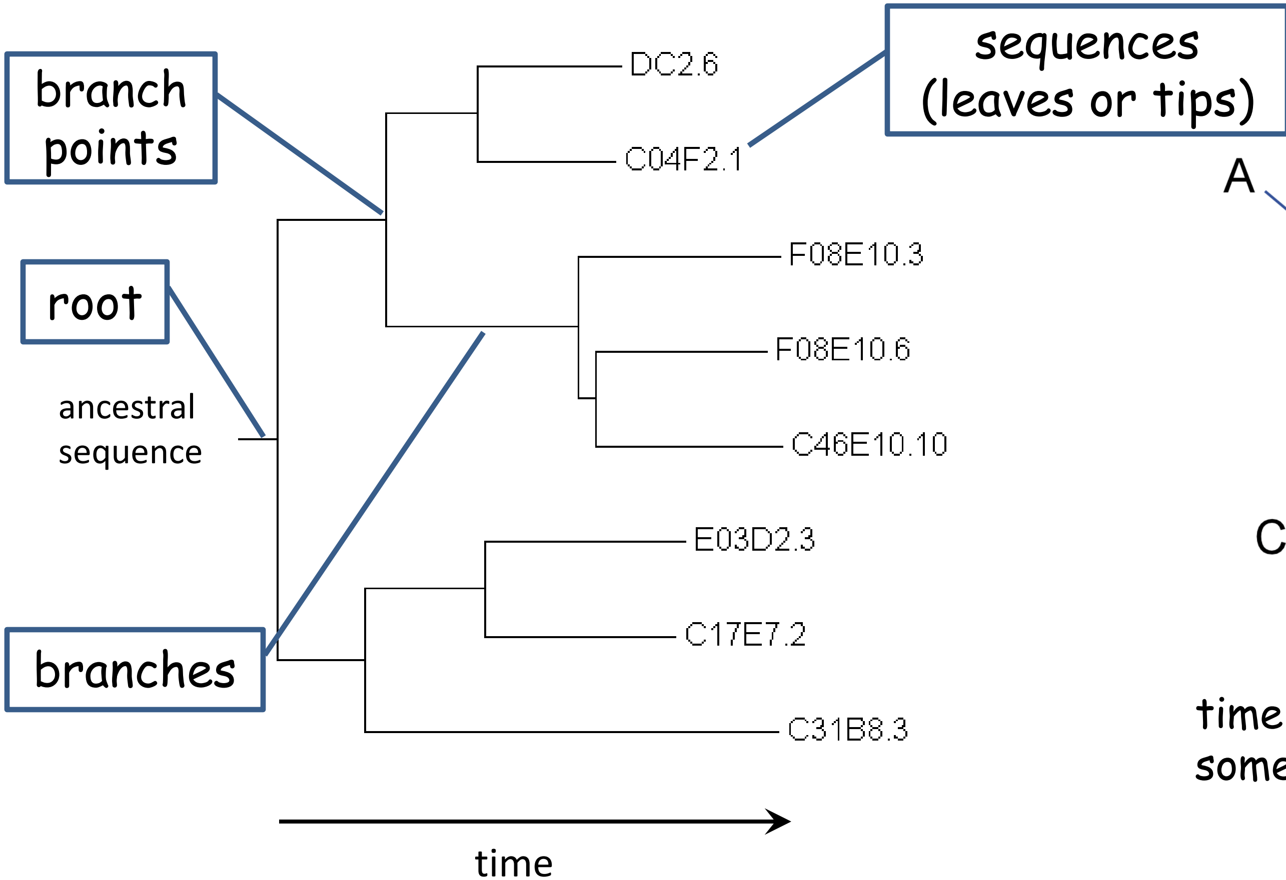
Computing a tree: I

Genome 559: Introduction to Statistical and Computational Genomics

Prof. James H. Thomas

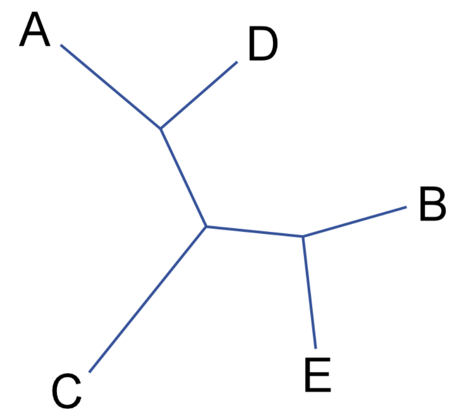
Defining what a tree means

rooted tree (all real trees are rooted):



