if (runif(1, 0, 1) < params[4]) {
    background.process<-FALSE
  }
  if (background.process) {
    newdisplacement <- rnorm(n=length(states),mean=0,sd=params[1])
    return(newdisplacement)
  }
  else {
    newdisplacement <- rnorm(n=length(states), mean=params[3],
      sd=params[2])
    return(newdisplacement)
  }
}
```

```
pollinatorShiftIntrinsic <-function(params, states, timefrompresent){
 #params[1] is sd for normal process,
 #params[2] is sd for jump size of shift,
 #params[3] is mean of shift (mean of normal process is zero),
 #params[4] is per generation probability of shift
 background.process <- TRUE
 if (runif(1, 0, 1) < params[4]) {
  background.process<-FALSE
 }
 if (background.process) {
  newdisplacement <- rnorm(n=length(states),mean=0,sd=params[1])
  return(newdisplacement)
 }
 else {
  newdisplacement <- rnorm(n=length(states), mean=params[3],
   sd=params[2])
  return(newdisplacement)
 }
}
```

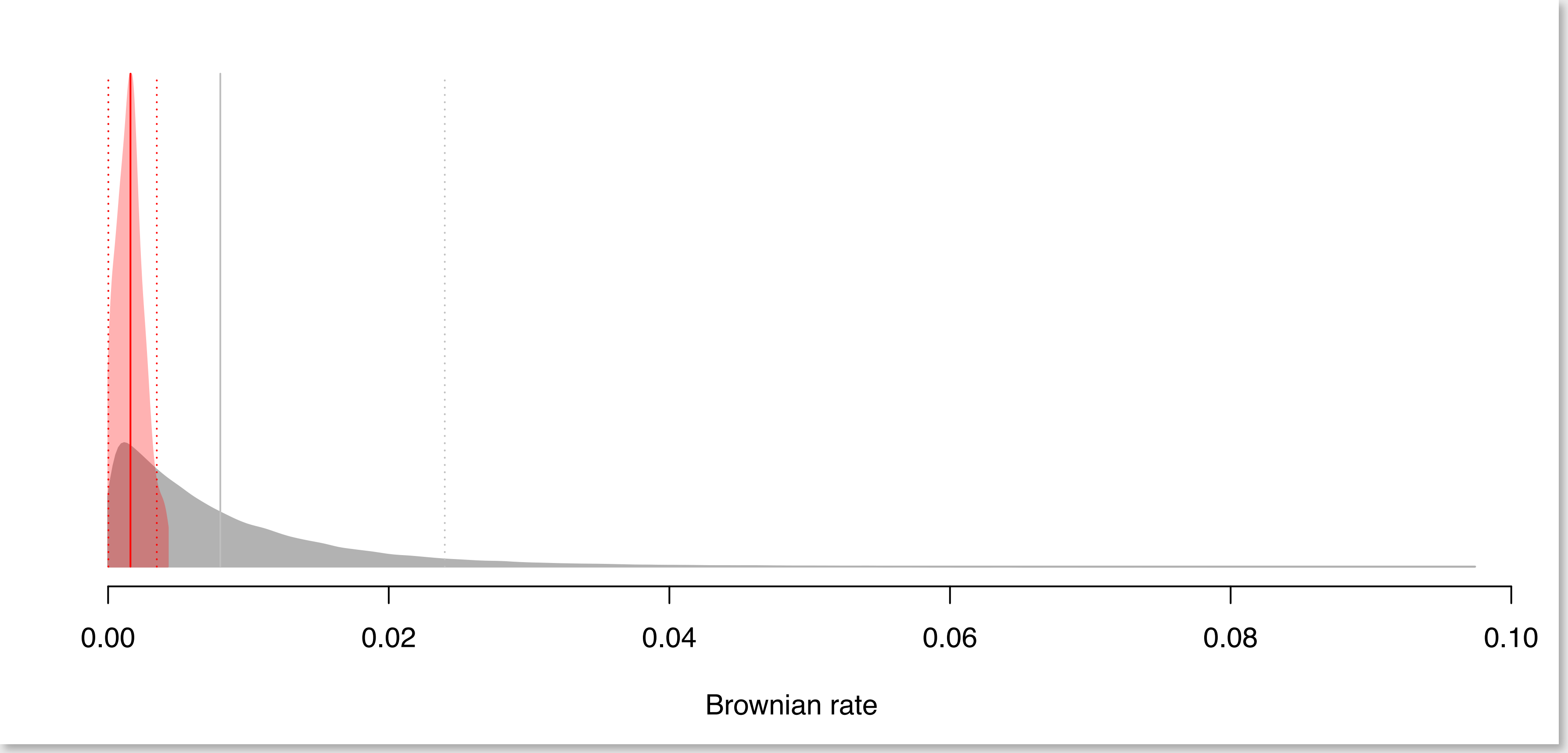
```
pollinatorShiftIntrinsic <-function(params, states, timefrompresent){
  #params[1] is sd for normal process,
  #params[2] is sd for jump size of shift,
  #params[3] is mean of shift (mean of normal process is zero),
  #params[4] is per generation probability of shift
  background.process <- TRUE
  if (runif(1, 0, 1) < params[4]) {
    background.process<-FALSE
  }
  if (background.process) {
    newdisplacement <- rnorm(n=length(states),mean=0,sd=params[1])
    return(newdisplacement)
  }
  else {
    newdisplacement <- rnorm(n=length(states), mean=params[3],
      sd=params[2])
    return(newdisplacement)
  }
}
```

