

# 30<sup>th</sup> Annual Workshop in Molecular Evolution

## Phylogenetic Considerations

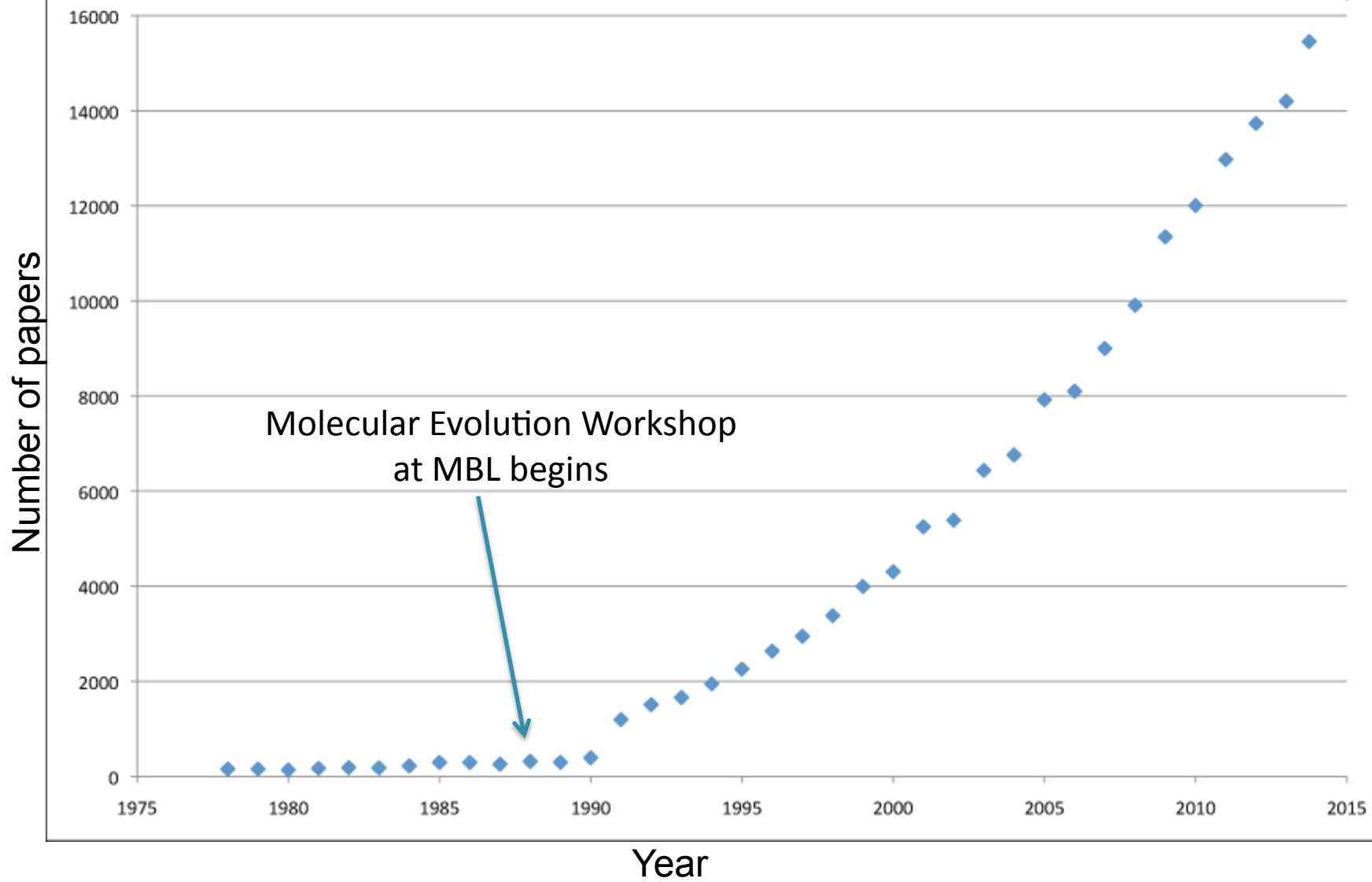
*David M. Hillis, Biodiversity Center,  
University of Texas at Austin*

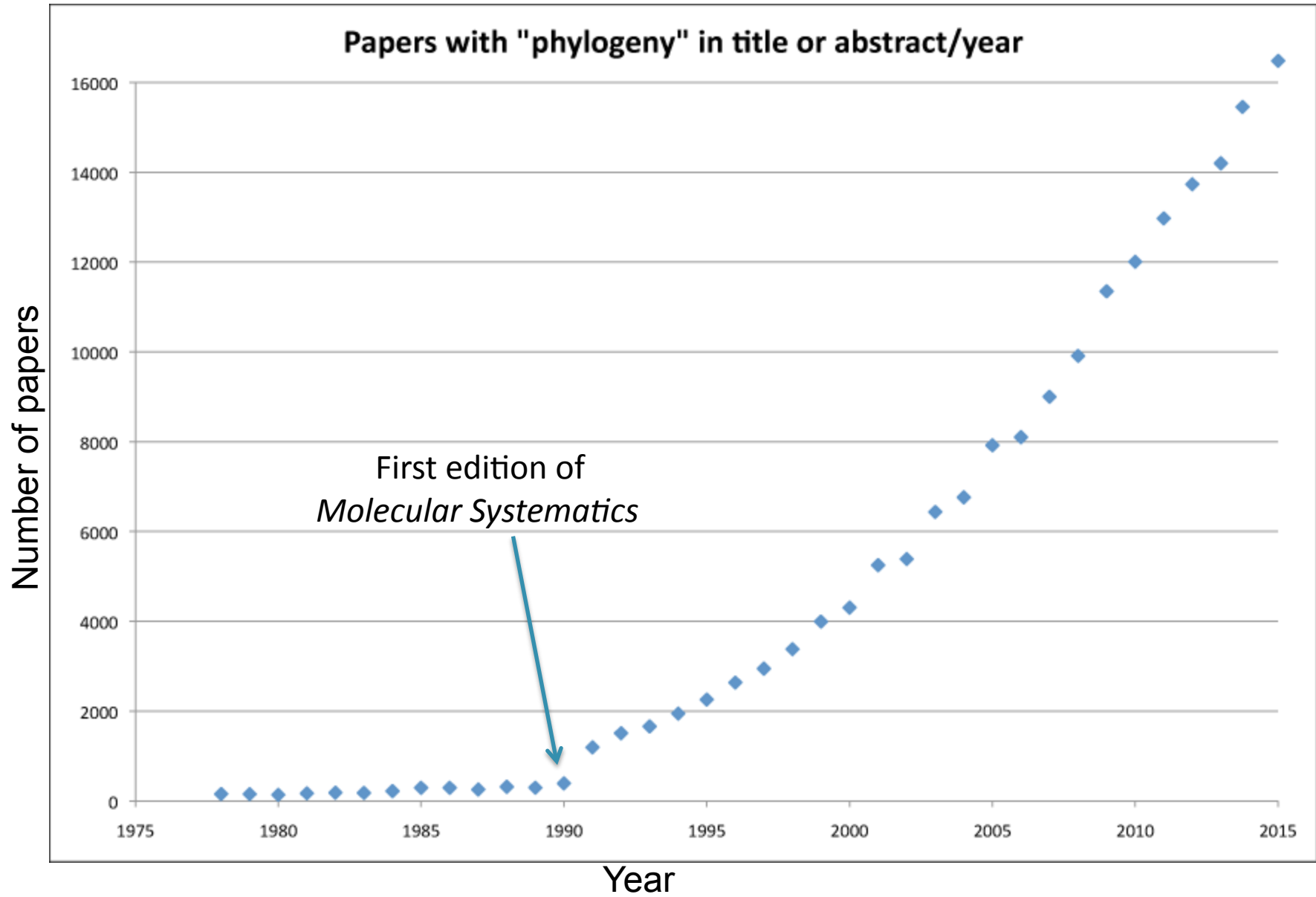
**Marine Biological Lab, Woods Hole  
2017**

# Molecular Evolution

- Using biomolecules to understand evolutionary history and evolutionary processes
- Phylogenetic trees are critical for studying molecular evolution, because many biological phenomena of interest can be modeled as bifurcating processes

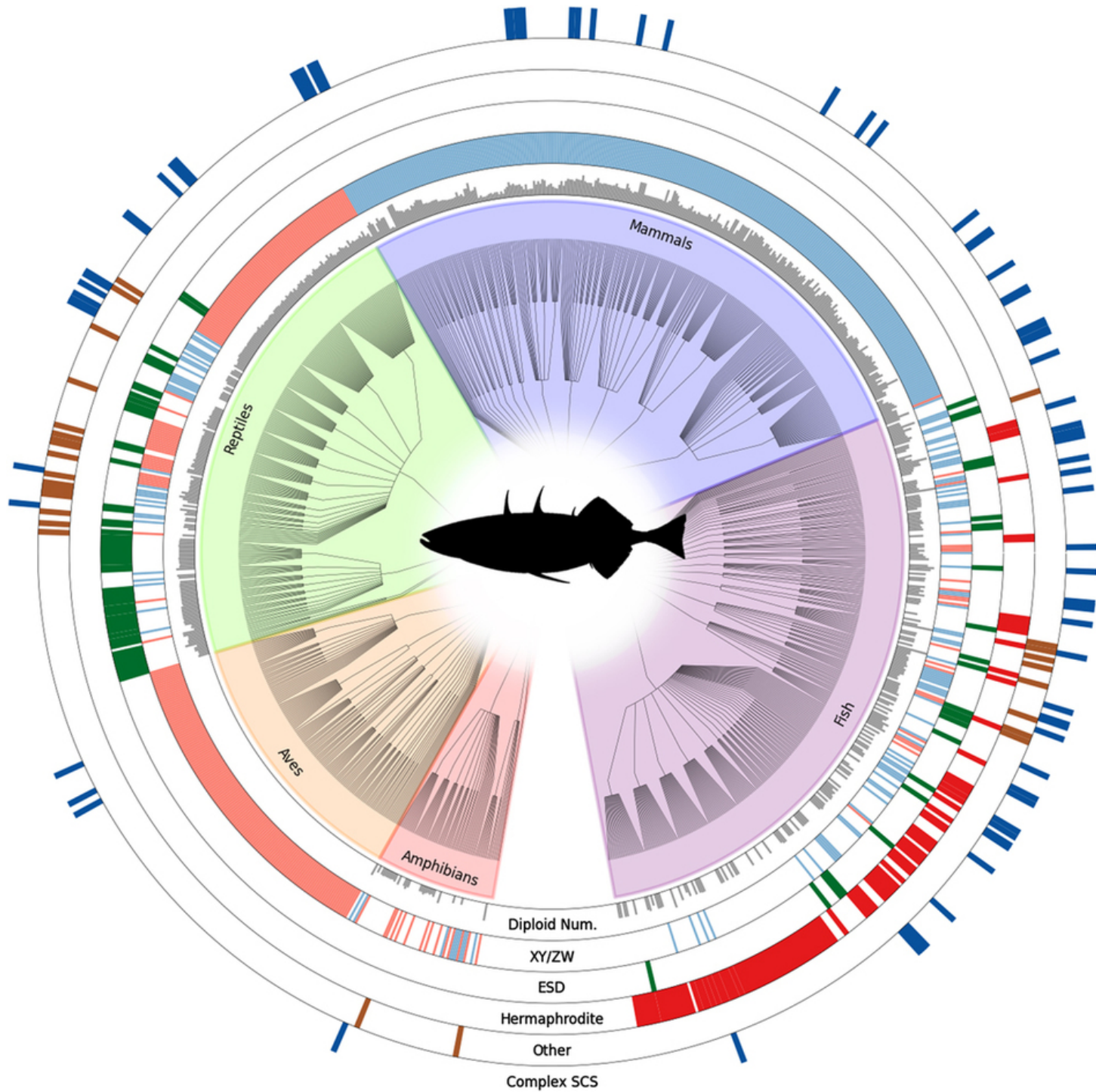
Papers with "phylogeny" in title or abstract/year

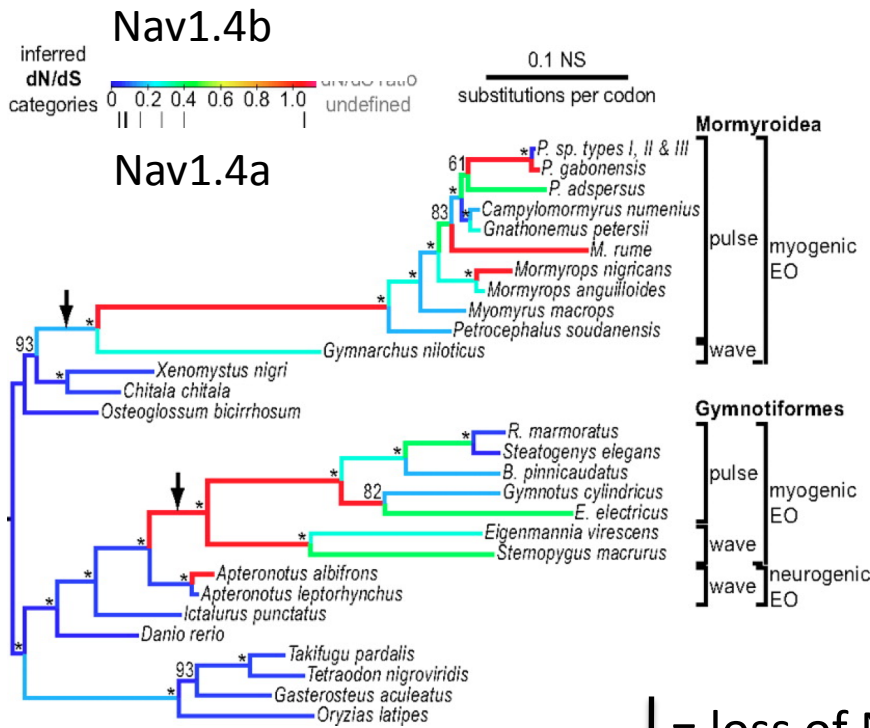
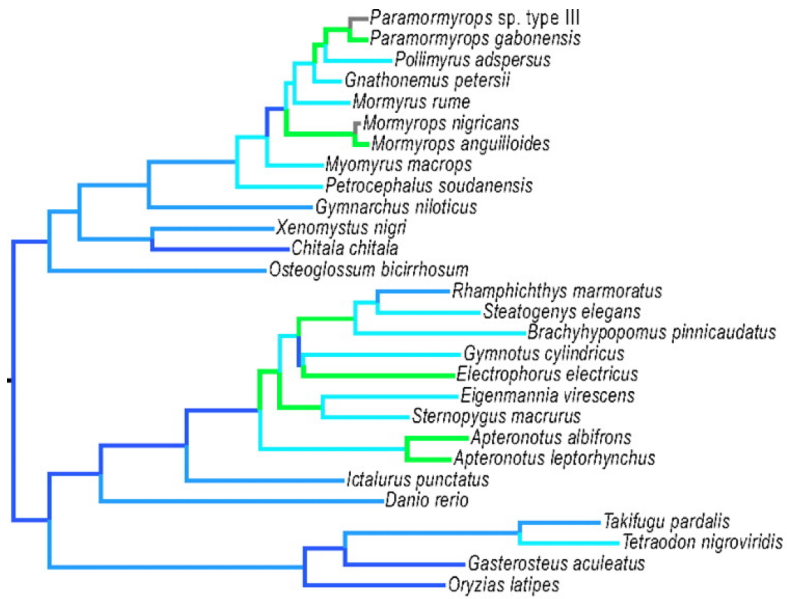




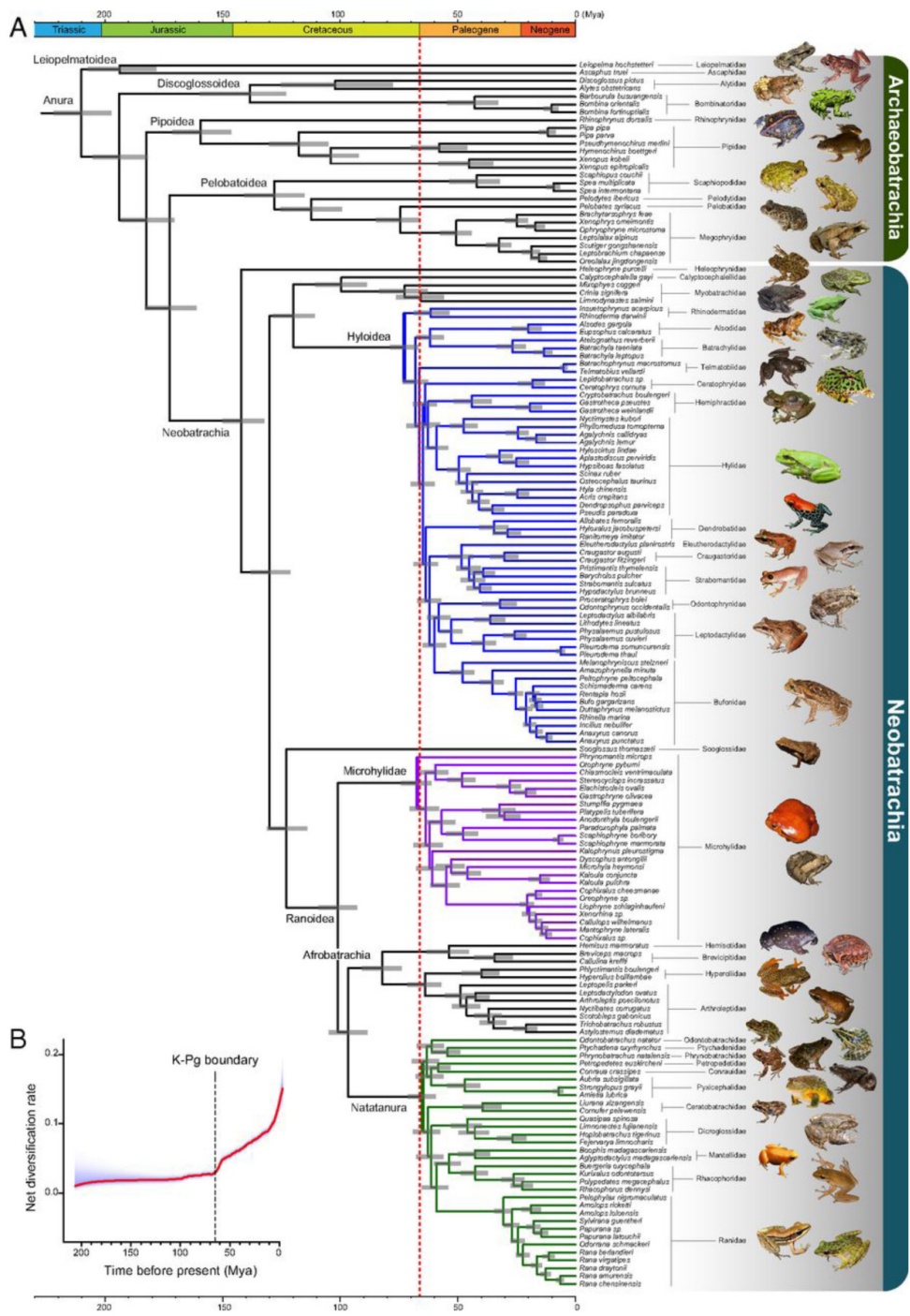
# Major Uses of Phylogenetic Trees

- The relationships are often informative about evolution (where genes came from, how and where viruses are transmitted, the origins of particular structures or processes)
- Trees allow estimation of time for various evolutionary events
- Trees facilitate analysis of evolutionary processes, such as selection, gene flow, and speciation
- Trees allow appropriate comparative biology (identify appropriate comparisons)
- Trees are informative about ancestral states and state transitions
- Trees are informative about species delimitation and biogeography





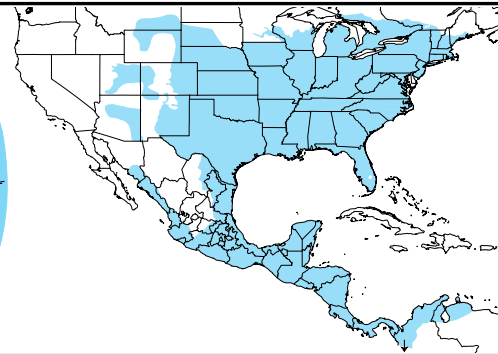
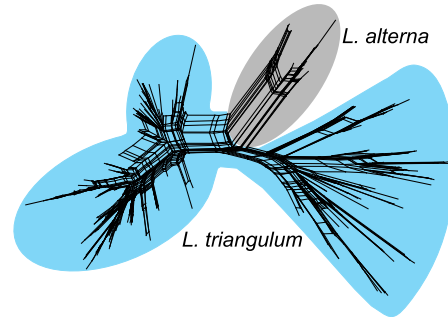
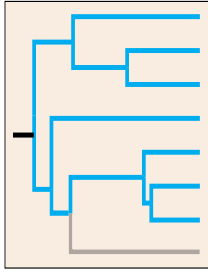
↓ = loss of Nav1.4a expression in muscle



