

Lecture 11

Molecular phylogenetics



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Lecture 11 outline

Last time: regex

This time: phylogenetics

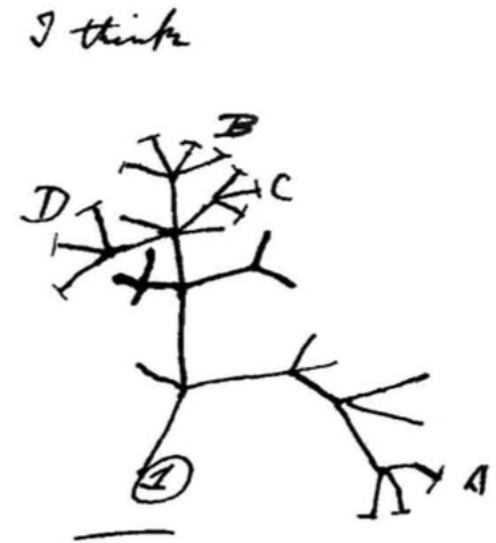
- interpreting trees
- tree-thinking
- inferring trees
- inference methods

Phylogenetics

Phylogenetics studies the relationships among evolutionary lineages (often called **taxa**)

Phylogenies are useful for

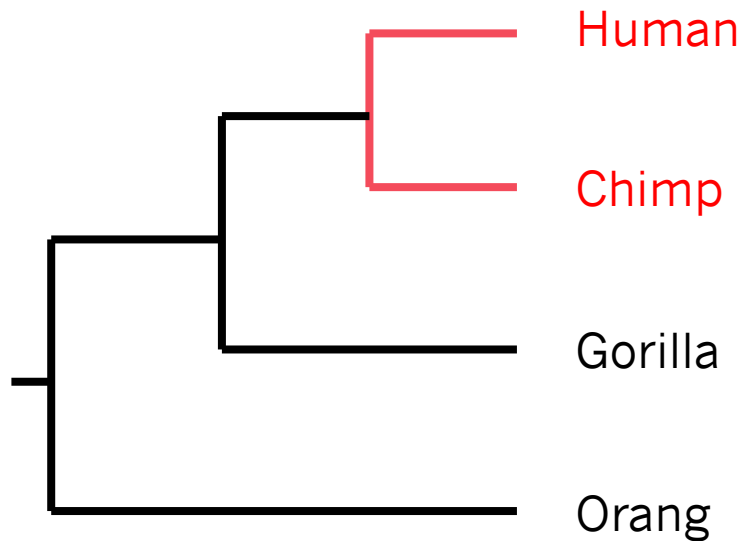
- gene annotation
- tracking viral spread
- identifying zoonosis
- reconstructing tumorigenesis
- conservation biology assays
- inferring species relationships



phylogeny sketch
by Darwin

Reading a phylogeny

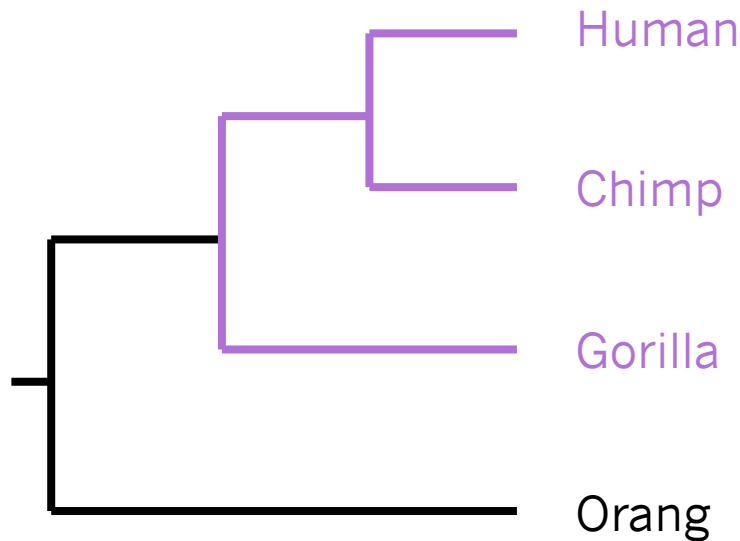
Phylogenetic relationships are hierarchical,
and most often represented as bifurcating **trees**



Human and Chimp are
more closely related to
each other than to
Gorilla or Orang

Reading a phylogeny

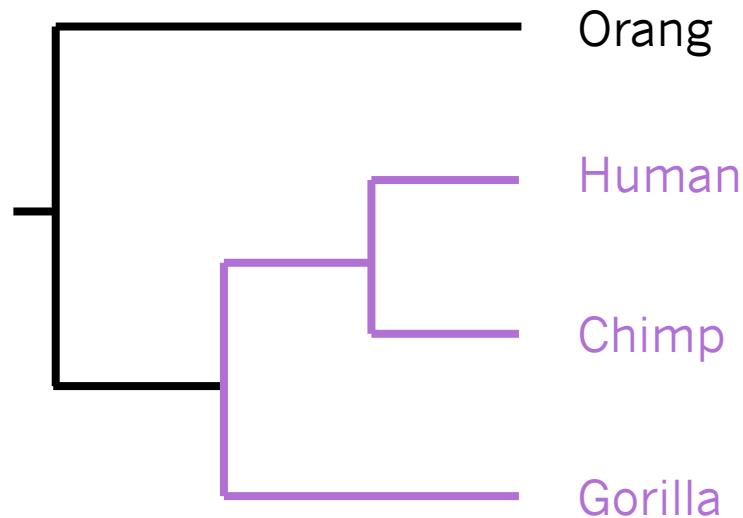
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Reading a phylogeny

Phylogenetic relationships are hierarchical, and most often represented as bifurcating **trees**

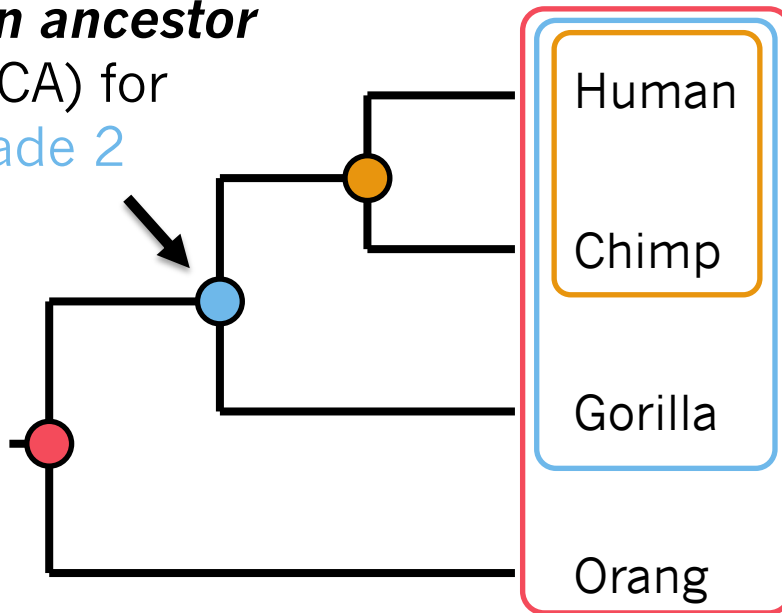


Human, Chimp and Gorilla are more closely related to each other than to Orang

Reading a phylogeny

Taxa that are more closely related to one another, over any other taxa, are called **clades**

