

Parsimony methods

- **A given tree is more likely if it requires less rather than more evolutionary changes in character states**
- **Find the tree that minimizes the number of evolutionary changes required**
- **Parsimony works best when changes are rare**

a → a

inference is clear

a → b

inference is clear

a → b → a

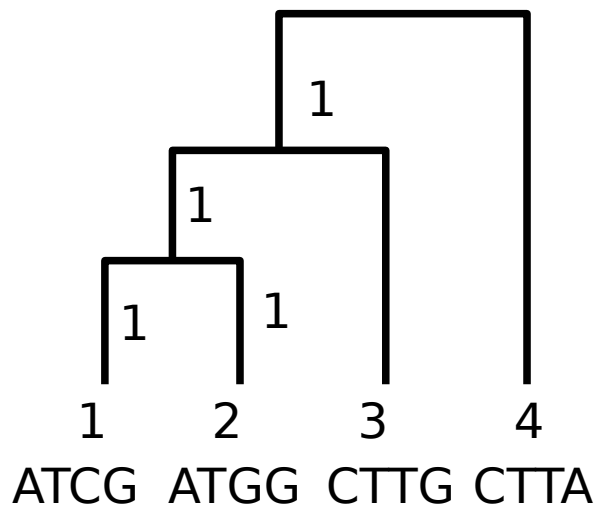
inference is lost unless "b" is known

Homoplasy

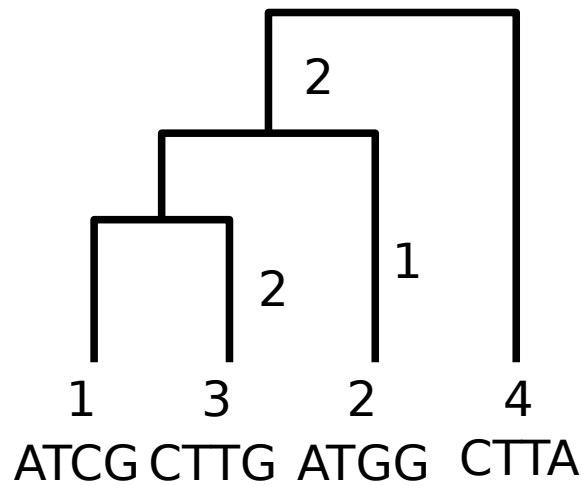
Parsimony methods

Building the tree corresponding to this alignment:

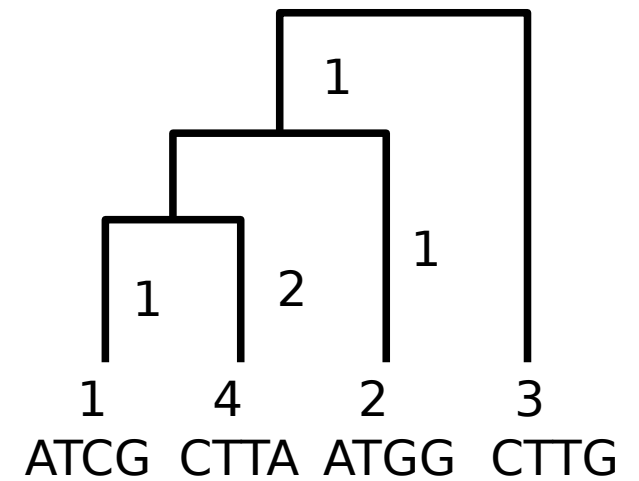
species 1 ATCG
species 2 ATGG
species 3 CTTG
species 4 CTTA



