

TME2 - PHYG

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1 Exercise 1 : Parsimony

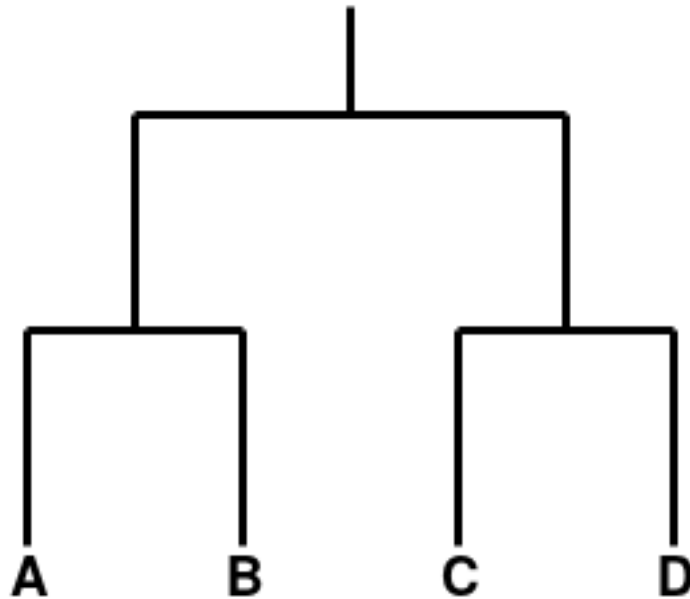
1.1 Question 1

1.2 Question 2

1.3 Question 3

1.4 Question 4

We assume that the topogy of the graph is the following :



Lets compute the parsimony scores of that tree with the Sankoff and fitch algorithms.

- Sankoff

We compute score tree nucleotide by nucleotide.