```
pollinatorShiftIntrinsic <-function(params, states, timefrompresent){
  #params[1] is sd for normal process,
  #params[2] is sd for jump size of shift,
  #params[3] is mean of shift (mean of normal process is zero),
  #params[4] is per generation probability of shift
  background.process <- TRUE
  if (runif(1, 0, 1) < params[4]) {
    background.process<-FALSE
  }
  if (background.process) {
    newdisplacement <- rnorm(n=length(states),mean=0,sd=params[1])
    return(newdisplacement)
  }
  else {
    newdisplacement <- rnorm(n=length(states), mean=params[3],
      sd=params[2])
    return(newdisplacement)
  }
}
```

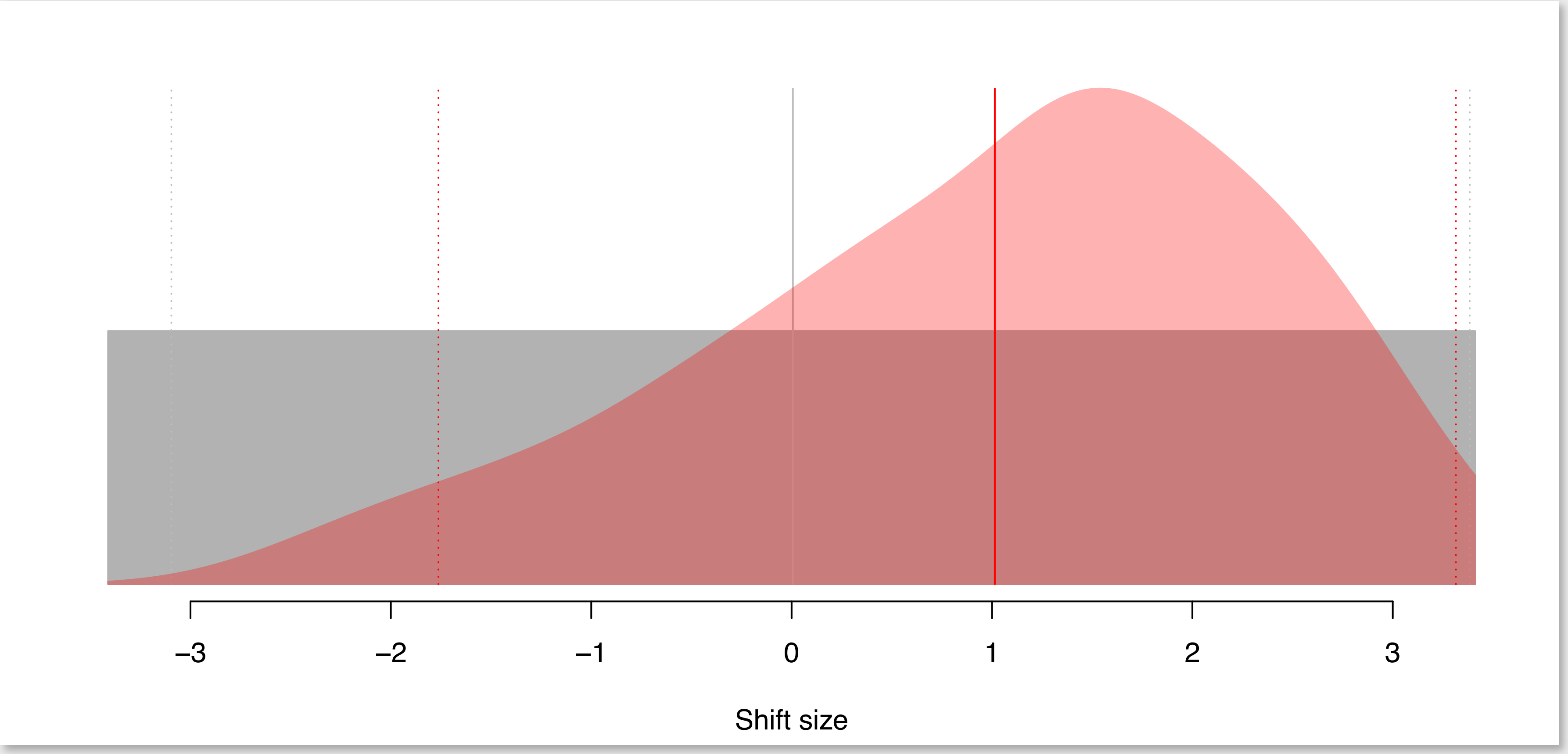
```
pollinatorShiftIntrinsic <-function(params, states, timefrompresent){
  #params[1] is sd for normal process,
  #params[2] is sd for jump size of shift,
  #params[3] is mean of shift (mean of normal process is zero),
  #params[4] is per generation probability of shift
  background.process <- TRUE
  if (runif(1, 0, 1) < params[4]) {
    background.process<-FALSE
  }
  if (background.process) {
    newdisplacement <- rnorm(n=length(states),mean=0,sd=params[1])
    return(newdisplacement)
  }
  else {
    newdisplacement <- rnorm(n=length(states), mean=params[3],
      sd=params[2])
    return(newdisplacement)
  }
}
```

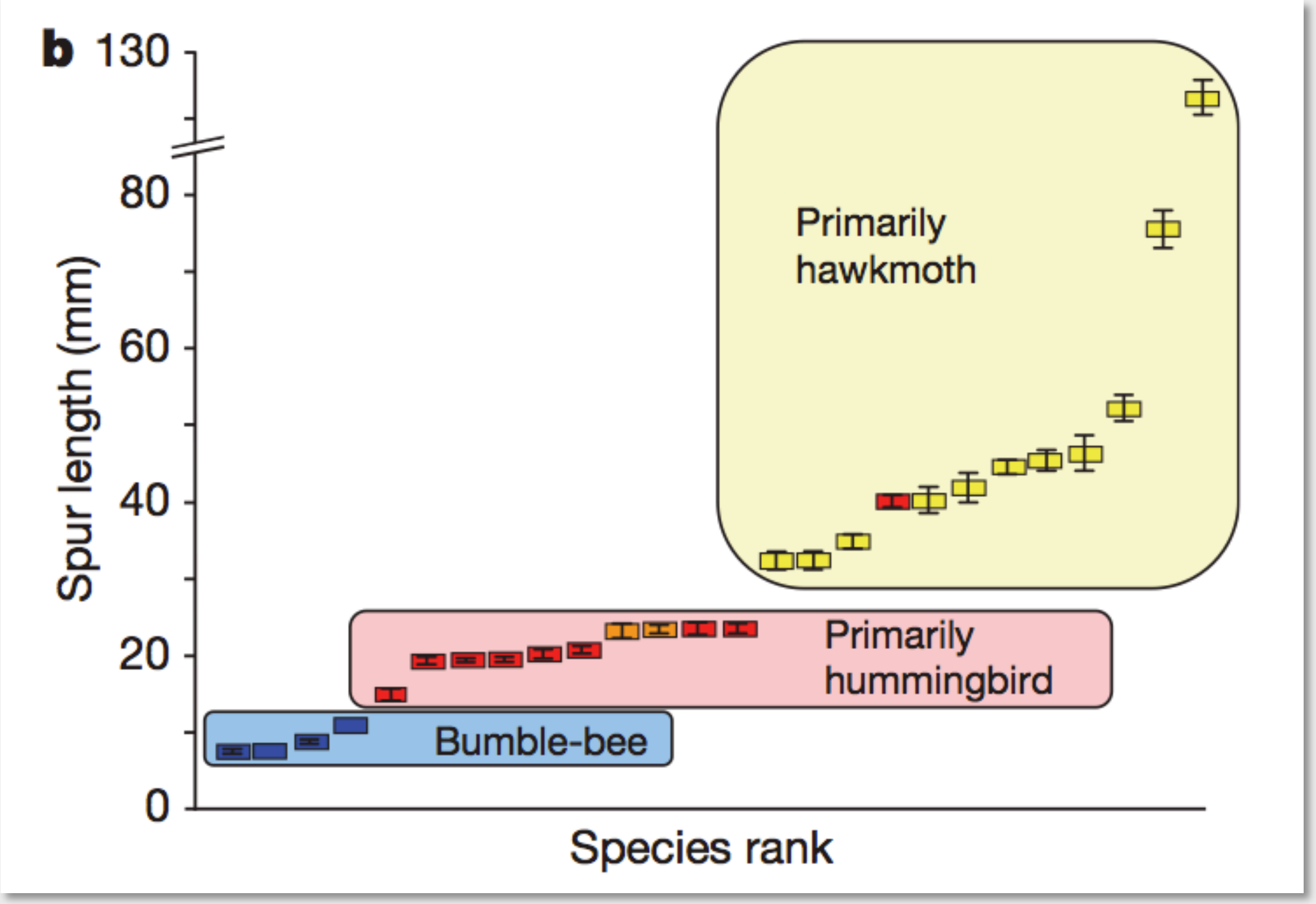
Parameter	**Prior**
Tree height	**Fixed** at 300,000 generations (~3MY for radiation, ~10 years/generation (Cooper et al. 2010))
Root state	**Fixed** at minimum spur length (proxy for using outgroup info)
Background rate for length	**Exponential**, mean set to rough guess based on max difference between taxa
Variation in displacement with pollinator shift	**Fixed** at zero
Mean displacement with pollinator shift	**Uniform**, bounds are +/- the biggest difference in trait values
Frequency of pollinator shift	**Exponential**, mean set to rough guess based on observed distribution (7 shifts over entire tree)

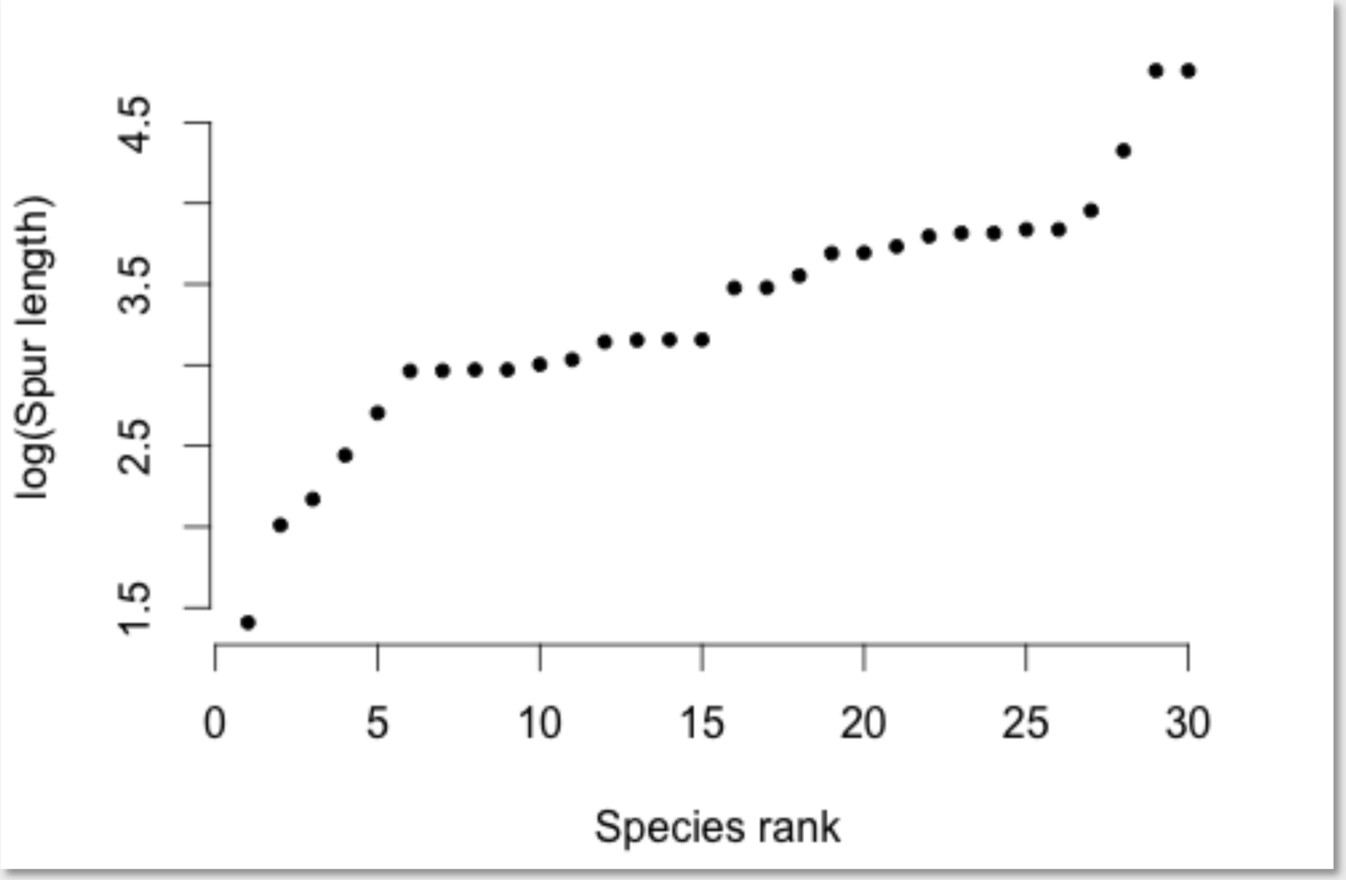
Brownian rate for background



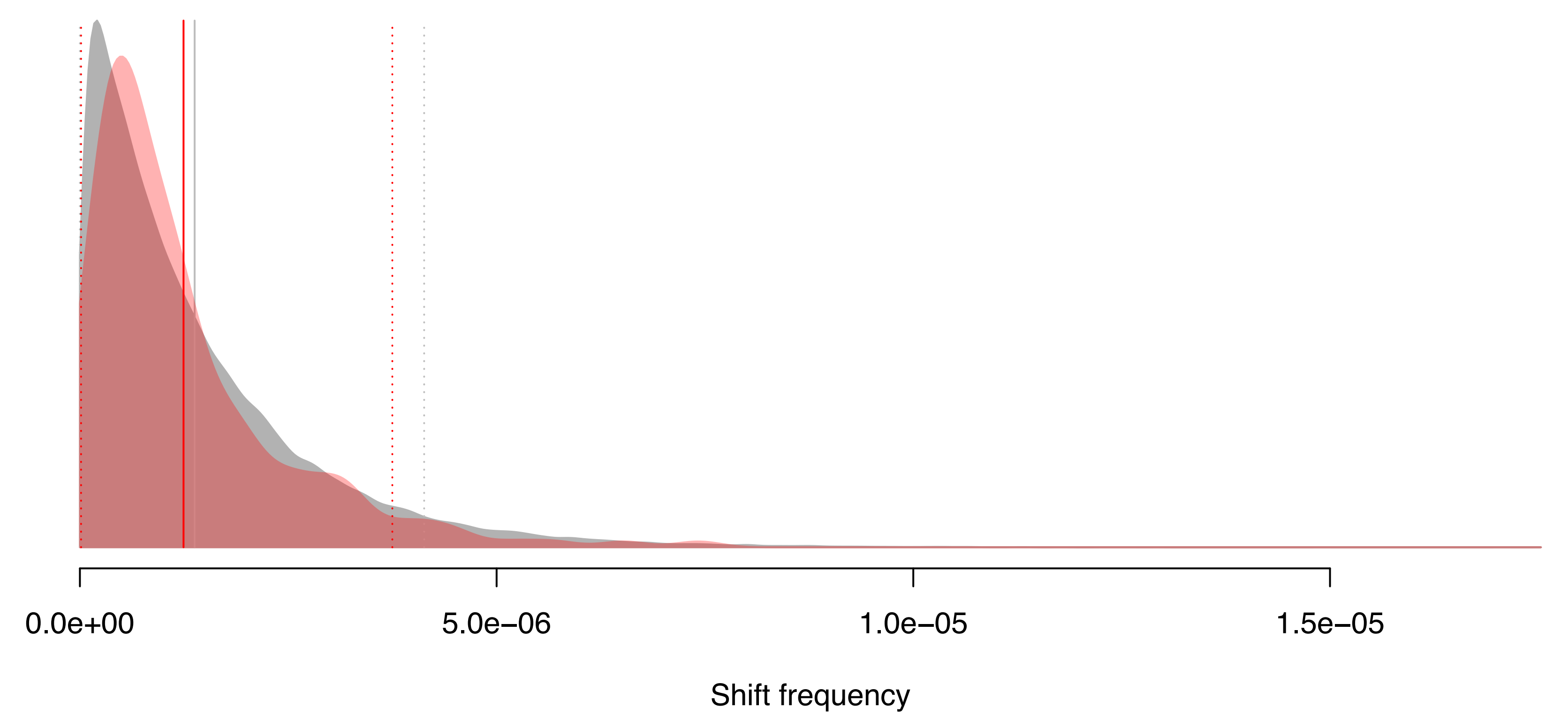
Nectar spur change at pollinator shift



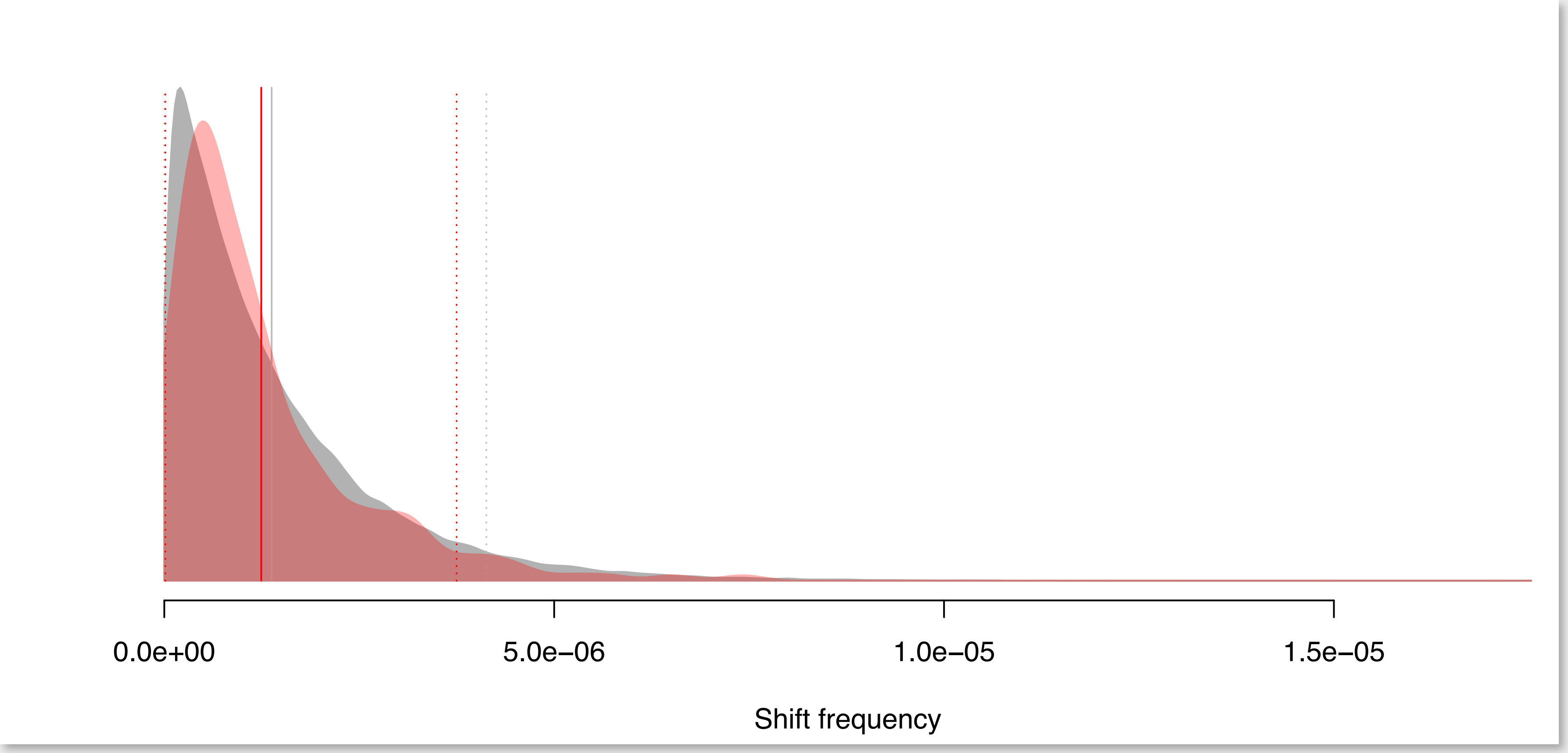




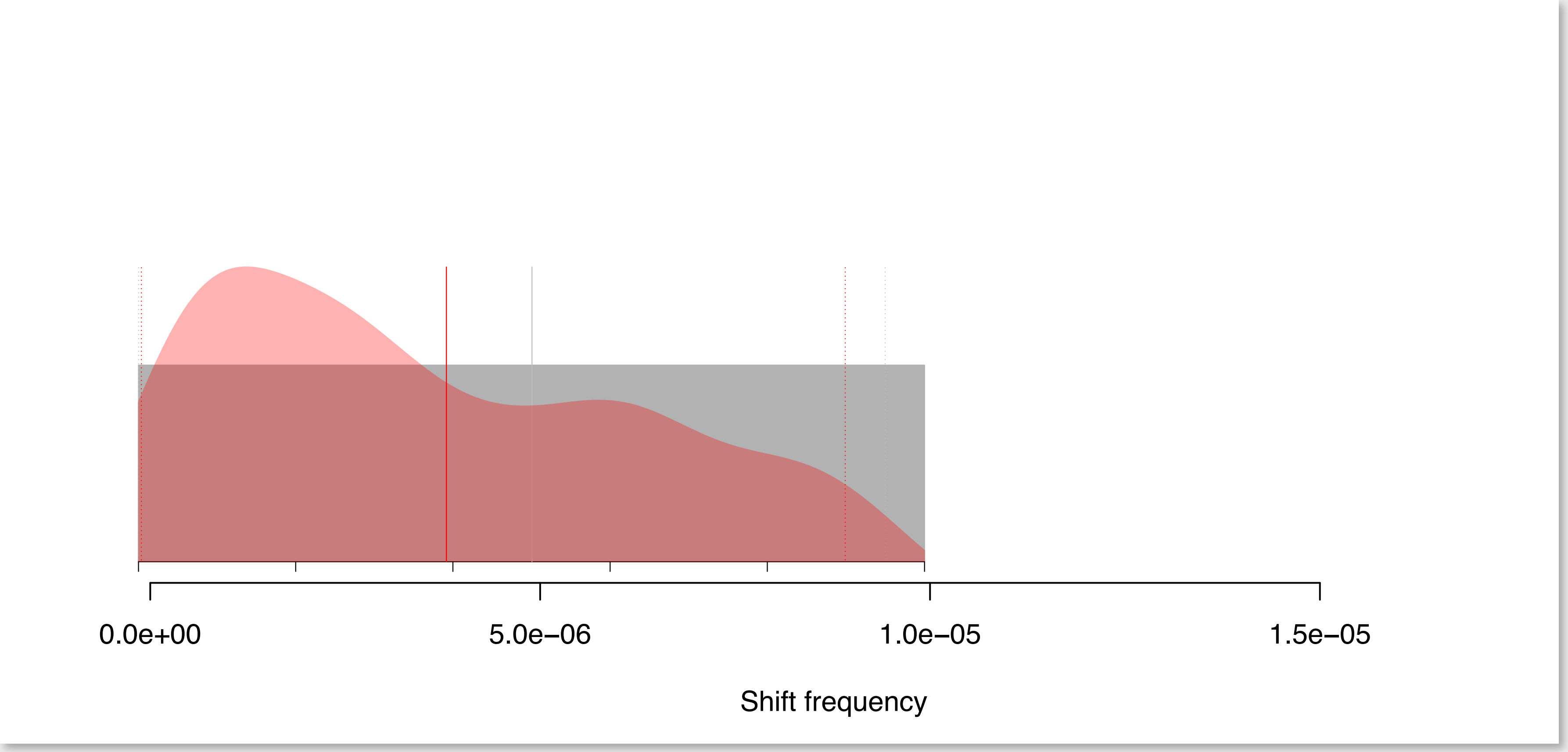
Frequency of pollinator shift (per generation)



Frequency of pollinator shift (exponential prior)



Frequency of pollinator shift (uniform prior)



Advantages

- Bayesian
- Flexible: make your own model
- Somewhat robust to user ~~laziness~~ efficient behavior
- Gets faster as computers get faster

Disadvantages

- Bayesian
- Far slower than closed form solutions where they are available
- No checking for model feasibility (i.e., inferring a trend on an ultrametric tree)
- More still to discover

A selection of ongoing work

Floral evolution

O'Meara*, Stacey Smith*, Armbruster, Harder, Hardy, Hileman, Hufford, Litt, Magallon, Stephen Smith, Stevens, Fenster, Diggle

Flexible trait evolution

O'Meara and Banbury[P]

Phylogeographic models

O'Meara, Jackson[P], Morales-Garcia, Carstens

