

Sequence alignment

```
>seq1
ATC---CCCTGGACC
>seq2
ATCGTTCACTC---
>seq3
ATC---CCCTGGATC
```

Presence/absence file

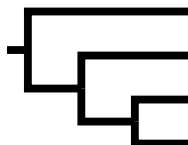
```
>seq1
000111000000000
>seq2
000000000000111
>seq3
000111000000000
```



IQ-TREE
command 1



Phylogenetic tree



IQ-TREE
command 3



INDEL reconstruction

```
>Node1
000111000000000
>Node2
000111000000000
```



IQ-TREE
command 2



Ancestral sequence reconstruction

```
>Node1
ATCGTTCCCTGGATC
>Node2
ATCGTTCCCTGGACC
```



Merged sequences

```
>Node1
ATC---CCCTGGATC
>Node2
ATC---CCCTGGACC
```