**most recent
common ancestor**
(MRCA) for
Clade 2



Clade 1: H+C

Clade 2: H+C+G

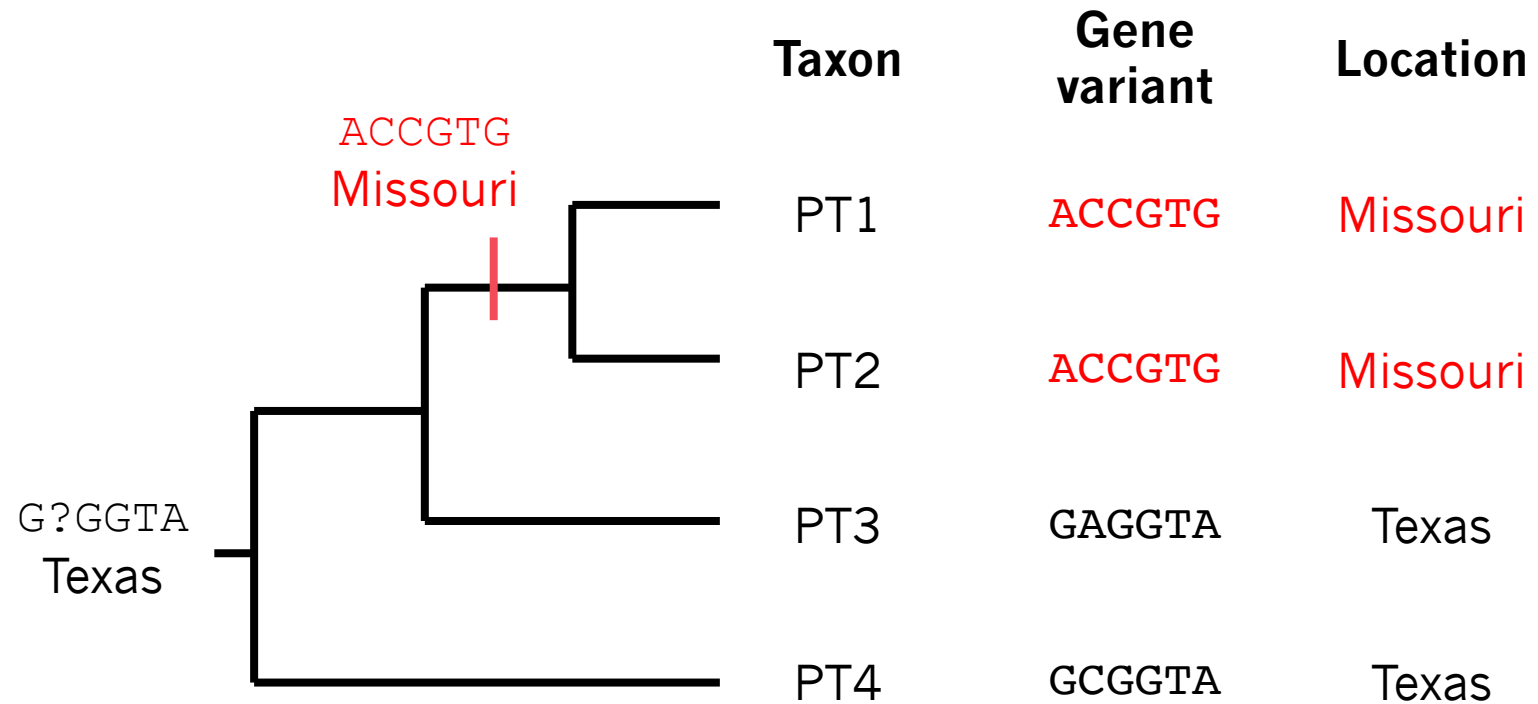
Clade 3: H+C+G+O

“Tree-thinking”

Taxon	Gene variant	Location
PT1	ACCGTG	Missouri
PT2	ACCGTG	Missouri
PT3	GAGGTA	Texas
PT4	GCGGTA	Texas

Four sequences,
but no historical context

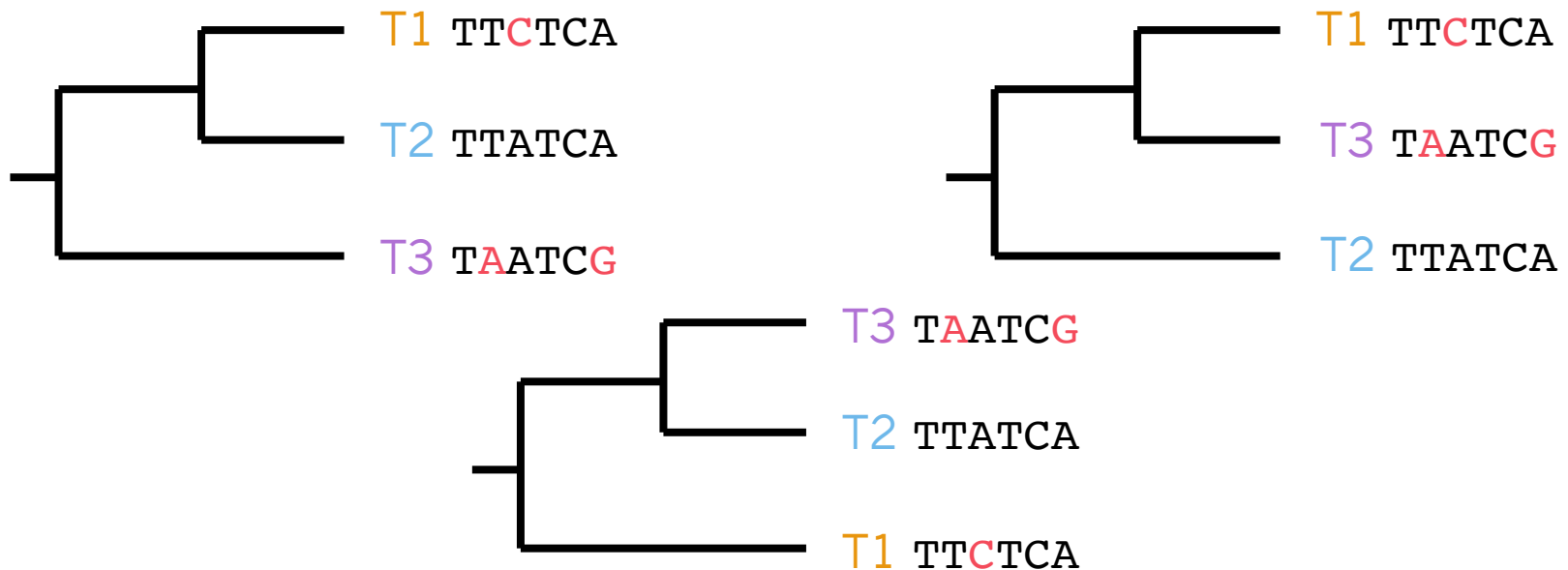
“Tree-thinking”



Phylogeny informs when and where variation arose,
which can guide future research

Inferring phylogeny

How are taxa T1, T2, and T3 related?



Which phylogeny generated the observed pattern of molecular variation?

Inferring phylogeny

Phylogenetic inference methods take a matrix of characters (e.g. *DNA alignment*) as input

Measure how well any possible phylogenetic estimate explains the data matrix pattern by assigning a **cost** to each considered estimate

Methods generally **optimize** the cost to estimate the phylogeny with the lowest cost for the provided data matrix

Phylogenetic method types

Most methods used to infer phylogenies compute scores based on

1. pattern distances (e.g. ***neighbor joining***)
2. event counting (***parsimony***)
3. event probabilities (***likelihood***)

Method choice often relates to concerns regarding accuracy, speed, scalability, etc.

Tree-space is large

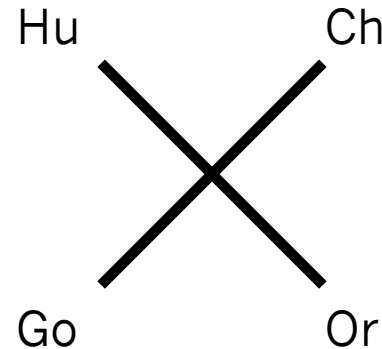
# taxa	# rooted trees
3	3
4	15
5	105
6	945
7	10395
8	135135
9	2027025
10	34459425

A major challenge: how to efficiently search
for trees with optimal scores?