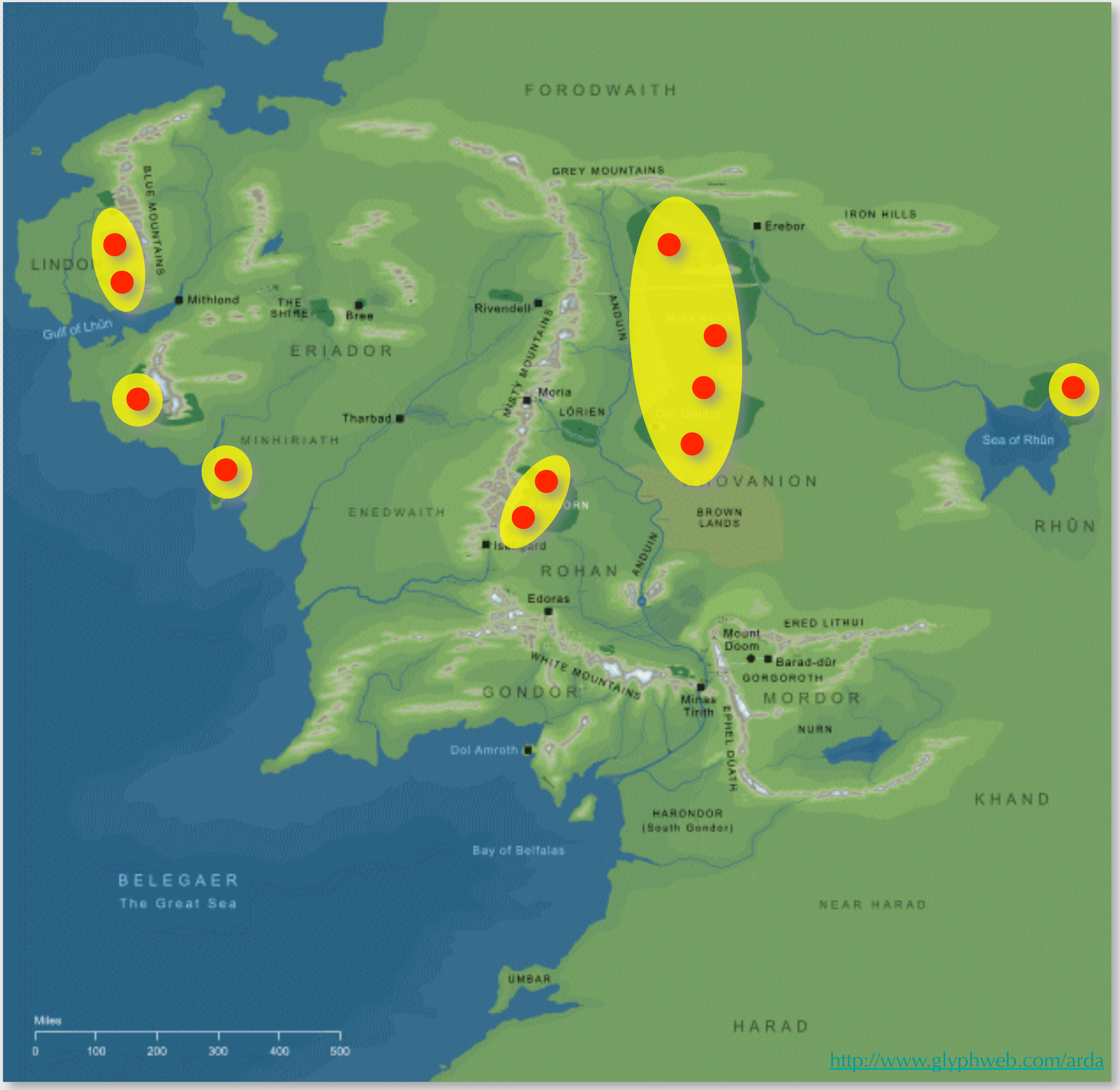
* = equal lead authors
[P] = postdoc mentee

http://www.glyphweb.com/arda

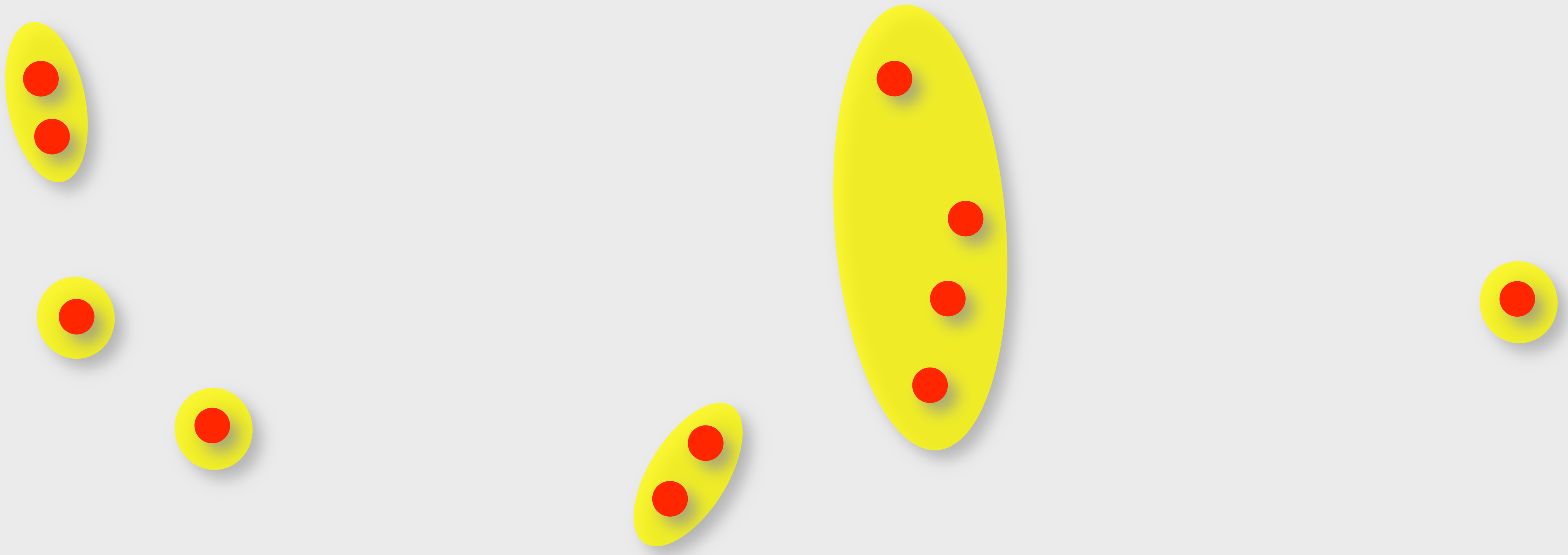
http://www.glyphweb.com/arda

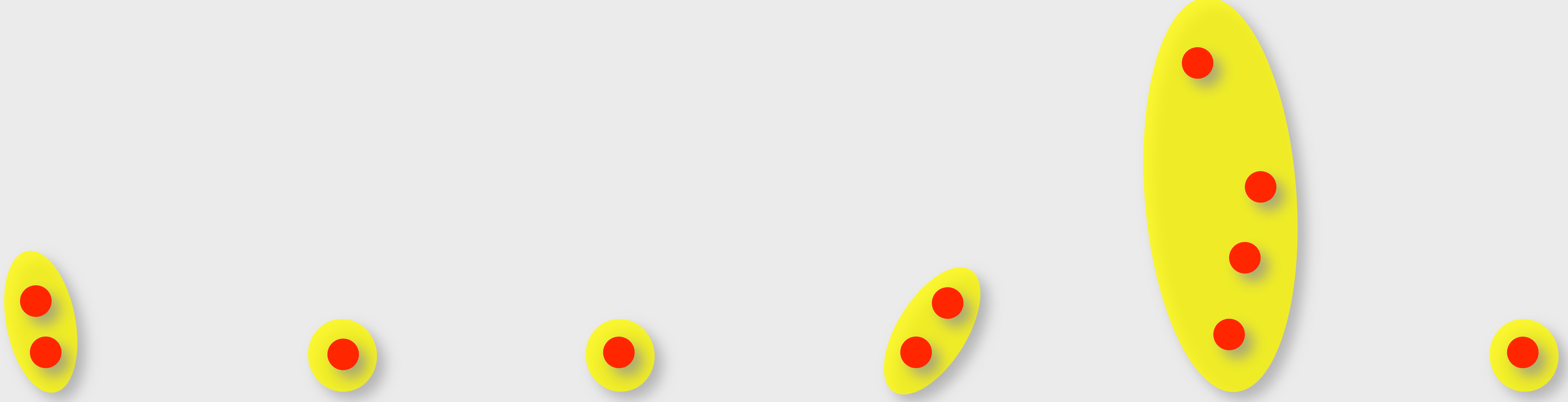
http://www.glyphweb.com/arda

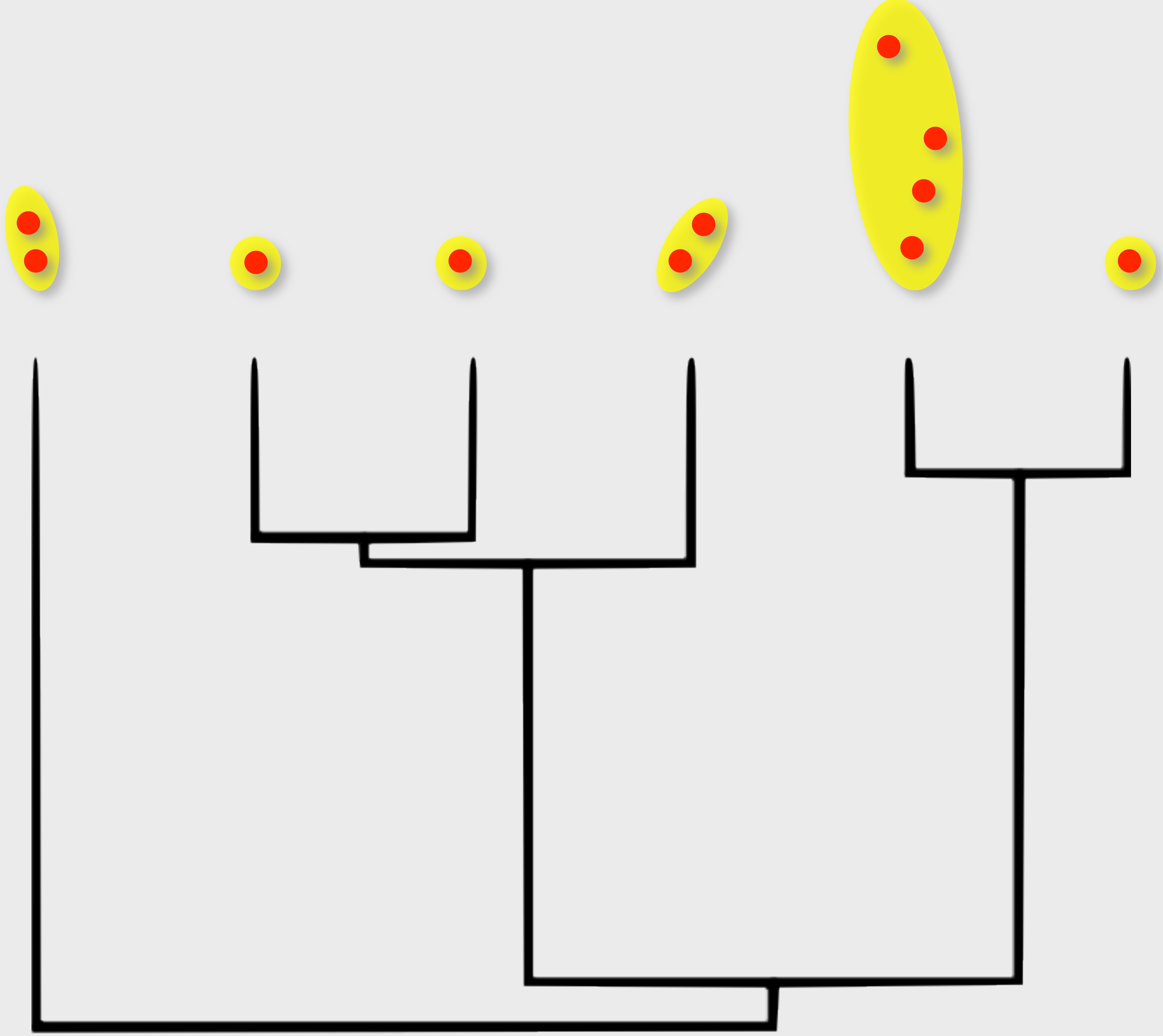
http://www.glyphweb.com/arda

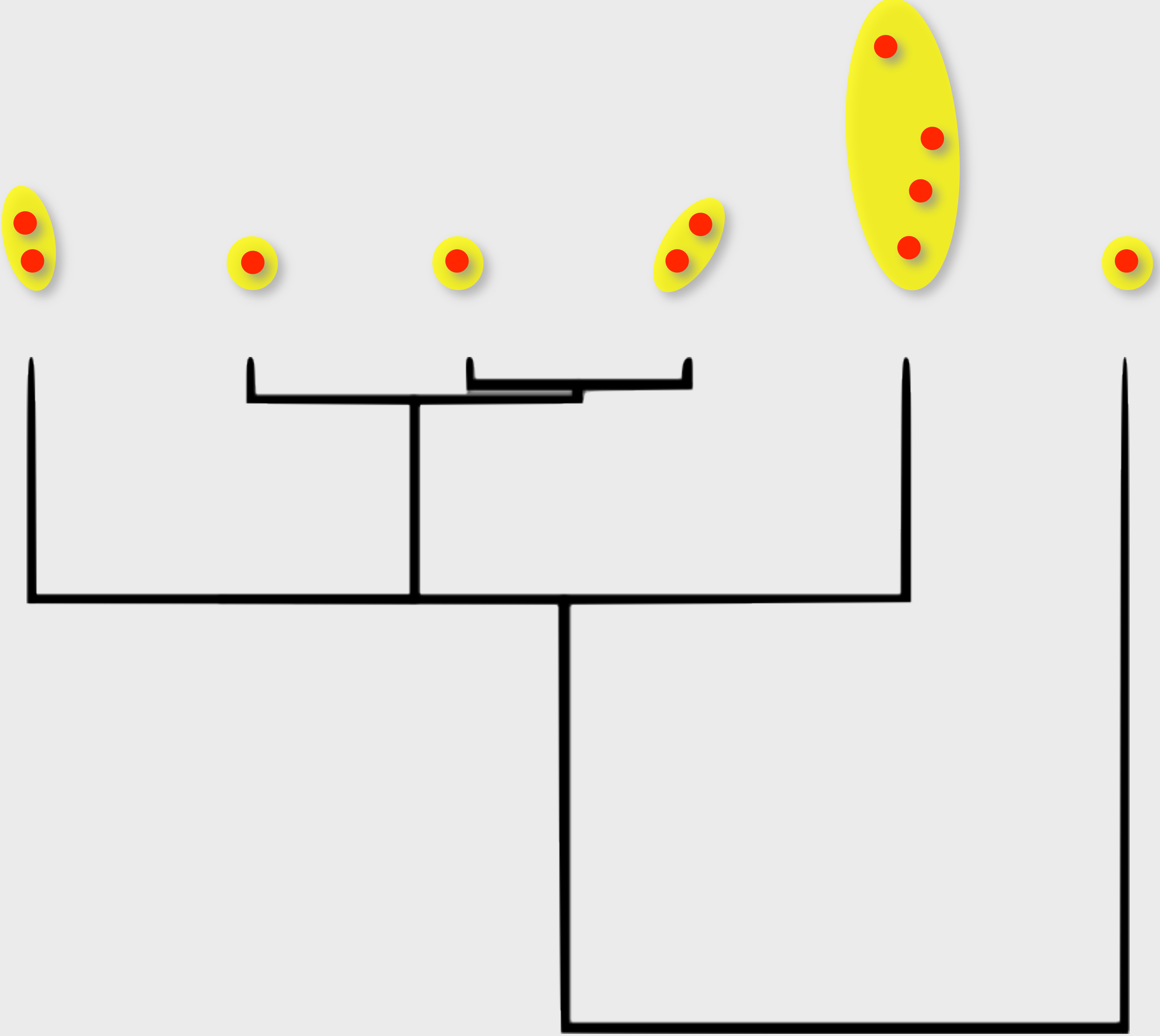


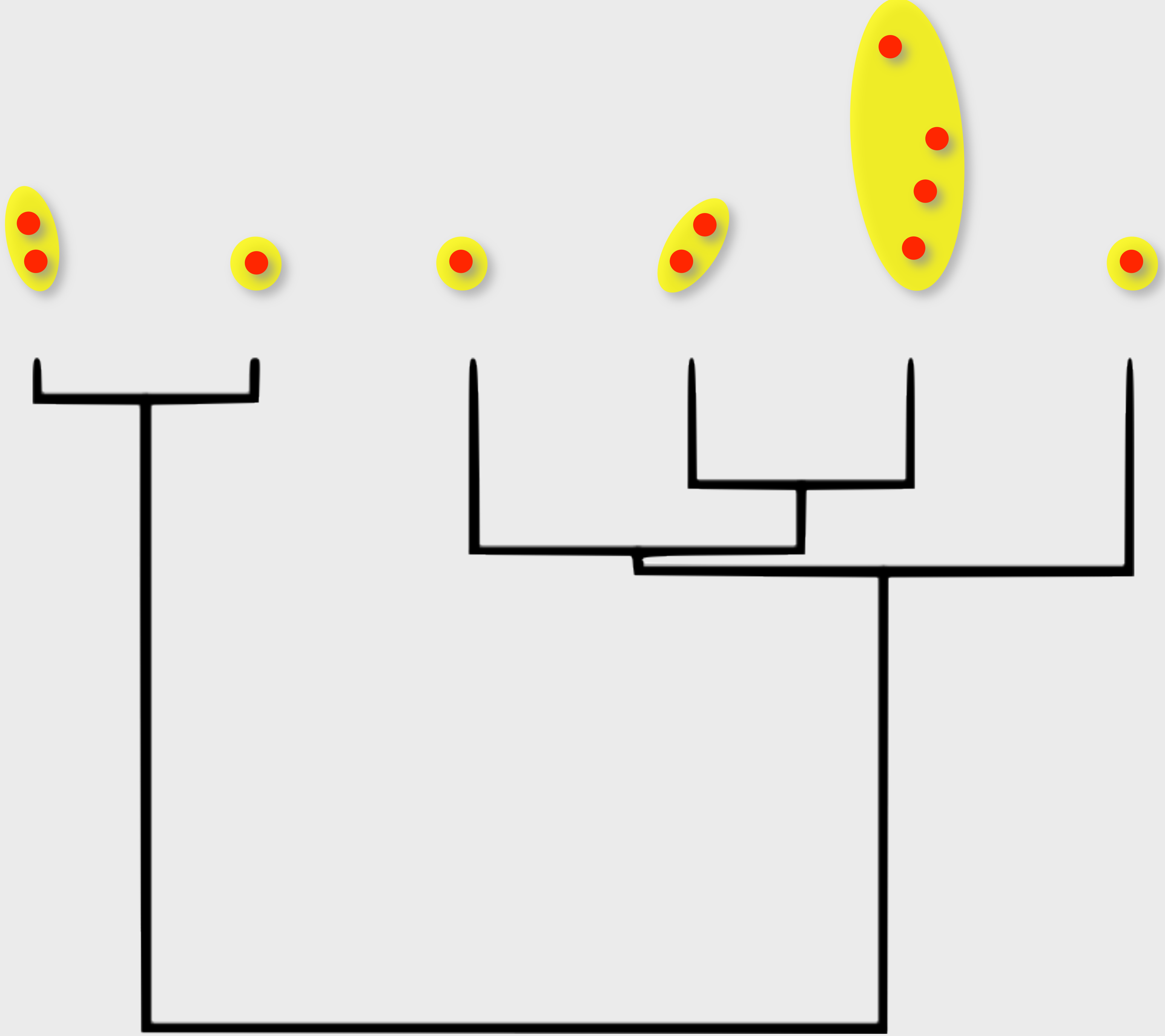
http://www.glyphweb.com/arda

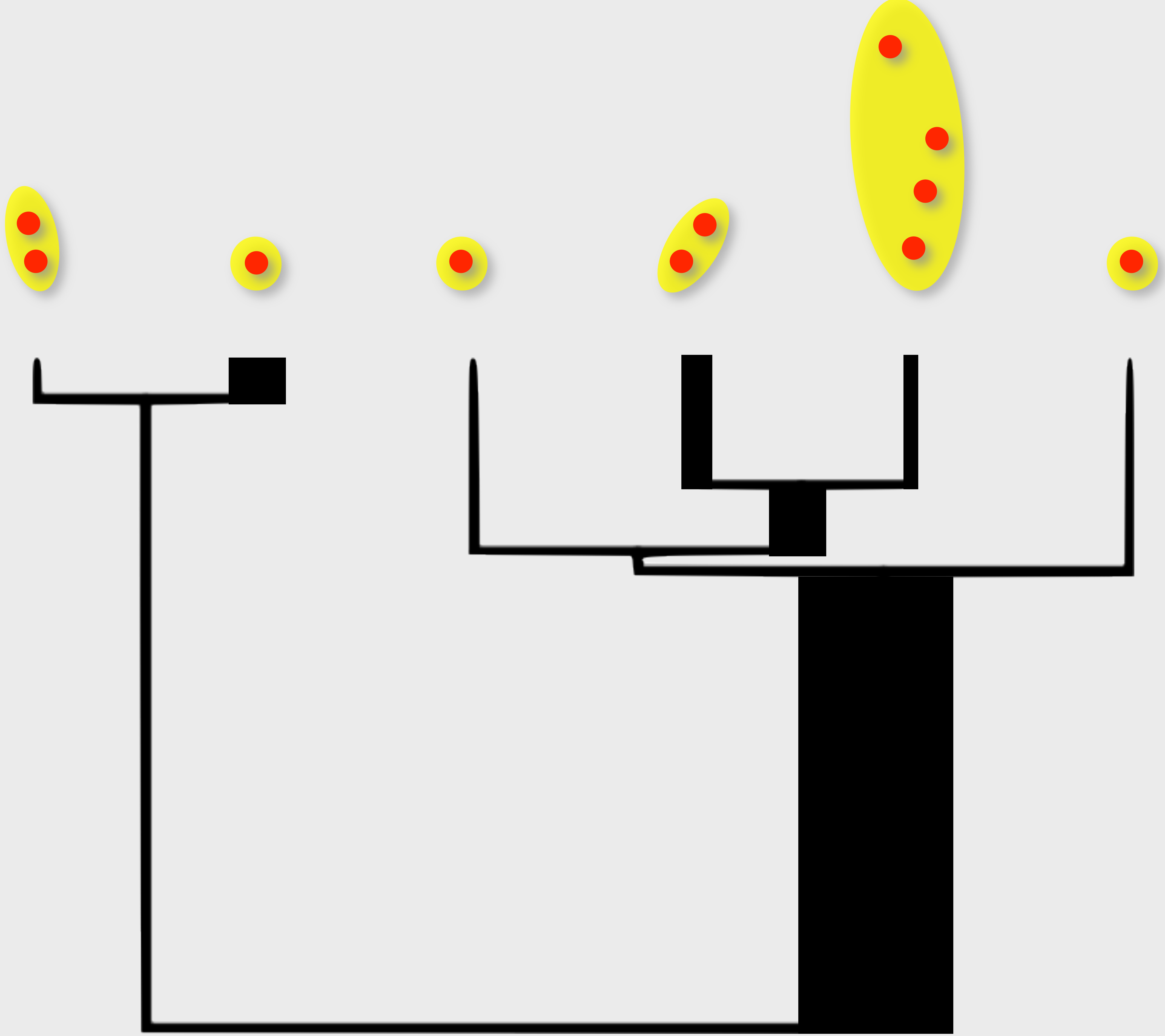


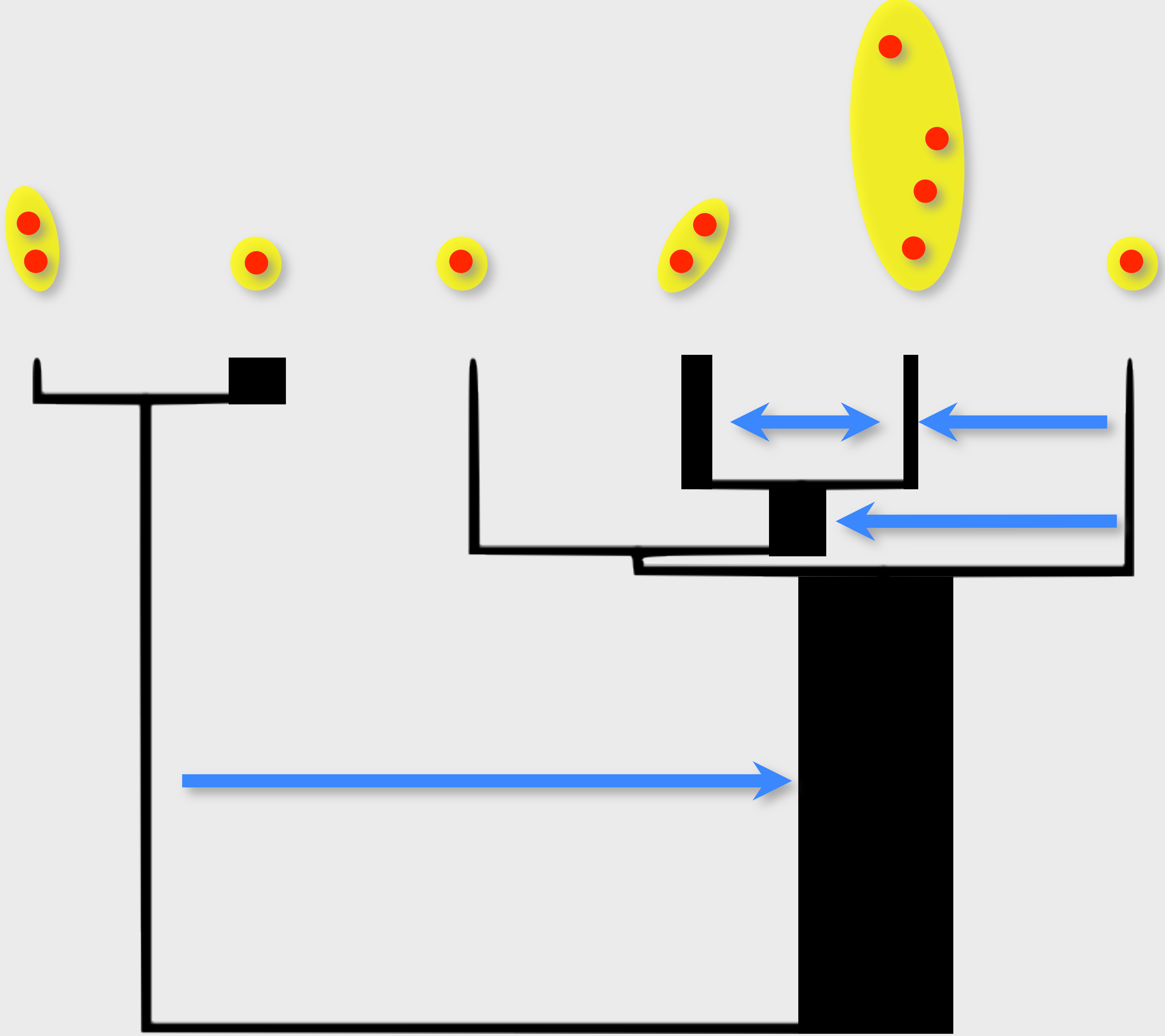


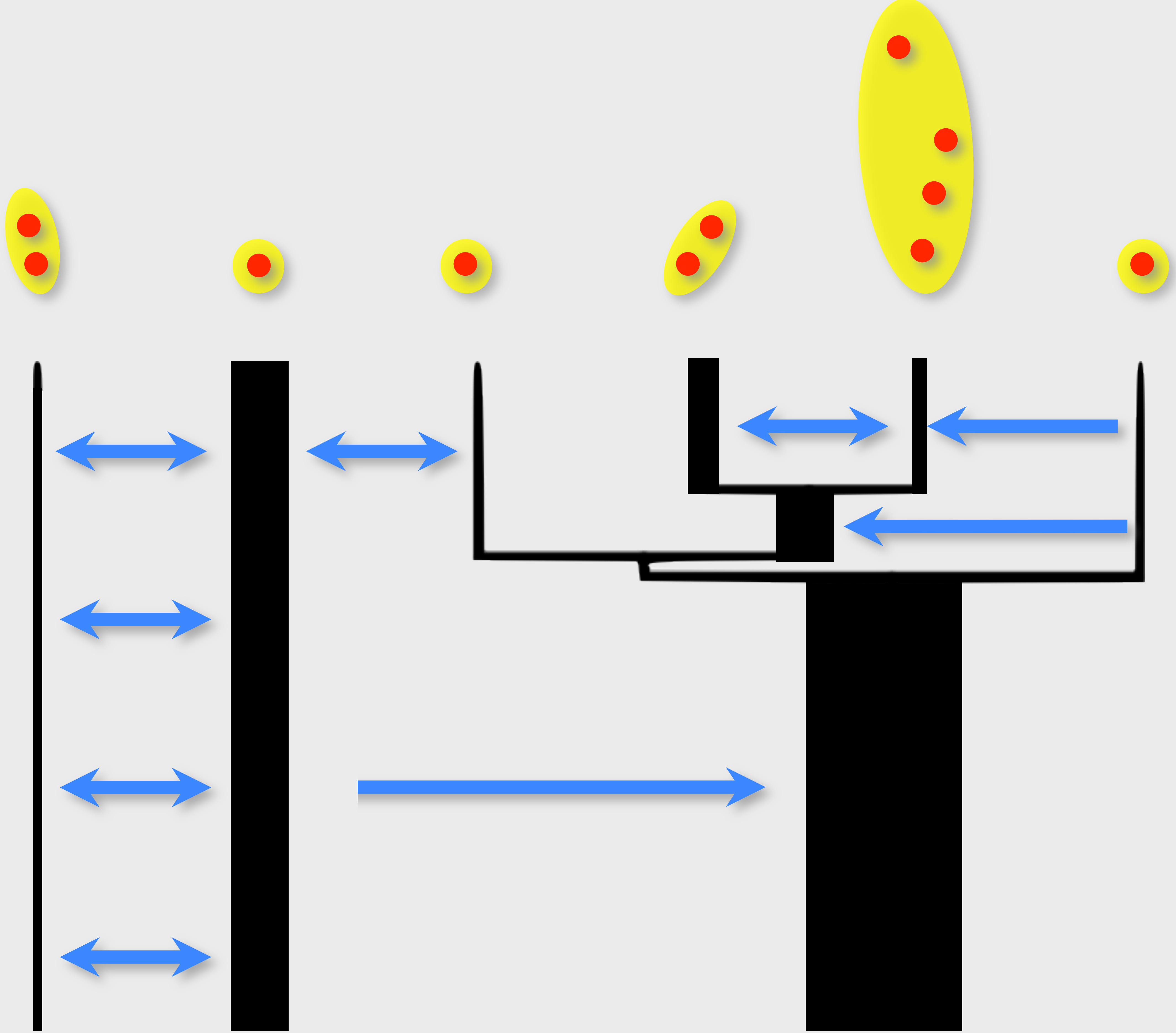


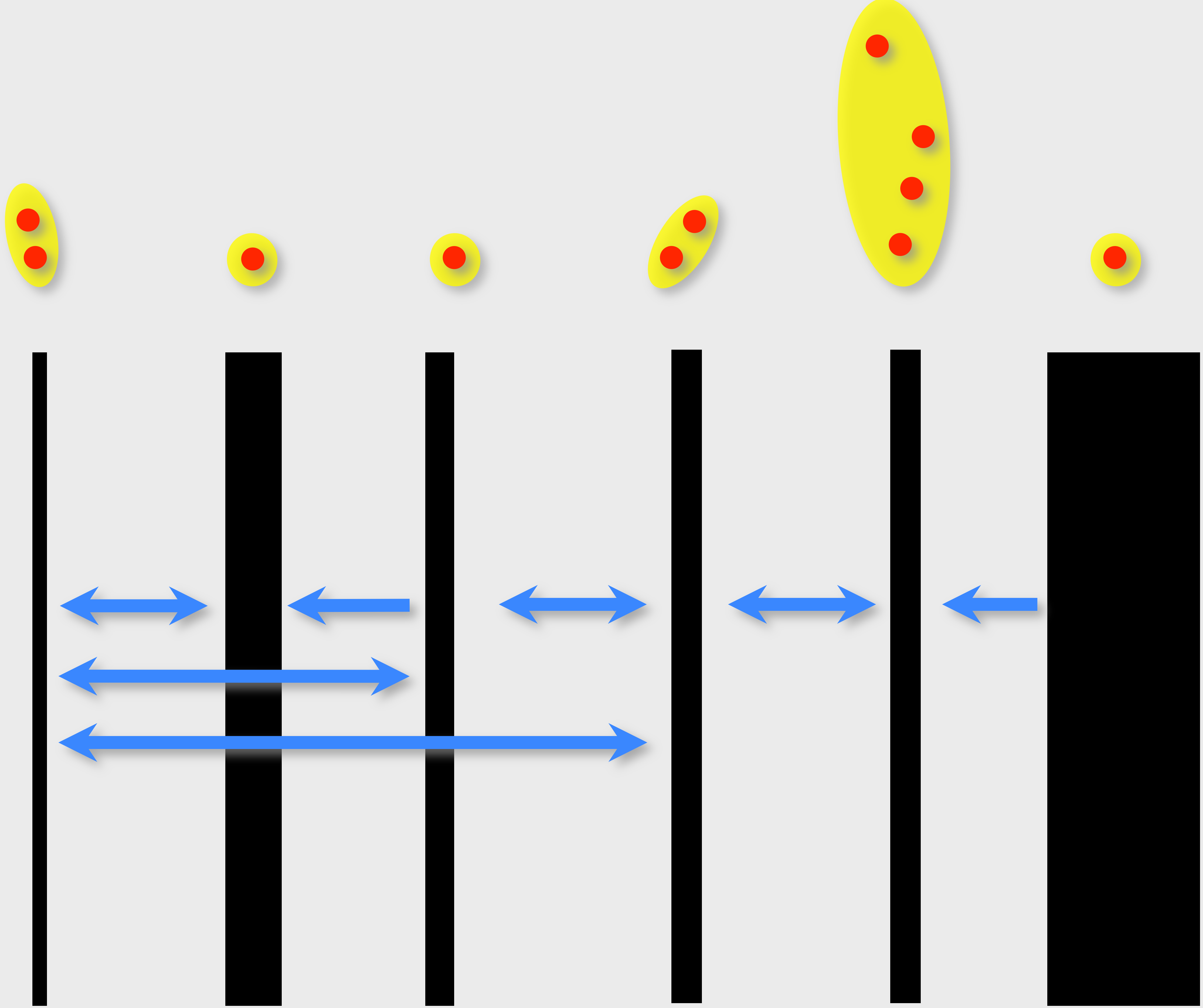




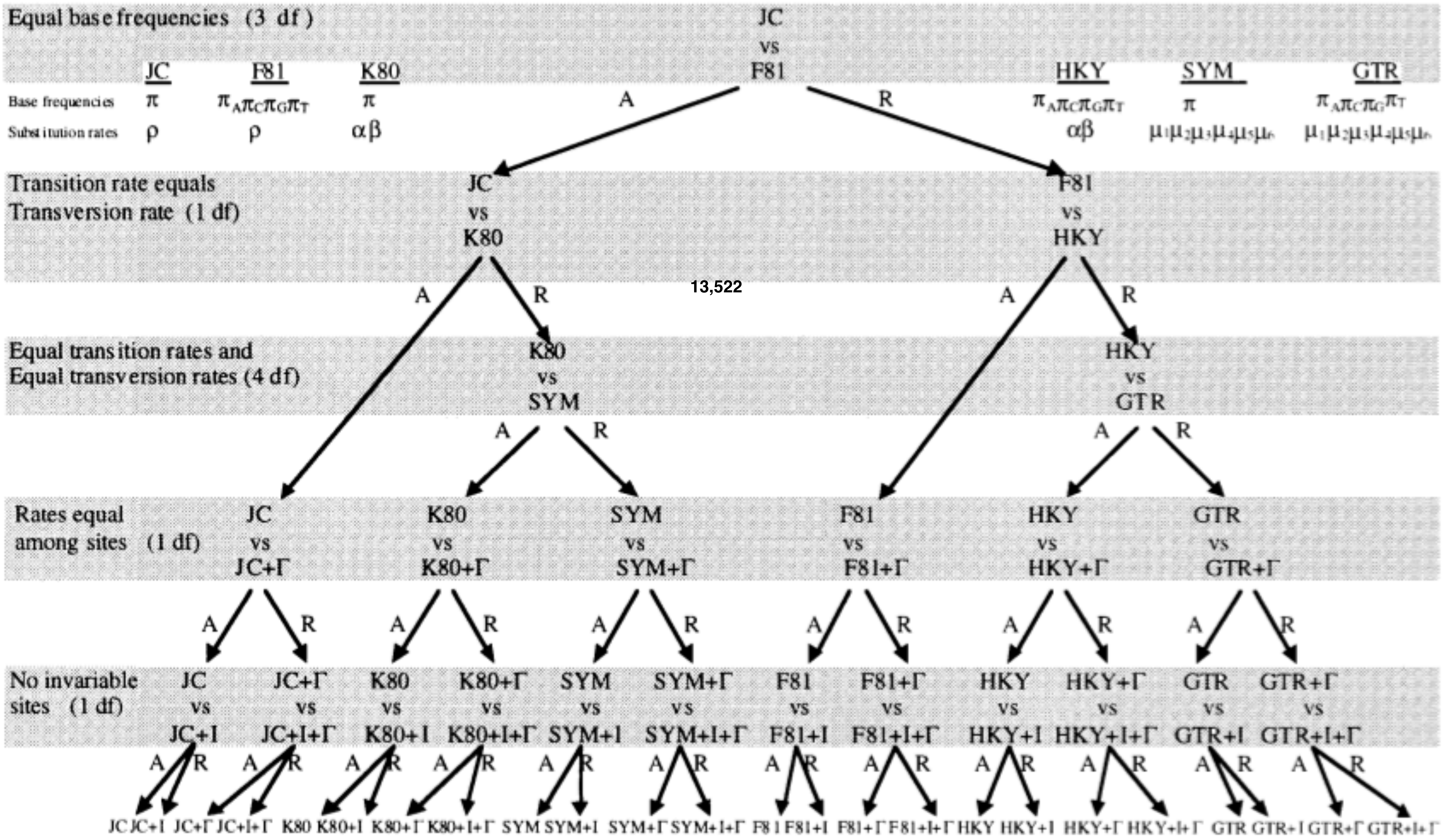








13,522 citations of first ModelTest paper (Posada and Crandall 1998) alone



Posada and Crandall 1998

Question	**Specified hypothesis method**	**Try all method**
DNA model	PAML	ModelTest
AA model	PAML	ProtTest
Continuous trait model	OUCH, Brownie (traits), OUWie	SURFACE, auteur
Diversification model	laser	Medusa
Phylogeographic	various ABC approaches	**phrapl**

phrapl

phylogeographic infe**r**ence using **ap**proximated **l**ikelihoods

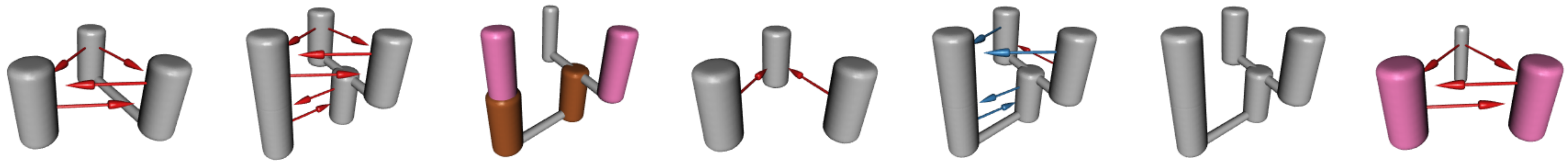
Input:
gene topologies
assignments of samples to populations

Jargon
N = number of populations
K = number of free parameters (as in AIC)

1

Generate all possible models

Given *N* populations, ≤*K* free parameters

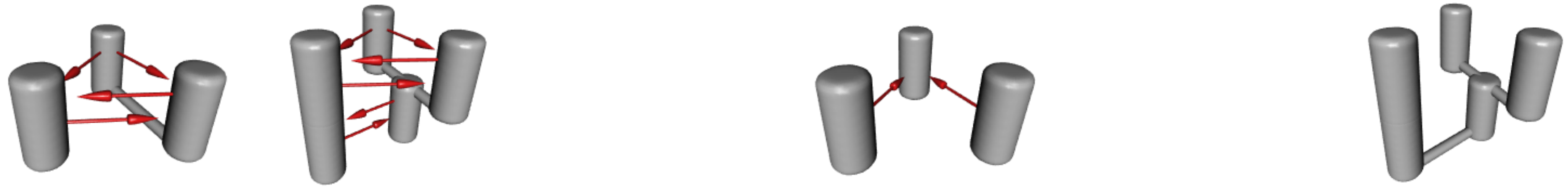


↓

2

Filter

(only tree models, no more than two migration rates, etc.)

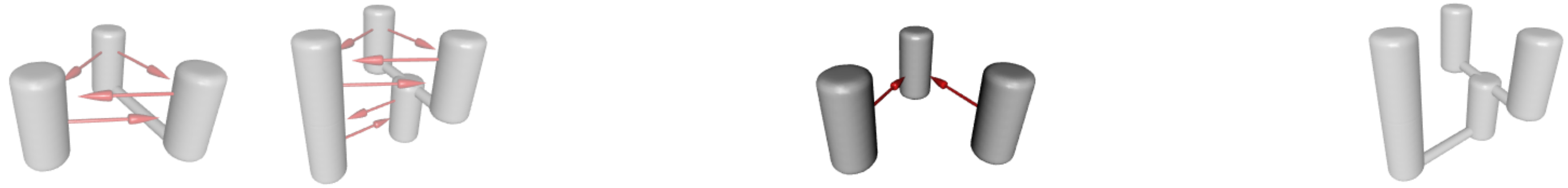


↓

3

Analyze

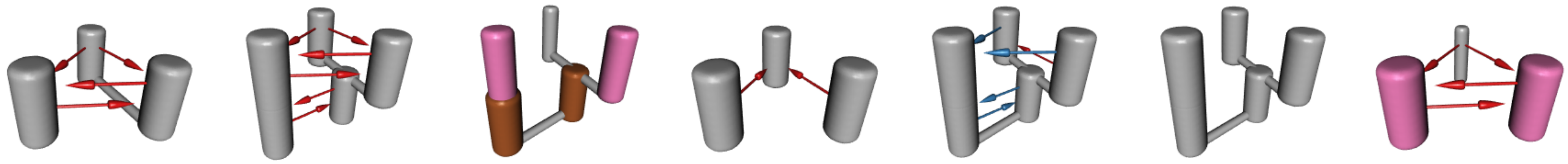
(find best, find AIC for all



1

Generate all possible models

Given *N* populations, ≤*K* free parameters



2

Filter

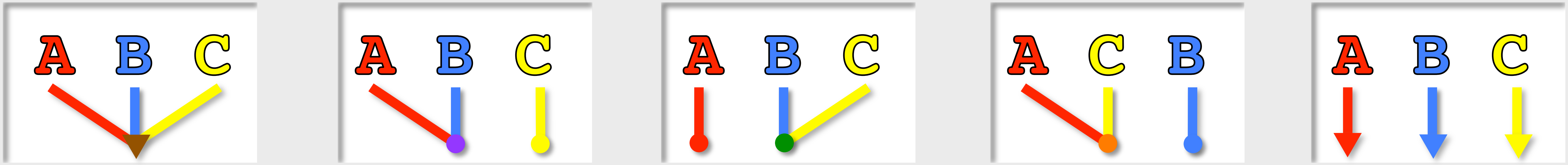
(only tree models, no more than two migration rates, etc.)

3

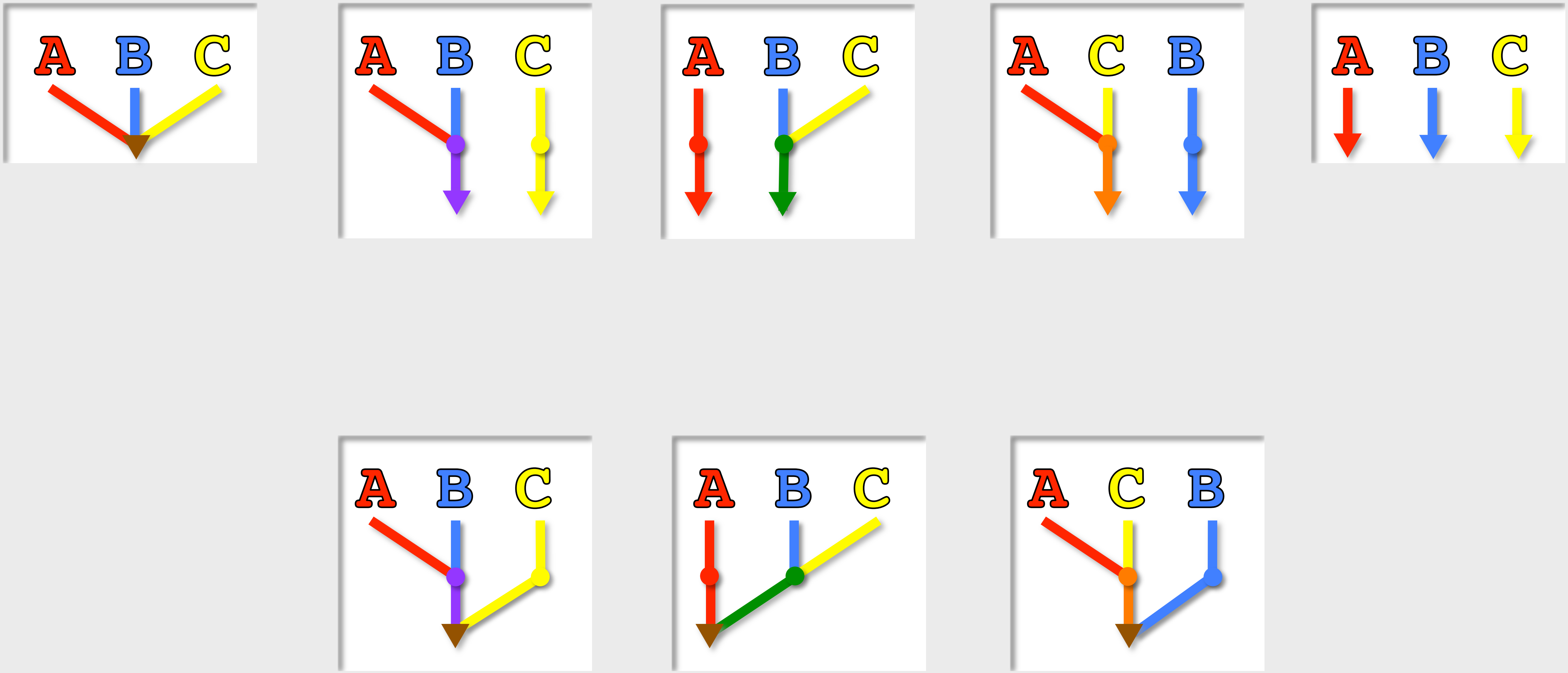
Analyze

(find best, find AIC for all

Coalescence of populations

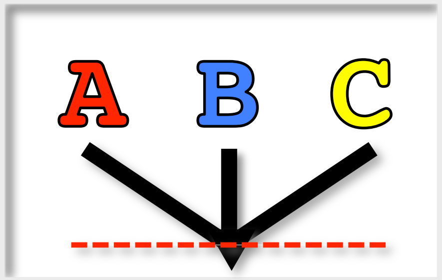


Coalescence of populations

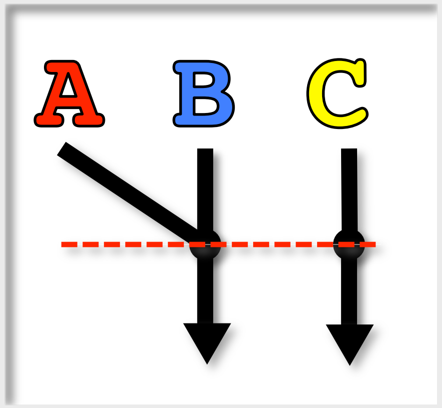


Coalescence of populations

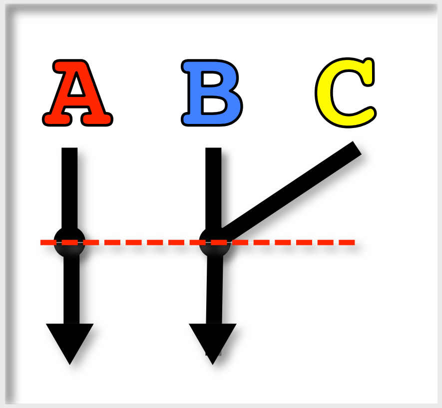
K=1



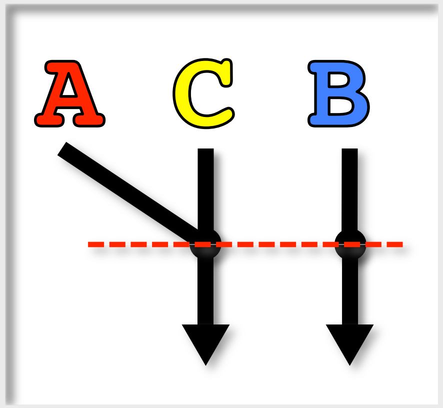
K=1



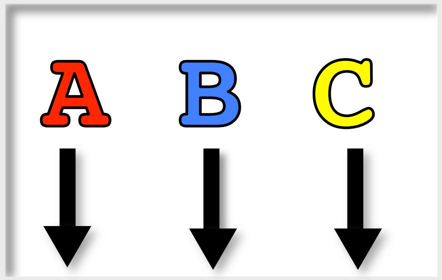
K=1



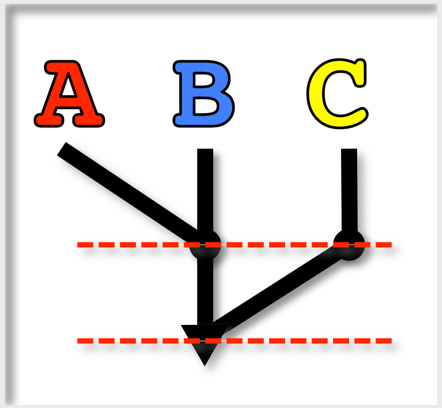
K=1



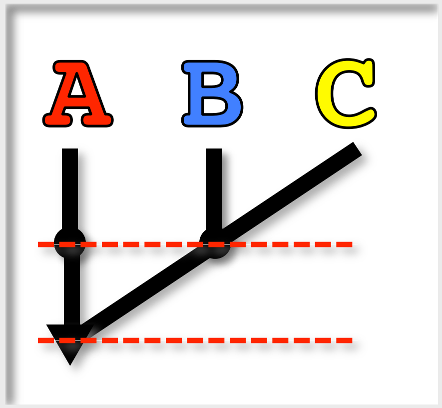
K=0



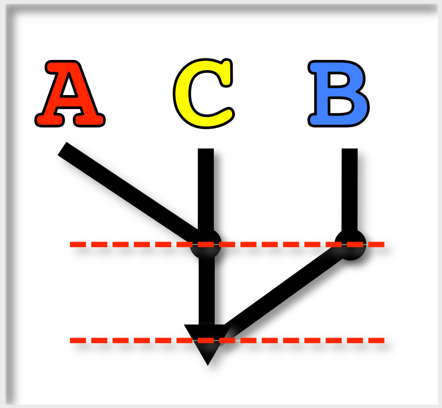
K=2

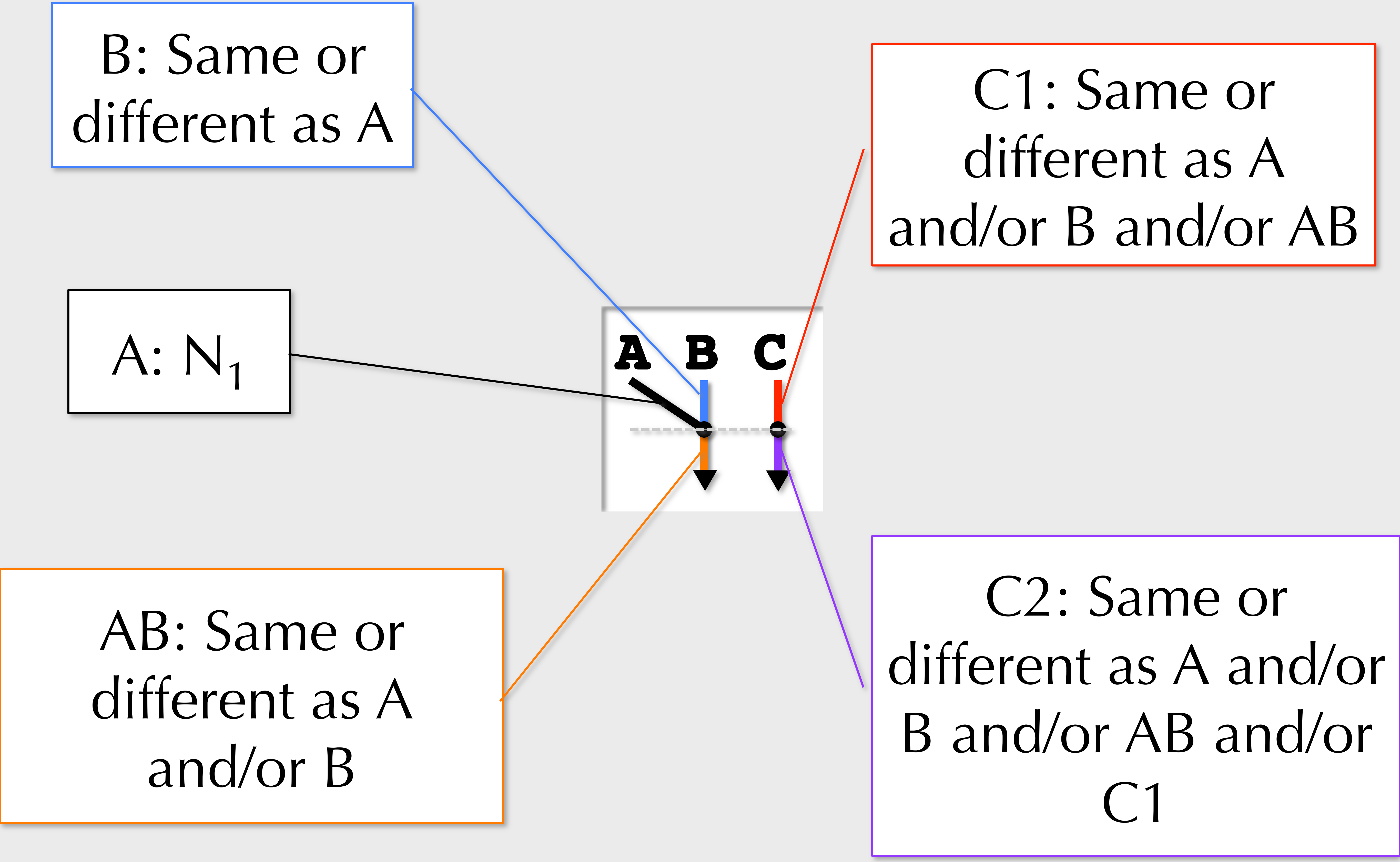


K=2



K=2





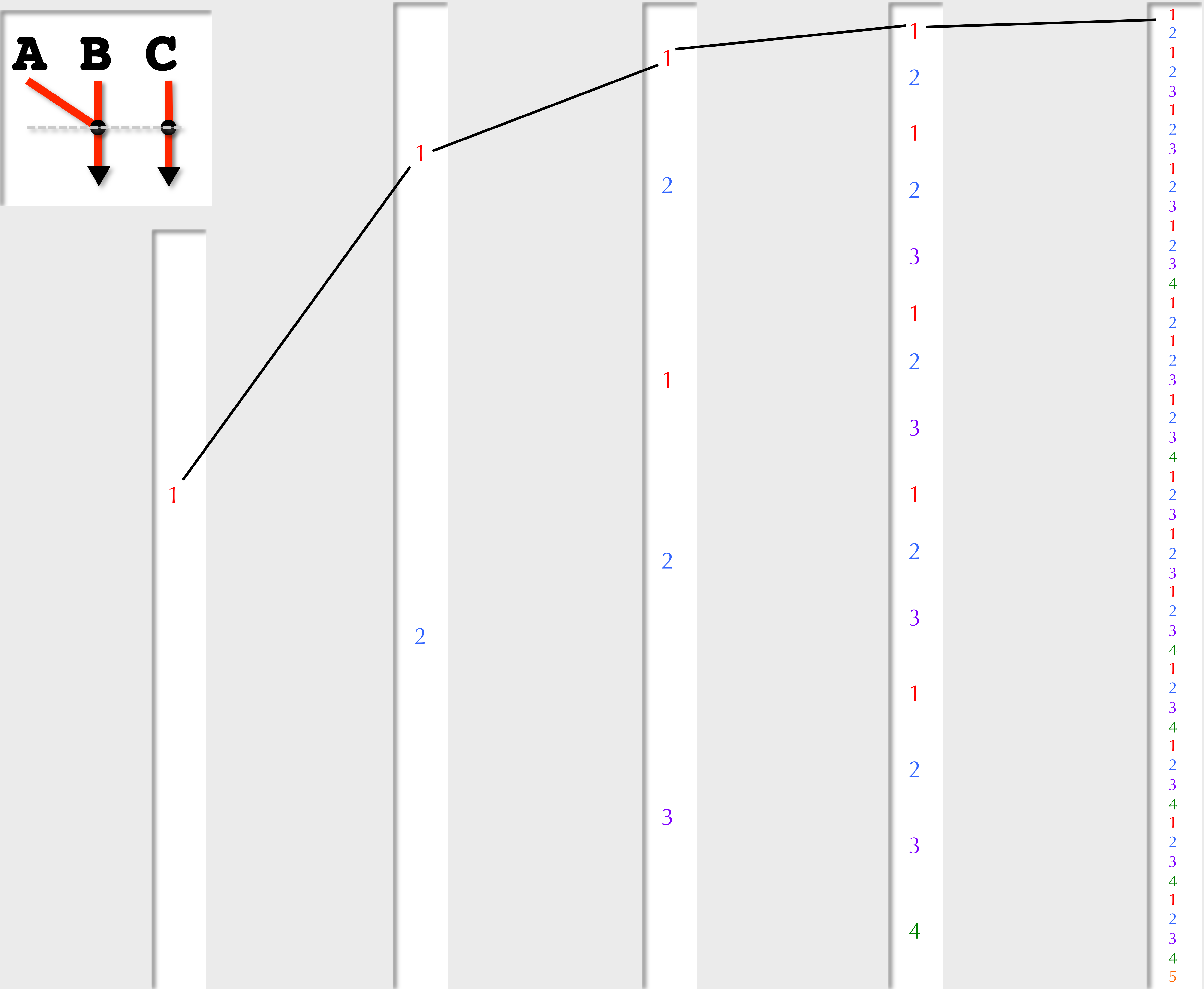
B: Same or different as A

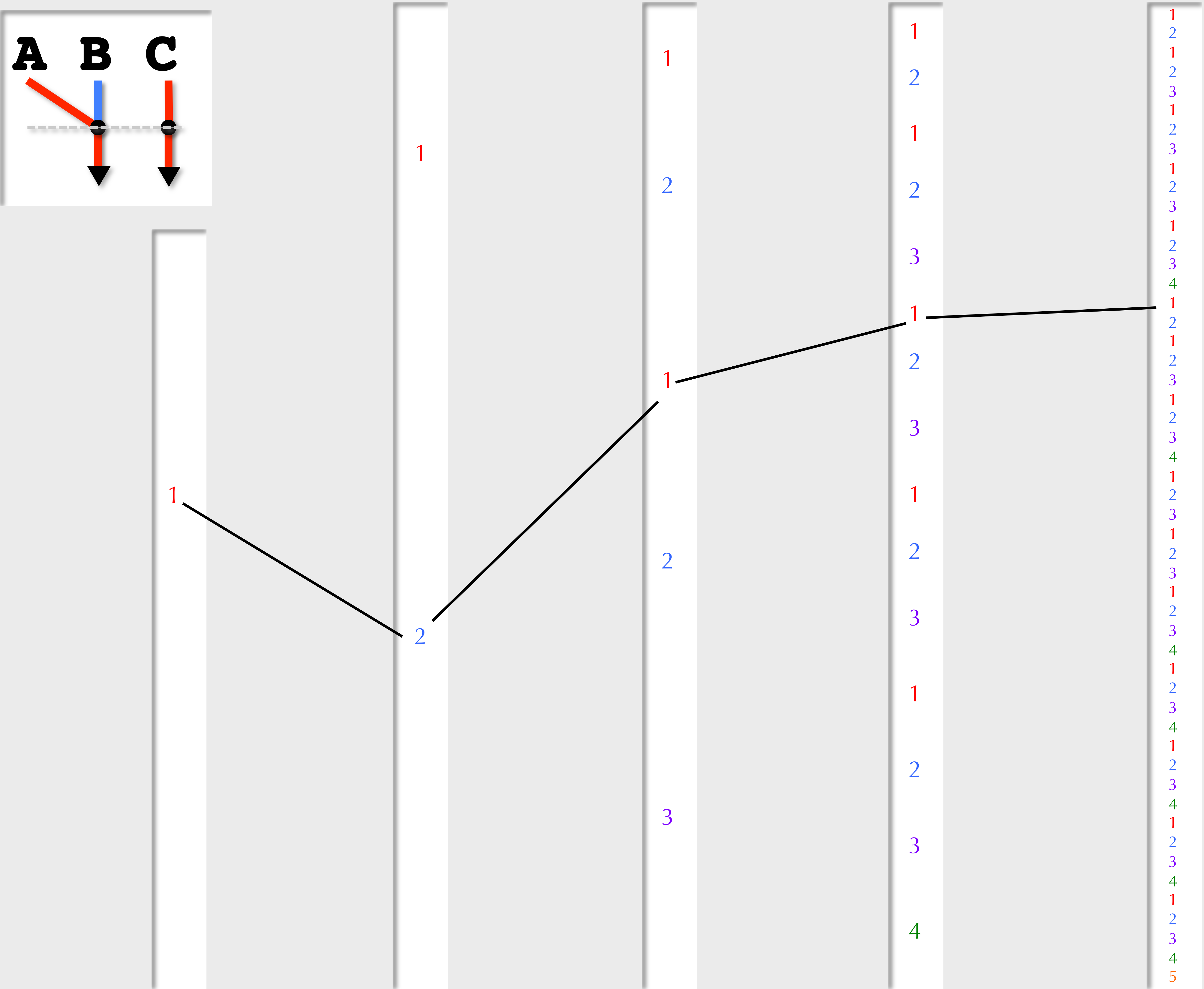
A: N_1

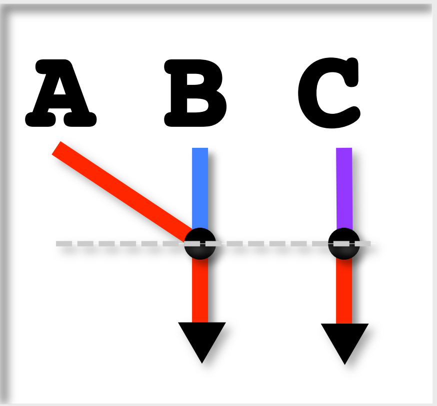
AB: Same or different as A and/or B

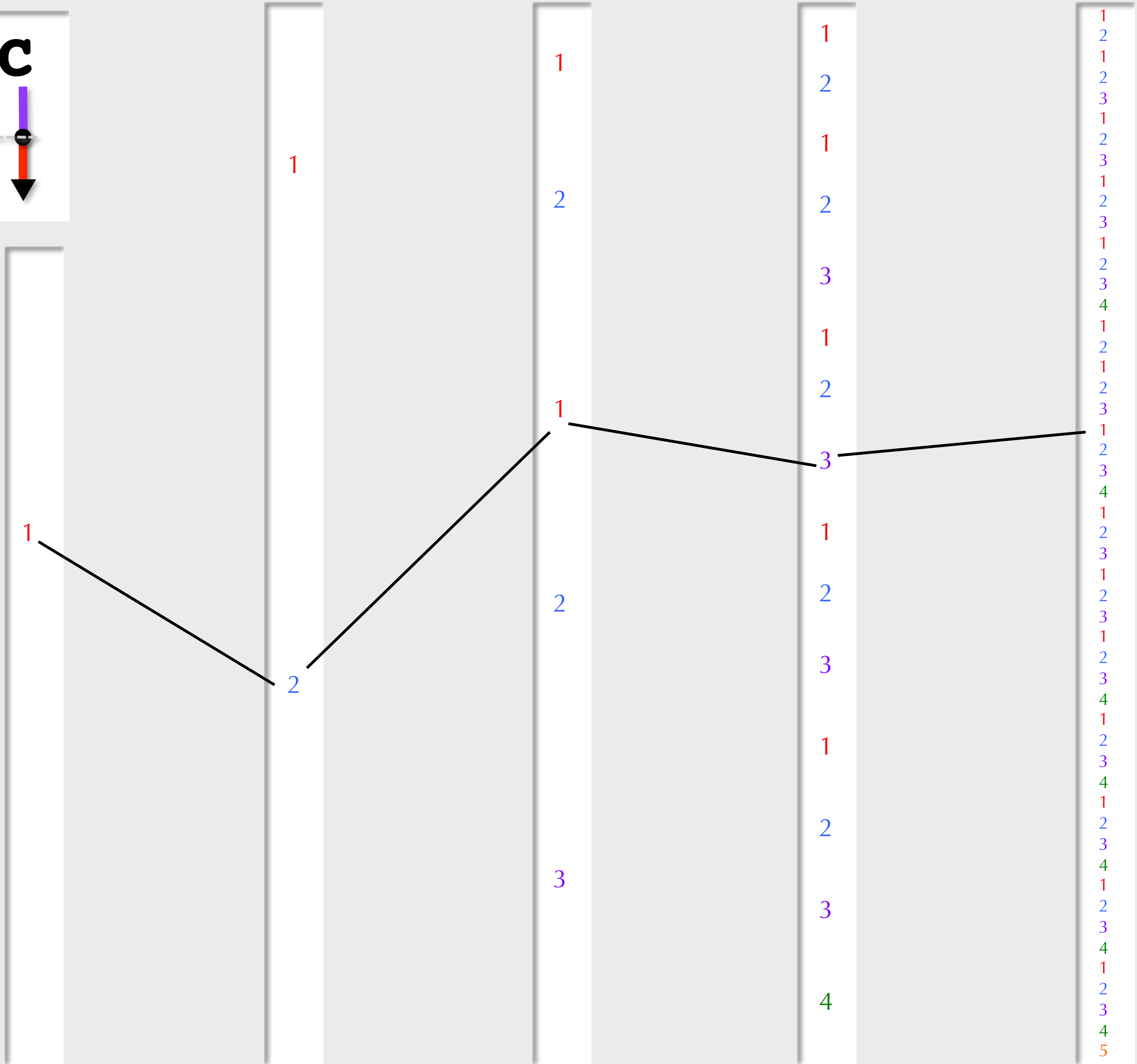
C1: Same or different as A and/or B and/or AB

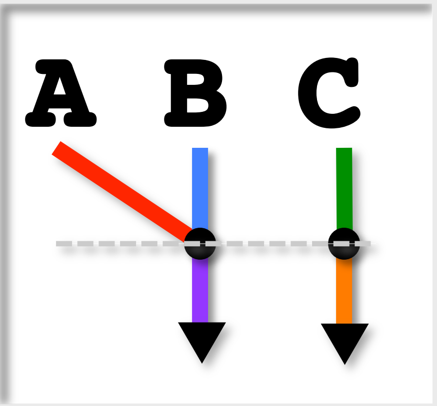
C2: Same or different as A and/or B and/or AB and/or C1

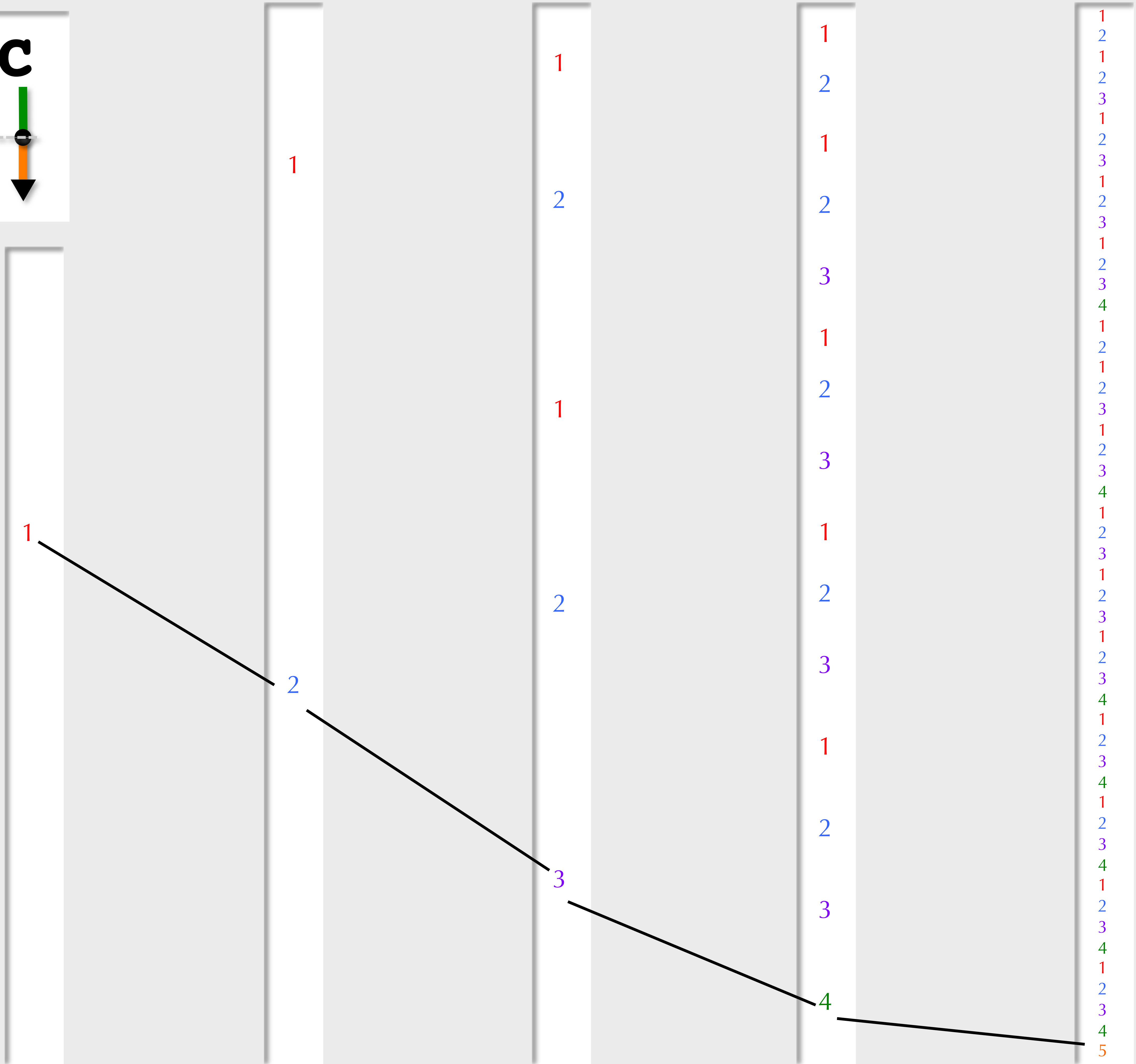

A
B
C
1
1 2
1 2 1 2 3
1 2 1 2 3 1 2 3 1 2 3 1 2 3 4
1 2 1 2 3 1 2 3 1 2 3 1 2 3 4 1 2 1 2 3 1 2 3 4 1 2 3 1 2 3 1 2 3 4 1 2 3 4 1 2 3 4 1 2 3 4 1 2 3 4 5