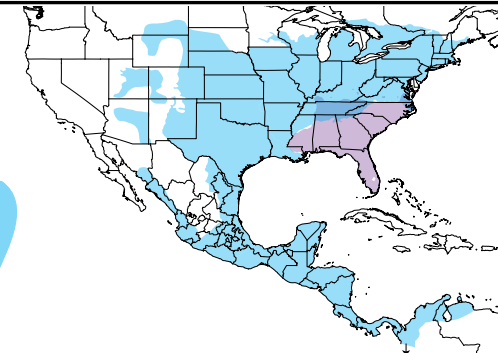
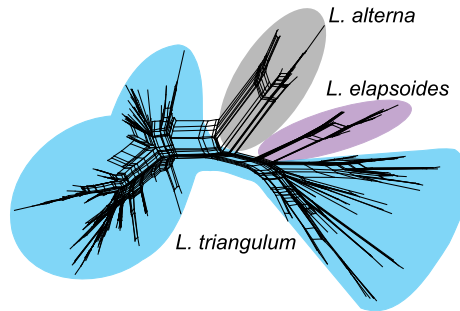
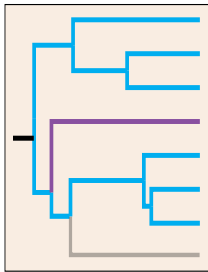
Yan-Jie Feng et al. PNAS doi:10.1073/pnas.1704632114



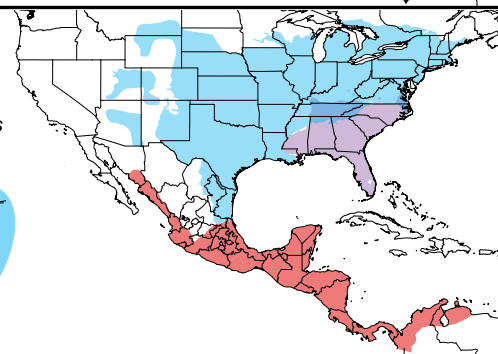
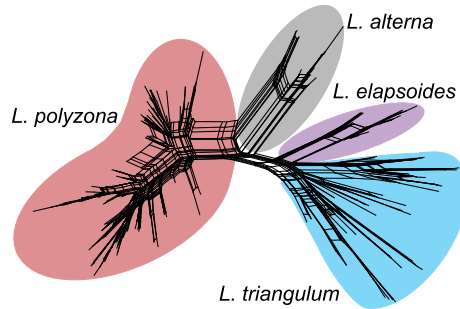
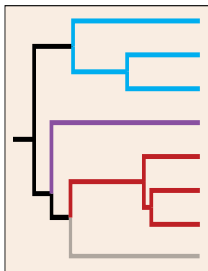
### Hypothesis 1



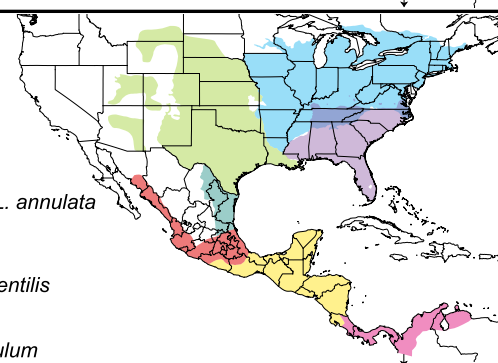
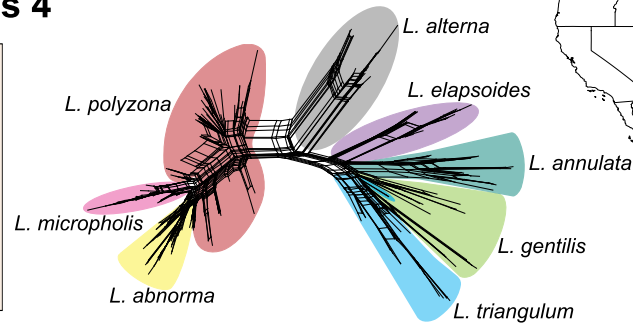
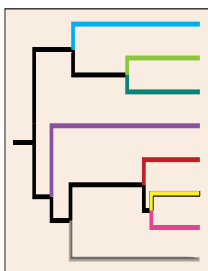
### Hypothesis 2



### Hypothesis 3



### Hypothesis 4



# *30<sup>th</sup> Workshop on Molecular Evolution*

Focus:

70% models and methods of analysis

10% on data acquisition

20% on applications

Why this emphasis on models and  
methods of analysis?

# Where were/are the problems?

- 1970s and 1980s: we badly needed more data
- 1990s and 2000s: we badly needed better sampling of taxa (also more loci)
- In the 2010s, we are finally getting some pretty good data sets. But are our models and methods up to the task of analyzing the data?
- Are we over-confident in the conclusions from existing models and methods?

*What are the sources of error in statistical inference?*

Population

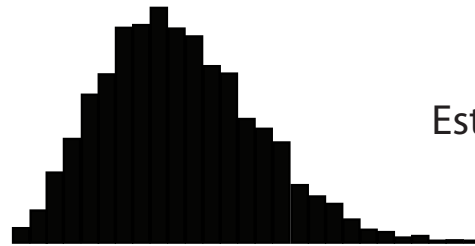


Draw sample from  
(unknown) true  
distribution

Stochastic sampling error  
(decreasing with increased sample size)



Sample



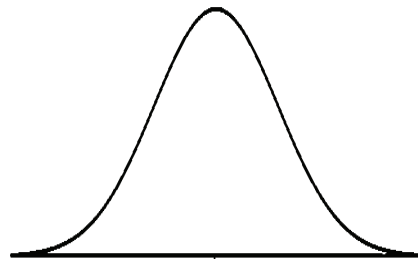
Estimate of true distribution:  
Better with more data

Inferences about  
true distribution

Systematic error in model assumptions  
(does not decrease with increasing sample size)



Inference



Our estimate of the true distribution  
(includes sampling error and systematic error)

True (unknown) distribution



Sampling (data acquisition)

Data



Model/assumptions (methods of analysis)

Inference

*Some people seem to think that with enough data (say, whole genomes from everything), we can stop worrying about inference error. Why are they mistaken?*

# True (unknown) distribution



If sample is large enough, sampling error may indeed approach 0%

## Data



But even if we have 100% confidence that our data are representative of the underlying population, we may still have 0% confidence in our model assumptions

## Inference

# True (unknown) distribution



If sample is large enough, sampling error may approach 0%

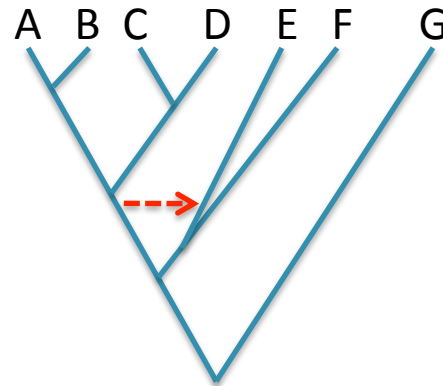
## Data



Even if we have 100% confidence that our data are representative of the underlying population, we may still have 0% confidence in our model assumptions

## Inference

$(100\% \text{ confidence in sample}) \times (0\% \text{ confidence in model assumptions}) = 0\% \text{ confidence in inference}$



True evolutionary history and processes  
(unknown)



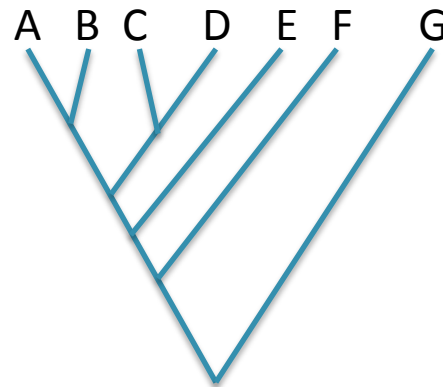
Universe of possible genomes of A-G, given true phylogeny and evolutionary processes



Samples drawn from genomes A-G (subject to sampling error, decreasing with increasing data)

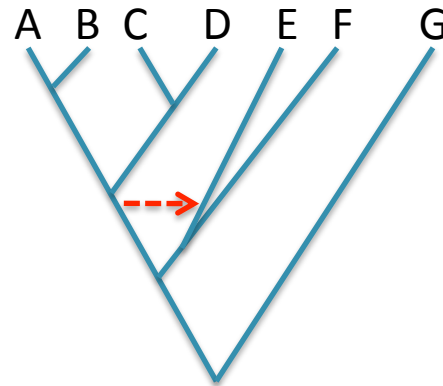


Estimate phylogeny, based on model assumptions  
(subject to systematic error)



If we collect enough data, we will have  
100% bootstrap proportions or Bayesian  
posterior probabilities for our inference.





True evolutionary history and processes  
(unknown)



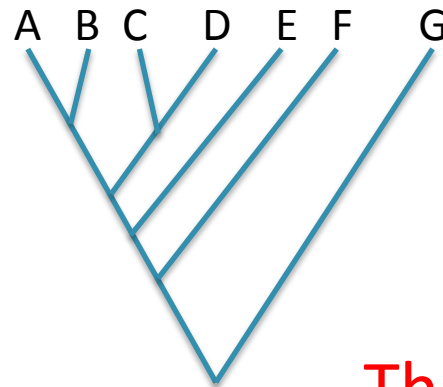
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Estimate phylogeny, based on model assumptions  
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If we collect enough data, we will have  
100% bootstrap proportions or Bayesian  
posterior probabilities for our inference.

**That doesn't mean it is correct**

## Sampling error: Relatively easy to assess

Bootstrapping, Bayesian posterior probabilities  
(This is what most people do, because it is easy.)

## Systematic error: Harder to assess

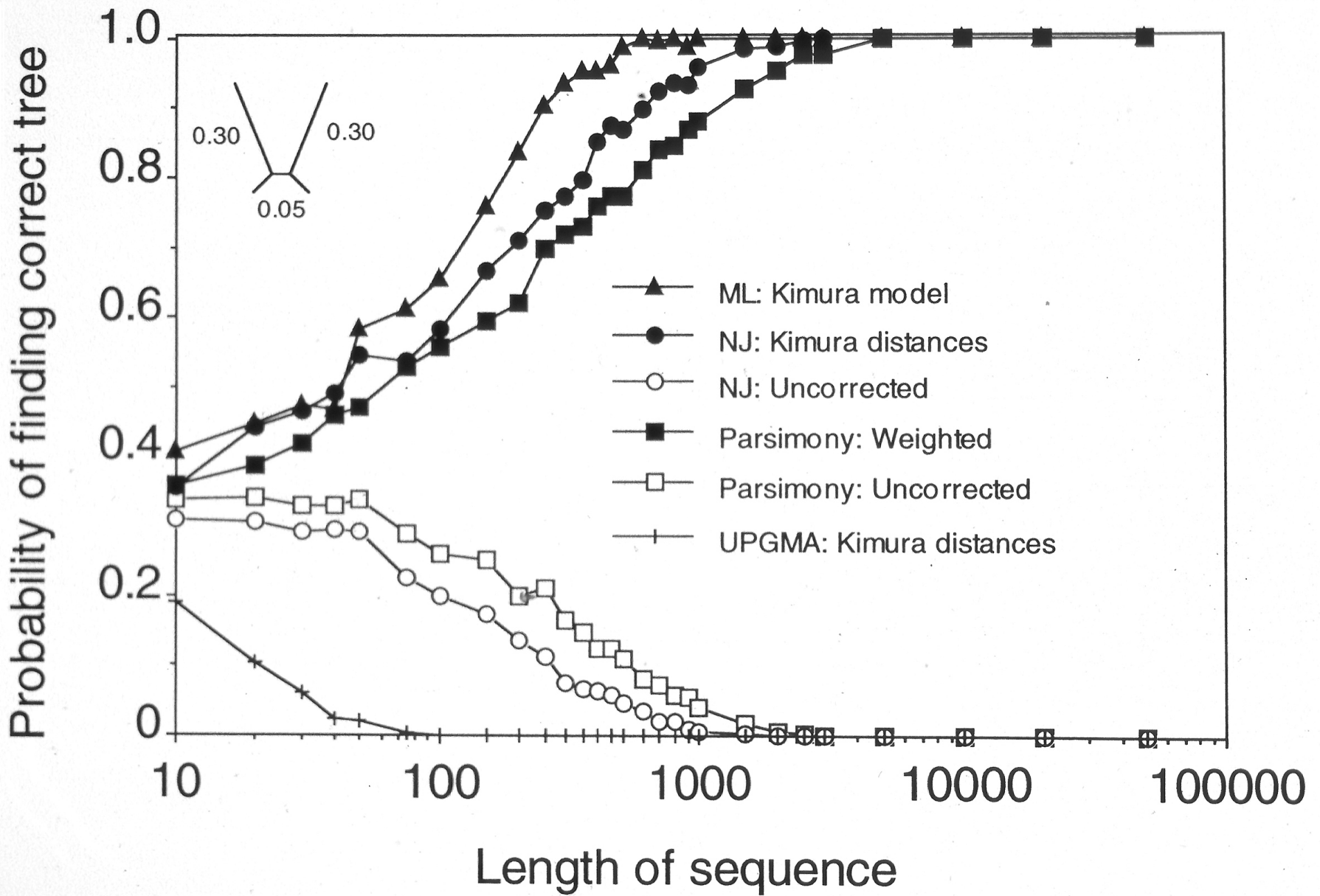
Examine sensitivity to model assumptions;  
develop and compare more complex models  
(This is what many people ignore, because it is hard)

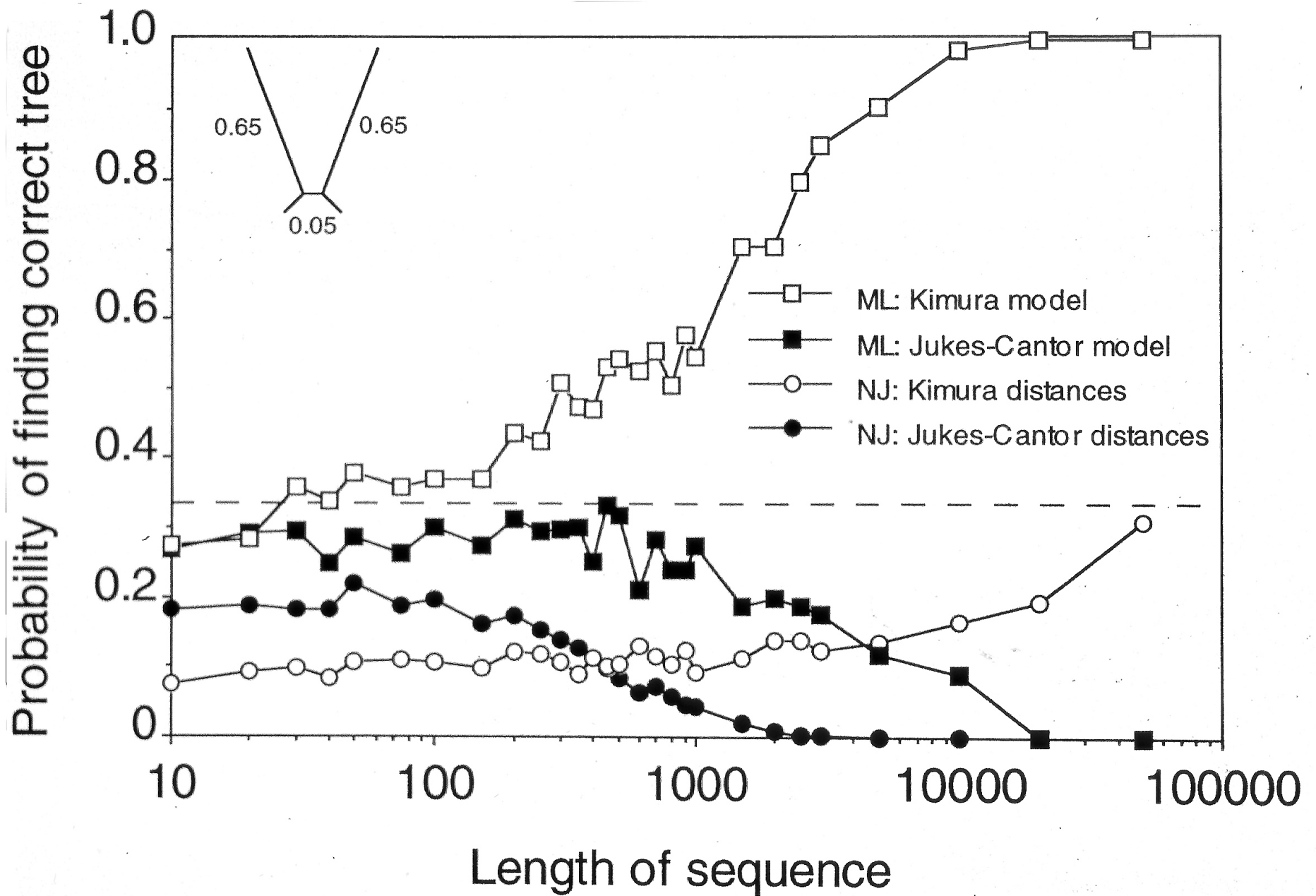
# What do we mean by more data?

## More sequences, or more taxa?

- Yes: both are very important
- Early days of molecular systematics: very short sequences, very few genes, lots of sampling error

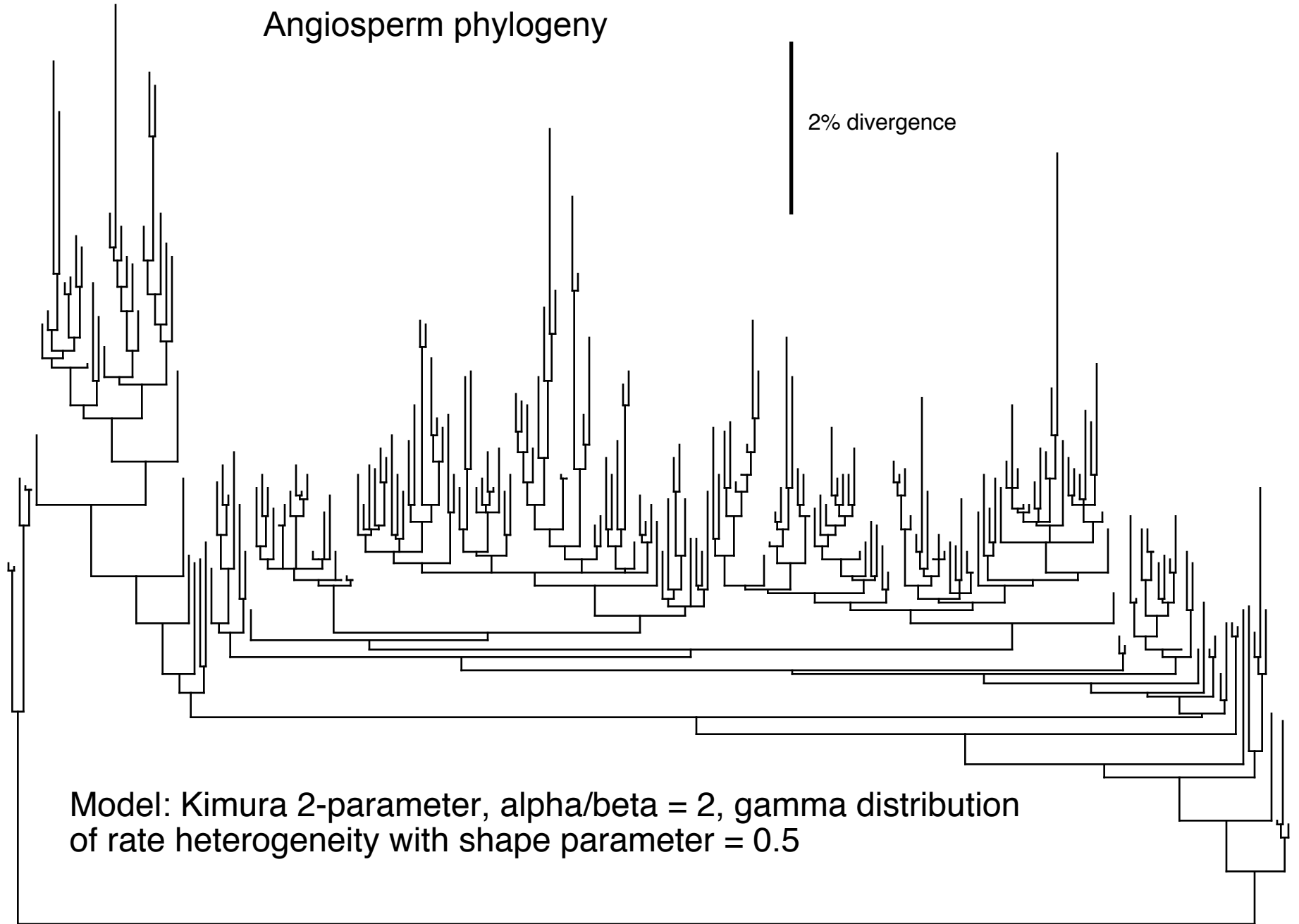
Emphasis was on increasing sequence length, because we didn't have enough data for our simple models