Neighbor-joining

	Hu	Ch	Go	Or
Hu	0	1	3	5
Ch	1	0	3	5
Go	3	3	0	2
Or	5	5	2	0

divergence matrix
for sequence pairs

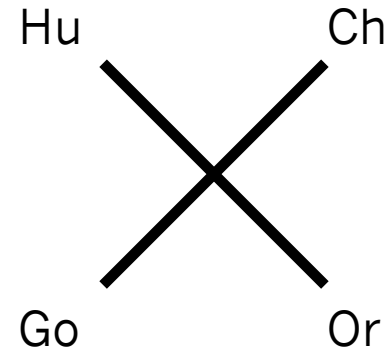


Divergence matrix is
based on relative distances
among sequences

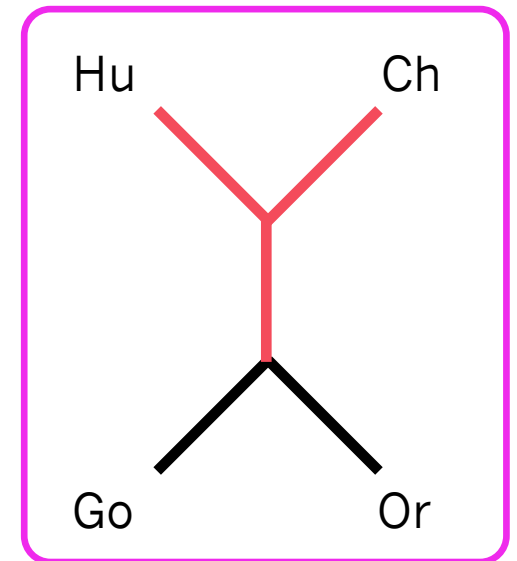
Neighbor-joining

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divergence matrix
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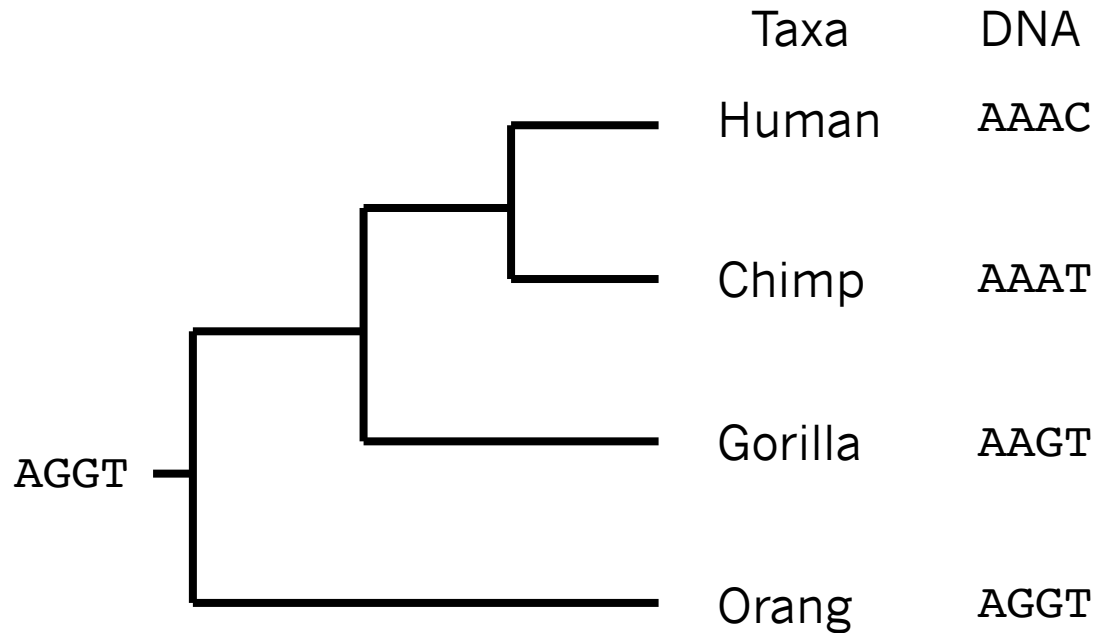


Hu and Ch
form a cluster



Join sequences with least divergence as
clade, assign length to new branch that
minimizes other divergence scores

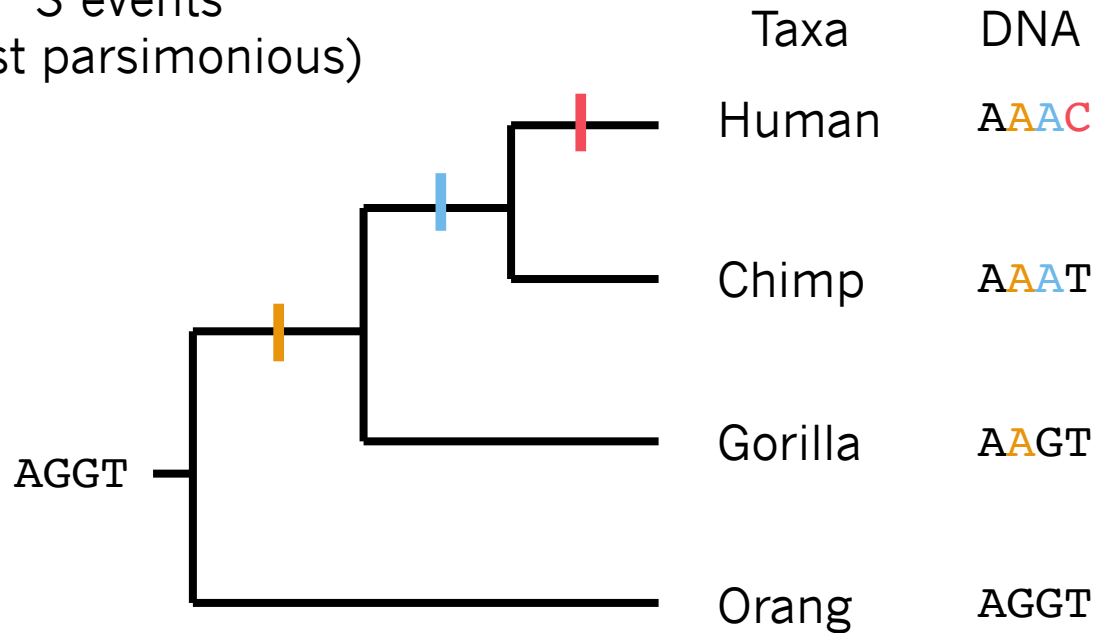
Parsimony



What phylogeny requires the fewest character change events?

Parsimony

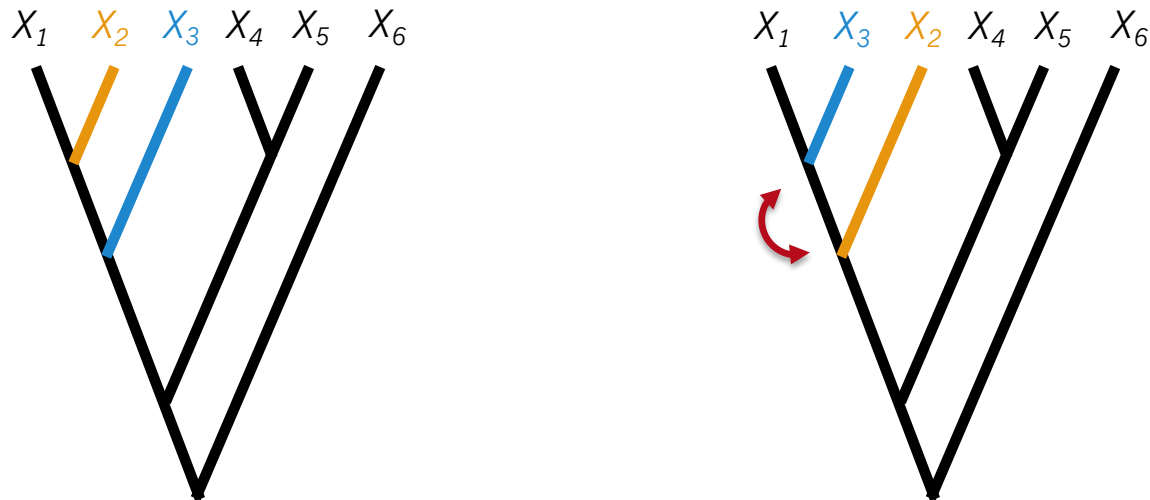
3 events
(most parsimonious)



What phylogeny requires the fewest
character change events?

