CSE 527
Lecture 10

Parsimony and
Phylogenetic Footprinting

Phylogenies
(aka Evolutionary Trees)

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

-- Dobzhansky

- A Complex Question:

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

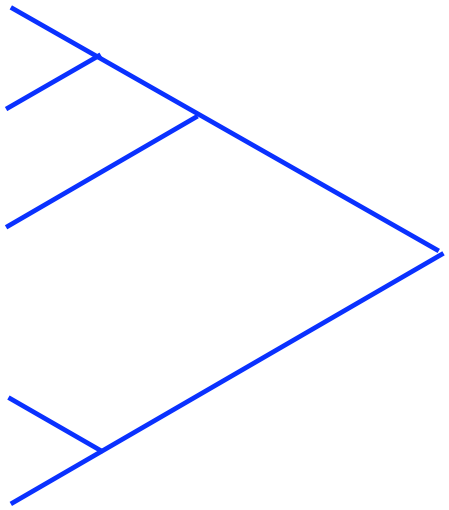
- A Simpler Question:

  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	...



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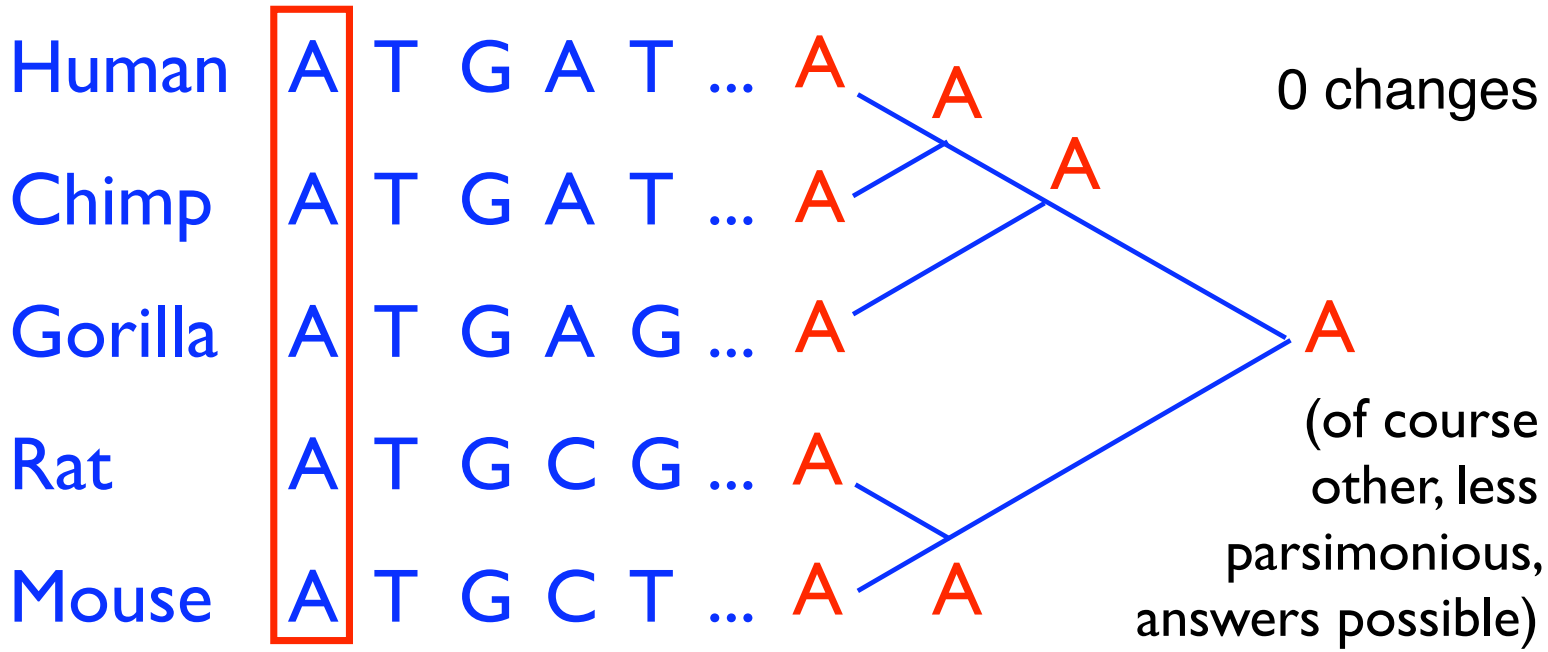