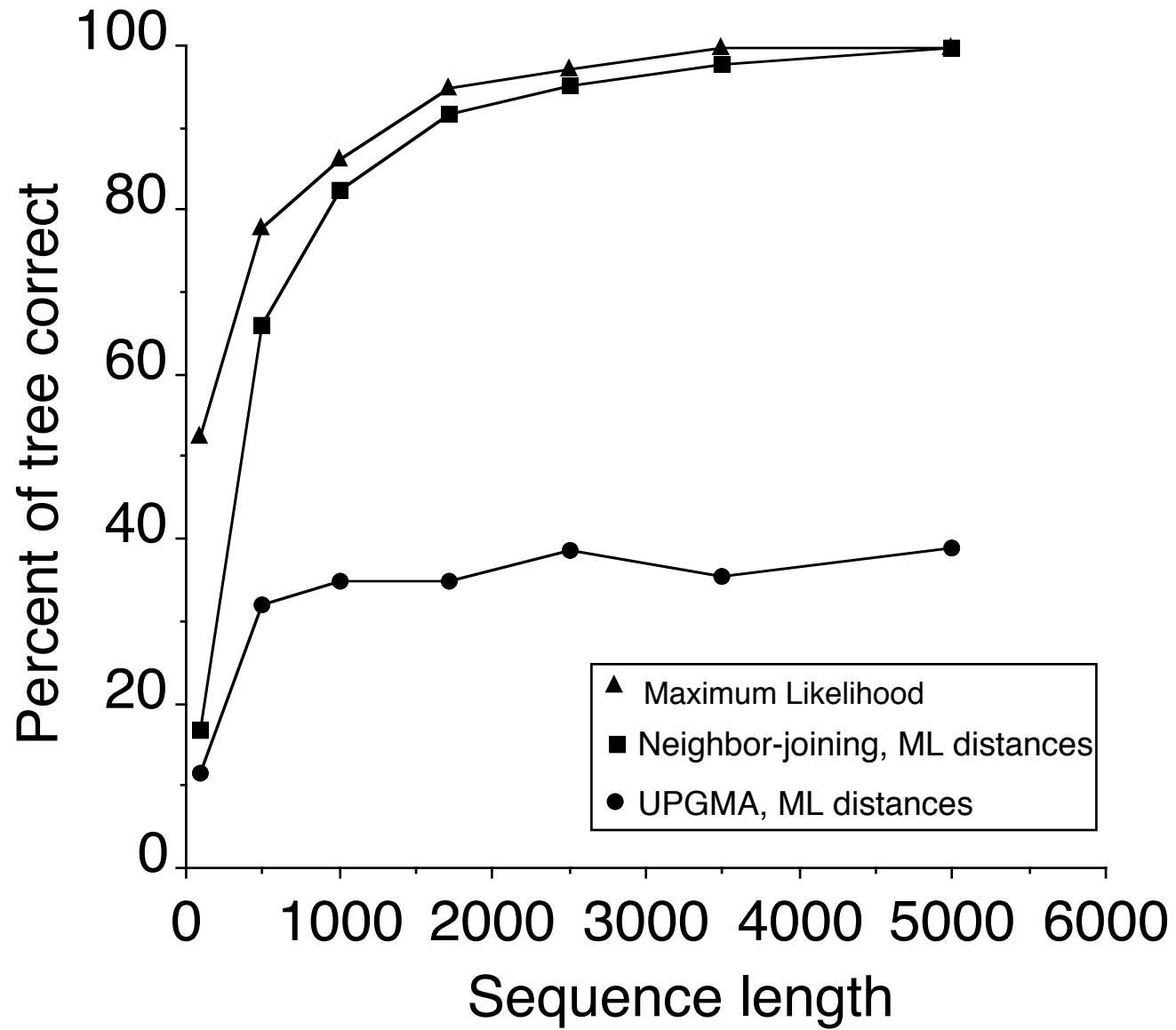
# Angiosperm phylogeny

2% divergence



Model: Kimura 2-parameter,  $\alpha/\beta = 2$ , gamma distribution  
of rate heterogeneity with shape parameter = 0.5

Figure from Hillis, 1996. Inferring complex phylogenies. Nature 383:130-131.



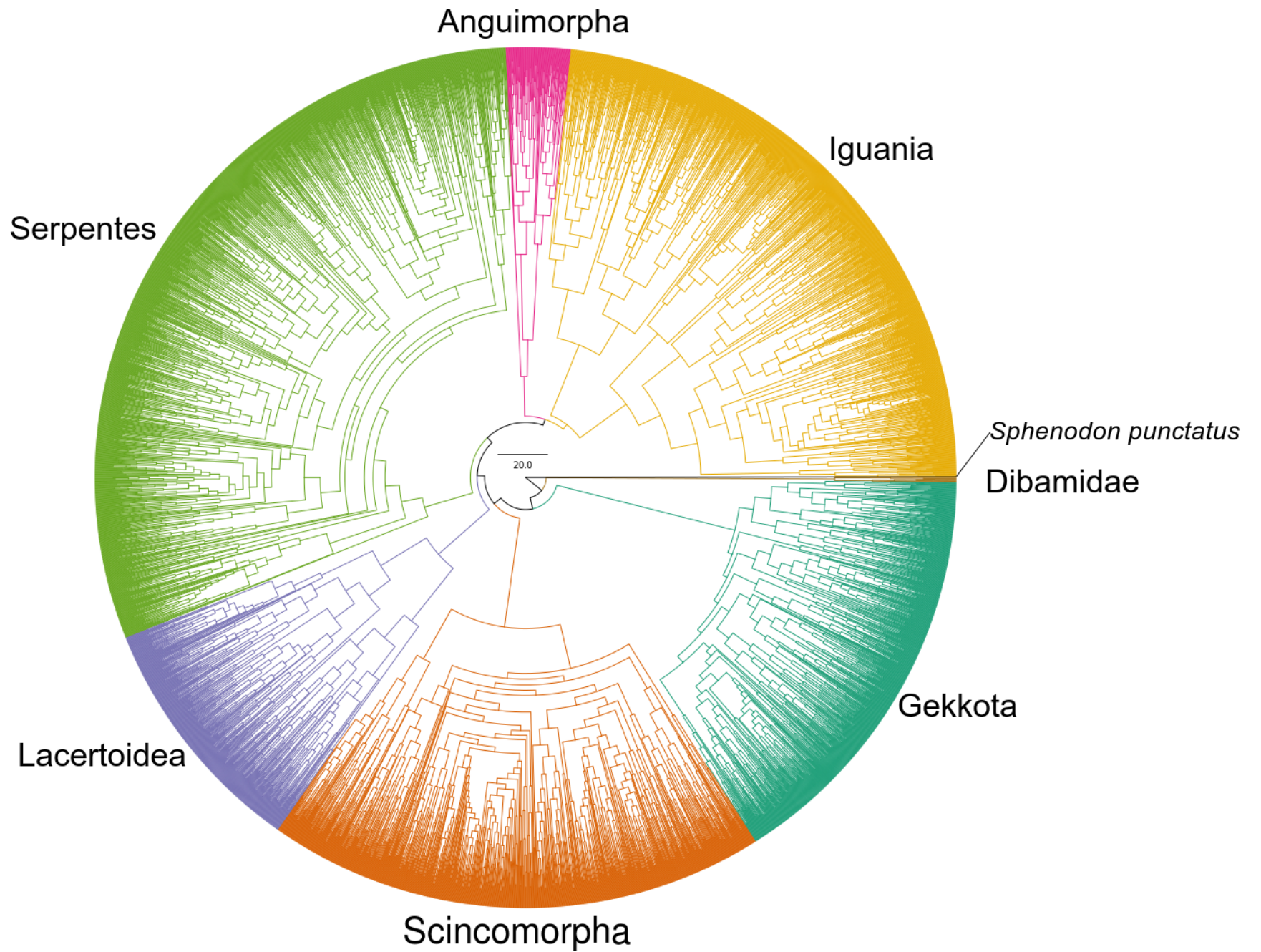
# Dense sampling of taxa greatly reduces systematic error

- Using many loci is also critical, to sort out differences between gene trees and species trees
- But even with lots of genes, poor taxon sampling results in large systematic error (fewer taxa means more reliance on overly simplistic models to infer multiple changes along long branches)

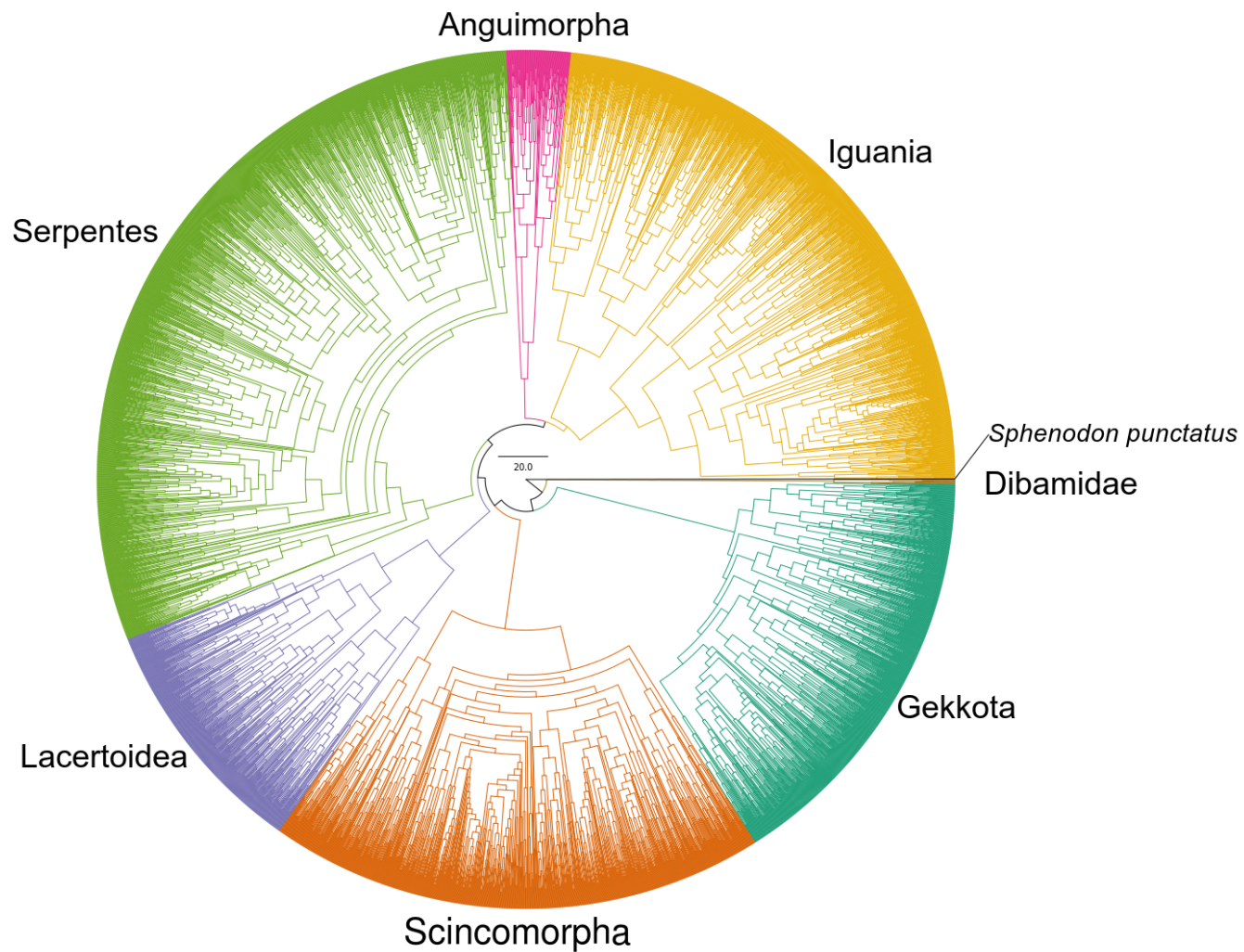


# Where are we today?

- Many studies use a large sample of genes
- Many studies sample taxa very broadly
- (Often with LOTS of missing data)
- Sampling error tends to be very low
- Bootstrap proportions and BPPs are often near 100%
- But are we over-confident in our model assumptions? ( $100 \times 0 = 0$ )



Data from Pyron et al., 2014; Figure from Wright et al., 2015



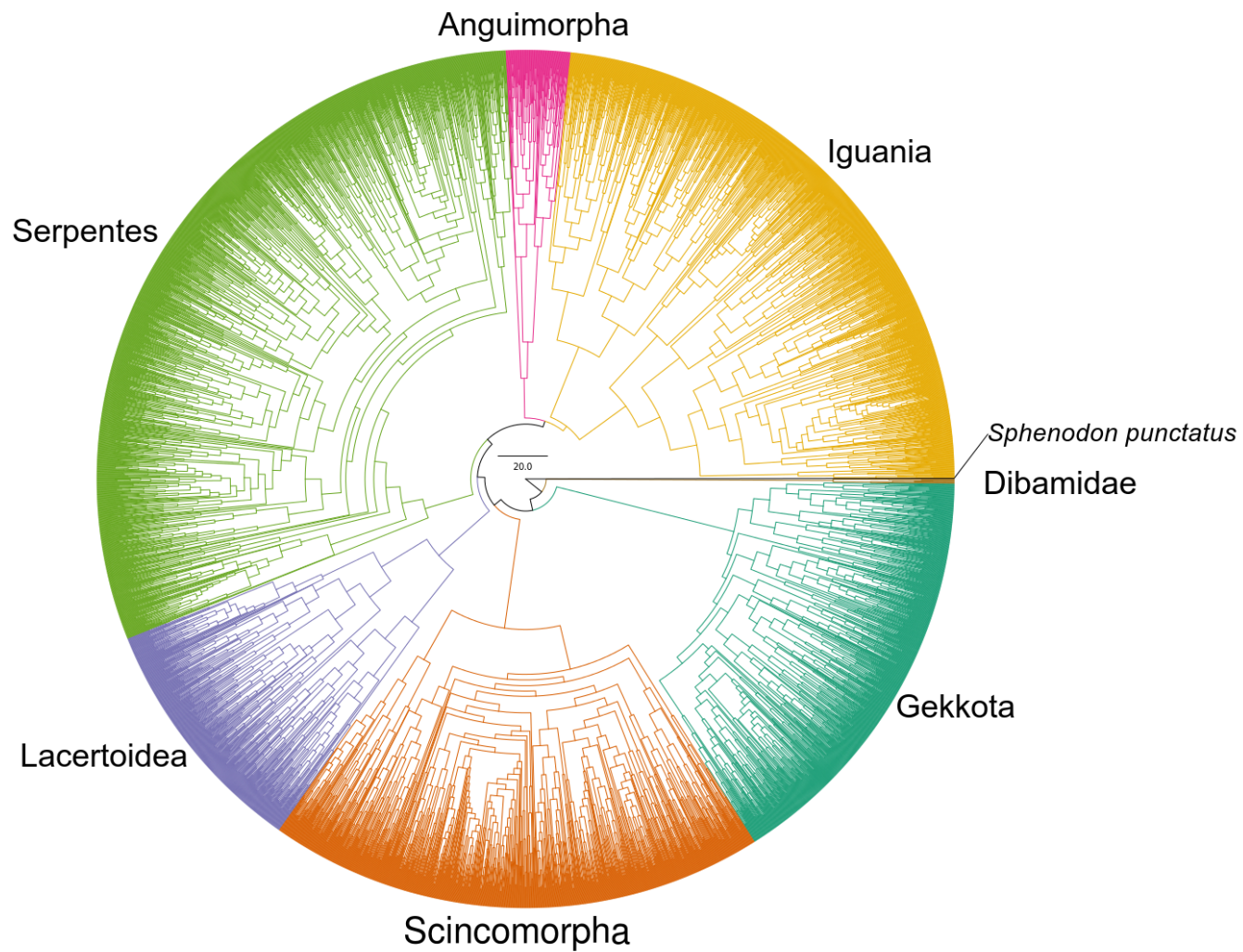
### Good:

- About 4,000 species
- Multiple nuclear and mitochondrial genes

### But worrisome:

- 81% missing data
- Biases in missing data (most taxa only have fragments of mtDNA)

How do biases in missing data affect our models?

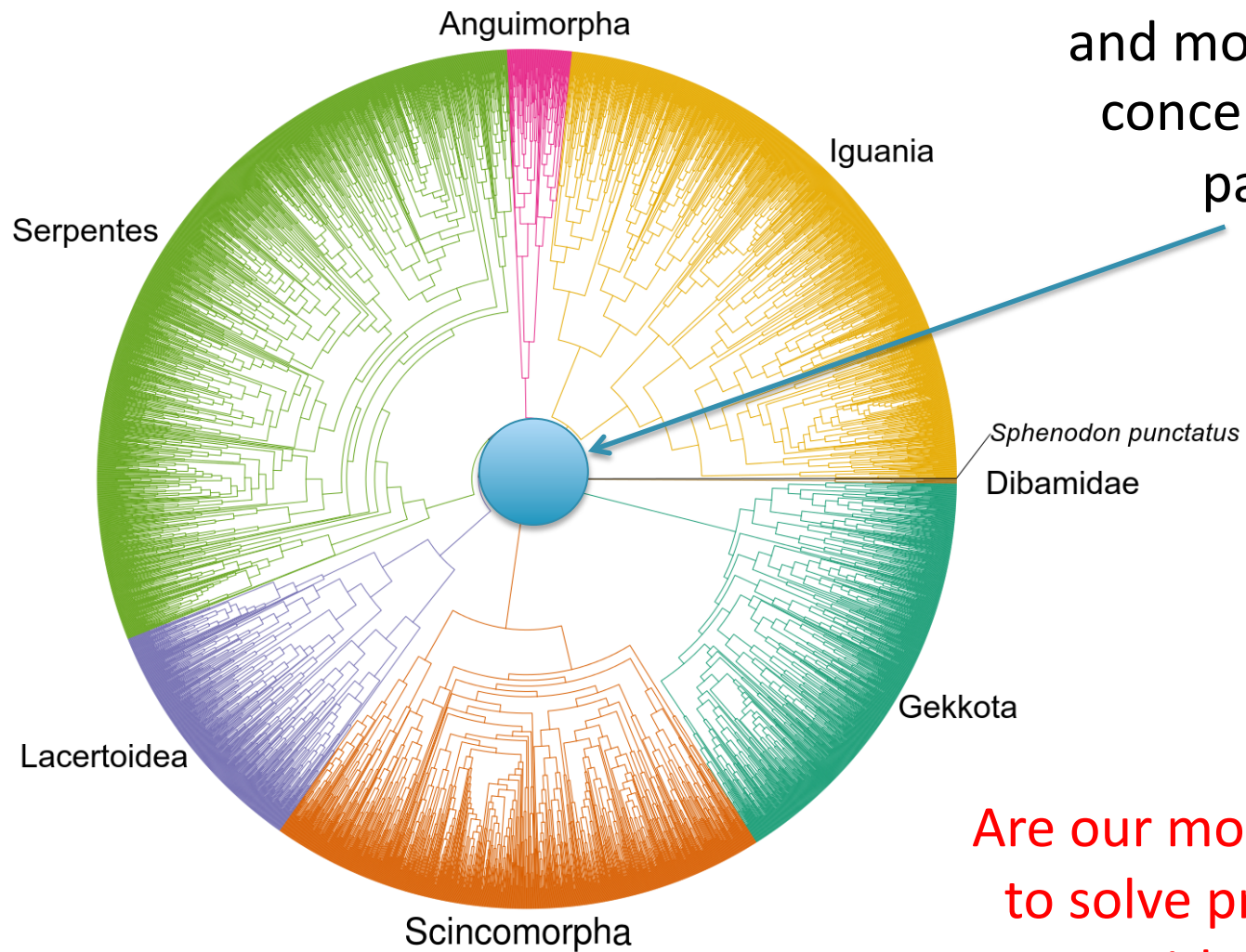


Tree conflicts with morphology, which places iguanians as the sister group of remaining squamates.

How confident should we be in this tree?