…divergence time is the sum of (horizontal) branch lengths

unrooted tree (used when the root isn't known):

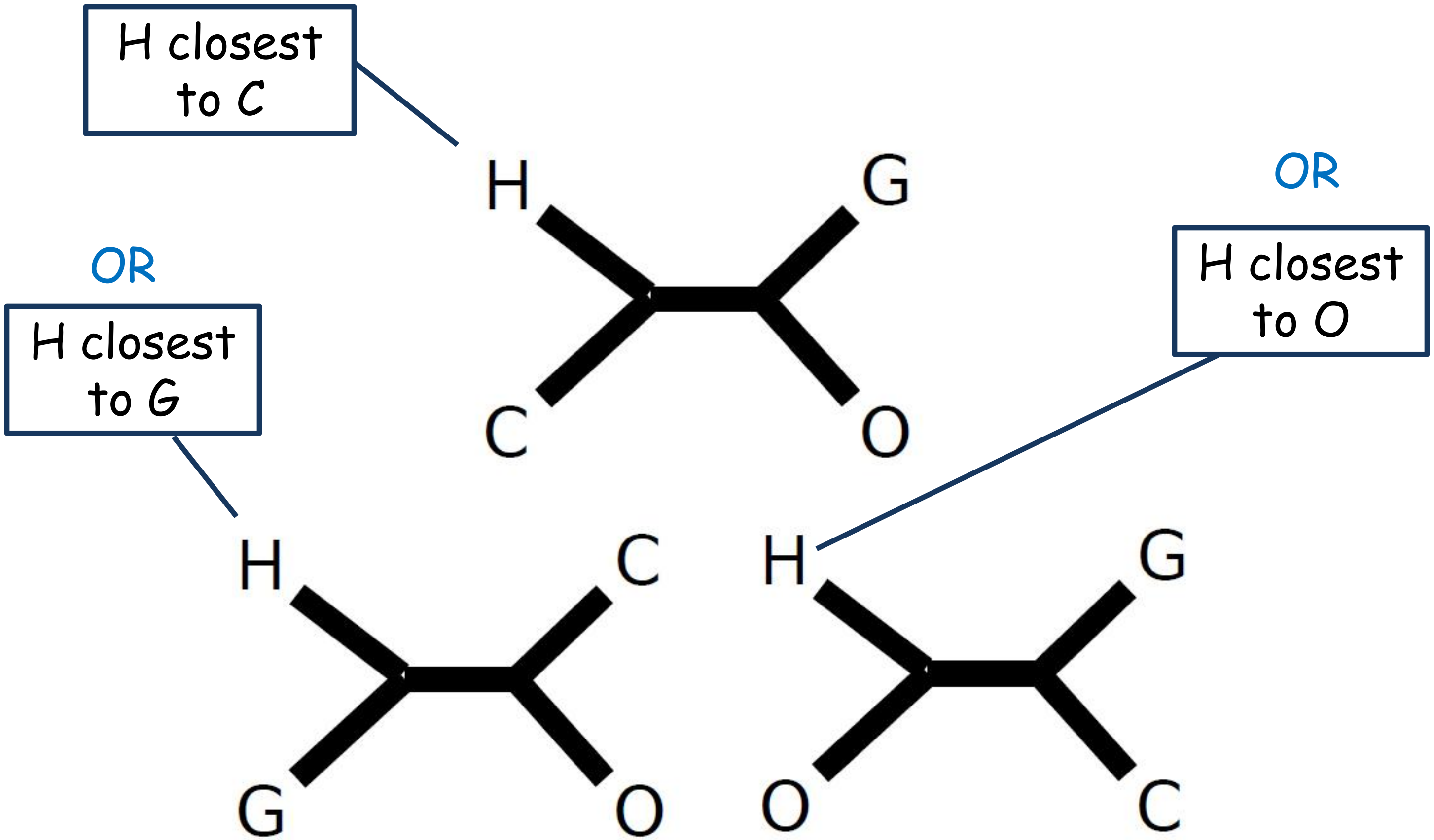


time vaguely radiates out from somewhere near the center

Parsimony principle

Find the tree that requires the fewest changes

Consider 4 sequences - all possible unrooted trees

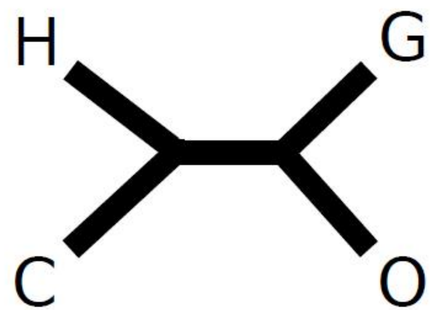


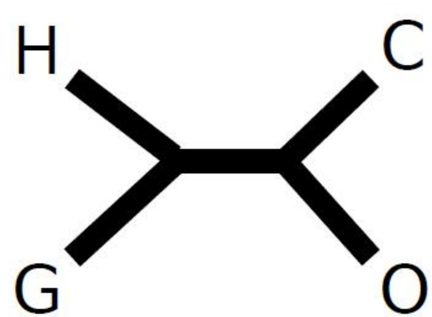
Consider 4 sequences - all possible unrooted trees

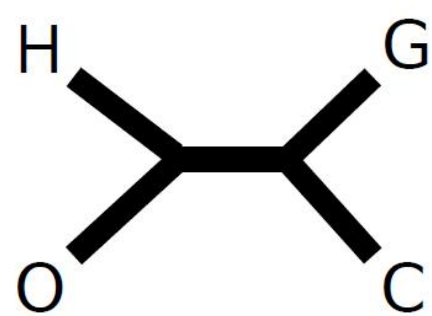
positions in alignment (usually called "sites"

	1	2	3	4	5	6
human	a	g	t	c	t	c
chimp	a	g	a	g	t	c
gorilla	c	g	g	c	a	g
orangutan	c	g	g	g	a	c

sequences represented on the tree







Consider site 1

	1	2	3	4	5	6
human	a	g	t	c	t	c
chimp	a	g	a	g	t	c
gorilla	c	g	g	c	a	g
orangutan	c	g	g	g	a	c

Consider site 1

	1	2	3	4	5	6
human	a	g	t	c	t	c
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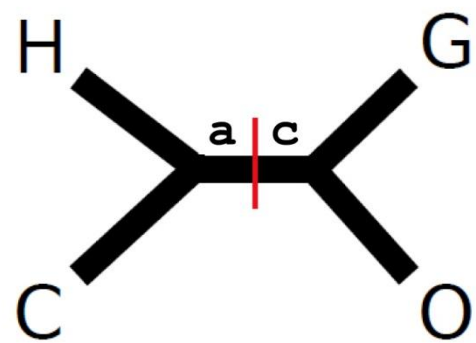
gorilla	c	g	g	c	a	g
orangutan	c	g	g	g	a	c