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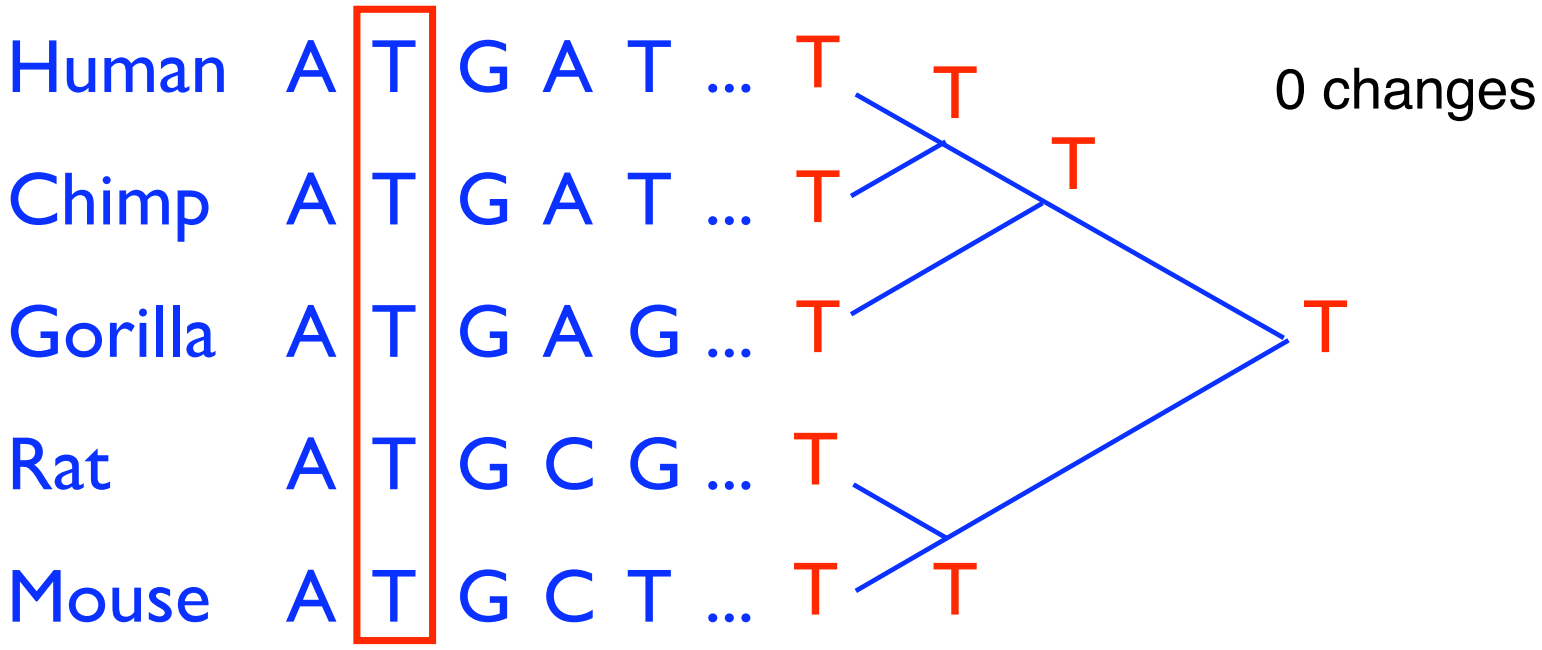