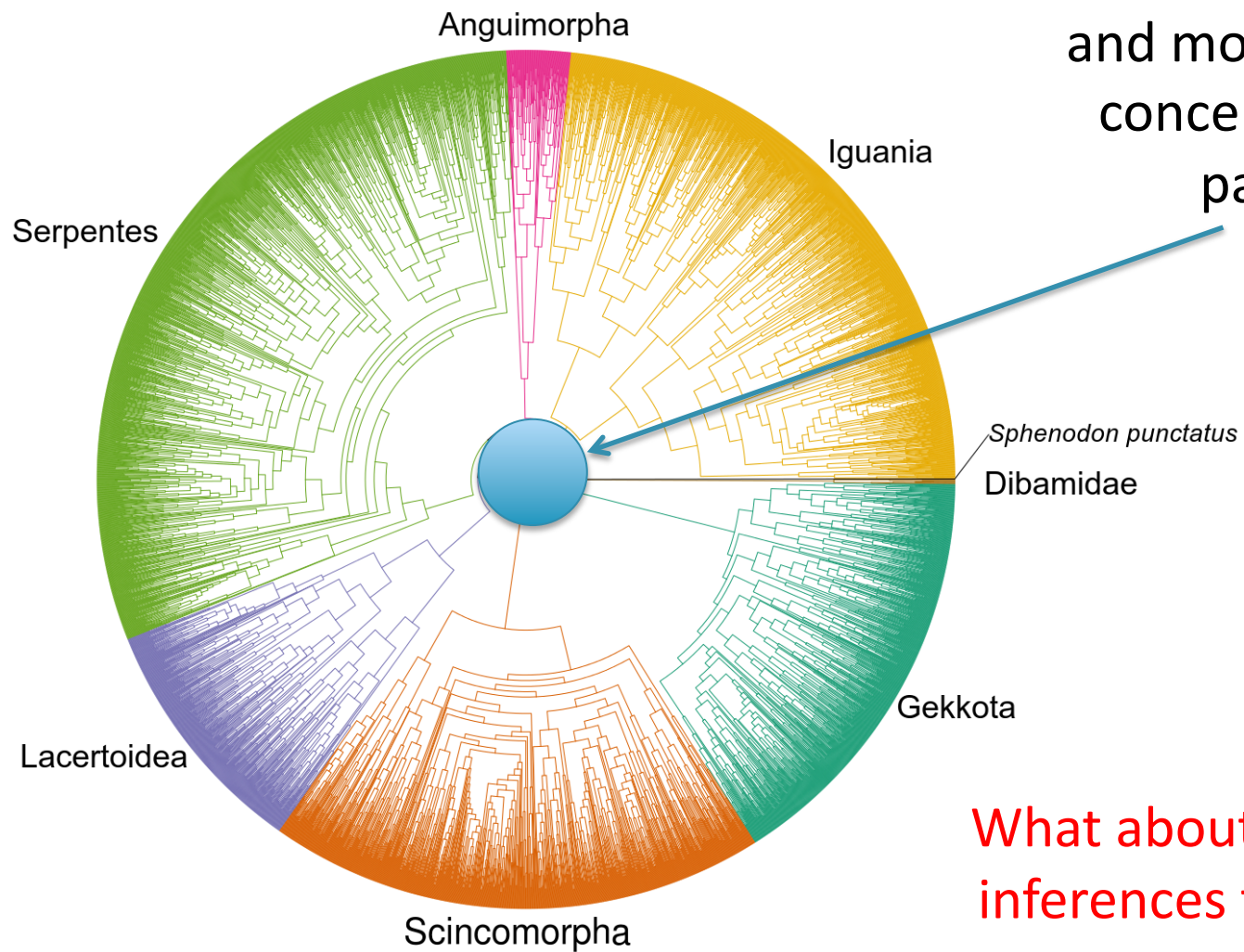


All the arguments between morphologists and molecular systematists concern branches in this part of the tree.



Are our models good enough to solve problems like this, with these data?

All the arguments between morphologists and molecular systematists concern branches in this part of the tree.



What about our evolutionary inferences from these trees?

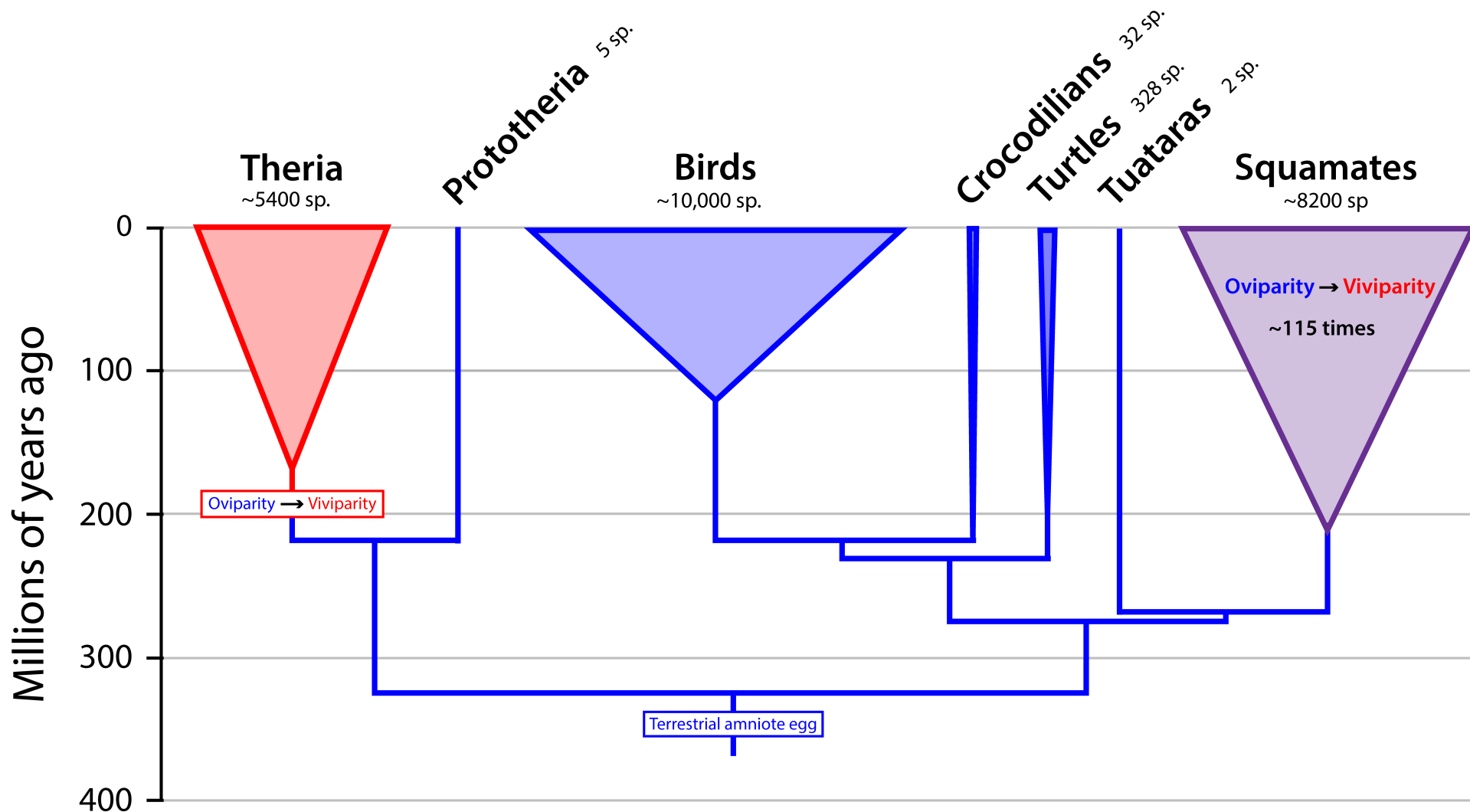
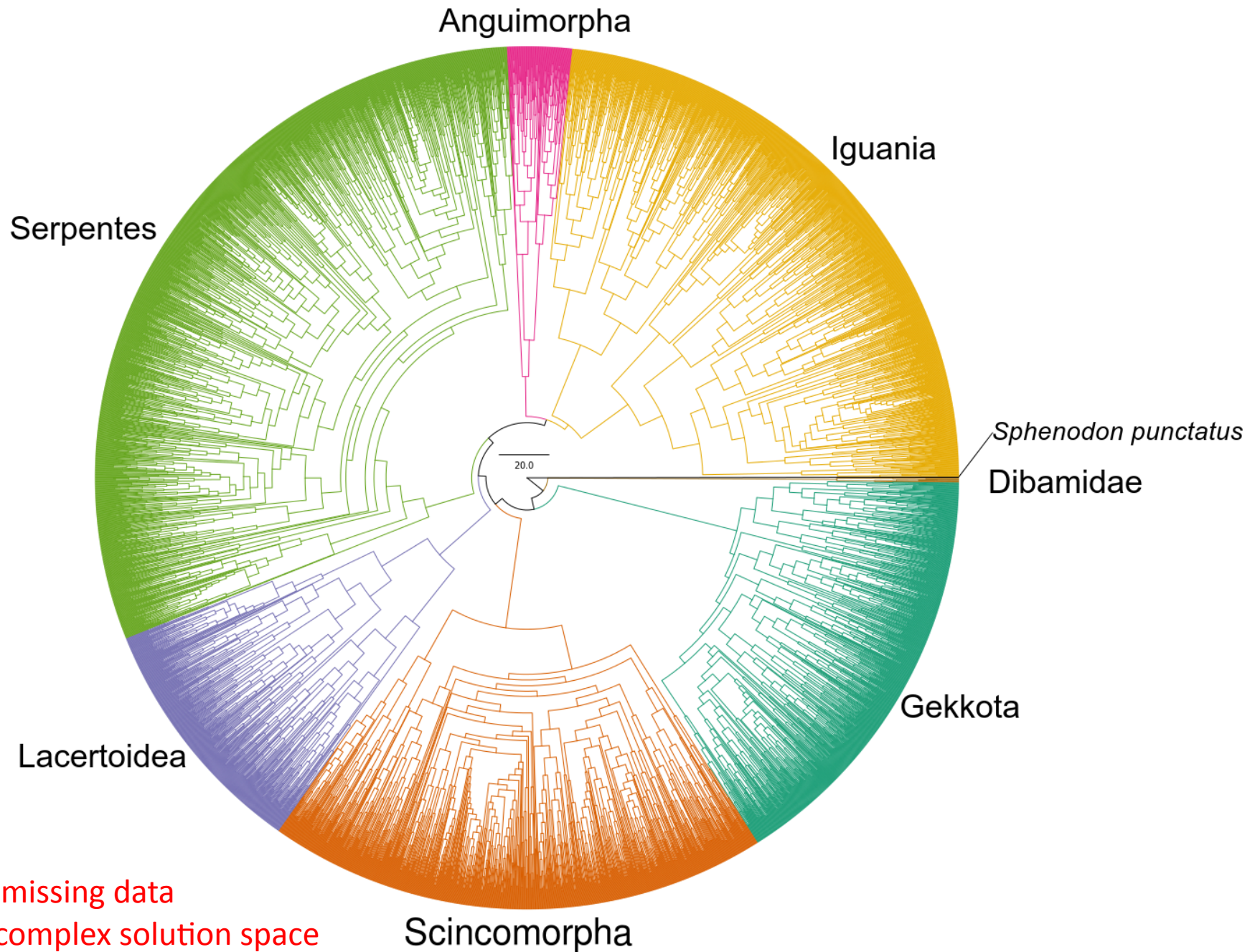


Figure from Wright et al., 2015





Data from Pyron et al., 2014; Figure from Wright et al., 2015

Best tree so far (improvement of >83,796 ln-L units)

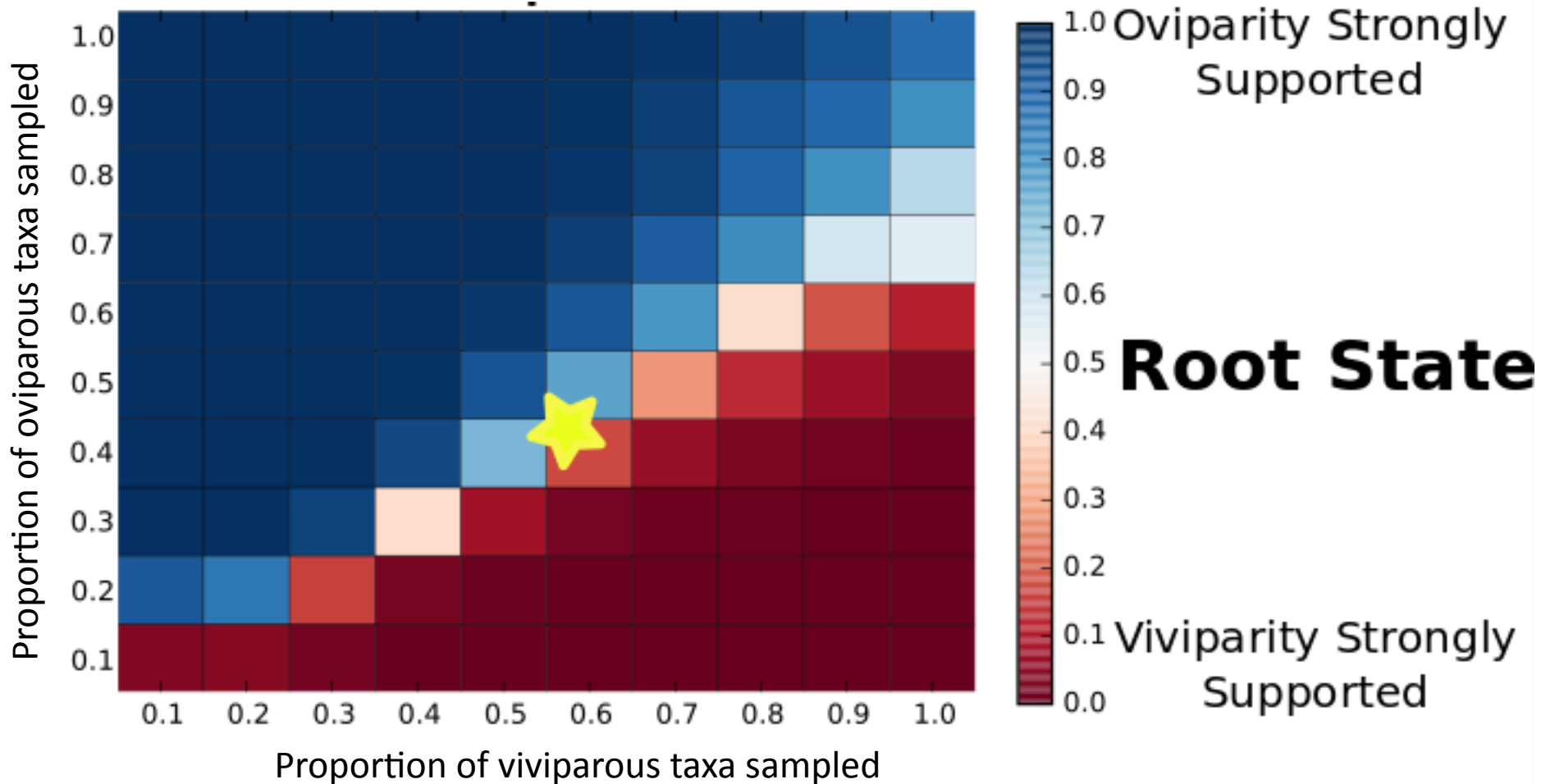


Figure from Wright et al., 2015

Parameter of model (e.g.,  $\alpha$  parameter of  $\Gamma$  distribution)

0

$\infty$

Parameter of model (e.g.,  $\alpha$  parameter of  $\Gamma$  distribution)



Assumed or estimated value of parameter leads to inference **Red**.  
How confident should we be in answer **Red**?

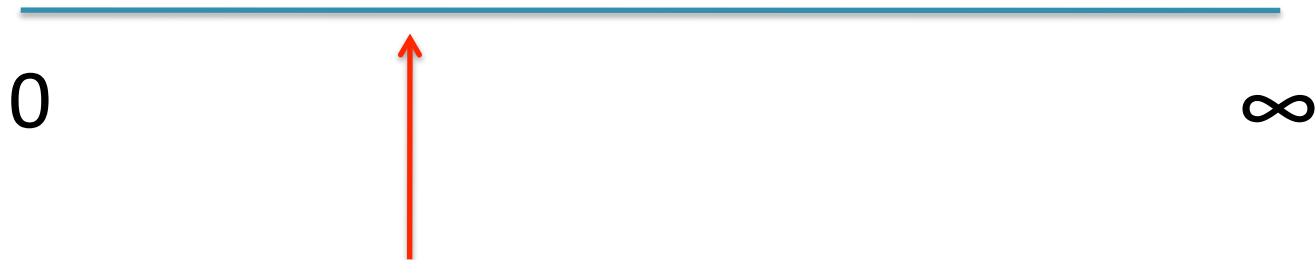
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Assumed or estimated value of parameter leads to inference **Red**.  
How confident should we be in answer **Red**?

1. We should be concerned with the sampling error that led to this estimated value of  $\alpha$ . (This is all that many people do).

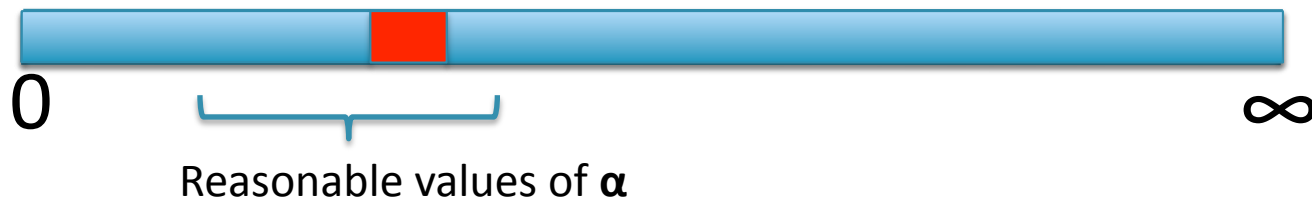
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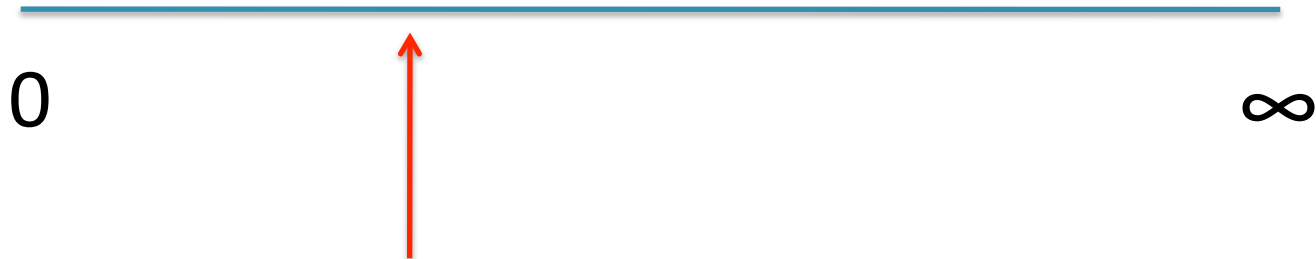
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How confident should we be in answer **Red**?

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2. We should be concerned with the sensitivity of the answer to this parameter value.