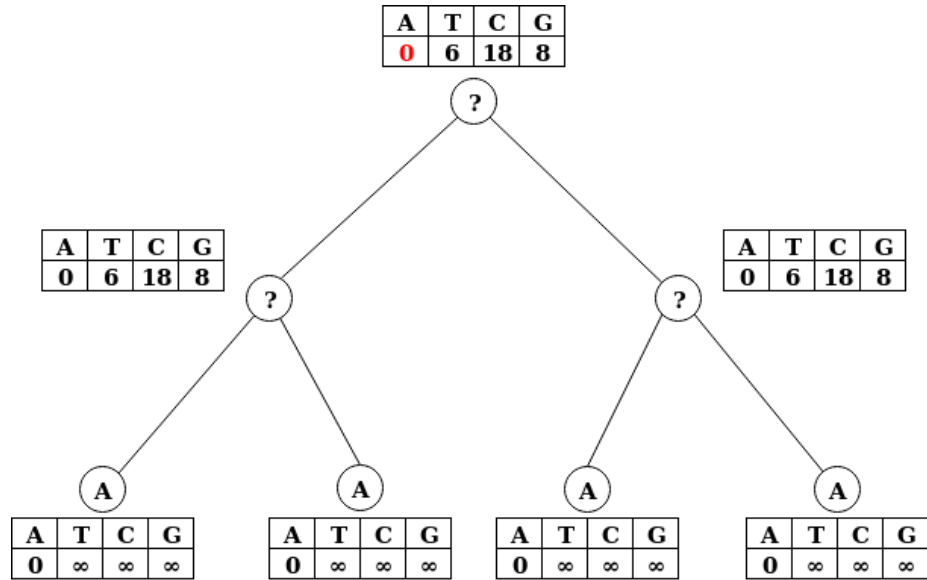


Figure 1: Sankoff score tree for the first nucleotide

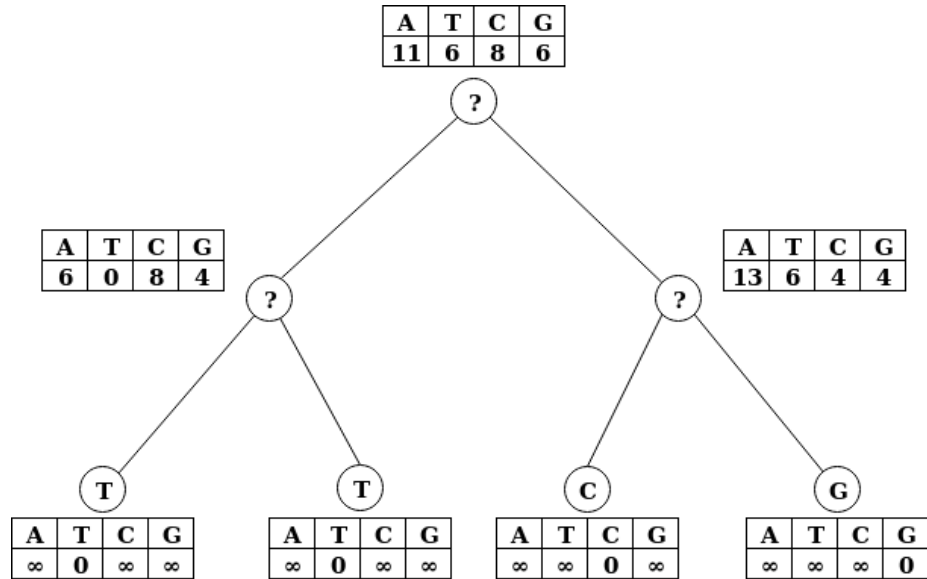


Figure 2: Sankoff score tree for the second nucleotide

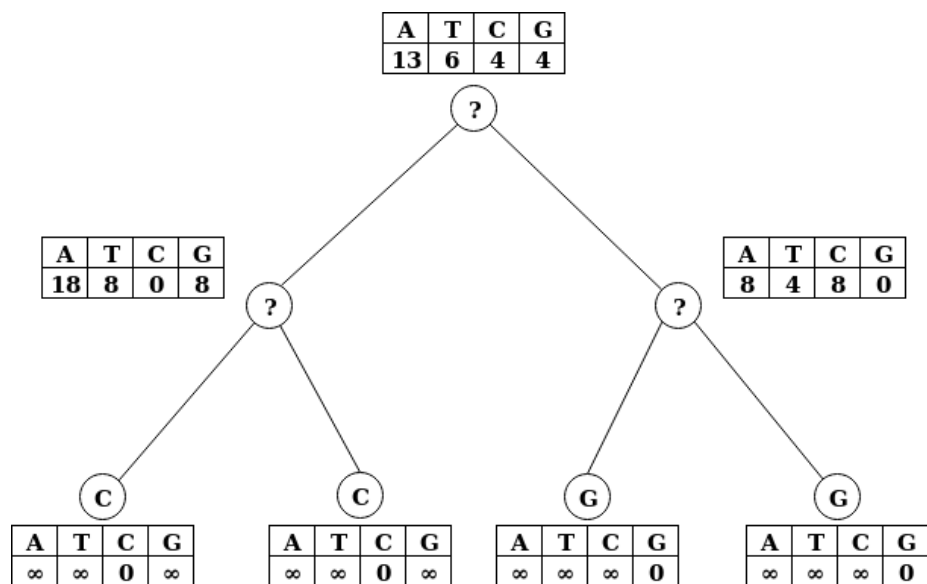


Figure 3: Sankoff score tree for the third and fourth nucleotide

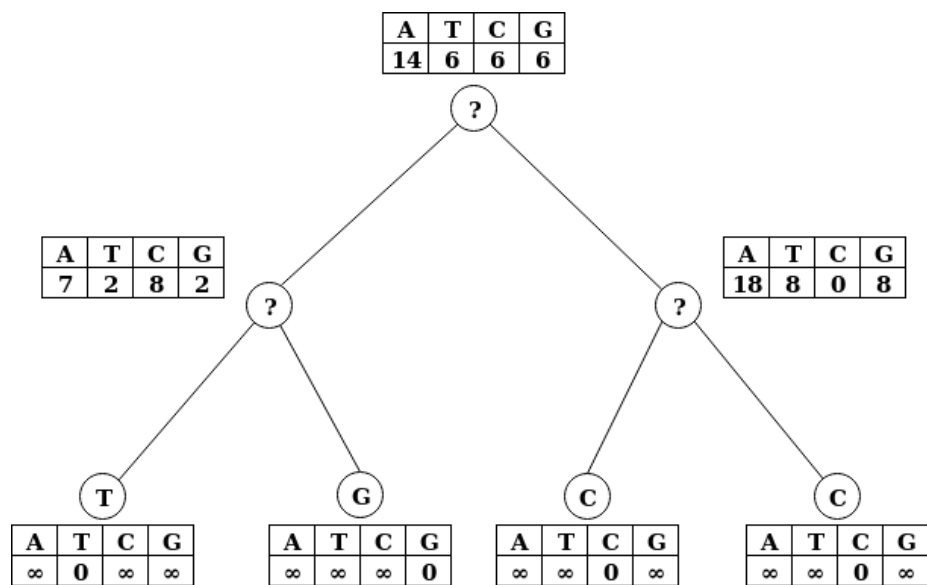


Figure 4: Sankoff score tree for the fifth nucleotide