Score= 4



Score= 5

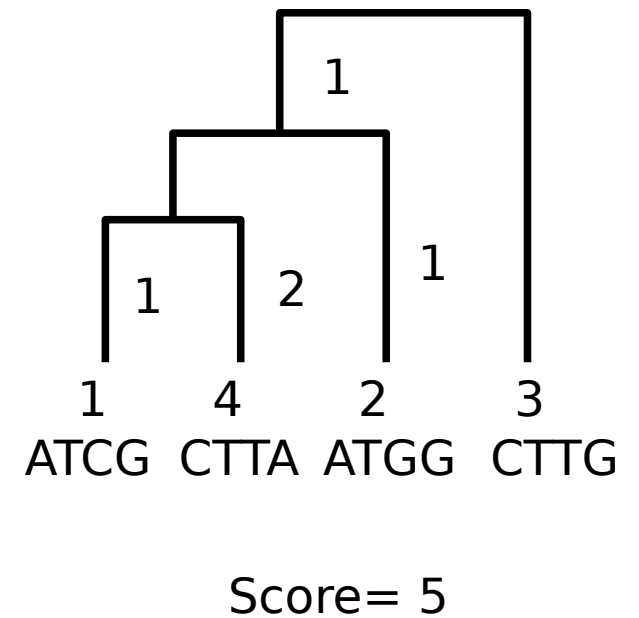
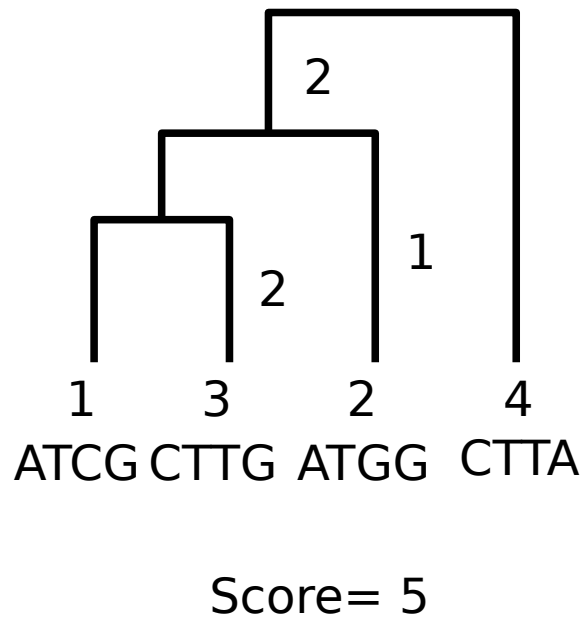
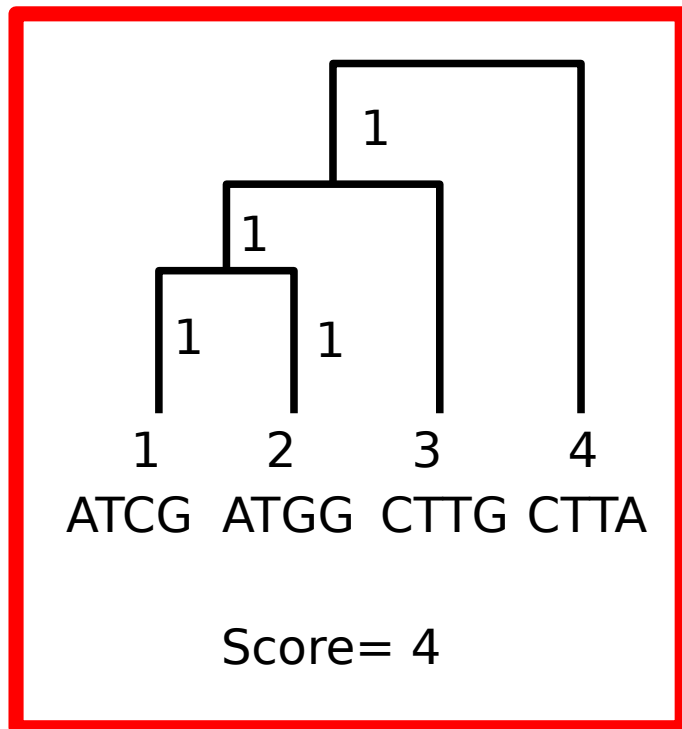