Consider site 1

	1	2	3	4	5	6
human	a	g	t	c	t	c
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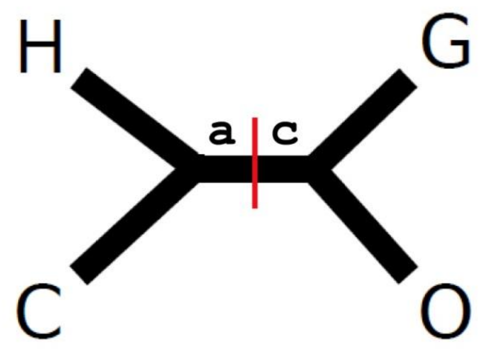
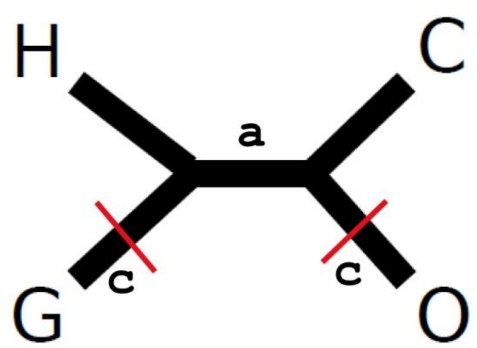
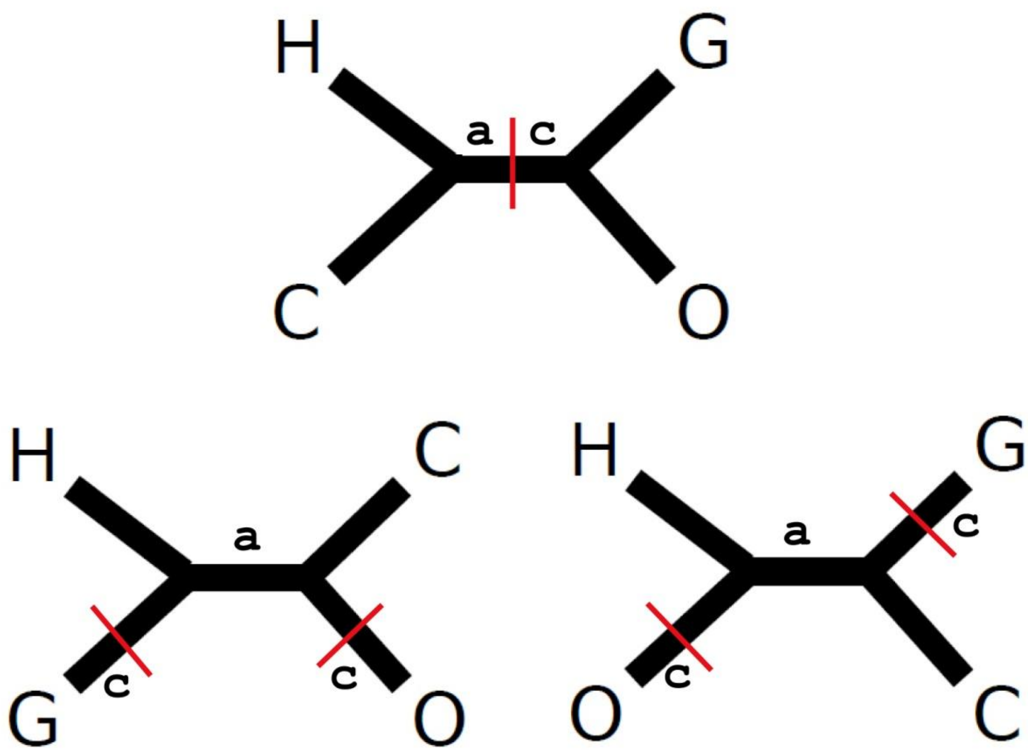




Consider site 1

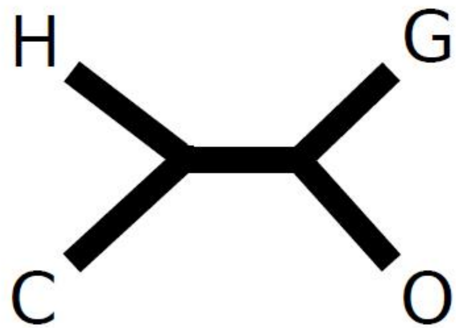
	1	2	3	4	5	6
human	a	g	t	c	t	c
chimp	a	g	a	g	t	c
gorilla	c	g	g	c	a	g
orangutan	c	g	g	g	a	c

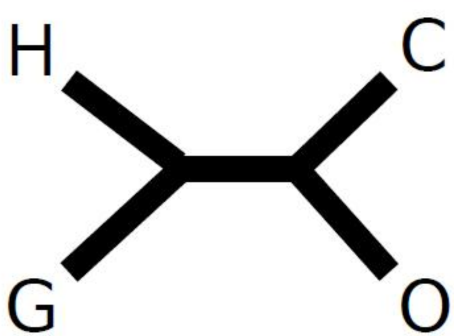


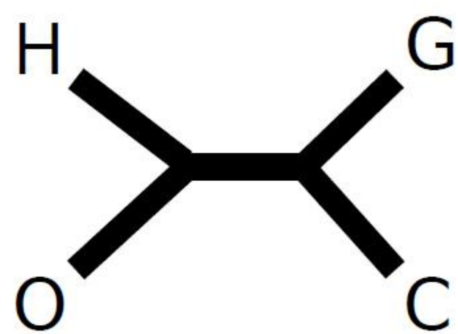
Consider site 2

	1	2	3	4	5	6
human	a	g	t	c	t	c
chimp	a	g	a	g	t	c
gorilla	c	g	g	c	a	g
orangutan	c	g	g	g	a	c