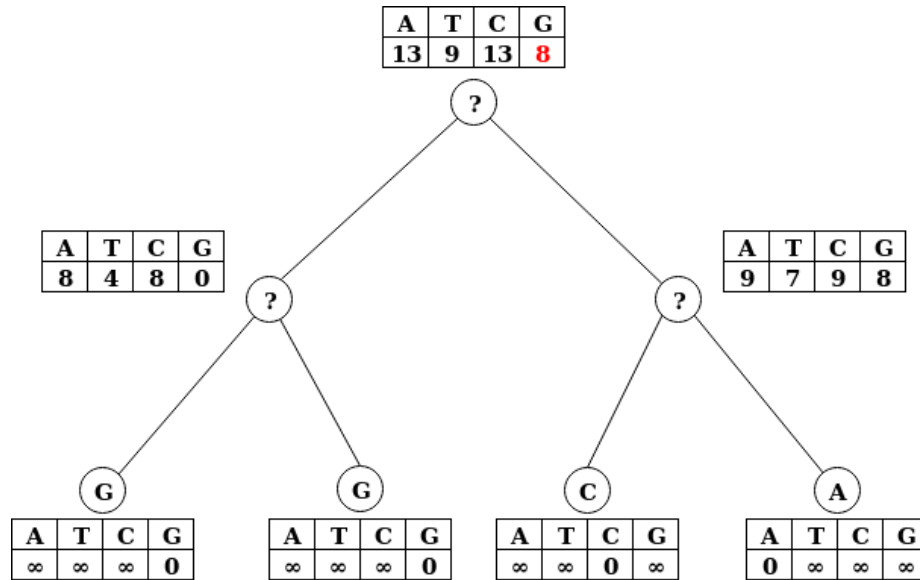


Figure 5: Sankoff score tree for the sixth nucleotide

- **Sankoff**

Again we proceed nucleotide by nucleotide.

1.5 Question 5

2 Exercise 2 : Reconstruction using reversal distances

2.1 Question 1

So we launch an entire genome comparison between human and mouse with the human as a reference.

Mouse-Human:
 Number of syntenic blocks: 891
 Reversal Distance: 330
 Breakpoint Reuse: 1.58