Score= 5

Parsimony methods

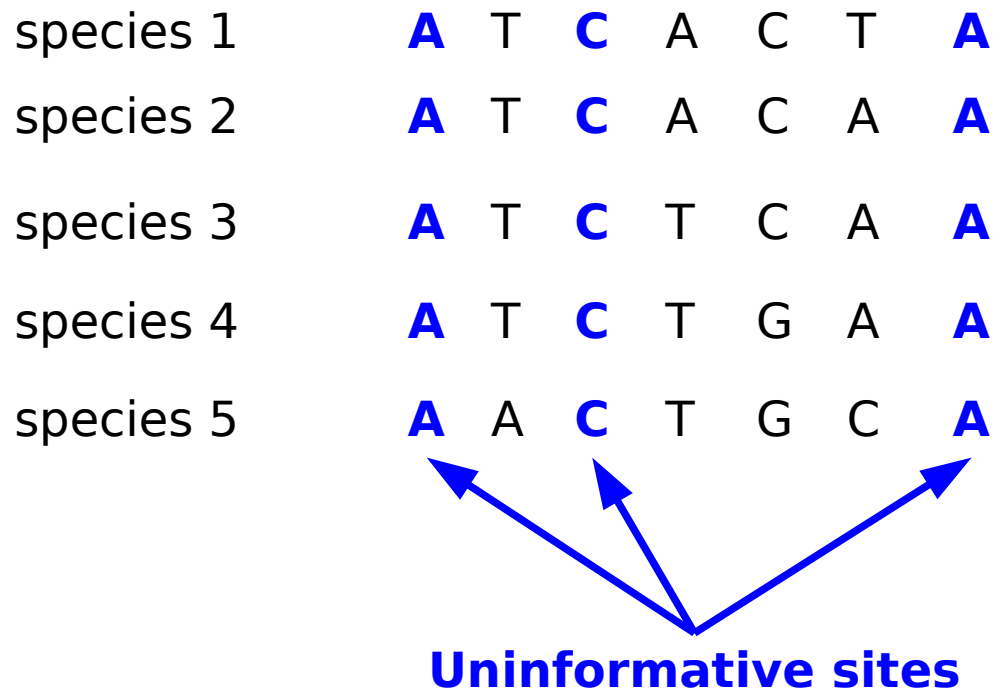
Building the tree corresponding to this alignment:

species 1 ATCG
species 2 ATGG
species 3 CTTG
species 4 CTTA



Parsimony methods

In order to infer the **topology** of the tree parsimony methods use only informative sites, discarding uninformative sites



Parsimony methods

In order to infer the **topology** of the tree parsimony methods use only informative sites, discarding uninformative sites

species 1	A	T	C	A	C	T	A
species 2	A	T	C	A	C	A	A
species 3	A	T	C	T	C	A	A
species 4	A	T	C	T	G	A	A
species 5	A	A	C	T	G	C	A

Uninformative sites



Parsimony methods

In order to infer the **topology** of the tree parsimony methods use only informative sites, discarding uninformative sites

species 1	A	T	C	A	C	T	A
species 2	A	T	C	A	C	A	A
species 3	A	T	C	T	C	A	A
species 4	A	T	C	T	G	A	A
species 5	A	A	C	T	G	C	A

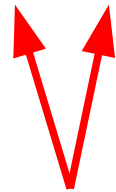


Informative sites

Parsimony methods

In order to infer the **topology** of the tree parsimony methods use only informative sites, discarding uninformative sites

species 1	A	T	C	A	C	T	A
species 2	A	T	C	A	C	A	A
species 3	A	T	C	T	C	A	A
species 4	A	T	C	T	G	A	A
species 5	A	A	C	T	G	C	A