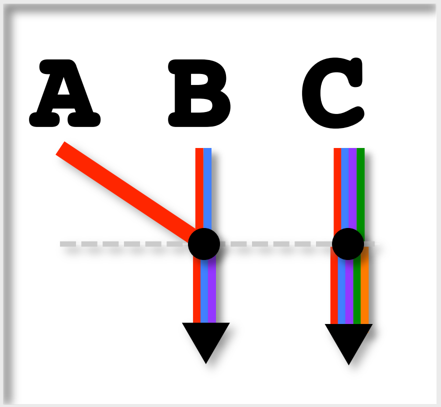

A
B
C
1
1 2
1 2 1 2 3
1 2 1 2 3 1 2 3 1 2 3 1 2 3 4
1 2 1 2 3 1 2 3 1 2 3 1 2 3 4 1 2 1 2 3 1 2 3 4 1 2 3 1 2 3 1 2 3 4 1 2 3 4 1 2 3 4 1 2 3 4 1 2 3 4 5

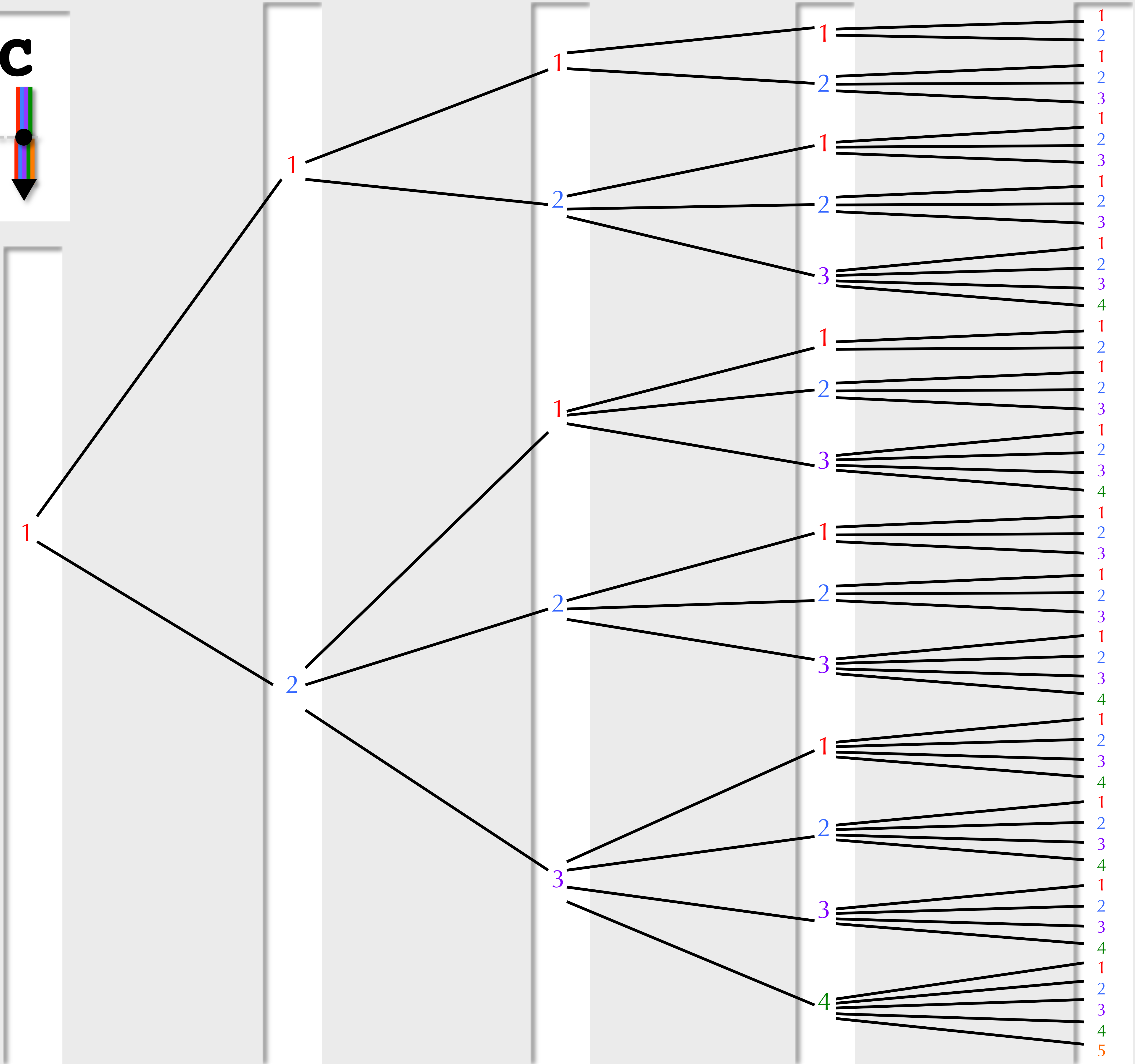

A
B
C

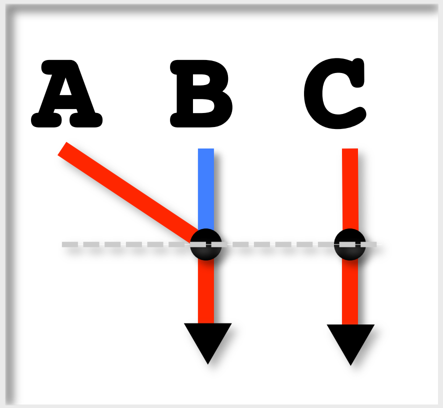

1
1
2
1
2
1
2
3
1
2
1
2
3
1
2
3
1
2
3
1
2
3
4
1
2
1
2
3
1
2
3
1
2
3
1
2
3
4
1
2
1
2
3
1
2
3
4
1
2
3
1
2
3
1
2
3
4
1
2
3
4
1
2
3
4
1
2
3
4
1
2
3
4
5


A
B
C

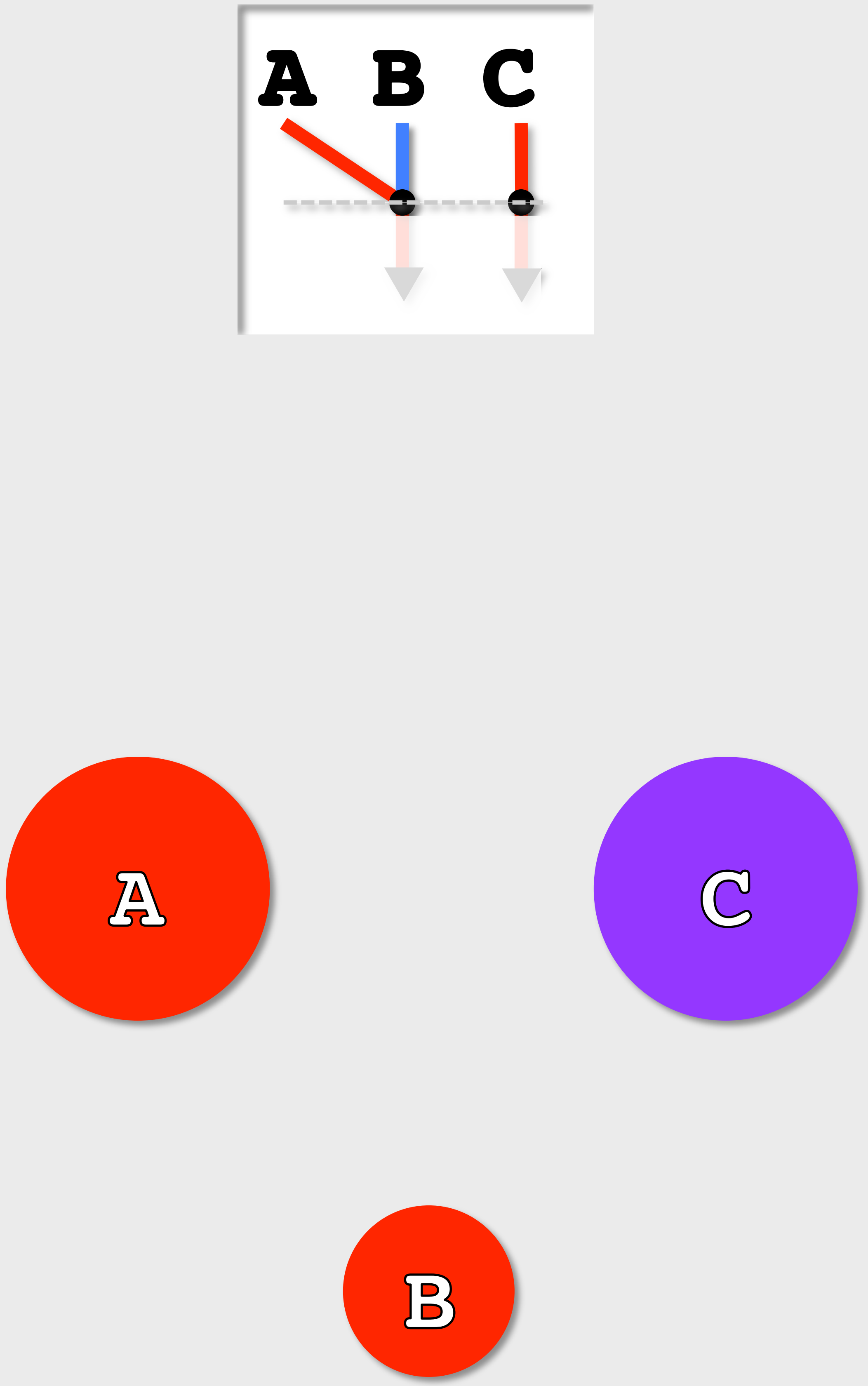

1
1 2
1 2 1 2 3
1 2 1 2 3 1 2 3 1 2 3 1 2 3 4
1 2 1 2 3 1 2 3 1 2 3 1 2 3 4 1 2 1 2 3 1 2 3 4 1 2 3 1 2 3 1 2 3 4 1 2 3 4 1 2 3 4 1 2 3 4 1 2 3 4 5

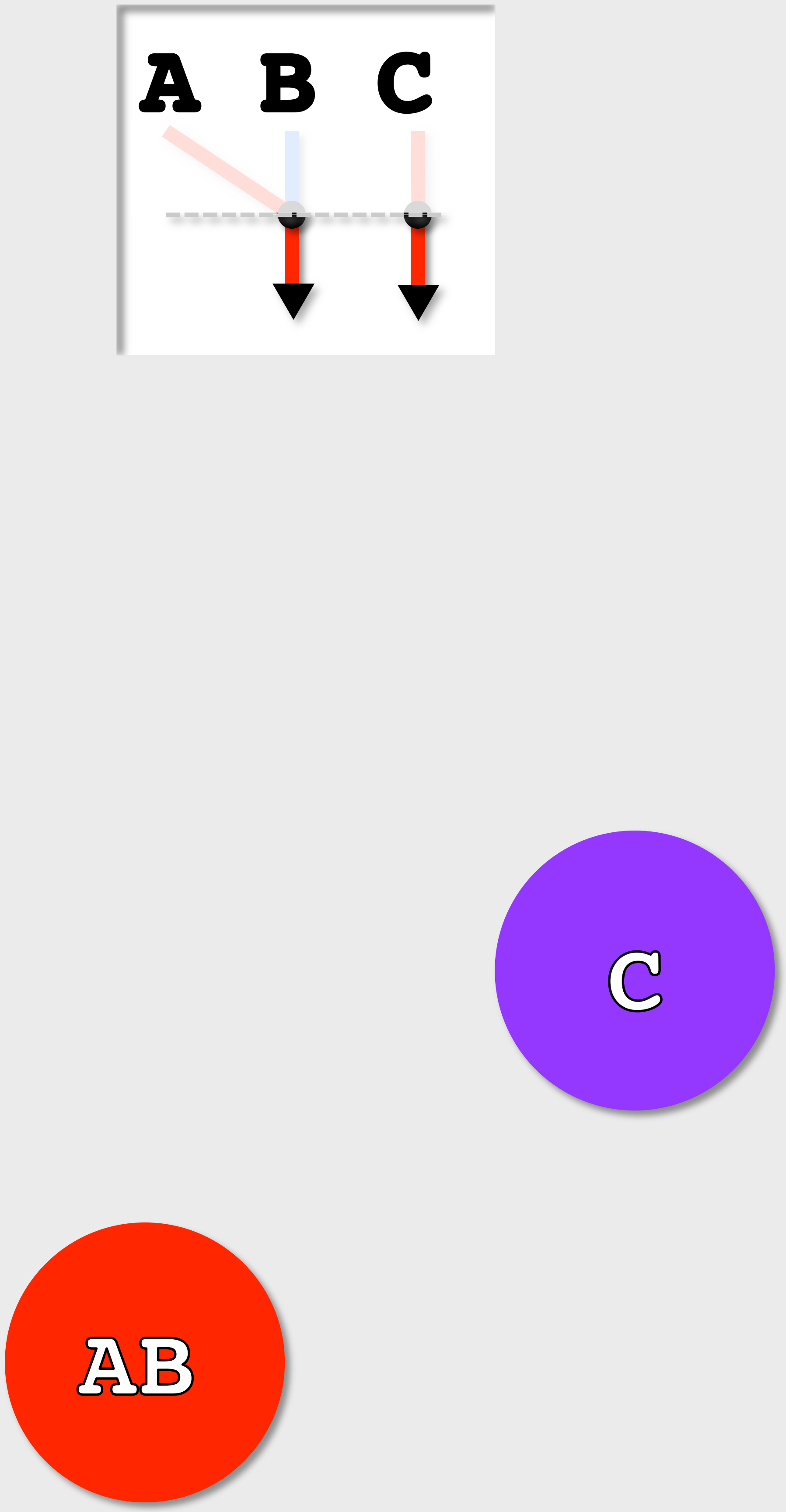

A
B
C

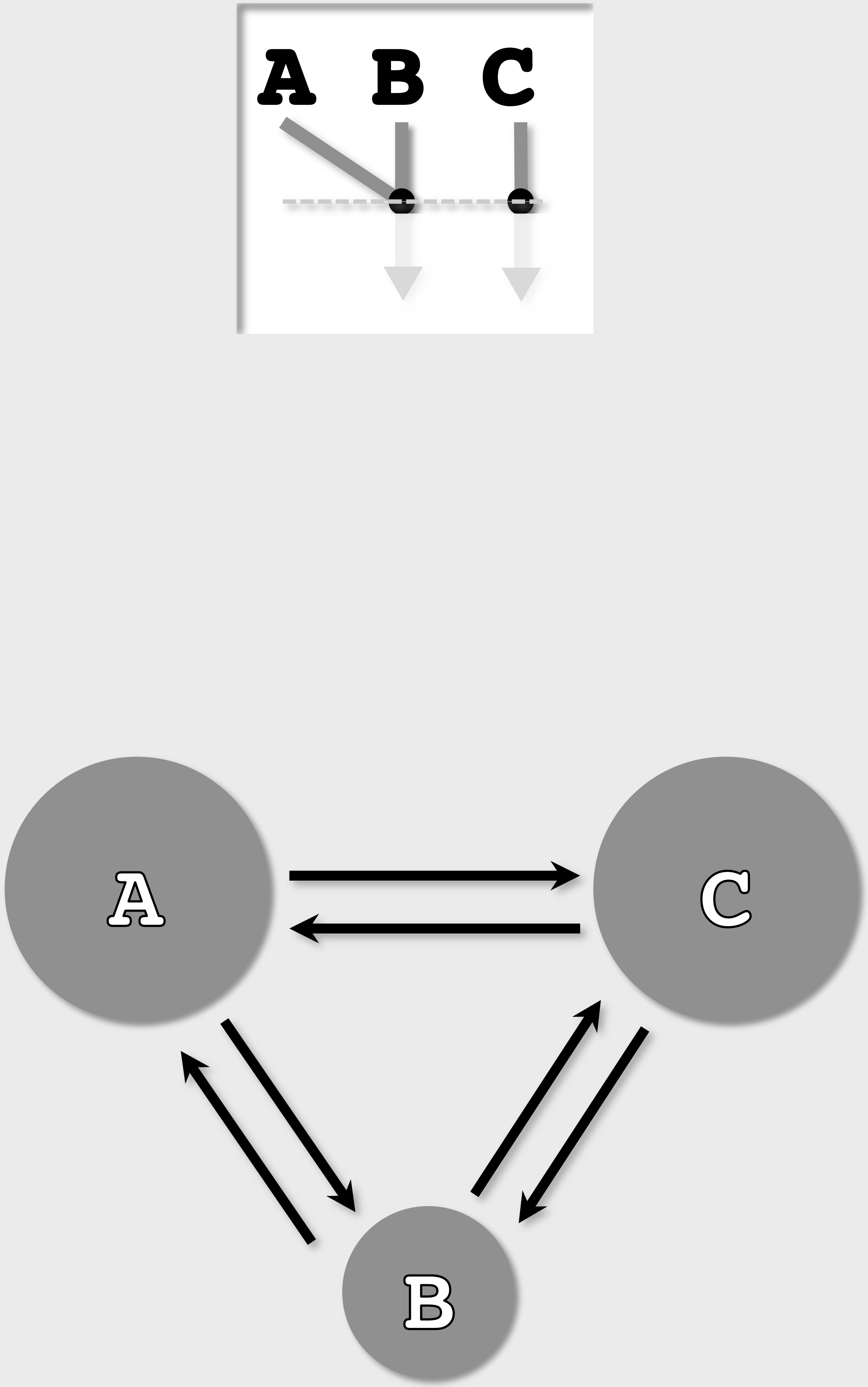

1
1 2
1 2 1 2 3
1 2 1 2 3 1 2 3 1 2 3 1 2 3 4
1 2 1 2 3 1 2 3 1 2 3 1 2 3 4 1 2 1 2 3 1 2 3 4 1 2 3 1 2 3 1 2 3 4 1 2 3 4 1 2 3 4 1 2 3 4 1 2 3 4 5

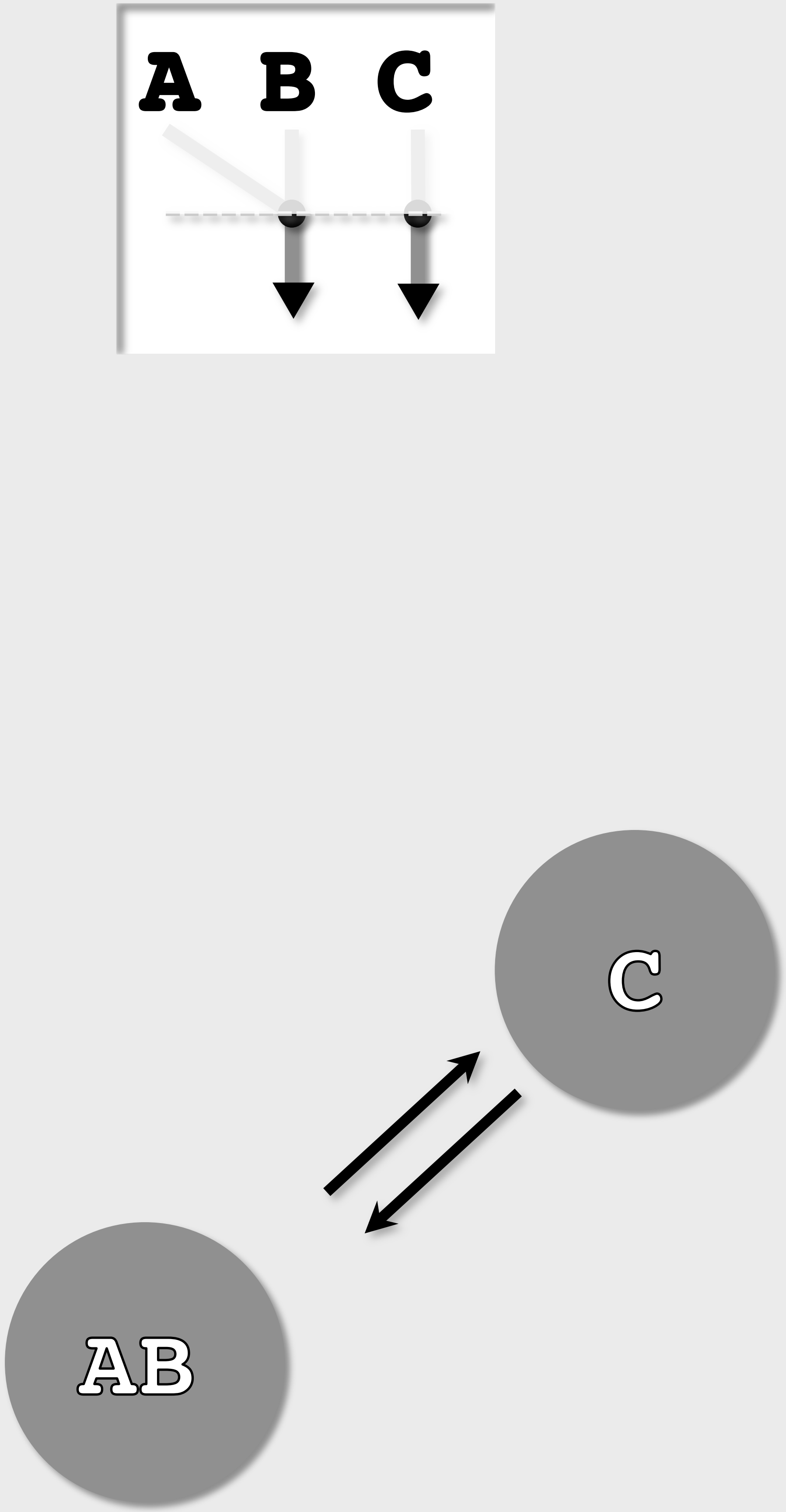


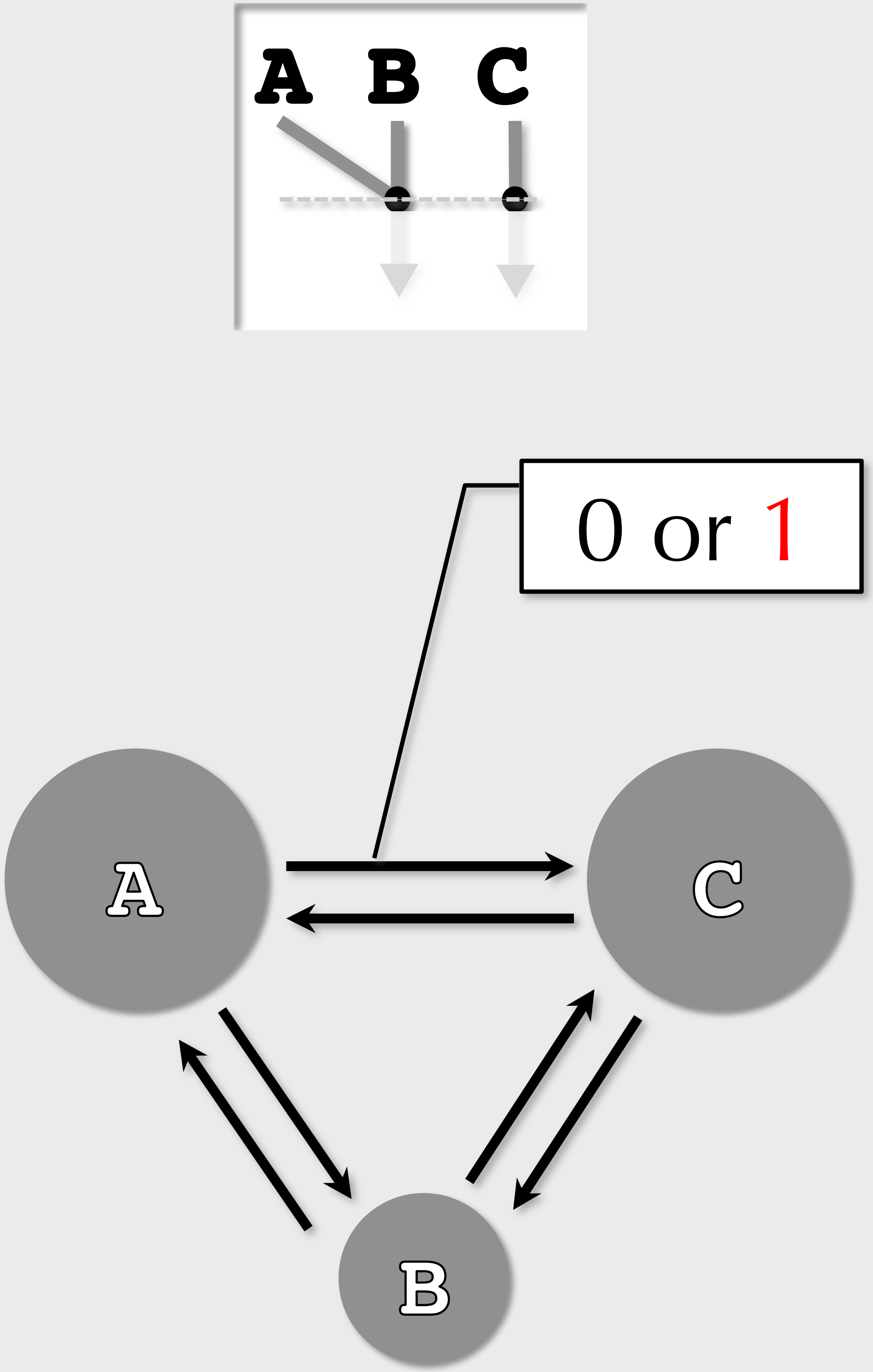
1 collapse parameter
2 population size parameters


A
B
C
A
C
B

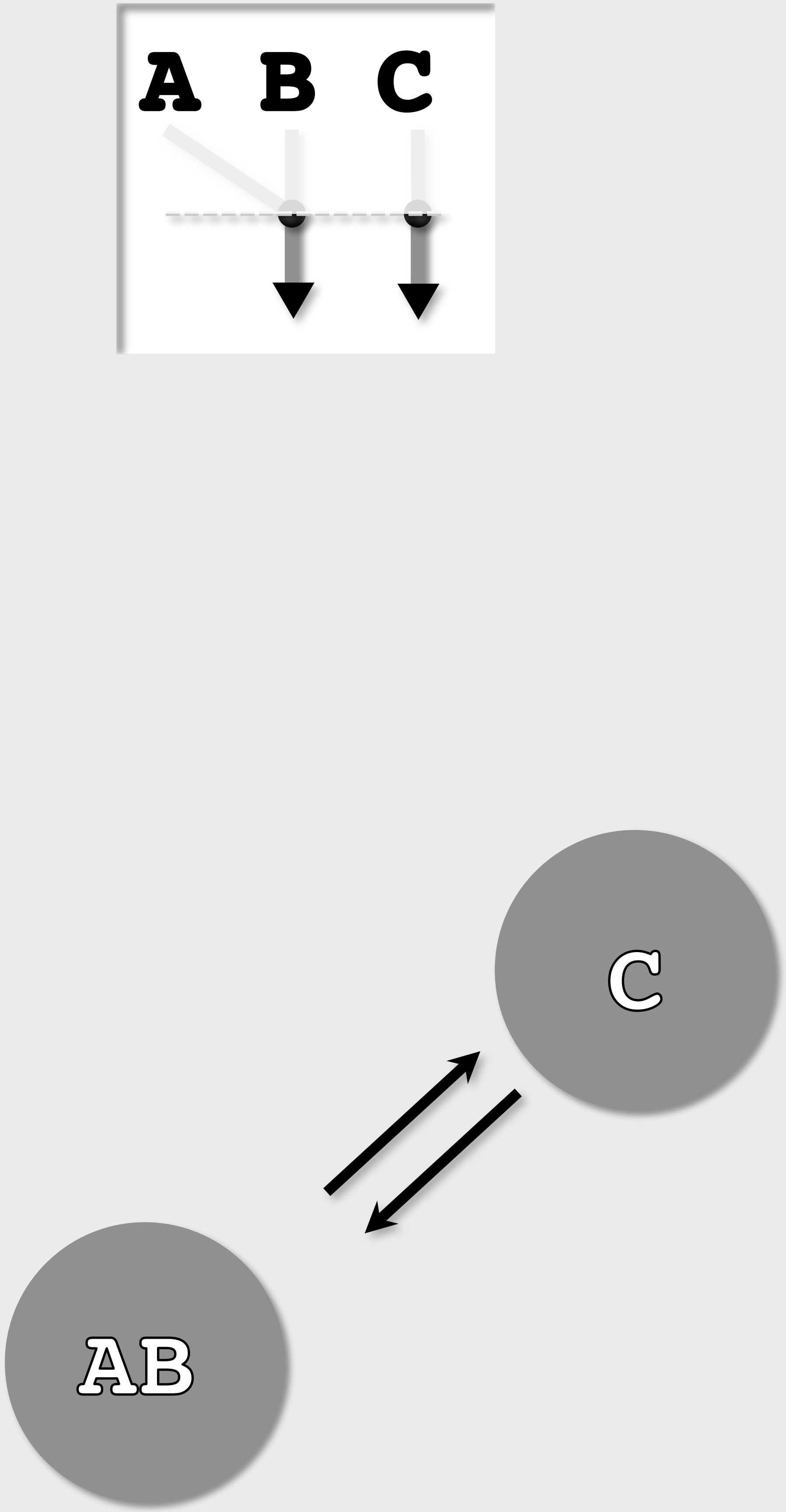

A
B
C
C
AB

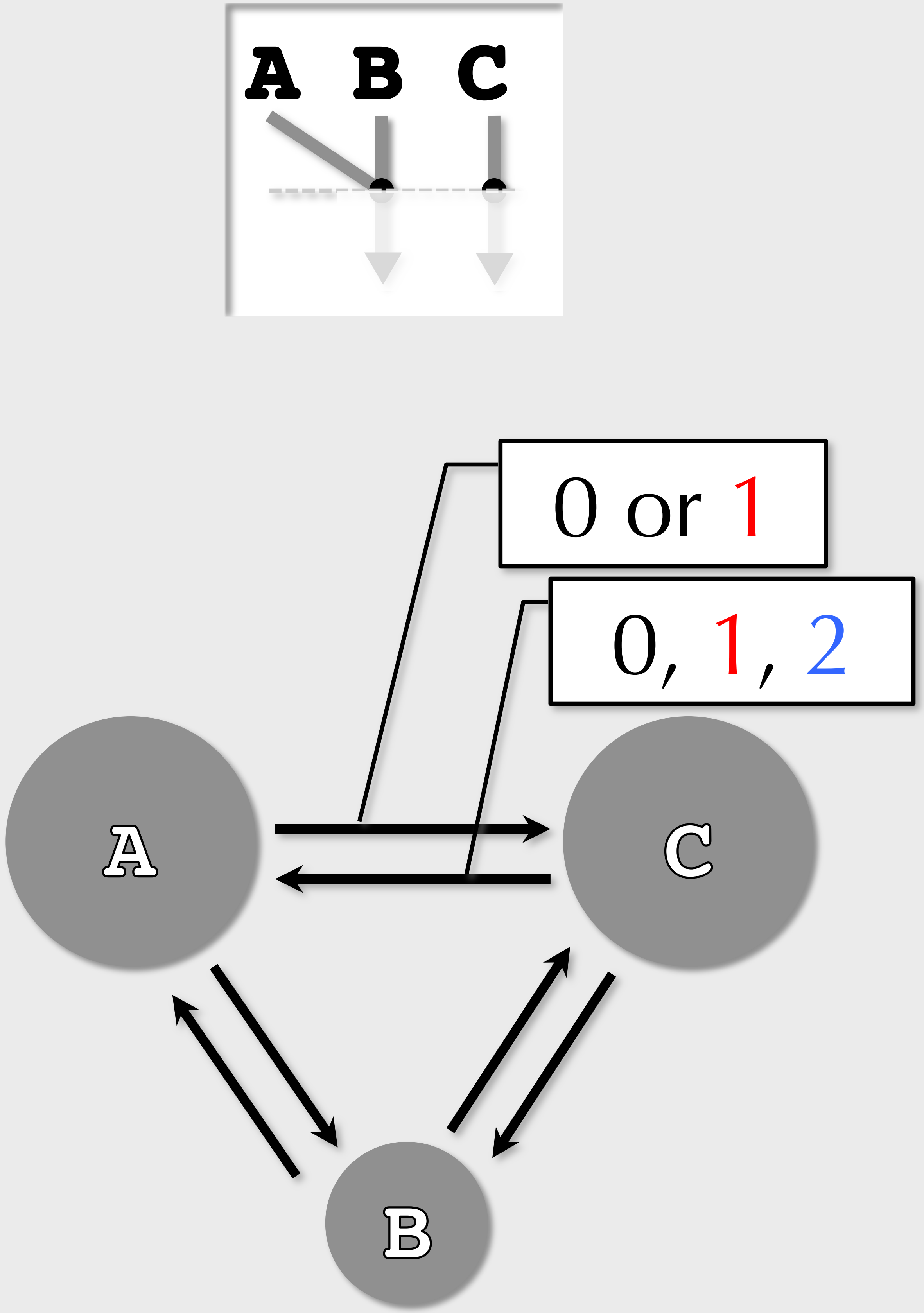

A B C
A
C
B

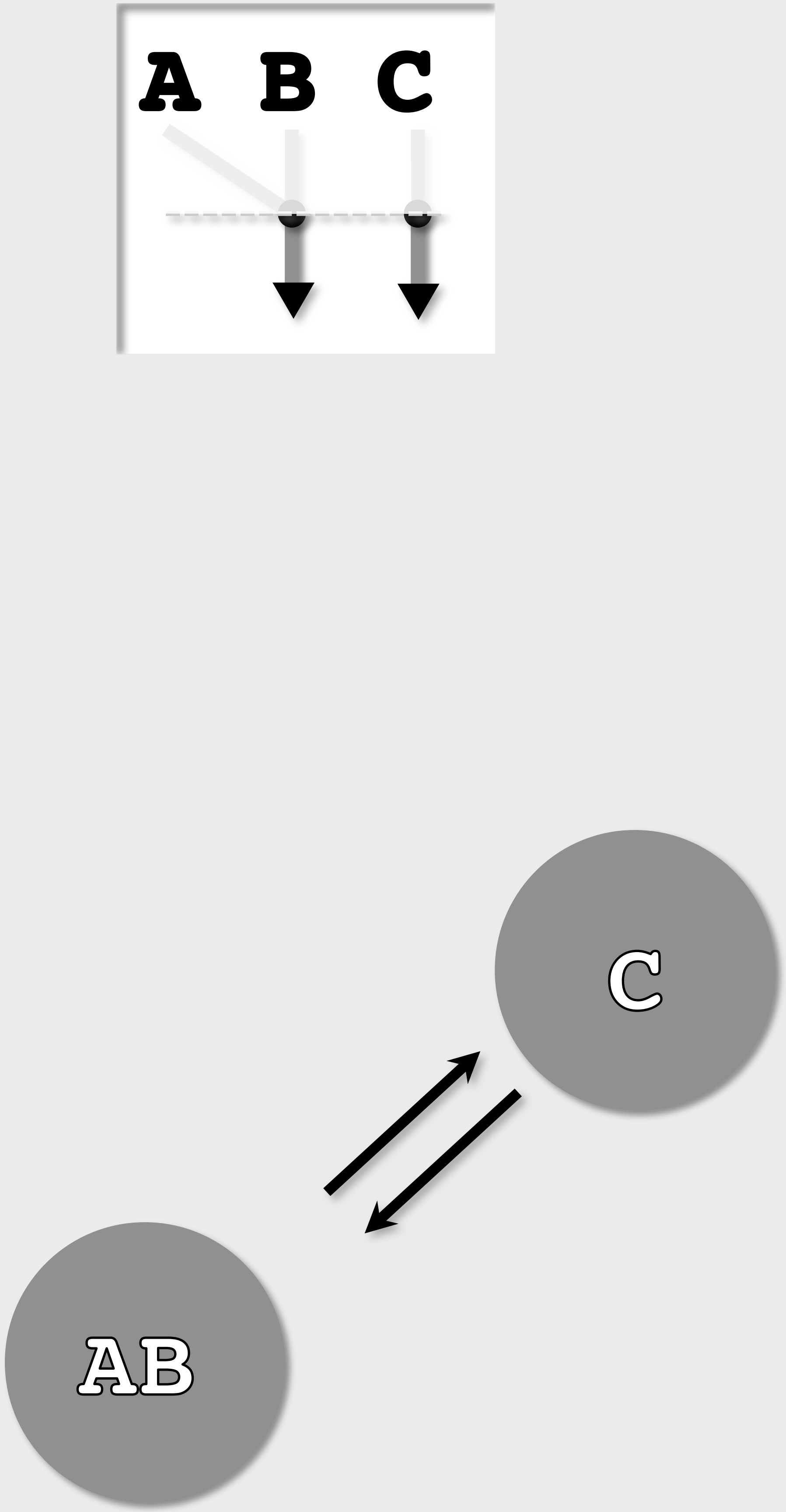

A B C
C
AB

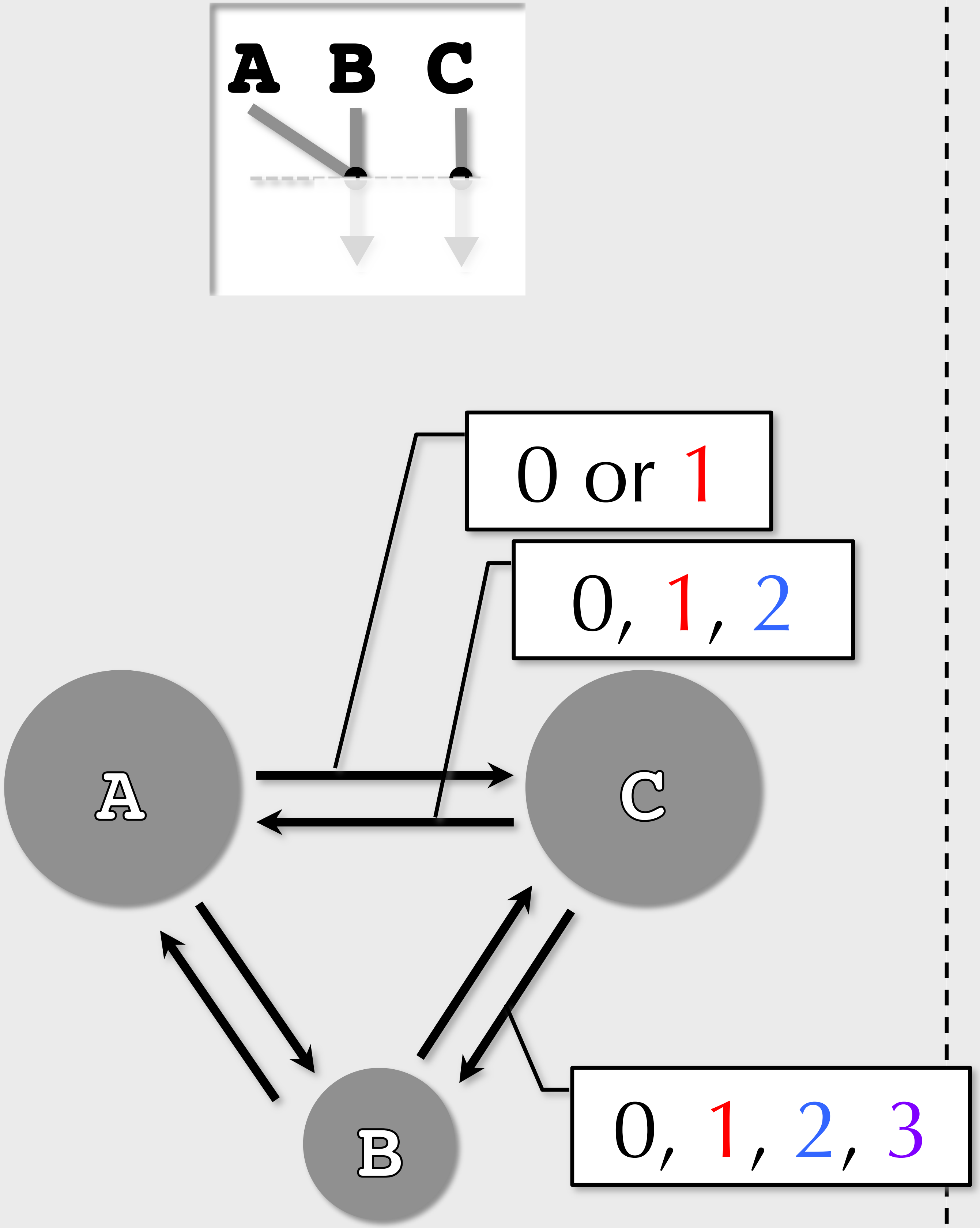


0 or 1




A B C
0 or 1
0, 1, 2
A
C
B

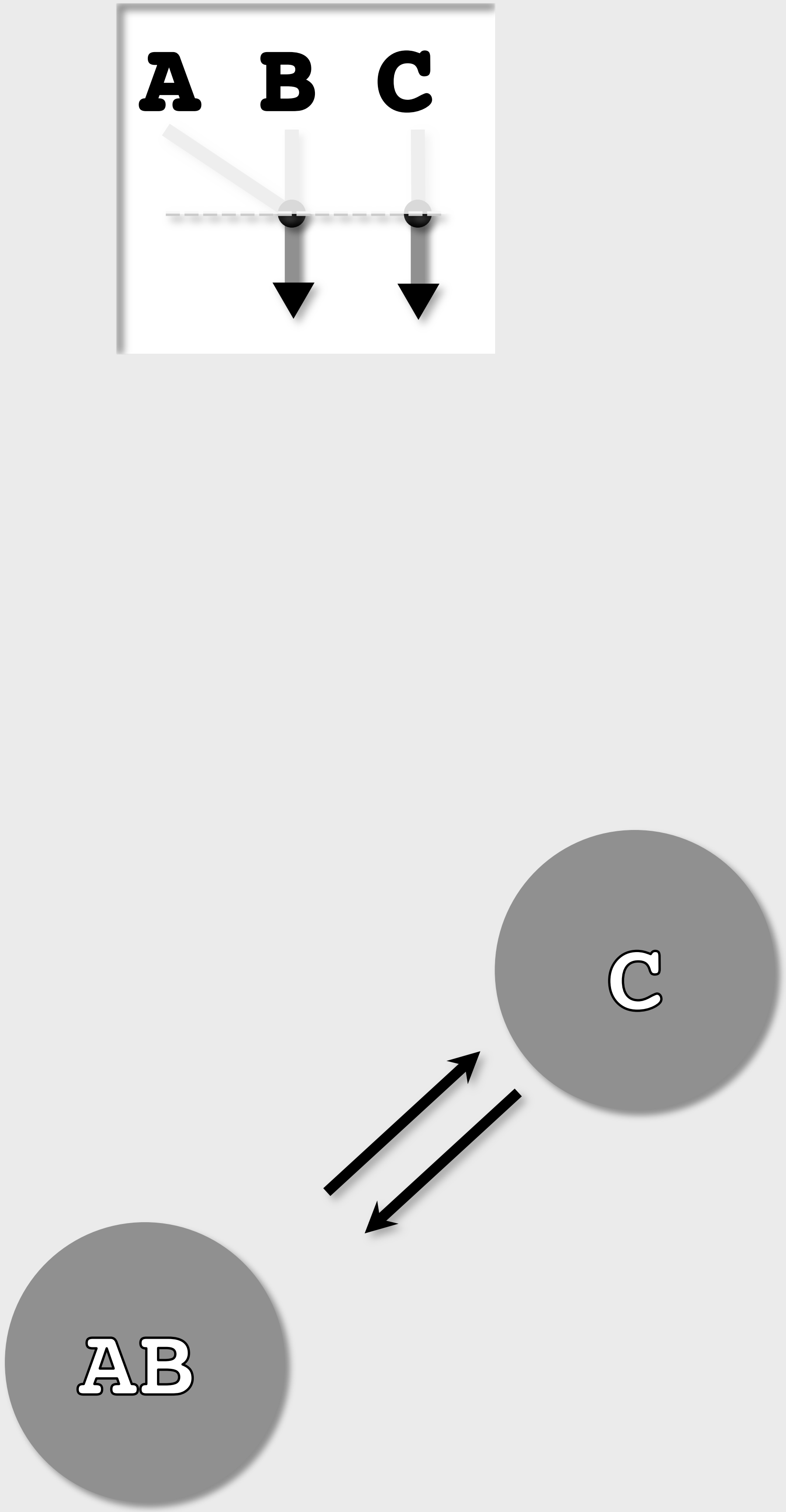

A B C
C
AB

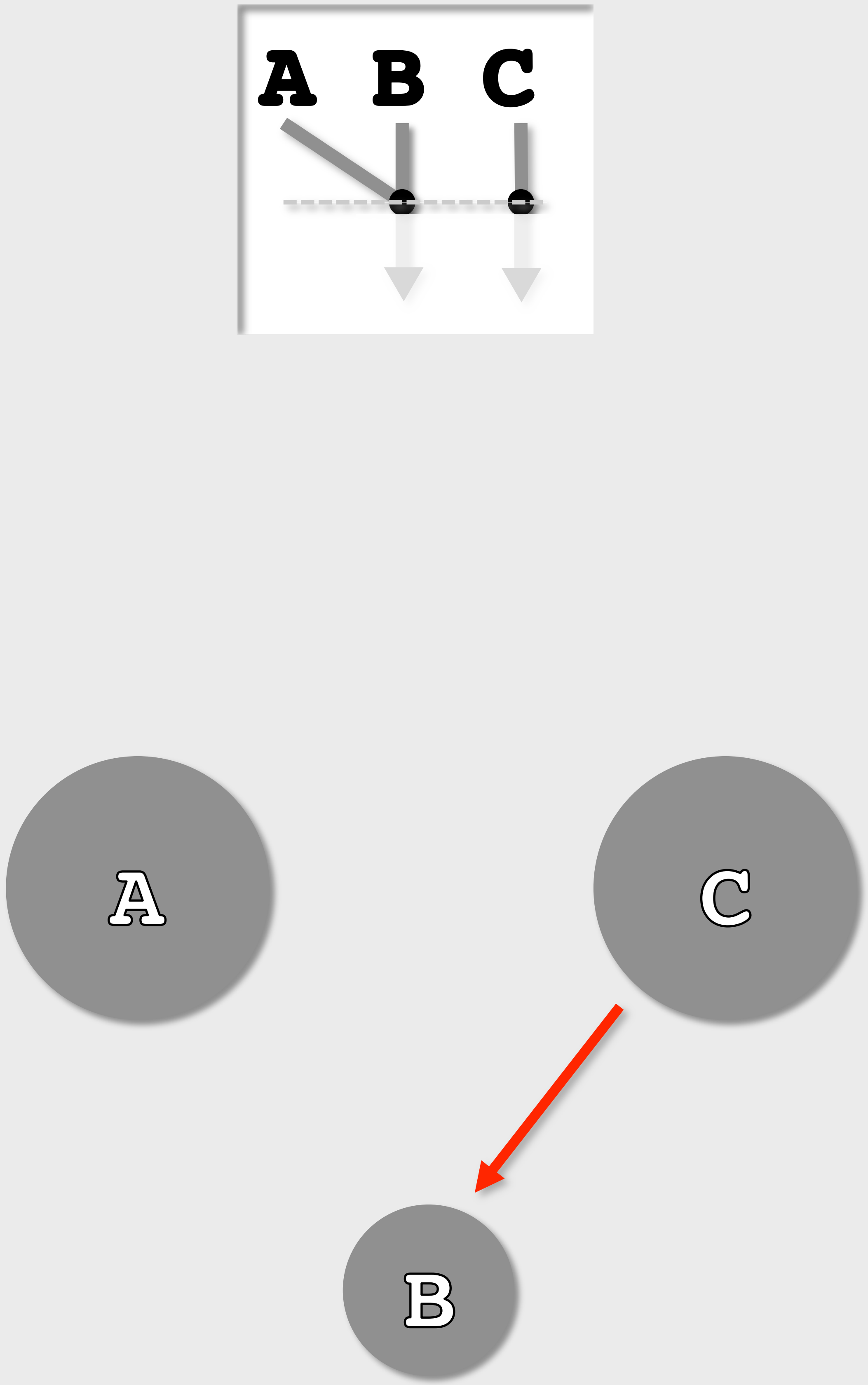


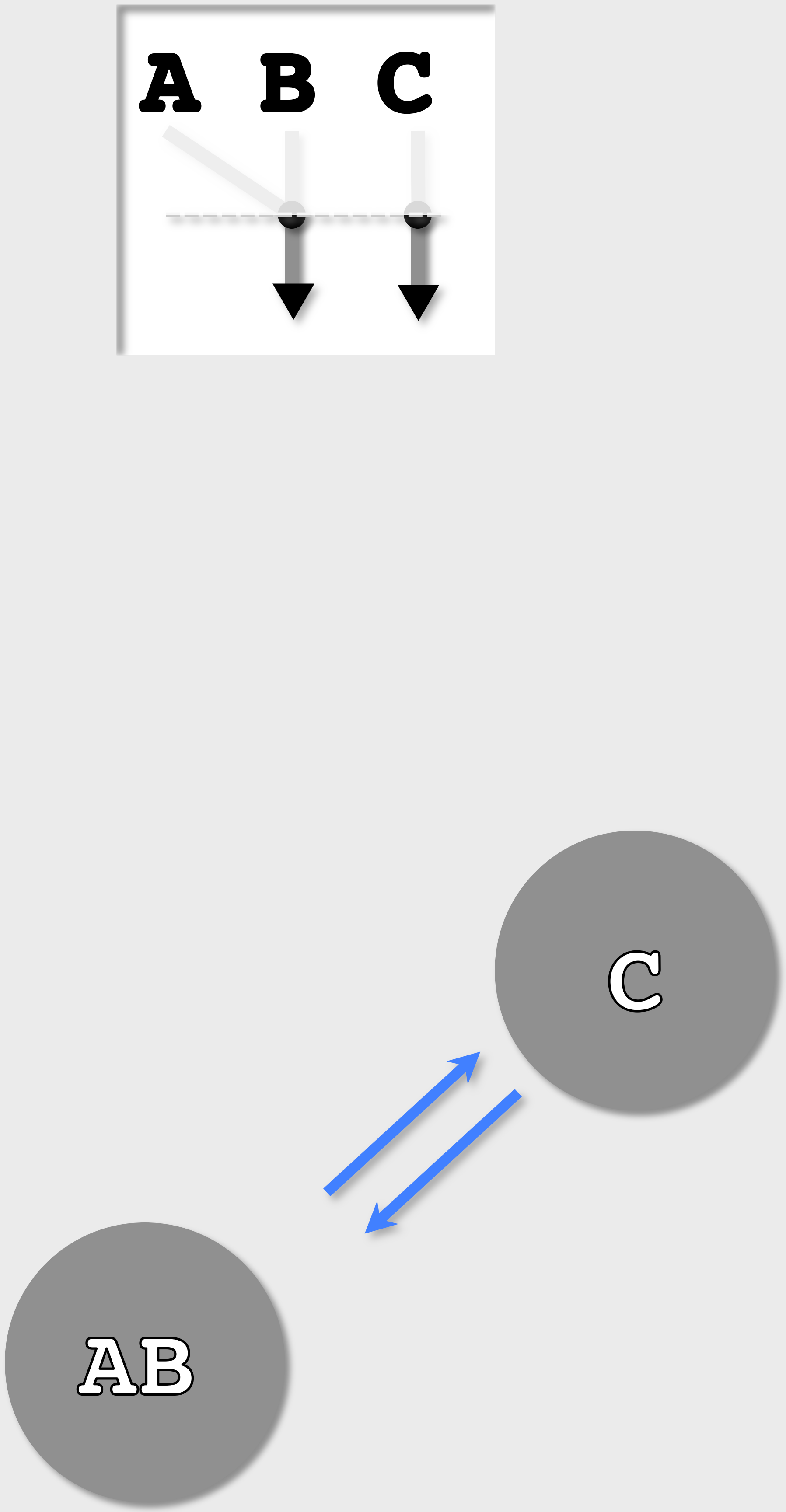
0 or 1

0, 1, 2

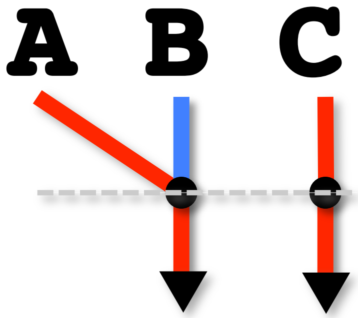
0, 1, 2, 3

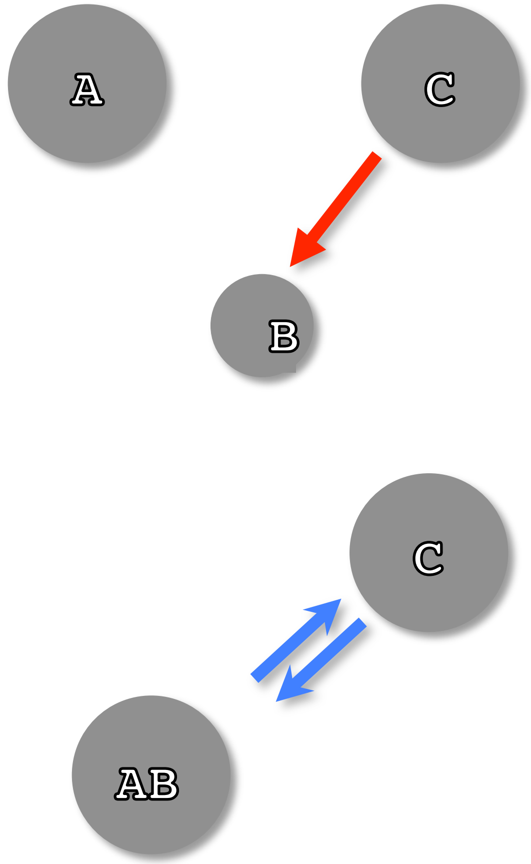


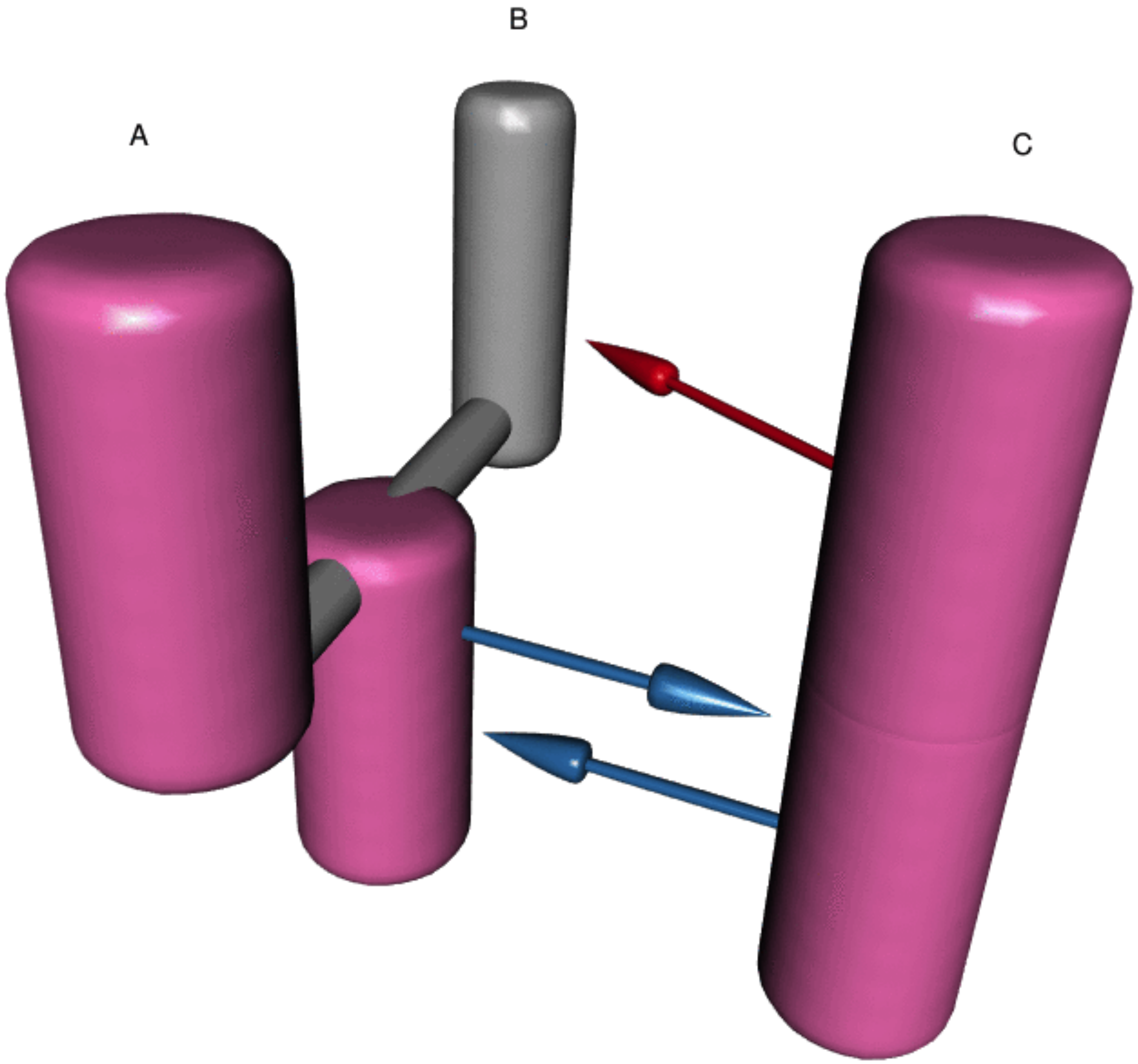

A B C
A
C
B

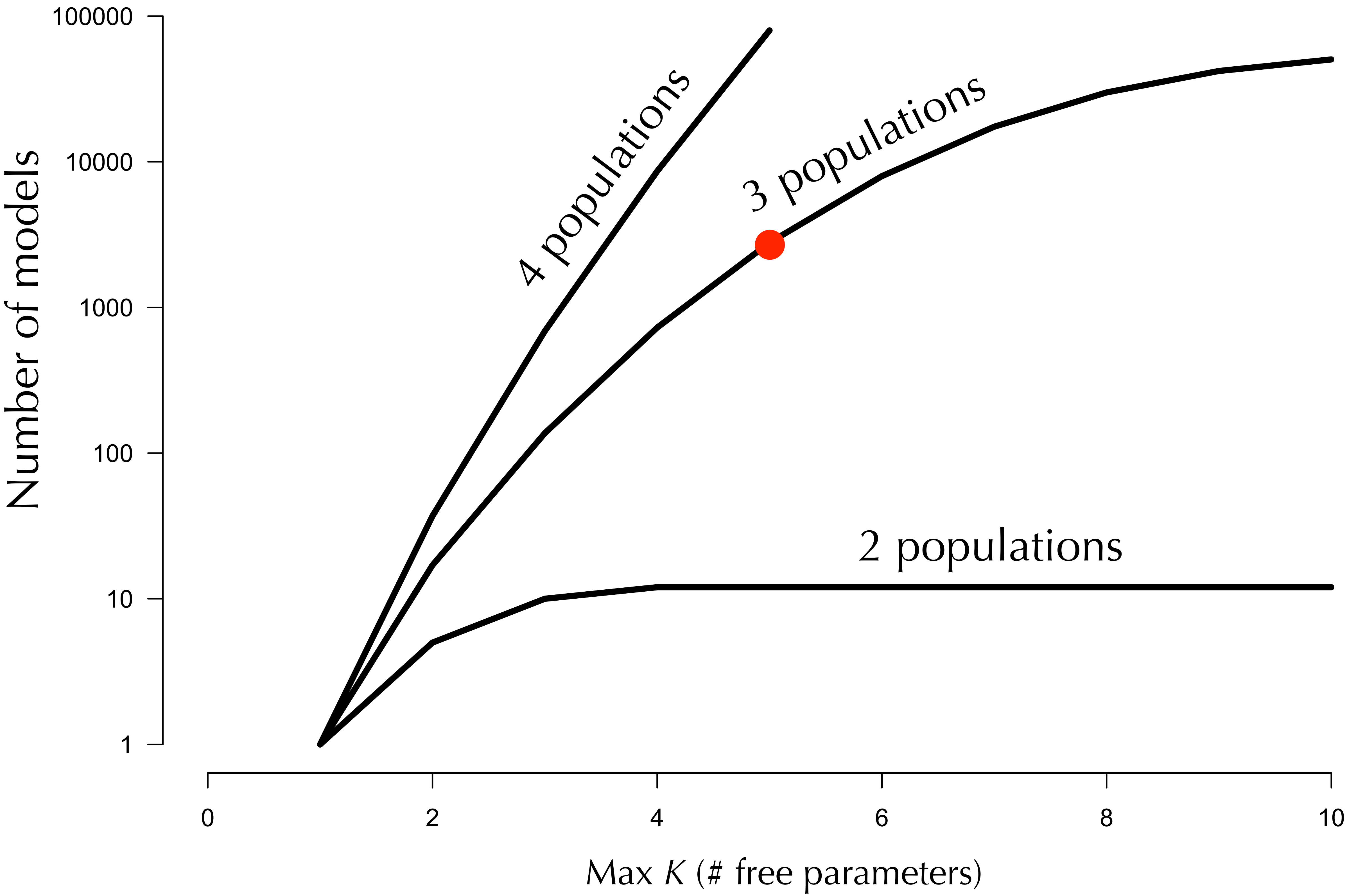

A B C
C
AB

1 collapse parameter
2 population size parameters
2 migration parameters





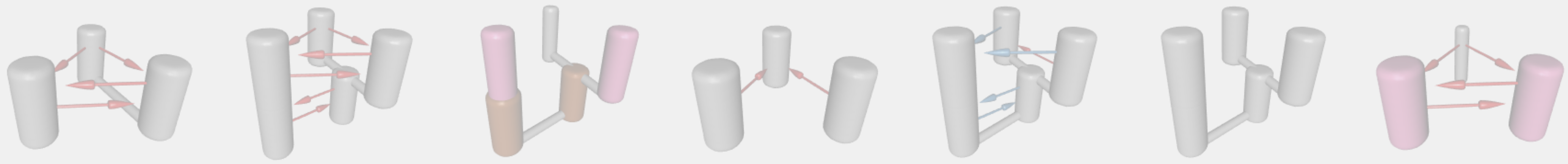



Number of models
100000
10000
1000
100
10
1
0
2
4
6
8
10
Max *K* (# free parameters)
4 populations
3 populations
2 populations

1

Generate all possible models

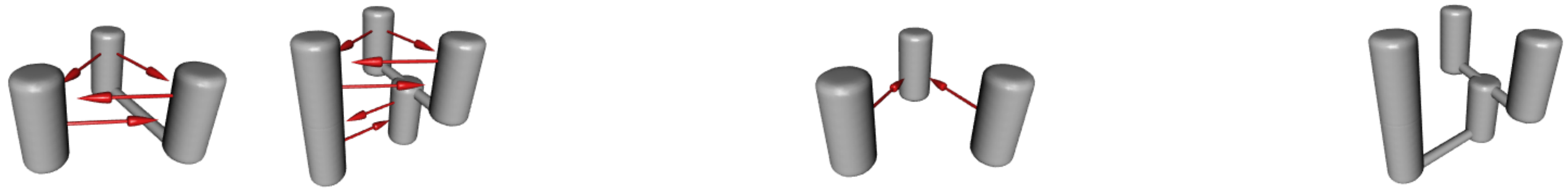
Given *N* populations, ≤*K* free parameters



2

Filter

(only tree models, no more than two migration rates, etc.)



3

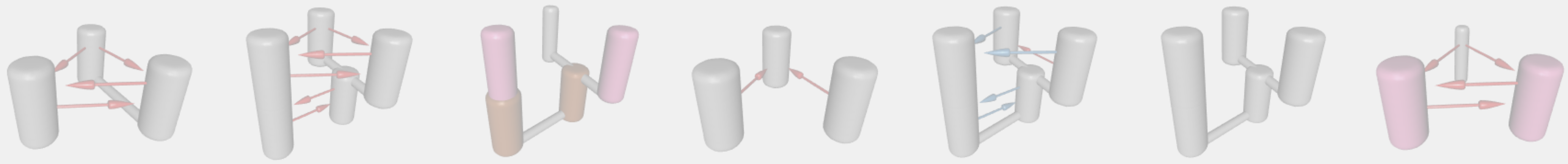
Analyze

(find best, find AIC for all

1

Generate all possible models

Given N populations, $\leq K$ free parameters



↓

2

Filter

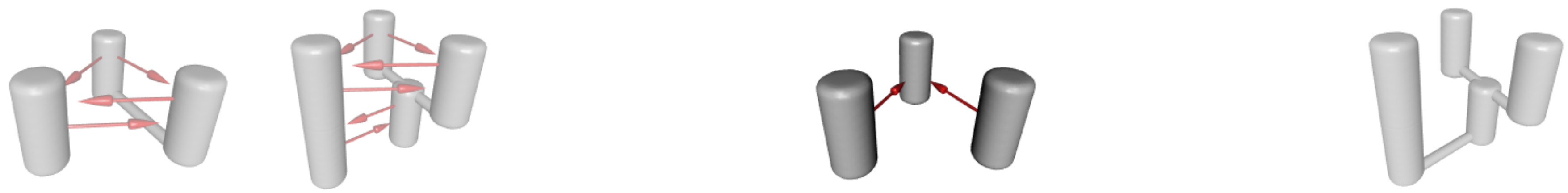
(only tree models, no more than two migration rates, etc.)

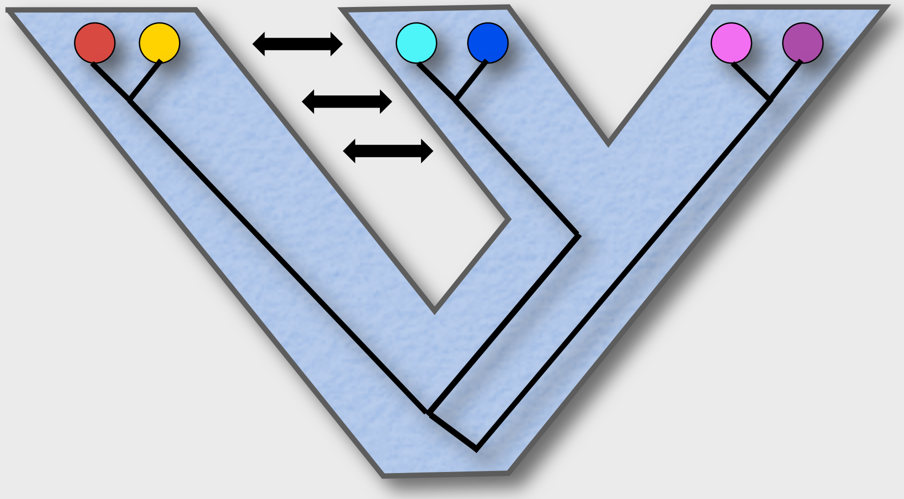
↓

3

Analyze

(find best, find AIC for all

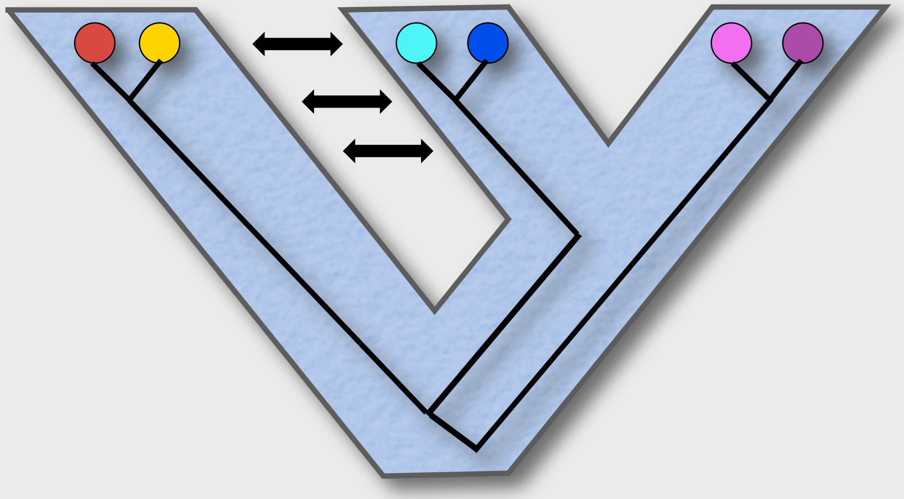




Exact likelihood: P(gene tree | population history)

COAL (Degnan and Salter 2005), STEM (Kubatko et al. 2009), BPP (Yang and Rannala 2010), IM (Nielsen and Wakely 2001), etc.

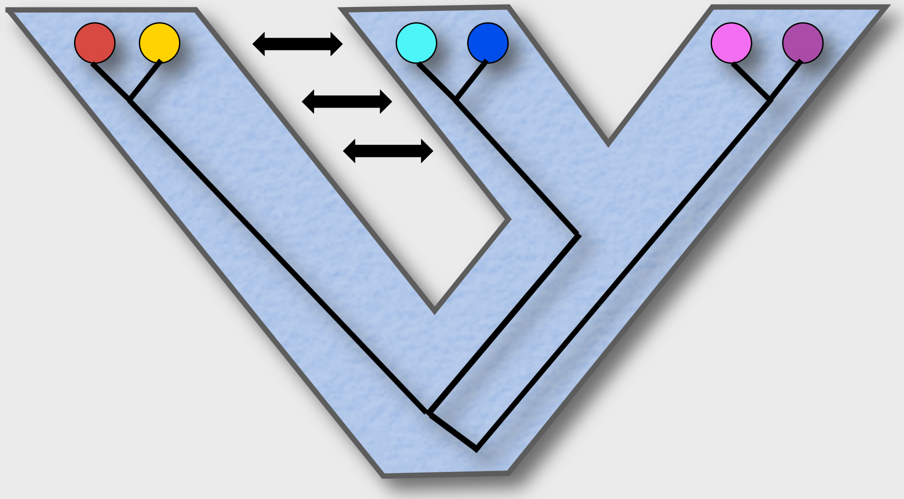
Issue: Not all models (currently) have analytical solutions, and it's always simpler to simulate (think of selection). But if it does work, can use it.



Approximate Bayesian Computation

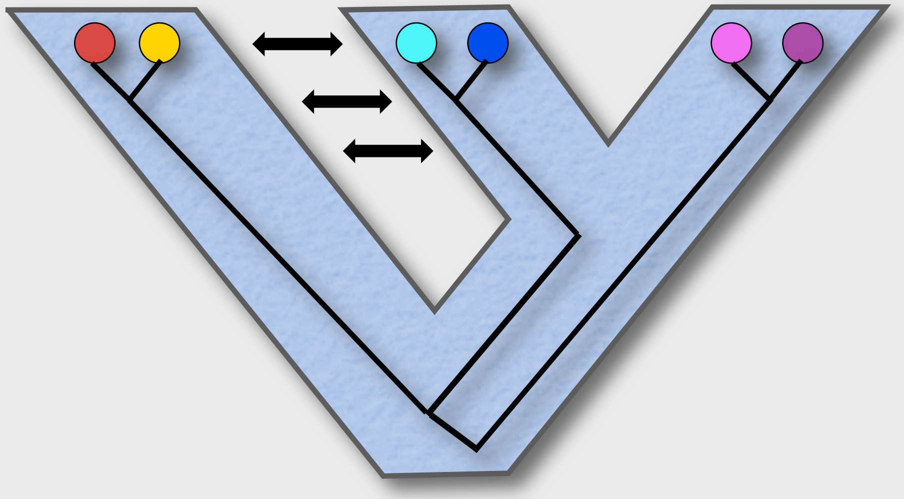
Carmago et al. 2012, DIYABC (Cornuet et al. 2010), PopABC (Lopes et al. 2009)