Uninformative
(no changes)

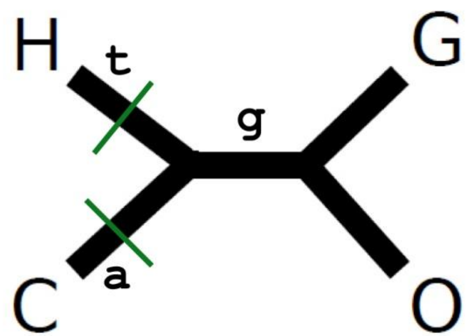


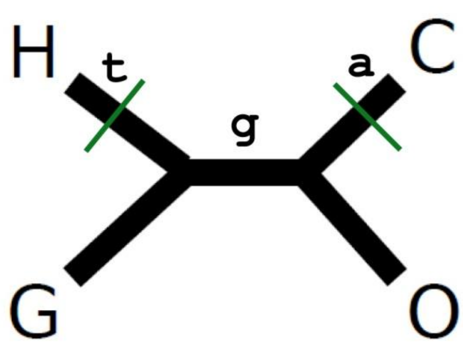


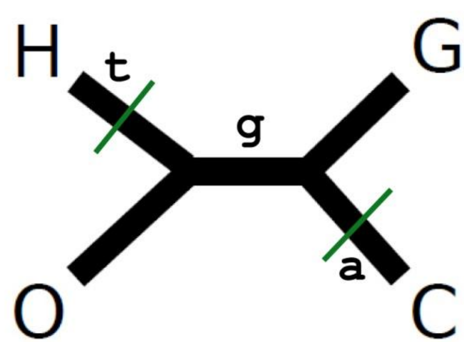


Consider site 3

	1	2	3	4	5	6
human	a	g	t	c	t	c
chimp	a	g	a	g	t	c
gorilla	c	g	g	c	a	g
orangutan	c	g	g	g	a	c

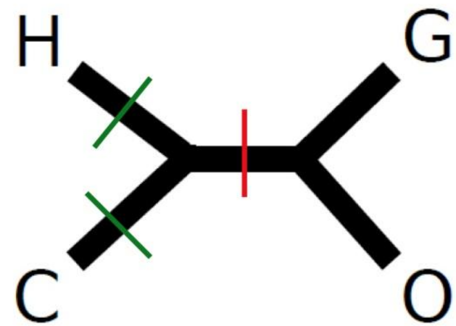


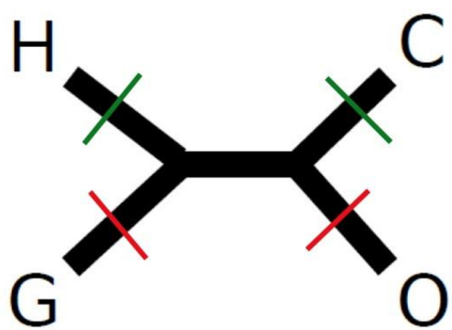


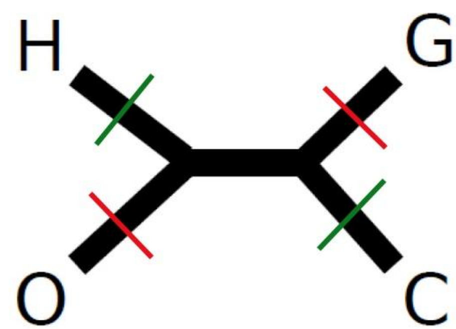


Put sites 1 and 3 together

	1	2	3	4	5	6
human	a	g	t	c	t	c
chimp	a	g	a	g	t	c
gorilla	c	g	g	c	a	g
orangutan	c	g	g	g	a	c

