CSE 527
Autumn 2009

10. Parsimony and Phylogenetic Footprinting

Phylogenies
(aka Evolutionary Trees)

"Nothing in biology makes sense, except in the light of evolution"

-- Theodosius Dobzhansky, 1973

A Complex Question:

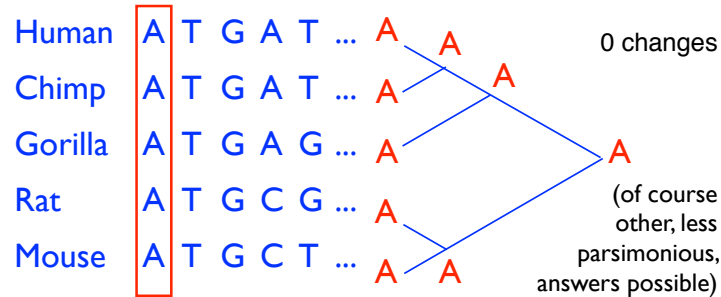Given data (sequences, anatomy, ...) infer the phylogeny

A Simpler Question:

Given data *and a phylogeny*, evaluate "how much change" is needed to fit data to tree

Parsimony

General idea ~ Occam's Razor:
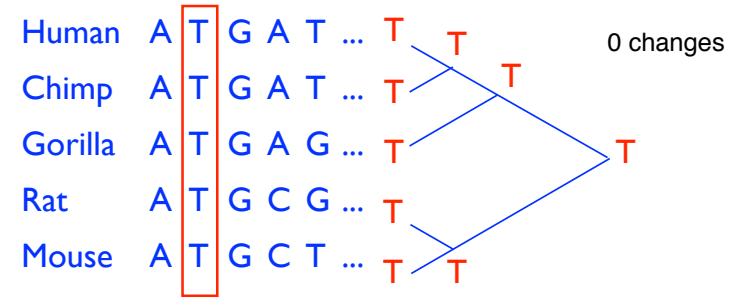Given data where change is rare, prefer an explanation that requires few events

Human	A T G A T ...
Chimp	A T G A T ...
Gorilla	A T G A G ...
Rat	A T G C G ...
Mouse	A T G C T ...

Parsimony

General idea ~ Occam's Razor:
Given data where change is rare, prefer
an explanation that requires few events

Human   A T G A T ... A   A   0 changes
Chimp   A T G A T ... A   A
Gorilla A T G A G ... A   A
Rat   A T G C G ... A
Mouse   A T G C T ... A   A
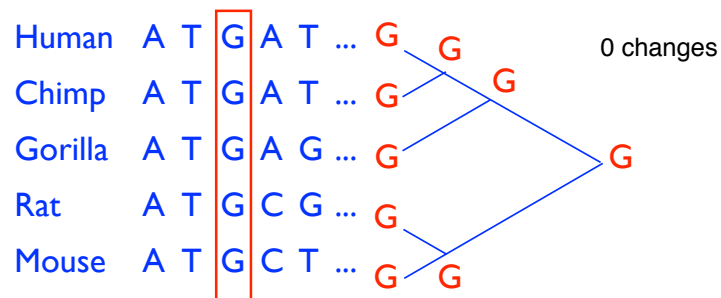
(of course
other, less
parsimonious,
answers possible)

Parsimony

General idea ~ Occam's Razor:
Given data where change is rare, prefer
an explanation that requires few events

Human   A T G A T ... T   T   0 changes
Chimp   A T G A T ... T   T
Gorilla A T G A G ... T   T
Rat   A T G C G ... T
Mouse   A T G C T ... T   T

Parsimony

General idea ~ Occam's Razor:
Given data where change is rare, prefer
an explanation that requires few events

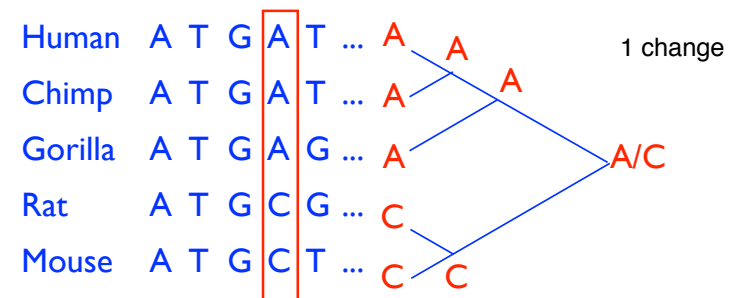Human   A T G A T ... G   G   0 changes
Chimp   A T G A T ... G   G
Gorilla A T G A G ... G   G
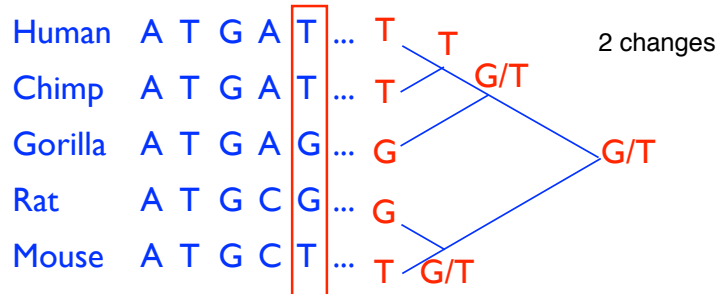Rat   A T G C G ... G
Mouse   A T G C T ... G   G