Informative sites

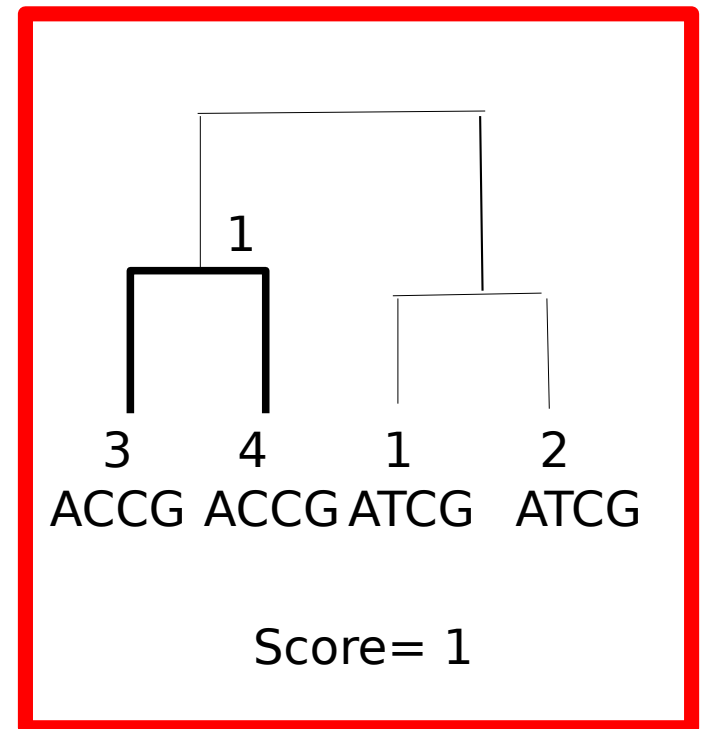
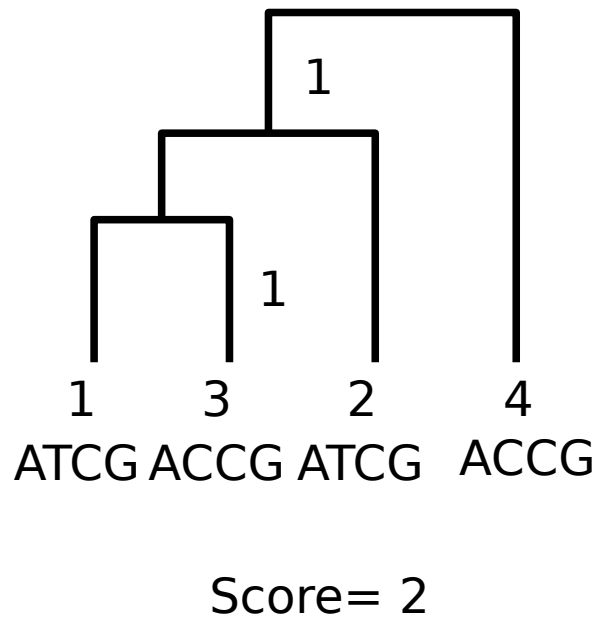
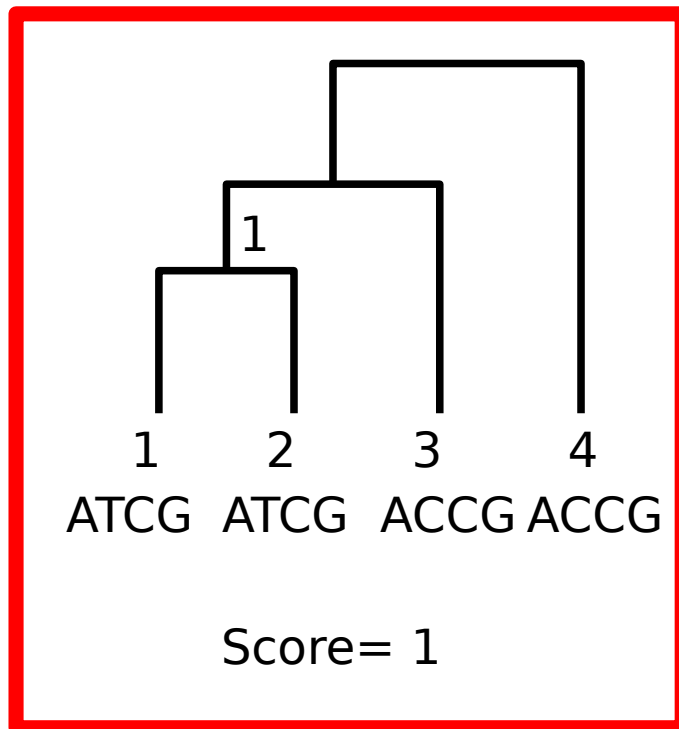
Do not forget that ALL the sites are used to compute the branch lengths

Parsimony methods

Building the tree corresponding to this alignment:

species 1 ATCG
species 2 ATCG
species 3 ACCG
species 4 ACCG

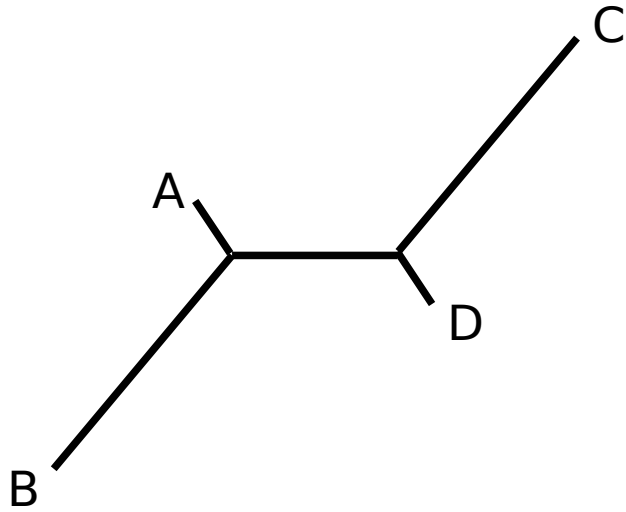
In some cases more than one parsimonious tree can be found