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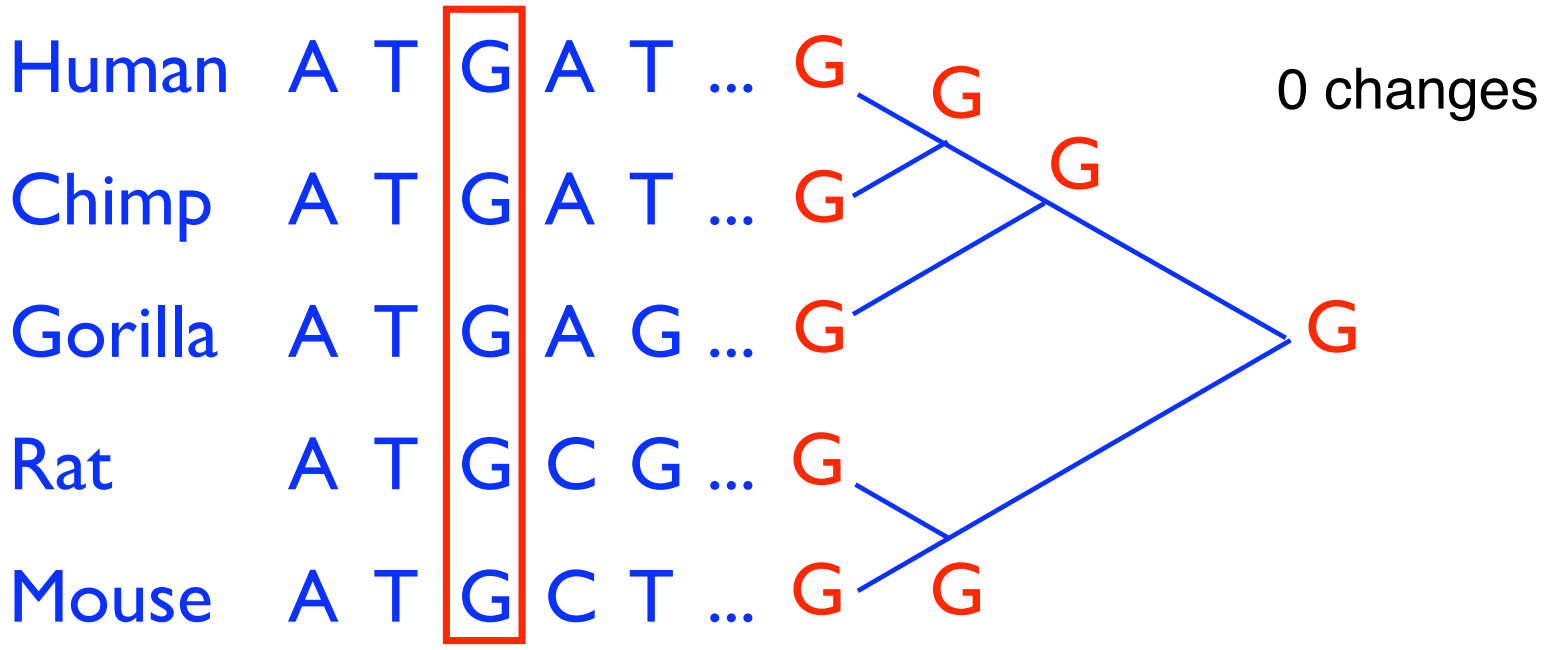