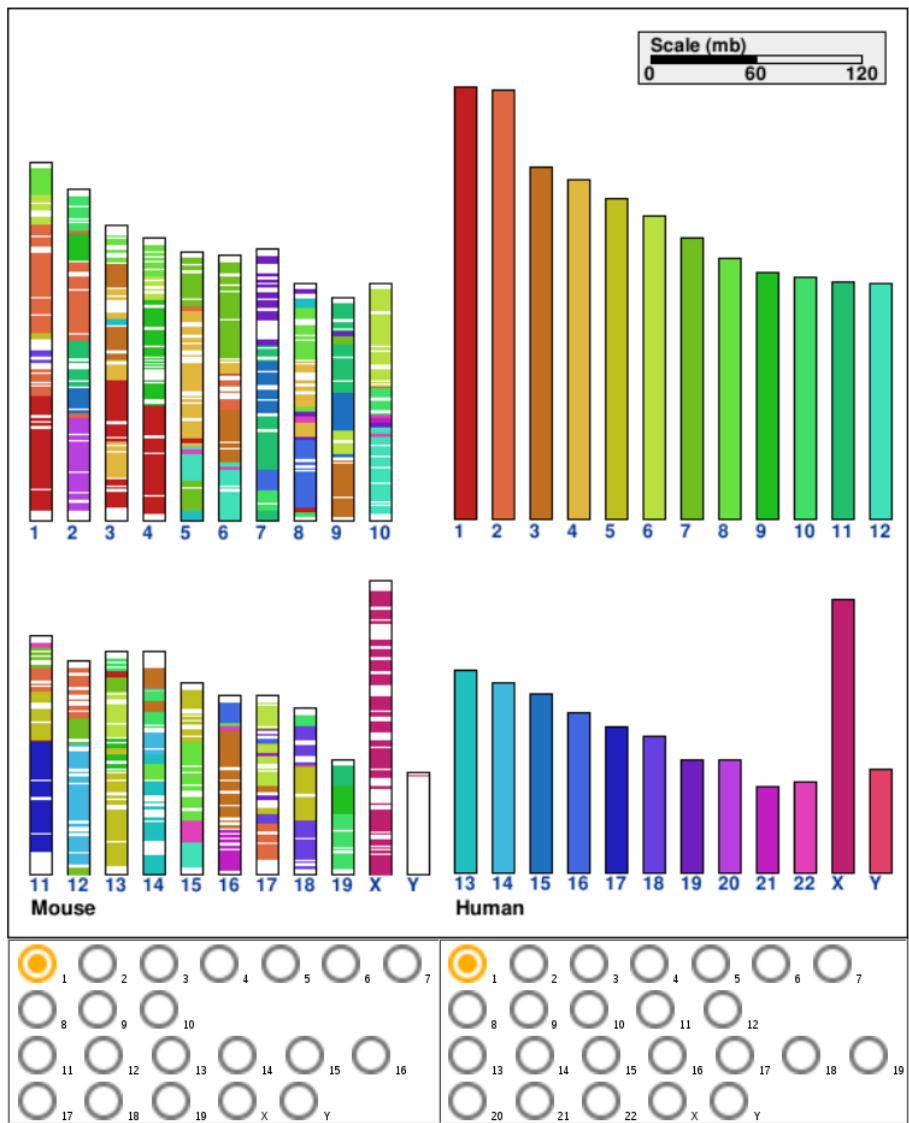


Figure 6: Genome comparison between human (reference) and mouse

As we can see, most of the genome is the same between this two species. However the genes are not in the same chromosomes and they seems mixed by recombination.

2.2 Question 2

So now we look at the homologous genes in the first human chromosome and the fourth mouse chromosome.