Parameter of model (e.g.,  $\alpha$  parameter of  $\Gamma$  distribution)



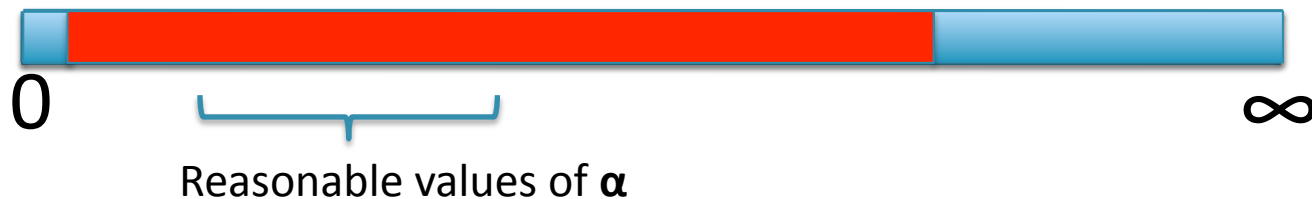
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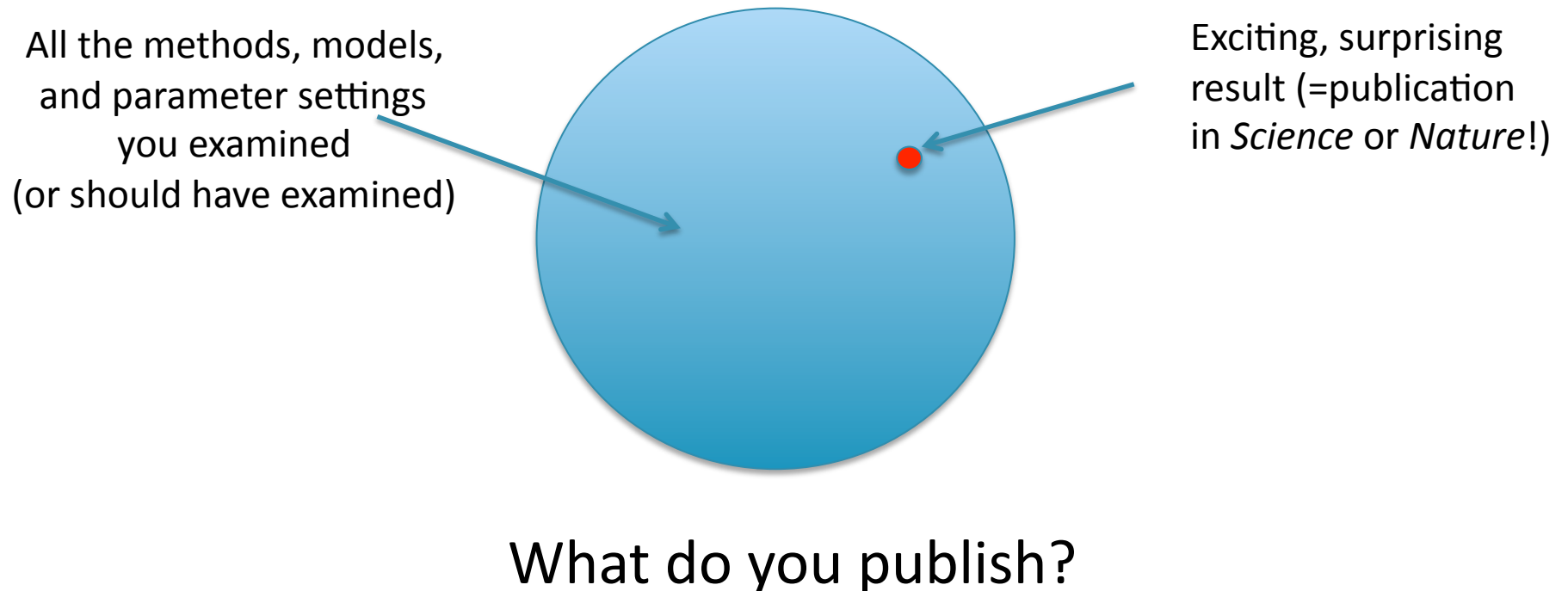
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# *Ethics of Data Presentation and Analysis*

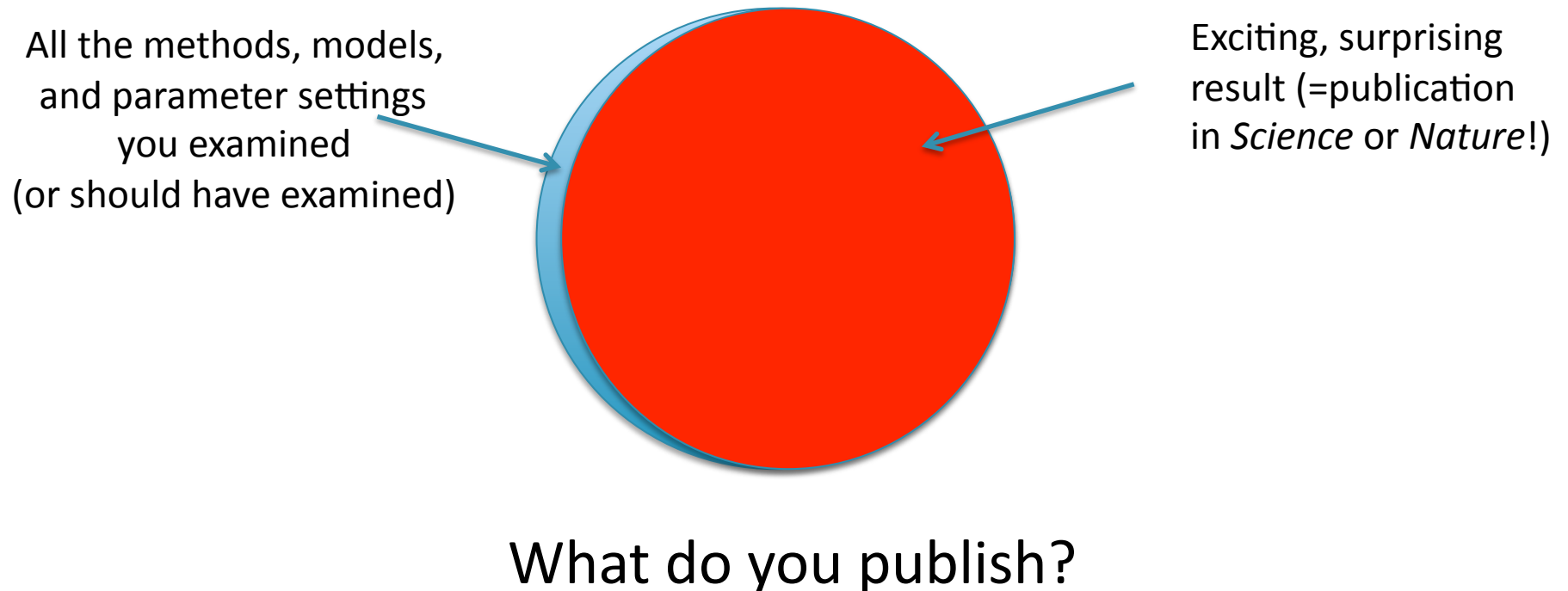
- Assume you analyze your data with multiple models, methods, or parameter settings:





# *Ethics of Data Presentation and Analysis*

- Assume you analyze your data with multiple models, methods, or parameter settings:



# How can our models be improved?

- Pretty much done:

Simple reversible models of nucleotide substitution under stationary conditions (GTR family of models) and bifurcating evolutionary lineages

# How can our models be improved?

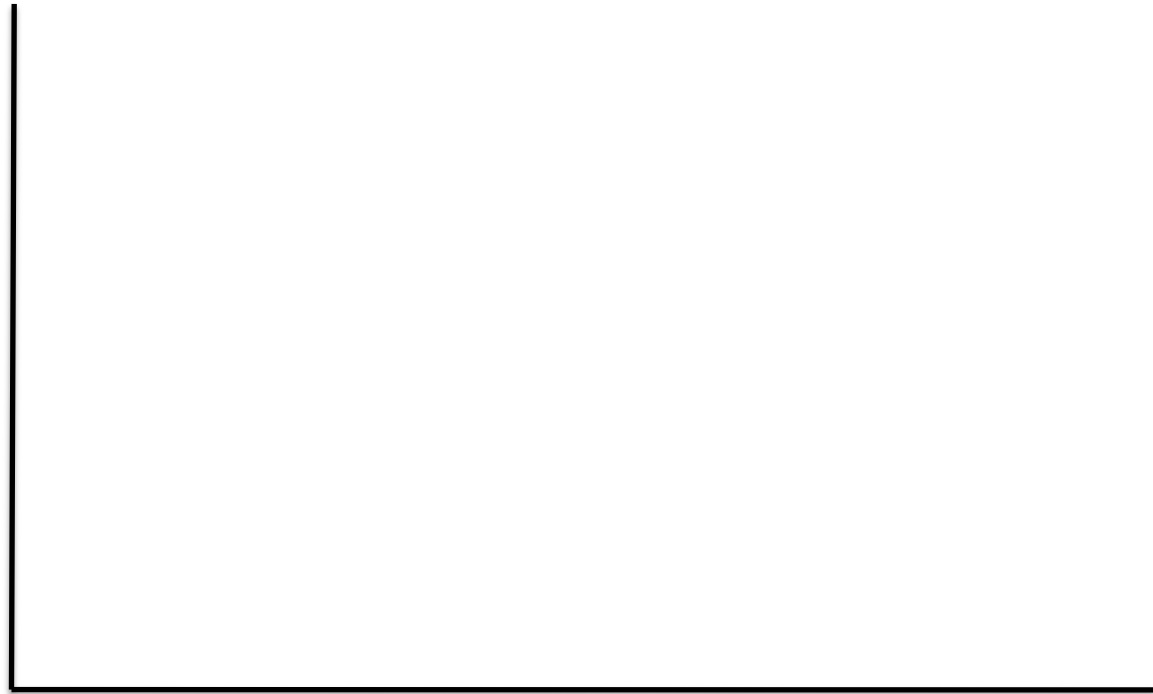
Still lots of work to do:

- Non-stationary models
- Codon biases
- Interactions among sites and genes
- Orthology, paralogy, and xenology
- Alignment within homologous genes
- Reticulation, lateral gene transfer
- Models for morphology and non-sequence data
- Methods for assessing confidence in our solutions