Exploring tree space

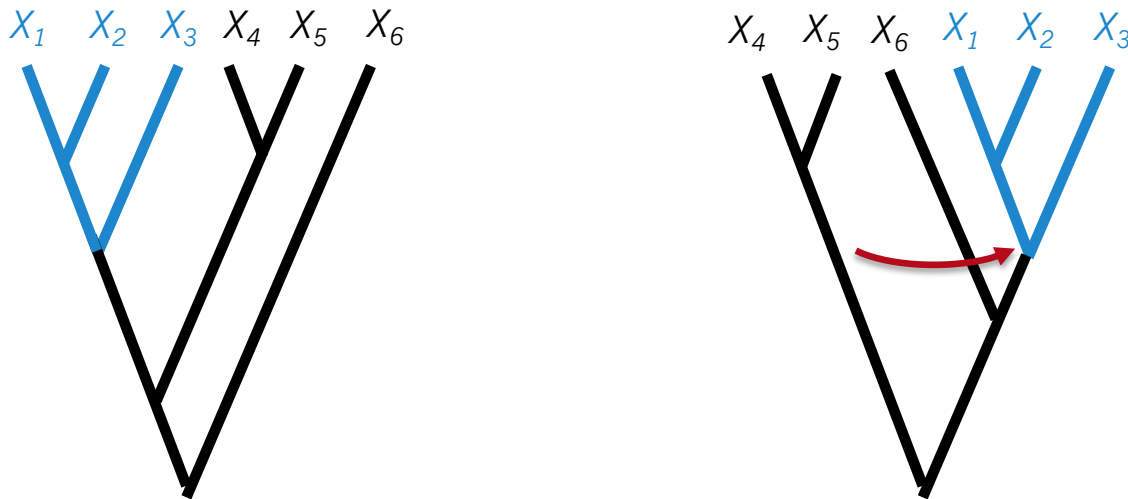
Define stochastic “moves” that modify topology,
prefer moves that improve tree score



Nearest neighbor interchange (NNI)

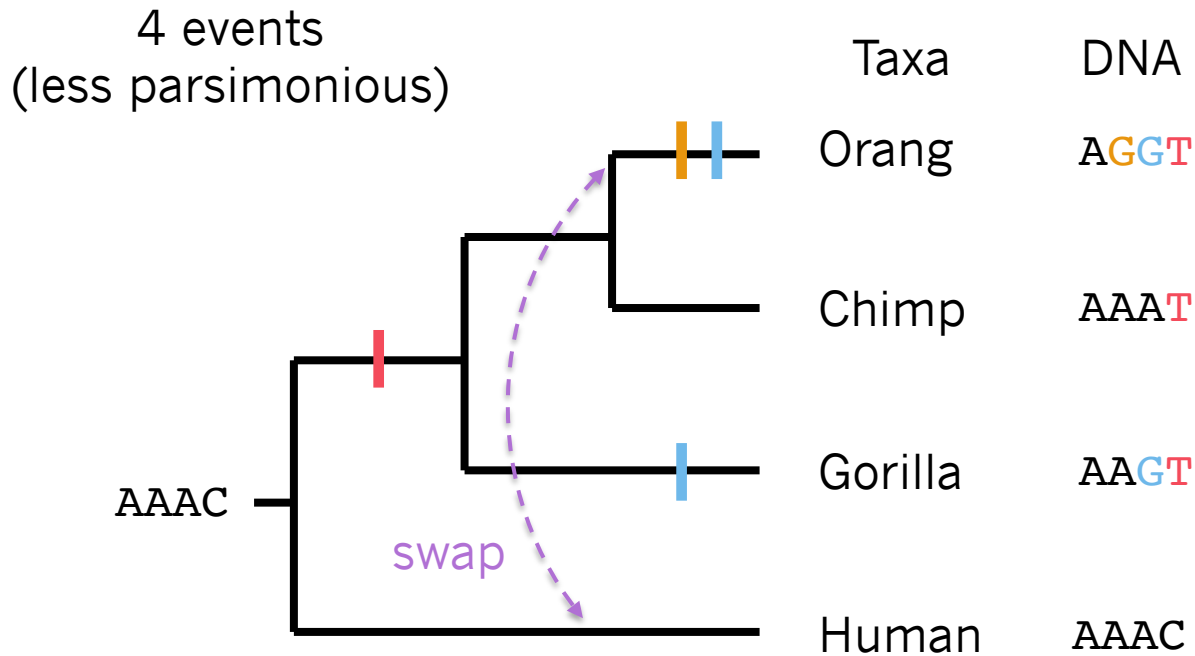
Exploring tree space

Define stochastic “moves” that modify topology,
prefer moves that improve tree score



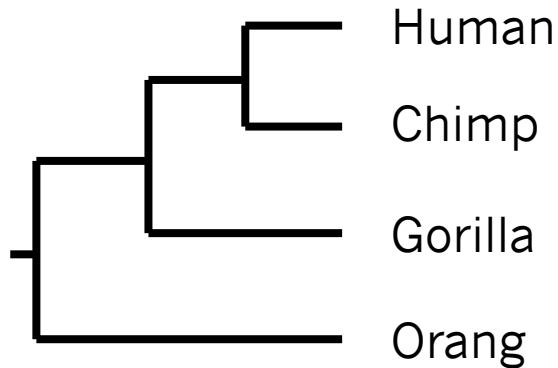
Subtree-prune-regraft (SPR)

Parsimony

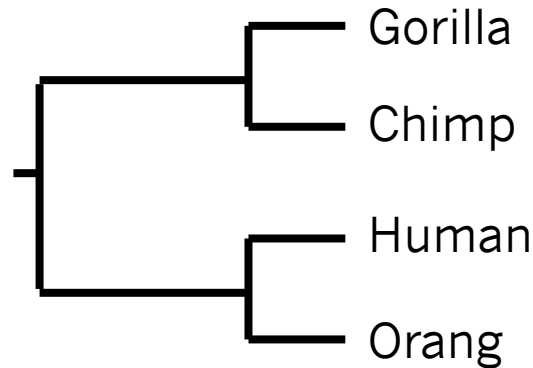


What phylogeny requires the fewest character change events?