```
for (many reps) {
     sample parameters (or models) from prior
     simulate dataset using these parameters
     if (|(summary(dataset) – summary(observed)|< ε ){
          count as match, save these parameters
     }
}

plot(saved parameters) #or other way to summarize
```



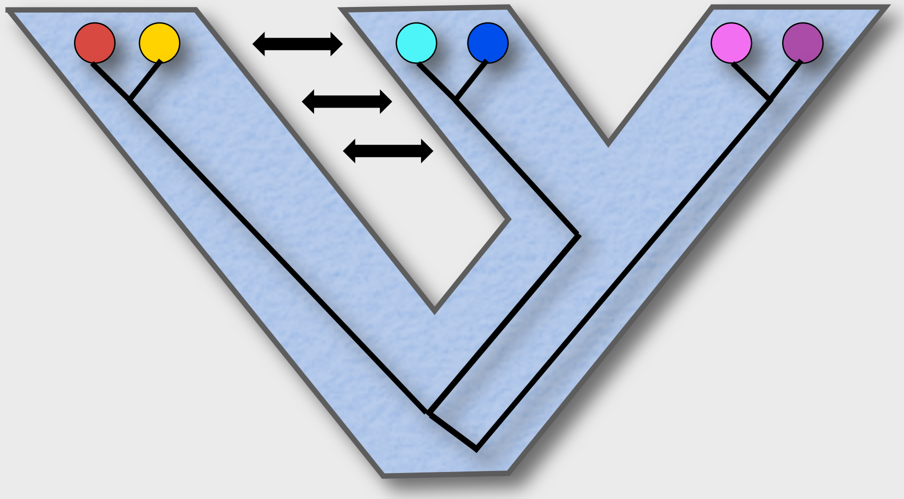
Approximate Likelihood

Estimate probability of data
counting exact matches



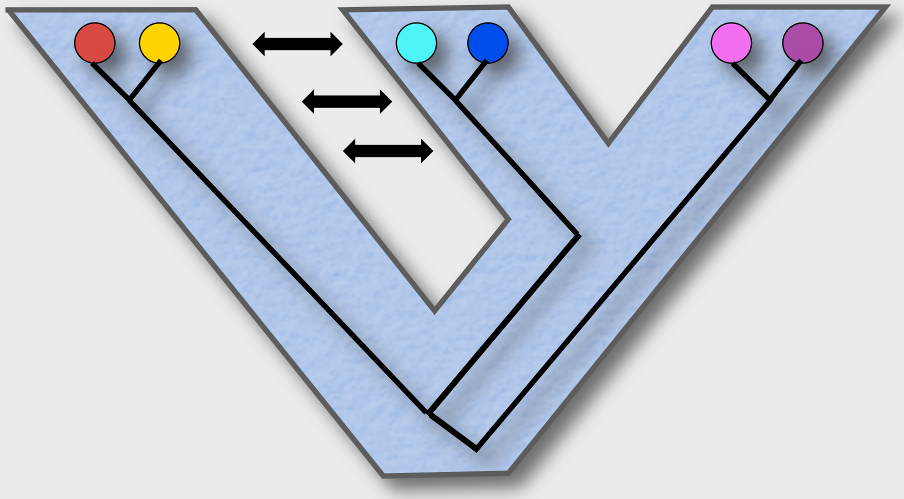
Approximate Likelihood