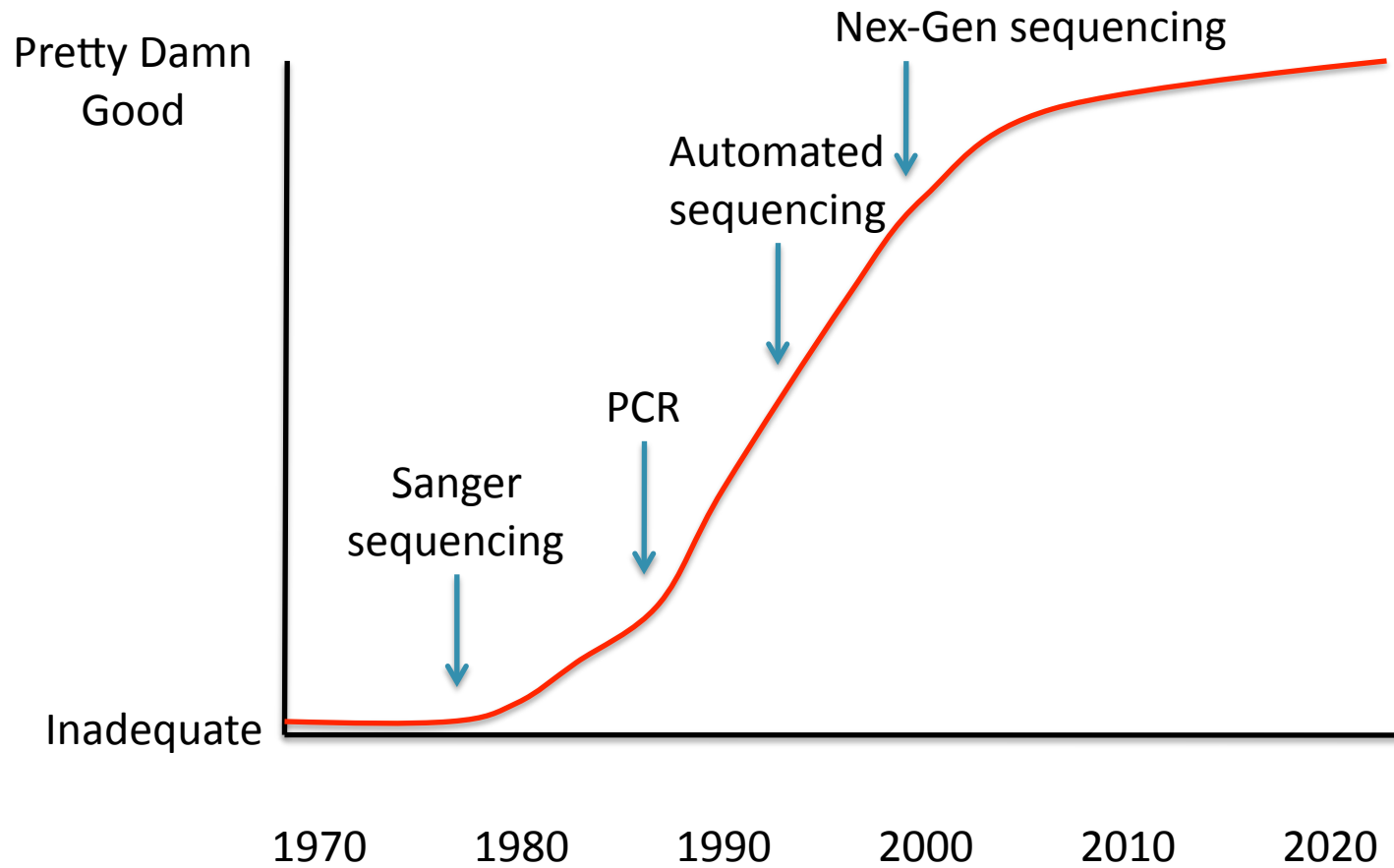
Pretty Damn  
Good

Inadequate

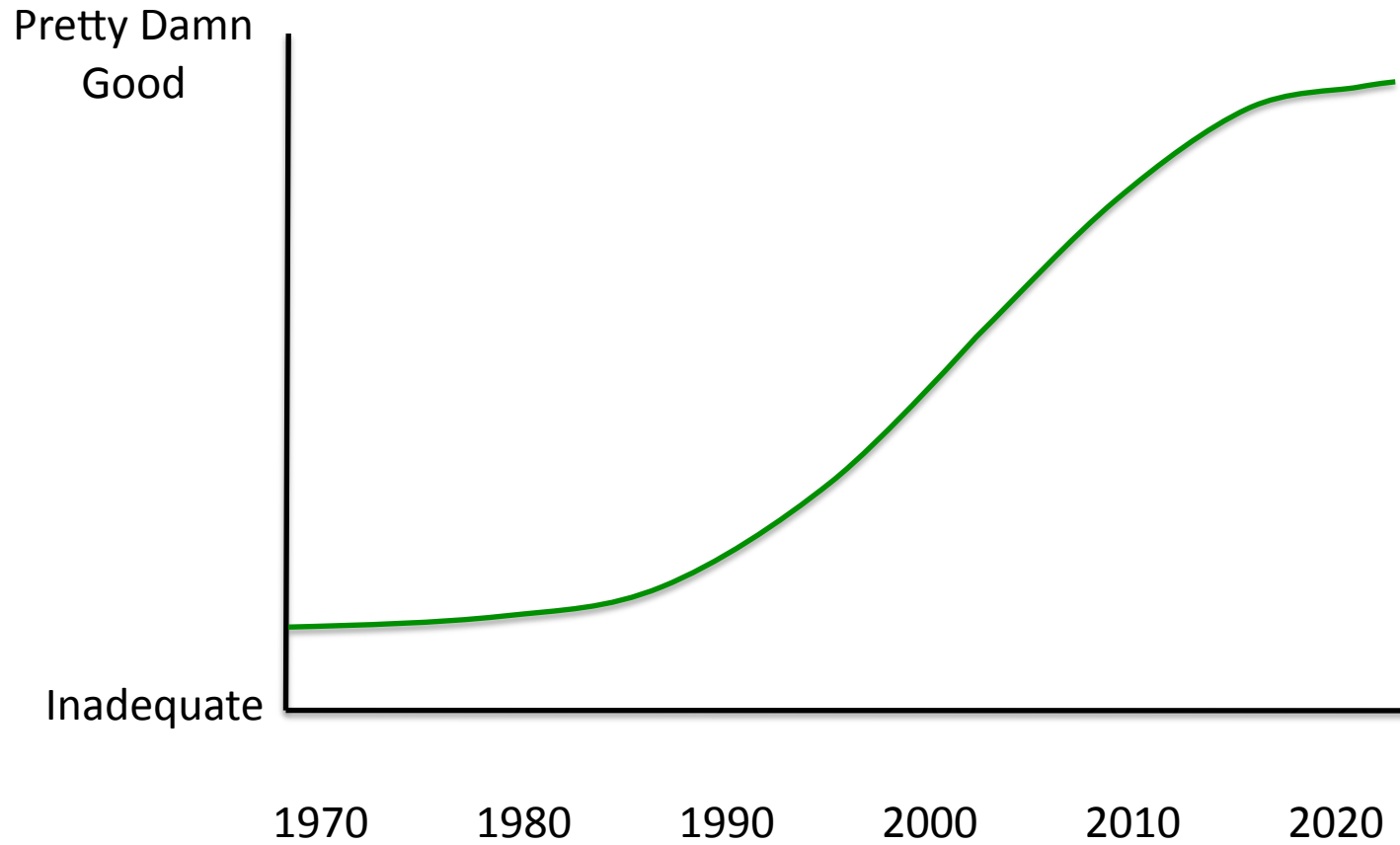
1970 1980 1990 2000 2010 2020



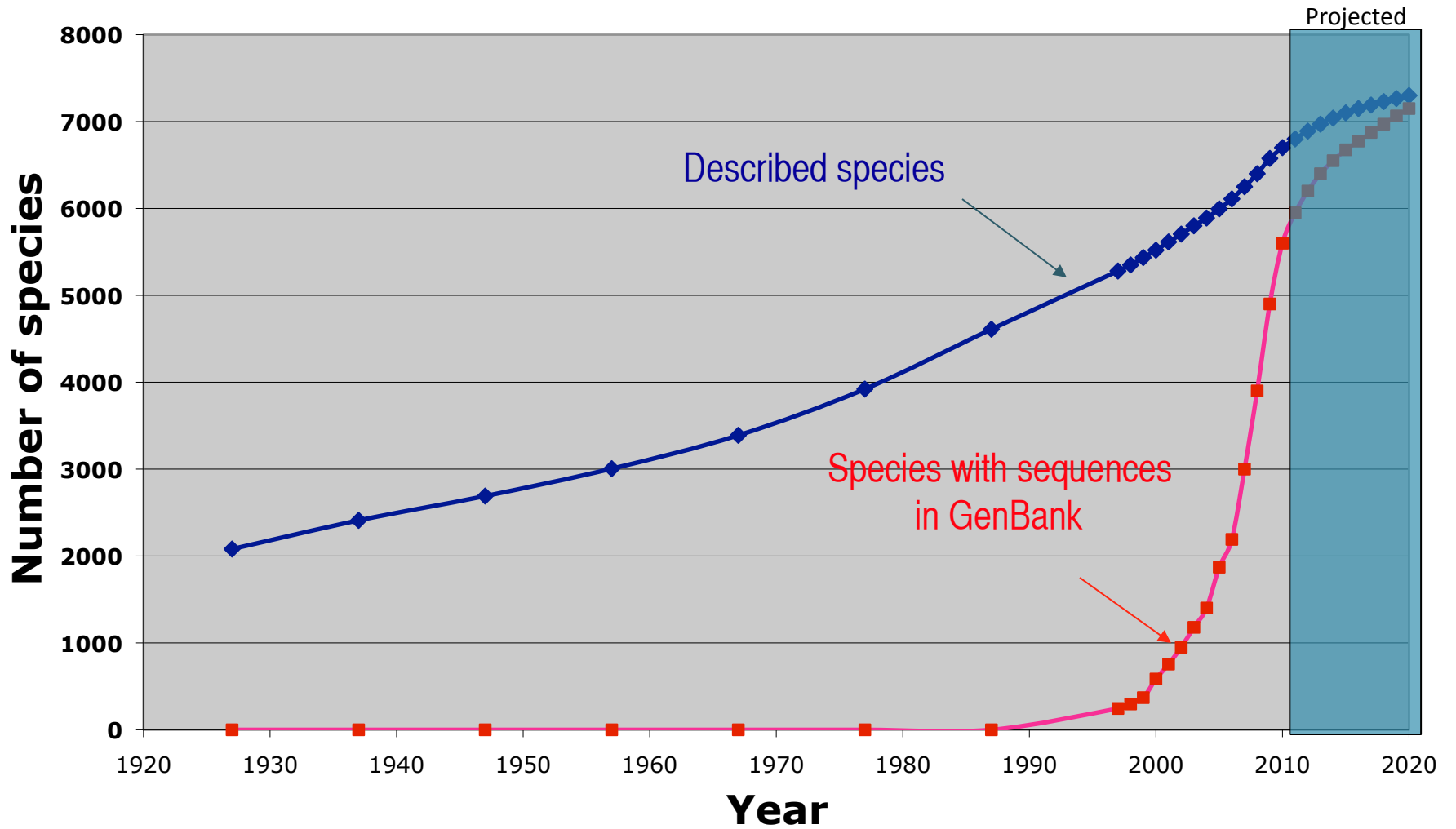
# Sequence length and number of loci



# Taxon sampling (at least for some genes in some taxa)

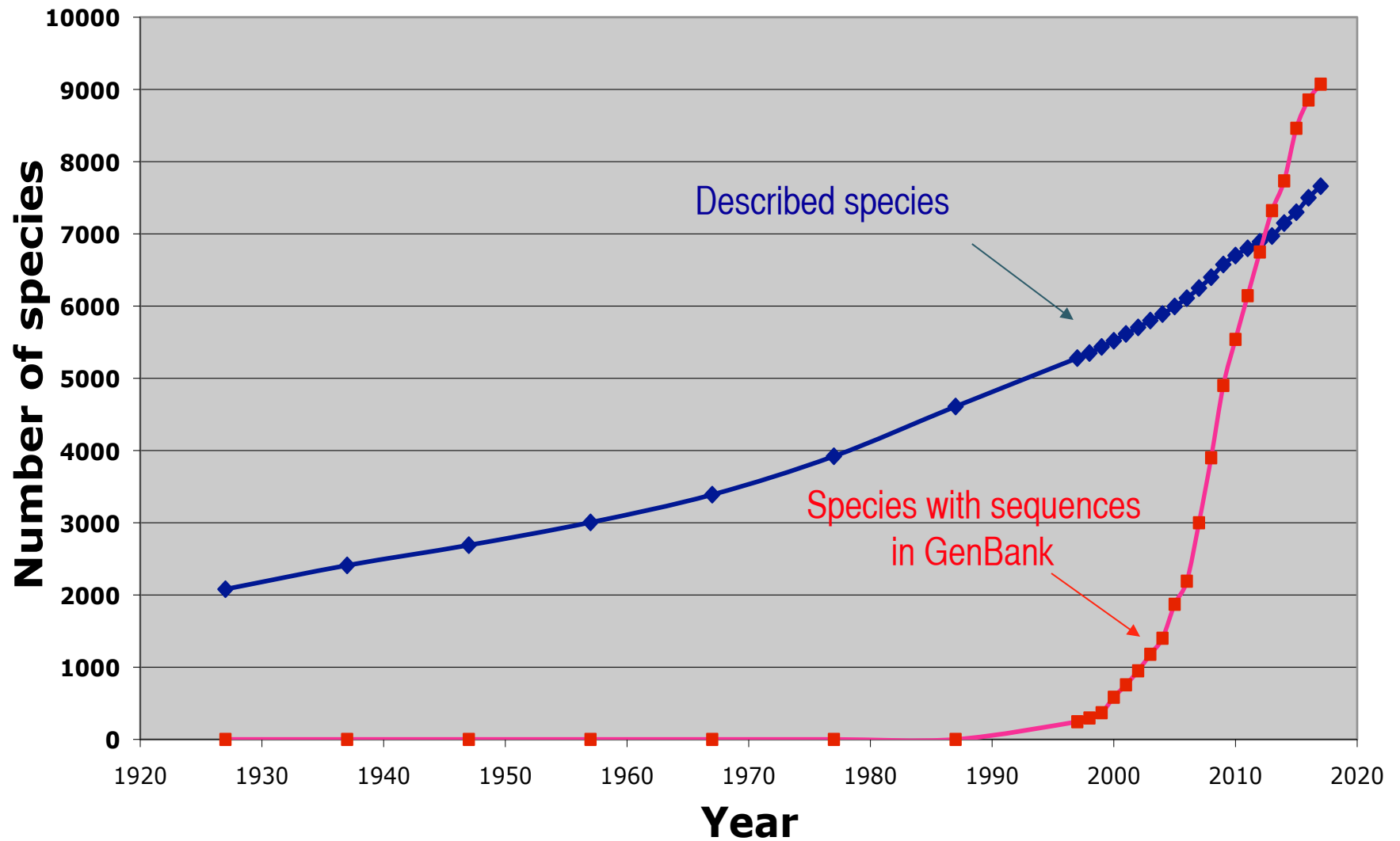


# Amphibian species and sequences



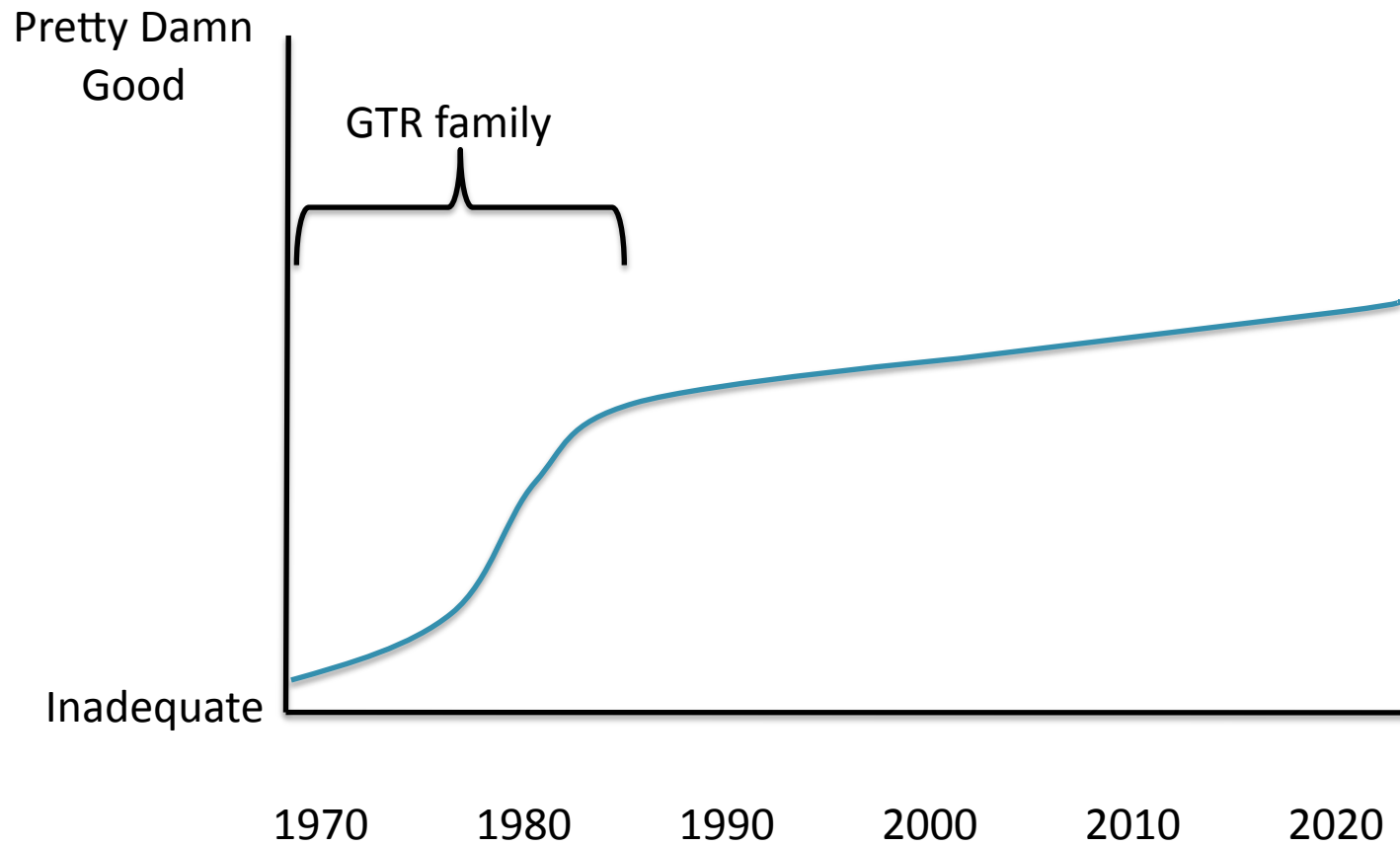
From Hillis, 2010. *in* Evolution Since Darwin: The First 150 Years, Sinauer.

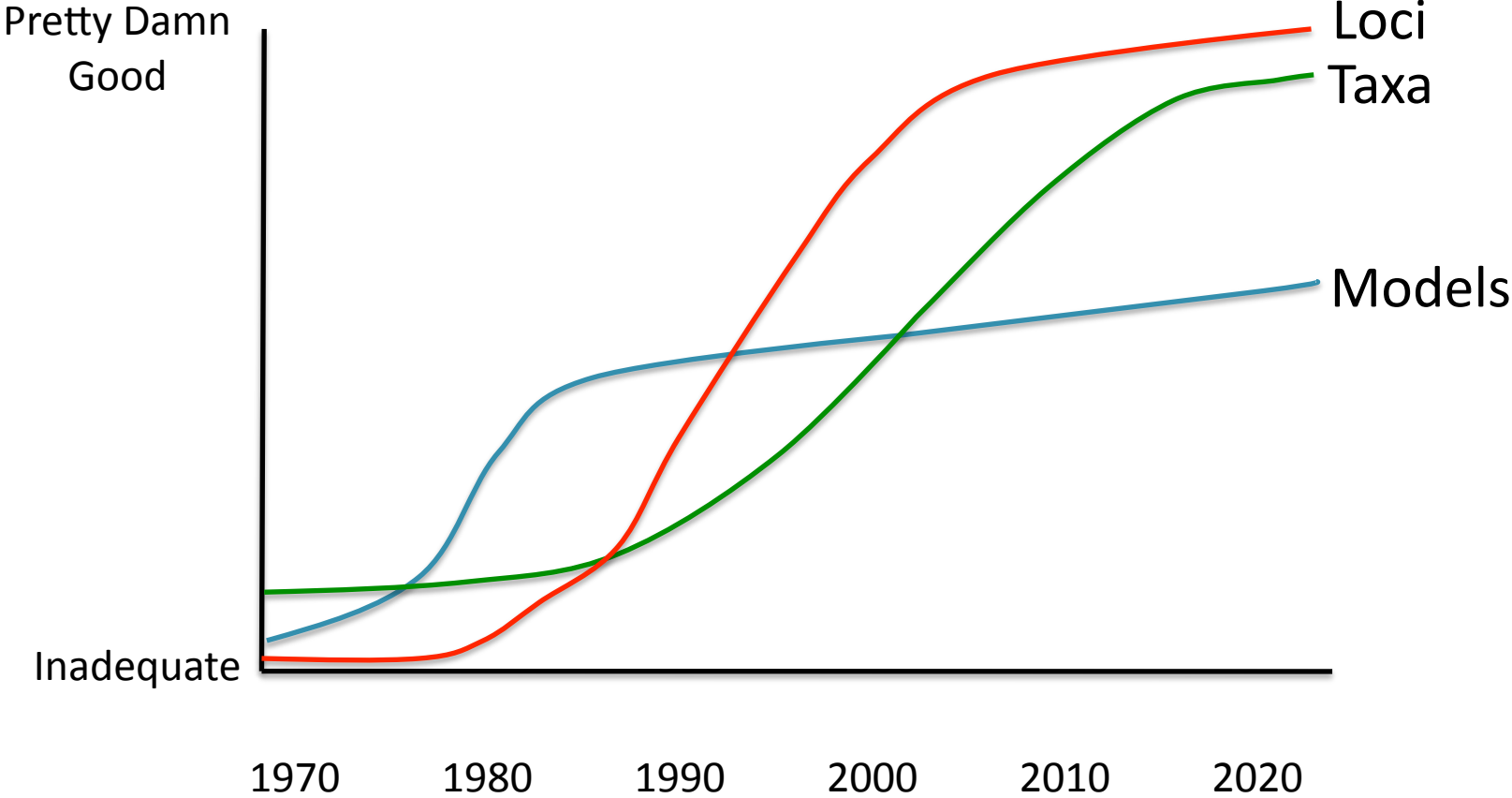
# Amphibian species and sequences





# Models of sequence evolution





# Do we need more data, or better analyses (models and methods)?

- The short answer is “yes, we need both”
- 1970s and 1980s: we badly needed more data
- 1990s and 2000s: we badly needed denser sampling of taxa (also more loci)
- In the 2010s, we are finally getting some pretty good data sets. But are our models up to the task of analyzing the data we have?
- Are we over-confident in the conclusions from the models that we have?

# *Ethics of Data Presentation and Analysis*

- All data, method descriptions, scripts, and programs must be publicly available in a way that all your analyses can be repeated, checked, and extended

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  - Not just sequences in GenBank and a statement that you used a particular program for analysis!

# *Ethics of Data Presentation and Analysis*

- All data, method descriptions, scripts, and programs must be publicly available in a way that all your analyses can be repeated, checked, and extended
  - Not just sequences in GenBank and a statement that you used a particular program for analysis!
  - Include alignments, parameter settings, scripts with program settings, and information on the range of methods, models, and parameter settings examined.

# *Ethics of Data Presentation and Analysis*

- Where can you put all this information?
  - Most journals allow online Supplementary Information
  - There may be discipline specific data repositories (such as *TreeBase* for phylogenetic analyses; <http://treebase.org>)
  - Public, archival databases such as *Dryad*, a digital data repository (<http://datadryad.org/>)
  - Individual websites are not the best solution, since long-term access and archiving are serious problems

# An Introduction to Phylogenetic Methods

- An optimality criterion defines how we measure the fit of data to a given solution
- Tree-searching is a separate step; this is how we search through possible solutions (which we then evaluate with the chosen optimality criterion)



# Phylogenetic methods

*Three main classes of optimality criteria:*

- Nonparametric methods: parsimony and related approaches
- Semi-parametric methods: pairwise distance approaches
- Parametric methods: Likelihood and Bayesian approaches

# Advantages of each

## Parsimony methods

- Widely applicable to many discrete data types (often used to combine analyses of different data types)
- Requires no explicit model of evolutionary change
- Computationally relatively fast
- Relatively easy interpretation of character change
- Perform well with many data sets

## Pairwise distance methods

- Can be used with pairwise distance data (e.g., non-discrete characters)
- Can incorporate an explicit model of evolution in estimation of pairwise distances
- Computationally relatively fast (especially for single-point estimates)

## Likelihood-based methods

- Fully based on explicit model of evolution
- Most efficient method under widest set of conditions
- Consistent (converges on correct answer with increasing data, as long as assumptions are met)
- Most straightforward statistical assessment of results; probabilistic assessment of ancestral character states

# Disadvantages of each

## Parsimony methods

- No explicit model of evolution; often less efficient
- Nonparametric statistical approaches for assessing results often have poorly understood properties
- Can provide misleading results under some fairly common conditions
- Do not provide probabilistic assessment of alternative solutions

## Pairwise distance methods

- Model of evolution applied locally (to pairs of taxa), rather than globally
- Statistical interpretation not straightforward
- Can provide misleading results under some fairly common conditions (but not as sensitive as parsimony)
- Do not provide probabilistic assessment of alternative solutions

## Likelihood-based methods

- Require an explicit model of evolution, which may not be realistic or available for some data types
- Computationally most intense

# Parsimony Criterion

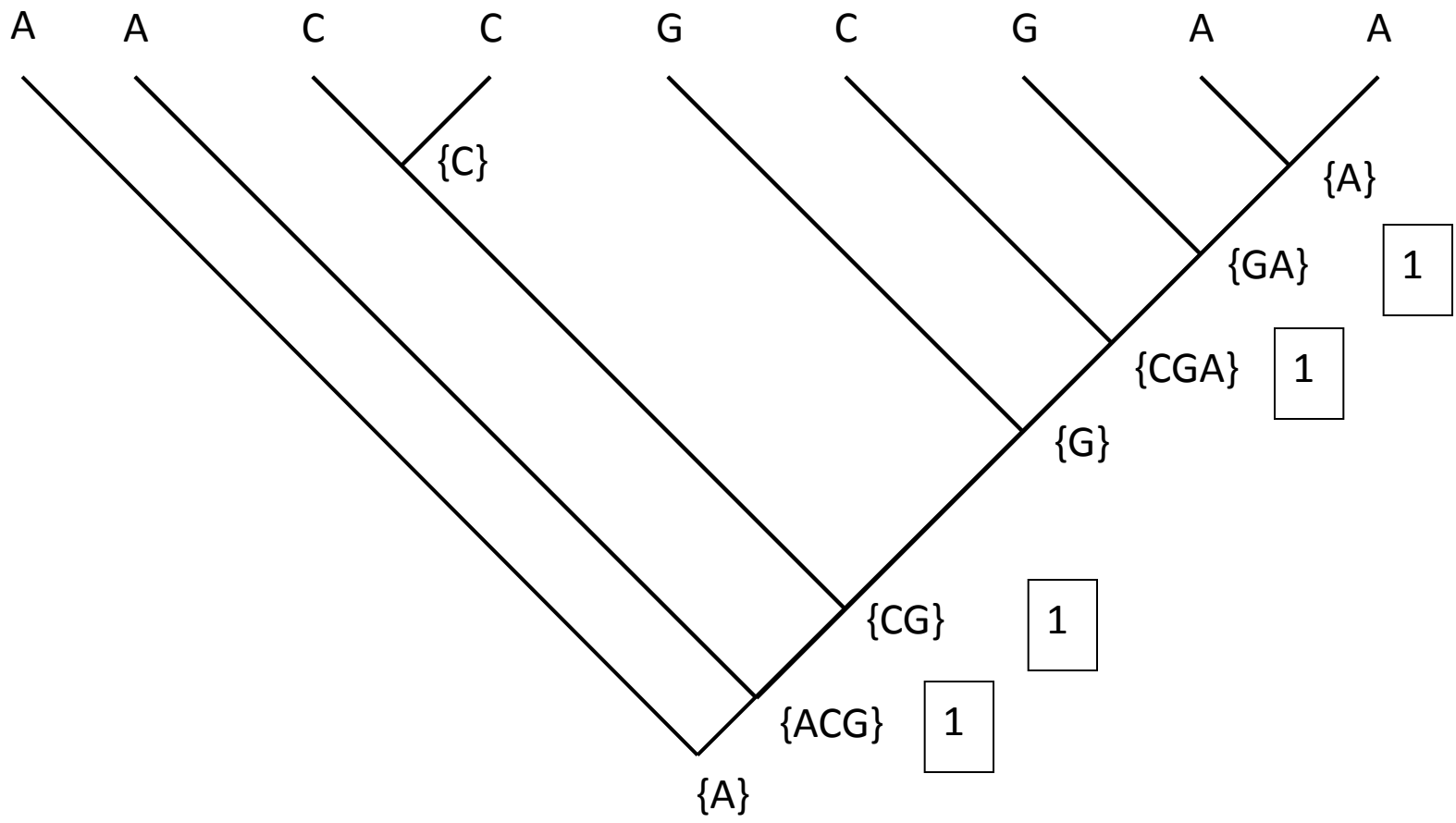
- Under the **parsimony criterion**, the optimal tree (the shortest or minimum-length tree) is the one that minimizes the sum of the lengths of all characters in terms of evolutionary steps (a step is a change from one character-state to another).
- For a given tree, find the length of each character, and sum these lengths; this is the **tree length**.
- The tree with the minimum length is the **most-parsimonious tree**.
- The most parsimonious tree provides the **best fit** of the data set under the parsimony criterion.

# Optimal versus True Tree

There is no guarantee that any criterion will necessarily identify the “true” tree. These are simply criteria for choosing which tree best fits a dataset

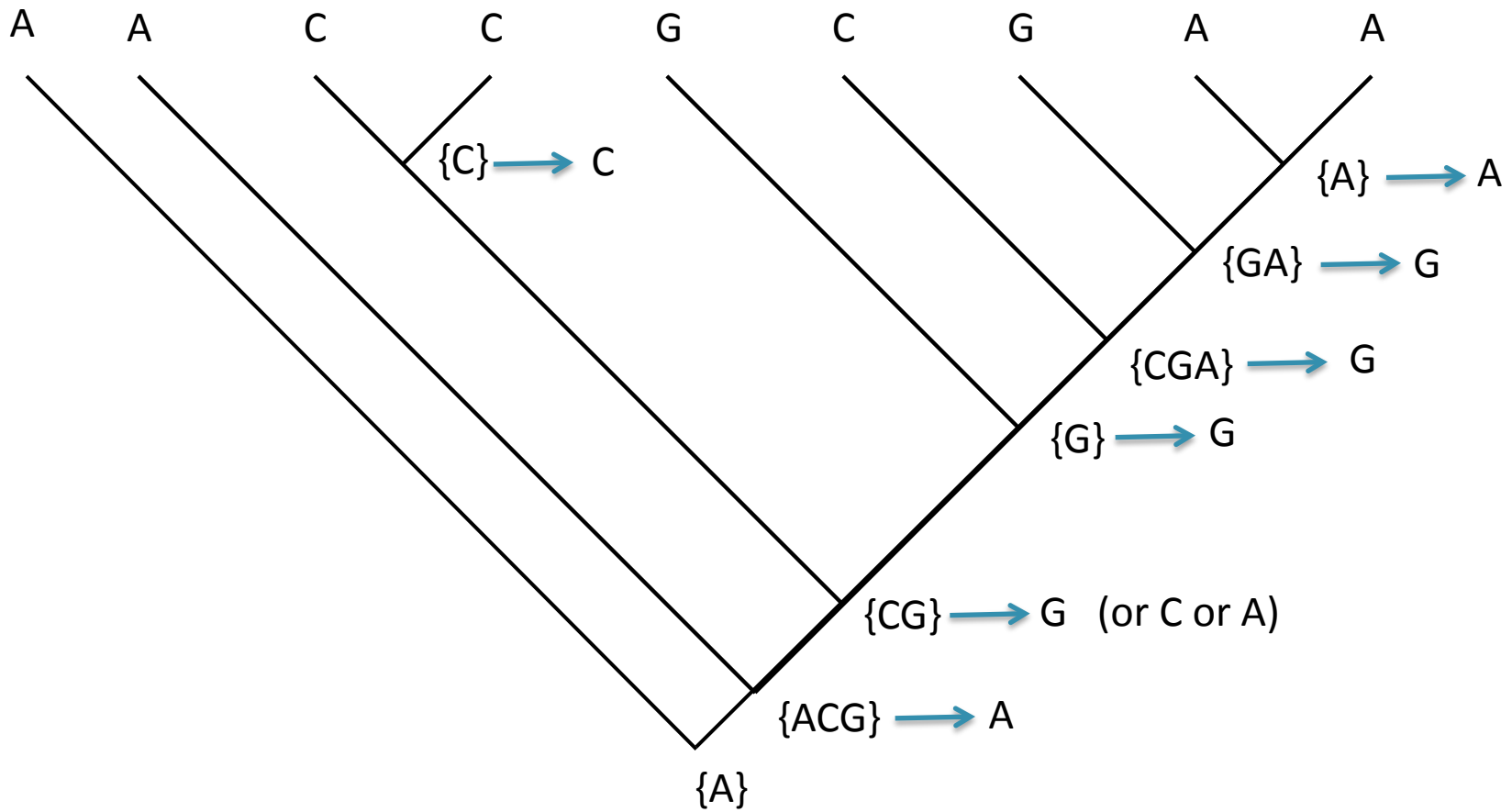
# Optimization

- In parsimony, this involves minimizing the number of changes of a character across a tree (the *length* of the character)
- The optimization involves estimating the state at all internal nodes.
- It is possible for a character to have more than one best optimization.