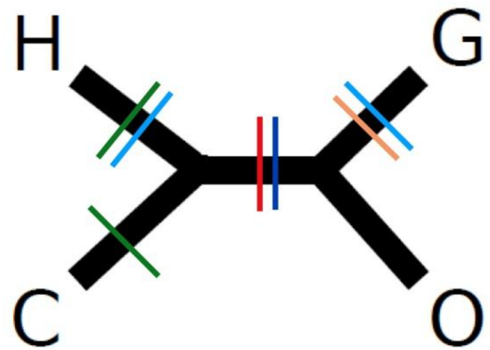




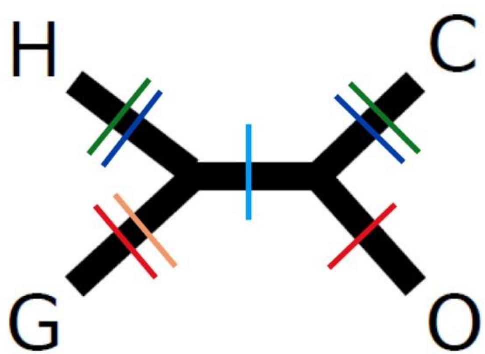


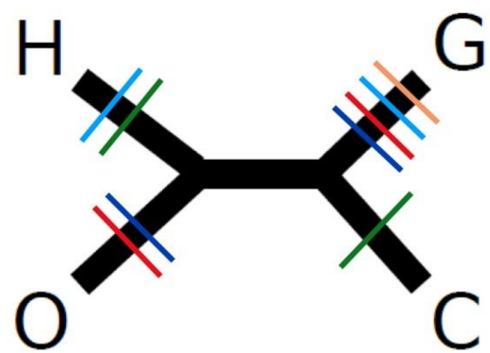
Now put all of them together

	1	2	3	4	5	6
human	a	g	t	c	t	c
chimp	a	g	a	g	t	c
gorilla	c	g	g	c	a	g
orangutan	c	g	g	g	a	c



Which tree is most parsimonious?





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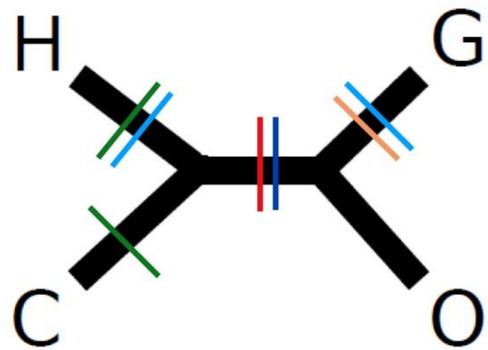

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parsimony score

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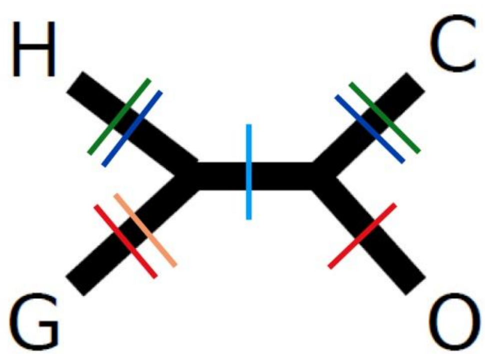

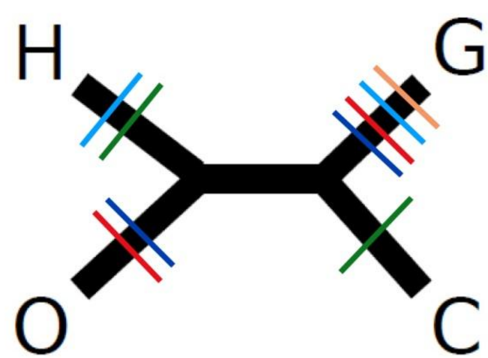

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Parsimony algorithm

1) Construct all possible trees

2) For each informative site in alignment
   count changes on each tree

3) Add them all up for each tree

4) Pick the lowest scoring

Distance trees

- Measure pairwise distance between each pair of sequences.

- Use a clustering method to build up a tree, starting with the closest pair (next lecture).

	1	2	3	4	5	6
human	a	g	t	c	t	c
chimp	a	g	a	g	t	c
gorilla	c	g	g	c	a	g
orangutan	c	g	g	g	a	c

human - chimp has 2 changes out of 6 sites
human - orang has 4 changes of out 6 sites
etc.