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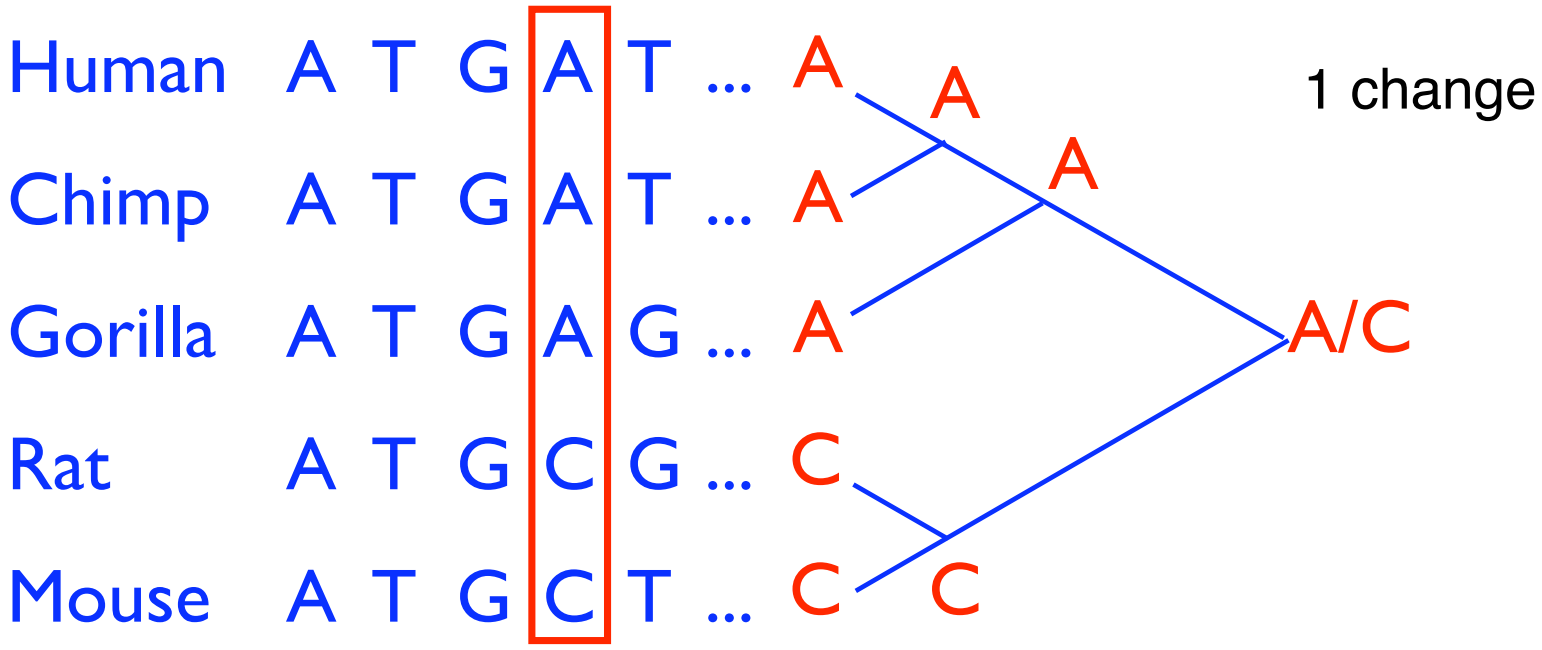