Parsimony methods

Long branch attraction

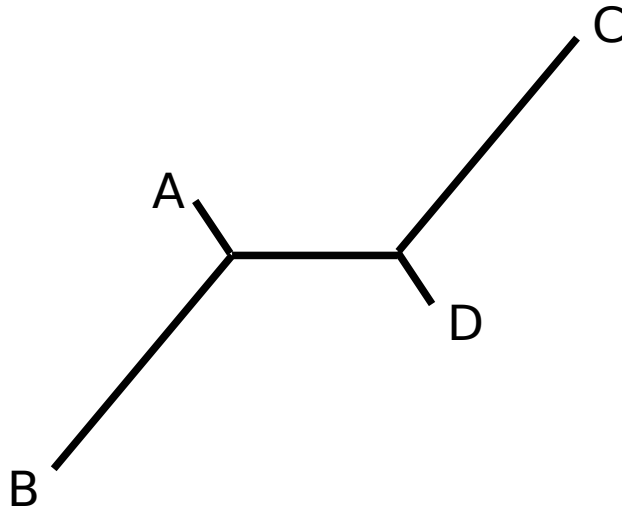
True tree



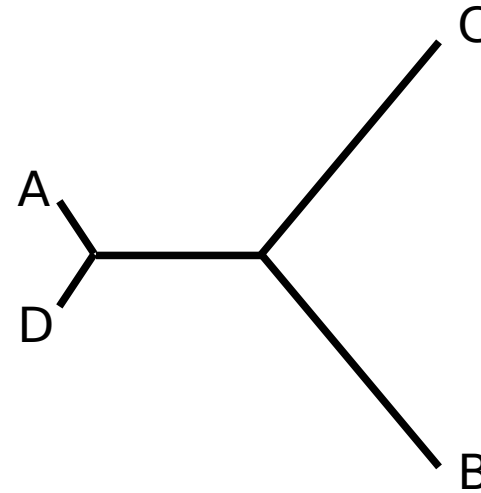
Parsimony methods

Long branch attraction

True tree



Maximum parsimony tree



Maximum parsimony

- The maximum parsimony result will converge to a maximum likelihood result when the rates of evolution along each branch are small
- Parsimony does not require constancy in the rates of change between branches if the number of substitutions per site is small. If the number is large serious errors will be made.
- If the number of substitution per site is small, a large proportion of the substitutions are autapomorphic and therefore uninformative (distance method may perform better in such a case)

Compatibility methods

- The number of individuals characters/sites that are strictly compatible with a given tree is used
- The tree with the most compatible sites is chosen.
- Compatibility for two characters will be assumed if these characters could evolve without any state having to arise more than once (homoplasy)
- Will give good results if the level of homoplasy is low

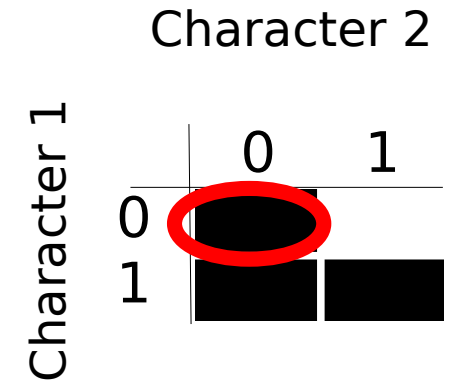
Characters

		Characters					
		1	2	3	4	5	6
Species	A	1	0	0	1	1	0
	B	0	0	1	0	0	0
	C	1	1	0	0	0	0
	D	1	1	0	1	1	1
	E	0	0	1	1	1	0
	F	0	0	0	0	0	0