Downpass (postorder traversal)

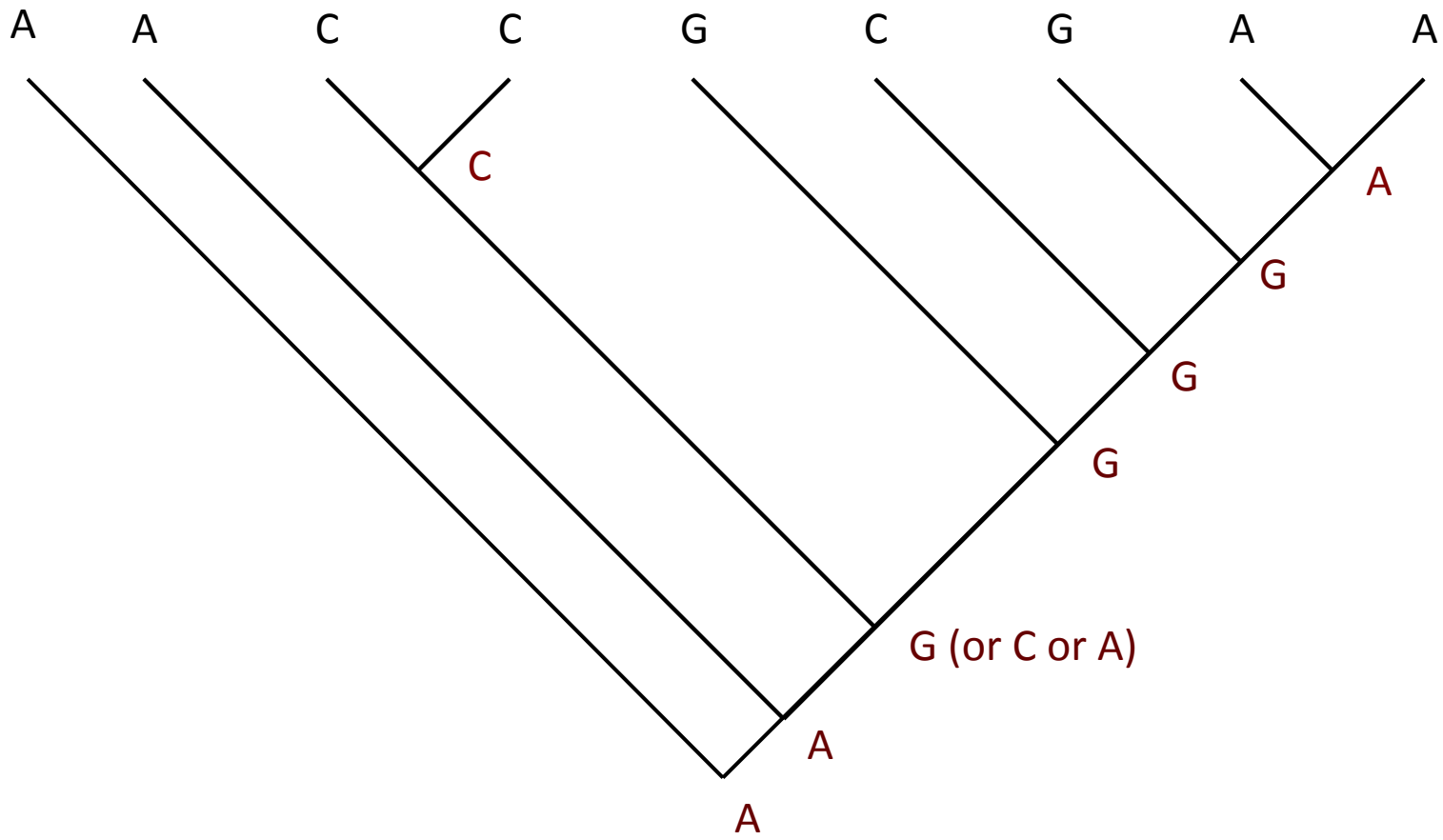
Length = 4

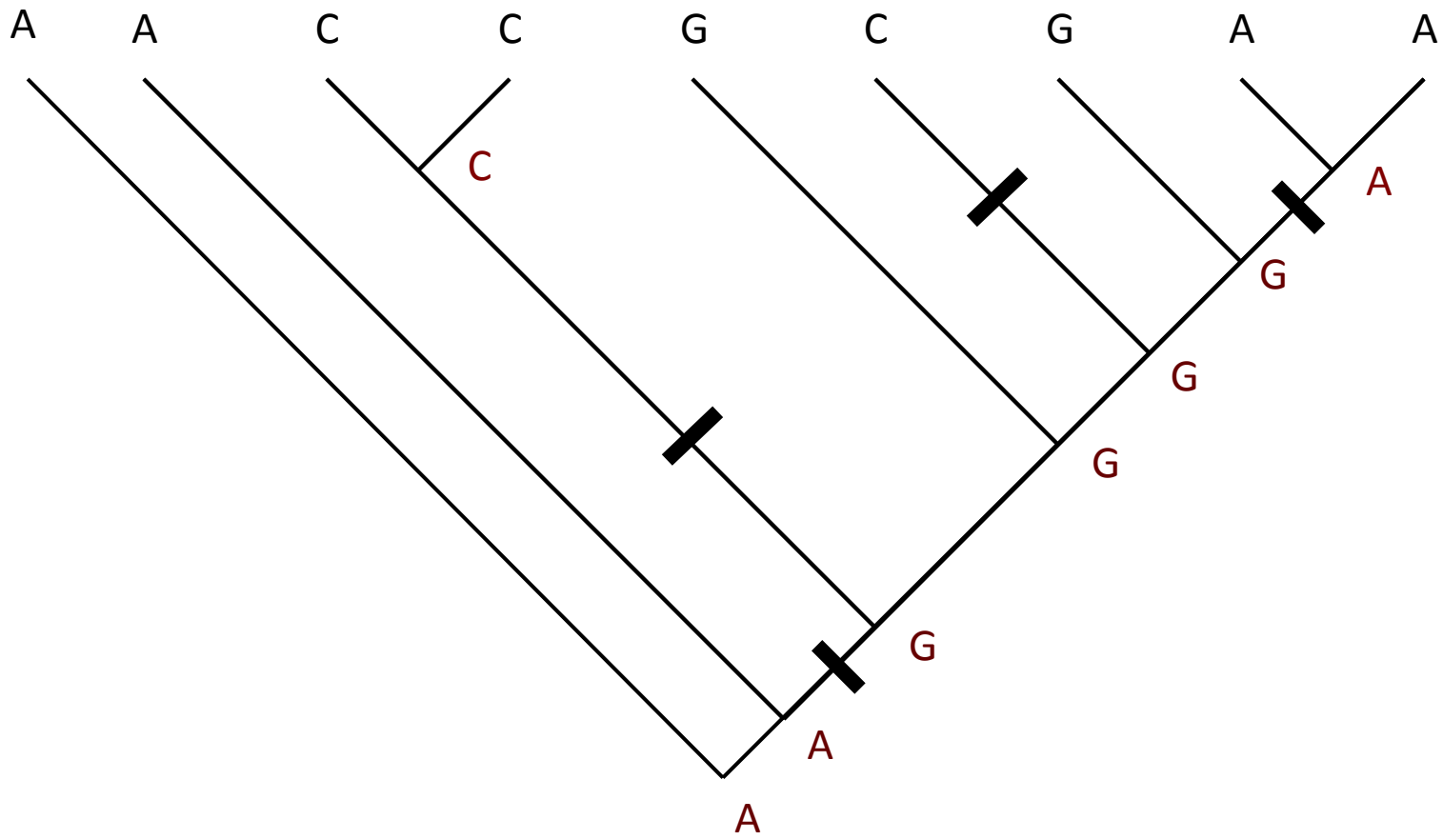


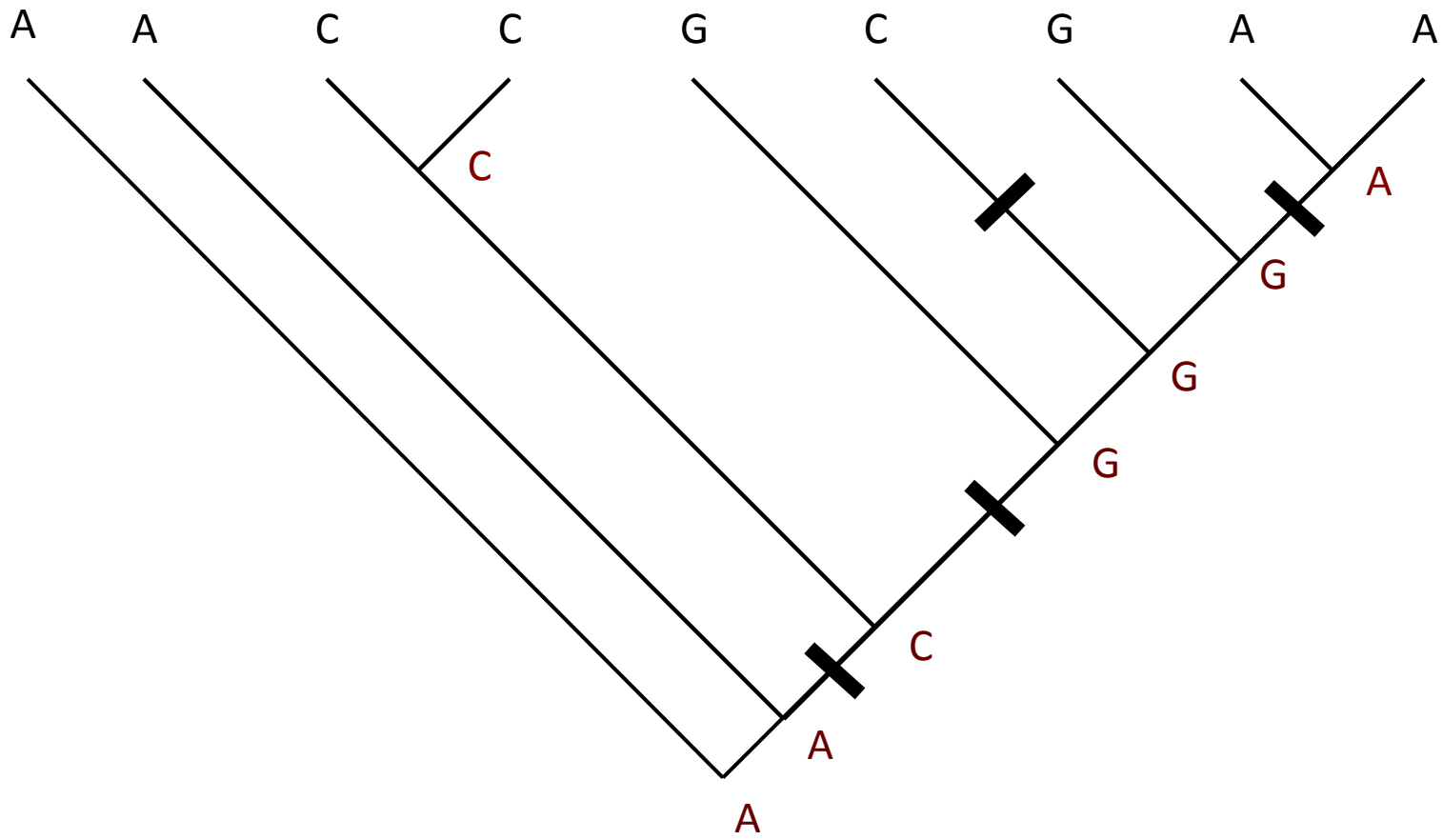
Up-Pass (preorder traversal)

Length = 4









# Weighted Parsimony

- Transformations among character-states do not need to be weighted equally
- Can account for different weights between transitions and transversions, for example
- A way to approximately incorporate some aspects of models of evolution

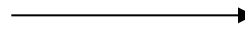
# Pairwise distances

- Distances summarize character differences between objects (terminals, taxa).
- Pairwise distances are computationally quick to calculate.
- Character differences cannot be recovered from distances, because different combinations of character states can yield the same distance.
- Characters cannot be compared individually, as in discrete character analyses.
- The distances in a matrix are not independent of each other, and errors are often compounded in fitting distances to a tree.

	Characters				
Taxa	1	2	3	4	5
one	A	G	C	G	A
two	A	G	C	G	T
three	C	T	C	G	T
four	C	T	C	A	A

Start with a data matrix of the usual form

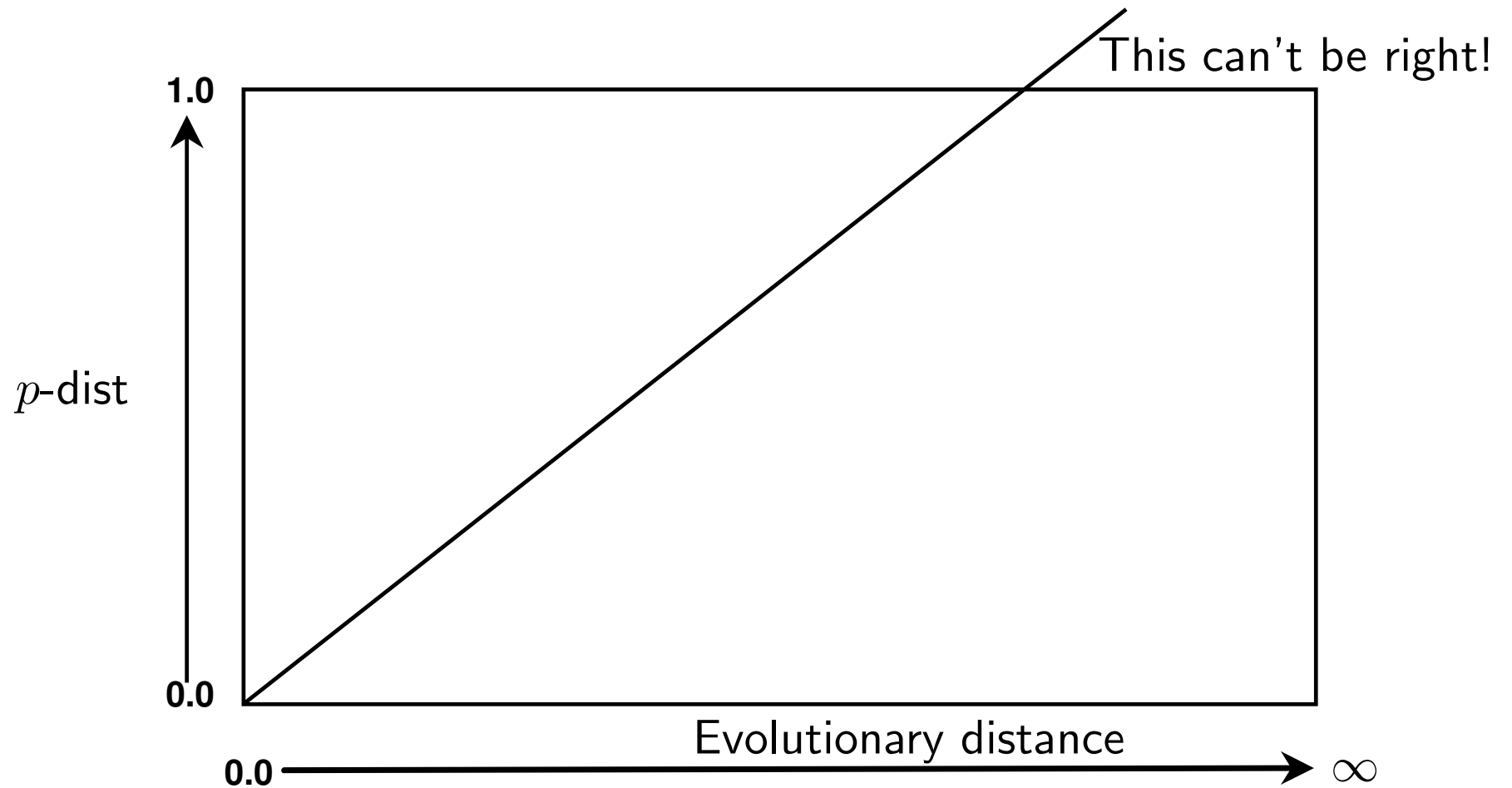
	Characters				
Taxa	1	2	3	4	5
one	A	G	C	G	A
two	A	G	C	G	T
three	C	T	C	G	T
four	C	T	C	A	A



	one	two	three	four
one	-	.2	.6	.6
two		-	.4	.8
three			-	.4
four				-

Compute a distance matrix of observed *proportional* distances

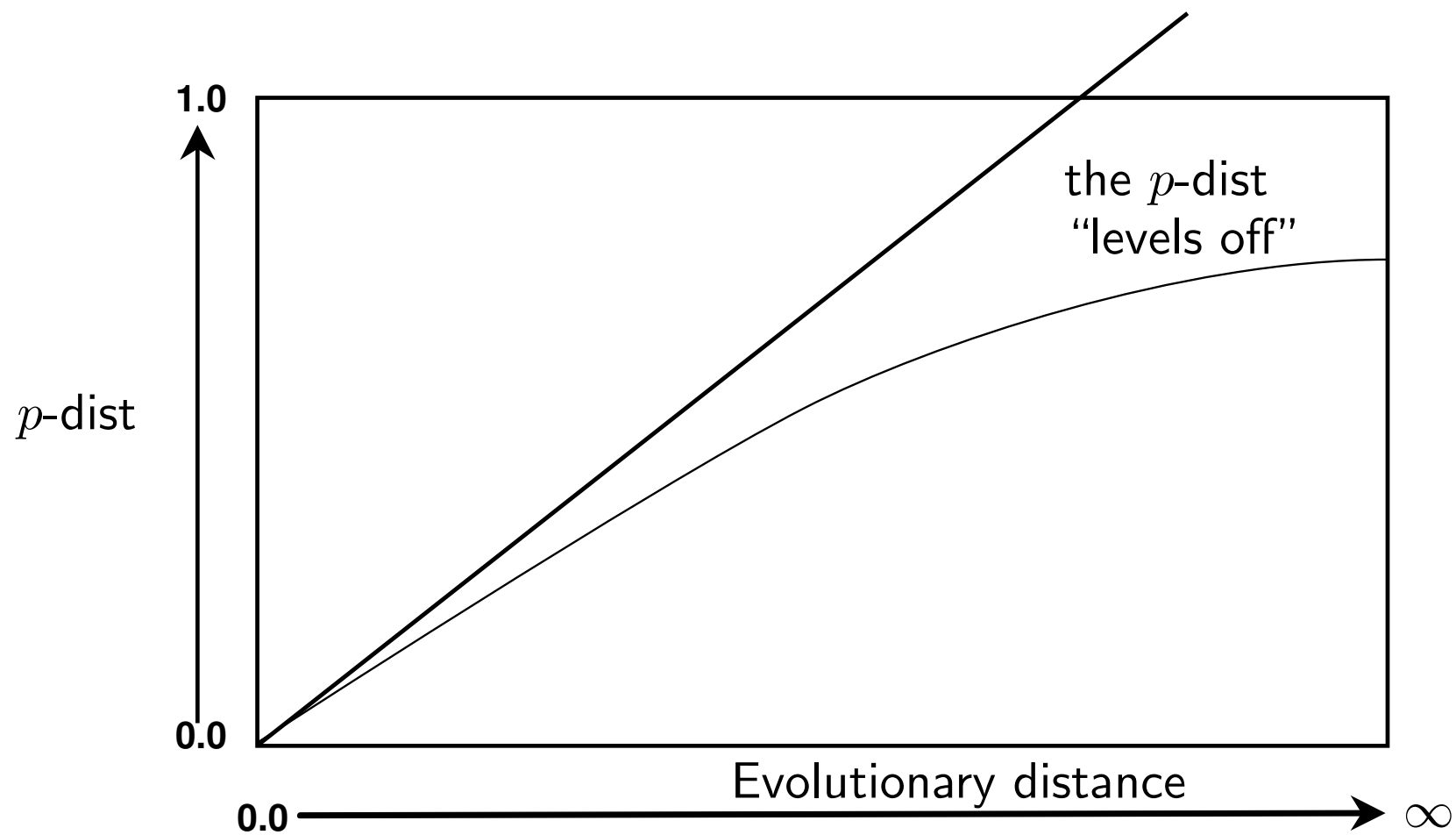
## Intuition of sequence divergence vs evolutionary distance