Number of syntenic blocks: 14

Reversal Distance: 1

Breakpoint Reuse: 1.00

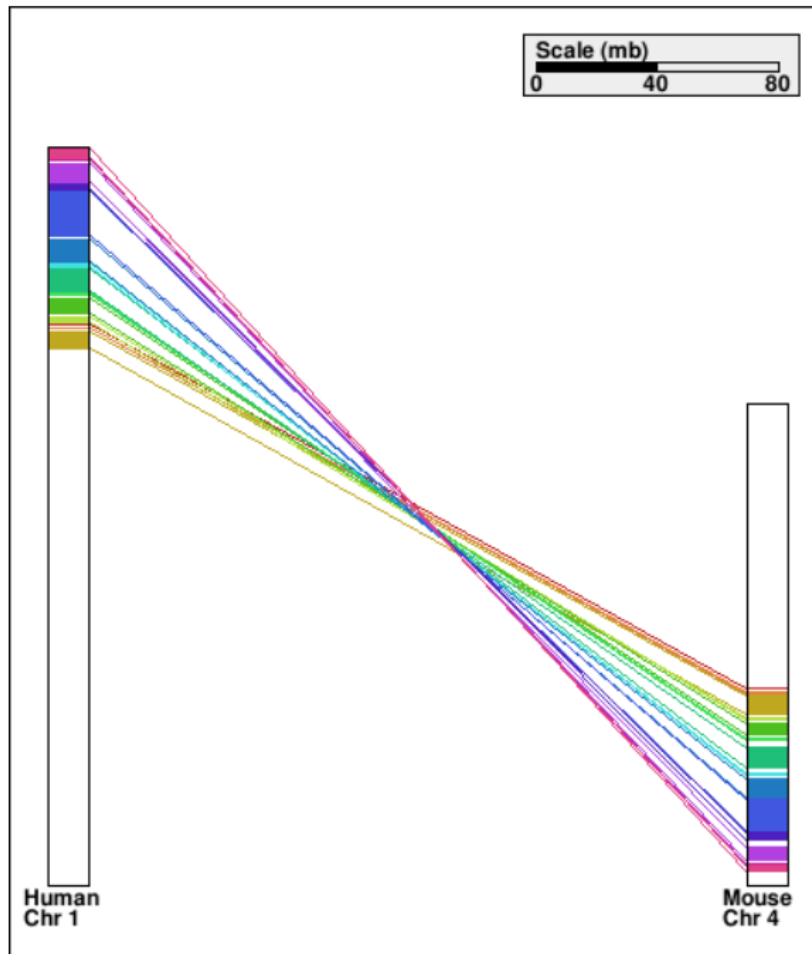


Figure 7: Genome comparison of the first human chromosome and fourth mouse chromosome

So we can see that there is the same alignment of genes in the two chromosomes, but it is reverse. The reversal distance is about one, that means that at least one event (recombination) is needed to go from a chromosome to another.

2.3 Question 3

	Human	Mouse	Cow	Chimp
Human	0	302	257	18
Mouse	302	0	360	306
Cow	257	360	0	261
Chimp	18	306	261	0

2.4 Question 4

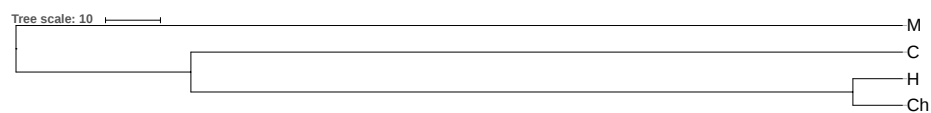


Figure 8: UPGMA tree according to the matrix above

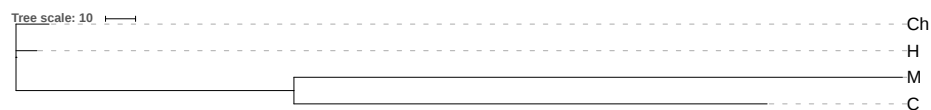


Figure 9: Neighbor-Joining tree according to the matrix above

2.5 Question 5

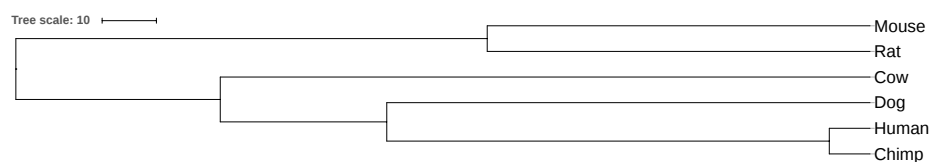


Figure 10: Neighbor-Joining tree for all mammals

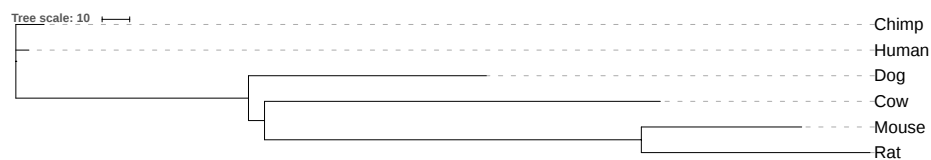


Figure 11: Neighbor-Joining tree for all mammals

2.6 Question 6

3 Exercise 3 : Reconstruction using characters

3.1 Question 1

3.2 Question 2

3.3 Question 3

3.4 Question 4