```
for (many reps) {
      sample parameters (or models) from prior
      simulate dataset using these parameters
      if (|(summary(dataset) – summary(observed)|< $\varepsilon$ ){
            count as match, save these parameters
      }
}

plot(saved parameters) #or other way to summarize
```



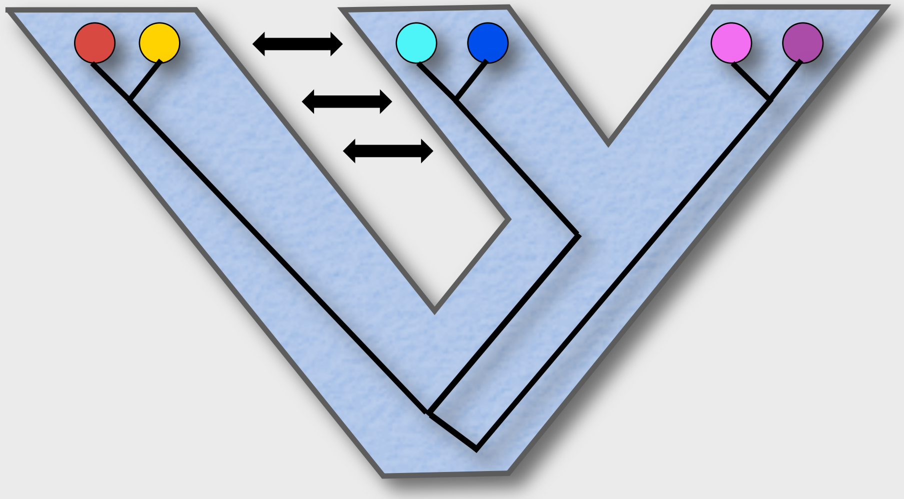
Approximate Likelihood

```
sample parameters ~~(or models)~~ from ~~prior~~ guesses
for (many reps) {
     ~~sample parameters (or models) from prior~~
     simulate dataset using these parameters
     if (|(summary(dataset) – summary(observed)|< $\varepsilon$ ){
          count as match, save these parameters
     }
}

plot(saved parameters) #or other way to summarize
```



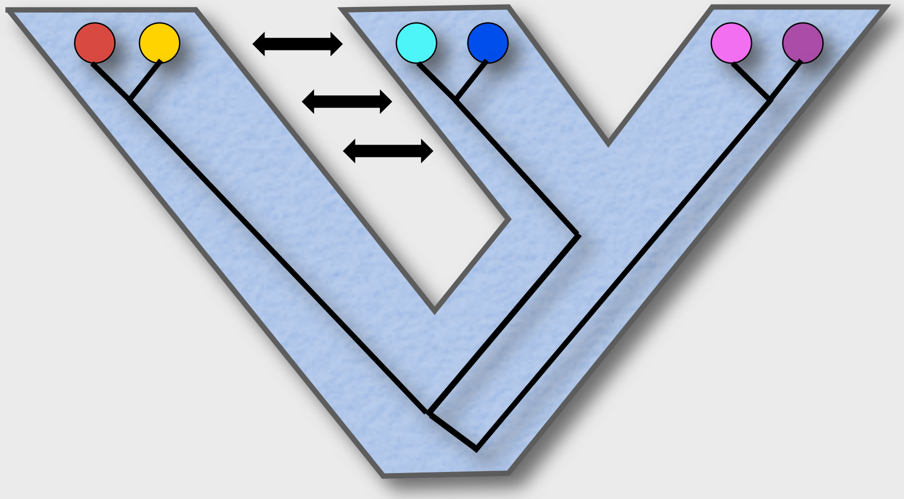
Approximate Likelihood

```
sample parameters ~~(or models)~~ from ~~prior~~ guesses
for (many reps) {
     ~~sample parameters (or models) from prior~~
     simulate dataset using these parameters
     if (  topology(dataset) == topology(observed)  ){
          count as match, save these parameters
     }
}

plot(saved parameters) #or other way to summarize
```



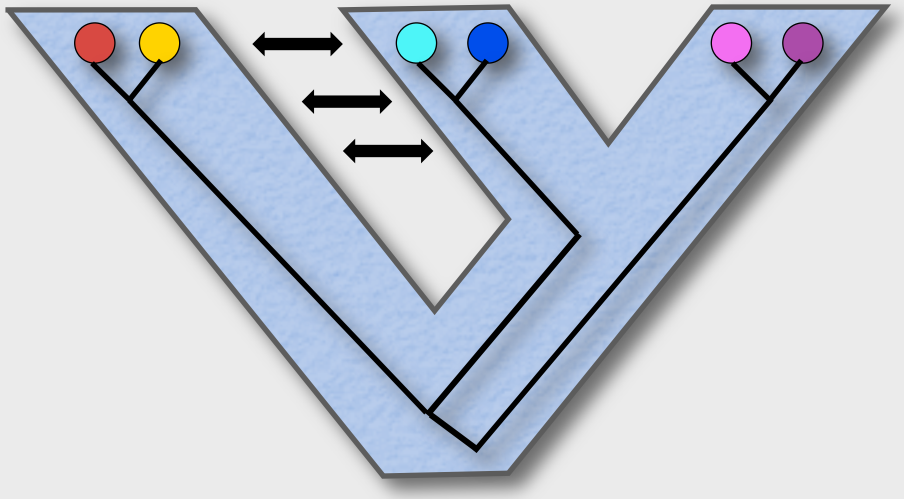
Approximate Likelihood