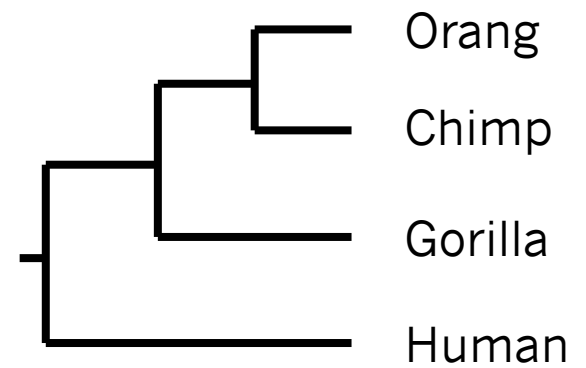
Parsimony



3 events



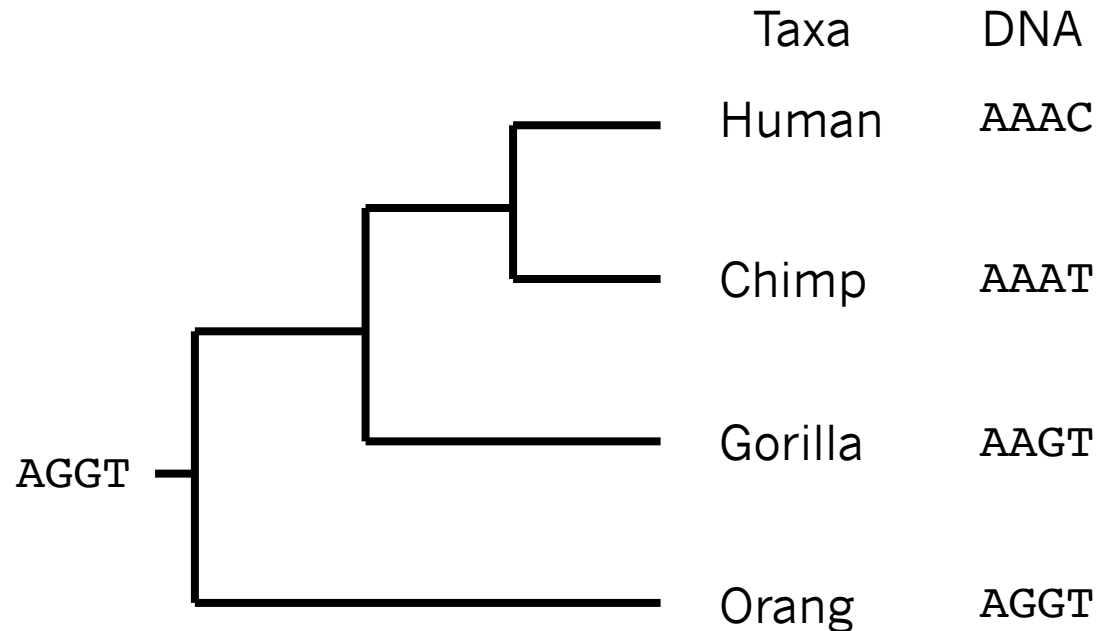
7 events



4 events

What phylogeny requires the fewest character change events?

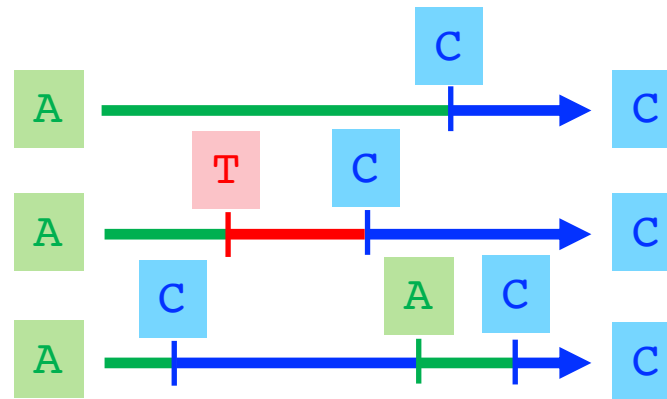
Likelihood



What phylogeny and model of evolution is *most likely* to generate the character data?

Likelihood for single site and single branch

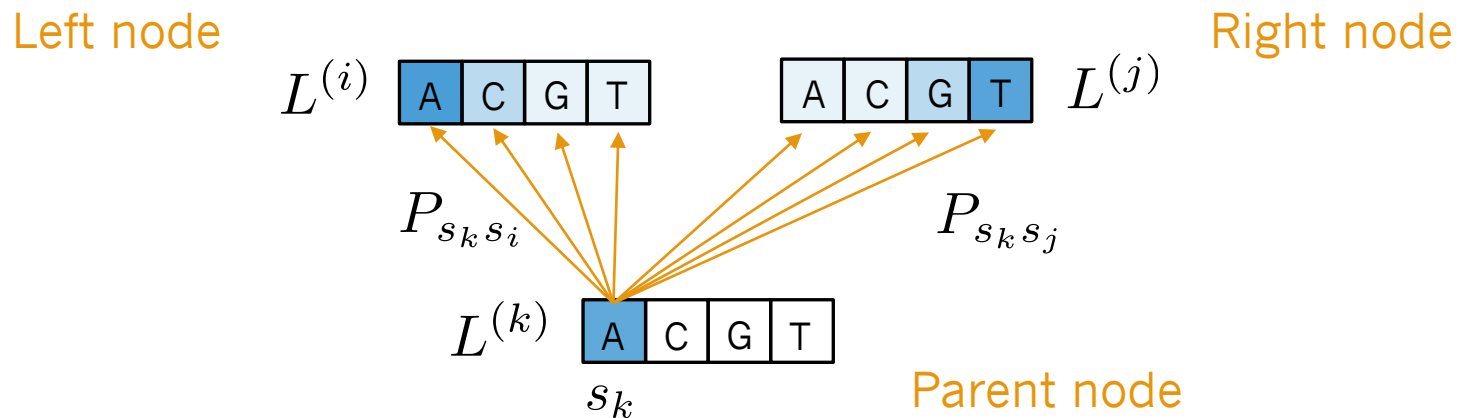
A single site is in one four discrete states: A, C, G, T



(possible evolutionary histories)

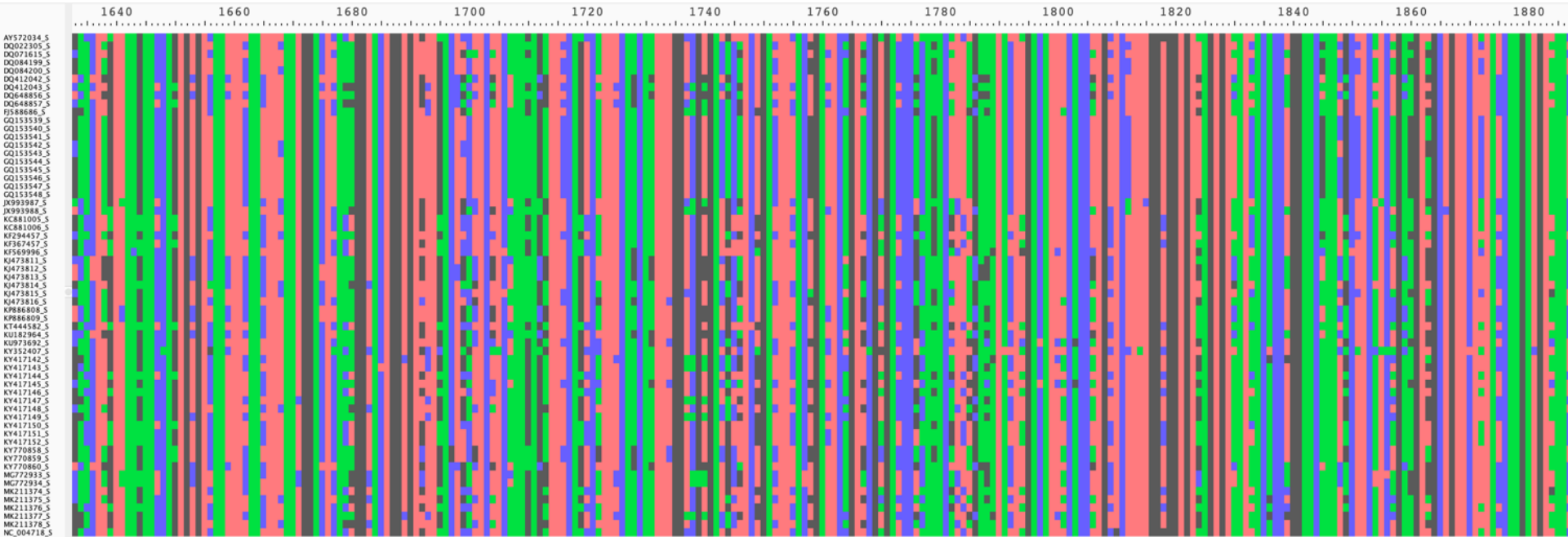
What is the probability to start in state **A** and end in state **C** along branch of length t ?