Parsimony

General idea ~ Occam's Razor:
Given data where change is rare, prefer
an explanation that requires few events

Human   A T G A T ... A   A   1 change
Chimp   A T G A T ... A   A
Gorilla A T G A G ... A   A/C
Rat   A T G C G ... C
Mouse   A T G C T ... C   C

Parsimony

General idea ~ Occam's Razor:
Given data where change is rare, prefer
an explanation that requires few events

Human	A	T	G	A	T	...	T	T
Chimp	A	T	G	A	T	...	T	G/T
Gorilla	A	T	G	A	G	...	G	G/T
Rat	A	T	G	C	G	...	G	
Mouse	A	T	G	C	T	...	T	G/T

2 changes

Counting Events Parsimoniously

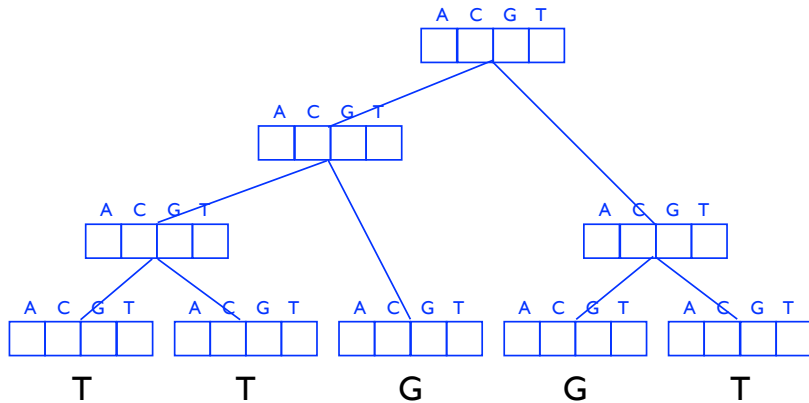Lesson of example – no unique reconstruction

But there is a unique minimum number, of course

How to find it?

Early solutions 1965-75

Sankoff & Rousseau, '75

$P_u(s)$ = best parsimony score of subtree rooted at node u, assuming u is labeled by character s

```
        A C G T
      ┌─┬─┬─┬─┐
      └─┴─┴─┴─┘
    A C G T
  ┌─┬─┬─┬─┐
  └─┴─┴─┴─┘
A C G T          A C G T
┌─┬─┬─┬─┐      ┌─┬─┬─┬─┐
└─┴─┴─┴─┘      └─┴─┴─┴─┘
```

A C G T   A C G T   A C G T   A C G T   A C G T

  T   T   G   G   T

Sankoff-Rousseau Recurrence

$P_u(s)$ = best parsimony score of subtree rooted at node u, assuming u is labeled by character s

For Leaf u:

$$P_u(s) = \begin{cases} 0 & \text{if } u \text{ is a leaf labeled } s \\ \infty & \text{if } u \text{ is a leaf not labeled } s \end{cases}$$

For Internal node u:

$$P_u(s) = \sum_{v \in \text{child}(u)} \min_{t \in \{A,C,G,T\}} \text{cost}(s,t) + P_v(t)$$

Time: O(alphabet² x tree size)

Sankoff & Rousseau, '75

$P_u(s) =$ best parsimony score of subtree rooted at node u, assuming u is labeled by character s

$$P_u(s) = \sum_{v \in \text{child}(u)} \min_{t \in \{A,C,G,T\}} \text{cost}(s,t) + P_v(t)$$

s	v	t	cost(s,t)+P_v(t)	min
	v_1	A		
		C		
		G		
		T		
	v_2	A		
		C		
		G		
		T		
		sum: P_u(s) =		