```
sample parameters ~~(or models)~~ from ~~prior~~ guesses
for (many reps) {
     ~~sample parameters (or models) from prior~~
     simulate dataset using these parameters
     if (  topology(dataset) == topology(observed)  ){
          count as match~~, save these parameters~~
     }
}

plot(saved parameters) #or other way to summarize
```



Approximate Likelihood

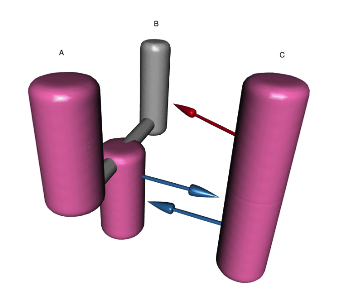
```
sample parameters ~~(or models)~~ from ~~prior~~ guesses
for (many reps) {
      ~~sample parameters (or models) from prior~~
      simulate dataset using these parameters
      if (  topology(dataset) == topology(observed)  ){
            count as match~~, save these parameters~~
      }
}

Likelihood ≡ prob(topology(observed)| parameters)
```



Approximate Likelihood

```
sample parameters (or models) from prior guesses
for (many reps) {
    sample parameters (or models) from prior
    simulate dataset using these parameters
    if ( topology(dataset) == topology(observed) ){
        count as match, save these parameters
    }
}

Likelihood = prob(topology(observed)| parameters) ≈ #matches / #reps
```

Approximate Bayesian Computation	**Approximate Likelihood**
Summary stats as functions of the data	Topologies (= the data)
Simulation	Simulation
Approximate match	Exact match
Priors	Starting values, but optimize
Integration	Maximum

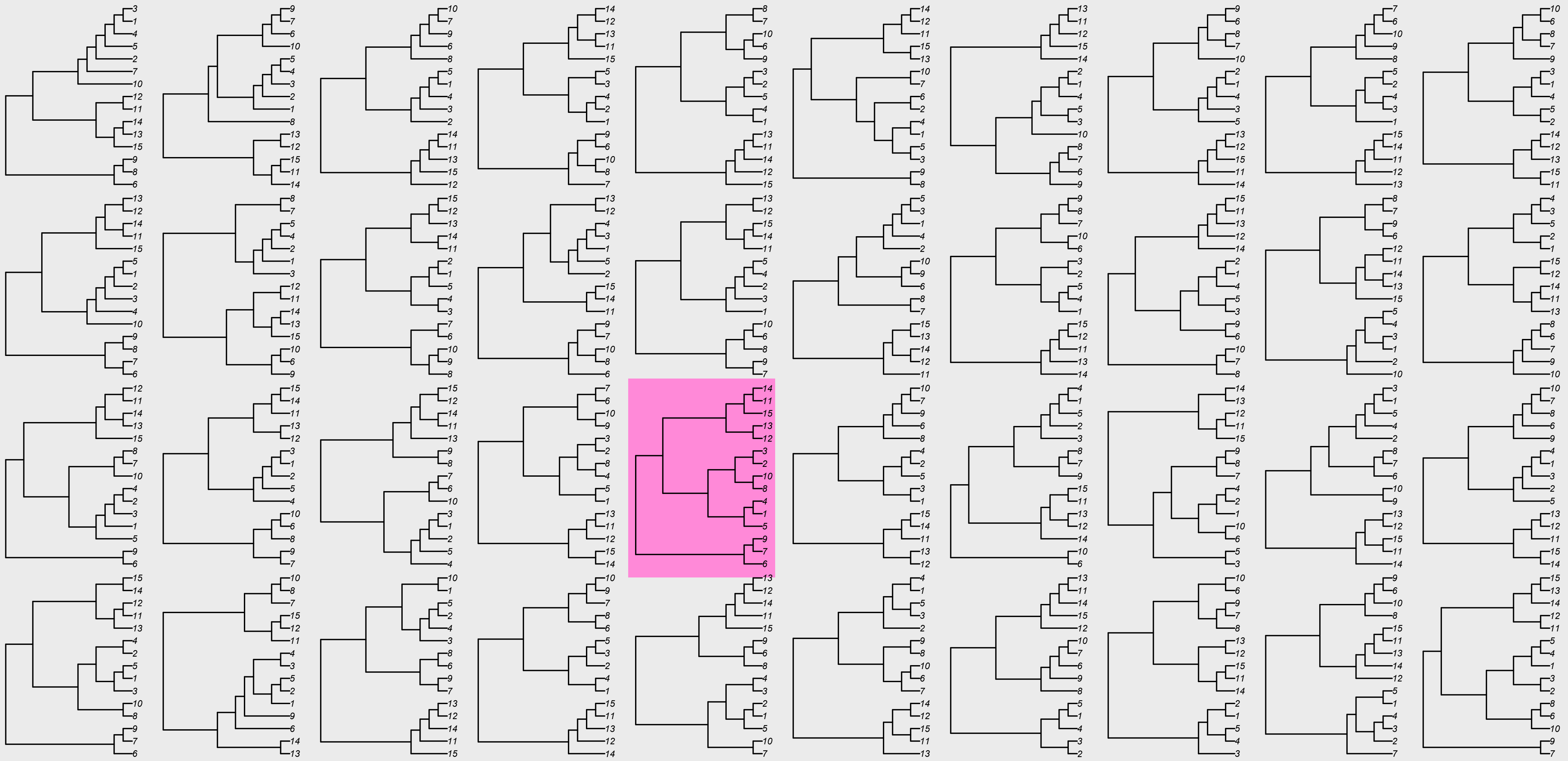


Collapse 1	Pop size 1	Pop size 2	Migration 1	Migration 2
4	1	3	0.2	0.6

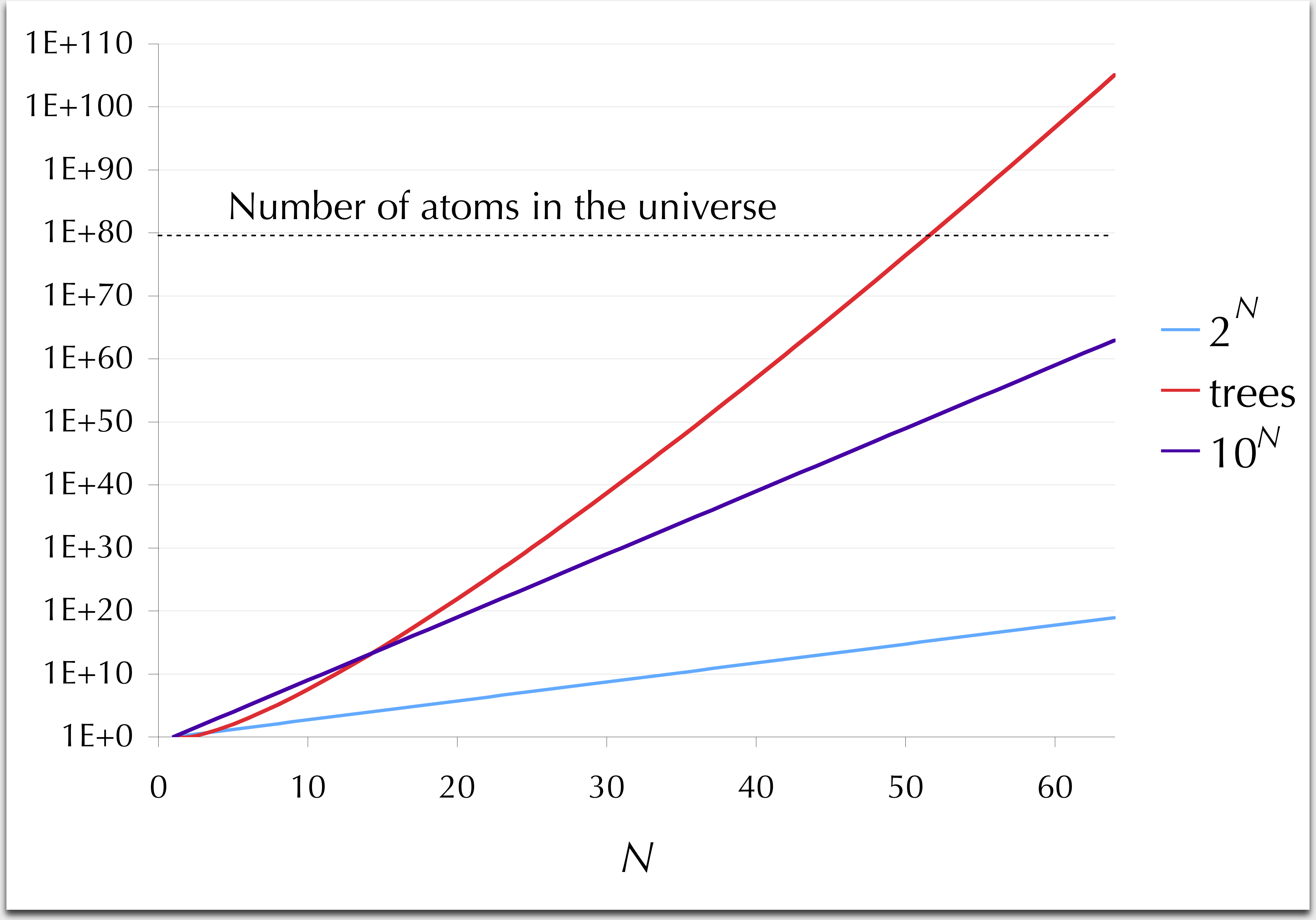
Generate 100,000 trees, three populations, five samples per population (~5 sec):