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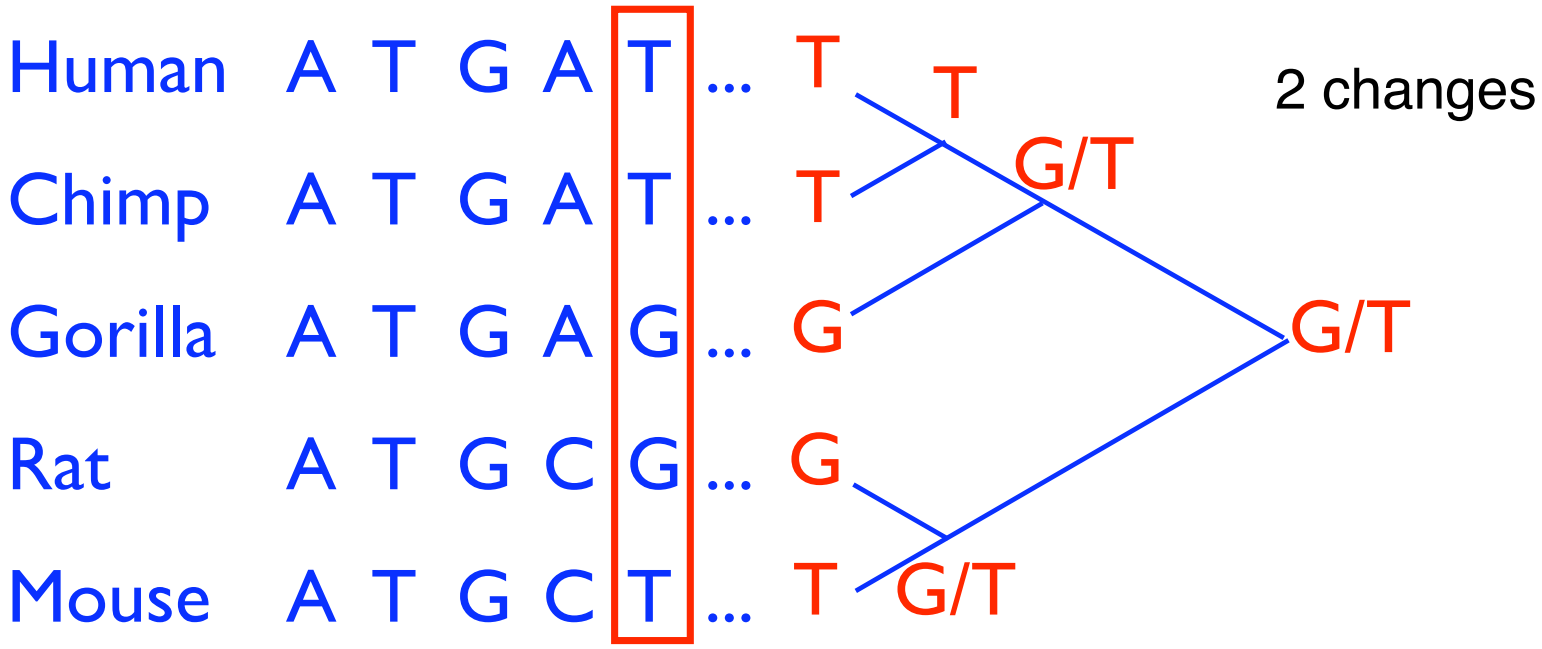
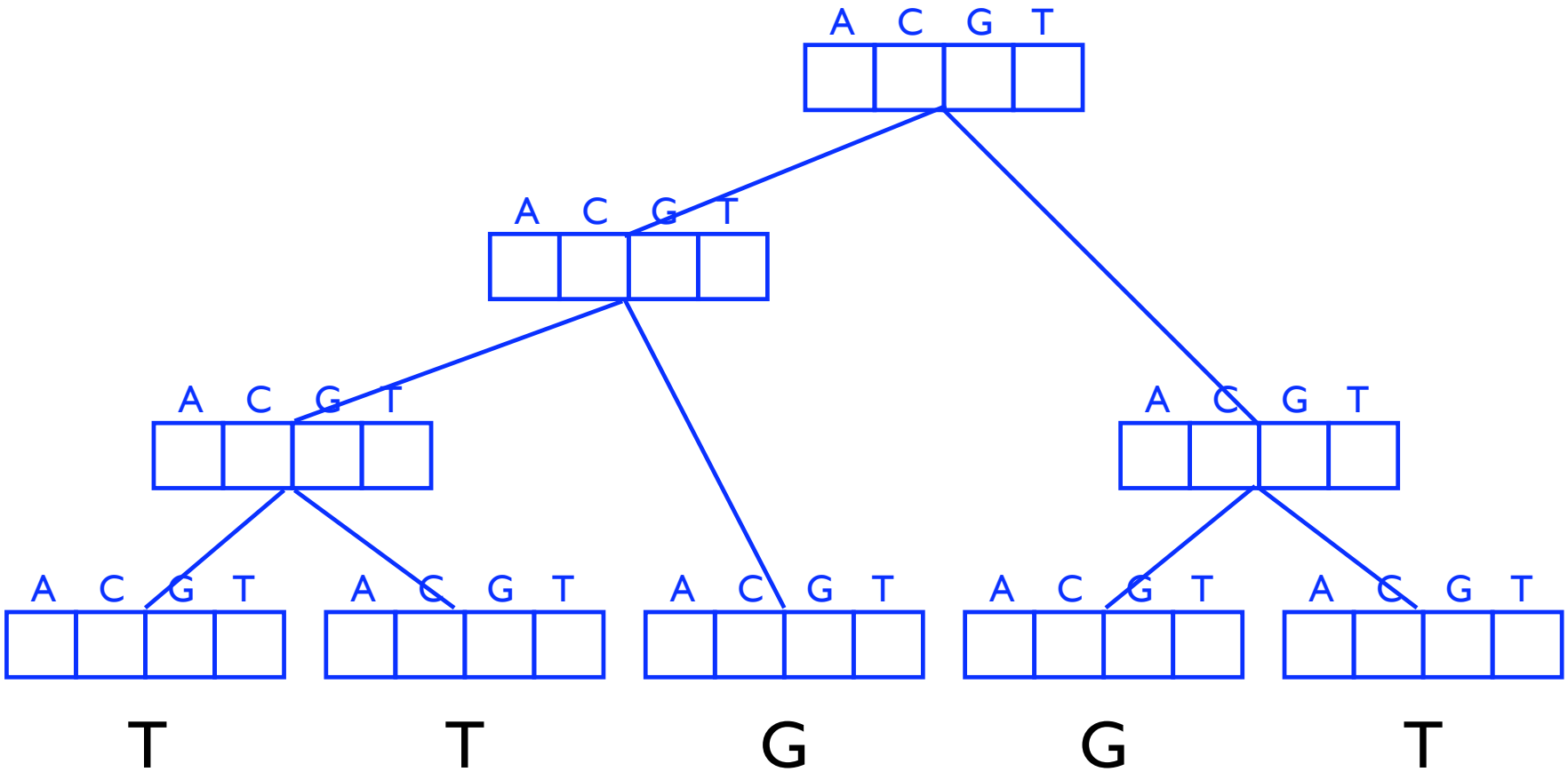