Sankoff & Rousseau, '75

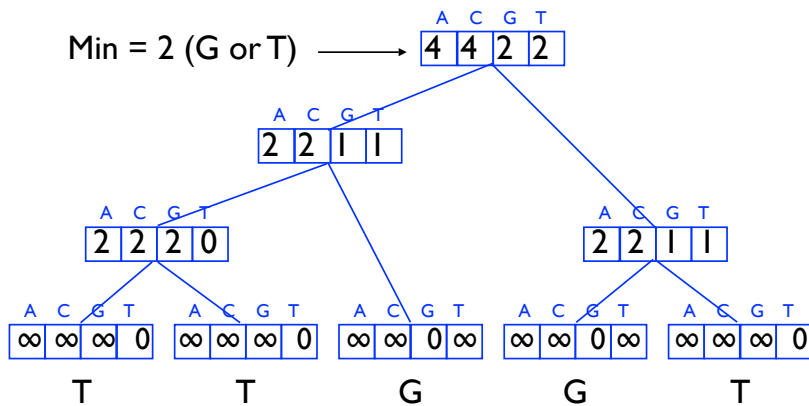$P_u(s) =$ best parsimony score of subtree rooted at node u, assuming u is labeled by character s

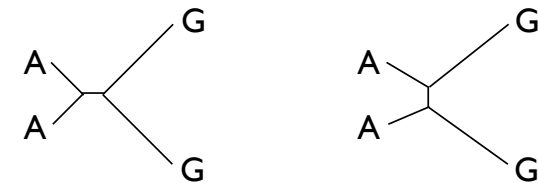$$P_u(s) = \sum_{v \in \text{child}(u)} \min_{t \in \{A,C,G,T\}} \text{cost}(s,t) + P_v(t)$$

s	v	t	cost(s,t)+P_v(t)	min
A	v_1	A	0 + ∞	
		C	1 + ∞	1
		G	1 + ∞	
		T	1 + 0	
	v_2	A	0 + ∞	
		C	1 + ∞	1
		G	1 + ∞	
		T	1 + 0	
		sum: P_u(s) =		2

Sankoff & Rousseau, '75

$P_u(s) =$ best parsimony score of subtree rooted at node u, assuming u is labeled by character s

Min = 2 (G or T) ⟶
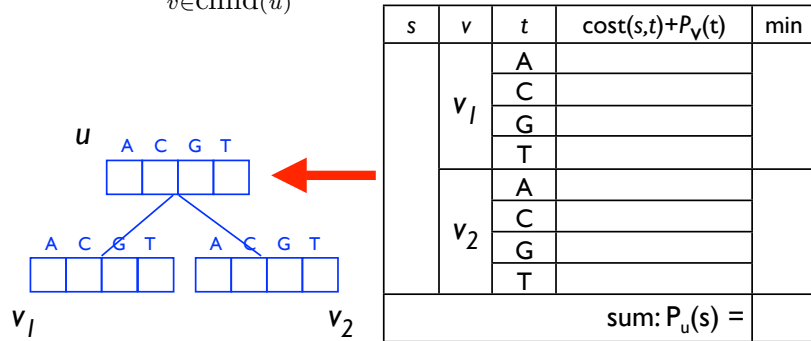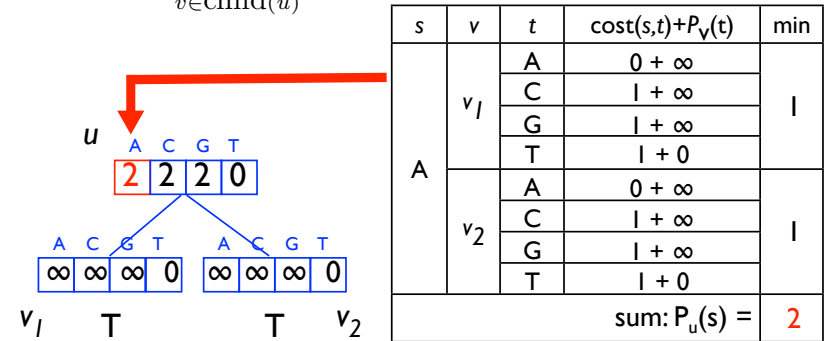
Which tree is better?

Which has smaller parsimony score?

Which is more likely, assuming edge length proportional to evolutionary rate?

Parsimony – Generalities

Parsimony is not the best way to evaluate a phylogeny (maximum likelihood generally preferred - as previous slide suggests)

But it is a natural approach, works well in many cases, and is fast.

Finding the best tree: a much harder problem

Much is known about these problems; *Inferring Phylogenies* by Joe Felsenstein is a great resource.

Phylogenetic Footprinting

See link to Tompa's slides on course web page
http://www.cs.washington.edu/homes/tompa/papers/ortho.ppt