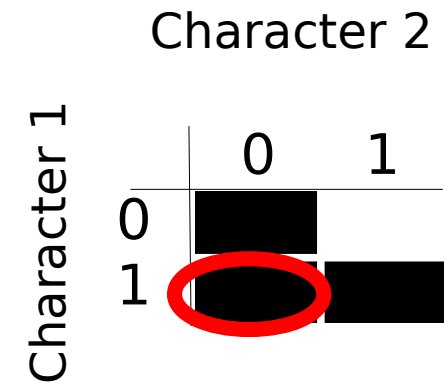
Characters

		1	2	3	4	5	6
Species	A	1	0	0	1	1	0
	B	0	0	1	0	0	0
	C	1	1	0	0	0	0
	D	1	1	0	1	1	1
	E	0	0	1	1	1	0
	F	0	0	0	0	0	0



Characters

	1	2	3	4	5	6
A	1	0	0	1	1	0
B	0	0	1	0	0	0
C	1	1	0	0	0	0
D	1	1	0	1	1	1
E	0	0	1	1	1	0
F	0	0	0	0	0	0



Characters

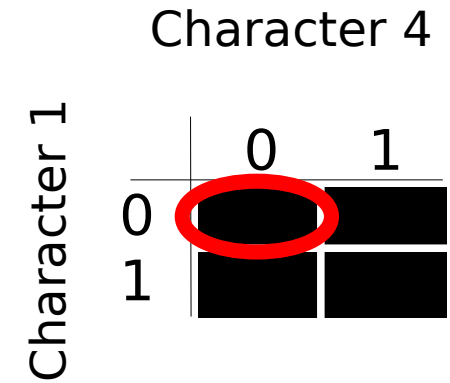
	1	2	3	4	5	6
A	1	0	0	1	1	0
B	0	0	1	0	0	0
C	1	1	0	0	0	0
D	1	1	0	1	1	1
E	0	0	1	1	1	0
F	0	0	0	0	0	0

	0	1
0	■	
1	■	●

Characters 1 and 2 are compatible

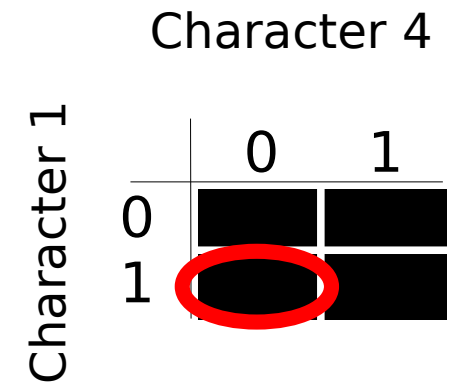
Characters

	1	2	3	4	5	6
A	1	0	0	1	1	0
B	0	0	1	0	0	0
C	1	1	0	0	0	0
D	1	1	0	1	1	1
E	0	0	1	1	1	0
F	0	0	0	0	0	0



Characters

	1	2	3	4	5	6
A	1	0	0	1	1	0
B	0	0	1	0	0	0
C	1	1	0	0	0	0
D	1	1	0	1	1	1
E	0	0	1	1	1	0
F	0	0	0	0	0	0



Characters

		1	2	3	4	5	6
Species	A	1	0	0	1	1	0
	B	0	0	1	0	0	0
	C	1	1	0	0	0	0
	D	1	1	0	1	1	1
	E	0	0	1	1	1	0
	F	0	0	0	0	0	0

		Character 4	
		0	1
Character 1	0	■	■
	1	■	■

Characters 1 and 4 are incompatible as one characters has at least changed twice

Characters

		1	2	3	4	5	6
Species	A	1	0	0	1	1	0
	B	0	0	1	0	0	0
	C	1	1	0	0	0	0
	D	1	1	0	1	1	1
	E	0	0	1	1	1	0
	F	0	0	0	0	0	0

		Character 4	
		0	1
Character 1	0	■	■
	1	■	■

Characters 1 and 4 are incompatible as one characters has at least changed twice

Characters

	1	2	3	4	5	6
A	1	0	0	1	1	0
B	0	0	1	0	0	0
C	1	1	0	0	0	0
D	1	1	0	1	1	1
E	0	0	1	1	1	0
F	0	0	0	0	0	0

Character 4

	0	1
0	■	■
1	■	■

Compatibility matrix

	1	2	3	4	5	6
1	■	■	■	□	□	■
2	■	■	■	□	□	■
3	■	■	■	□	□	■
4	□	□	□	■	■	■
5	□	□	□	■	■	■
6	■	■	■	■	■	■

The characters 4 and 5 will not be used for the phylogenetic reconstruction as they are not compatible with 1, 2, 3 and 6

Tree