Counting Events Parsimoniously

- 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



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(alphabet^2 x tree size)

Sankoff & Rousseau, '75

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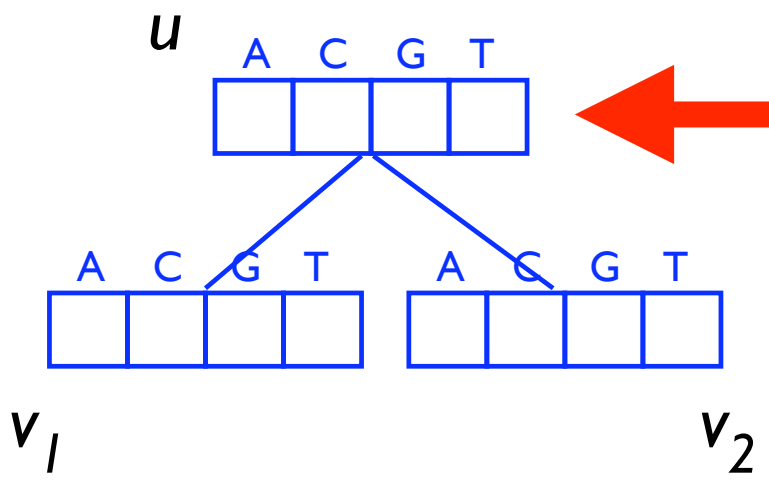
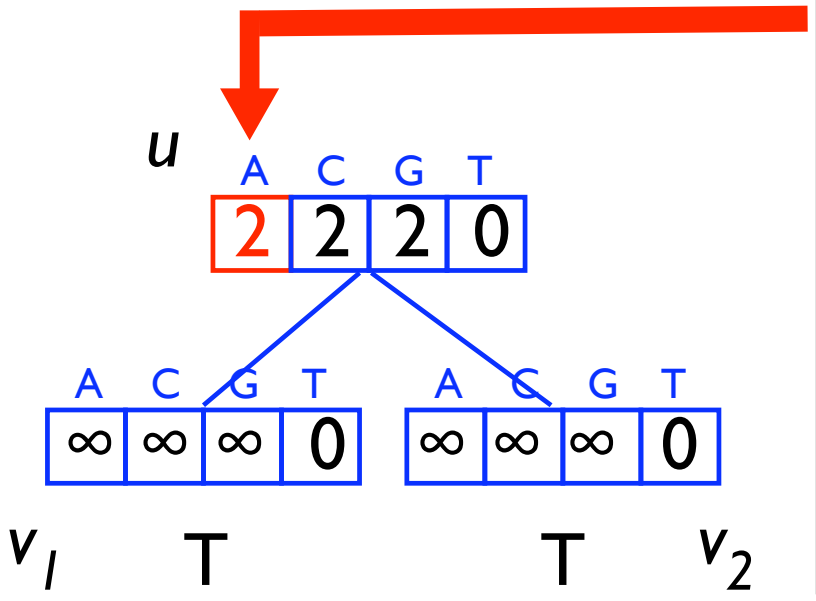


s	v	t	cost(s,t)+P_v(t)	min
	v_1	A		
		C		
		G		
		T		
	v_2	A		
		C		
		G		
		T		
			sum: P_u(s) =	

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 + ∞	1
		C	1 + ∞	
		G	1 + ∞	
		T	1 + 0	
	v_2	A	0 + ∞	1
		C	1 + ∞	
		G	1 + ∞	
		T	1 + 0	
			sum: P_u(s) =	2