Phylogenetic marginalization



Using the **pruning algorithm** to move “backwards in time”;
compute the **partial likelihood** for each ancestral node state
based on its descendants' states

Phylogenetic likelihood

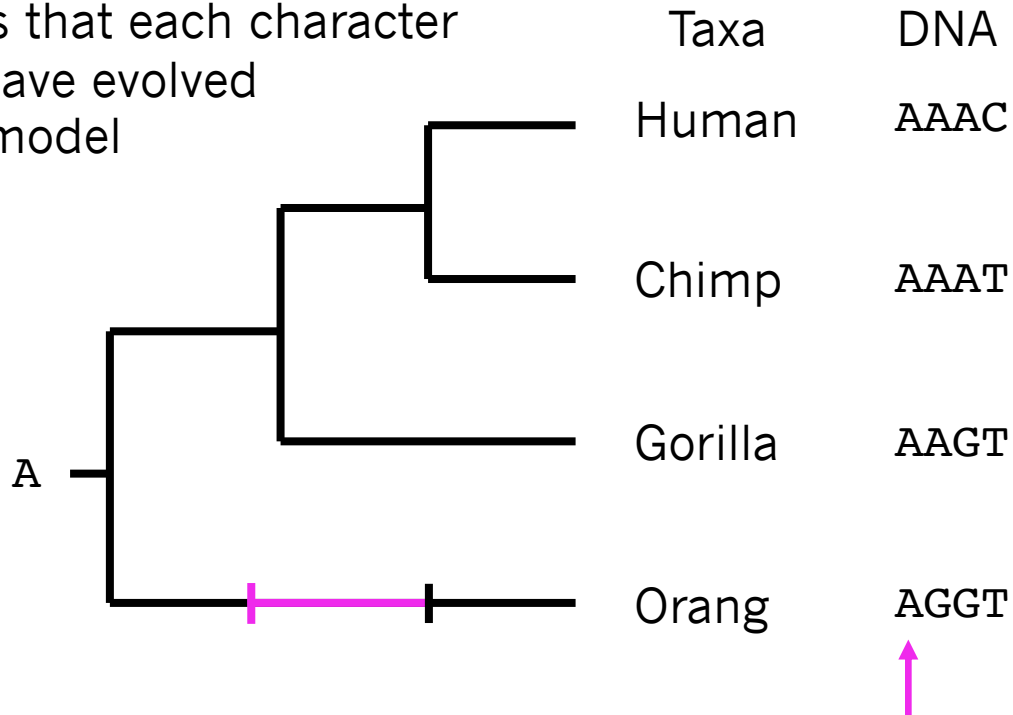


↑
single
site

Compute the total phylogenetic likelihood as
the product of likelihoods across all sites

Likelihood

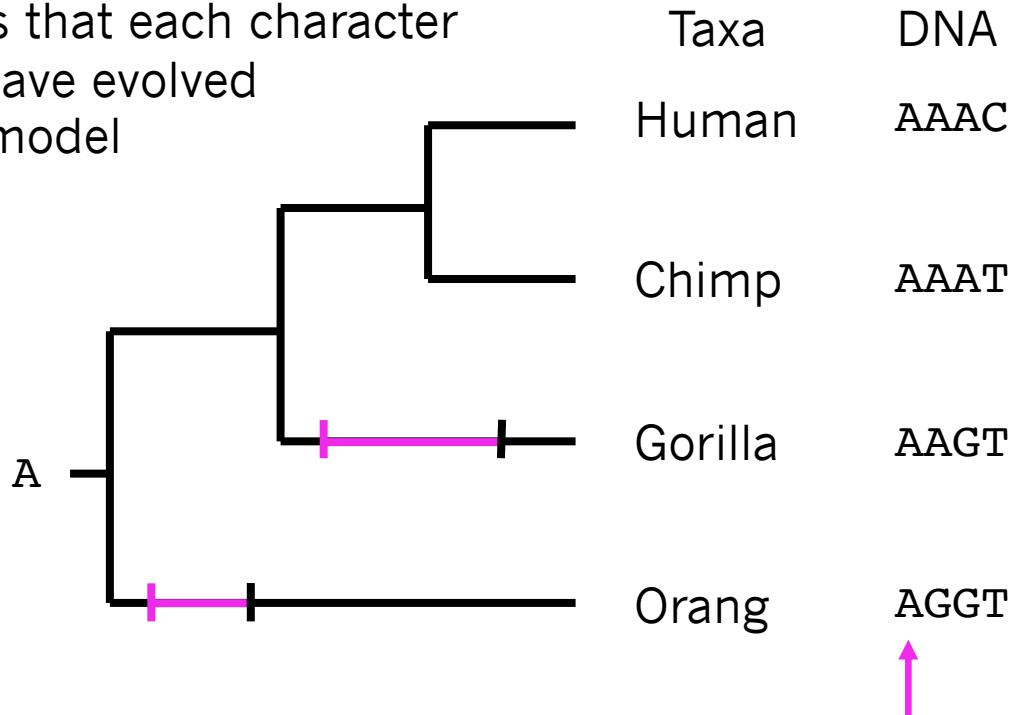
Compute probability for
all ways that each character
could have evolved
under model



What phylogeny and model of evolution is
most likely to generate the character data?

Likelihood

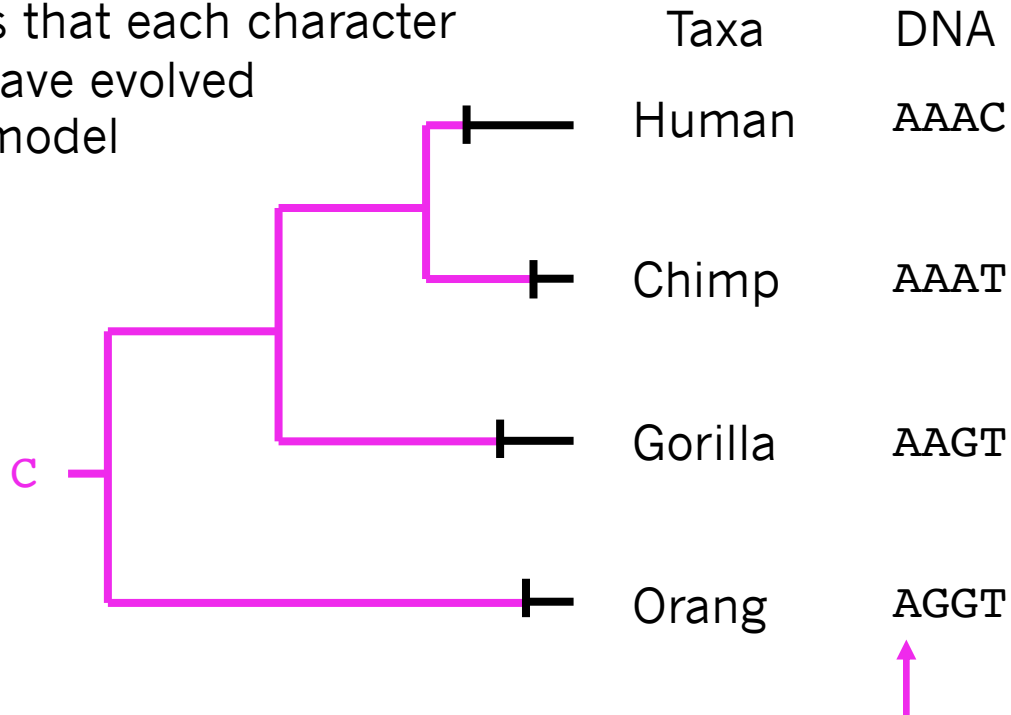
Compute probability for
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What phylogeny and model of evolution is
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Likelihood