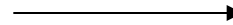


## Sequence divergence vs evolutionary distance

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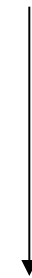


	Characters				
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one	A	G	C	G	A
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three	C	T	C	G	T
four	C	T	C	A	A



	one	two	three	four
one	-	.2	.6	.6
two		-	.4	.8
three			-	.4
four				-

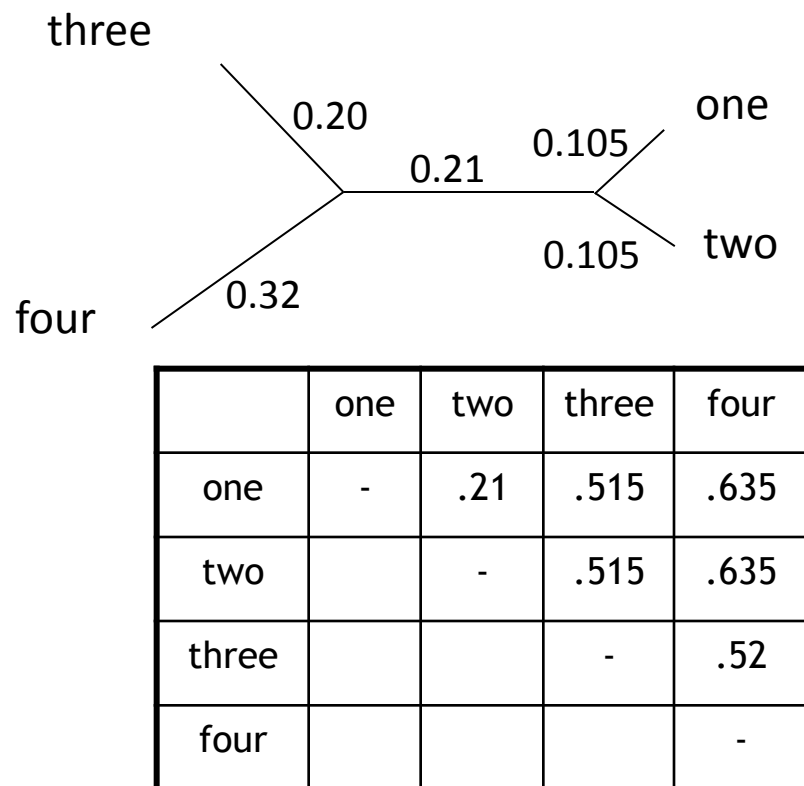
Model of evolution



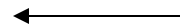
Transform the distance matrix ( $d_{ij}$ ) into a matrix of evolutionary (corrected) distances, using a model of evolution to account for superimposed changes (reversal, convergences, multiple changes, etc.). This is where the parametric model is applied (to many separate 2-taxon “trees”).

	one	two	three	four
one	-	.21	.63	.63
two		-	.42	.85
three			-	.42
four				-

Find the tree and branch lengths that result in the best match (using an objective function) between the corrected distance matrix ( $d_{ij}$ ) and the patristic distance matrix ( $p_{ij}$ ) (the matrix of path-length distances)



	one	two	three	four
one	-	.21	.63	.63
two		-	.42	.85
three			-	.42
four				-



# Optimality Criteria using Pairwise Distances

- Two commonly used **objective functions**:
  - Fitch-Margoliash
  - Minimum Evolution
- The general strategy is to find a set of patristic distances (path-length distances) for the branches so as to minimize the difference between the evolutionary distances and the patristic distances.

# Pairwise Distance Methods

- Fitch-Margoliash family

$$Fit = \sum_{1 \leq i < j < n} \omega_{ij} |d_{ij} - p_{ij}|^{\alpha}$$

i = taxon i

j = taxon j, up to n

d = evolutionary distance

p = patristic or tree distance

w = weight

Exponent: 2 = least squares

1 = absolute difference

## Common weights

$$w_{ij} = 1$$

$$w_{ij} = 1/d_{ij}$$

$$w_{ij} = 1/d_{ij}^2$$

# Pairwise Distance Methods

- Minimum Evolution

$$Fit = \sum_{1 \leq i < j < n} \omega_{ij} |d_{ij} - p_{ij}|^{\alpha}$$

1. Use  $w = 1$  and  $\alpha = 2$  to fit branch lengths  $l_i$
2. Pick the tree that minimizes the sum of the branch lengths,  $L$ , over all branches (this is parsimony in spirit):

$$L = \sum_{i=1}^{2n-3} l_i$$

# Algorithmic Methods for Distance Trees

- UPGMA--unweighted pair-group method using arithmetic means  
(not widely used anymore...assumes equal rates of change)
- Neighbor-joining--an approximation method for the minimum evolution criterion

# Likelihood

- Imagine that we are given a coin, and flip it  $n$  times, getting  $h$  heads: these are our data ( $D$ )
- We can explore various hypotheses ( $H$ ) about the coin, which may have implicit and explicit components:
  - The coin has a  $p_h$  probability of landing on heads
  - The coin has a heads side and a tails side
  - Successive flips of the coin are independent
  - The flipping process is fair
  - etc.



# Coin flipping

- The likelihood ( $L$ ) is proportional to the probability of observing our data, given our hypothesis:

$$L(H | D) \propto P(D | H)$$

- The probability of getting the outcome  $h$  heads on  $n$  flips is given by the binomial distribution:

$$P(h, n | p_h) = \binom{n}{h} (p_h)^h (1 - p_h)^{n-h}$$

(Likelihood score)

# Coin flipping

- The expression  $\binom{n}{h}$  gives the binomial coefficients, or the number of different ways to (for example) get 4 heads in 10 flips
- We can ignore that term to look at the probability of a particular sequence of heads and tails (to make it more like the case of a particular observed sequence of nucleotides)

# Coin flipping

- Let's try applying this to some data
  - Dataset 1 : A particular sequence of  
H T H T T T H T T H
- Assume a particular hypothesis
  - Try  $p_h = 0.5$
- This gives us a likelihood score of

$$L(p_h = 0.5 | obs) = (0.5)^4 (0.5)^6 = 0.000976563$$

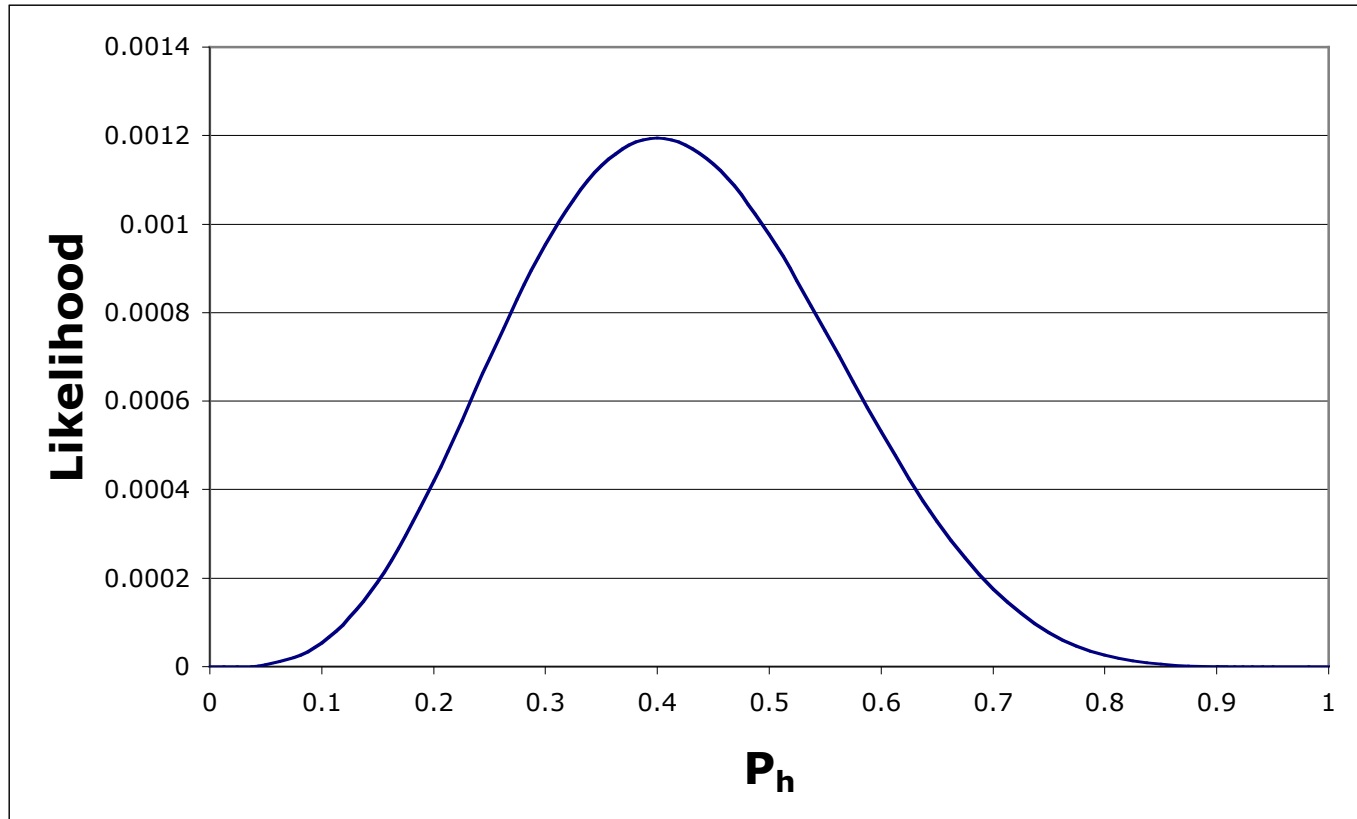
# Coin flipping

- What does the likelihood score tell us about the likelihood of our hypothesis? In isolation, nothing, because the score is dependent on the particular data set. The score will get smaller as we collect more data (flip the coin more times).
- Only the *relative* likelihood scores for various hypotheses, evaluated using the same data, are useful to us.
- What are some other models?

$$L(p_h = 0.6 | obs) = (0.6)^4 (0.4)^6 = 0.000530842$$

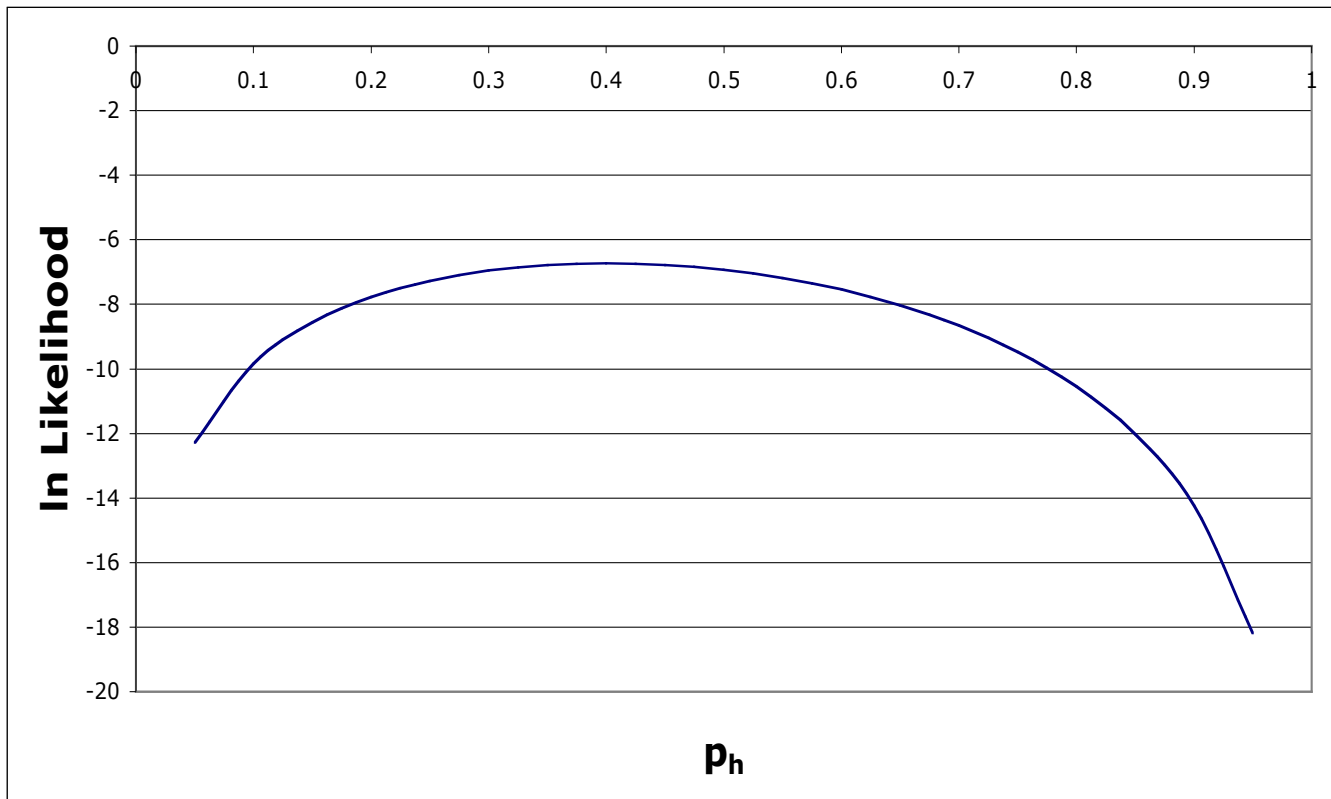
$$L(p_h = 0.4 | obs) = (0.4)^4 (0.6)^6 = 0.001194394$$

# The likelihood surface



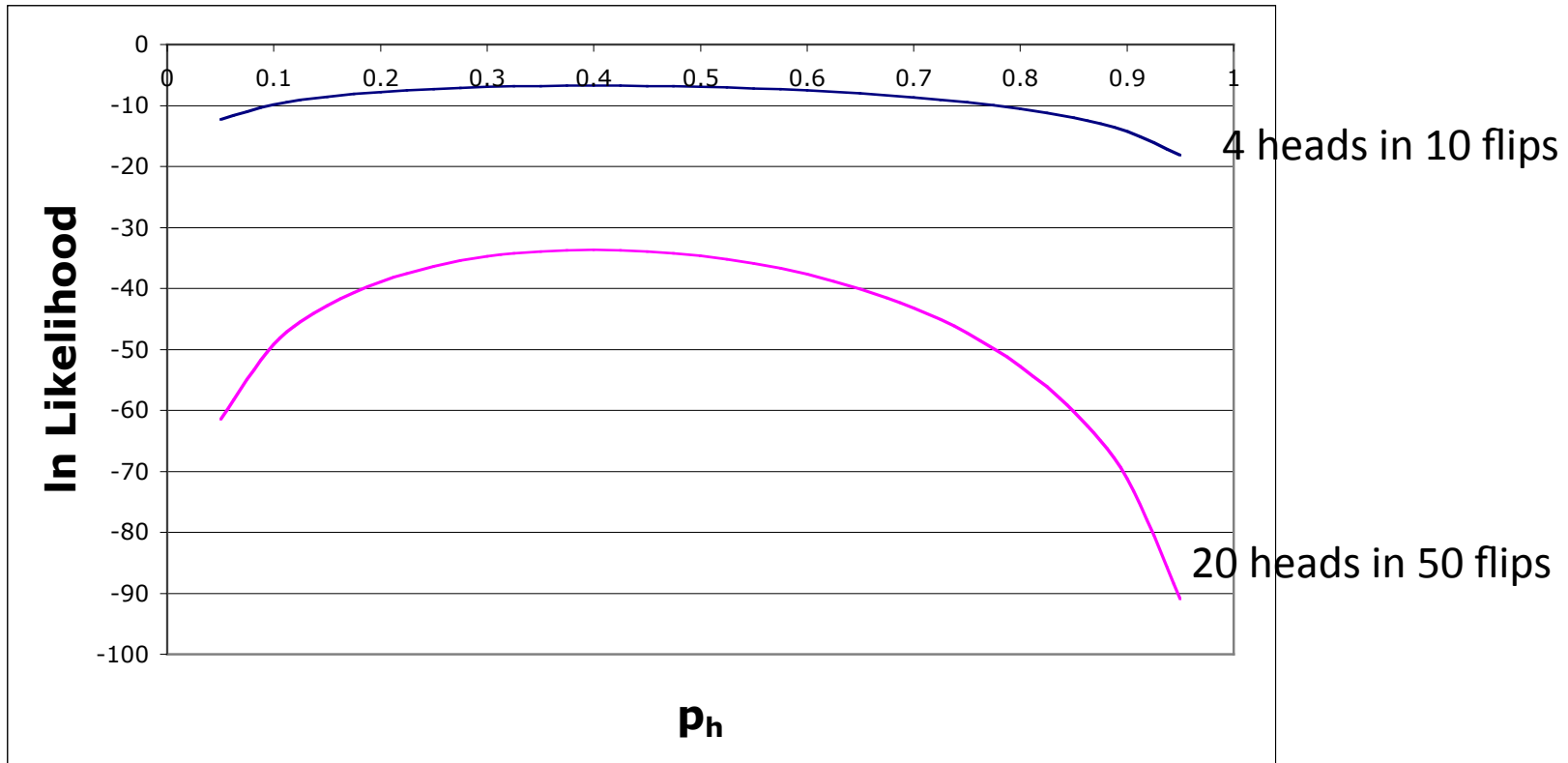
Data: H T H T T T H T T H

# The log likelihood surface



Data: HTHTTHTTH

# Other data



# Likelihood

- Likelihood ( $H|D$ ) is proportional to  $P(D|H)$
- Components of the hypothesis can be explicit and implicit
- Only relative likelihoods are important in evaluating hypotheses
- The point on the likelihood curve that maximizes the likelihood score (the MLE) is our best estimate given the data at hand
- Likelihood scores shouldn't be compared between datasets
- More data lead to more peaked surfaces (i.e., better ability to discriminate among hypotheses)



# Likelihood in Phylogenetics

- In phylogenetics, the **data** are the observed characters (e.g., DNA sequences) as they are distributed across taxa
- The **hypothesis** consists of the tree topology, a set of specified branch lengths, and an explicit model of character evolution.
- Calculating the likelihood score for a tree requires a very large number of calculations

# Bayesian Approaches

- Take prior information into account

$$P(A|B) = \frac{P(B|A) P(A)}{P(B)}$$

(Bayes Theorem)



Reverend Thomas Bayes, 1701-1761

# Bayesian Approaches

- Take prior information into account

$$P(A|B) = \frac{P(B|A) P(A)}{P(B)}$$

Posterior probability

# Bayesian Approaches

- Take prior information into account

$$P(A|B) = \frac{P(B|A)P(A)}{P(B)}$$

The support that  $B$  provides for  $A$

# Bayesian Approaches

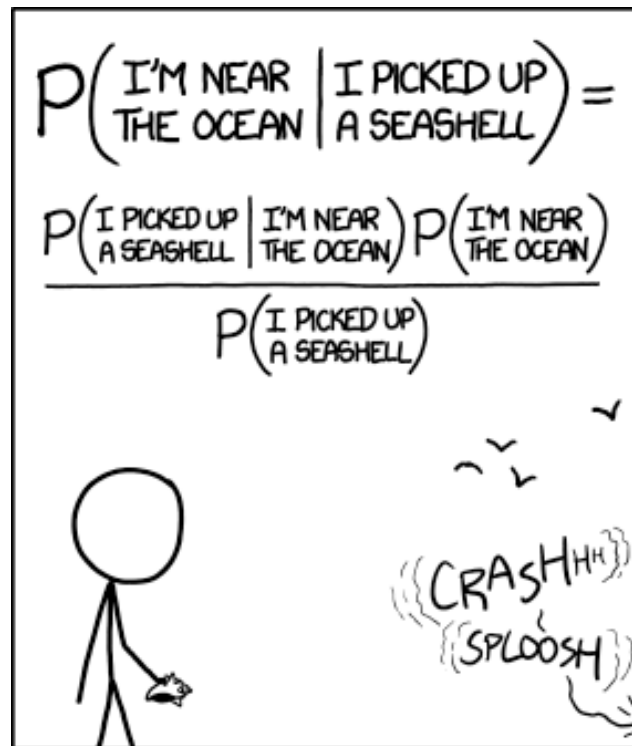
- Take prior information into account

$$P(A|B) = \frac{P(B|A) \boxed{P(A)}}{P(B)}$$

Prior information about A  
(the initial expectation for A)

# Bayesian Approaches

- An example:



STATISTICALLY SPEAKING, IF YOU PICK UP A SEASHELL AND DON'T HOLD IT TO YOUR EAR, YOU CAN PROBABLY HEAR THE OCEAN.

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- Optimality criterion (likelihood-based methods have best performance, as long as assumptions of model are met)

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- Sampling density of genes (more genes provide more information, and allow resolution of species trees from gene trees)
- Sampling density of taxa (more thorough taxon sampling produces better estimates of parameters and results in better estimates of trees)