Sankoff & Rousseau, '75

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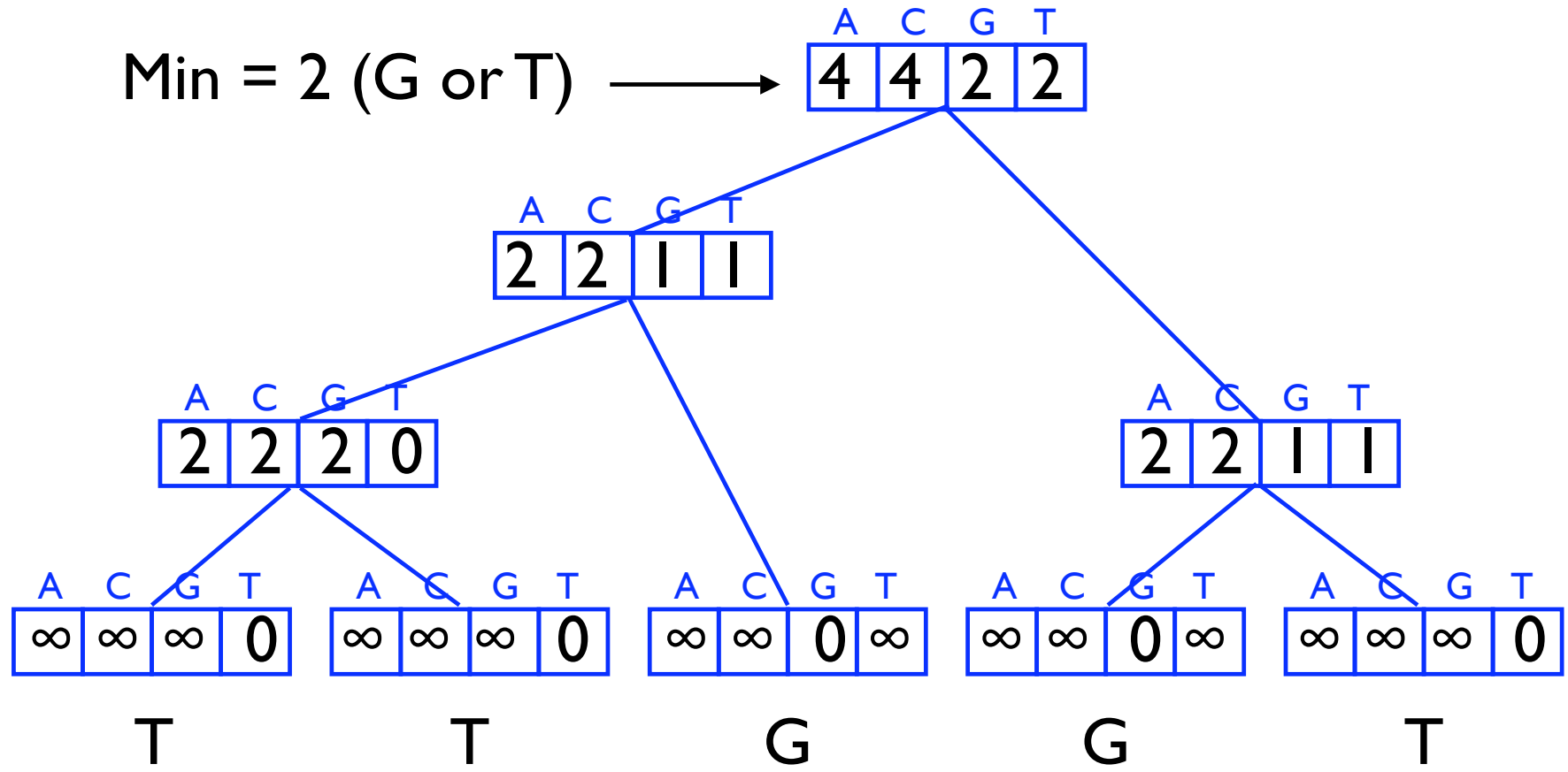

Parsimony – Generalities

- Parsimony is not necessarily the best way to evaluate a phylogeny (maximum likelihood generally preferred)
- But it is a natural approach, & 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