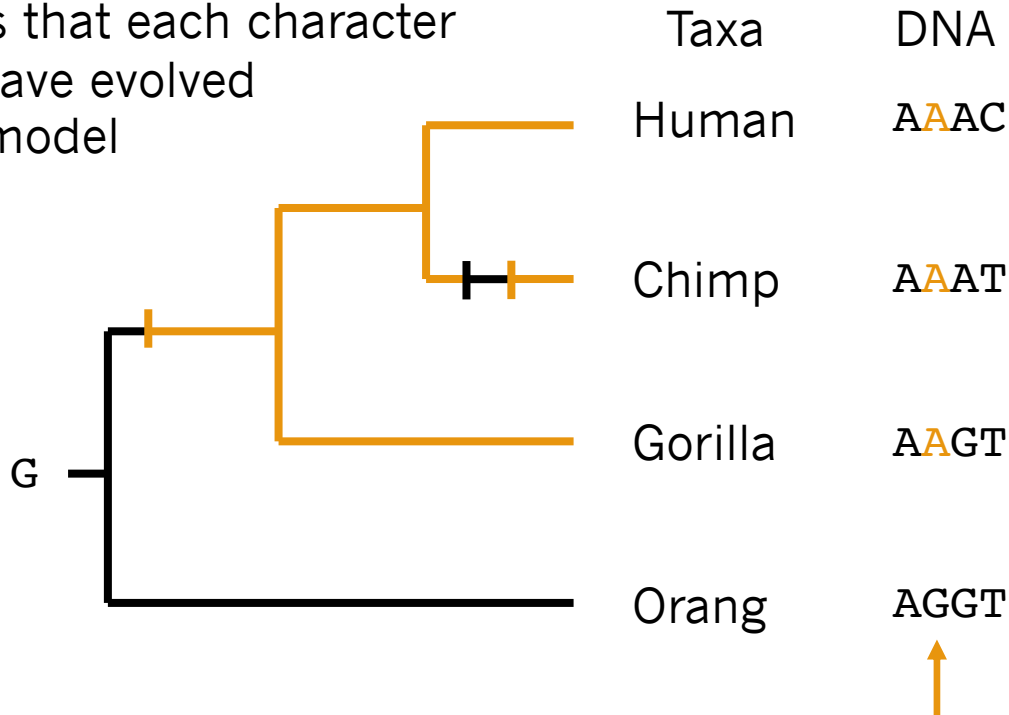
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What phylogeny and model of evolution is
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Likelihood

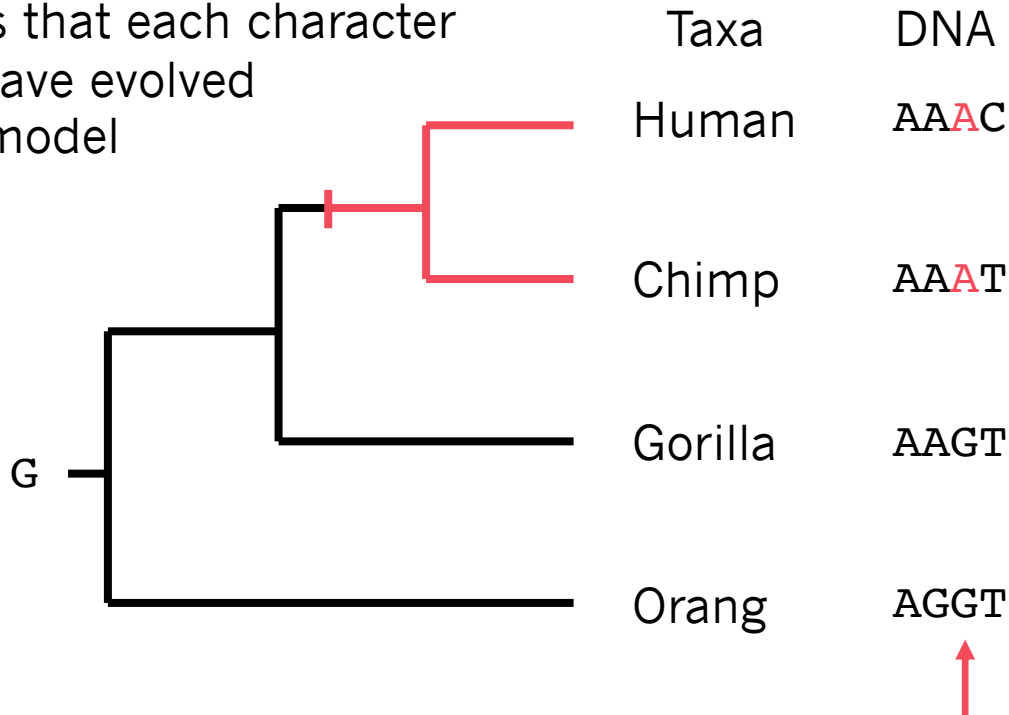
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Likelihood

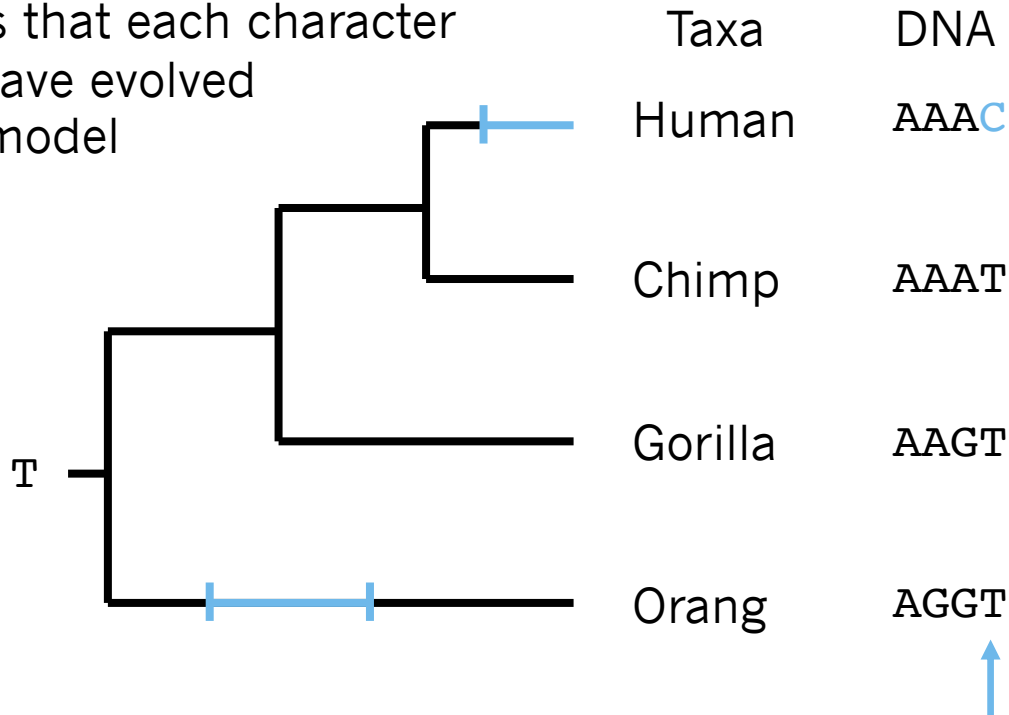
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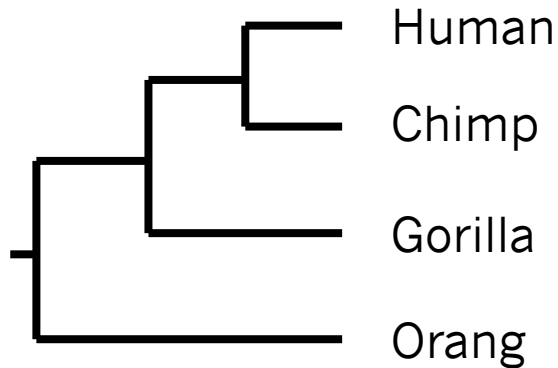
Likelihood

Compute probability for all ways that each character could have evolved under model

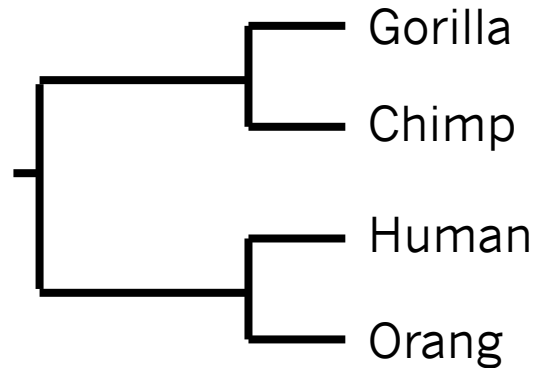


What phylogeny and model of evolution is *most likely* to generate the character data?