```
ms 15 100000 -T -I 3 5 5 5  -n 1 1.0 -n 2 3.0 -n 3 3.0 -ma x 0.0 0.0 0.2 x 0.0 0.0 0.0 x
     -ej 4.0 3 1 -en 4.0 1 3.0 -en 4.0 2 3.0 -em 4.0 1 2 0.6 -em 4.0 2 1 0.6
```

ms (Hudson 2002)

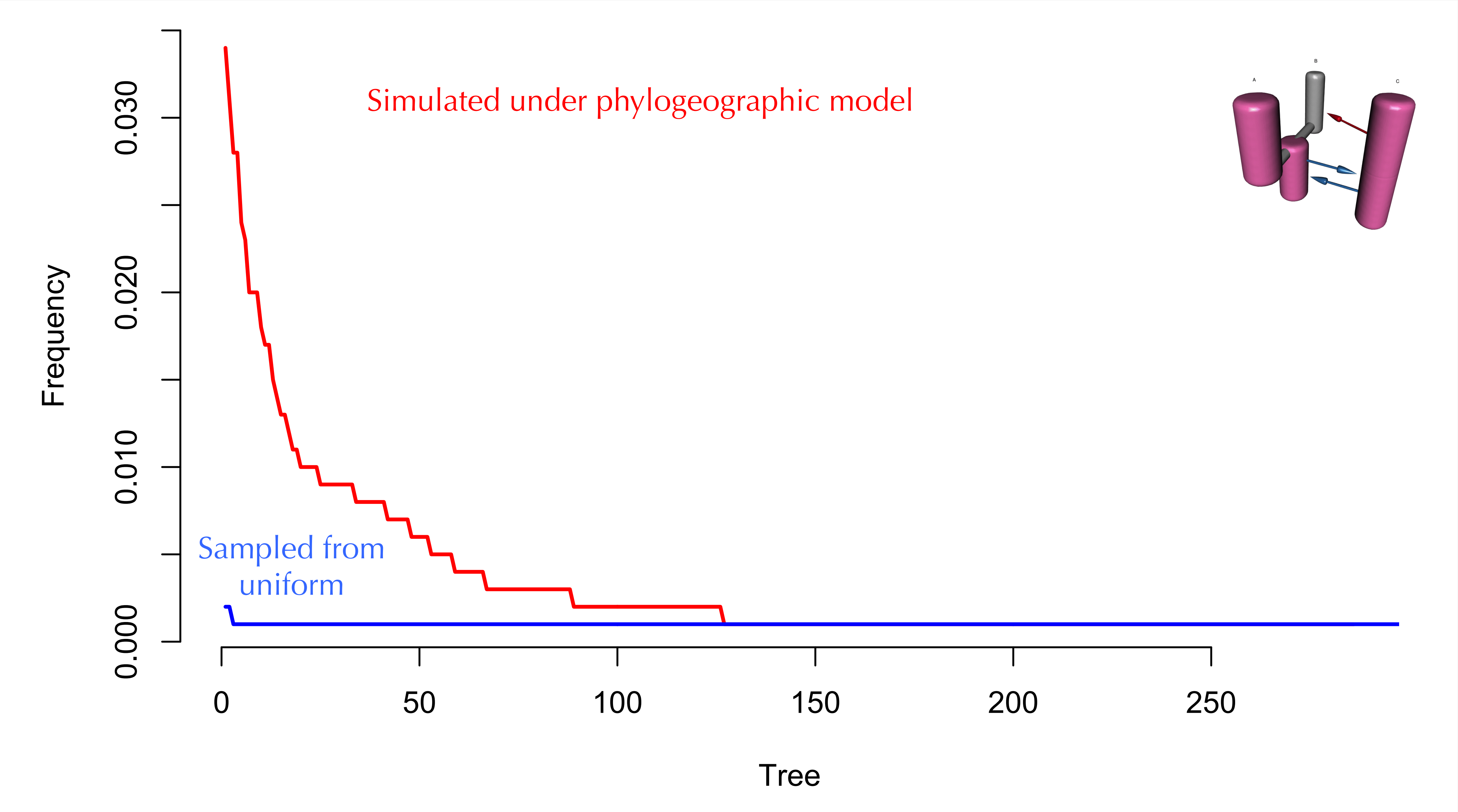


A dumb idea?


1E+110
1E+100
1E+90
1E+80
1E+70
1E+60
1E+50
1E+40
1E+30
1E+20
1E+10
1E+0
Number of atoms in the universe
0
10
20
30
40
50
60
N
2^N
trees
10^N

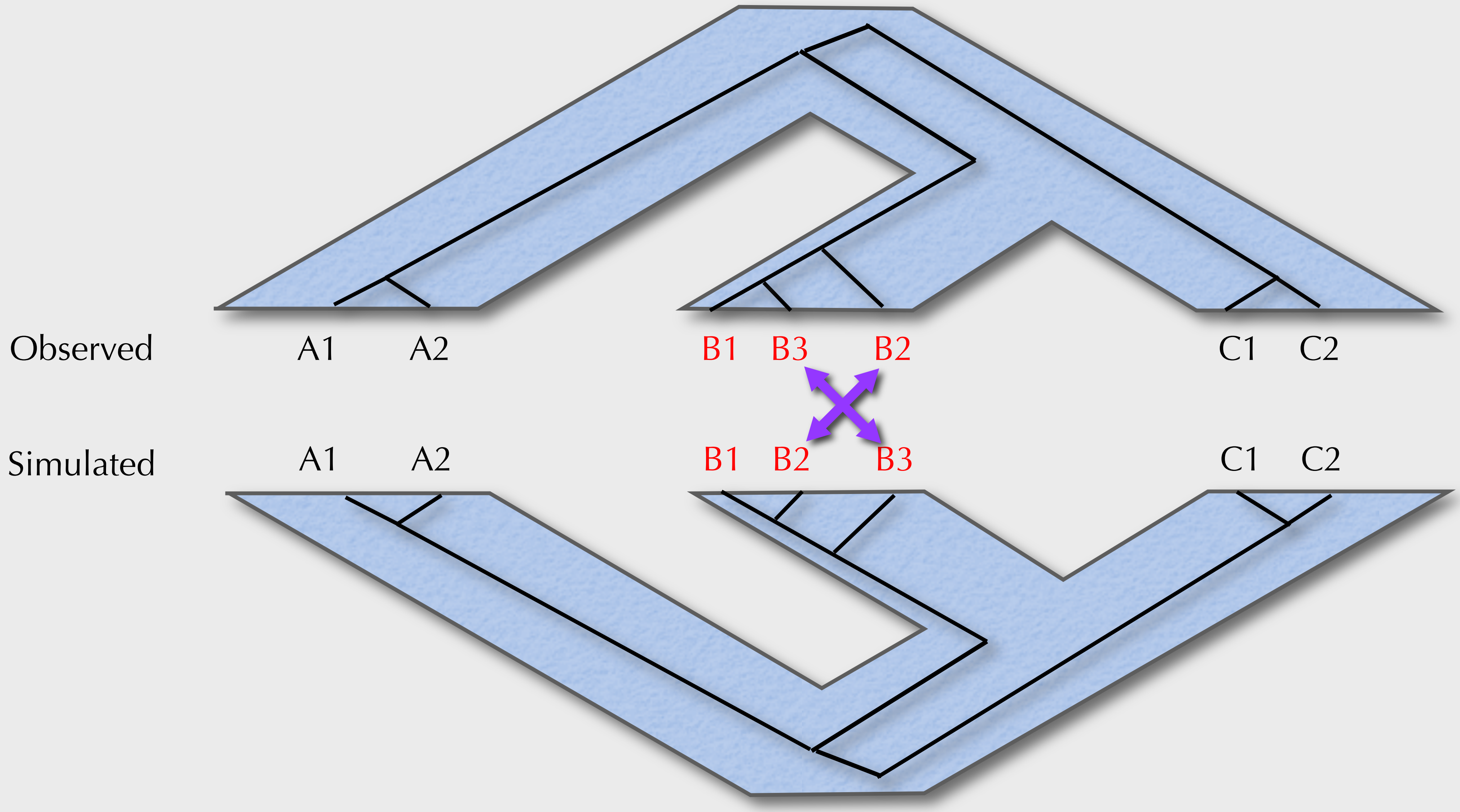
A dumb idea?

Tree probabilities not uniform (some trees *much* more likely than others)



A dumb idea?

Clever idea 1: Sample labels within populations arbitrary

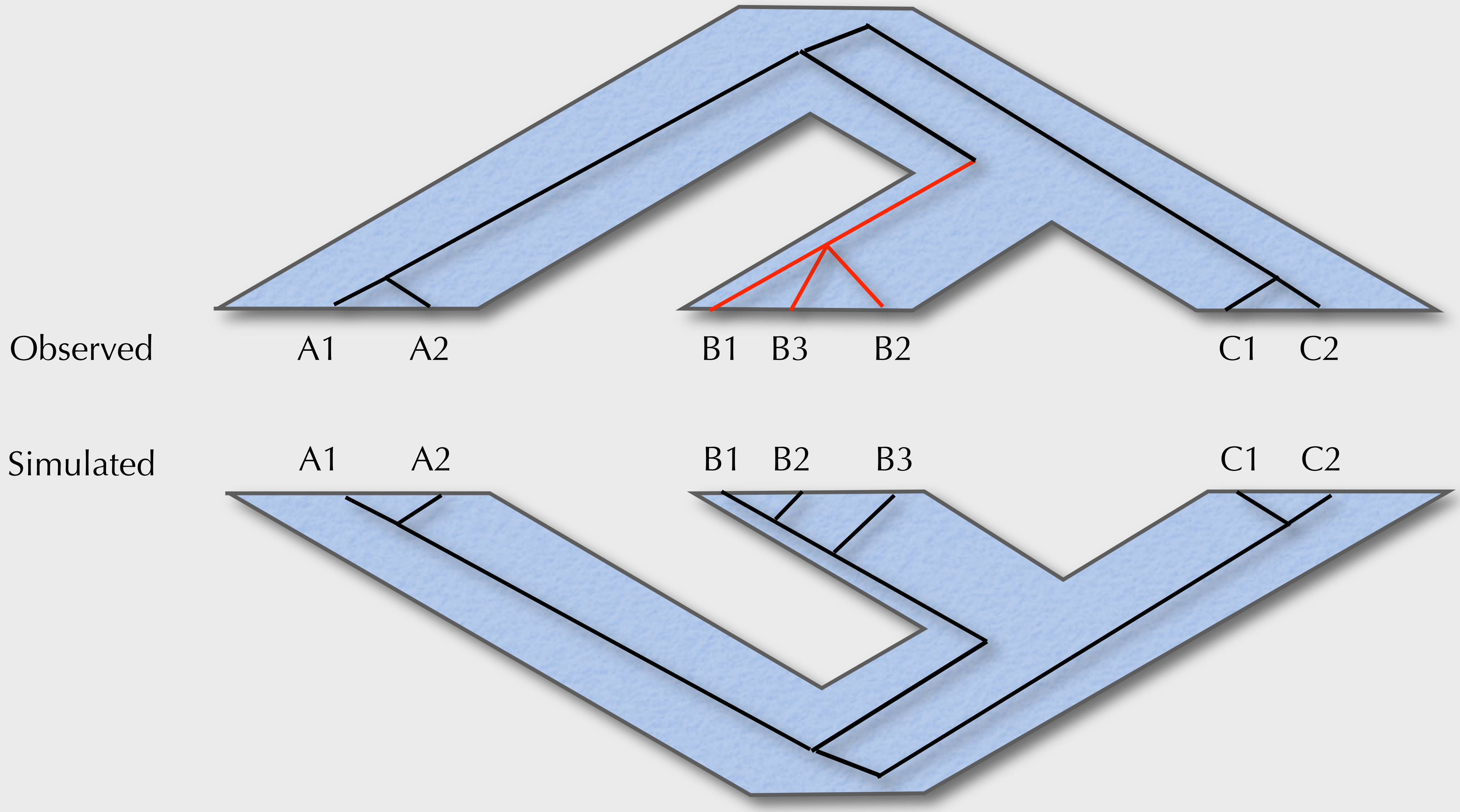


Match based on all possible labeling, then correct for this

i.e., three possible permutations, so if there is a match divide by 3 to get probability

A dumb idea?

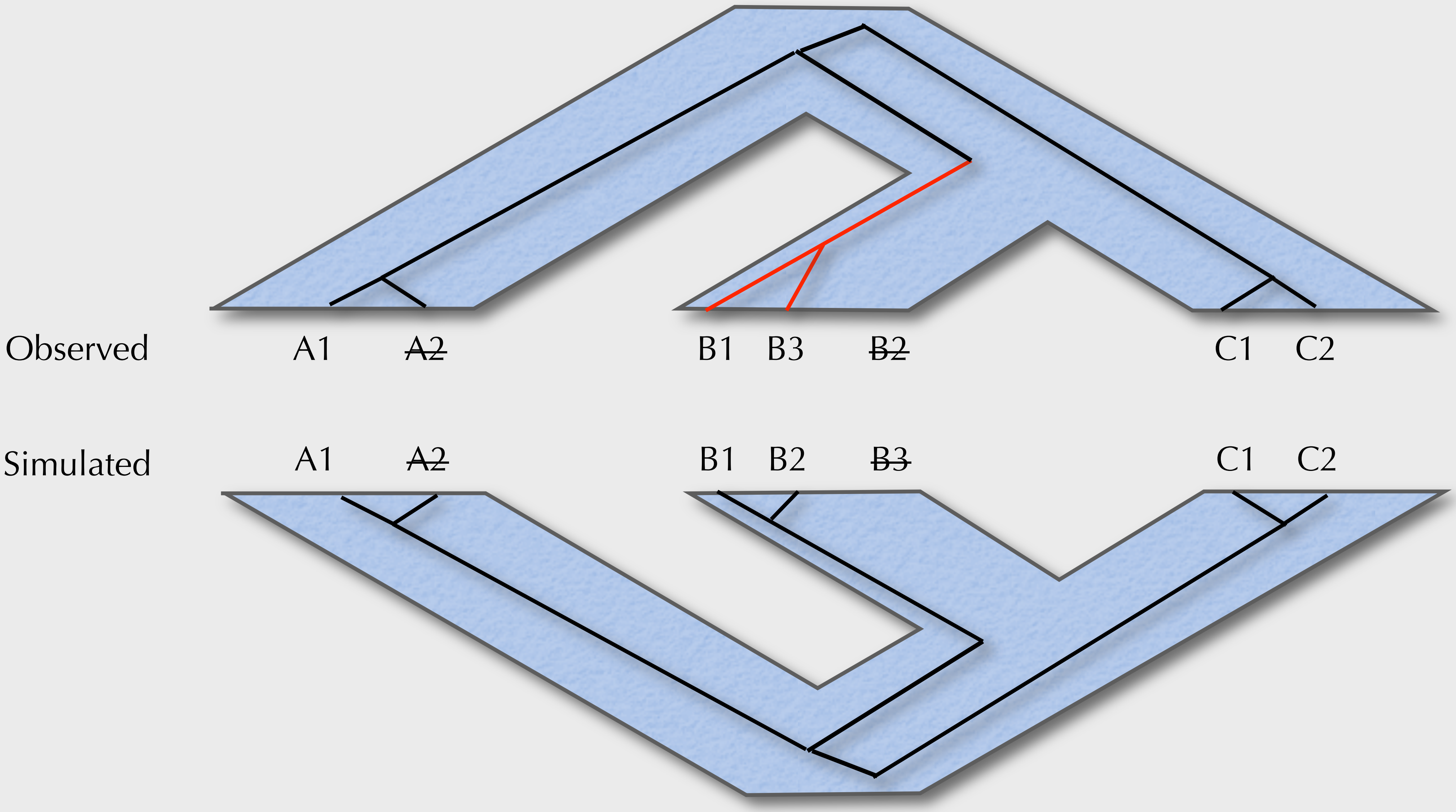
Clever idea 2: Polytomies are soft in gene trees (optional)



Match based on all possible resolutions, then correct for this

A dumb idea?

Clever idea 3: Subsample



Reduce the gene tree size (speed gain, precision loss)

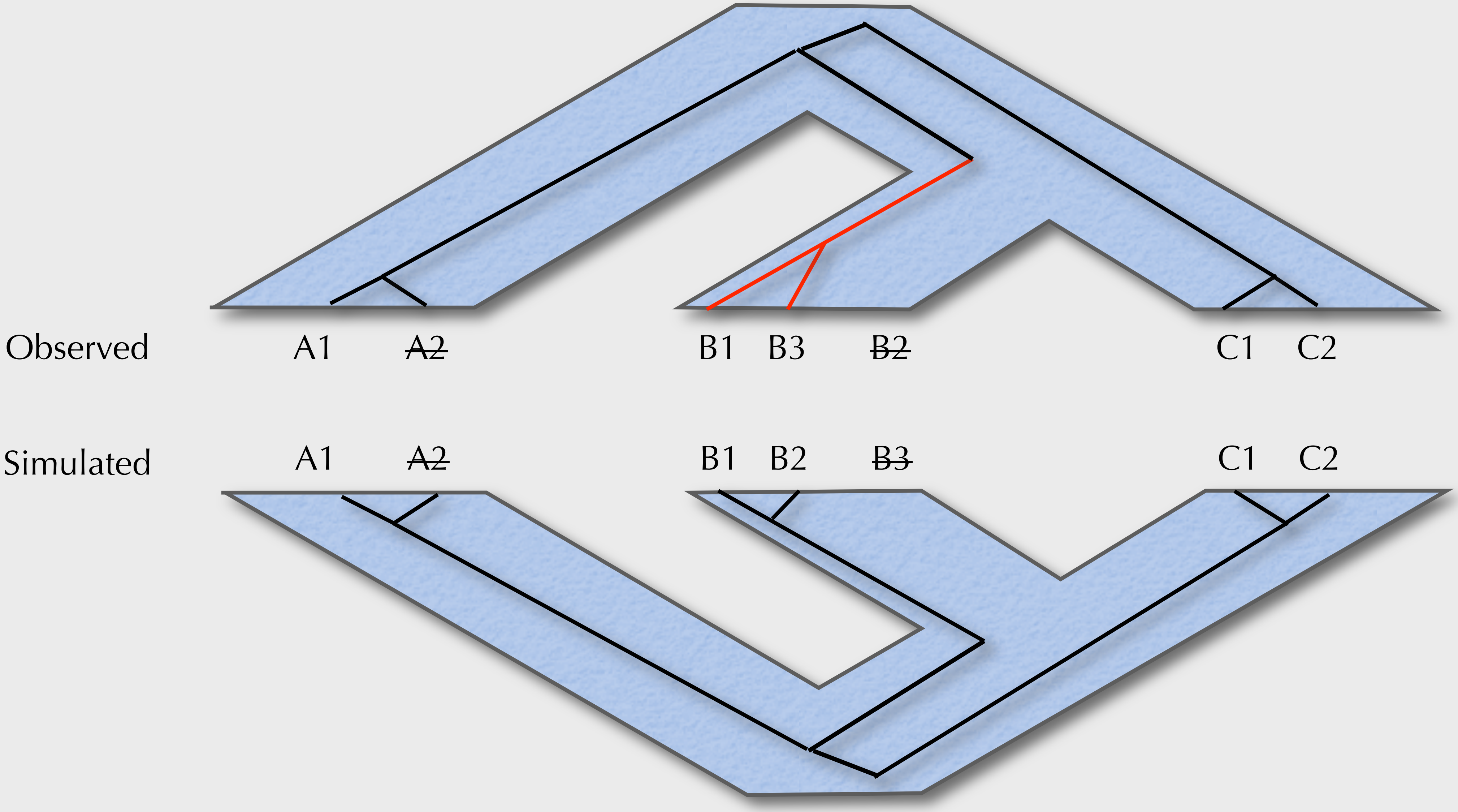
A dumb idea?

Clever idea 4: Do many empirical loci, some are the same

The run time should increase linearly or better with number of gene trees.

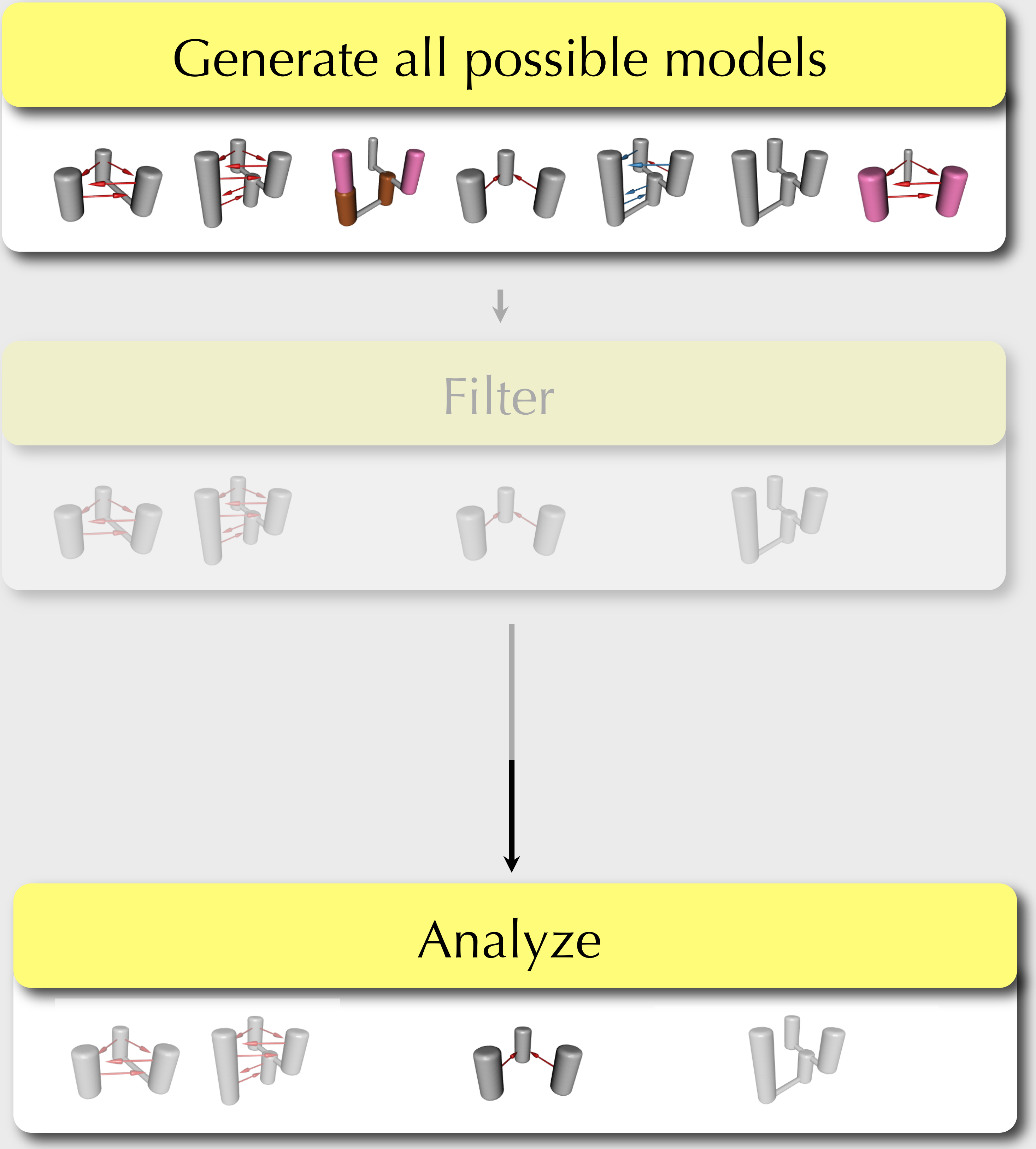
A dumb idea?

Clever idea 5: Your suggestion.....



Grows (quickly) with number of populations

Grows quickly with number of samples per population, but only linearly with number of genes



Simulate gene trees

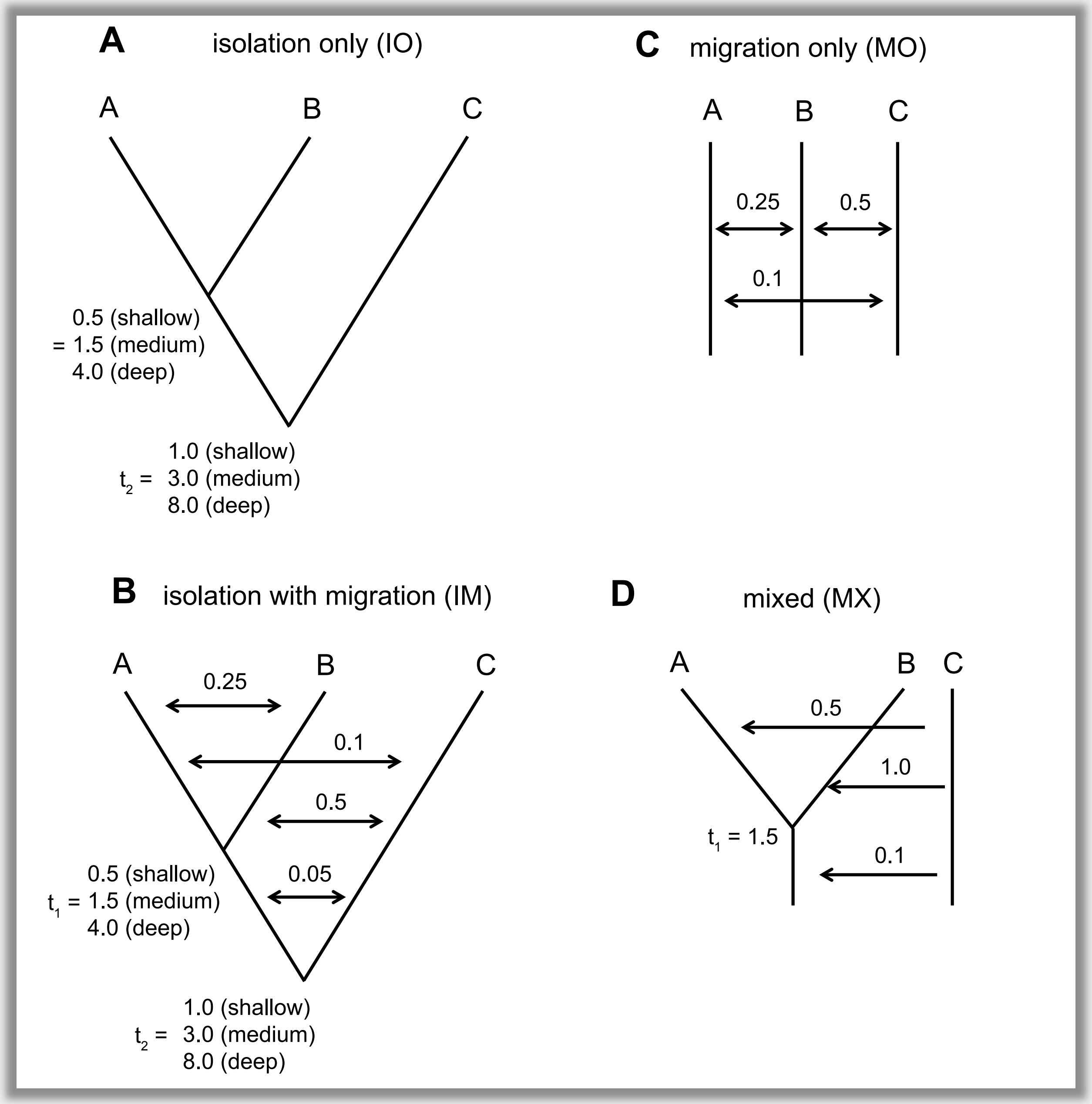
Simulate DNA

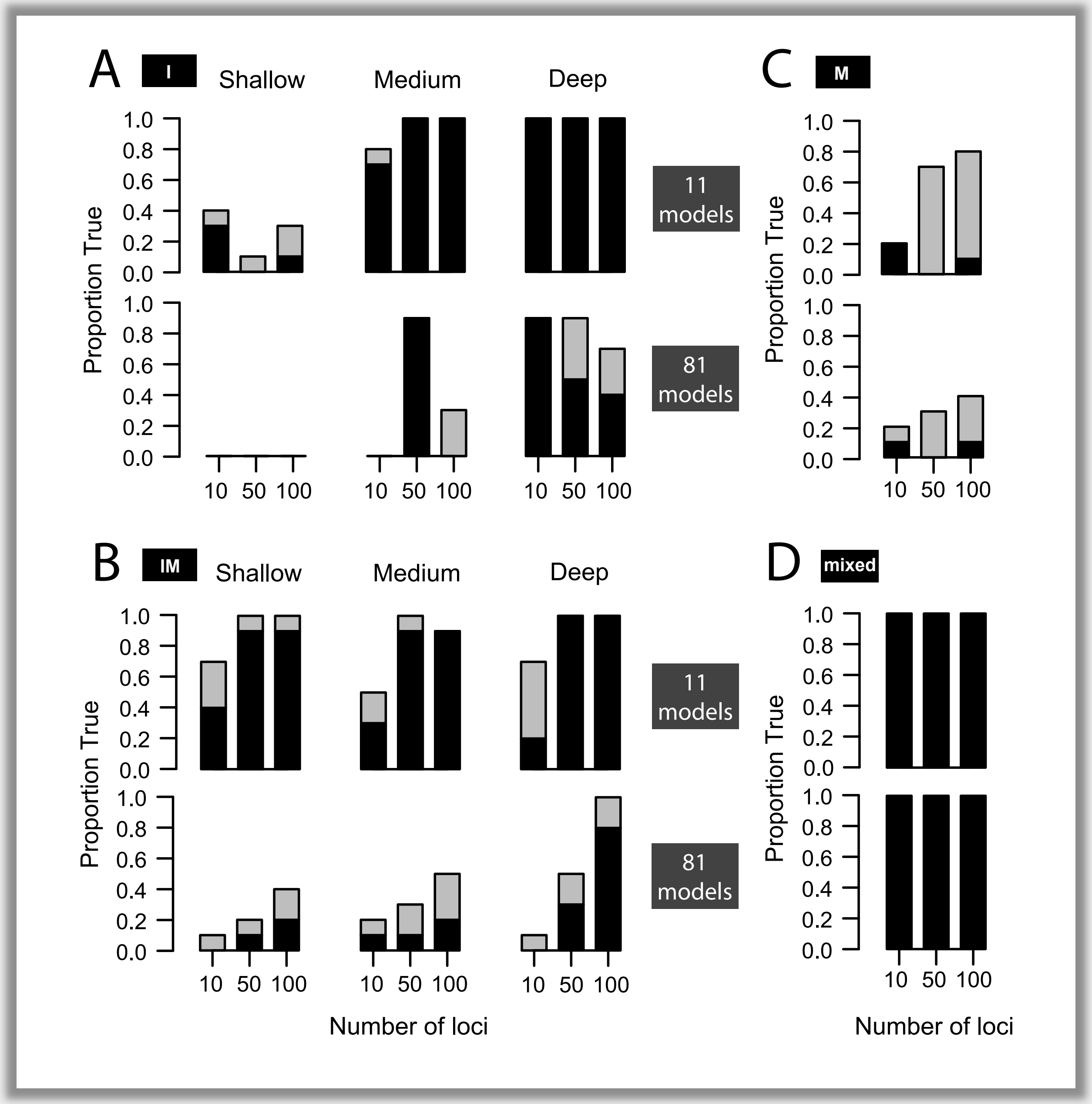
Infer gene trees

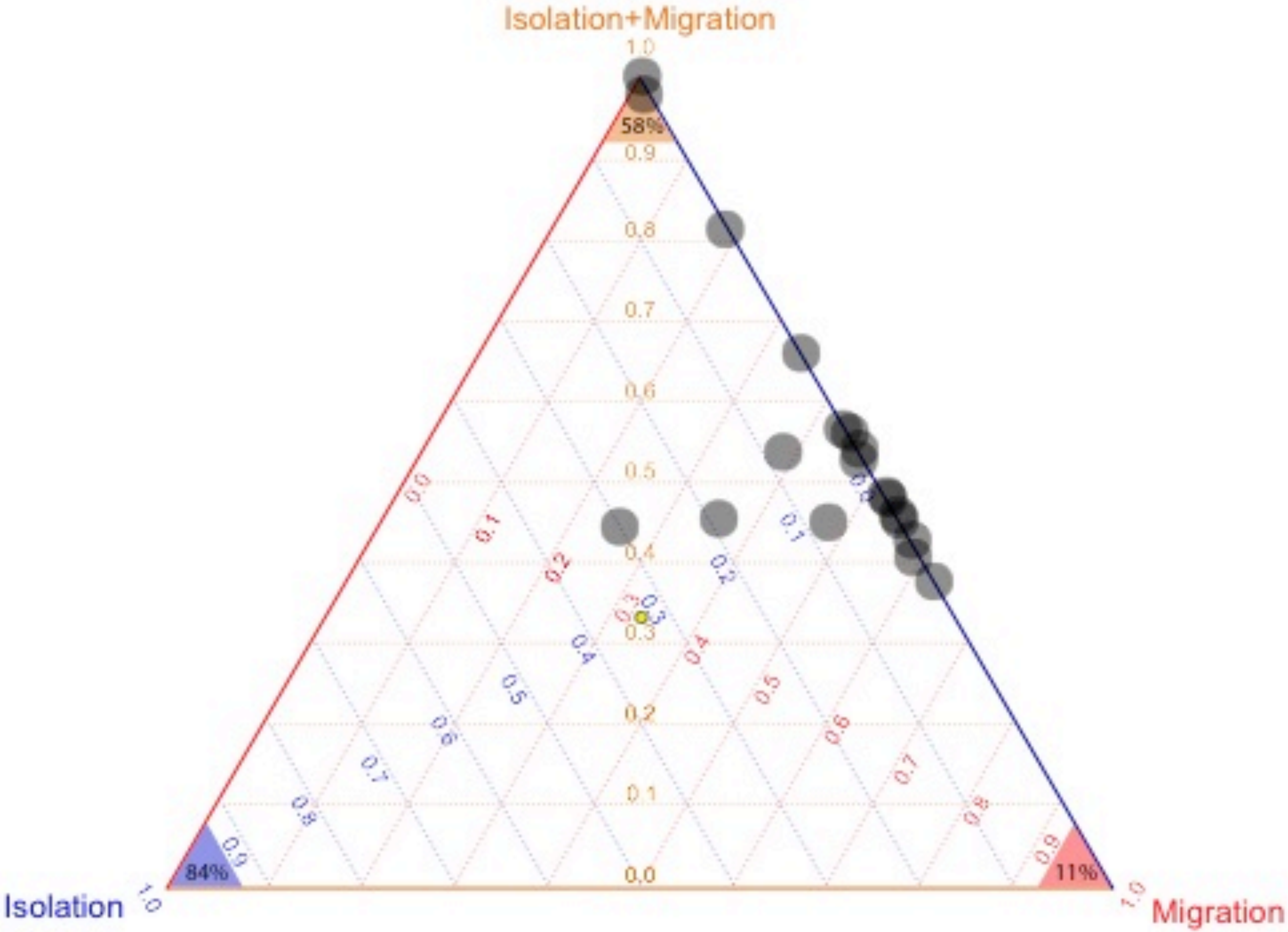
Run PHRAPL

True model

Inferred model






Isolation+Migration
Isolation
Migration
58%
84%
11%
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0

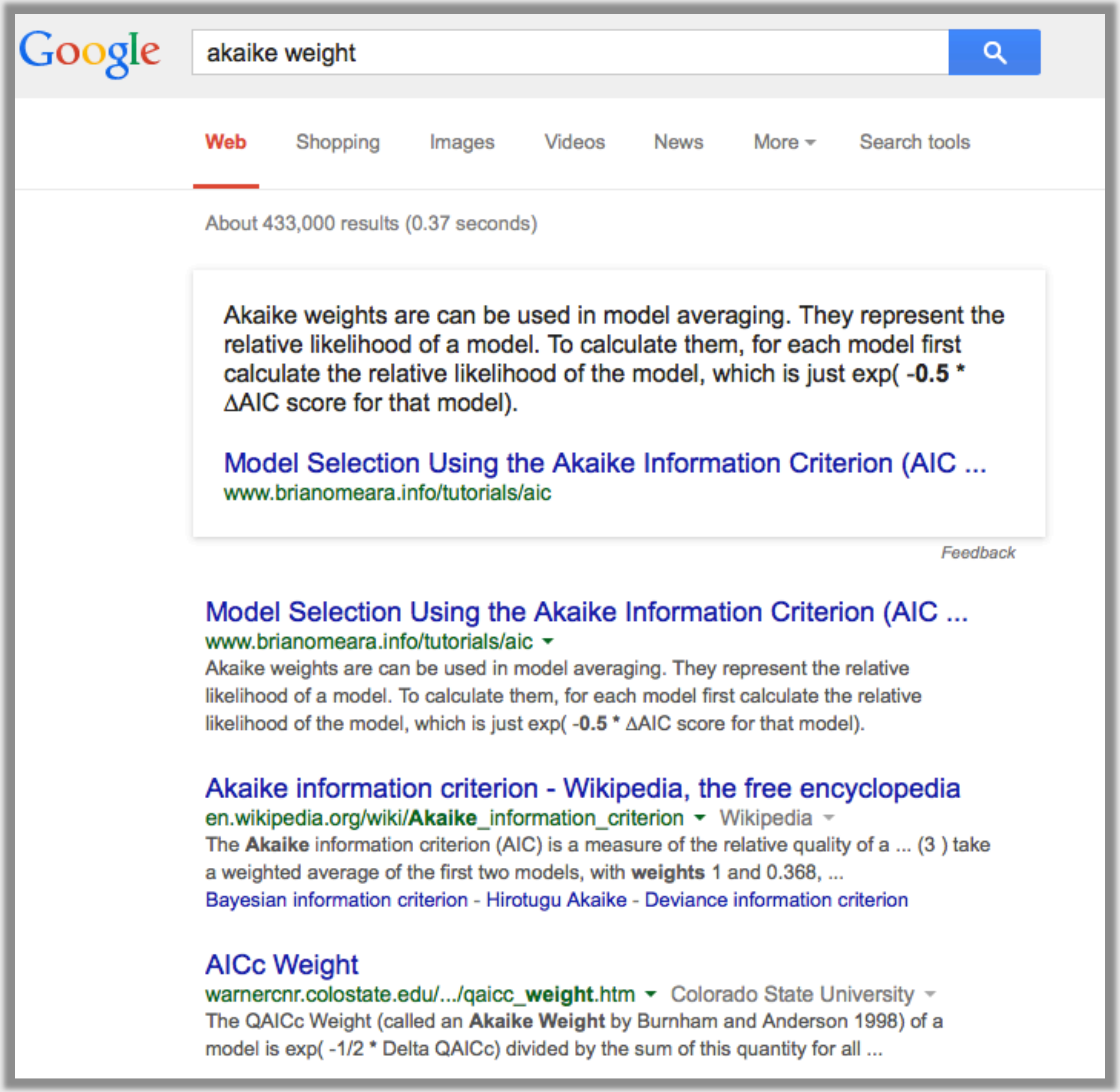
Summary

- Way to create many models
- Evaluate many models
- Prior free, but complementary with other approaches
- Should scale better than linearly with gene number (due to multiple identical histories)

Conclusion

- Addressed questions about how species move through landscapes, what limits rates of evolution, predictability of evolution, competition between organisms, and more
- Creation of methods and open software to deal with rate heterogeneity for discrete characters, more flexible ways of dealing with continuous characters, simulating millions of species, examining correlations, and much more
- Taught hundreds of students to think critically and to understand science as a process
- Mentored 4 students and 10 postdocs
- 28 grant proposals (including 16 full and 5 preproposals to NSF), $1.4M in external funds
- Service in improving representation of women in science, Darwin Day outreach, numerous workshops, hackathons, and conferences

End



akaike weight

About 433,000 results (0.37 seconds)

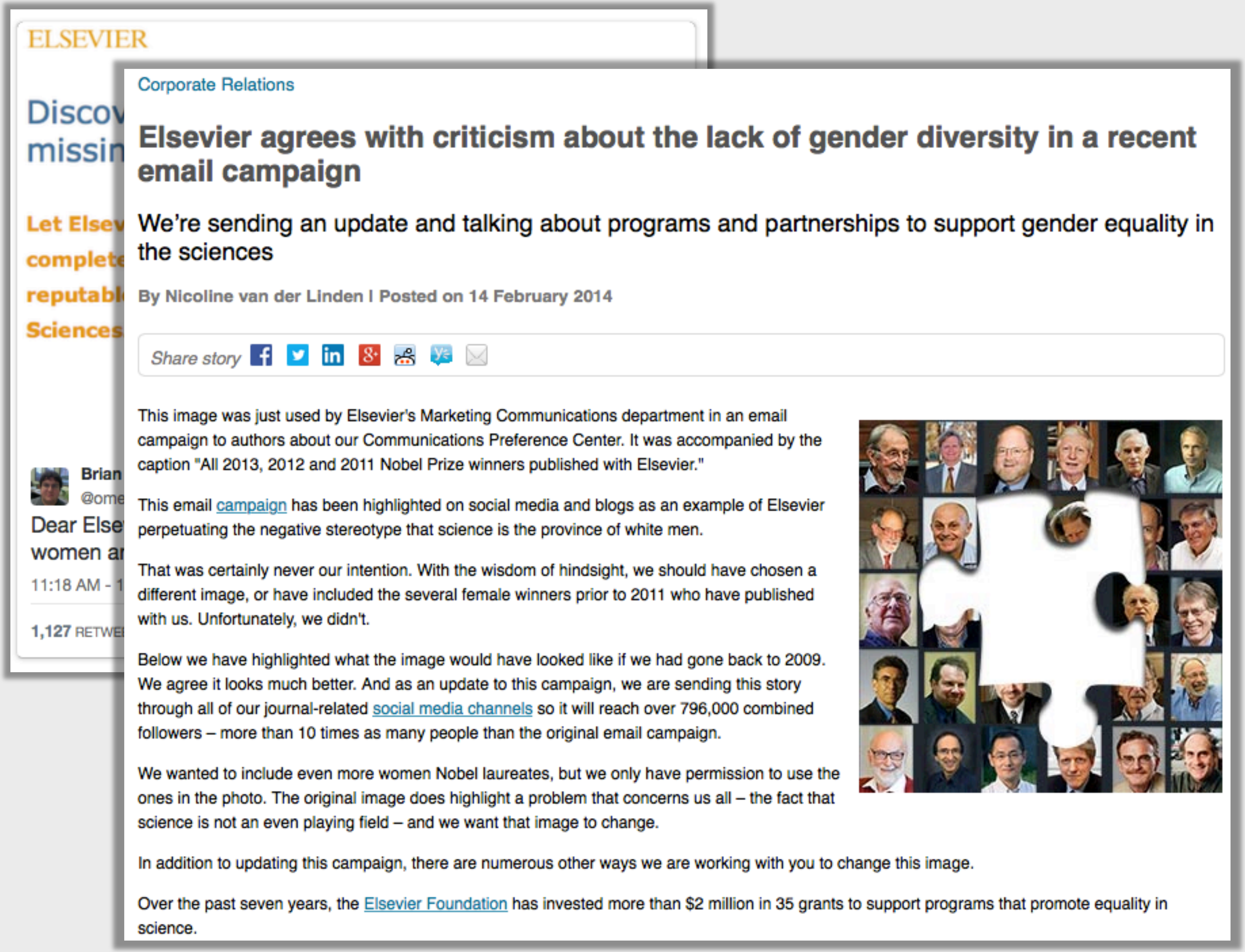
Akaike weights are can be used in model averaging. They represent the relative likelihood of a model. To calculate them, for each model first calculate the relative likelihood of the model, which is just exp(**-0.5** * ΔAIC score for that model).

Model Selection Using the Akaike Information Criterion (AIC ...
www.brianomeara.info/tutorials/aic

Model Selection Using the Akaike Information Criterion (AIC ...
www.brianomeara.info/tutorials/aic
Akaike weights are can be used in model averaging. They represent the relative likelihood of a model. To calculate them, for each model first calculate the relative likelihood of the model, which is just exp(**-0.5** * ΔAIC score for that model).

Akaike information criterion - Wikipedia, the free encyclopedia
en.wikipedia.org/wiki/**Akaike**_information_criterion Wikipedia
The **Akaike** information criterion (AIC) is a measure of the relative quality of a ... (3) take a weighted average of the first two models, with **weights** 1 and 0.368, ...
Bayesian information criterion - Hirotugu Akaike - Deviance information criterion

AICc Weight
warnercnr.colostate.edu/.../qaicc_**weight**.htm Colorado State University
The QAICc Weight (called an **Akaike Weight** by Burnham and Anderson 1998) of a model is exp(-1/2 * Delta QAICc) divided by the sum of this quantity for all ...



ELSEVIER

Discov
missin

Let Else
complete
reputabl
Sciences

Brian
@ome

Dear Else
women ar

11:18 AM - 1

1,127 RETWE

Corporate Relations

Elsevier agrees with criticism about the lack of gender diversity in a recent email campaign

We're sending an update and talking about programs and partnerships to support gender equality in the sciences

By Nicoline van der Linden | Posted on 14 February 2014

Share story

This image was just used by Elsevier's Marketing Communications department in an email campaign to authors about our Communications Preference Center. It was accompanied by the caption "All 2013, 2012 and 2011 Nobel Prize winners published with Elsevier."

This email campaign has been highlighted on social media and blogs as an example of Elsevier perpetuating the negative stereotype that science is the province of white men.

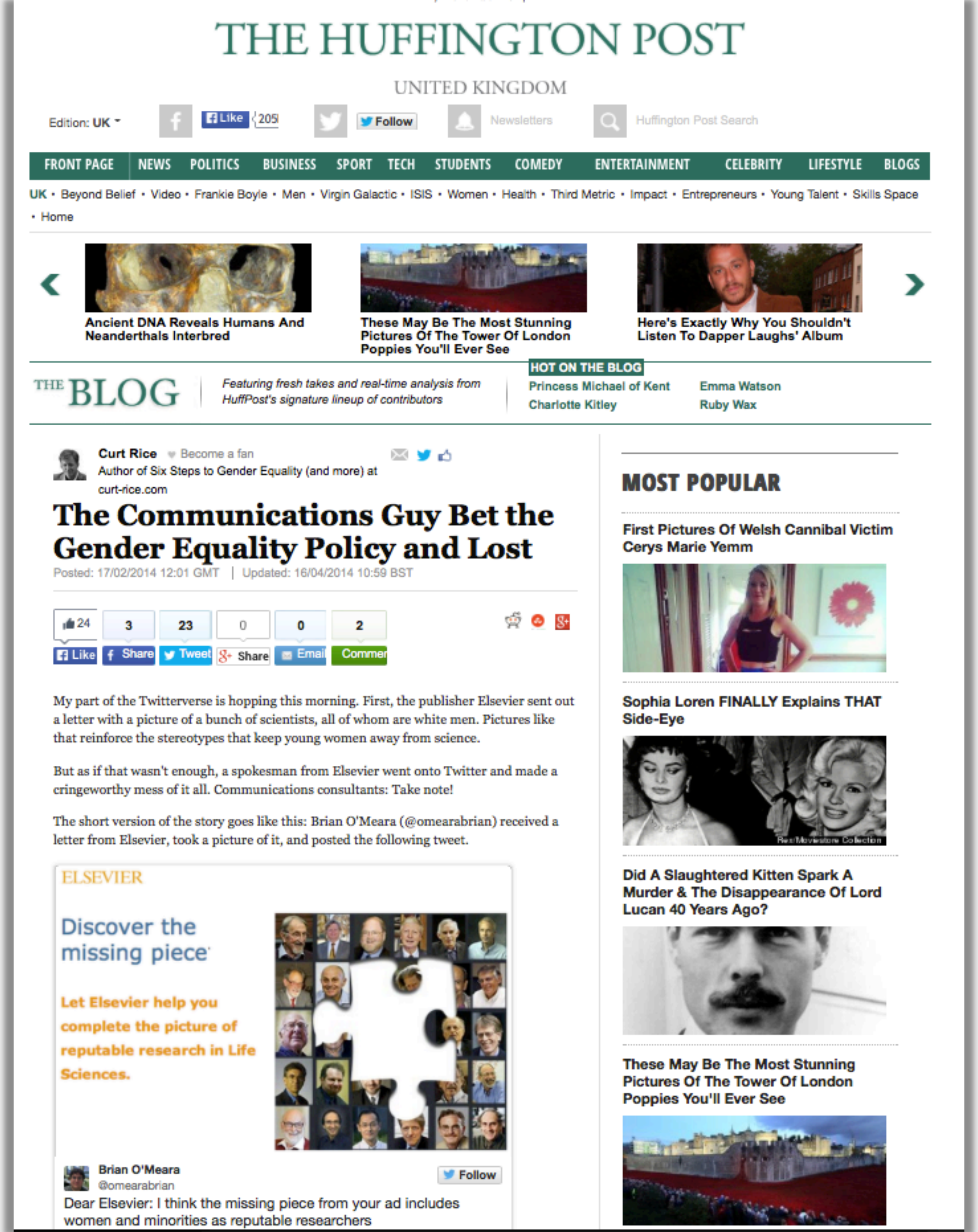
That was certainly never our intention. With the wisdom of hindsight, we should have chosen a different image, or have included the several female winners prior to 2011 who have published with us. Unfortunately, we didn't.

Below we have highlighted what the image would have looked like if we had gone back to 2009. We agree it looks much better. And as an update to this campaign, we are sending this story through all of our journal-related social media channels so it will reach over 796,000 combined followers – more than 10 times as many people than the original email campaign.

We wanted to include even more women Nobel laureates, but we only have permission to use the ones in the photo. The original image does highlight a problem that concerns us all – the fact that science is not an even playing field – and we want that image to change.

In addition to updating this campaign, there are numerous other ways we are working with you to change this image.

Over the past seven years, the Elsevier Foundation has invested more than $2 million in 35 grants to support programs that promote equality in science.



THE HUFFINGTON POST

UNITED KINGDOM

Edition: UK ˅ Like 205 Follow Newsletters Huffington Post Search

FRONT PAGE NEWS POLITICS BUSINESS SPORT TECH STUDENTS COMEDY ENTERTAINMENT CELEBRITY LIFESTYLE BLOGS

UK • Beyond Belief • Video • Frankie Boyle • Men • Virgin Galactic • ISIS • Women • Health • Third Metric • Impact • Entrepreneurs • Young Talent • Skills Space • Home

Ancient DNA Reveals Humans And Neanderthals Interbred

These May Be The Most Stunning Pictures Of The Tower Of London Poppies You'll Ever See

Here's Exactly Why You Shouldn't Listen To Dapper Laughs' Album

THE BLOG | *Featuring fresh takes and real-time analysis from HuffPost's signature lineup of contributors*

HOT ON THE BLOG
Princess Michael of Kent
Charlotte Kitley
Emma Watson
Ruby Wax

Curt Rice Become a fan
Author of Six Steps to Gender Equality (and more) at curt-rice.com

The Communications Guy Bet the Gender Equality Policy and Lost

Posted: 17/02/2014 12:01 GMT | Updated: 16/04/2014 10:59 BST

24 Like | 3 Share | 23 Tweet | 0 Share | 0 Email | 2 Comment

My part of the Twitterverse is hopping this morning. First, the publisher Elsevier sent out a letter with a picture of a bunch of scientists, all of whom are white men. Pictures like that reinforce the stereotypes that keep young women away from science.

But as if that wasn't enough, a spokesman from Elsevier went onto Twitter and made a cringeworthy mess of it all. Communications consultants: Take note!

The short version of the story goes like this: Brian O'Meara (@omearabrian) received a letter from Elsevier, took a picture of it, and posted the following tweet.

ELSEVIER

Discover the missing piece

Let Elsevier help you complete the picture of reputable research in Life Sciences.

Brian O'Meara
@omearabrian
Follow

Dear Elsevier: I think the missing piece from your ad includes women and minorities as reputable researchers

MOST POPULAR

First Pictures Of Welsh Cannibal Victim Cerys Marie Yemm

Sophia Loren FINALLY Explains THAT Side-Eye

Did A Slaughtered Kitten Spark A Murder & The Disappearance Of Lord Lucan 40 Years Ago?

These May Be The Most Stunning Pictures Of The Tower Of London Poppies You'll Ever See