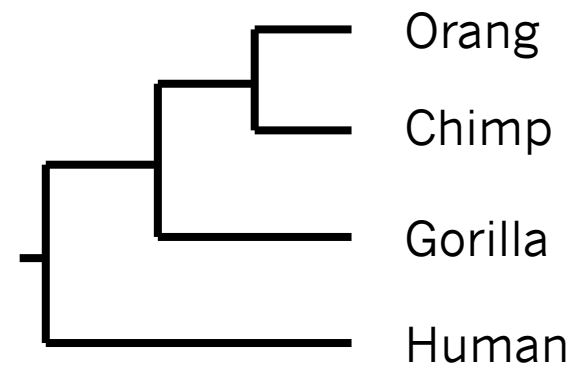
Likelihood



log-likelihood = -32.14



log-likelihood = -42.77



log-likelihood = -39.08

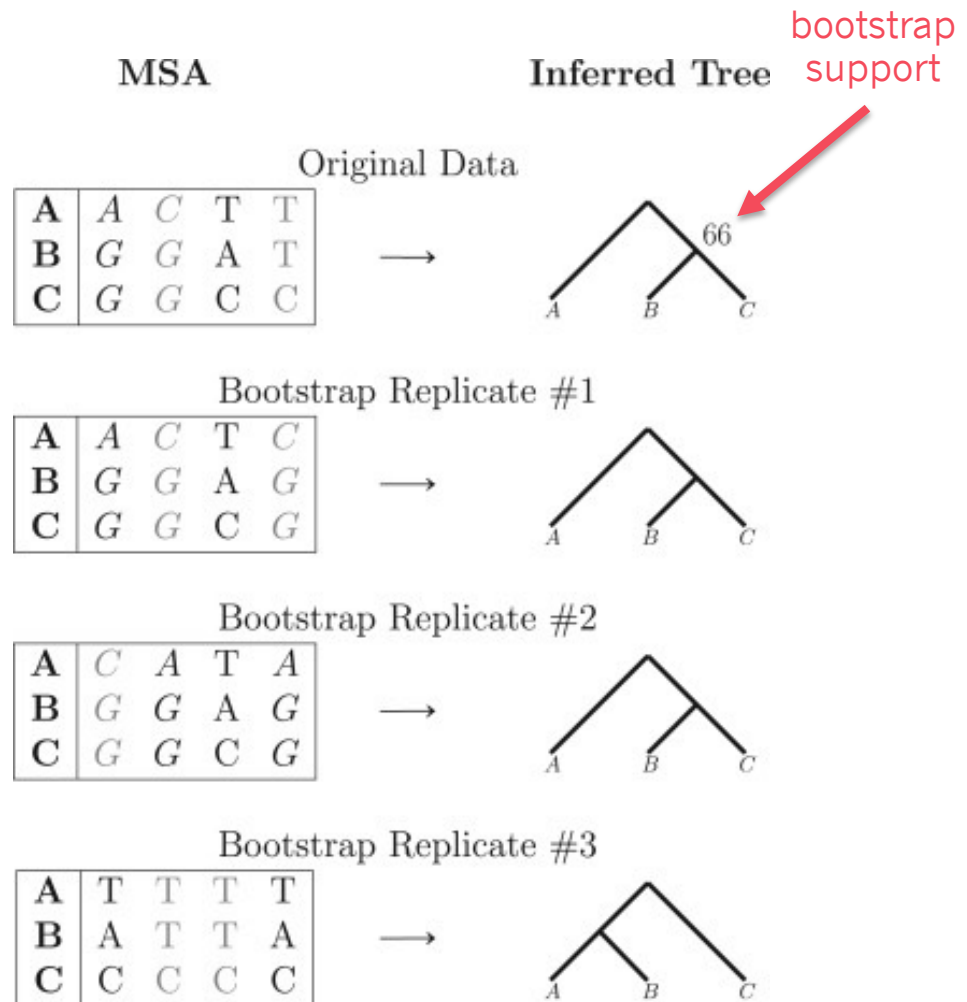
What phylogeny and model of evolution is *most likely* to generate the character data?

Clade support

Clade support measures our statistical confidence for each clade

Bootstrap support:

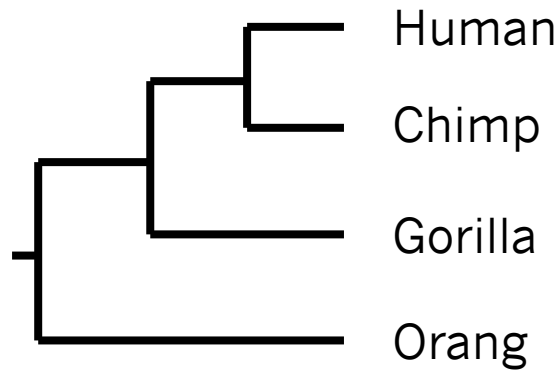
1. estimate a tree from the original dataset
2. simulate K replicate datasets by resampling sites *with replacement* from the original dataset
3. estimate a new tree for each of the K replicates
4. report the frequency (k/K %) for each clade in the original tree



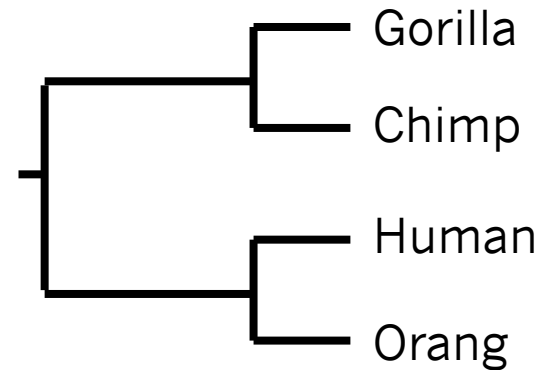
Method comparison

Method	Pros	Cons
Neighbor-joining	Extremely fast Scalable	Does not use evolutionary events to infer tree
Parsimony	Intuitive Fairly fast	Assumes change is rare; Event costs are arbitrary
Likelihood	Most accurate Most realistic Can simulate data	Slower Complex theory + algorithms

Newick strings



`((Human,Chimp),Gorilla),Orang);`



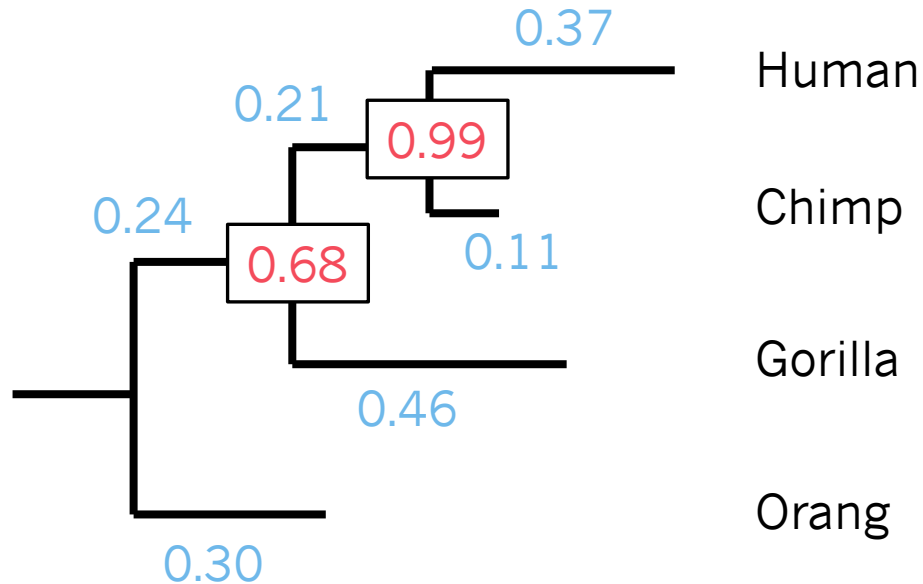
`((Gorilla,Chimp),(Human,Orang));`

Taxa in parentheses define clades;
commas define divergence events

Newick strings

Branch lengths measure molecular distances in expected # substitutions per site

Clade support measures reliability of clade in a tree estimate



```
((Human:0.37,Chimp:0.11)0.99:0.21,  
Gorilla:0.46)0.68:0.24,Orang:0.30);
```

Overview for Lab 11